# DIVERSITY OF VIRUSES INFECTING TOMATO AND WEED PLANTS IN AGROECOSYSTEMS

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**Doctoral Dissertation**
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# RAZNOLIKOST VIRUSOV PARADIŽNIKA IN PLEVELNIH RASTLIN V KMETIJSKIH EKOSISTEMIH

**Doktorska disertacija**

**Supervisor:** Dr. Denis Kutnjak

**Co-Supervisor:** Prof. Dr. Maja Ravnikar

Ljubljana, Slovenia, July 2022

*To my family and friends who never ceased to support my career and personal pursuits and to all anonymous foreign students and researchers 'of color' who are struggling to put their talents in good use in a non-native country, and yet discriminated, neglected, and attacked, the triumph of talent, hard work and perseverance culminating in this scientific work is specially dedicated to all of you.*

# Acknowledgments

This work would not be possible without the generous financial support from our funding sources. I am very grateful for the Horizon 2020 Marie Skłodowska-Curie Actions Innovative Training Network (MSCA-ITN) project "Innovative Network for Next Generation Training and Sequencing of Virome (INEXTVIR)" (GA 813542), for funding this research, the research visits, conferences and workshops attended, my living expenses, and other costs related to obtaining my doctoral degree. I am also thankful for the additional support from the Administration of the Republic of Slovenia for Food Safety, Veterinary Sector and Plant Protection and Slovenian Research Agency (ARRS) core funding (P4-0165, P4-0407).

I would like to thank all the persons who directly or indirectly contributed to this research, spanning almost three memorable years, during the most difficult part of the COVID-19 pandemic.

First of all, I would like to express my gratitude to my supervisor, Denis Kutnjak, for his thorough guidance, hours of dedication, and very useful professional and personal pieces of advice. Our Monday morning of supervision meetings were rewarding and memorable learning experiences. I am likewise thankful to Maja Ravnikar, who co-supervised my doctoral research, especially for putting our goals in practical perspective and in sharing wisdom in academic research and collaboration. Their supervision instilled in me the practice of thorough and high quality research, which I am very thankful for, and will for sure greatly help me in my future scientific endeavors. I would also like to thank the members of my thesis evaluation board, David Dobnik, Jernej Jakše, and Thierry Candresse, for taking some of their precious time to critically read this dissertation, and for their participation in my defense. I appreciate all their comments and suggestions, that made this dissertation the best version it could be.

I would like to thank the members of Department of Biotechnology and Systems Biology, National Institute of Biology (NIB-FITO) for their contributions: Ion Gutierrez-Aguirre, Nataša Mehle, Anja Pecman, Katarina Bačnik, Olivera Maksimović Carvalho Ferreira, Ana Vučurović, Gabrijel Seljak, Magda Tušek-Žnidaric, Zala Kogej and Živa Lengar. I am thankful for the help in sampling and sample processing by Meta Ješelnik, Lija Fajdiga, Miha Kitek, and Anja Cerovšek; Živa Ramšak and Henrik Krnec for helping in setting up bioinformatics programs; and Nejc Jakoš and Tjaša Jakomin for training me during my first months at NIB-FITO. I am of course thankful to the rest of NIB-FITO that indirectly helped in administrative tasks related to the achievement of the goals in this doctoral research.

I am also grateful to the viroid discovery community led by Benjamin Lee and Uri Neri, with Grigorii Sukhurokov, Simon Roux, Yuri Wolf, and Antonio Camargo for the insightful discussions on viroid discovery. I am thankful for the plant virus ecology journal club led by Carolyn Malmstrom, with Kerry Mauck, Adrian Fox, Rene van der Vlugt, Sebastien Massart, *et al.* for the informative and stimulating discussions on virology that contributed useful insights to this study. Looking back at my first research stint in Europe before starting this doctoral research, I am very grateful to Santiago F. Elena, Rubén González, Anamarija Butković, and the rest of the Evolutionary Systems Virology group at I$^2$SysBio-UV-CSIC for hosting my unforgettable and very productive stay in Valencia, Spain. My research experience with them made a pivotal role in my research trajectory and inspired me to pursue high quality and impactful research in plant virology.

This doctoral research experience is not complete without its unforgettable highlights: the very enjoyable and scientifically productive research visits I made in France and Spain. I am very thankful to Thierry Candresse and Armelle Marais for hosting me at INRAE, Bordeaux, France, and for introducing me to classical and advanced plant virus disease etiology techniques. If not for the friendly and untiring help from Chantal Faure, Laurence Svanella-Dumas, Thierry Maduit, Christophe Higelin, Marie Lefebvre, Maryam Khalili, and Deborah Schöenegger, my research in INRAE would not be successful. I would also like to thank Miguel Aranda of CEBAS-CSIC and Yolanda Hernandez of Abiopep, S.L. for hosting me in Murcia, Spain, and introducing me to molecular plant virology and diversity concepts and techniques. I am especially thankful to Ayoub Maachi, Livia Donaire, Joan Bernabe, Covadonga Latorre, and Ginés Gil Pardo for dedicating their time, expertise and effort in training and helping me throughout my stay. My stays in Bordeaux and Murcia would not be definitely fun without the company of the remaining members of each group, whom I failed to mention here due to lack of space.

I am also thankful to Sebastien Massart, Nuria Fontdevilla, Johan Rollin, Coline Temple, and the rest of their group in Gembloux AgroBiotech, University of Leige in Belgium, for hosting me for a few days of research and personal excursion. I am also thankful for the visits made by Nuria, Coline, Grigorii, and Ayoub at NIB-FITO, during which I enriched my perspectives and skills, while enjoying their great companies, which were perhaps the best I had during my doctoral research. I am also thankful to meet, to be able to talk to, and be in the same research network with other prominent plant virologist within the INEXTVIR project (*i.e.* Fernando Garcia-Arenal, Neil Boonham, Adrian Fox). For sure, I will cherish all the friendships and collaborations I made during these stays, and throughout my entire doctoral experience.

I am of course very grateful to the Jesuit community that I shared a roof, hanged-out with, and checked-up on me regularly during my stay in Ljubljana. They made my stay less stressful during the peak of the COVID-19 pandemic, and of course memorable, especially during the after mass Agape gatherings and Sunday lunch that we shared. Last, but definitely not the least, I would like to thank my loving family (Nanay Celsa, Tatay Joseph, Kel, and Ceres) and my best of friends (Ate Beth, Ate Sha, and Ate Nia) way back in the Philippines and Indonesia. Their unconditional support, encouragements, and time dedicated to just hearing my struggles and experiences, kept me going in my doctoral research, despite the difficulties of the COVID-19 pandemic and the stress of being away from home.

My lasting and sincerest gratitude goes out to you all!

# Abstract

Viruses, satellite viruses, viroids, virusoids, and satellite nucleic acids (herewith, referred to collectively or in part as 'viruses') comprise the virosphere and are perhaps the most diverse and abundant, yet still under-sampled, microbes on Earth. They are primarily regarded as pathogens or parasites of their eukaryotic or prokaryotic hosts. In agroecosystems, viruses are particularly well known for their devastating effects on crops, and thus research on their diversity, biology, ecology, epidemiology, and evolution focuses primarily on pathogenic viruses. In recent years, the availability of cost effective high-throughput sequencing technologies (HTS), improved experimental approaches and computational tools has gradually shifted virology towards non-targeted studies on virus sequences in metagenomic data (*i.e.,* viromics). In this doctoral research, we focused on tomato (*Solanum lycopersicum* L.) agroecosystems, including surrounding weeds, as a model to demonstrate the use of HTS for uncovering portions of the vast virome diversity, and to describe aspects of virus biology, epidemiology, and ecology. First, we gained a strong foundation by conducting a meta-analysis on tomato viruses worldwide by searching through the literature and databases. We found and curated 312 tomato-associated viruses, and showed that this number was underestimated in previous publications, and is still growing based on very recent reports. We showed that HTS accelerated the discovery and post-discovery characterization of tomato viruses. We synthesized pertinent information on economically important tomato viruses, and presented insights that HTS can bring forth. We then used this informational foundation to efficiently investigate the viromes of tomato and weeds in an agroecosystem setting. We detected and characterized the genomes of 125 known and novel viruses in 293 tomato samples and 143 weed plant samples (representing 59 different plant species). We did phylogenetic and diversity analyses to classify the viruses in known taxa, and found that the vast majority of novel viruses were detected in weeds. Ten viruses with probable wide host range were detected in both tomato and weeds. We demonstrated an association between plant rhabdoviruses and their taxonomically-related hosts, which provided hints to possible co-evolutionary relationships. We further characterized and showed infectivity of a novel *Tobamovirus* species in host plants from family Solanaceae. We determined the diversity of novel and previously undetected tomato viruses wherein we observed high genome-wide diversity for populations of two novel tomato viruses due to presence of two divergent lineages, while populations of other known tomato viruses showed variable diversities. Lastly, we demonstrated that HTS can be used to reveal previously undetected viruses circulating in crops, such as the case of Ranunculus white mottle ophiovirus (RWMV). We showed variable diversity of RWMV isolates from several localities in Slovenia collected since 2017, which is also the first time it was detected in tomato and pepper crops. Overall, our studies reported for the first time four known viruses in Slovenia and discovered ten novel viruses associated with tomato. We also report known or novel members of *Albetovirus*, *Vitivirus*, *Picornaviridae*, and *Lispiviridae* for the first time in tomato. Our HTS-based viromic studies and in-depth analyses, revealed vast undiscovered portions of the virosphere of tomato agroecosystems, predominantly present in weed plants, which has important implications in weed management decisions. Finally, it is pertinent to further characterize these viruses to aid in uncovering possible emergences and their influence on tomato health.

# Povzetek

Virusi, satelitni virusi, viroidi, virusoidi in satelitne nukleinske kisline (v tem odstavku poenostavljeno imenovani virusi) sestavljajo virosfero in so verjetno najbolj raznoliki in pogosti, a vendar premalo raziskani mikrobi na Zemlji. Najpogosteje jih obravnavamo kot patogene mikrobe ali parazite njihovih evkariontskih ali prokariontskih gostiteljev. V kmetijskih ekosistemih viruse poznamo zlasti zaradi njihovih uničujočih učinkov na poljščine, zato se večina raziskav njihove raznolikosti, biologije, ekologije, epidemiologije in evolucije osredotoča prav na patogene vrste. V zadnjih letih sta dostopnost tehnologij visokozmogljivega sekvenciranja in napredek v pristopih analize podatkov povzročila premik raziskav v virologiji k bolj netarčnim raziskavam virusnih zaporedij oziroma viromov v metagenomskih setih podatkov. V predloženem doktorskem delu smo se osredotočili na kmetijske ekosisteme, v katerih gojijo paradižnik (*Solanum lycopersicum* L.), vključujoč tudi plevelne rastline, ki smo jih uporabili kot model za odkrivanje še neznanih deležev viromov v takih sistemih s pomočjo visokozmogljivega sekvenciranja. Pri tem smo opisali tudi določene vidike virusne biologije, epidemiologije in ekologije. V začetku smo z metaanalizo znanja o virusih paradižnika (na podlagi literature in baz podatkov) pridobili pregled in temeljne podatke za nadaljnje raziskave. Pri tem smo našli vsaj 312 virusov, ki so bili povezani s paradižnikom, in pokazali, da je bilo ocenjeno število virusov na paradižniku v prejšnjih objavah na to temo podcenjeno ter da še vedno narašča. Opazili smo, da je uporaba visokozmogljivega sekvenciranja pospešila odkrivanje virusov paradižnika kot tudi nekaterih vidikov karakterizacije novo odkritih virusov. Pri tem smo tudi povzeli pomembne informacije o ekonomsko najpomembnejših virusih paradižnika in predstavili pomen uporabe visokozmogljivega sekvenciranja pri raziskavah teh virusov. Na osnovi pridobljenega znanja smo v drugem delu načrtovali in izvedli viromsko analizo paradižnika in plevelnih rastlin v kmetijskih ekosistemih. V 293 vzorcih paradižnika in 143 vzorcih plevelnih rastlin (vključujoč 59 različnih rastlinskih vrst) smo zaznali 125 znanih in novih virusov ter okarakterizirali njihove genome. S pomočjo filogenetskih analiz in poravnav genomskih zaporedij smo viruse uvrstili v obstoječe taksone. Večino novih virusov smo zaznali samo v plevelnih rastlinah. Deset virusov smo zaznali tako v vzorcih paradižnika kot tudi v vzorcih plevelnih rastlin. Opazili smo povezave med skupino rabdovirusov in skupino sorodnih gostiteljskih rastlin, kar nakazuje na možnost njihove koevolucije. Bolj podrobno smo okarakterizirali tobamovirus trpotca 1 in dokazali njegovo kužnost v rastlinah iz družine razhudnikovk. Raziskali smo tudi raznolikosti virusov zaznanih na paradižniku in pri tem opazili veliko raznolikost znotraj izolatov dveh novih, prej še nepoznanih, virusov paradižnika ter nizko do zmerno raznolikost znotraj izolatov znanih vrst. Prikazali smo tudi uporabo visokozmogljivega sekvenciranja za odkrivanje virusov, ki prej še niso bili zaznani v poljščinah, na primeru virusa bele lisavosti zlatice. Opazili smo zmerno raznolikost med izolati tega virusa, vzorčenimi na več lokacijah v Sloveniji od leta 2017 dalje. Pri tem smo virus prvič zaznali na paradižniku in papriki. Skupno smo v okviru raziskave prvič poročali o štirih znanih virusih in odkrili deset novih virusov v paradižniku. Prav tako smo prvič v paradižniku odkrili znane ali nove viruse iz taksonov *Albetovirus*, *Vitivirus*, *Picornaviridae* in *Lispiviridae*. S tako celostno viromsko raziskavo in inadaljnjimi analizami smo razkrili velik delež prej še neznae raznolikosti virosfere v izbranih kmetijskih ekosistemih. To nakazuje na pomen takšnih raziskav in kliče k nadaljnji karakterizaciji odkritih virusov, ki bo doprinesla k razumevanju njihove vloge v ekosistemu in vpliva na zdravje paradižnika.

# Contents

# Chapter 1

# Introduction

## 1.1 The Impact of High-throughput Sequencing (HTS) on the Discovery of Plant Viruses

Virology traces back its origins to the discovery of the first virus, the plant-infecting tobacco mosaic virus, by Martinus Willem Beijerinck together with the seminal work by Dmitry Iosifovich Ivanovsky around 120 years ago (Ivanovsky, 1892; Beijerinck, 1898; Creager et al., 1999; Lecoq, 2001). From this single virus, the understanding of virus diversity has largely expanded, resulting in the formation of 15 orders of megataxonomy (Gorbalenya et al., 2020), spanning six Realms of the virosphere delineated by the virus' (or virus-like agents') replicative nature (Koonin et al., 2021). As of March 2022, 10,434 viruses, viroids, and satellite viruses were recognized by the International Committee on the Taxonomy of Viruses (ICTV) as indicated in their Master Species List (ICTV, 2022; Lefkowitz et al., 2018). Beyond this number are thousands more viruses still awaiting naming, characterization, and finally, ratification by the ICTV (Kuhn et al., 2019). This includes the thousands of viruses discovered through metagenomic exploration of invertebrates (Shi et al., 2016) and global ocean samples (Gregory et al., 2019; Zayed et al., 2022). In addition to this, hundreds of thousands of viruses were discovered through *in silico* exploration of global nucleotide sequencing datasets (Edgar et al., 2022; Lee et al., 2022; Mifsud et al., 2022; Tisza et al., 2020). With the increasing use metagenomics based on cost-effective high-throughput sequencing (HTS) (Bertran, 2022; NIH-NHGRI, 2021), innovations in experimental approaches in virome studies (Call et al., 2021; S. E. Smith et al., 2022; Y.-Z. Zhang et al., 2018), and the continuous improvement of various computational methods (Pappas et al., 2021; Sharma et al., 2015), it is possible that in the next decades, hundreds of thousands more viruses could be discovered, out of the estimated several millions of species (Carroll et al., 2018; Geoghegan & Holmes, 2017).

Several HTS-based virus explorations in plants were reported in recent years. The most notable ones involved the sampling of crop plants or their wild relatives in extended geographical scales, such as tomatoes (*Solanum lycopersicum*) from China (Xu et al., 2017) and Brazil (de Nazaré Almeida dos Reis et al., 2020), and tomatoes and *Solanum nigrum* from France (Ma et al., 2020); peas (*Pisum sativum*) from the UK (Fowkes et al., 2021) and peas and surrounding plants from Germany (Gaafar et al., 2020); sweet potatoes (*Ipomoea batatas*) from Barbados (Alleyne et al., 2019); papayas (*Carica papaya*) from Mexico (Alcalá-Briseño et al., 2020); wild *Solanum* species from South Africa (Mahlanza et al., 2022); various wild plants from France (Ma et al., 2019); and the pollen of various wild plants from the USA (Fetters et al., 2022). These studies have contributed vast information on the distribution, ecology, epidemiology, and previously unknown phylogenetic relationships of new virus species. Additionally, out of the thousands of known viruses, only 3,206 species were associated with plant hosts, based on the information from the One Thousand Plant Transcriptomes project (1KP) and the National Center for Biotechnology Information (NCBI) GenBank database (Benson et al., 2015; Leebens-Mack et al., 2019; Wu et al., 2022). Moreover, search for new viruses in NCBI's Sequence Read Archive (SRA) identified additional 11,001 putative new plant viruses globally from nucleotide sequences of samples from different ecosystems (Edgar et al., 2022). Furthermore, 104 new plant viruses were identified from the 1KP project (Mifsud et al., 2022). Driven by HTS, plant virology has gradually shifted from a simple concept of individual plant virus species, to the concept of 'viromes', or the collection of all viruses, satellite viruses, viroids, and virus-like sequences in a metagenomic dataset from single or pooled plant samples (Roossinck et al., 2015). Furthermore, with the vast amount of virus genomic data and ecological and environmental metadata collected from these studies, plant virology has transitioned from the traditional focus only on symptomatic virus diseases, to the entire set of viruses present in a phytobiome or agroecosystem, regardless of pathogenicity (Lefeuvre et al., 2019; Maclot et al., 2020; Sommers et al., 2021).

### 1.1.1 Discovery of numerous plant viruses using HTS and deciphering previously unknown evolutionary relationships

Viruses are primarily studied using targeted detection techniques such as ELISA, PCR and Sanger sequencing (Katsarou et al., 2019). These methods are widely used in molecular plant pathology or virology laboratories, but the development of these methods requires *a priori* information on viral nucleotide sequences or serological properties. Recently, the study of the entire set of viral genomes from populations of viruses (*i.e.*, viromes), became possible due to the rapid decrease in HTS costs (NIH-NHGRI, 2021), and the availability of improved computational tools (Sharma et al., 2015; Villamor et al., 2019). These advancements surpassed the challenges of targeted detection, and uncovered vast virus diversity, discovered new species, revealed new phylogenetic relationships, thereby expanding the known plant virus taxa. Early instances of the use of HTS for studying plant viruses can be traced to more than a decade ago (Donaire et al., 2009; Kreuze et al., 2009; Rwahnih et al., 2011). Nowadays, HTS is establishing its position as one of the preferred approaches in plant virology research and diagnostics laboratories (Massart et al., 2019).

HTS-driven virus diversity and discovery studies in plants mainly focused on a single plant or crop species (Villamor et al., 2019) or a set of species in a family in natural or wild setting (Hasiów-Jaroszewska et al., 2021). Early efforts that used HTS for plant virus discovery investigated tomato samples and detected both known and a few novel viruses. HTS was demonstrated to be a useful tool in recovering virus genomes in sweet potatoes (Kreuze et al., 2009), and in various plant hosts (Donaire et al., 2009), differentiating strains of pepino mosaic virus and discovering a novel potyvirus in tomato (R. Li et al., 2012). Discovery of novel viruses also led to the establishment of novel species or family. Recently, two new *Potyviridae* members discovered in *Stylosanthes guianensis*, were suggested to be members of putative new genera within the family (Mendes De Souza et al., 2021). Furthermore, several cile-like viruses were discovered in *Solanum violifolium* and three species of *Ligustrum* from Brazil. These discoveries resolve phylogenetic relationships between plant-infecting *Kitaviridae* species, thus determining *Kitaviridae* as a monophyletic group and phylogenetically delineating its members from the related and primarily animal-associated negeviruses (Ramos-González et al., 2022). This study suggested the establishment of novel genera within the *Kitaviridae* family, but this warrants further characterization of its understudied members.

Most viruses, even multi-host ones, may have evolved and settled for a specialist or host-selective lifestyle, (Malpica et al., 2006), due to inherent fitness trade-offs and evolutionary constraints of a generalist lifestyle (Elena et al., 2009). Nevertheless, the prevalence of both specialist (*i.e.,* with narrow host range) and generalist (*i.e.,* with wide host range) viruses in an ecosystem or habitat has not yet been exhaustively investigated. Attempts to uncover plant viromes at the ecosystem level mainly focused on discovery, and its epidemiological or ecological implications (Gaafar et al., 2020; Ma et al., 2020; Xu et al., 2017). Knowing which virus species are present in an agroecosystem and to what extent they influence the host fitness landscape, while factoring in influence of environmental conditions, will greatly aid in the prediction of possible virus emergences (McLeish et al., 2019).

Overall, HTS-based viromics and *in silico* exploration of databases have uncovered phylogenetic or evolutionary relationships of numerous previously uncharacterized plant viruses and viroids (Edgar et al., 2022; Lee et al., 2022; Mifsud et al., 2022; Neri et al., 2022; Paez-Espino et al., 2016; Shi et al., 2016). However, viruses in the tropics and subtropics (*i.e.*, global South) remain under-explored, as demonstrated by the global distribution of virus detections in SRA (Edgar et al., 2022). In the future, a globally coordinated effort to explore viromes of plants, especially in these under-represented areas, would greatly contribute to expanding knowledge on plant virus diversity, ecology, epidemiology, and evolutionary relationships.

### 1.1.2 Establishing complex links between viruses, crop and non-crop plants, vectors, and the environment using HTS

Post-discovery characterization of new viruses is a pertinent step towards understanding their biological and ecological properties, which are important for assessing their potential quarantine and economic importance (Hou et al., 2020; Massart et al., 2017). Aspects of post-discovery characterization include, but are not limited to, gene and genome diversity, infectivity and host range, and survey of the distribution at different geographical scales (Massart et al., 2017). HTS-based viromics, has facilitated the discovery and detection of plant viruses in a broad geographical scale, leading to an expanded view of virus diversity, host range, epidemiology and other ecological properties (Maclot et al., 2020). Specifically, using vast data from HTS, viromes of weeds or volunteer plants, and alternative eukaryotic hosts or vectors, and possible exchanges among those parts of an ecosystem, can be deduced (Roossinck, 2015). HTS-based virome studies of plants and nearby wild plant species that can serve as reservoirs for viruses (Hančinský et al., 2020; Hasiów-Jaroszewska et al., 2021), and environmental samples, such as water that might serve as transmission pathway of still infective plant viruses (Bačnik et al., 2020), can also enhance our understanding of the epidemiology and ecology of plant viruses.

Plant virus disease outbreaks are usually associated with the introduction of plants into new environments, where plants can encounter indigenous viruses, or with the introduction and/or rapid adaptation of a novel, mutated, or recombinant virus into a new geographical region (Jones, 2021). These viruses could be brought by the introduction of their arthropod vectors, weed or ornamental hosts to new regions, or through contaminated water, soil and other environmental media (Jones, 2018). With the use of HTS and bioinformatics tools, it is now possible to trace the origins and evolution of emerging viruses causing disease pandemics in crops, and contribute in predicting disease emergence (McLeish et al., 2020, 2021). It is likewise possible to monitor the diversity of weeds and wild plants in relation to their cultivated relatives, which aids in predicting possible emergences (Alexander et al., 2014; García-Arenal & Zerbini, 2019).

A metagenomic survey of viruses in wild *Solanum* species from South Africa, revealed that, despite the close proximity of their habitats, the major viruses of cultivated *Solanum* plants were not prevalent in wild species, with the exception of potato virus Y (PVY) (Mahlanza et al., 2022). However, several known viruses of other non-Solanaceae crop plants were present in wild *Solanum* species, indicating their possible role as reservoirs for crop-infecting viruses. The study also suggested that through future and constant encounter with cultivated solanaceous plants, these viruses could have breakthrough infections and eventual emergence in crop plants. In France, the presence of PVY and Solanum nigrum ilarvirus 1 (SnIV1) in cultivated tomato plants and wild *Solanum nigrum* was demonstrated (Ma et al., 2020), indicating potential exchange of the two viruses in the wild and cultivated compartments. The same study detected the presence of broad bean wilt virus 1 (BBWV1) only in *S. nigrum.* A previous study demonstrated that it could be mechanically transmitted to tomato (Carpino et al., 2019). An extensive HTS-based exploration of viruses at the interface between cultivated and uncultivated ecosystems revealed the influence of agriculture on the distribution of plant viruses across wide areas in South Africa and France with similar climate profiles (Bernardo et al., 2018). The study also discovered 94 putative novel viruses, suggesting a large diversity of viruses in wild or weed plants that remains to be characterized. Overall, weed and wild plant viruses represent a big gap in plant virus research. Estimates indicate that only a small portion (17%) of described plant viruses are associated with weeds or wild plants (Wren et al., 2006). Thus, exploration of their viromes, in conjunction with their cultivated relatives will help close this gap.

Several known and novel plant viruses were also detected in an HTS-based exploration of viromes of arthropods. A vast survey of viruses in arthropods from China detected 1,445 novel viruses, some of which are phylogenetically-related to known plant viruses (Shi et al., 2016). Nevertheless, it is also possible that several of these viruses were wrongly assigned to arthropod hosts because they can be present as contaminations or as part of the arthropods' diets. Studies on the viromes of honeybees (*Apis mellifera*) (Roberts, Anderson, et al., 2018; Roberts, Ireland, et al., 2018), other wild pollinators (N. Li et al., 2022), whiteflies (*Bemesia tabaci*) (Huang et al., 2021), and thrips species (*Frankliniella occidentalis* and *Thrips tabaci*) (Chiapello et al., 2021) revealed the presence of plant viruses such arthropods could transmit. These studies also revealed novel viruses that are phylogenetically related to plant viruses and might be plant-infecting as well. In all these cases, host assignation is difficult due to the tight associations between plant hosts, vectors, and viruses. Nevertheless, these studies provided valuable insights into the possible interconnectivity between plants, arthropods, and viruses. Using HTS, wastewater was also explored as a possible transmission pathway of infective plant viruses in Slovenia (Bačnik et al., 2020). This study detected several plant viruses that were not reported before in Slovenia and indicated their possible distribution within the region. Another study on papaya orchards in Mexico used HTS-based network analyses to assess links of viruses to weeds, insects, and papaya, and provided valuable insights that aided in formulating virus disease management strategies (Alcalá-Briseño et al., 2020).

Post-discovery characterization of these plant and arthropod viruses, followed by in-depth and extensive studies of their links or exchanges with nearby cropping areas, could potentially result to invaluable ecological and epidemiological information. Collectively, establishing these plant-weed-vector-environment links will greatly aid in elucidating holistic understanding of virus population dynamics in an agroecosystem, and guide future studies, and disease management practices (Garrett et al., 2018; Shates et al., 2019).

## 1.2 Tomato Virome Studies and Research Gaps Addressed by HTS

In global agriculture, the expanding connectivity of international trade and commerce has driven the introduction and emergence of viruses and other pathogens in new geographical areas (Jones, 2009, 2021; Xing et al., 2020). Additionally, due to the innate high mutation rates and propensity for structural genomic changes in viruses, the emergence of more virulent strains more possible than not (Elena et al., 2014). Changes in habitats such as ecosystem conversion and simplification, combined with the modulation of environmental factors and warming climate, could highly influence the population dynamics of plant viruses and their arthropod vectors (Fraile & García-Arenal, 2016; Islam et al., 2020; Jones, 2016; Roossinck & García-Arenal, 2015; Trebicki, 2020)). All these interplaying factors of plant viruses, along plant pests and diseases, continuously threaten global food security, especially in highly vulnerable areas where population density and food demand are high (Ristaino et al., 2021).

Approximately half of the emerging crop diseases can be attributed to viruses (Anderson et al., 2004), and their economic damages are estimated to be around a quarter of the overall attainable yields in major crops, including tomato (Oerke, 2006). Global economic losses caused by virus diseases in crops were roughly estimated, with costs ranging from 30 to 50 billion US dollars annually (Sastry, 2013). Tomato production, which is one of the most economically valuable vegetables worldwide and has the highest volume of production (FAO, 2021), is affected by numerous pathogens and among them, viruses are considered an important limiting factor (Hanssen et al., 2010; Ong et al., 2020; Souiri et al., 2019). Thus, it is becoming increasingly important that tomato virus diversity should be well-studied, and routine monitoring and diagnostics should be done to limit possible emergence and spread of virus diseases.

A comprehensive review of the existing knowledge on tomato virus diversity and their characterization was published 12 years ago (Hanssen et al., 2010), and recent reviews have focused only on selected aspects of tomato viruses, such as genomic diversity and in relation to viruses of other plant species from family Solanaceae (Hančinský et al., 2020; Ong et al., 2020). Since then, HTS has significantly advanced tomato virus discovery, and is starting to be a commonly used tool in studies on diversity, ecology and epidemiology. A survey of over a hundred tomatoes showing virus disease-like symptoms from major tomato-growing areas in China uncovered the prevalence of 22 viruses, a few of which were not reported before in tomato, including one new rhabdovirus (Xu et al., 2017). In 2017-2018, a survey of viruses in tomato and in surrounding *S. nigrum* from different locations in France, unveiled the presence of PVY (*Potyvirus*) and SnIV1 (*Ilarvirus*) between the two related plants, between the wild and cultivated ecological zones, suggesting possible virus exchanges (Ma et al., 2020). Using HTS, similar studies reported known and novel virus species associated with individual tomato plants or a collection of tomato samples (de Nazaré Almeida dos Reis et al., 2020; Fontenele et al., 2017; Rego-Machado et al., 2019; Saqib et al., 2015). Findings from these studies have significantly contributed to the characterization of the global tomato virome and presented several insights that an HTS-based viromics survey can provide regarding the diversity, ecology and evolution of tomato viruses. These findings can be used as a baseline for post-discovery characterizations of viruses and their population dynamics, which could facilitate predicting virus emergences and disease outbreaks.

## 1.3 Scientific Problems and Research Aims

With the increasing number of reports on the impacts and predicted risks of virus diseases globally, whether in plants (Jones, 2021; Ristaino et al., 2021), humans or animals (Carlson et al., 2022; Morens et al., 2020), there is indeed an urgent need to collect and synthesize the current knowledge, and decipher the still less understood diversity of viruses across habitats and ecosystems. Better awareness of the current global status of virus diseases will help us to better prepare for future virus disease pandemics. The most recent comprehensive review of tomato viruses is more than a decade old (Hanssen et al., 2010), thus an update on the vast diversity of information regarding tomato viruses, including a summary of their genomic, biological and ecological properties, is needed. Moreover, the impact of HTS on the discovery of tomato viruses and their subsequent characterization has not yet been assessed in any literature. A meta-analysis of the current body of knowledge on tomato viruses is needed and should be made accessible to plant virologists, plant protection officers, and students worldwide.

Moreover, to date, no study has used an HTS-based viromics approach to simultaneously uncover the diversity and distribution of viruses and other virus-like agents, in tomato and the diverse set of weeds within or surrounding tomato-growing areas. Furthermore, no study on a nation-wide scale has been done in Slovenia, nor with any symptomatic and asymptomatic crops in association with diverse weed plants surrounding or within the crop-growing areas. The vast quantities of virome datasets that will be gained from such studies will help deduce diverse virus genome organizations, genetic and genome-wide population diversity, phylogenetic relationships and possible co-evolutionary links between certain groups of viruses with their host. Overall, these information contribute invaluable insights on plant viruses at the ecosystem level, specifically, their diversity and dynamics at the wild-cultivated agroecological interface, a known zone for disease spill-overs (Alexander et al., 2014; Elena et al., 2014). Such virome datasets could also serve as baseline information that will aid in future tomato virus disease monitoring, thus contributing to the prevention future virus epidemics in tomato in the region.

This doctoral research focuses on virus diversity associated with crops and surrounding flora in an agroecosystem. With the use of HTS, uncovering the diversity and monitoring virus evolution through extended time and space became easily implementable. Thus, in this research, we focused on tomato agroecosystems, on a nation-wide scale, as a model to demonstrate the use of HTS in addressing the above-mentioned knowledge gaps in plant virology. We sought to achieve the following general and specific aims:

1. To assess the current body of knowledge on tomato viruses and how HTS influenced their discovery and characterization. Specifically:
   a. to comprehensively collect all the information on viruses reported to infect or be associated with tomato, and highlight the economically important viruses,
   b. to assess how HTS influenced the rate of tomato virus discovery in the past decade (2010–2020) and how it provided insights into the epidemiology and ecology of viruses, and
   c. to evaluate the extent of follow-up characterization studies (*i.e.*, based on genetic, biological or ecological properties) implemented on newly discovered tomato viruses, based on a published characterization framework and criteria.

2. To uncover the diversity of known and novel viruses, satellite RNAs, and viroid-like sequences in tomato, and weeds within or surrounding selected tomato growing areas. Specifically:
   a. to obtain metagenomes from tomato and weed plants, and assemble, identify, and characterize genomes of known and novel viruses from these metagenomes,
   b. to distinguish viruses as novel or known based on demarcation criteria set by the ICTV, and
   c. to identify viroid-like circular RNAs from tomato and weed plant metagenomes.

3. To examine phylogenetic relationships and host associations of selected virus groups, genera, or families, identified in tomatoes and weeds. Specifically:
   a. to identify specific host(s) of selected known and novel viruses,
   b. to decipher overlap of virus presence in weeds and tomatoes,
   c. to determine placement of novel viruses within known virus taxa, and
   d. to determine associations of phylogenetically-related viruses with their taxonomically-related plant hosts.

4. To characterize properties of novel viruses. Specifically:
   a. to examine the virion morphology of a novel virus, and
   b. to determine the mechanical transmissibility, and infectivity of a novel virus in selected plant hosts.

5. To determine the distribution and genetic and genome-wide diversity of selected viruses. Specifically:
   a. to determine the distribution of previously undetected viruses possibly circulating in tomatoes or other crops, and
   b. to determine the genetic and genome-wide diversity of previously undetected and predominantly detected viruses in tomatoes.

## 1.4 Research Hypotheses

In this doctoral research, we hypothesized that:

1. the number of tomato viruses is probably underestimated and represents one of the largest numbers of distinct viruses associated with a plant species,
2. there is still a vast undiscovered diversity of viruses, especially novel virus species, in tomatoes and various species of weed plants in tomato agroecosystems,
3. there are overlaps in the presence of viruses in tomato and weed plants within or surrounding tomato-farming areas,
4. certain groups of evolutionarily-related viruses are associated with specific groups of taxonomically-related plant hosts, marking virus/host long-term co-evolution,
5. a known or novel virus from a family with a known wide host range found in weed plant(s) will be able to infect plants from a botanical family different from the original weed host, and
6. there are previously undetected viruses are already circulating in tomato and other economically-important crops and can be uncovered using HTS data across years of collection and from different locations.

## 1.5 Publications Included and Candidate's Contribution

The first publication, "Global Advances in Tomato Virome Research: Current Status and the Impact of High-Throughput Sequencing", was published in *Frontiers in Microbiology* vol. 12 (2021), doi: 10.3389/fmicb.2021.671925. This review and meta-analyses is the most comprehensive and systematic review of all tomato viruses so far. It highlights tomato virus studies from the most recent decade (2011-2020), and evaluates how HTS has impacted the discovery of tomato viruses and how it can contribute to their further characterization, according to a published characterization framework and criteria (Hou et al., 2020; Massart et al., 2017). It also provides a comprehensive and detailed summary of the current widespread, emergent and economically important viruses of tomato, which will be a useful reference for researchers, students, and private companies that are interested in studying viruses of tomato. In this study, we addressed the first aim (see Section 1.3) and first hypothesis of this dissertation (see Section 1.4). The doctoral candidate contributed to the conceptualization the research topic. He did the data mining and analyses, wrote the first draft of the manuscript, and contributed to editing the final version of the published manuscript.

The second publication "In-depth study of tomato and weed viromes reveals undiscovered plant virus diversity in an agroecosystem", is a submitted article available as a preprint in *bioRxiv* doi: 10.1101/2022.06.30.498278, and its supplementary materials are available at *Figshare* doi: 10.6084/m9.figshare.20200769. This research. to date, comprises the largest concurrent virome survey of tomato and diverse species of weed in Slovenia, and worldwide. It has discovered a considerable number of novel viruses, for which it has provided in-depth characterization of their genomes, phylogenetic relationships with known taxa, biology, and links to plant hosts. Collectively, this study helped to illuminate the vast unknown diversity of viruses in tomato agroecosystems, at least in Slovenia, which could serve as baseline for further biological studies and further virus monitoring in the region. In this study, we addressed the second to fourth aims, a part of the fifth aim (see Section 1.3), and second to fifth hypotheses of this dissertation (see Section 1.4). The doctoral candidate contributed to the formulation and design of the study. He did the laboratory and greenhouse work, analyzed the data, wrote the first draft of the manuscript, and contributed to editing the final version of the manuscript.

The third publication, “First report of Ranunculus white mottle ophiovirus in Slovenia in pepper with yellow leaf curling symptom and in tomato”, was published in *Plant Disease* vol. 106, no. 7 (2022), doi: 10.1094/PDIS-08-21-1624-PDN. This research demonstrated the use of HTS to identify a previously undetected virus in crops that might be circulating and contributing to losses or emerging and expanding its geographical distribution. This paper addressed a part of the fifth aim (see Section 1.3) and the sixth hypothesis of this dissertation (see Section 1.4). The doctoral candidate contributed to the formulation and design of the study and to the laboratory work, analyzed the data, wrote the first draft of the manuscript, and contributed to editing the final version of the manuscript.

# Chapter 2

# Scientific Publications

## 2.1 Global Advances in Tomato Virome Research: Current Status and the Impact of High-Throughput Sequencing

Authors: **Mark Paul Selda Rivarez**, Ana Vučurović, Nataša Mehle, Maja Ravnikar, and Denis Kutnjak

Published in: *Frontiers in Microbiology*, vol. 12 (2021),
doi: 10.3389/fmicb.2021.671925

frontiers in Microbiology

REVIEW
published: 21 May 2021
doi: 10.3389/fmicb.2021.671925

# Global Advances in Tomato Virome Research: Current Status and the Impact of High-Throughput Sequencing

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Viruses cause a big fraction of economically important diseases in major crops, including tomato. In the past decade (2011–2020), many emerging or re-emerging tomato-infecting viruses were reported worldwide. In this period, 45 novel viral species were identified in tomato, 14 of which were discovered using high-throughput sequencing (HTS). In this review, we first discuss the role of HTS in these discoveries and its general impact on tomato virome research. We observed that the rate of tomato virus discovery is accelerating in the past few years due to the use of HTS. However, the extent of the post-discovery characterization of viruses is lagging behind and is greater for economically devastating viruses, such as the recently emerged tomato brown rugose fruit virus. Moreover, many known viruses still cause significant economic damages to tomato production. The review of databases and literature revealed at least 312 virus, satellite virus, or viroid species (in 22 families and 39 genera) associated with tomato, which is likely the highest number recorded for any plant. Among those, here, we summarize the current knowledge on the biology, global distribution, and epidemiology of the most important species. Increasing knowledge on tomato virome and employment of HTS to also study viromes of surrounding wild plants and environmental samples are bringing new insights into the understanding of epidemiology and ecology of tomato-infecting viruses and can, in the future, facilitate virus disease forecasting and prevention of virus disease outbreaks in tomato.

**Keywords: tomato, virome, high-throughput sequencing, metagenomics, virus diversity, virus discovery, virus ecology, virus epidemiology**

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***Specialty section:***
*This article was submitted to Virology, a section of the journal Frontiers in Microbiology*

***Received:*** *24 February 2021*
***Accepted:*** *12 April 2021*
***Published:*** *21 May 2021*

***Citation:***
*Rivarez MPS, Vučurović A, Mehle N, Ravnikar M and Kutnjak D (2021) Global Advances in Tomato Virome Research: Current Status and the Impact of High-Throughput Sequencing. Front. Microbiol. 12:671925. doi: 10.3389/fmicb.2021.671925*

## INTRODUCTION

Tomato (*Solanum lycopersicum* L.) is one of the most economically valuable fruit or vegetable crops worldwide, valued at 93.9 billion US dollars in 2018, with yield estimated at 180.8 million tons in 2019 (FAOSTAT, 2020). Tomato production is affected by numerous diseases and, among them, viruses are considered an important production-limiting factor (Hanssen et al., 2010b; Souiri et al., 2019; Hančinský et al., 2020; Ong et al., 2020). It was estimated that almost half of the emerging crop diseases can be attributed to plant viruses (Anderson et al., 2004), which could amount up to around a quarter of the overall attainable yields in major crops, including tomato (Oerke, 2006). Worldwide economic damages caused by viruses in crops are difficult to estimate; however, rough approximations indicate yield losses range from 30 to 50 billion US dollars annually (Sastry, 2013). Yield and economic losses due to virus diseases in tomato vary greatly and are often dependent on the virus species and growing region.

Until a decade ago, viruses were mostly analyzed using targeted detection techniques such as ELISA, PCR, and Sanger sequencing (Katsarou et al., 2019). These methods are widely available in molecular biology labs, but they require *a priori* information on viral genomes or serological properties of viral species that might be present in a sample. The study of a whole community of viruses (i.e., viromes), including unknown ones, became possible due to the rapid decrease in high-throughput sequencing (HTS) costs (NIH-NHGRI, 2019) and the availability of the improved data analysis tools (Villamor et al., 2019). This circumvented challenges of targeted detection of plant viruses and contributed useful ecological and epidemiological insights. First examples of the use of HTS for detection of plant viruses are now over a decade old (Adams et al., 2009a; Al Rwahnih et al., 2009; Donaire et al., 2009; Kreuze et al., 2009). Currently, HTS is used for discovery of many novel viruses and is now establishing its position as one of the classical approaches in plant virology research and diagnostics laboratories (Massart et al., 2019). HTS is often employed with one of the possible nucleic acid preparation approaches, such as sequencing of double-stranded (ds)RNA, small (s)RNAs, total (tot)DNA after rolling circle amplification, virion-associated RNA (VANA), and total (tot)RNA after ribosomal (r)RNA depletion (Pecman et al., 2017; Ma et al., 2019; de Nazaré Almeida dos Reis et al., 2020; Gaafar and Ziebell, 2020). Each method has its pros and cons (Roossinck, 2017) and should be selected according to the aims of the study; e.g., sequencing rRNA depleted totRNA or sRNA might be the most straightforward and generic approaches for detection of a wide range of viruses in single samples or relatively small sample pools (Pecman et al., 2017). On the other hand, dsRNA or VANA might be beneficial, when trying to enrich for viruses in, e.g., large pools of starting plant material (Ma et al., 2019).

Both classical (Sanger) sequencing and HTS are regularly used for discovery of new viruses in tomato; however, the usage of the latter is evidently increasing in the past few years. In the first part of this review, we discuss the discovery of 45 novel virus species in tomato within the 2011–2020 period and contextualize the role of HTS in these findings. Moreover, a post-discovery characterization of new viruses represents an important step toward understanding their biological and/or economical relevance (Massart et al., 2017; Hou et al., 2020); thus, we also systematically reviewed to which extent such characterization have been performed for newly discovered viruses associated with tomato. Beyond discovering and detecting viruses in tomato, HTS can enable a broader look into the virome of tomato on a defined geographical scale, a virome of surrounding plants and vectors, and possible exchanges among those communities. HTS-based virome studies of tomato and surrounding wild plant species (which can serve as reservoirs for viruses) (Hančinský et al., 2020; Ma et al., 2020), and environmental samples, such as water (which might serve as transmission pathway) (Bačnik et al., 2020), can also bring important insights into the understanding of the epidemiology of some tomato viruses.

Review of the past and recent discoveries of viruses in tomato shows that tomato is currently associated with at least 312 different viral species, which is likely, according to our knowledge, the largest recorded number known for any cultivated plant. Among those, many known and several recently discovered viruses cause significant economic damage in tomato production in different parts of the world. In the second part of this review, we focus on important tomato viruses, which caused significant economic losses in tomato production in the past decade and new virus discoveries in tomato, for which limited or no knowledge about potential impact on tomato health is available.

## HTS HAS BECOME AN IMPORTANT TOOL IN TOMATO VIRUS DISCOVERY AND EPIDEMIOLOGY STUDIES

Forty-five novel virus species were discovered in tomato in the recent decade (2011–2020) (**Table 1**). Majority of these discoveries were made in Neotropic and Palearctic countries and just in recent years (**Figure 1**). Out of this set, 14 were discovered using HTS, and in 2020 alone, seven novel species were discovered just by three HTS-based studies (Ciuffo et al., 2020; de Nazaré Almeida dos Reis et al., 2020; Ma et al., 2020). In this period, also four viral families were associated with tomato for the first time, in four HTS-based studies, i.e., *Iflaviridae* (Saqib et al., 2015), *Phenuiviridae* (Lecoq et al., 2019), *Kitaviridae* (Ciuffo et al., 2020), and *Genomoviridae* (de Nazaré Almeida dos Reis et al., 2020). Specifically, more than half of the RNA viruses were discovered using HTS (7/13), while most of the DNA viruses (including satellite virus species) were discovered using a non-HTS approach (24/32). Overall, non-HTS-based discovery approaches remain widely used for targeted, single species plant virus discoveries, while HTS has become a tool to discover multiple species, without *a priori* knowledge about possibly present viruses. In this section, the impact of HTS as an important tool in tomato viromics is further contextualized, from the discovery of viruses in individual plants, through the post-discovery characterization of new viruses, to the holistic analysis of plant viromes in agroecosystems.

### Discovery and Generic Detection of Viruses in Tomato Using HTS

Fourteen new tomato viruses or virus satellites were detected using HTS in recent years (**Table 1**). As an example, HTS was used to characterize the diversity of viruses and viroids in tomato-growing areas of Mexico, where a novel tobamovirus, tomato mild mottle virus (ToMMV), and a novel potyvirus, tomato necrotic stunt virus (ToNStV), were discovered (Li et al., 2012, 2013). In the extensive study of the diversity of tomato viruses

**TABLE 1** | Novel virus species discovered from 2011 to 2020 and associated with tomato.

| Family | Genus | Virus name | Acronym | Baltimore Group[1] | HTS-based discovery? | Sample and library preparation approach[2]/ Sequencing platform | Country(ies) where first reported | Publication |
|---|---|---|---|---|---|---|---|---|
| *Alphasatellitidae* | Unspecified | "New alphasatellite" | – | ssDNA | Yes | Total DNA-RCA/HiSeq 2500 | Brazil | de Nazaré Almeida dos Reis et al., 2020 |
| | *Colecusatellite* | Tomato leaf curl Cameroon alphasatellite | ToLCCMA | ssDNA | No | – | Cameroon | Leke et al., 2011 |
| *Bromoviridae* | *Ilarvirus* | Solanum nigrum ilarvirus 1 | SnIV1 | (+)ssRNA | Yes | dsRNA/HiSeq 3000 | France | Ma et al., 2020 |
| | | Tomato necrotic streak virus | TomNSV | (+)ssRNA | No | – | USA | Adkins et al., 2015 |
| *Geminiviridae* | *Begomovirus* | "New begomovirus species #1" | – | ssDNA | Yes | Total DNA-RCA/HiSeq 2500 | Brazil | de Nazaré Almeida dos Reis et al., 2020 |
| | | "New begomovirus species #2" | – | ssDNA | Yes | Total DNA-RCA/HiSeq 2500 | Brazil | de Nazaré Almeida dos Reis et al., 2020 |
| | | "New begomovirus species #3" | – | ssDNA | Yes | Total DNA-RCA/HiSeq 2500 | Brazil | de Nazaré Almeida dos Reis et al., 2020 |
| | | Pepper leafroll virus | PepLRV | ssDNA | No | – | Peru | Martínez-Ayala et al., 2014 |
| | | Pepper yellow leaf curl Aceh virus | PepYLCAV | ssDNA | No | – | Indonesia | Kesumawati et al., 2019 |
| | | Tomato apical leaf curl virus | ToALCV | ssDNA | No | – | Argentina | Vaghi Medina et al., 2018 |
| | | Tomato chlorotic leaf curl virus | ToCLCV | ssDNA | No | – | Brazil | Quadros et al., 2019 |
| | | Tomato chlorotic leaf distortion virus | TCLDV | ssDNA | No | – | Venezuela | Zambrano et al., 2011 |
| | | Tomato dwarf leaf virus | ToDLV | ssDNA | No | – | Argentina | Vaghi Medina and López Lambertini, 2012 |
| | | Tomato interveinal chlorosis virus | ToICV | ssDNA | No | – | Brazil | Albuquerque et al., 2012 |
| | | Tomato interveinal chlorosis virus-2 | ToICV2 | ssDNA | Yes | Total DNA-RCA/HiSeq 2000 | Brazil | Rego-Machado et al., 2019 |
| | | Tomato latent virus | TLV | ssDNA | No | – | Cuba | Fuentes et al., 2016 |
| | | Tomato leaf curl Burkina Faso virus | ToLCBFV | ssDNA | No | - | Burkina Faso | Ouattara et al., 2017 |
| | | Tomato leaf curl Cameroon virus | ToLCCMV | ssDNA | No | – | Cameroon | Leke et al., 2011 |
| | | Tomato leaf curl Kunene virus | ToLCKunV | ssDNA | No | – | Namibia | Lett et al., 2020 |
| | | Tomato leaf curl Liwa virus | ToLCLV | ssDNA | No | – | Oman | Khan et al., 2014 |
| | | Tomato leaf curl Mahé virus | ToLCMahV | ssDNA | No | – | Seychelles | Scussel et al., 2018 |
| | | Tomato leaf curl Oman virus | ToLCOMV | ssDNA | No | – | Oman | Idris et al., 2011 |
| | | Tomato leaf curl purple vein virus | ToLCPVV | ssDNA | No | – | Brazil | Macedo et al., 2018 |

*(Continued)*

**TABLE 1** | Continued

| Family | Genus | Virus name | Acronym | Baltimore Group[1] | HTS-based discovery? | Sample and library preparation approach[2]/ Sequencing platform | Country(ies) where first reported | Publication |
|---|---|---|---|---|---|---|---|---|
| | | Tomato leaf deformation virus | ToLDeV | ssDNA | No | – | Peru | Márquez-Martín et al., 2011 |
| | | Tomato mottle wrinkle virus | ToMoWV | ssDNA | No | – | Argentina | Vaghi Medina et al., 2015 |
| | | Tomato rugose yellow leaf curl virus | ToRYLCV | ssDNA | No | – | Uruguay | Márquez-Martín et al., 2012 |
| | | Tomato twisted leaf virus | ToTLV | ssDNA | No | – | Venezuela | Romay et al., 2019 |
| | | Tomato vein clearing leaf deformation virus | ToVCLDeV | ssDNA | No | – | Argentina | Vaghi Medina et al., 2020 |
| | | Tomato wrinkled mosaic virus | ToWMV | ssDNA | No | – | Venezuela | Romay et al., 2018 |
| | | Tomato yellow margin leaf curl virus | TYMLCV | ssDNA | No | – | Venezuela | Nava et al., 2013 |
| | Unassigned | "Tomato associated geminivirus 1" | TaGV1 | ssDNA | Yes | Total DNA-RCA/HiSeq 2500 | Brazil | Fontenele et al., 2017 |
| *Genomoviridae* | *Gemycirculavirus* | "Plant-associated genomovirus 2" | – | ssDNA | Yes | Total DNA-RCA/HiSeq 2500 | Brazil | de Nazaré Almeida dos Reis et al., 2020 |
| *Iflaviridae* | *Iflavirus* | Tomato matilda virus | TMaV | (+)ssRNA | Yes | Total RNA/GA IIx | Australia | Saqib et al., 2015 |
| *Kitaviridae* | *Blunervirus* | Tomato fruit blotch virus | ToFBV | ( + )ssRNA | Yes | Total RNA-RD/unspecified | Italy, Australia | Ciuffo et al., 2020 |
| *Phenuiviridae* | *Tenuivirus* | Melon chlorotic spot virus | MeCSV | (–)ssRNA | Yes | Small RNA/HiSeq | France | Lecoq et al., 2019 |
| *Potyviridae* | *Potyvirus* | Tomato necrotic stunt virus | ToNStV[3] | (+)ssRNA | Yes | Small RNA/GA IIx | Mexico | Li et al., 2012 |
| *Rhabdoviridae* | *Cytorhabdovirus* | Tomato yellow mottle-associated virus | TYMaV | (–)ssRNA | Yes | Small RNA/HiSeq 2500 | China | Xu et al., 2017 |
| *Tollecusatellitidae* | *Betasatellite* | Tomato leaf curl Hajipur betasatellite | ToLCHLB | ssDNA | No | – | India | Kumar et al., 2013 |
| | | Tomato leaf curl Togo betasatellite | ToLCTGB | ssDNA | No | – | Togo | Kon and Gilbertson, 2012 |
| *Tospoviridae* | *Orthotospovirus* | Pepper necrotic spot virus | PNSV | (–)ssRNA | No | – | Peru | Torres et al., 2012 |
| | | Tomato necrotic ringspot virus | TNRSV | (-)ssRNA | No | – | Thailand | Seepiban et al., 2011 |
| | | Tomato necrotic spot virus[4] | TNSV | (–)ssRNA | No | – | China | Yin et al., 2014 |
| *Tymoviridae* | *Tymovirus* | Tomato blistering mosaic tymovirus | ToBMV | (+)ssRNA | No | – | Brazil | De Oliveira et al., 2013 |
| *Virgaviridae* | *Tobamovirus* | Tomato brown rugose fruit virus | ToBRFV | (+)ssRNA | No | – | Jordan | Salem et al., 2016 |
| | | Tomato mottle mosaic virus | ToMMV | (+)ssRNA | Yes | Small RNA/HiSeq 2000 | Mexico | Li et al., 2013 |

*Viruses are grouped according to virus family and genus, with its genome type indicated. The sample and library preparation approach and sequencing platform used are indicated for viruses discovered using HTS. Lastly, the country where the virus was first discovered and the corresponding publication and year are also indicated. [1]ssDNA: circular, positive sense, single-stranded DNA (Group I), (+)ssRNA: linear, positive sense, single-stranded RNA (Group IV), (–)ssRNA: linear, negative sense, single-stranded RNA (Group V); [2]total DNA-RCA: total DNA with rolling circle amplification, total RNA-RD: total RNA with rRNA depletion; [3]Taken from recent literature, ToNSV and TNSV were previously also used in literature; however, they are also used for other viruses. [4]The same name is used also for another virus from the genus Ilarvirus (family Bromoviridae).*

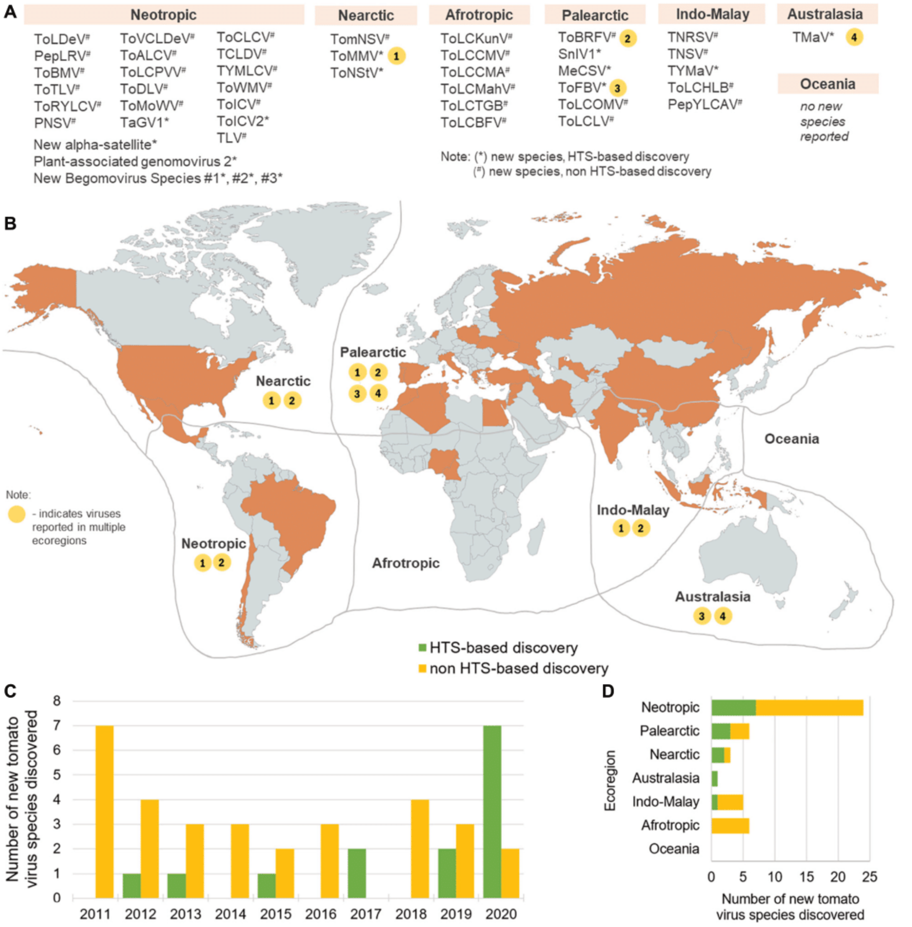

**FIGURE 1 |** Global distribution of virus species newly discovered in the 2011 to 2020 period. Abbreviated virus names (see **Table 1**) are shown in groups corresponding to the ecozones in which they were discovered (Antarctic is not shown, for simplicity, China and Indonesia are included in Indo-Malay, and Mexico is included in the Neotropic ecoregion) **(A)**. In the map **(B)**, ecoregions are delimited by gray lines and countries colored in orange are top producers of tomato in the 2008–2018 period, recording at least 8.14 million tons of total tomato produced (FAOSTAT, 2020). Viruses detected in more than one ecozone are shown on the map as number-coded yellow circles (1–4) corresponding to the virus species designated in the list in **(A)**. The numbers of annual new tomato virus discoveries in the 2011–2020 period are shown in **(C)** and the numbers of new tomato virus discoveries per ecoregion in this time period are shown in **(D)**. The map was created using www.mapchart.net under the CC BY-SA 4.0 license.

in China, a novel cytorhabdovirus, named tomato yellow mottle-associated virus (TYMaV), was discovered (Xu et al., 2017). In France, a novel ilarvirus was found in tomatoes and *Solanum nigrum*, named Solanum nigrum ilarvirus 1 (SnIV1) (Ma et al., 2020). Three begomoviruses, a gemycircularvirus, and a new alpha satellite were discovered by HTS in tomatoes in Brazil (de Nazaré Almeida dos Reis et al., 2020). A novel begomovirus named tomato-associated geminivirus 1 (TaGV1) was discovered using HTS in Brazil and was suggested as a member of a putative new genus closely related to *Capulavirus* (Fontenele et al., 2017). In Italy and Australia, a new blunervirus (*Kitaviridae*), named tomato fruit blotch virus (ToFBV), was discovered by HTS (Ciuffo et al., 2020). Tomato matilda virus (TMaV) (*Iflaviridae*), first detected in Australia using HTS (Saqib et al., 2015), was also detected in tomatoes grown in Italy, based on sequences deposited in GenBank (accession number MK517476) (**Table 1** and **Figure 1**). The infectivity of ToFBV and TMaV in tomato, other biological characteristics, and their impact on tomato yield are not yet known.

Aside from discovery of new viruses, HTS was also used to detect known viruses for the first time in tomato. In China, six known viruses, namely, potato virus A, tobacco vein banding mosaic virus (*Potyviridae*), potato virus H, potato virus S, potato virus M (*Betaflexiviridae*), and turnip yellows virus (*Luteoviridae*) were reported for the first time in tomato (Xu et al., 2017). In Germany, Physostegia chlorotic mottle virus (PhCMoV) was detected for the first time in tomato using HTS (Gaafar et al., 2018), and in the United States, cherry rasp leaf virus was detected (Bratsch et al., 2020) in tomato. In a survey of tomato and pepper viruses in Vietnam, pepper chlorotic spot orthotospovirus (*Tospoviridae*) and Lindernia anagallis yellow vein virus (*Geminiviridae*) were associated with tomato for the first time (Choi et al., 2020). A known virus, discovered in henbane in 1932 in England, called henbane mosaic virus (HMV), but later on rarely detected, was found using HTS for the first time in tomatoes from Slovenia (Pecman et al., 2018). In the same study, HTS was also used to reconstruct complete genomic sequences of the isolate from tomato and historic isolates from virus collections, since only partial genomic sequence of the virus was available before.

## Post-discovery Characterization of New Tomato Viruses

Even though HTS advanced our ability for generic detection and discovery of novel viruses, it can only provide us with genomic information of the virus. For a meaningful biological characterization, classical virology tools are still very much needed, which include plant bioassays (i.e., infectivity and transmission assays), electron microscopy, and targeted diagnostics. Virus characterization is a time- and resource-intensive task that often requires efforts from different institutions, sometimes at an international scale. A framework for biological characterization of viruses discovered by HTS was proposed to facilitate this part of the research pipeline (Massart et al., 2017). We used this framework to review how the 45 new viruses discovered in tomato, both through HTS and through other methods, were characterized. The same approach was recently employed for fruit tree infecting viruses (Hou et al., 2020), where fulfillment of 14 characterization categories were reviewed. We analyzed 53 publications on novel tomato viruses (41 reporting viruses for the first time and 12 follow-up studies) from the 2011–2020 period contributing to characterization of newly discovered viruses associated with tomato, reviewing the fulfillment of 14 characterization categories (**Figure 2A**; for details, see **Supplementary Table 1**).

Our review showed that, e.g., for majority (>60%) of the HTS-based new virus discoveries, whole genome sequence was determined, primers for detection of the virus with PCR were designed, local survey of prevalence was done, and co-infection with other viruses was checked (**Figure 2A**). Comparing HTS-based and non-HTS-based virus discoveries, there were fewer infectivity studies done on the original host and other natural or indicator hosts for HTS-based discoveries compared to that of non-HTS discoveries. Moreover, vector transmission was studied in very few cases and possibility of latent infections has not been studied for any of the newly discovered viruses. Practically, completeness of virus characterization greatly depended on the phytosanitary priority level of a virus. For tomato brown rugose fruit virus (ToBRFV), which is an emerging virus with significant economic importance, 13 of 14 characterization criteria were fulfilled in less than 4 years after the discovery, included in five publications after its first report. On the other hand,

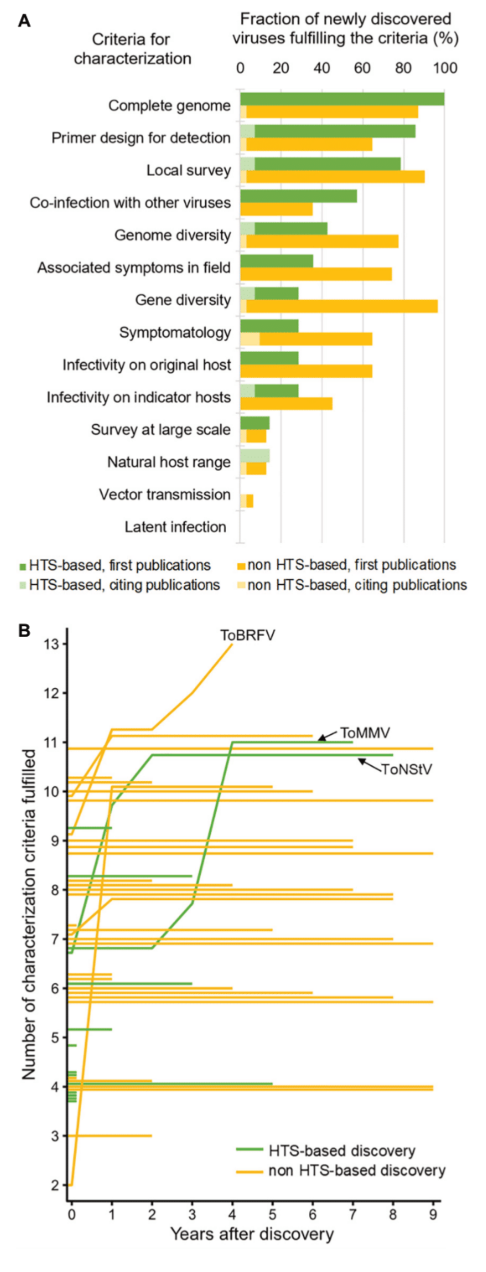

**FIGURE 2 |** Post-discovery characterization of new tomato-infecting viruses according to the literature review. Percentages of newly discovered virus species fulfilling each of the 14 characterization criteria are shown for viruses discovered by HTS or other methods **(A)**. Fulfillment of characterization criteria plotted through the years elapsed since the first report is shown as a line plot **(B)**, wherein each line represents a single virus and the evolution of its characterization; the lines corresponding to the emerging tomato brown rugose fruit virus (ToBRFV), and the first two tomato viruses discovered through HTS, tomato mottle mosaic virus (ToMMV) and tomato necrotic stunt virus (ToNStV), are labeled.

ToNStV and ToMMV, which were the first tomato-infecting viruses discovered using small RNA sequencing, were more extensively characterized after 7–8 years. Finally, many viruses were not followed up at all after the initial discovery and first publication (**Figure 2B**).

## Looking Outside Tomato: Vectors, Weeds, Water, and Epidemiological Implications of HTS

Spatially, crop lands are always in conjunction with the wild or urban ecosystems bound by an agroecological interface, which is characterized by active biological interactions and exchange of materials, including pests and pathogens (Alexander et al., 2014). Nevertheless, it was just in the recent decade that plant virologists started to explore more intensively the diversity of viruses in wild ecosystems. Plant virus ecology and epidemiology include studies on viruses infecting weeds and other wild plants (Malmstrom and Alexander, 2016; Shates et al., 2019) as well as water as potential channel for plant virus spread (Mehle and Ravnikar, 2012). In this context, HTS is a well-suited tool, which allows generic investigation of viromes in a diverse set of sample matrices, from an array of different plant species to environmental samples, such as water and soil.

Weeds and other wild plants could act as reservoirs from which plant viruses can spill to crops, or vice versa (Malmstrom and Alexander, 2016). The association of tomato viruses with weeds also implies increased chances of survival for the viruses because weeds have high reproductive rates and are environmentally persistent (Cooper and Jones, 2006). These findings imply importance of weeds in plant-virus pathosystems and the importance of their inclusion in epidemiological studies. A recent review of viruses infecting plants from the *Solanaceae* family highlights the importance of studying the virome of both wild and cultivated plants to fully understand the plant virus impact on the agroecological scale (Hančinský et al., 2020). For tomato-infecting viruses, several studies were done to elucidate the role of wild plants as virus reservoirs, more specifically referred to in Section "Emerging and endemic viruses and viroids causing significant economic damages in tomato production in the past decade."

The first extensive tomato virome HTS-based study was done in major tomato-growing areas in China (Xu et al., 2017), resulting in a lot of new knowledge about occurrence of tomato viruses in the region and revealed several previously unknown associations of known plant viruses with tomato. It also suggested that some viruses originally associated with insect hosts (Wuhan insect virus 4, 5, and 6) (Li et al., 2015) might in fact be plant viruses, since they were found in tomato and they cluster with other plant viruses in phylogenetic analysis (Xu et al., 2017). This study did not look into virome of wild plants growing nearby. On the other hand, a recent large-scale virome study of tomato in France also included its wild relative, *S. nigrum* or European black nightshade (Ma et al., 2020). The study suggested the likely exchange of some viruses between tomato and *S. nigrum*; a newly discovered SnIV1 was found in both species, as well as potato virus Y (PVY), for which there was a strong evidence for a likely spillover from tomato to *S. nigrum*. On the other hand, a possible biological and ecological barrier was proposed for a spread of broad bean wilt virus (known to be able to infect both hosts) from *S. nigrum* to tomato, since high incidence and diversity of this virus was observed in *S. nigrum*; however, the virus was not detected in tomato in this study. Moreover, discovery of Euphorbia caput-medusae latent virus by HTS in South Africa in wild plant *Euphorbia caput-medusae*, which was shown to be infective in tomato and *Nicotiana benthamiana*, led to the establishment of a new genus, *Capulavirus*, in the family *Geminiviridae* (Bernardo et al., 2013).

Even prior to the application of HTS-based methods for detection of plant viruses, several studies detected plant viruses outside of the host, in environmental samples, such as water (Mehle and Ravnikar, 2012) and in soil (Fillhart et al., 1998). Several plant viruses are stable in the environment and can survive long periods of time outside the host (Mehle et al., 2018). Water can serve as virus transmission channel that have the potential to create new infection foci and to spread viruses in a wide range of host species and at long distances (Jones, 2018). HTS-based virome studies of different environmental waters all over the world reported the presence of plant virus nucleic acids in various types of samples. With the use of HTS, viruses in wastewater, irrigation water, and potable water can be monitored in extended areas over a regular period of time, which can provide a useful info for predicting or following disease outbreaks (Mehle et al., 2018). A recent virome study focusing on plant viruses in wastewater in Slovenia gave insights into diverse economically important plant viruses that might be circulating in the area. Wastewater treatment plant influents and effluents contained nucleic acids of at least 47 viruses, both previously known and also unknown to be present in the region. Tobamoviruses were highly represented in the samples, and for three of them, all of which can infect tomato [pepper mild mottle virus, tobacco mild green mosaic virus and tomato mosaic virus (ToMV)], the infectivity was confirmed (Bačnik et al., 2020). Alongside other detected plant viruses, nucleic acids of ToBRFV, which is currently one of the major threats in tomato production worldwide, were also detected in this study; however, ToBRFV was still not detected in the plants in the area. Moreover, pollinators, specifically honeybees (*Apis mellifera*), were studied as possible effective ecological "samplers" of plant viruses. HTS was employed in a recent study of honeybee-assisted surveillance in Australia to investigate the presence of plant viruses, and cucumber green mottle mosaic virus was detected on bees in several states of Australia before its subsequent detection in diseased plant material (Roberts et al., 2018).

High-throughput sequencing can also be used to rapidly obtain complete genome sequences of many viral isolates of the same species and thus follow the molecular epidemiology of viruses in real time. As such, HTS was used in a recent comprehensive study of whole genome sequences of ToBRFV from the Netherlands, which revealed the existence of three virus phylogenetic clusters in the country, which are hypothesized

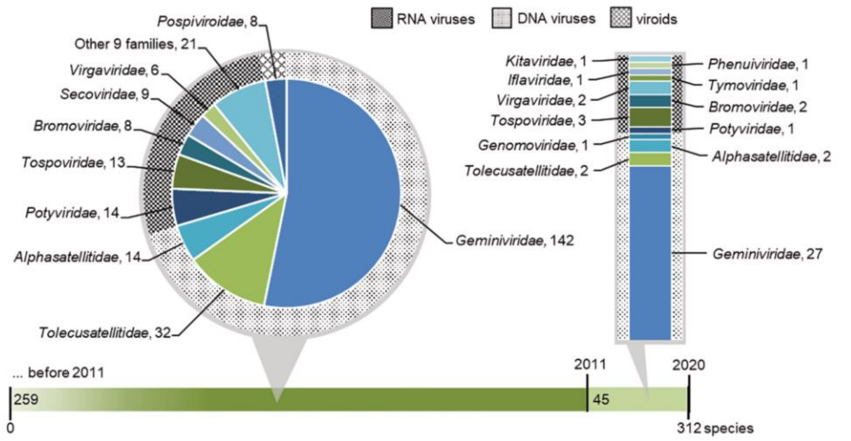

**FIGURE 3 |** Taxonomic distribution of virus and viroid species that were reported to infect or were associated with tomato. The green horizontal bar represents tomato viruses discovered before 2011 and within the 2011–2020 period. Known species reported before 2011 (including all known viruses that were first associated in tomato within the 2011–2020 period) are shown in the dark green portion on the left and extended in pie chart callout, where their distribution across viral families is shown. Species newly discovered in 2011–2020 are shown in the light green portion of the bar and extended in bar chart callout, where their distribution across viral families is shown. In both callouts, families of DNA viruses, RNA viruses, and viroids are designated with differently hatched backgrounds.

to represent three different introduction sources of the virus (van de Vossenberg et al., 2020).

## EMERGING AND ENDEMIC VIRUSES AND VIROIDS CAUSING SIGNIFICANT ECONOMIC DAMAGES IN TOMATO PRODUCTION IN THE PAST DECADE

We collected a list of viruses and viroids with tomato indicated as host (**Supplementary Table 2**). A total of 312 species of tomato viruses (including satellite viruses) and viroids were verified. They are classified across 39 genera and 22 families (**Figure 3**). Among the species in the list, 220 species of tomato viruses (including satellite viruses) have DNA genomes and are classified in three families. Due to the high species count within a genus, the majority of viral species infecting tomato belongs to the *Begomovirus* genus (DNA viruses) and associated satellites. On the other hand, a greater richness of tomato viruses is found for RNA viruses, for which 84 known species are classified in 18 families. Finally, eight viroids, from a single family, are known to infect tomato (**Figure 3**).

Virus can be considered as emerging if it recently has changed or appeared to occupy and spread within a new niche (Rojas and Gilbertson, 2008). In general, emergence is connected to ecological change or intensive agricultural practices (Elena et al., 2014). Complex virus epidemiology, especially insect transmission (by, e.g., whiteflies, aphids, and thrips), and constant evolution of virus populations are key factors associated with emergence and outbreaks of viruses. Emerging pathogens and pests in crop plants are often accompanied by significant yield or economic losses (Savary et al., 2019). In addition, changes in global climate conditions, e.g., increasing temperatures, are predicted to generally exacerbate spread of plant virus diseases in many regions and can cause changes in the severity of the disease symptoms (Canto et al., 2009; Jones, 2016, 2021; Trebicki, 2020). As an example, tomato yellow leaf curl virus (TYLCV) invasion risk analysis under different climate scenarios predicted emergence of the virus and its primary vector, *B. tabaci*, in tomatoes cultivated in open fields worldwide (Ramos et al., 2019). Another study showed that, indeed, heat stress accompanied by the infection of TYLCV resulted in lower stress response efficiency in tomatoes and higher aggregation of TYLCV proteins and DNA (Anfoka et al., 2016). Higher day–night temperature regimes were also shown to favor virion accumulation of tomato spotted wilt orthotospovirus (TSWV) in solanaceous weeds (Llamas-Llamas et al., 1998), and pepper plants that are heterozygous for the *Tsw* resistance gene showed susceptibility at higher temperatures (Moury et al., 1998). Pepper plants with tobamovirus resistance genes were also shown to be susceptible to ToBRFV, when grown in infected soil at 32°C (Luria et al., 2017).

Over the past decades, significant damages to tomato production were caused by viruses described as emerging or re-emerging, such as a few criniviruses, pepino mosaic virus (PepMV), tomato torrado virus (ToTV), tomato leaf curl New Delhi virus (ToLCNDV), and ToBRFV (Hanssen et al., 2010b; Navas-Castillo et al., 2011; Gómez et al., 2012; Moodley et al., 2019, 2020; Oladokun et al., 2019). On the other hand, significant yield losses in tomato could also be associated with widespread, endemic viruses, such as PVY or cucumber mosaic virus (CMV) (Quenouille et al., 2013; Tepfer and García-Arenal, 2019). In the following sections, we review the available information about an array of important emergent or endemic viruses and viroids in tomato, as well as some recently discovered viruses with yet unclear role in tomato health.

## Begomoviruses and Their Satellite Viruses

*Begomovirus* (*Geminiviridae*) is the biggest and one of the most studied genera of plant viruses, comprising 162 known species infecting tomato. Seven viral species belonging to other genera from the family *Geminiviridae* are also known to infect tomato (**Figure 3**). Virions of viruses belonging to *Geminiviridae* are typically twinned ("geminate"). Begomoviruses have monopartite or bipartite genomes (Zerbini et al., 2017). The most important way of the transmission of begomoviruses is by the whiteflies *Bemisia tabaci,* a cryptic species complex, which can infest many crops and is now globally widespread (Stansly et al., 2010; Fiallo-Olivé et al., 2020).

Among the tomato-infecting begomoviruses, ToLCNDV and TYLCV are the most widespread and economically important (Zaidi et al., 2017; Prasad et al., 2020). ToLCNDV is a re-emerging bipartite begomovirus known to infect around 47 different plant species, predominantly crops and weeds from *Solanaceae* and *Cucurbitaceae* (Moriones et al., 2017) families. ToLCNDV, distinct species with two strains (ToLCNDV and ToLCNDV-ES), was first described in India (Padidam et al., 1995) and it is mainly present in Asia where many host plants and various isolates were described (Zaidi et al., 2017). In the Mediterranean basin, the ToLCNDV-ES recombinant strain was identified in tomatoes showing stunting, yellowing, and/or curling in apical leaves (Fortes et al., 2016). ToLCNDV was then reported to spread in Africa and in European countries (e.g., Spain, Italy, Greece, Portugal) (EPPO GD, 2020). Furthermore, the monopartite TYLCV has several widespread strains that are altogether considered as most devastating for tomato production in the tropical and subtropical tomato-growing regions (Mabvakure et al., 2016). Severe yield losses of up to 100% were frequently recorded in tomato yellow leaf curl virus-infected susceptible cultivars showing typical symptoms, such as stunting, upward curling of leaves, chlorosis, and reduction in leaf size (Prasad et al., 2020). For instance, losses due to TYLCV outbreaks in the Dominican Republic were estimated at over 10 million US dollars (Gilbertson et al., 2007), and in China, the virus was reported to be widely spreading and causing unprecedented losses (Pan et al., 2012). Several resistance genes (e.g.*, Ty-1, Ty-2, Ty-3*) identified from wild tomato relatives are used to breed for tolerant varieties against ToLCNDV, TYLCV, and other begomoviruses and multi-gene resistance is currently considered to increase the level of resistance and prevent its breakdown (Zaidi et al., 2017; Prasad et al., 2020).

Circular ssDNA satellite viruses (i.e., alphasatellites, betasatellites, and deltasatellites) are often associated with begomoviruses (Rao and Kalantidis, 2015). They can influence helper virus (i.e., begomovirus) multiplication and disease severity (Gnanasekaran and Chakraborty, 2018). Their replication, cell-to-cell movement and vector transmission are dependent on helper virus, except for independently replicating alphasatellites (Gnanasekaran and Chakraborty, 2018). Several betasatellites were connected with enhancement of symptom severity of TYLCV, e.g., cotton leaf curl Gezira betasatellite, tobacco leaf curl Japan betasatellite, honey-suckle yellow vein mosaic betasatellite (Ito et al., 2009), and tomato leaf curl Philippines betasatellite (Sharma et al., 2011). Co-inoculation experiments of several betasatellites with ToLCNDV resulted in enhancement of symptom severity (Jyothsna et al., 2013), while, in one experiment, co-inoculation of an alphasatellite, betasetellite, and TYLCV resulted in reduction of the accumulation of betasatellite and symptoms induced by TYLCV (Idris et al., 2011) in *N. benthamiana*.

In the last 10 years, several novel begomovirus species were described in different parts of the world (**Table 1** and **Figure 1**). From the Afrotropic ecoregion, tomato leaf curl Kunene virus (Lett et al., 2020), tomato leaf curl Mahé virus (Scussel et al., 2018), and tomato leaf curl Burkina Faso virus (Ouattara et al., 2017) were recently discovered. Numerous begomoviruses were discovered in Neotropic countries, which include four novel species: tomato leaf deformation virus (ToLDeV; Márquez-Martín et al., 2011), tomato apical leaf curl virus (Vaghi Medina et al., 2018), tomato twisted leaf virus (Romay et al., 2019), and pepper leafroll virus (PepLRV; Melgarejo et al., 2013; Martínez-Ayala et al., 2014). Initial surveys suggest that ToLDeV and PepLRV are the predominant pathogens causing the tomato leaf curl disease complex in the Ecuadorian and Peruvian regions (Melgarejo et al., 2013). In Brazil, tomato severe rugose fruit virus (ToSRV) and tomato mottle leaf curl virus (ToMoLCV) were found to be prevalent in tomato crops (Souza et al., 2020).

Reports were made on the potential of wild plants to act as hosts for important tomato-infecting begomoviruses (Prajapat et al., 2014). In Cyprus, a large-scale survey of more than a hundred weed species in major tomato-growing areas revealed the presence of TYLCV in 49 species (in 15 families), suggesting inclusion of these possible reservoir hosts in control measures (Papayiannis et al., 2011). A recent study focused on ToLCNDV found the virus in 5 out of 24 investigated wild plant species in Spain. In that study, HTS was used to characterize the genomes of 80 isolates from different plant species and analyze within-plant virus population diversities for some of them, hinting at some differences between the isolates from wild and cultivated (cucurbit) plants. Tomato chlorotic mottle virus (TCMV) was also found in several weed species in Brazil (Ambrozevicius et al., 2002). In Spain, *S. nigrum* was shown to harbor four known begomoviruses associated with tomato yellow leaf curl disease. Through infectivity assays, tomato severe rugose virus was shown to be infective and harbored in common weeds, such as *Nicandra physaloides*, *Datura stramonium*, and *Sida* sp., which are found surrounding the tomato-growing areas in Brazil (Barreto et al., 2013; Gorayeb et al., 2020).

## Tobamoviruses

Tobamoviruses (*Virgaviridae*) are among the most environmentally stable viruses that remain viable for a long time outside of their host plant in various environmental media (e.g., water, soil) (Fillhart et al., 1998; Mehle and Ravnikar, 2012).

A positive-sense single-stranded RNA [(+)ssRNA] genome of tobamoviruses is around 6.5 kb long and coated in rigid rod virion (Adams et al., 2009b). They are efficiently transmitted mechanically (e.g., by wounding and contact) and can be spread also passively through water and soil, and vertically through seeds (Dombrovsky and Smith, 2017; Mehle et al., 2018). Six tobamoviruses are known to infect tomato, and two of them are known to be globally widespread for many years, namely, tobacco mosaic virus (TMV) and ToMV. Since the discovery and deployment of three resistance genes, *Tm-1*, *Tm-2,* and *Tm-2*$^2$, the economic damages caused by these two viruses reduced dramatically (Pfitzner, 2006).

The most recent virus outbreaks with significant losses in tomato production worldwide were connected to the emergence of two new tobamovirus species, ToMMV (Li et al., 2013, 2017; Sui et al., 2016) and ToBRFV (Salem et al., 2016; Luria et al., 2017). Many research efforts are directed in studies of these viruses, particularly ToBRFV, and significant efforts are directed to limit their spread with appropriate quarantine and phytosanitary measurements (EPPO, 2020a,b).

ToBRFV was first detected in field-cultivated tomatoes showing typical mosaic symptoms as well as narrowing of leaves (Luria et al., 2017) and strong brown rugose spots on fruits (Salem et al., 2016). ToBRFV was found in tomatoes in Jordan in 2015 (Salem et al., 2016) and in 2014 in tomatoes from Israel, where ToBRFV was also shown to break the *Tm-2*$^2$ resistance in some tomato cultivars (Luria et al., 2017). ToBRFV likely emerged as a recombinant between TMV and ToMMV (Salem et al., 2016). It can infect up to 100% of plants at a location and amounts to around 70% tomato yield losses due to symptoms expressed in the fruits (EPPO, 2020a). After its first detection in Israel and in Jordan, it has rapidly spread into many other countries (**Figure 1**). It was recently reported in the United States (Ling et al., 2019), Mexico (Camacho-Beltrán et al., 2019), China (Yan et al., 2019), Palestine (Alkowni et al., 2019), Turkey (Fidan et al., 2019), Germany (Menzel et al., 2019), Netherlands (van de Vossenberg et al., 2020), France (Verdin et al., 2020), Greece (Beris et al., 2020), Italy (Panno et al., 2019), the United Kingdom (Skelton et al., 2019), Egypt (Amer and Mahmoud, 2020), and Spain (Alfaro-Fernández et al., 2021). ToBRFV can be easily transmitted through mechanical contact or can be transmitted by bumblebees (Levitzky et al., 2019), similar to what was reported for TMV (Okada et al., 2000). ToBRFV can overcome known resistance genes against tobamoviruses and there are currently no commercially available ToBRFV-resistant tomato varieties; thus, it remains an imminent threat to tomato production worldwide (EPPO, 2020a). Currently, the only possible control measures are the ones directed at eradication and containment of the infections, such as restriction of access to the production site, disposal of infested plant material, and sanitation measures (EPPO, 2020a). Moreover, a recent research reported that co-infection of ToBRFV with mild strain PepMV resulted in enhanced PepMV accumulation and symptoms characteristic for an aggressive PepMV strain (Klap et al., 2020), bringing additional concerns about the impact of ToBRFV on tomato production.

ToMMV was first isolated from infected greenhouse-grown tomatoes showing mosaic and leaf distortion in Mexico in 2013 (Li et al., 2013). Later on, ToMMV was reported to occur across three ecoregions, specifically in the United States (Padmanabhan et al., 2015a), Israel (Turina et al., 2016a), Spain (Ambrós et al., 2017), China (Che et al., 2018), Brazil (Nagai et al., 2019), Iran, and Czech Republic (EPPO GD, 2020). Interception of ToMMV introduction in Australia through infected pepper seeds was made in biosecurity checks (Lovelock et al., 2020), highlighting the importance of preventive measures in preventing virus spread. ToMMV was shown to successfully infect a small portion of ToMV-resistant plants (Sui et al., 2016) but did not successfully infect some cultivars with *Tm-2*$^2$ gene, (Nagai et al., 2019). Further assessment is needed to ascertain yield loss and economic impact of ToMMV.

Through mechanical inoculation, ToBFRV was shown to be able to infect various hosts, aside from crops from genus *Solanum*, also *Chenopodium* spp., *Petunia hybrida*, and wild relative of tomato, *S. nigrum* (Luria et al., 2017; Alkowni et al., 2019; Yan et al., 2019). ToMMV was experimentally shown to infect various species from family Solanaceae (Ambrós et al., 2017), causing systemic necrosis and death in *Datura stramonium* (Sui et al., 2016). No further studies were conducted yet on the possibility of these alternative hosts to act as natural reservoir of these viruses.

## Orthotospoviruses

The genus *Orthotospovirus* (*Tospoviridae*) is currently composed of 26 species and is the only plant-infecting genus in the order *Bunyavirales* (Oliver and Whitfield, 2016; ICTV, 2020). Orthotospoviruses have a single-stranded negative-sense RNA [(−)ssRNA] genome, divided into three segments, and are capable of replication both in the plant host and in thrips (Riley et al., 2011). Economically, the most important orthotospovirus infecting tomato is the re-emerging TSWV. In the case of TSWV outbreaks, up to 95% losses in total market value can be recorded due to tomato fruits showing typical necrotic spots and concentric rings (Sherwood et al., 2003; Sevik and Arli-Sokmen, 2012).

TSWV has one of the widest host ranges of all plant viruses with more than 1000 known host species from 85 families (Parrella et al., 2003). In large-scale surveys of weeds in United States, several were proven to harbor TSWV, and, among them, *Sonchus asper*, *Taraxacum officinale*, *Ranunculus sardous*, *Aster* sp., *Senecio vulgaris*, and *S. nigrum* were shown to have the highest potential to be an inoculum source of TSWV (Chatzivassiliou et al., 2001; Groves et al., 2002). Four weed species surrounding tomato-growing areas in Kenya were also shown to be hosts of TSWV (Macharia et al., 2016). TSWV was found in all known ecozones of the world, affecting numerous crops (Butković et al., 2021). Orthotospoviruses are transmitted in a persistent propagative and circulative manner by thrips, the most important of which is western flower thrips (*Frankliniella occidentalis*). This insect vector remains a global problem due to inefficient insecticidal control (Riley et al., 2011), thus contributing to continuous emergence of orthotospoviruses worldwide (Oliver and Whitfield, 2016).

Several resistance genes have been identified and employed to confer resistance against TSWV in tomato, *Sw-5b* offering the most durable and broad resistance to different orthotospovirus species (Turina et al., 2016b).

Tomato spotted wilt orthotospovirus resistance-breaking (RB) strains were first discovered in the early 2000s, and since then, they are occurring sporadically in many regions causing significant damages. These strains overcome TSWV resistance regulated by hypersensitivity genes: *Tsw* (in pepper) and *Sw-5* (in tomato). This further worsened the economic losses caused by TSWV in tomato and pepper, which were previously estimated at more than 1 billion US dollars annually (Prins and Goldbach, 1998). Currently, there is no new resistance gene discovered against TSWV (Turina et al., 2016b).

Among other orthotospoviruses, important viruses reported in tomato in the past decade are tomato chlorotic spot virus (TCSV), groundnut ringspot virus (GRSV), capsicum chlorosis virus (CaCV), and tomato yellow ring virus (TYRV) (**Table 1** and **Figure 1**). TCSV was reported to be actively spreading in the Nearctic countries such as United States (Sui et al., 2017; Poudel et al., 2019), Puerto Rico (Webster et al., 2013) and GRSV was reported in tomatoes and other vegetables in the United States (Webster et al., 2010, 2014). CaCV is expanding its distribution in Indo-Malay and Australasian ecoregions as it was detected in Taiwan (Huang et al., 2010), China (Yin et al., 2015), and Australia (Sharman et al., 2020). TYRV was reported in Kenya (Birithia et al., 2012) and Poland (Zarzyñska-Nowak et al., 2016). Other novel orthotospoviruses recently identified are tomato necrotic ring virus (TNRV) from Thailand (Hassani-Mehraban et al., 2011), pepper necrotic spot virus (PNSV) from Peru (Torres et al., 2012), and tomato necrotic spot virus (TNSV; as a word of caution, an ilarvirus was named identically, but has another acronym: ToNSV) from China (Yin et al., 2014). These viruses were not yet associated with significant or large-scale outbreaks.

## Potyviruses

*Potyvirus* (*Potyviridae*) is one of the largest genera of plant-infecting viruses, with 183 recognized species (ICTV, 2020), 15 of which are known to infect tomato (**Figure 3**). Potyviruses are characterized by a (+)ssRNA genome (∼9.7 kb), which is coated in a flexible filamentous virion. PVY is an economically important potyvirus infecting solanaceous crops. It is efficiently transmitted by *Myzus persicae* and other aphid species (Revers and García, 2015; Gadhave et al., 2020). PVY is widespread in several tomato-growing regions worldwide, based on recent large-scale studies (Soler et al., 2010; Al-Kuwaiti et al., 2016; Xu et al., 2017; Nikolić et al., 2018; Ignatov et al., 2020; Ma et al., 2020). Recently, PVY strain C was detected in tomatoes showing leaf necrosis in Kenya (Chikh-Ali et al., 2015). Symptoms of PVY infection in tomato ranges from faint mottling to necrosis but varies depending on plant age, environmental conditions, PVY strain, and co-infecting viruses (Sastry et al., 2019). Aside from tomato, PVY was shown to infect weed species from *Asteraceae, Chenopodiaceae, Geraniaceae,* and *Lamiaceae* families (Kaliciak and Syller, 2009).

In recent years, three other potyviruses infecting tomato were reported, namely, chili veinal mottle virus (ChiVMV), pepper mottle virus (PepMoV), and pepper veinal mottle virus (PVMV). PepMoV infection in tomatoes in Hawaii resulted in unmarketable fruits with mottling symptoms (Melzer et al., 2012) and, recently, the virus was detected in India (Sharma et al., 2019). ChiVMV was detected in several provinces in southwest China, with recorded incidence of up to 90% in some areas (Zhao et al., 2014; Zhu et al., 2017). PVMV was reported to cause considerable epidemics in tomato-growing areas in Mali in 2010 and is now under consideration in tomato disease resistance breeding programs (Tsai et al., 2010). HMV was recently reported to naturally infect field tomatoes in Slovenia (Pecman et al., 2018).

## Cucumoviruses and Other Members of Family *Bromoviridae*

Cucumber mosaic virus (genus *Cucumovirus*, family *Bromoviridae*) is an important tomato-infecting virus. Cucumoviruses have a spherical virion encapsidating a tripartite (+)ssRNA genome. Some CMV strains encapsidate subviral RNAs termed satellite RNAs (satRNAs) (Masuta, 2014). In nature, CMV and other cucumoviruses are non-persistently transmitted by aphid species, the most important of which are *Myzus persicae* and *Aphis gossypii.* They were also shown to be transmitted through seeds of some species, but not tomato (Palukaitis and García-Arenal, 2003). CMV has a very broad host range, able to infect more than 1200 plant species across 100 botanical families (Mochizuki and Ohki, 2012). Several weed species surrounding tomato production areas were shown to harbor CMV and could serve as reservoir or alternative host of the virus. Such weeds include, e.g., *Convolvulus arvensis*, *Malva sylvestris*, and *Sonchus tenerrimus*, reported from Spain (Lavina et al., 1996), and other nine diverse weeds from Pakistan (Akhtar et al., 2019). Due to its very broad host range, transmissibility through seeds of some species, and ubiquitous presence of its aphid vectors (Jacquemond, 2012), CMV became a globally distributed species that still causes significant damages in many crops, especially in tomato.

Outbreaks of CMV infection in tomato-growing areas were reported, and some of these were associated with satellite RNAs (satRNAs) that induce systemic necrotic symptoms, referred to as lethal necrosis (Garcìa-Arenal and Palukaitis, 1999; Xu et al., 2003). This disease was reported in Italy between 1988 and 1993 (Cillo et al., 1994; Grieco et al., 1997) and in Croatia in 1993 (Škoric et al., 1996). Recently, CMV-satRNA infection was reported in legume crops in Greece (Chatzivassiliou et al., 2016), and was shown to cause lethal necrosis in tomato through mechanical inoculation (Giakountis et al., 2018). Also, during a 4-year survey in Serbia (2012–2015), CMV satRNAs were identified from collected tomato samples showing systemic necrosis accompanied by fruit malformation (Stanković et al., 2021). Cultivated crops are important reservoir of CMV satRNAs (Gallitelli, 2000), and thus, strategic intercropping should be taken into consideration to prevent devastating CMV lethal necrosis outbreaks in tomato.

Tomato aspermy virus (TAV) is another cucumovirus that naturally infects tomato. TAV was recently reported in tomato samples from China; however, its economic impact was not recorded (Xu et al., 2017). TAV was reported as a major pathogen of ornamentals such as chrysanthemums that are grown in subtropical Asia (Verma et al., 2009; Maddahian et al., 2017).

Tomato necrotic spot virus (ToNSV) and the novel species named tomato necrotic streak virus (TomNSV) are tomato-infecting ilarviruses within *Bromoviridae* family. Detections of these viruses were reported in the United States (Batuman et al., 2009; Adkins et al., 2015; Badillo-Vargas et al., 2016; Bratsch et al., 2018, 2019). Both viruses caused necrotic symptoms in leaves, stem or fruits of tomatoes. In France, a novel ilarvirus, named SnIV1, was discovered in both tomato and its wild relative, *S. nigrum* (Ma et al., 2020). However, the transmission routes, possible reservoir or alternative hosts, and economic impact are yet to be determined for ToNSV, TomNSV, and SnIV1 (Badillo-Vargas et al., 2016; Bratsch et al., 2019; Ma et al., 2020). Moreover, a re-emerging ilarvirus named parietaria mottle virus (PMoV) was suggested to be a threat to tomatoes, which showed rings and bright necrotic mosaic on young leaves upon infection. It was reported in Europe, particularly in the Mediterranean countries such as Italy, France, Greece, and Spain (Aparicio et al., 2018). Outbreaks of PMoV were recently reported in Sardinia, Italy (Parrella et al., 2020) and research on possible sources of resistance against the virus already started (Parrella, 2020). Lastly, two other members of *Bromoviridae* known to infect tomato and a variety of other crops are alfalfa mosaic virus (*Alfamovirus*), causing necrotic yellows disease on tomato (Finetti Sialer et al., 1997; Nikolić et al., 2018) and pelargonium zonate spot virus causing mild mosaic, leaf malformation, and severe stunting of the plants (Finetti-Sialer and Gallitelli, 2003; Lapidot et al., 2010).

## Potexvirus: Pepino Mosaic Virus (PepMV)

PepMV belongs to genus *Potexvirus* (*Alphaflexiviridae*) and has an unsegmented (+)ssRNA genome coated in a flexuous rod virion. PepMV was first described in Peru, and since its first detection in tomato in Netherlands in 1999, it quickly spread in Europe (van der Vlugt et al., 2000; Hanssen and Thomma, 2010). It is efficiently transmitted mechanically (e.g., contaminated tools and whitefly feeding) (Hanssen and Thomma, 2010; Noël et al., 2014) with occasional transmission through seeds (Hanssen et al., 2010c), as well as through water (Mehle et al., 2014). PepMV was originally discovered to infect pepino (*Solanum muricatum*) (Jones et al., 1980), and it quickly became endemic in tomato since its first discovery in this plant in 1999 (van der Vlugt et al., 2000; van der Vlugt and Stijger, 2021). In tomato, fruit marbling symptoms are considered as the most important cause of significant economic losses around the world (Hanssen and Thomma, 2010; Hanssen et al., 2010b). PepMV is present in major tomato-growing areas of the Mediterranean (Gómez et al., 2012) and was recently reported in United States and Mexico (Ling and Zhang, 2011), South Africa (Carmichael et al., 2011), Spain and Morocco (Gómez-Aix et al., 2019), and Serbia (Stanković et al., 2020).

To date, there are five strains identified for PepMV, namely, (1) the Peruvian (LP) strain, originally found infecting pepino (*S. muricatum*) and wild *Solanum* spp.; (2) the European EU-tomato (EU) strain; (3) the American US1 strain; (4) the Chilean-2 (CH2) strain; and (5) the PES strain, described in wild tomato populations in Peru (Moreno-Perez et al., 2014). PepMV was reported to infect a wide range of crops and weed species (Gómez et al., 2012); its infectivity and symptom expression are also dependent on the virus strain and host species or cultivar (Kazinczi et al., 2005; Hanssen et al., 2009; Blystad et al., 2015).

Due to the extensive damages caused by PepMV infections, and since there are currently no commercially available PepMV-resistant tomato varieties available, efforts have been made to produce efficient cross-protection strategies against the virus, particularly for the strains circulating in Europe (Pechinger et al., 2019). Other than host resistance, cross-protection is one of the most effective methods of virus disease management, which entails "pre-immunization" of susceptible genotypes by inoculation of mild strain of a particular virus (Ziebell and Carr, 2010). Successful applications of PepMV mild strain cross-protection were reported in the laboratory or greenhouse in the past years (Hanssen et al., 2010a; Schenk et al., 2010; Vermunt and Kaarsemaker, 2017). Recently, successful protection of field tomatoes against PepMV were reported using two mild strains of the virus (Agüero et al., 2018).

## Criniviruses

Criniviruses from genus *Crinivirus* (*Closteroviridae*) are whitefly transmitted viruses with bipartite genome composed of two (+)ssRNA genome segments that are separately coated in filamentous virions (Kiss et al., 2013). Their infection in plants can be mistaken for nutritional disorders and phytotoxicity because of the obvious interveinal leaf yellowing and leaf brittleness, resulting in reduced overall yield (Tzanetakis et al., 2013). Two widespread tomato-infecting criniviruses are tomato infectious chlorosis virus (TICV) and tomato chlorosis virus (ToCV). TICV was first described in 1996 in the United States (Duffus et al., 1996), and recently reported to cause yield losses in Mexico (Méndez-Lozano et al., 2012), Greece (Orfanidou et al., 2014), and Serbia (Vučurović et al., 2019). ToCV was first described in 1998 (Wisler et al., 1998) and is now present globally causing yield losses due to fruit size reduction (Fiallo-Olivé and Navas-Castillo, 2019). ToCV was shown to infect 25 species of crops and weeds (Fariña et al., 2019), while TICV was shown to be infective in 22 species of weeds that may serve as reservoir of the virus (Alfaro-Fernández et al., 2008). Lastly, another crinivirus that was first reported to infect tomato in China is lettuce chlorosis virus; however, its economic impact has not yet been assessed (Zhang et al., 2017).

## Rhabdoviruses

Rhabdoviruses (*Rhabdoviridae*) can propagate inside either a leafhopper, an aphid, or mite vector or a plant. Rhabdoviruses are composed of large bacilliform virions encapsulating an (−)ssRNA genome of around 13–15 kbp. There are currently three known species of rhabdoviruses that infect or are associated with tomato: the newly discovered TYMaV in genus *Cytorhabdovirus* (Xu et al., 2017) and, in genus *Alphanucleorhabdovirus*, the eggplant mottled dwarf virus (Mavrič et al., 2006) and the recently discovered PhCMoV. PhCMoV was first detected in *Physostegia* sp. sampled in 2014 in Austria (Menzel et al., 2018) and was recently detected in Germany from two tomato samples 12 years apart (2003 and 2015) that showed typical fruit marbling and discoloration symptoms (Gaafar et al., 2018). Within this period, PhCMoV was also detected in tomato samples showing leaf and fruit mottling and uneven ripening of fruits collected in 2012 at three locations in Serbia (Vučurović et al., 2021), indicating extended presence of the virus in the country. Findings of PhCMoV in three different countries in two different plant species in recent years could indicate the emerging status, and the presence of this virus needs to be assessed in the future, to determine its potential impact on tomato production.

## *Secoviridae*: Nepoviruses and Torradoviruses

Family *Secoviridae* contains insect or nematode transmitted viruses, nine of which are known to infect tomato. These viruses have mono- or bipartite 9- to 13.7-kbp-long (+)ssRNA genomes encapsidated in an icosahedral virion (Thompson et al., 2017). Several viruses of this group were reported in recent years, namely, tomato black ring virus (TBRV) from genus *Nepovirus* and ToTV and tomato marchitez virus (ToMarV), both from genus *Torradovirus.* TBRV was recently reported infecting tomatoes in Poland showing chlorotic and/or necrotic ringspots and was found to be associated with eight satellite RNAs, but no assessment about economic losses were made (Rymelska et al., 2013; Zarzyñska-Nowak et al., 2020). Moreover, ToTV is reported to spread globally since its discovery in 2007 in tomatoes from Spain showing systemic necrosis or burnt-like symptoms (Verbeek et al., 2007). ToTV was recently reported to be present in South Africa (Moodley et al., 2016, 2020) and Colombia (Verbeek and Dullemans, 2012), which are first reports of the virus in the Afrotropic and Neotropic ecoregions. ToTV was also reported in tomato-growing areas in the Mediterranean basin (e.g., Spain and Italy), in Poland, Hungary, and Australia (Hanssen et al., 2010a; Hanssen and Lapidot, 2012) and recently in Serbia (Vučurović et al., 2021). On the contrary, since the discovery of ToMarV in tomatoes from Mexico showing severe leaf necrosis and necrotic rings on fruits in 2007 (Verbeek et al., 2008), natural infection of ToMarV was only reported in pepper in Mexico (Camacho-Beltrán et al., 2015).

## Other Known Viruses Associated With Tomato

Several other tomato viruses were recently reported worldwide. Necrotic foliar symptoms in greenhouse grown tomatoes in Poland were associated with an alphanecrovirus (*Tombusviridae*) named olive latent virus 1 (OLV1); however, its economic impact has not been assessed (Borodynko et al., 2010). Aside from its original host, olive, OLV1 was also reported to infect citrus and tulip (Varanda et al., 2014).

In 2015, TMaV, classified in the family *Iflaviridae*, which is currently known to contain members that infect arthropod hosts (Valles et al., 2017), was reported to be associated with tomato (Saqib et al., 2015). The virus was discovered in a single asymptomatic tomato sample in which no presence of a probable arthropod pest was observed under the microscope and in BLAST search of the assembled contigs from small RNA sequencing. Among the artificially inoculated plants, TMaV was detected in non-inoculated leaves, reported to cause symptomless infection in *S. lycopersicum* and *S. melongena*, but showed mild symptomatic infection in *Capsicum annum* (Saqib et al., 2015). Further research is needed to ascertain the role of TMaV in tomato and also to investigate its possible replication in arthropod hosts.

In Brazil, tomato blistering mosaic virus (ToBMV) (*Tymoviridae*) was discovered in field tomatoes that exhibited severe leaf mosaic and blistering symptoms (De Oliveira et al., 2013). Later, analyses confirmed the presence of ToBMV in the tobacco sample from 1986 (Melo et al., 2014). ToBMV was also reported in tomatoes from Argentina (Ferrand et al., 2016) and in a weed relative of tomato, *Solanum violaefolium* (Blawid et al., 2016). These studies may imply possible emergent status of ToBMV in the Neotropics and further investigations are therefore needed.

Southern tomato virus (STV) (family *Amalgaviridae*, genus *Amalgavirus*), a double-stranded (ds) RNA virus, was first detected in tomato plants in United States and Mexico exhibiting stunting of the growing tips, fruit discoloration, and reduced fruit size (Sabanadzovic et al., 2009). Since then, it was also reported in several European countries (Iacono et al., 2015; Verbeek et al., 2015; Pecman et al., 2018; Gaafar et al., 2019; HortDaily, 2019; WUR, 2019), Bangladesh (Padmanabhan et al., 2015c), China (Padmanabhan et al., 2015b), and South Korea (Oh et al., 2018), and so far only in tomato plants. STV co-infections with other viruses are frequent, as well as detections of STV in asymptomatic tomatoes (Alcalá-Briseño et al., 2017). STV virions were not yet observed (Tzanetakis et al., 2020), and the epidemiology of STV remains unclear, as it is only known to be vertically transmitted through seeds at high rates (70–90%) (Sabanadzovic et al., 2009). A recent study showed that STV infection alone did not induce symptoms and cellular ultrastructure changes; however, it modified expression of certain microRNAs (Elvira-González et al., 2020).

## Pospiviroids

Viroids are naked, non-coding, circular (+)ssRNA molecules, around 246–401 bp long, and are the smallest entities known to infect any living organisms. They are known to infect only plants (Kovalskaya and Hammond, 2014). They can induce disease symptoms, resulting in significant economic damages in different crops and ornamentals (Navarro et al., 2012). Viroid infection in tomatoes results in growth reduction or stunting accompanied by leaf distortion or epinasty, although symptoms vary greatly among viroid strains and tomato cultivars (Mackie et al., 2019). Aside from tomato and other crops and ornamentals (van Brunschot et al., 2014a), pospiviroids were also found to be harbored in several weed species, which were reported as their natural reservoir (Van Bogaert et al., 2015; Mackie et al., 2016). Majority of viroids are transmitted mechanically through infected tools and seldom through seeds or pollen; however, the most efficient transmission of viroids is through vegetative propagation of infected material (Flores et al., 2005). Viroids were reported to cause significant losses in tomato production in a few countries over the last decade. Out of the nine recognized pospiviroids (*Pospiviroidae*), eight are known to infect tomato. Among these viroids, potato spindle tuber viroid (PSTVd) and tomato chlorotic dwarf viroid (TCDVd) are the most prevalent and economically important (Verhoeven et al., 2010; van Brunschot et al., 2014b). Several introductions of viroids were reported recently, such as in Italy and Norway, where phytosanitary authorities were able to eradicate PSTVd and TCDVd upon the detection in established tomato crops (Navarro et al., 2009; Fox et al., 2013). In order to prevent introduction of viroids, all imported lots of tomato and pepper seeds are tested in Australia (Constable et al., 2019). Since testing of seeds is needed to prevent the introduction of pospiviroids into new areas, many efforts have already been done to optimize diagnostic protocols that enable their detection at low concentration, which is expected in case of seed infestation (Mehle et al., 2017).

## CONCLUSION AND FUTURE PROSPECTS

New discoveries and studies on emergence of tomato viruses in the recent decade contributed to our understanding of the tomato virome, its diversity, virus ecology, and epidemiology. Tomato is likely associated with the highest number of viruses and viroids known for any plant species to date, currently amounting to at least 312 known species. Because of the absence of resistant varieties for some viruses, global spread of insect vectors, emergence of RB viral strains, increased global movement of plant materials, such as seeds, and high stability and environmental persistence of some viruses, viral diseases in tomato cause massive yield and economic losses. Begomoviruses and associated satellite viruses represent the most numerous group of tomato viruses. ToLCNDV and TYLCV are two of the most important begomoviruses, with ToLCNDV currently prevailing as an emergent and damaging species worldwide (Zaidi et al., 2017; Prasad et al., 2020). On the other hand, a diverse array of RNA viruses cause high economic losses in tomato globally. The most striking example is the recent emergence of ToBRFV that quickly caused outbreaks in several regions all around the world, within just few years after its discovery. According to our review, 45 novel virus species have been discovered in tomato in the past decade and several known viruses have been associated with tomato for the first time. The discovery and first detections of viruses in tomato are increasing in recent years also because of the prevalent use of HTS as a generic virus detection technique. This faster discovery rate is often not paralleled with virus characterization studies, biological or ecological, for newly discovered tomato viruses. In-depth characterization studies are mostly performed for viruses with high phytosanitary and economic importance. At the agroecological scale, the first extensive HTS-based tomato virome studies were conducted in China (Xu et al., 2017) and France (Ma et al., 2020), the latter also addressing the link between the virome of tomato and wild plants. In addition, by the use of HTS, viable tomato-infecting tobamoviruses were detected in the environment outside their hosts, specifically in untreated and treated wastewater (Bačnik et al., 2020).

The increasing knowledge on the virome of tomato, the environment, and the surrounding wild plants contributes to better understanding of virus disease emergence and epidemiology of viruses associated with tomato. Moreover, an increase in viral sequence information in databases can enable more rapid development of targeted diagnostic tests. A tailored approach in studies of plant virus diseases is needed because each crop species or family has its distinctive virome (McLeish et al., 2020b). At the agroecological scale, a holistic view of the virome would include viruses in crops, wild plants, vectors, or in the surrounding environment. This is important to consider for tomato that is associated with a very high number of virus species, which are transmitted by numerous vectors and harbored in wild plants and some remain stable in the environment. HTS-based viromics approach enables collection of ecosystem-level genomic data in extended spatiotemporal scales (McLeish et al., 2020a,b). Furthermore, the use of long-read (or single molecule) portable sequencing platforms, such as Oxford Nanopore Technologies MinIon, is expected to bring HTS even closer to the end-users (e.g., small research and diagnostics laboratories) and contribute to new viral discoveries in plants, including tomato (Bronzato Badial et al., 2018; Boykin et al., 2019; Chalupowicz et al., 2019). Approaches such as virome network analysis can finally be used to, e.g., associate viromes of the crops to that of the insect vectors or wild plants and can consider biogeographical features of the cropping area (Alcalá-Briseño et al., 2020). With such analyses, new insights can be generated that could be useful in possible forecasting and eventual prevention of virus disease emergence and outbreaks in the future (Garrett et al., 2018; McLeish et al., 2020a).

## AUTHOR CONTRIBUTIONS

MPSR and DK conceptualized the review topic. MPSR did the data mining and analysis and wrote the first draft of the manuscript, including the table, figures, and **Supplementary Material**. DK contributed in making and editing the table and figures. DK and AV edited initial drafts of the manuscript. DK, AV, NM, and MR edited the final draft of the manuscript. All authors significantly contributed to the writing and editing of the manuscript.

## FUNDING

This work was supported by the funding from Horizon 2020 Marie Skłodowska-Curie Actions Innovative Training Network (H2020 MSCA-ITN) project “INEXTVIR” (GA 813542) under the management of the European Commission-Research Executive Agency and from the Slovenian Research Agency (ARRS), Republic of Slovenia project (L7-2632), and core financing (P4-0407 and P4-0165).

## SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fmicb.2021.671925/full#supplementary-material

**Supplementary Table 1 |** Meta-analysis of the extent of characterization of novel viruses discovered in tomato from 2011 to 2020.

**Supplementary Table 2 |** Summary list of all viruses with tomato indicated as host based on review of literature and different databases.

## REFERENCES

Adams, I. P., Glover, R. H., Monger, W. A., Mumford, R., Jackeviciene, E., Navalenskiene, M., et al. (2009a). Next-generation sequencing and metagenomic analysis: a universal diagnostic tool in plant virology. *Mol. Plant Pathol.* 10, 537–545. doi: 10.1111/j.1364-3703.2009.00545.x

Adams, M. J., Antoniw, J. F., and Kreuze, J. (2009b). Virgaviridae: a new family of rod-shaped plant viruses. *Arch. Virol.* 154, 1967–1972. doi: 10.1007/s00705-009-0506-6

Adkins, S., Baker, C. A., Badillo-Vargas, I. E., Frantz, G., Mellinger, H. C., Roe, N., et al. (2015). Necrotic streak disease of tomato in florida caused by a new ilarvirus species related to tulare apple mosaic virus. *New Dis. Rep.* 31:16. doi: 10.5197/j.2044-0588.2015.031.016

Agüero, J., Gómez-Aix, C., Sempere, R. N., García-Villalba, J., García-Núñez, J., Hernando, Y., et al. (2018). Stable and broad spectrum cross-protection against pepino mosaic virus attained by mixed infection. *Front. Plant Sci.* 9:1810. doi: 10.3389/fpls.2018.01810

Akhtar, K. P., Anwer, M., Saleem, M. Y., Yousaf, S., Ullah, N., Cheema, H. M. N., et al. (2019). Identification of natural weed hosts of cucumber mosaic virus subgroup-I and the absence of seed transmission in weed hosts in pakistan. *J. Hortic. Sci. Biotechnol.* 94, 468–474. doi: 10.1080/14620316.2019.1565947

Al Rwahnih, M., Daubert, S., Golino, D., and Rowhani, A. (2009). Deep sequencing analysis of RNAs from a grapevine showing syrah decline symptoms reveals a multiple virus infection that includes a novel virus. *Virology* 387, 395–401. doi: 10.1016/j.virol.2009.02.028

Albuquerque, L. C., Varsani, A., Fernandes, F. R., Pinheiro, B., Martin, D. P., de Tarso Oliveira Ferreira, P., et al. (2012). Further characterization of tomato-infecting begomoviruses in Brazil. *Arch. Virol.* 157, 747–752. doi: 10.1007/s00705-011-1213-7

Alcalá-Briseño, R. I., Casarrubias-Castillo, K., López-Ley, D., Garrett, K. A., and Silva-Rosales, L. (2020). Network analysis of the papaya orchard virome from two agroecological regions of chiapas, mexico. *mSystems* 5, e419–e423. doi: 10.1128/msystems.00423-19

Alcalá-Briseño, R. I., Coşkan, S., Londoño, M. A., and Polston, J. E. (2017). Genome sequence of southern tomato virus in asymptomatic tomato 'Sweet Hearts'. *Genome Announc.* 5, e1316–e1374. doi: 10.1128/genomeA.01374-16

Alexander, H. M., Mauck, K. E., Whitfield, A. E., Garrett, K. A., and Malmstrom, C. M. (2014). Plant-virus interactions and the agro-ecological interface. *Eur. J. Plant Pathol.* 138, 529–547. doi: 10.1007/s10658-013-0317-1

Alfaro-Fernández, A., Castillo, P., Sanahuja, E., Rodríguez-Salido, M. C., and Font, M. I. (2021). First report of tomato brown rugose fruit virus in tomato in spain. *Plant Dis.* 105, 515–515. doi: 10.1094/PDIS-06-20-1251-PDN

Alfaro-Fernández, A., Córdoba-Sellés, C., Cebrián, M. C., Herrera-Vásquez, J. A., Sánchez-Navarro, J. A., Juárez, M., et al. (2008). First report of tomato torrado virus on weed hosts in Spain. *Plant Dis.* 92, 831. doi: 10.1094/PDIS-92-5-0831B

Alkowni, R., Alabdallah, O., and Fadda, Z. (2019). Molecular identification of tomato brown rugose fruit virus in tomato in Palestine. *J. Plant Pathol.* 101, 719–723. doi: 10.1007/s42161-019-00240-7

Al-Kuwaiti, N. A., Maruthi, M. N., and Seal, S. E. (2016). Molecular characterization of potyviruses infecting potato and vegetables in Iraq. *J. Plant Pathol.* 98, 603–606.

Ambrós, S., Martínez, F., Ivars, P., Hernández, C., de la Iglesia, F., and Elena, S. F. (2017). Molecular and biological characterization of an isolate of Tomato mottle mosaic virus (ToMMV) infecting tomato and other experimental hosts in eastern Spain. *Eur. J. Plant Pathol.* 149, 261–268. doi: 10.1007/s10658-017-1180-2

Ambrozevicius, L. P., Calegario, R. F., Fontes, E. P. B., De Carvalho, M. G., and Zerbini, F. M. (2002). Genetic diversity of begomovirus infecting tomato and associated weeds in southeastern Brazil. *Fitopatol. Bras.* 27, 372–377. doi: 10.1590/s0100-41582002000400006

Amer, M. A., and Mahmoud, S. Y. (2020). First report of tomato brown rugose fruit virus on tomato in Egypt. *New Dis. Rep.* 41:24. doi: 10.5197/j.2044-0588.2020.041.024

Anderson, P. K., Cunningham, A. A., Patel, N. G., Morales, F. J., Epstein, P. R., and Daszak, P. (2004). Emerging infectious diseases of plants: pathogen pollution, climate change and agrotechnology drivers. *Trends Ecol. Evol.* 19, 535–544. doi: 10.1016/j.tree.2004.07.021

Anfoka, G., Moshe, A., Fridman, L., Amrani, L., Rotem, O., Kolot, M., et al. (2016). Tomato yellow leaf curl virus infection mitigates the heat stress response of plants grown at high temperatures. *Sci. Rep.* 6:19715. doi: 10.1038/srep19715

Aparicio, F., Aramburu, J., Herranz, M. C., Pallás, V., and López, C. (2018). Parietaria mottle virus: a potential threat for tomato crops? *Acta Hortic.* 1207, 261–268. doi: 10.17660/ActaHortic.2018.1207.36

Bačnik, K., Kutnjak, D., Pecman, A., Mehle, N., Tušek Žnidarič, M., Gutiérrez Aguirre, I., et al. (2020). Viromics and infectivity analysis reveal the release of infective plant viruses from wastewater into the environment. *Water Res.* 177:115628. doi: 10.1016/j.watres.2020.115628

Badillo-Vargas, I. E., Baker, C. A., Turechek, W. W., Frantz, G., Mellinger, H. C., Funderburk, J. E., et al. (2016). Genomic and biological characterization of tomato necrotic streak virus, a novel subgroup 2 ilarvirus infecting tomato in Florida. *Plant Dis.* 100, 1046–1053. doi: 10.1094/PDIS-12-15-1437-RE

Barreto, S. S., Hallwass, M., Aquino, O. M., and Inoue-Nagata, A. K. (2013). A study of weeds as potential inoculum sources for a tomato-infecting begomovirus in central Brazil. *Phytopathology* 103, 436–444. doi: 10.1094/PHYTO-07-12-0174-R

Batuman, O., Miyao, G., Kuo, Y. W., Chen, L. F., Davis, R. M., and Gilbertson, R. L. (2009). An outbreak of a necrosis disease of tomato in california in 2008 was caused by a new ilarvirus species related to parietaria mottle virus. *Plant Dis.* 93:546. doi: 10.1094/PDIS-93-5-0546C

Beris, D., Malandraki, I., Kektsidou, O., Theologidis, I., Vassilakos, N., and Varveri, C. (2020). First report of tomato brown rugose fruit virus infecting tomato in Greece. *Plant Dis.* 104:2035. doi: 10.1094/PDIS-01-20-0212-PDN

Bernardo, P., Golden, M., Akram, M., Naimuddin, K., Nadarajan, N., Fernandez, E., et al. (2013). Identification and characterisation of a highly divergent geminivirus: evolutionary and taxonomic implications. *Virus Res.* 177, 35–45. doi: 10.1016/j.virusres.2013.07.006

Birithia, R., Subramanian, S., Villinger, J., Muthomi, J. W., Narla, R. D., and Pappu, H. R. (2012). First report of tomato yellow ring virus (tospovirus, bunyaviridae) infecting tomato in kenya. *Plant Dis.* 96, 1384–1384. doi: 10.1094/PDIS-05-12-0462-PDN

Blawid, R., Hayashi, E. A. I., Rezende, J. A. M., Kitajima, E. W., and Nagata, T. (2016). A highly divergent isolate of tomato blistering mosaic virus from solanum violaefolium. *Virus Genes* 52, 294–298. doi: 10.1007/s11262-016-1288-z

Blystad, D. R., van der Vlugt, R., Alfaro-Fernández, A., del Carmen Córdoba, M., Bese, G., Hristova, D., et al. (2015). Host range and symptomatology of pepino mosaic virus strains occurring in Europe. *Eur. J. Plant Pathol.* 143, 43–56. doi: 10.1007/s10658-015-0664-1

Borodynko, H., Hasiów-Jaroszewska, B., and Pospieszny, H. (2010). Identification and characterization of an olive latent virus 1 isolate from a new host: solanum lycopersicum. *J. Plant Pathol.* 92, 789–792. doi: 10.4454/jpp.v92i3.328

Boykin, L. M., Sseruwagi, P., Alicai, T., Ateka, E., Mohammed, I. U., Stanton, J. A. L., et al. (2019). Tree lab: portable genomics for early detection of plant viruses and pests in sub-saharan africa. *Genes (Basel).* 10:632. doi: 10.3390/genes10090632

Bratsch, S. A., Creswell, T. C., and Ruhl, G. E. (2018). First report of tomato necrotic spot virus infecting tomato in indiana. *Plant Heal. Prog.* 19, 224–225. doi: 10.1094/PHP-05-18-0019-BR

Bratsch, S. A., Grinstead, S., Creswell, T. C., Ruhl, G. E., and Mollov, D. (2019). Characterization of tomato necrotic spot virus, a subgroup 1 ilarvirus causing necrotic foliar, stem, and fruit symptoms in tomatoes in the united states. *Plant Dis.* 103, 1391–1396. doi: 10.1094/PDIS-11-18-2112-RE

Bratsch, S. A., Grinstead, S., Lockhart, B., and Mollov, D. (2020). Biological properties and genomic sequence of an isolate of cherry rasp leaf virus from tomato. *J. Plant Pathol.* 102, 843–848. doi: 10.1007/s42161-020-00522-5

Bronzato Badial, A., Sherman, D., Stone, A., Gopakumar, A., Wilson, V., Schneider, W., et al. (2018). Nanopore sequencing as a surveillance tool for plant pathogens in plant and insect tissues. *Plant Dis.* 102, 1648–1652. doi: 10.1094/PDIS-04-17-0488-RE

Butković, A., González, R., and Elena, S. F. (2021). Revisiting orthotospovirus phylogeny using full-genome data and testing the contribution of selection, recombination and segment reassortment in the origin of members of new species. *Arch. Virol.* 166, 491–499. doi: 10.1007/s00705-020-04902-1

Camacho-Beltrán, E., Armenta-Chávez, R., Romero-Romero, J. L., Magallanes-Tapia, M. A., Leyva-López, N. E., Apodaca-Sánchez, M. Á., et al. (2015). First report of pepper as a natural new host for tomato marchitez virus in sinaloa, mexico. *Can. J. Plant Pathol.* 37, 384–389. doi: 10.1080/07060661.2015.1078412

Camacho-Beltrán, E., Pérez-Villarreal, A., Leyva-López, N. E., Rodríguez-Negrete, E. A., Ceniceros-Ojeda, E. A., and Méndez-Lozano, J. (2019). Occurrence of tomato brown rugose fruit virus infecting tomato crops in mexico. *Plant Dis.* 103, 1440–1440. doi: 10.1094/PDIS-11-18-1974-PDN

Canto, T., Aranda, M. A., and Fereres, A. (2009). Climate change effects on physiology and population processes of hosts and vectors that influence the spread of hemipteran-borne plant viruses. *Glob. Chang. Biol.* 15, 1884–1894. doi: 10.1111/j.1365-2486.2008.01820.x

Carmichael, D. J., Rey, M. E. C., Naidoo, S., Cook, G., and van Heerden, S. W. (2011). First report of pepino mosaic virus infecting tomato in south africa. *Plant Dis.* 95:767. doi: 10.1094/PDIS-01-11-0036

Chalupowicz, L., Dombrovsky, A., Gaba, V., Luria, N., Reuven, M., Beerman, A., et al. (2019). Diagnosis of plant diseases using the nanopore sequencing platform. *Plant Pathol.* 68, 229–238. doi: 10.1111/ppa.12957

Chatzivassiliou, E. K., Boubourakas, I., Drossos, E., Eleftherohorinos, I., Jenser, G., Peters, D., et al. (2001). Weeds in greenhouses and tobacco fields are differentially infected by tomato spotted wilt virus and infested by its vector species. *Plant Dis.* 85, 40–46. doi: 10.1094/PDIS.2001.85.1.40

Chatzivassiliou, E. K., Giakountis, A., Kumari, S. G., and Makkouk, K. M. (2016). Viruses affecting lentil (lens culinaris medik.) in greece; incidence and genetic variability of bean leafroll virus and pea enation mosaic virus. *Phytopathol. Mediterr.* 55, 239–252. doi: 10.2307/44809330

Che, H. Y., Luo, D. Q., and Cao, X. R. (2018). First report of tomato mottle mosaic virus in tomato crops in china. *Plant Dis.* 102:2051. doi: 10.1094/PDIS-03-18-0538-PDN

Chikh-Ali, M., Naidu, R. A., and Karasev, A. V. (2015). First report of potato virus Y (PVY) strain PVY C associated with a tomato disease in kenya. *Plant Dis.* 100:864. doi: 10.1094/PDIS-08-15-0890-PDN

Choi, H., Jo, Y., Cho, W. K., Yu, J., Tran, P.-T., Salaipeth, L., et al. (2020). Identification of viruses and viroids infecting tomato and pepper plants in vietnam by metatranscriptomics. *Int. J. Mol. Sci.* 21:7565. doi: 10.3390/ijms21207565

Cillo, F., Barbarossa, L., Grieco, F., and Gallitelli, D. (1994). Lethal necrosis, fruit necrosis and top stunting: molecular- biological aspects of three cucumber mosaic virus-induced diseases of processing tomatoes in Italy. *Acta Hortic.* 379, 369–376. doi: 10.17660/ActaHortic.1994.376.51

Ciuffo, M., Kinoti, W. M., Tiberini, A., Forgia, M., Tomassoli, L., Constable, F. E., et al. (2020). A new blunervirus infects tomato crops in italy and australia. *Arch. Virol.* 165, 2379–2384. doi: 10.1007/s00705-020-04760-x

Constable, F., Chambers, G., Penrose, L., Daly, A., Mackie, J., Davis, K., et al. (2019). Viroid-infected tomato and capsicum seed shipments to Australia. *Viruses* 11:98. doi: 10.3390/v11020098

Cooper, I., and Jones, R. A. C. (2006). Wild plants and viruses: under-investigated ecosystems. *Adv. Virus Res.* 67, 1–47. doi: 10.1016/S0065-3527(06)67001-2

de Nazaré Almeida dos Reis, L., Fonseca, M. E. N., Ribeiro, S. G., Naito, F. Y. B., Boiteux, L. S., and Pereira-Carvalho, R. C. (2020). Metagenomics of neotropical single-stranded DNA viruses in tomato cultivars with and without the Ty-1 gene. *Viruses* 12:819. doi: 10.3390/v12080819

De Oliveira, V. C., Nagata, T., Guimarães, F. C., Ferreira, F. A., Kitajima, E. W., Nicolini, C., et al. (2013). Characterization of a novel tymovirus on tomato plants in Brazil. *Virus Genes* 46, 190–194. doi: 10.1007/s11262-012-0830-x

Dombrovsky, A., and Smith, E. (2017). "Seed Transmission of Tobamoviruses: Aspects of Global Disease Distribution," in *Advances in Seed Biology*, ed. J. C. Jimenez-Lopez (London: InTech).

Donaire, L., Wang, Y., Gonzalez-Ibeas, D., Mayer, K. F., Aranda, M. A., and Llave, C. (2009). Deep-sequencing of plant viral small RNAs reveals effective and widespread targeting of viral genomes. *Virology* 392, 203–214. doi: 10.1016/j.virol.2009.07.005

Duffus, J. E., Liu, H.-Y., and Wisler, G. C. (1996). Tomato infectious chlorosis virus — a new clostero-like virus transmitted by trialeurodes vaporariorum. *Eur. J. Plant Pathol.* 102, 219–226. doi: 10.1007/BF01877960

Elena, S. F., Fraile, A., and García-Arenal, F. (2014). *"Evolution and Emergence of Plant Viruses," in Advances in Virus Research*. Amsterdam: Elsevier, 161–191.

Elvira-González, L., Medina, V., Rubio, L., and Galipienso, L. (2020). The persistent southern tomato virus modifies miRNA expression without inducing symptoms and cell ultra-structural changes. *Eur. J. Plant Pathol.* 156, 615–622. doi: 10.1007/s10658-019-01911-y

EPPO (2020a). *Tomato brown rugose fruit virus (TOBRFV)[Datasheet]*| *EPPO Global Database*. Available Online at: https://gd.eppo.int/taxon/TOBRFV/datasheet [Accessed January 5, 2021].

EPPO (2020b). *Tomato mottle mosaic virus*. Available Online at: https://www.eppo.int/ACTIVITIES/plant_quarantine/alert_list_viruses/tomato_mottle_mosaic_virus [Accessed January 5, 2021]

EPPO GD (2020). *EPPO Global Database*. Available Online at: https://gd.eppo.int [Accessed January 5, 2021].

FAOSTAT (2020). *Statistics Division of the Food and Agricultural Organization of the United Nations*. Availabe Online at: http://www.fao.org/faostat/en/ Accessed December 31, 2020

Fariña, A. E., Rezende, J. A. M., and Wintermantel, W. M. (2019). Expanding knowledge of the host range of *Tomato chlorosis virus* and host plant preference of *Bemisia tabaci* MEAM1. *Plant Dis.* 103, 1132–1137. doi: 10.1094/PDIS-11-18-1941-RE

Ferrand, L., Nome, C., Orílio, A. F., García, M. L., Nagata, T., Ronco, L. B., et al. (2016). First report of tomato blistering mosaic virus infecting tomato in Argentina. *Plant Dis.* 100:1026. doi: 10.1094/PDIS-07-15-0782-PDN

Fiallo-Olivé, E., and Navas-Castillo, J. (2019). Tomato chlorosis virus, an emergent plant virus still expanding its geographical and host ranges. *Mol. Plant Pathol.* 20, 1307–1320. doi: 10.1111/mpp.12847

Fiallo-Olivé, E., Pan, L.-L., Liu, S.-S., and Navas-Castillo, J. (2020). Transmission of begomoviruses and other whitefly-borne viruses: dependence on the vector species. *Phytopathology* 110, 10–17. doi: 10.1094/PHYTO-07-19-0273-FI

Fidan, H., Sarikaya, P., and Calis, O. (2019). First report of tomato brown rugose fruit virus on tomato in Turkey. *New Dis. Rep.* 39:18. doi: 10.5197/j.2044-0588.2019.039.018

Fillhart, R. C., Bachand, G. D., and Castello, J. D. (1998). Detection of infectious tobamoviruses in forest soils. *Appl. Environ. Microbiol.* 64, 1430–1435. doi: 10.1128/aem.64.4.1430-1435.1998

Finetti Sialer, M., Di Franco, A., Papanice, M. A., and Gallitelli, D. (1997). Tomato necrotic yellows induced by a novel strain of alfalfa mosaic virus. *J. Plant Pathol.* 79, 115–120.

Finetti-Sialer, M., and Gallitelli, D. (2003). Complete nucleotide sequence of pelargonium zonate spot virus and its relationship with the family bromoviridae. *J. Gen. Virol.* 84, 3143–3151. doi: 10.1099/vir.0.19391-0

Flores, R., Hernández, C., Alba, A. E. M., de Daròs, J.-A., and Serio, F. D. (2005). Viroids and viroid-host interactions. *Annu. Rev. Phytopathol.* 43, 117–139. doi: 10.1146/annurev.phyto.43.040204.140243

Fontenele, R. S., Lamas, N. S., Lacorte, C., Lacerda, A. L. M., Varsani, A., and Ribeiro, S. G. (2017). A novel geminivirus identified in tomato and cleome plants sampled in Brazil. *Virus Res.* 240, 175–179. doi: 10.1016/j.virusres.2017.08.007

Fortes, I. M., Sánchez-Campos, S., Fiallo-Olivé, E., Díaz-Pendón, J. A., Navas-Castillo, J., and Moriones, E. (2016). A novel strain of tomato leaf curl new delhi virus has spread to the mediterranean basin. *Viruses* 8:307. doi: 10.3390/v8110307

Fox, A., Daly, M., Nixon, T., Brurberg, M. B., Blystad, D.-R., Harju, V., et al. (2013). First report of tomato chlorotic dwarf viroid (TCDVd) in tomato in norway and subsequent eradication. *New Dis. Rep.* 27:8. doi: 10.5197/j.2044-0588.2013.027.008

Fuentes, A., Carlos, N., Ruiz, Y., Callard, D., Sánchez, Y., Ochagavía, M. E., et al. (2016). Field trial and molecular characterization of RNAi-transgenic tomato plants that exhibit resistance to tomato yellow leaf curl geminivirus. *Mol. Plant-Microbe Interact.* 29, 197–209. doi: 10.1094/MPMI-08-15-0181-R

Gaafar, Y., Lüddecke, P., Heidler, C., Hartrick, J., Sieg-Müller, A., Hübert, C., et al. (2019). First report of southern tomato virus in german tomatoes. *New Dis. Rep.* 40:1. doi: 10.5197/j.2044-0588.2019.040.001

Gaafar, Y. Z. A., Abdelgalil, M. A. M., Knierim, D., Richert-Pöggeler, K. R., Menzel, W., Winter, S., et al. (2018). First report of physostegia chlorotic mottle virus on tomato (*Solanum lycopersicum*) in germany. *Plant Dis.* 102, 255–255. doi: 10.1094/PDIS-05-17-0737-PDN

Gaafar, Y. Z. A., and Ziebell, H. (2020). Comparative study on three viral enrichment approaches based on RNA extraction for plant virus/viroid detection using high-throughput sequencing. *PLoS One* 15:e0237951. doi: 10.1371/journal.pone.0237951

Gadhave, K. R., Gautam, S., Rasmussen, D. A., and Srinivasan, R. (2020). Aphid transmission of Potyvirus: the largest plant-infecting RNA virus genus. *Viruses* 12:773. doi: 10.3390/v12070773

Gallitelli, D. (2000). The ecology of cucumber mosaic virus and sustainable agriculture. *Virus Res.* 71, 9–21. doi: 10.1016/S0168-1702(00)00184-2

Garcìa-Arenal, F., and Palukaitis, P. (1999). Structure and functional relationships of satellite RNAs of cucumber mosaic virus. *Curr. Top. Microbiol. Immunol.* 239, 37–63. doi: 10.1007/978-3-662-09796-0_3

Garrett, K. A., Alcalá-Briseño, R. I., Andersen, K. F., Buddenhagen, C. E., Choudhury, R. A., Fulton, J. C., et al. (2018). Network analysis: a systems framework to address grand challenges in plant pathology. *Annu. Rev. Phytopathol.* 56, 559–580. doi: 10.1146/annurev-phyto-080516-035326

Giakountis, A., Tsarmpopoulos, I., and Chatzivassiliou, E. K. (2018). Cucumber mosaic virus isolates from greek legumes are associated with satellite RNAs that are necrogenic for tomato. *Plant Dis.* 102, 2268–2276. doi: 10.1094/PDIS-08-17-1259-RE

Gilbertson, R. L., Rojas, M. R., Kon, T., and Jaquez, J. (2007). "Introduction of Tomato Yellow Leaf Curl Virus into the Dominican Republic: the Development of a Successful Integrated Pest Management Strategy," in *Tomato Yellow Leaf Curl Virus Disease: Management, Molecular Biology, Breeding for Resistance*, ed. H. Czosnek (Dordrecht: Springer), 279–303.

Gnanasekaran, P., and Chakraborty, S. (2018). Biology of viral satellites and their role in pathogenesis. *Curr. Opin. Virol.* 33, 96–105. doi: 10.1016/j.coviro.2018.08.002

Gómez, P., Sempere, R., and Aranda, M. A. (2012). Pepino mosaic virus and tomato torrado virus: two emerging viruses affecting tomato crops in the mediterranean basin. *Adv. Virus Res.* 84, 505–532. doi: 10.1016/B978-0-12-394314-9.00014-2

Gómez-Aix, C., Alcaide, C., Agüero, J., Faize, M., Juárez, M., Díaz-Marrero, C. J., et al. (2019). Genetic diversity and population structure of pepino mosaic virus in tomato crops of spain and morocco. *Ann. Appl. Biol.* 174, 284–292. doi: 10.1111/aab.12491

Gorayeb, E. S., Bello, V. H., Cruciol, G. C. D., Watanabe, L. F. M., Dovigo, L. H., Sartori, M. M. P., et al. (2020). Evaluation of datura stramonium and nicandra physaloides as reservoirs of tomato severe rugose virus and whiteflies. *Plant Pathol.* 69, 569–575. doi: 10.1111/ppa.13139

Grieco, F., Lanave, C., and Gallitelli, D. (1997). Evolutionary dynamics of cucumber mosaic virus satellite RNA during natural epidemics in Italy. *Virology* 229, 166–174. doi: 10.1006/viro.1996.8426

Groves, R. L., Walgenbach, J. F., Moyer, J. W., and Kennedy, G. G. (2002). The role of weed hosts and tobacco thrips, *Frankliniella fusca*, in the epidemiology of tomato spotted wilt virus. *Plant Dis.* 86, 573–582. doi: 10.1094/PDIS.2002.86.6.573

Hančinský, R., Mihálik, D., Mrkvová, M., Candresse, T., and Glasa, M. (2020). Plant viruses infecting solanaceae family members in the cultivated and wild environments: a review. *Plants* 9:667. doi: 10.3390/plants9050667

Hanssen, I. M., Gutiérrez-Aguirre, I., Paeleman, A., Goen, K., Wittemans, L., Lievens, B., et al. (2010a). Cross-protection or enhanced symptom display in greenhouse tomato co-infected with different pepino mosaic virus isolates. *Plant Pathol.* 59, 13–21. doi: 10.1111/j.1365-3059.2009.02190.x

Hanssen, I. M., Lapidot, M., and Thomma, B. P. H. J. (2010b). Emerging viral diseases of tomato crops. *Mol. Plant-Microbe Interact.* 23, 539–548. doi: 10.1094/MPMI-23-5-0539

Hanssen, I. M., Mumford, R., Blystad, D.-R., Cortez, I., Hasiów-Jaroszewska, B., Hristova, D., et al. (2010c). Seed transmission of pepino mosaic virus in tomato. *Eur. J. Plant Pathol.* 126, 145–152. doi: 10.1007/s10658-009-9528-x

Hanssen, I. M., and Lapidot, M. (2012). Major tomato viruses in the mediterranean basin. *Adv. Virus Res.* 84, 31–66. doi: 10.1016/B978-0-12-394314-9.00002-6

Hanssen, I. M., Paeleman, A., Vandewoestijne, E., Van Bergen, L., Bragard, C., Lievens, B., et al. (2009). Pepino mosaic virus isolates and differential symptomatology in tomato. *Plant Pathol.* 58, 450–460. doi: 10.1111/j.1365-3059.2008.02018.x

Hanssen, I. M., and Thomma, B. P. H. J. (2010). Pepino mosaic virus: a successful pathogen that rapidly evolved from emerging to endemic in tomato crops. *Mol. Plant Pathol.* 11, 179–189. doi: 10.1111/j.1364-3703.2009.00600.x

Hassani-Mehraban, A., Cheewachaiwit, S., Relevante, C., Kormelink, R., and Peters, D. (2011). Tomato necrotic ring virus (TNRV), a recently described tospovirus species infecting tomato and pepper in Thailand. *Eur. J. Plant Pathol.* 130, 449–456. doi: 10.1007/s10658-011-9771-9

HortDaily (2019). *Southern Tomato Virus reported in the UK*. Available Online at: https://www.hortidaily.com/article/9103907/southern-tomato-virus-reported-in-the-uk/ [Accessed August 3, 2020]

Hou, W., Li, S., and Massart, S. (2020). Is there a "biological desert" with the discovery of new plant viruses? a retrospective analysis for new fruit tree viruses. *Front. Microbiol.* 11:592816. doi: 10.3389/fmicb.2020.592816

Huang, C.-H., Zheng, Y.-X., Cheng, Y.-H., Lee, W.-S., and Jan, F.-J. (2010). First report of capsicum chlorosis virus infecting tomato in Taiwan. *Plant Dis.* 94:1263. doi: 10.1094/PDIS-04-10-0275

Iacono, G., Hernandez-Llopis, D., Alfaro-Fernandez, A., Davino, M., Font, M., Panno, S., et al. (2015). First report of southern tomato virus in tomato crops in Italy. *New Dis. Rep.* 32, 27–27. doi: 10.5197/j.2044-0588.2015.032.027

ICTV (2020). *ICTV Master Species List 2019.v1*. Available Online at: https://talk.ictvonline.org/files/master-species-lists/m/msl/9601 (accessed June 1, 2020).

Idris, A. M., Shahid, M. S., Briddon, R. W., Khan, A. J., Zhu, J. K., and Brown, J. K. (2011). An unusual alphasatellite associated with monopartite begomoviruses attenuates symptoms and reduces betasatellite accumulation. *J. Gen. Virol.* 92, 706–717. doi: 10.1099/vir.0.025288-0

Ignatov, A. N., Gritsenko, V. V., and Dzhalilov, F. S. (2020). Risks of new tomato virus diseases spreading in the russian federation. *Potato Veg.* 5:3. doi: 10.25630/PAV.2020.80.51.001

Ito, T., Kimbara, J., Sharma, P., and Ikegami, M. (2009). Interaction of tomato yellow leaf curl virus with diverse betasatellites enhances symptom severity. *Arch. Virol.* 154, 1233–1239. doi: 10.1007/s00705-009-0431-8

Jacquemond, M. (2012). "Cucumber Mosaic Virus," in *Viruses and Virus Diseases of Vegetables in the Mediterranean Basin*, eds G. Loebenstein and H. Lecoq (Cambridge,MA: Academic Press), 439–504.

Jones, R. A. C. (2016). *"Future Scenarios for Plant Virus Pathogens as Climate Change Progresses," in Advances in Virus Research*. Cambridge,MA: Academic Press Inc, 87–147.

Jones, R. A. C. (2018). *"Plant and Insect Viruses in Managed and Natural Environments: Novel and Neglected Transmission Pathways," in Advances in Virus Research*. Cambridge,MA: Academic Press Inc, 149–187.

Jones, R. A. C. (2021). Global plant virus disease pandemics and epidemics. *Plants* 10:233. doi: 10.3390/plants10020233

Jones, R. A. C., Koenig, R., and Lasemann, D. E. (1980). Pepino mosaic virus, a new potexvirus from pepino (solanum muricatum). *Ann. Appl. Biol.* 94, 61–68. doi: 10.1111/j.1744-7348.1980.tb03896.x

Jyothsna, P., Haq, Q. M. I., Singh, P., Sumiya, K. V., Praveen, S., Rawat, R., et al. (2013). Infection of tomato leaf curl New Delhi virus (ToLCNDV), a bipartite begomovirus with betasatellites, results in enhanced level of helper virus components and antagonistic interaction between DNA B and betasatellites. *Appl. Microbiol. Biotechnol.* 97, 5457–5471. doi: 10.1007/s00253-012-4685-9

Kaliciak, A., and Syller, J. (2009). New hosts of potato virus Y (PVY) among common wild plants in Europe. *Eur. J. Plant Pathol.* 124, 707–713. doi: 10.1007/s10658-009-9452-0

Katsarou, K., Bardani, E., Kallemi, P., and Kalantidis, K. (2019). Viral detection: past, present, and future. *Bioessays* 41:e1900049. doi: 10.1002/bies.201900049

Kazinczi, G., Takács, A. P., Horváth, J., Gáborjányi, R., and Béres, I. (2005). Susceptibility of some weed species to pepino mosaic virus (PepMV). *Commun. Agric. Appl. Biol. Sci.* 70, 489–491.

Kesumawati, E., Okabe, S., Homma, K., Fujiwara, I., Zakaria, S., Kanzaki, S., et al. (2019). Pepper yellow leaf curl aceh virus: a novel bipartite begomovirus isolated from chili pepper, tomato, and tobacco plants in indonesia. *Arch. Virol.* 164, 2379–2383. doi: 10.1007/s00705-019-04316-8

Khan, A. J., Akhtar, S., Singh, A. K., Al-Shehi, A. A., Al-Matrushi, A. M., Ammara, U., et al. (2014). Recent evolution of a novel begomovirus causing tomato leaf curl disease in the Al-batinah region of oman. *Arch. Virol.* 159, 445–455. doi: 10.1007/s00705-013-1853-x

Kiss, Z. A., Medina, V., and Falk, B. W. (2013). Crinivirus replication and host interactions. *Front. Microbiol.* 4:99. doi: 10.3389/fmicb.2013.00099

Klap, C., Luria, N., Smith, E., Hadad, L., Bakelman, E., Sela, N., et al. (2020). Tomato brown rugose fruit virus contributes to enhanced pepino mosaic virus titers in tomato plants. *Viruses* 12:879. doi: 10.3390/v12080879

Kon, T., and Gilbertson, R. L. (2012). Two genetically related begomoviruses causing tomato leaf curl disease in togo and nigeria differ in virulence and host range but do not require a betasatellite for induction of disease symptoms. *Arch. Virol.* 157, 107–120. doi: 10.1007/s00705-011-1139-0

Kovalskaya, N., and Hammond, R. W. (2014). Molecular biology of viroid–host interactions and disease control strategies. *Plant Sci.* 228, 48–60. doi: 10.1016/j.plantsci.2014.05.006

Kreuze, J. F., Perez, A., Untiveros, M., Quispe, D., Fuentes, S., Barker, I., et al. (2009). Complete viral genome sequence and discovery of novel viruses by deep sequencing of small RNAs: a generic method for diagnosis, discovery and sequencing of viruses. *Virology* 388, 1–7. doi: 10.1016/j.virol.2009.03.024

Kumar, J., Gunapati, S., Singh, S. P., Kumar, A., Lalit, A., Sharma, N. C., et al. (2013). A new betasatellite associated with cotton leaf curl burewala virus infecting tomato in india: influence on symptoms and viral accumulation. *Arch. Virol.* 158, 1349–1353. doi: 10.1007/s00705-013-1613-y

Lapidot, M., Guenoune-Gelbart, D., Leibman, D., Holdengreber, V., Davidovitz, M., MacHbash, Z., et al. (2010). Pelargonium zonate spot virus is transmitted vertically via seed and pollen in tomato. *Phytopathology* 100, 798–804. doi: 10.1094/PHYTO-100-8-0798

Lavina, A., Aramburu, J., and Moriones, E. (1996). Occurrence of tomato spotted wilt and cucumber mosaic viruses in field-grown tomato crops and associated weeds in northeastern Spain. *Plant Pathol.* 45, 837–842. doi: 10.1111/j.1365-3059.1996.tb02893.x

Lecoq, H., Wipf-Scheibel, C., Verdin, E., and Desbiez, C. (2019). Characterization of the first tenuivirus naturally infecting dicotyledonous plants. *Arch. Virol.* 164, 297–301. doi: 10.1007/s00705-018-4057-6

Leke, W. N., Kvarnheden, A., Ngane, E. B., Titanji, V. P. K., and Brown, J. K. (2011). Molecular characterization of a new begomovirus and divergent alphasatellite from tomato in Cameroon. *Arch. Virol.* 156, 925–928. doi: 10.1007/s00705-011-0957-4

Lett, J.-M., Ncho, J., Claverie, S., Hoareau, M., Lefeuvre, P., De Cauwer, V., et al. (2020). Tomato leaf curl kunene virus: a novel tomato-infecting monopartite begomovirus from namibia. *Arch. Virol.* 165, 1887–1889. doi: 10.1007/s00705-020-04666-8

Levitzky, N., Smith, E., Lachman, O., Luria, N., Mizrahi, Y., Bakelman, H., et al. (2019). The bumblebee bombus terrestris carries a primary inoculum of tomato brown rugose fruit virus contributing to disease spread in tomatoes. *PLoS One* 14:e0210871. doi: 10.1371/journal.pone.0210871

Li, C. X., Shi, M., Tian, J. H., Lin, X. D., Kang, Y. J., Chen, L. J., et al. (2015). Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative-sense RNA viruses. *Elife* 4:e05378. doi: 10.7554/eLife.05378

Li, R., Gao, S., Fei, Z., and Ling, K.-S. (2013). Complete genome sequence of a new tobamovirus naturally infecting tomatoes in Mexico. *Genome Announc.* 1, e713–e794. doi: 10.1128/genomeA.00794-13

Li, R., Gao, S., Hernandez, A. G., Wechter, W. P., Fei, Z., and Ling, K.-S. (2012). Deep sequencing of small RNAs in tomato for virus and viroid identification and strain differentiation. *PLoS One* 7:e37127. doi: 10.1371/journal.pone.0037127

Li, Y., Wang, Y., Hu, J., Xiao, L., Tan, G., Lan, P., et al. (2017). The complete genome sequence, occurrence and host range of tomato mottle mosaic virus chinese isolate. *Virol. J.* 14:15. doi: 10.1186/s12985-016-0676-2

Ling, K.-S., Tian, T., Gurung, S., Salati, R., and Gilliard, A. (2019). First report of tomato brown rugose fruit virus infecting greenhouse tomato in the united states. *Plant Dis.* 103:1439. doi: 10.1094/pdis-11-18-1959-pdn

Ling, K.-S., and Zhang, W. (2011). First report of pepino mosaic virus infecting tomato in Mexico. *Plant Dis.* 95, 1035–1035. doi: 10.1094/PDIS-04-11-0334

Llamas-Llamas, M. E., Zavaleta-Mejia, E., Gonzalez-Hernandez, V. A., Cervantes-Diaz, L., Santizo-Rincon, J. A., and Ochoa-Martinez, D. L. (1998). Effect of temperature on symptom expression and accumulation of tomato spotted wilt virus in different host species. *Plant Pathol.* 47, 341–347. doi: 10.1046/j.1365-3059.1998.00249.x

Lovelock, D. A., Kinoti, W. M., Bottcher, C., Wildman, O., Dall, D., Rodoni, B. C., et al. (2020). Tomato mottle mosaic virus intercepted by australian biosecurity in capsicum annuum seed. *Aust. Plant Dis. Notes* 15:8. doi: 10.1007/s13314-020-0378-x

Luria, N., Smith, E., Reingold, V., Bekelman, I., Lapidot, M., Levin, I., et al. (2017). A new Israeli tobamovirus isolate infects tomato plants harboring Tm-22 resistance genes. *PLoS One* 12:e0170429. doi: 10.1371/journal.pone.0170429

Ma, Y., Marais, A., Lefebvre, M., Faure, C., and Candresse, T. (2020). Metagenomic analysis of virome cross-talk between cultivated *Solanum lycopersicum* and wild *Solanum nigrum. Virology* 540, 38–44. doi: 10.1016/j.virol.2019.11.009

Ma, Y., Marais, A., Lefebvre, M., Theil, S., Svanella-Dumas, L., Faure, C., et al. (2019). Phytovirome analysis of wild plant populations: comparison of double-stranded RNA and virion-associated nucleic acid metagenomic approaches. *J. Virol.* 94, e1419–e1462. doi: 10.1128/JVI.01462-19

Mabvakure, B., Martin, D. P., Kraberger, S., Cloete, L., van Brunschot, S., Geering, A. D. W., et al. (2016). Ongoing geographical spread of tomato yellow leaf curl virus. *Virology* 498, 257–264. doi: 10.1016/j.virol.2016.08.033

Macedo, M. A., Albuquerque, L. C., Maliano, M. R., Souza, J. O., Rojas, M. R., Inoue-Nagata, A. K., et al. (2018). Characterization of tomato leaf curl purple vein virus, a new monopartite new world begomovirus infecting tomato in northeast Brazil. *Arch. Virol.* 163, 737–743. doi: 10.1007/s00705-017-3662-0

Macharia, I., Backhouse, D., Wu, S. B., and Ateka, E. M. (2016). Weed species in tomato production and their role as alternate hosts of tomato spotted wilt virus and its vector frankliniella occidentalis. *Ann. Appl. Biol.* 169, 224–235. doi: 10.1111/aab.12297

Mackie, A. E., Barbetti, M. J., Rodoni, B., McKirdy, S. J., and Jones, R. A. C. (2019). Effects of a potato spindle tuber viroid tomato strain on the symptoms, biomass, and yields of classical indicator and currently grown potato and tomato cultivars. *Plant Dis.* 103, 3009–3017. doi: 10.1094/PDIS-02-19-0312-RE

Mackie, A. E., Rodoni, B. C., Barbetti, M. J., McKirdy, S. J., and Jones, R. A. C. (2016). Potato spindle tuber viroid: alternative host reservoirs and strain found in a remote subtropical irrigation area. *Eur. J. Plant Pathol.* 145, 433–446. doi: 10.1007/s10658-016-0857-2

Maddahian, M., Massumi, H., Heydarnejad, J., Hosseini Pour, A., and Varsani, A. (2017). Characterization of iranian tomato aspermy virus isolates with a variant 2b gene sequence. *Trop. Plant Pathol.* 42, 475–484. doi: 10.1007/s40858-017-0173-1

Malmstrom, C. M., and Alexander, H. M. (2016). Effects of crop viruses on wild plants. *Curr. Opin. Virol.* 19, 30–36. doi: 10.1016/j.coviro.2016.06.008

Márquez-Martín, B., Aragón-Caballero, L., Fiallo-Olivé, E., Navas-Castillo, J., and Moriones, E. (2011). Tomato leaf deformation virus, a novel begomovirus associated with a severe disease of tomato in Peru. *Eur. J. Plant Pathol.* 129, 1–7. doi: 10.1007/s10658-010-9699-5

Márquez-Martín, B., Maeso, D., Martínez-Ayala, A., Bernal, R., Teresa Federici, M., Vincelli, P., et al. (2012). Diverse population of a new bipartite begomovirus infecting tomato crops in uruguay. *Arch. Virol.* 157, 1137–1142. doi: 10.1007/s00705-012-1262-6

Martínez-Ayala, A., Sánchez-Campos, S., Cáceres, F., Aragón-Caballero, L., Navas-Castillo, J., and Moriones, E. (2014). Characterisation and genetic diversity of pepper leafroll virus, a new bipartite begomovirus infecting pepper, bean and tomato in Peru. *Ann. Appl. Biol.* 164, 62–72. doi: 10.1111/aab.12074

Massart, S., Candresse, T., Gil, J., Lacomme, C., Predajna, L., Ravnikar, M., et al. (2017). A framework for the evaluation of biosecurity, commercial, regulatory, and scientific impacts of plant viruses and viroids identified by NGS technologies. *Front. Microbiol.* 8:45. doi: 10.3389/fmicb.2017.00045

Massart, S., Chiumenti, M., De Jonghe, K., Glover, R., Haegeman, A., Koloniuk, I., et al. (2019). Virus detection by high-throughput sequencing of small RNAs: Large-scale performance testing of sequence analysis strategies. *Phytopathology* 109, 488–497. doi: 10.1094/PHYTO-02-18-0067-R

Masuta, C. (2014). Molecular biology of cucumber mosaic virus and its satellite RNA. *J. Gen. Plant Pathol.* 80, 514–518. doi: 10.1007/s10327-014-0547-x

Mavrič, I., Tušek Žnidarič, M., Viršček Marn, M., Dolničar, P., Mehle, N., Lesemann, D.-E., et al. (2006). First report of eggplant mottled dwarf virus in potato and tomato in Slovenia. *Plant Pathol.* 55, 566. doi: 10.1111/j.1365-3059.2006.01414.x

McLeish, M. J., Fraile, A., and García-Arenal, F. (2020a). Population genomics of plant viruses: the ecology and evolution of virus emergence. *Phytopathology* 111, 32–39. doi: 10.1094/PHYTO-08-20-0355-FI

McLeish, M. J., Fraile, A., and García-Arenal, F. (2020b). Trends and gaps in forecasting plant virus disease risk. *Ann. Appl. Biol.* 176, 102–108. doi: 10.1111/aab.12553

Mehle, N., Gutiérrez-Aguirre, I., Kutnjak, D., and Ravnikar, M. (2018). Water-mediated transmission of plant, animal, and human viruses. *Adv. Virus Res.* 101, 85–128. doi: 10.1016/bs.aivir.2018.02.004

Mehle, N., Gutiérrez-Aguirre, I., Prezelj, N., Delić, D., Vidic, U., and Ravnikar, M. (2014). Survival and transmission of potato virus Y, pepino mosaic virus, and potato spindle tuber viroid in water. *Appl. Environ. Microbiol.* 80, 1455–1462. doi: 10.1128/AEM.03349-13

Mehle, N., Kogovšek, P., Rački, N., Jakomin, T., Gutiérrez-Aguirre, I., Kramberger, P., et al. (2017). Filling the gaps in diagnostics of *Pepino mosaic virus* and *Potato spindle tuber viroid* in water and tomato seeds and leaves. *Plant Pathol.* 66, 1191–1201. doi: 10.1111/ppa.12710

Mehle, N., and Ravnikar, M. (2012). Plant viruses in aqueous environment - survival, water mediated transmission and detection. *Water Res.* 46, 4902–4917. doi: 10.1016/j.watres.2012.07.027

Melgarejo, T. A., Kon, T., Rojas, M. R., Paz-Carrasco, L., Zerbini, F. M., and Gilbertson, R. L. (2013). Characterization of a new world monopartite begomovirus causing leaf curl disease of tomato in ecuador and peru reveals a new direction in geminivirus evolution. *J. Virol.* 87, 5397–5413. doi: 10.1128/jvi.00234-13

Melo, F. L., Fernandes, J. E. A., Ribeiro, B. M., and Ribeiro, S. G. (2014). Complete genome sequence of a tobacco-infecting, tomato blistering mosaic virus. *Genome Announc.* 2, 701–715. doi: 10.1128/genomeA.00701-14

Melzer, M. J., Sugano, J. S., Cabanas, D., Dey, K. K., Kandouh, B., Mauro, D., et al. (2012). First report of pepper mottle virus infecting tomato in Hawaii. *Plant Dis.* 96:917. doi: 10.1094/PDIS-02-12-0147-PDN

Méndez-Lozano, J., Magallanes-Tapia, M. A., Romero-Romero, J. L., Camacho-Beltrán, E., Vega, W. L. O., Leyva-López, N. E., et al. (2012). Tomato infectious chlorosis virus associated with tomato diseases in baja california, mexico. *Plant Dis.* 96:1229. doi: 10.1094/PDIS-02-12-0196-PDN

Menzel, W., Knierim, D., Winter, S., Hamacher, J., and Heupel, M. (2019). First report of tomato brown rugose fruit virus infecting tomato in Germany. *New Dis. Rep.* 39:1. doi: 10.5197/j.2044-0588.2019.039.001

Menzel, W., Richert-Pöggeler, K. R., Winter, S., and Knierim, D. (2018). Characterization of a nucleorhabdovirus from physostegia. *Acta Hortic.* 1193, 29–38. doi: 10.17660/ActaHortic.2018.1193.5

Mochizuki, T., and Ohki, S. T. (2012). Cucumber mosaic virus: viral genes as virulence determinants. *Mol. Plant Pathol.* 13, 217–225. doi: 10.1111/j.1364-3703.2011.00749.x

Moodley, V., Gubba, A., and Mafongoya, P. L. (2016). First report of tomato torrado virus on tomato (*Solanum lycopersicum*) in south africa. *Plant Dis.* 100:231. doi: 10.1094/PDIS-06-15-0683-PDN

Moodley, V., Gubba, A., and Mafongoya, P. L. (2019). A survey of whitefly-transmitted viruses on tomato crops in south africa. *Crop Prot.* 123, 21–29.

Moodley, V., Gubba, A., and Mafongoya, P. L. (2020). Emergence and full genome analysis of tomato torrado virus in south africa. *Viruses* 12:1167. doi: 10.3390/v12101167

Moreno-Perez, M. G., Pagan, I., Aragon-Caballero, L., Caceres, F., Fraile, A., and Garcia-Arenal, F. (2014). Ecological and genetic determinants of pepino mosaic virus emergence. *J. Virol.* 88, 3359–3368. doi: 10.1128/JVI.02980-13

Moriones, E., Praveen, S., and Chakraborty, S. (2017). Tomato leaf curl new delhi virus: an emerging virus complex threatening vegetable and fiber crops. *Viruses* 9:264. doi: 10.3390/v9100264

Moury, B., Gebre Selassie, K., Marchoux, G., Daubčze, A. M., and Palloix, A. (1998). High temperature effects on hypersensitive resistance to tomato spotted wilt tospovirus (TSWV) in pepper (capsicum chinense jacq.). *Eur. J. Plant Pathol.* 104, 489–498. doi: 10.1023/A:1008618022144

Nagai, A., Duarte, L. M. L., Chaves, A. L. R., Peres, L. E. P., and dos Santos, D. Y. A. C. (2019). Tomato mottle mosaic virus in brazil and its relationship with Tm-22 gene. *Eur. J. Plant Pathol.* 155, 353–359. doi: 10.1007/s10658-019-01762-7

Nava, A., Londoño, A., and Polston, J. E. (2013). Characterization and distribution of tomato yellow margin leaf curl virus, a begomovirus from venezuela. *Arch. Virol.* 158, 399–406. doi: 10.1007/s00705-012-1501-x

Navarro, B., Gisel, A., Rodio, M.-E., Delgado, S., Flores, R., and Di Serio, F. (2012). Viroids: how to infect a host and cause disease without encoding proteins. *Biochimie* 94, 1474–1480. doi: 10.1016/j.biochi.2012.02.020

Navarro, B., Silletti, M. R., Trisciuzzi, V. N., and Di Serio, F. (2009). Identification and characterization of potato spindle tuber viroid infecting tomato in italy. *J. Plant Pathol.* 91, 723–726.

Navas-Castillo, J., Fiallo-Olivé, E., and Sánchez-Campos, S. (2011). Emerging virus diseases transmitted by whiteflies. *Annu. Rev. Phytopathol.* 49, 219–248. doi: 10.1146/annurev-phyto-072910-095235

NIH-NHGRI (2019). *DNA sequencing costs: data*. Available Online at: https://www.genome.gov/about-genomics/fact-sheets/DNA-Sequencing-Costs-Data [Accessed July 8, 2020]

Nikolić, D., Vučurović, A., Stanković, I., Radović, N., Zečević, K., Bulajić, A., et al. (2018). Viruses affecting tomato crops in Serbia. *Eur. J. Plant Pathol.* 152, 225–235. doi: 10.1007/s10658-018-1467-y

Noël, P., Hance, T., and Bragard, C. (2014). Transmission of the pepino mosaic virus by whitefly. *Eur. J. Plant Pathol.* 138, 23–27. doi: 10.1007/s10658-013-0313-5

Oerke, E. C. (2006). Crop losses to pests. *J. Agric. Sci.* 144, 31–43. doi: 10.1017/S0021859605005708

Oh, J., Lee, H.-K., Park, C.-Y., Yeom, Y.-A., Min, H.-G., Yang, H.-J., et al. (2018). First report of southern tomato virus in tomato (*Solanum lycopersicum*) in Korea. *Plant Dis.* 102:1467. doi: 10.1094/PDIS-09-17-1499-PDN

Okada, K., Kusari, S., Kawaratani, M., Negoro, J., Ohki, S. T., and Osaki, T. (2000). Tobacco mosaic virus is transmissible from tomato to tomato by pollinating bumblebees. *J. Gen. Plant Pathol.* 66, 71–74. doi: 10.1007/pl00012924

Oladokun, J. O., Halabi, M. H., Barua, P., and Nath, P. D. (2019). Tomato brown rugose fruit disease: current distribution, knowledge and future prospects. *Plant Pathol.* 68, 1579–1586. doi: 10.1111/ppa.13096

Oliver, J. E., and Whitfield, A. E. (2016). The genus tospovirus: emerging bunyaviruses that threaten food security. *Annu. Rev. Virol.* 3, 101–124. doi: 10.1146/annurev-virology-100114-055036

Ong, S. N., Taheri, S., Othman, R. Y., and Teo, C. H. (2020). Viral disease of tomato crops (*Solanum lycopesicum* L.): an overview. *J. Plant Dis. Prot.* 127, doi: 10.1007/s41348-020-00330-0

Orfanidou, C. G., Dimitriou, C., Papayiannis, L. C., Maliogka, V. I., and Katis, N. I. (2014). Epidemiology and genetic diversity of criniviruses associated with tomato yellows disease in Greece. *Virus Res.* 186, 120–129. doi: 10.1016/j.virusres.2013.12.013

Ouattara, A., Tiendrébéogo, F., Lefeuvre, P., Claverie, S., Hoareau, M., Traoré, E. V., et al. (2017). Tomato leaf curl burkina faso virus: a novel tomato-infecting monopartite begomovirus from burkina faso. *Arch. Virol.* 162, 1427–1429. doi: 10.1007/s00705-017-3231-6

Padidam, M., Beachy, R. N., and Fauquet, C. M. (1995). Tomato leaf curl geminivirus from India has a bipartite genome and coat protein is not essential for infectivity. *J. Gen. Virol.* 76, 25–35. doi: 10.1099/0022-1317-76-1-25

Padmanabhan, C., Zheng, Y., Li, R., Martin, G. B., Fei, Z., and Ling, K. S. (2015a). Complete genome sequence of a tomato-infecting tomato mottle mosaic virus in New York. *Genome Announc.* 3, 151–152. doi: 10.1128/genomeA.01523-15

Padmanabhan, C., Zheng, Y., Li, R., Sun, S.-E., Zhang, D., Liu, Y., et al. (2015b). Complete genome sequence of southern tomato virus identified in china using next-generation sequencing. *Genome Announc.* 3, 1226–1241. doi: 10.1128/genomeA.01226-15

Padmanabhan, C., Zheng, Y., Li, R., Fei, Z., and Ling, K.-S. (2015c). Complete genome sequence of southern tomato virus Naturally infecting tomatoes in bangladesh. *Genome. Announc.* 3, 1522–1537. doi: 10.1128/genomeA.01522-15

Palukaitis, P., and García-Arenal, F. (2003). Cucumoviruses. *Adv. Virus Res.* 62, 241–323. doi: 10.1016/S0065-3527(03)62005-1

Pan, H., Chu, D., Yan, W., Su, Q., Liu, B., Wang, S., et al. (2012). Rapid spread of tomato yellow leaf curl virus in china is aided differentially by two invasive whiteflies. *PLoS One* 7:e34817. doi: 10.1371/journal.pone.0034817

Panno, S., Caruso, A. G., and Davino, S. (2019). First report of tomato brown rugose fruit virus on tomato crops in italy. *Plant Dis.* 103:1443. doi: 10.1094/PDIS-12-18-2254-PDN

Papayiannis, L. C., Katis, N. I., Idris, A. M., and Brown, J. K. (2011). Identification of weed hosts of tomato yellow leaf curl virus in cyprus. *Plant Dis.* 95, 120–125. doi: 10.1094/PDIS-05-10-0346

Parrella, G. (2020). Sources of resistance in wild solanum germplasm (*Section lycopersicon*) to parietaria mottle virus, an emerging virus in the mediterranean basin. *Plant Pathol.* 69, 1018–1025. doi: 10.1111/ppa.13194

Parrella, G., Gognalons, P., Gebre-Selassie, K., Vovlas, C., and Marchoux, G. (2003). An update of the host range of tomato spotted wilt virus. *J. Plant Pathol.* 85, 227–264.

Parrella, G., Troiano, E., Cherchi, C., and Giordano, P. (2020). Severe outbreaks of parietaria mottle virus in tomato in sardinia, southern Italy. *J. Plant Pathol.* 102:915. doi: 10.1007/s42161-020-00492-8

Pechinger, K., Chooi, K. M., Macdiarmid, R. M., Ziebell, H., and Harper, S. J. (2019). A new era for mild strain cross-protection. *Viruses* 11, 1–17. doi: 10.3390/v11070670

Pecman, A., Kutnjak, D., Gutiérrez-Aguirre, I., Adams, I., Fox, A., Boonham, N., et al. (2017). Next generation sequencing for detection and discovery of plant viruses and viroids: comparison of two approaches. *Front. Microbiol.* 8:1998. doi: 10.3389/fmicb.2017.01998

Pecman, A., Kutnjak, D., Mehle, N., Žnidarič, M. T., Gutiérrez-Aguirre, I., Pirnat, P., et al. (2018). High-throughput sequencing facilitates characterization of a “forgotten” plant virus: the case of a henbane mosaic virus infecting tomato. *Front. Microbiol.* 9:2739. doi: 10.3389/fmicb.2018.02739

Pfitzner, A. J. P. (2006). ““Resistance to Tobacco Mosaic Virus and Tomato Mosaic Virus in Tomato,” in *Natural Resistance Mechanisms of Plants to Viruses*, eds G. Loebenstein and J. P. Carr (Dordrecht: Springer), 399–413.

Poudel, B., Abdalla, O. A., Liu, Q., Wang, Q., McAvoy, E., Seal, D., et al. (2019). Field distribution and disease incidence of tomato chlorotic spot virus, an emerging virus threatening tomato production in south Florida. *Trop. Plant Pathol.* 44, 430–437. doi: 10.1007/s40858-019-00305-z

Prajapat, R., Marwal, A., and Gaur, R. K. (2014). Begomovirus associated with alternative host weeds: a critical appraisal. *Arch. Phytopathol. Plant Prot.* 47, 157–170. doi: 10.1080/03235408.2013.805497

Prasad, A., Sharma, N., Hari-Gowthem, G., Muthamilarasan, M., and Prasad, M. (2020). Tomato yellow leaf curl virus: impact, challenges, and management. *Trends Plant Sci.* 25, 897–911. doi: 10.1016/j.tplants.2020.03.015

Prins, M., and Goldbach, R. (1998). The emerging problem of tospovirus infection and nonconventional methods of control. *Trends Microbiol.* 6, 31–35. doi: 10.1016/S0966-842X(97)01173-6

Quadros, A. F. F., Silva, J. P., Xavier, C. A. D., Zerbini, F. M., and Boari, A. J. (2019). Two new begomoviruses infecting tomato and hibiscus sp. in the amazon region of Brazil. *Arch. Virol.* 164, 1897–1901. doi: 10.1007/s00705-019-04245-6

Quenouille, J., Vassilakos, N., and Moury, B. (2013). Potato virus Y: a major crop pathogen that has provided major insights into the evolution of viral pathogenicity. *Mol. Plant Pathol.* 14, 439–452. doi: 10.1111/mpp.12024

Ramos, R. S., Kumar, L., Shabani, F., and Picanço, M. C. (2019). Risk of spread of tomato yellow leaf curl virus (TYLCV) in tomato crops under various climate change scenarios. *Agric. Syst.* 173, 524–535. doi: 10.1016/j.agsy.2019.03.020

Rao, A. L. N., and Kalantidis, K. (2015). Virus-associated small satellite RNAs and viroids display similarities in their replication strategies. *Virology* 479–480, 627–636. doi: 10.1016/j.virol.2015.02.018

Rego-Machado, C. M., Nakasu, E. Y. T., Blawid, R., Nagata, T., and Inoue-Nagata, A. K. (2019). Complete genome sequence of a new bipartite begomovirus infecting tomato in Brazil. *Arch. Virol.* 164, 2873–2875. doi: 10.1007/s00705-019-04380-0

Revers, F., and García, J. A. (2015). Chapter three - molecular biology of potyviruses. *Adv. Virus Res.* 92, 101–199. doi: 10.1016/bs.aivir.2014.11.006

Riley, D. G., Joseph, S. V., Srinivasan, R., and Diffie, S. (2011). Thrips vectors of tospoviruses. *J. Integr. Pest Manag.* 2, I1–I10. doi: 10.1603/IPM10020

Roberts, J. M. K., Ireland, K. B., Tay, W. T., and Paini, D. (2018). Honey bee-assisted surveillance for early plant virus detection. *Ann. Appl. Biol.* 173, 285–293. doi: 10.1111/aab.12461

Rojas, M. R., and Gilbertson, R. L. (2008). *“Emerging plant viruses: a diversity of mechanisms and opportunities,” in Plant virus evolution*. Amsterdam: Springer, 27–51.

Romay, G., Chirinos, D. T., Geraud-Pouey, F., Gillis, A., Mahillon, J., and Bragard, C. (2018). Complete genome sequence of two tomato-infecting begomoviruses in Venezuela: evidence of a putative novel species and a novel recombinant strain. *Arch. Virol.* 163, 555–558. doi: 10.1007/s00705-017-3611-y

Romay, G., Geraud-Pouey, F., Chirinos, D., Mahillon, M., Gillis, A., Mahillon, J., et al. (2019). Tomato twisted leaf virus: a novel indigenous new world monopartite begomovirus infecting tomato in Venezuela. *Viruses* 11:327. doi: 10.3390/v11040327

Roossinck, M. J. (2017). Deep sequencing for discovery and evolutionary analysis of plant viruses. *Virus Res.* 239, 82–86. doi: 10.1016/j.virusres.2016.11.019

Rymelska, N., Borodynko, N., Pospieszny, H., and Hasiów-Jaroszewska, B. (2013). Analysis of the biological and molecular variability of the polish isolates of tomato black ring virus (TBRV). *Virus Genes* 47, 338–346. doi: 10.1007/s11262-013-0941-z

Sabanadzovic, S., Valverde, R. A., Brown, J. K., Martin, R. R., and Tzanetakis, I. E. (2009). Southern tomato virus: the link between the families totiviridae and partitiviridae. *Virus Res.* 140, 130–137. doi: 10.1016/j.virusres.2008.11.018

Salem, N., Mansour, A., Ciuffo, M., Falk, B. W., and Turina, M. (2016). A new tobamovirus infecting tomato crops in Jordan. *Arch. Virol.* 161, 503–506. doi: 10.1007/s00705-015-2677-7

Saqib, M., Wylie, S. J., and Jones, M. G. K. (2015). Serendipitous identification of a new Iflavirus -like virus infecting tomato and its subsequent characterization. *Plant Pathol.* 64, 519–527. doi: 10.1111/ppa.12293

Sastry, K. S. (2013). *Plant Virus and Viroid Diseases in the Tropics*. Dordrecht: Springer.

Sastry, K. S., Mandal, B., Hammond, J., Scott, S. W., and Briddon, R. W. (2019). *Encyclopedia of Plant Viruses and Viroids*. New Delhi: Springer.

Savary, S., Willocquet, L., Pethybridge, S. J., Esker, P., McRoberts, N., and Nelson, A. (2019). The global burden of pathogens and pests on major food crops. *Nat. Ecol. Evol.* 3, 430–439. doi: 10.1038/s41559-018-0793-y

Schenk, M. F., Hamelink, R., van der Vlugt, R. A. A., Vermunt, A. M. W., Kaarsenmaker, R. C., and Stijger, I. C. C. M. M. (2010). The use of attenuated isolates of pepino mosaic virus for cross-protection. *Eur. J. Plant Pathol.* 127, 249–261. doi: 10.1007/s10658-010-9590-4

Scussel, S., Claverie, S., Hoareau, M., Moustache, R., Delatte, H., Lefeuvre, P., et al. (2018). Tomato leaf curl mahé virus: a novel tomato-infecting monopartite begomovirus from the seychelles. *Arch. Virol.* 163, 3451–3453. doi: 10.1007/s00705-018-4007-3

Seepiban, C., Gajanandana, O., Attathom, T., and Attathom, S. (2011). Tomato necrotic ringspot virus, a new tospovirus isolated in Thailand. *Arch. Virol.* 156, 263–274. doi: 10.1007/s00705-010-0856-0

Sevik, M. A., and Arli-Sokmen, M. (2012). Estimation of the effect of Tomato spotted wilt virus (TSWV) infection on some yield components of tomato. *Phytoparasitica* 40, 87–93. doi: 10.1007/s12600-011-0192-2

Sharma, P., Matsuda, N., Bajet, N. B., and Ikegami, M. (2011). Molecular analysis of new isolates of tomato leaf curl philippines virus and an associated betasatellite occurring in the Philippines. *Arch. Virol.* 156, 305–312. doi: 10.1007/s00705-010-0837-3

Sharma, S., Sharma, A., and Kaur, S. I. (2019). Occurrence of pepper mottle virus on tomato in India. *Virus Dis.* 30, 474–475. doi: 10.1007/s13337-019-00543-4

Sharman, M., Thomas, J. E., Tree, D., and Persley, D. M. (2020). Natural host range and thrips transmission of capsicum chlorosis virus in Australia. *Aust. Plant Pathol.* 49, 45–51. doi: 10.1007/s13313-019-00675-7

Shates, T. M., Sun, P., Malmstrom, C. M., Dominguez, C., and Mauck, K. E. (2019). Addressing research needs in the field of plant virus ecology by defining knowledge gaps and developing wild dicot study systems. *Front. Microbiol.* 9:3305. doi: 10.3389/fmicb.2018.03305

Sherwood, J. L., German, T. L., Moyer, J. W., and Ullman, D. E. (2003). Tomato spotted wilt. *Plant Heal. Instr.* doi: 10.1094/PHI-I-2003-0613-02

Skelton, A., Buxton-Kirk, A., Ward, R., Harju, V., Frew, L., Fowkes, A., et al. (2019). First report of Tomato brown rugose fruit virus in tomato in the united kingdom. *New Dis. Rep.* 40:12. doi: 10.5197/j.2044-0588.2019.040.012

Škoric, D., Krajacic, M., Barbarossa, L., Cillo, F., Grieco, F., Šaric, A., et al. (1996). Occurrence of cucumber mosaic cucumovirus with satellite RNA in lethal necrosis affected tomatoes in croatia. *J. Phytopathol.* 144, 543–549. doi: 10.1111/j.1439-0434.1996.tb00296.x

Soler, S., Prohens, J., López, C., Aramburu, J., Galipienso, L., and Nuez, F. (2010). Viruses infecting tomato in valčncia, spain: occurrence, distribution and effect of seed origin. *J. Phytopathol.* 158, 797–805. doi: 10.1111/j.1439-0434.2010.01706.x

Souiri, A., Khataby, K., Kasmi, Y., Zemzami, M., Amzazi, S., and Ennaji, M. M. (2019). "Emerging and reemerging viral diseases of solanaceous crops and management strategies for detection and eradication," in *Emerging and Reemerging Viral Pathogens*, ed. M. M. Ennaji (Cambridge, MA: Elsevier), 847–877.

Souza, T. A., Silva, J. M. F., Nagata, T., Martins, T. P., Nakasu, E. Y. T., and Inoue-Nagata, A. K. (2020). A temporal diversity analysis of brazilian begomoviruses in tomato reveals a decrease in species richness between 2003 and 2016. *Front. Plant Sci.* 11:1201. doi: 10.3389/fpls.2020.01201

Stanković, I., Vučurović, A., Zečević, K., Petrović, B., Nikolić, D., and Delibašić, G. (2021). Characterization of cucumber mosaic virus and its satellite RNAs associated with tomato lethal necrosis in Serbia. *Eur. J. Plant Pathol.* doi: 10.1007/s10658-021-02241-8

Stanković, I., Vučurović, A., Zečević, K., Petrović, B., Ristic, D., Vucurovic, I., et al. (2020). Short communication: pepino mosaic virus, a new threat for Serbia's tomatoes. *Spanish J. Agric. Res.* 18:e10SC05. doi: 10.5424/sjar/2020184-16244

Stansly, P. A., Naranjo, S. E., Brown, J. K., Horowitz, A. R., Legg, J. P., Polston, J. E., et al. (2010). *Bemisia: Bionomics and Management of a Global Pest*. Netherlands: Springer.

Sui, X., McGrath, M. T., Zhang, S., Wu, Z., and Ling, K.-S. (2017). First report of tomato chlorotic spot virus infecting tomato in New York. *Plant Dis.* 102:460. doi: 10.1094/PDIS-07-17-0991-PDN

Sui, X., Zheng, Y., Li, R., Padmanabhan, C., Tian, T., Groth-Helms, D., et al. (2016). Molecular and biological characterization of tomato mottle mosaic virus and development of RT-PCR detection. *Plant Dis.* 101, 704–711. doi: 10.1094/PDIS-10-16-1504-RE

Tepfer, M., and García-Arenal, F. (2019). "Chapter 3: Epidemiology and Ecology," in *Cucumber Mosaic Virus*, (Saint Paul,MN: The American Phytopathological Society), 37–45.

Thompson, J. R., Dasgupta, I., Fuchs, M., Iwanami, T., Karasev, A. V., Petrzik, K., et al. (2017). ICTV virus taxonomy profile: secoviridae. *J. Gen. Virol.* 98, 529–531. doi: 10.1099/jgv.0.000779

Torres, R., Larenas, J., Fribourg, C., and Romero, J. (2012). Pepper necrotic spot virus, a new tospovirus infecting solanaceous crops in Peru. *Arch. Virol.* 157, 609–615. doi: 10.1007/s00705-011-1217-3

Trebicki, P. (2020). Climate change and plant virus epidemiology. *Virus Res.* 286:198059. doi: 10.1016/j.virusres.2020.198059

Tsai, W. S., Abdourhamane, I. K., and Kenyon, L. (2010). First report of pepper veinal mottle virus associated with mosaic and mottle diseases of tomato and pepper in Mali. *Plant Dis.* 94, 378–378. doi: 10.1094/PDIS-94-3-0378B

Turina, M., Geraats, B. P. J., and Ciuffo, M. (2016a). First report of tomato mottle mosaic virus in tomato crops in Israel. *New Dis. Rep.* 33:1. doi: 10.5197/j.2044-0588.2016.033.001

Turina, M., Kormelink, R., and Resende, R. O. (2016b). Resistance to tospoviruses in vegetable crops: epidemiological and molecular aspects. *Annu. Rev. Phytopathol.* 54, 347–371. doi: 10.1146/annurev-phyto-080615-095843

Tzanetakis, I. E., Martin, R. R., and Wintermantel, W. M. (2013). Epidemiology of criniviruses: an emerging problem in world agriculture. *Front. Microbiol.* 4:119. doi: 10.3389/fmicb.2013.00119

Tzanetakis, I. E., Sabanadzovic, S., and Valverde, R. A. (2020). *"Amalgaviruses (Amalgaviridae)," in Reference Module in Life Sciences*. Amsterdam: Elsevier.

Vaghi Medina, C. G., Bornancini, V. A., and López Lambertini, P. M. (2020). Tomato vein clearing leaf deformation virus, a new begomovirus species infecting tomato in Argentina. *Eur. J. Plant Pathol.* 156, 285–290. doi: 10.1007/s10658-019-01835-7

Vaghi Medina, C. G., and López Lambertini, P. M. (2012). Tomato dwarf leaf virus, a new world begomovirus infecting tomato in Argentina. *Arch. Virol.* 157, 1975–1980. doi: 10.1007/s00705-012-1355-2

Vaghi Medina, C. G., Martin, D. P., and López Lambertini, P. M. (2015). Tomato mottle wrinkle virus, a recombinant begomovirus infecting tomato in Argentina. *Arch. Virol.* 160, 581–585. doi: 10.1007/s00705-014-2216-y

Vaghi Medina, C. G., Teppa, E., Bornancini, V. A., Flores, C. R., Marino-Buslje, C., and López Lambertini, P. M. (2018). Tomato apical leaf curl virus: a novel, monopartite geminivirus detected in tomatoes in Argentina. *Front. Microbiol.* 8:2665. doi: 10.3389/fmicb.2017.02665

Valles, S. M., Chen, Y., Firth, A. E., Guérin, D. M. A., Hashimoto, Y., Herrero, S., et al. (2017). ICTV virus taxonomy profile: iflaviridae. *J. Gen. Virol.* 98, 527–528. doi: 10.1099/jgv.0.000757

Van Bogaert, N., Smagghe, G., and De Jonghe, K. (2015). The role of weeds in the epidemiology of pospiviroids. *Weed Res.* 55, 631–638. doi: 10.1111/wre.12173

van Brunschot, S. L., Persley, D. M., Roberts, A., and Thomas, J. E. (2014a). First report of pospiviroids infecting ornamental plants in australia: potato spindle tuber viroid in solanum laxum (synonym S. jasminoides) and citrus exocortis viroid in petunia spp. *New Dis. Rep.* 29:3. doi: 10.5197/j.2044-0588.2014.029.003

van Brunschot, S. L., Verhoeven, J. T. J., Persley, D. M., Geering, A. D. W., Drenth, A., and Thomas, J. E. (2014b). An outbreak of potato spindle tuber viroid in tomato is linked to imported seed. *Eur. J. Plant Pathol.* 139, 1–7. doi: 10.1007/s10658-014-0379-8

van de Vossenberg, B. T. L. H., Visser, M., Bruinsma, M., Koenraadt, H. M. S., Westenberg, M., and Botermans, M. (2020). Real-time tracking of tomato brown rugose fruit virus (ToBRFV) outbreaks in the netherlands using nextstrain. *PLoS One* 15:e0234671. doi: 10.1371/journal.pone.0234671

van der Vlugt, R. A. A., Stijger, C., Verhoeven, J. T. J., and Lesemann, D.-E. (2000). First report of pepino mosaic virus on tomato. *Plant Dis.* 84:103. doi: 10.1094/pdis.2000.84.1.103c

van der Vlugt, R. A. A., and Stijger, C. C. M. M. (2021). *Pepino Mosaic Virus (Alphaflexiviridae), in Encyclopedia of Virology*. Amsterdam: Elsevier, 539–544.

Varanda, C. M. R., Nolasco, G., Clara, M. I., and Félix, M. R. (2014). Genetic diversity of the coat protein of olive latent virus 1 isolates. *Arch. Virol.* 159, 1351–1357. doi: 10.1007/s00705-013-1953-7

Verbeek, M., and Dullemans, A. M. (2012). First report of tomato torrado virus infecting tomato in colombia. *Plant Dis.* 96, 592–592. doi: 10.1094/PDIS-11-11-1000

Verbeek, M., Dullemans, A. M., Espino, A., Botella, M., Alfaro-Fernández, A., and Font, M. I. (2015). First report of southern tomato virus in tomato in the canary islands, spain. *J. Plant Pathol.* 97:392. doi: 10.4454/JPP.V97I2.038

Verbeek, M., Dullemans, A. M., Van Den Heuvel, J. F. J. M., Maris, P. C., and Van Der Vlugt, R. A. A. (2007). Identification and characterisation of tomato torrado virus, a new plant picorna-like virus from tomato. *Arch. Virol.* 152, 881–890. doi: 10.1007/s00705-006-0917-6

Verbeek, M., Dullemans, A. M., van den Heuvel, J. F. J. M., Maris, P. C., and van der Vlugt, R. A. A. (2008). Tomato marchitez virus, a new plant picorna-like virus from tomato related to tomato torrado virus. *Arch. Virol.* 153, 127–134. doi: 10.1007/s00705-007-1076-0

Verdin, E., Gentit, P., Steyer, S., Wetzel, T., Le Bourgeois, T., Balesdent, M.-H., et al. (2020). *Évaluation du risque simplifiée du tomato brown rugose fruit virus pour la France métropolitaine*. Available online at: https://hal.archives-ouvertes.fr/hal-02473673 [Accessed July 28, 2020].

Verhoeven, J. T. J., Jansen, C. C. C., Botermans, M., and Roenhorst, J. W. (2010). Epidemiological evidence that vegetatively propagated, *Solanaceous* plant species act as sources of potato spindle tuber viroid inoculum for tomato. *Plant Pathol.* 59, 3–12. doi: 10.1111/j.1365-3059.2009.02173.x

Verma, N., Kumar, K., Kulshrestha, S., Raikhy, G., Hallan, V., Ram, R., et al. (2009). Molecular studies on tomato aspermy virus isolates infecting chrysanthemums. *Arch. Phytopathol. Plant Prot.* 42, 99–111. doi: 10.1080/03235400600951779

Vermunt, A. M. W., and Kaarsemaker, R. C. (2017). Multi-genotype cross-protection against pepino mosaic virus in tomato. *Crop Prot.* 96, 116–122. doi: 10.1016/j.cropro.2017.02.007

Villamor, D. E. V., Ho, T., Al Rwahnih, M., Martin, R. R., and Tzanetakis, I. E. (2019). High throughput sequencing for plant virus detection and discovery. *Phytopathology* 109, 716–725. doi: 10.1094/PHYTO-07-18-0257-RVW

Vučurović, A., Kutnjak, D., Mehle, N., Stanković, I., Pecman, A., Bulajić, A., et al. (2021). Detection of four new tomato viruses in serbia using post-hoc high-throughput sequencing analysis of samples from a large-scale field survey. *Plant Dis.*

Vučurović, A., Stanković, I., Zečević, K., Petrović, B., Delibašić, G., and Krstić, B. (2019). *First report of Tomato infectious chlorosis virus on tomato in Serbia. B. Abstr. VIII Congr. Plant Prot. Integr. Plant Prot. Sustain. Crop Prod. For. Novemb. 25-29.2019., Zlatibor, Serbia, 188.*

Webster, C. G., de Jensen, C. E., Rivera-Vargas, L. I., Rodrigues, J. C. V., Mercado, W., Frantz, G., et al. (2013). First report of tomato chlorotic spot virus (TCSV) in tomato, pepper, and jimsonweed in puerto rico. *Plant Heal. Prog.* 14:47. doi: 10.1094/PHP-2013-0812-01-BR

Webster, C. G., Frantz, G., Reitz, S. R., Funderburk, J. E., Mellinger, H. C., McAvoy, E., et al. (2014). Emergence of groundnut ringspot virus and tomato chlorotic spot virus in vegetables in Florida and the southeastern united states. *Phytopathology* 105, 388–398. doi: 10.1094/PHYTO-06-14-0172-R

Webster, C. G., Perry, K. L., Lu, X., Horsman, L., Frantz, G., Mellinger, C., et al. (2010). First report of groundnut ringspot virus infecting tomato in south Florida. *Plant Heal. Prog.* 11:49. doi: 10.1094/PHP-2010-0707-01-BR

Wisler, G. C., Li, R. H., Liu, H.-Y., Lowry, D. S., and Duffus, J. E. (1998). Tomato chlorosis virus: a new whitefly-transmitted, phloem-limited, bipartite closterovirus of tomato. *Phytopathology* 88, 402–409. doi: 10.1094/PHYTO.1998.88.5.402

WUR (2019). *Southern tomato virus: hype or a real threat? - WUR.* Available Online at: https://www.wur.nl/en/newsarticle/Southern-tomato-virus-hype-or-a-real-threat.htm [Accessed August 3, 2020]

Xu, C., Sun, X., Taylor, A., Jiao, C., Xu, Y., Cai, X., et al. (2017). Diversity, distribution, and evolution of tomato viruses in china uncovered by small RNA sequencing. *J. Virol.* 91, e117–e173. doi: 10.1128/JVI.00173-17

Xu, P., Blancaflor, E. B., and Roossinck, M. J. (2003). In spite of induced multiple defense responses, tomato plants infected with cucumber mosaic virus and D satellite RNA succumb to systemic necrosis. *Mol. Plant-Microbe Interact.* 16, 467–476. doi: 10.1094/MPMI.2003.16.6.467

Yan, Z.-Y., Ma, H.-Y., Han, S.-L., Geng, C., Tian, Y.-P., and Li, X.-D. (2019). First report of tomato brown rugose fruit virus infecting tomato in china. *Plant Dis.* 103, 2973–2973. doi: 10.1094/PDIS-05-19-1045-PDN

Yin, Y., Zheng, K., Dong, J., Fang, Q., Wu, S., Wang, L., et al. (2014). Identification of a new tospovirus causing necrotic ringspot on tomato in china. *Virol. J.* 11:213. doi: 10.1186/s12985-014-0213-0

Yin, Y. Y., Li, T. T., Lu, X., Fang, Q., Ding, M., and Zhang, Z. K. (2015). First report of capsicum chlorosis virus infecting tomato in yunnan, southwest of china. *Plant Dis.* 100:230. doi: 10.1094/PDIS-01-15-0088-PDN

Zaidi, S. S.-E.-A., Martin, D. P., Amin, I., Farooq, M., and Mansoor, S. (2017). Tomato leaf curl new delhi virus: a widespread bipartite begomovirus in the territory of monopartite begomoviruses. *Mol. Plant Pathol.* 18, 901–911. doi: 10.1111/mpp.12481

Zambrano, K., Geraud-Pouey, F., Chirinos, D., Romay, G., and Marys, E. (2011). Tomato chlorotic leaf distortion virus, a new bipartite begomovirus infecting *Solanum lycopersicum* and capsicum chinense in venezuela. *Arch. Virol.* 156, 2263–2266. doi: 10.1007/s00705-011-1093-x

Zarzyñska-Nowak, A., Rymelska, N., Borodynko, N., and Hasiów-Jaroszewska, B. (2016). The occurrence of tomato yellow ring virus on tomato in Poland. *Plant Dis.* 100, 234–234. doi: 10.1094/PDIS-05-15-0521-PDN

Zarzyñska-Nowak, A., Hasiów-Jaroszewska, B., Budzyñska, D., and Trzmiel, K. (2020). Genetic variability of polish tomato black ring virus isolates and their satellite RNAs. *Plant Pathol.* 69, 1034–1041. doi: 10.1111/ppa.13188

Zerbini, F. M., Briddon, R. W., Idris, A., Martin, D. P., Moriones, E., Navas-Castillo, J., et al. (2017). ICTV virus taxonomy profile: geminiviridae. *J. Gen. Virol.* 98, 131–133. doi: 10.1099/jgv.0.000738

Zhang, S. B., Zhang, D. Y., Liu, Y., Luo, X. W., Liu, M. Y., Du, J., et al. (2017). First report of lettuce chlorosis virus infecting tomato in china. *Plant Dis.* 101, 846–846. doi: 10.1094/PDIS-09-16-1315-PDN

Zhao, F.-F., Xi, D.-H., Liu, J., Deng, X.-G., and Lin, H.-H. (2014). First report of chilli veinal mottle virus infecting tomato (*Solanum lycopersicum*) in China. *Plant Dis.* 98, 1589–1589. doi: 10.1094/PDIS-11-13-1188-PDN

Zhu, F., Che, Y.-P., Qian, K., Zhou, Y.-K., Xu, Y.-J., Zhao, Y.-Q., et al. (2017). First report of chilli veinal mottle virus infecting *Lycopersicon esculentum* in jiangsu province in China. *Plant Dis.* 102:462. doi: 10.1094/PDIS-07-17-1100-PDN

Ziebell, H., and Carr, J. P. (2010). *Cross-Protection.* 1st Edn. Amsterdam: Elsevier Inc.

**Conflict of Interest:** The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

## 2.2 In-depth Study of Tomato and Weed Viromes Reveals Undiscovered Plant Virus Diversity in an Agroecosystem

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Published in: This is a submitted article, publicly available at *bioRxiv* doi: 10.1101/2022.06.30.498278, with supplementary materials available at *Figshare* doi: 10.6084/m9.figshare.20200769

# In-depth study of tomato and weed viromes reveals undiscovered plant virus diversity in an agroecosystem

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## Abstract

**Background**: In agroecosystems, viruses are well known to influence crop health and a few cause phytosanitary and economic problems, but their diversity in non-crop plants and role outside the disease perspective is less known. An extensive virome exploration that includes both crop and diverse weed plants is therefore needed to better understand roles of viruses in agroecosystems. Such unbiased exploration is possible through viromics, which could generate biological and ecological insights from immense high-throughput sequencing (HTS) data.

**Results**: Here, we implemented HTS-based viromics to explore viral diversity in tomatoes and weeds in farming areas at a nation-wide scale. We detected 125 viruses, including 79 novel species, wherein 65 were found exclusively in weeds. This spanned 21 higher-level plant virus taxa dominated by *Potyviridae*, *Rhabdoviridae*, and *Tombusviridae,* and four non-plant virus families. We detected viruses of non-plant hosts and viroid-like sequences, and demonstrated infectivity of a novel tobamovirus in plants of Solanaceae family. Diversities of predominant tomato viruses were variable, in some cases, comparable to that of global isolates of same species. We phylogenetically classified novel viruses, and showed links between a subgroup of phylogenetically-related rhabdoviruses to their taxonomically-related host plants. Ten classified viruses detected in tomatoes were also detected in weeds, which might indicate possible role of weeds as their reservoirs, and that these viruses could be exchanged between the two compartments.

**Conclusions**: We showed that even in relatively well studied agroecosystems, such as tomato farms, a large part of very diverse plant viromes can still be unknown and is mostly present in understudied non-crop plants. The overlapping presence of viruses in tomatoes and weeds implicate possible presence of virus reservoir and possible exchange between the weed and crop compartments, which may influence weed management decisions. The observed variability and widespread presence of predominant tomato viruses and the infectivity of a novel tobamovirus in solanaceous plants, provided foundation for further investigation of virus disease dynamics and their effect on tomato health. The extensive insights we generated from such in-depth agroecosystem virome exploration will be valuable in anticipating possible emergences of plant virus diseases, and would serve as baseline for further post-discovery characterization studies.

**Keywords**: tomato, weed, virus, viroid, virome, virus discovery, virus diversity, phylogenetics, metagenomics, viromics

## Background

The awareness on the importance of virus diseases, especially amid an on-going COVID-19 pandemic [1], increased research interest on the exploration of virus diversity across ecosystems, assisted by high-throughput sequencing (HTS) [2–4], and by exploring global nucleotide databases [5–7]. In agroecosystems, viruses are ubiquitous microbes associated with eukaryotic hosts including crop and weed plants, fungi, oomycetes, arthropods, and nematodes, as well as prokaryotes such as bacteria [8,9]. Thus, viruses could influence dynamics of plant populations and individual phytobiomes, directly, or through modulation of other ecological or environmental factors [10]. Due to the parasitic nature, high transmissibility and adaptability of plant pathogenic viruses [11], it was estimated that they account for half of emerging diseases in plants [12], and losses equivalent to around a quarter of expected crop yield [13]. Tomato (*Solanum lycopersicum* L.), which has the highest volume of vegetable production globally [14], is associated with more than 300 viruses including several that are frequently associated with disease symptoms and yield losses [15]. In recent years plant virologists have witnessed a spread of emerging tomato viruses, such as tomato brown rugose fruit virus (ToBRFV) [16] and tomato leaf curl New Delhi virus (ToLCNDV) [17]. To study such a high diversity of viruses, HTS has become the tool of choice. HTS-based viromics, coupled with bioinformatics tools, enable inference of biological, evolutionary, and ecological insights [18], which impact also fields of virus diagnostics and epidemiology [19].

With HTS, plant virology has greatly shifted from traditional focus on disease-associated relationships [18], to a scalable and unbiased ecosystems-level approach [3]. The study of plant virus pathogenesis and emergence with an ecological approach has also integrated the modulation of various environmental factors. Specifically, studies, which have been collectively reviewed in recent literature [20–22], demonstrated the importance of unmanaged weed plants surrounding cultivated areas in the distribution, ecology and emergence of viruses [23,24]. In tomato, HTS has significantly advanced virus discovery, diversity, ecological and epidemiological studies [15]. Several HTS-based studies in the recent decade have contributed to the current known set of tomato viruses. A survey of tomatoes showing virus disease-like symptoms in China uncovered the presence of 21 known and one novel viruses [25]. Similar studies reported known and novel viruses associated with individual tomato plants or a collection of tomato samples using HTS [26–28]. Findings from these studies significantly contributed to the characterization of the global tomato virome and presented several insights that an HTS-based viromics survey can provide regarding the diversity, ecology and evolution of tomato viruses. In a survey of viruses in tomato and in surrounding *Solanum nigrum* from different locations in France possible exchanges of viruses were observed between wild and cultivated plant species [23]. This suggests that more extensive studies exploring the viromes of the vast diversity of weeds surrounding crop farming areas would be needed to better understand diversity and dynamics of plant viromes in an agroecosystem.

Studies that uncovered plant viromes at the ecosystem scale have focused mainly on discovery, and its epidemiological or ecological implications [23,25,29]. Knowing which species of viruses are present in an agroecosystem and to what extent they influence the host fitness landscape will greatly aid prediction of emergence [30]. To better understand plant virus diversity, ecology and possible emergence of plant virus diseases in an agroecosystem, we selected tomato as a model crop, and investigated a very diverse set of mostly broadleaf dicotyledonous volunteer plants, including weeds (designated simply 'weeds' hereafter) surrounding selected tomato production sites in Slovenia. We examined their viromes using an HTS-based approach, followed by virus characterization, to answer the following questions: (1) How diverse and prevalent are plant viruses and other virus-/viroid-like agents in tomatoes compared to that of surrounding weeds? (2) Are there overlaps of viruses detected in tomatoes and weeds? (3) Can we identify potential weed reservoirs of known crop viruses, and do weeds harbor an under-sampled virus diversity? (4) Can we identify some viruses in weeds, or those shared between tomatoes and weeds, which could potentially emerge in tomato? (5) What are the phylogenetic relationships of known and novel viruses to known taxa?

This study represented the largest simultaneous survey of viromes of diverse weed species and a crop (tomato) within a cropping system. Our approach can be used to gain insights on plant virus' diversity and dynamics in the wild-cultivated agroecological interface, a known zone for virus spillovers [11,31,32]. The virome dataset could also aid in future tomato virus disease monitoring, thus possibly contributing to the prevention of future virus epidemics in tomato.

## Methods

### Sample collection and processing

Tomato and weed plants, within or in the immediate surroundings of tomato farming fields or greenhouses were collected in Slovenia during summer of 2019 and 2020. Fourteen farms at six different localities were visited, spanning central (Dol pri Ljubljani, 1 farm), west (Miren-Kostanjevica, 2 farms; Nova Gorica, 1 farm), southwest (Koper, 4 farms; Piran, 3 farms), and southeast (Novo Mesto, 3 farms) regions of Slovenia. A total of 436 samples were collected, full details of which are in Supplementary Table 1. Asymptomatic tomatoes were randomly sampled within an area, while symptomatic tomatoes and weeds were selectively sampled based on appearance of virus disease-like symptoms most commonly shown as foliar discoloration (*e.g.,* chlorosis, mosaic, yellowing), leaf deformation (*e.g.,* folding, curling), fruit deformation (*e.g.,* mottling, marbling), and systemic symptoms (*e.g.,* general stunting, rosetting), among others. Selected photographs of collected plants, with a notion of associated detected viruses, are shown in Supplementary Fig. 3 and Supplementary Table 9. Most tomato samples collected were in the early fruiting or fruit harvesting stage, while the most weed plants were sampled at the mature or flowering stage. To aliquot tissues for RNA extraction, leaves or fruits were obtained equally from different parts of the plant to account for possible uneven distribution of viruses within the plants. Leaf and fruit tissues were separately aliquoted in cases where these were collected from a single plant. Collected tissues were stored at -80°C.

### RNA extraction and sequencing

Total RNAs were extracted from individual plant samples using RNeasy Plant Mini Kit (Qiagen, USA). RNA quality and quantity were checked using QuBit fluorometer (Thermo Fisher Scientific, USA), and NanoDrop spectrophotometer (Thermo Fisher Scientific, USA). RNAs were then pooled equimolarly into composite samples based on plant type (*i.e.*, tomato or weed), health status (*i.e.*, symptomatic or asymptomatic), and the sampling location (Supplementary Table 2). A total of 67 composite samples were cleaned, concentrated and treated with DNase (RNA Clean and Concentrator, Zymo Research, USA). Alien controls from total RNAs extracted from *Phaseolus vulgaris* infected with Phaseolus vulgaris alphaendornavirus 1, Phaseolus vulgaris alphaendornavirus 2 and Phaseolus vulgaris alphaendornavirus 3 were included into each sequencing run. The 2019 and 2020 sample set were separately sent to Macrogen, Inc. (South Korea), for library preparation and high-throughput sequencing. Sequencing libraries, including depletion of ribosomal RNA using Ribo-Zero rRNA Removal Kit (Plant) (Illumina, USA), were prepared suitable for 150 bp paired-end sequencing using TruSeq RNA Library Prep Kit (Illumina, USA) and sequenced using Illumina HiSeq 2500 platform.

Total RNAs from inoculated plants (discussed below) were extracted as mentioned above and depleted of ribosomal RNA using RiboMinus$^{TM}$ Plant Kit (Invitrogen, USA), then ligated with poly-A sequences using E. coli Poly(A) polymerase (NEB #M0276, UK). Library preparation was done using the PCR-cDNA Barcoding kit (SQK-PCB109, version 10Oct2019, Oxford Nanopore Technologies, UK), prior to sequencing using Oxford Nanopore Technologies MinION platform (Oxford Nanopore Technologies, UK) and base-calling following a previously described workflow [33].

### Sequence quality screening, trimming and virus genome assembly

Raw reads were trimmed, screened for quality and analyzed following a previously described pipeline for plant virus detection using HTS [34]. Contigs were primarily assembled from the filtered reads using CLC Genomics Workbench (GWB) v. 20 [34] (Qiagen, USA). Within the used pipeline, virus and virus-like reads and contigs were initially identified by mapping trimmed reads/contigs to virus RefSeq database (version from Jul. 2020) [35] and viral domains searches in contigs against pFam database v. 33. Candidate viral contigs were later confirmed by homology search using BLASTn against the NCBI nucleotide (nt) and BLASTx [36] against NCBI non-redundant protein (nr) databases from Dec. 2020. Assembly in metaSPAdes v. 3.14 [37] was also implemented to recover longer contigs in some cases, where these were not assembled in CLC-GWB. Consensus genome sequences of detected viruses were reconstructed using de-novo assembled contigs and/or iterative reads mapping to the most similar reference sequences obtained from NCBI GenBank. Since datasets were derived from pooled samples, consensus viral genomes were reconstructed only for the viruses with observed low to moderate population diversity (determined after manual inspection of the mapping files), indicative of infection with a single viral lineage. As a final checkup, mapping of reads of corresponding datasets to reconstructed consensus virus genomes was implemented (with 95% identity and read length fraction). Overall sequencing results and statistics, and information on sequencing read archive (SRA) metadata are given in Supplementary Table 3. The internal controls were used to check the prevalence of sequencing cross-talks. A threshold of <0.00001% of total reads in the library was set, based on the general virome composition of the internal controls, to classify sequences as either a possible contamination, crosstalk, or low titer virus infection.

For the sequences obtained from inoculated plants (discussed below) using MinION platform, quality screening was done following a customized workflow [33], that uses the programs from the NanoPack program [38] for quality screening and visualization. Reads were assembled using Racon [39]. The mapping program Minimap2 [40] run in Geneious Prime software v. 2022.1.1 (Dotmatics, USA), was used for mapping reads to viral RefSeq (version from May 2022) and consensus genomes of viruses detected in this study.

**Virus genome annotation and classification**

Genomes of detected viruses were annotated using the ORF prediction tool in CLC-GWB v. 20, and checked based on known genome organization and open reading frame composition reported in the ICTV website [41], and in peer-reviewed publications. InterProScan was used to identify known and unknown protein domains [42], and in the case of potyviruses, homology alignment in BLASTp (E-val<$10^{-4}$) with well-characterized known species was implemented to detect gene products and their start and cleavage sites [43]. Viruses were taxonomically classified based on the percent pairwise identity obtained in SDT v1. 2[44], and other genomic criteria imposed by the ICTV [41], as of Oct. 31, 2021. Multiple sequence alignments were made for each genus or family based on the recommended gene or genome segment by the ICTV. Unaligned ends were trimmed, and trimmed alignments were used for pairwise identity comparisons. Details of the genes or genome segments used, and the results of the pairwise identity comparisons are indicated in Supplementary Tables 23-42. Classifications were then confirmed by analyses of phylogenetic relationships with known virus taxa (described below).

### Genome assembly and screening for putative viroids

Viroid-like circular RNAs were assembled using the SLS-PFOR2 program [45]. BLASTn searches [36] against the NCBI nt database and BLASTx searches against NCBI nr database, from Dec. 2020, were implemented to filter out sequences from known organisms, and sequences that code for proteins (E-val$<10^{-4}$). Filtered contigs were re-examined by remapping (95% identity and read length fraction) virtually-diced reads (generated as a part of SLS-PFOR2 pipeline) and trimmed reads to the assembled circular RNAs. Contigs with average mapping depth below 10 were manually discarded. Contigs were again filtered based on the presence of two or more rotationally identical contigs of the same length (*i.e.*, indicating the presence of (+) and (-) strands). After selecting for rotational identical contigs, presence of viroid-like secondary structure motifs (*e.g.,* avsunviroid hammerhead ribozyme and rod-like pospiviroid structures) were predicted using forna [46]. Low structural Gibbs free energy and visual inspections such as high degree of base paring, or degree of branching were the criteria used to preliminarily select for putative novel viroids.

### RT-PCR assays and Sanger sequencing

PCR primers were designed using Primer3Plus [47], and RT-PCR assays were designed to identify individual plant host(s) of selected viruses detected using HTS of pooled samples (Supplementary Table 7). RT-PCRs were performed using OneStep RT-PCR kit (Qiagen, USA) with thermocycling program conditions given in Supplementary Table 8. To confirm genome circularity of viroid-like circular RNAs, abutting primers for inverse RT-PCR were manually designed as previously described [45] (Supplementary Fig. 2). Amplicons were visualized in 1% agarose gel, stained with ethidium bromide. When PCR amplicons need to be sequenced, to confirm sequence identity or circularity in the viroid-like sequences, they were purified using QIAquick PCR purification kit (Qiagen, USA), and sent at Eurofins Genomics, Germany. Amplicon sequences were visualized and trimmed in CLC-GWB v. 20. Final sequences were remapped (95% identity and read length fraction) to the target virus genome to confirm its identity, or to putative viroid genome to confirm its circularity (Supplementary Fig. 2). Photos of identified plant hosts are in Supplementary Fig. 3.

### Phylogenetic analyses

Phylogenetic analyses were performed to investigate taxonomic positions of detected newly discovered and known viruses from different taxonomic groups (Supplementary Table 10). Conserved amino acid sequences of viruses (mainly conserved parts of RNA-dependent RNA polymerase (RdRp) (methyl transferase, helicase or CP were used in some cases) for RNA viruses, replicase (C1) protein for geminivirus and reverse transcriptase (RT) for caulimovirus) detected in this study were aligned with corresponding viral RefSeq amino acid sequences of viruses within a recognized virus family, in addition to selected BLASTp hits (E-val$<10^{-4}$). For multiple sequence alignment, ClustalW [48] was used as implemented in CLC-GWB v. 20. Non-aligned sequences at both ends were trimmed after alignment. Realignment of trimmed sequences was done using MAFFT [49] and further processed with trimAI [50].

In the case of tobamoviruses, a nucleotide-based phylogenetic analyses were done on full genomes. Genomes of different isolates gathered from GenBank and viral RefSeq database, were aligned using MUSCLE [51], and checked for possible recombinants in RDP v. 4 [52]. All recombination events with $p$-val$<10^{-4}$ reported by at least four methods were considered significant. Phylogenetic analyses were performed on alignments free of recombinants.

For both, protein and nucleotide alignments, maximum likelihood phylogenetic analyses were inferred in MEGA X [53], after the selection of the most suitable substitution models. Details on the sequence sets for each analysis, and the parameters used in the analyses are in

Supplementary Table 10. The phylogenetic trees were visualized and edited in iToL v. 6.4 [54]. To investigate possible structuring of virus species in phylogenetic trees by associated host plants, plant host cladograms were generated in phyloT v. 2 (https://phylot.biobyte.de/) [54], based on NCBI Taxonomy. Host associations were based on information on the specific accession in NCBI GenBank of the virus isolate of tobamoviruses in Fig. 7, and all isolates of species for rhabdoviruses in Fig. 5. Connections were manually inferred between viral and plant phylogram and cladogram and visually inspected.

### Genome-wide molecular diversity analyses

Tomato viruses which have at least three isolates detected with full genomes reconstructed, including their isolates from weed samples, were included in the calculation of percent pairwise identities and polymorphisms. Full genome nucleotide sequences of selected viruses were aligned using MUSCLE [51] in MEGA X [53], and unaligned ends were trimmed thereafter. Genome segments of multi-segmented virus genomes were concatenated after trimming. Percent pairwise identities and number of polymorphic sites were calculated using SDT v. 1.2 [44]. For two newly discovered viruses, the aligned sequences were used to calculate genome-wide polymorphisms and nucleotide diversities ($\pi$) in DnaSP v. 6 [55] in sliding windows of 100 bases and step size of 5.

### Infectivity tests and transmission electron microscopy (TEM)

Further characterization studies were performed to test the infectivity and visualize the virions of newly discovered Plantago tobamovirus 1 (PTV1). Five plants each of *Solanum lycopersicum, Nicotiana benthamiana,* and *Nicotiana clevelandii,* were used in the inoculation experiments, with additional two plants each as mock inoculated controls. Plants were inoculated at the four-leaf stage. The source of inoculum for PTV1 was the original *Plantago major* infected sample from the field. Mechanical inoculation of infected plant sap, diluted 1:10

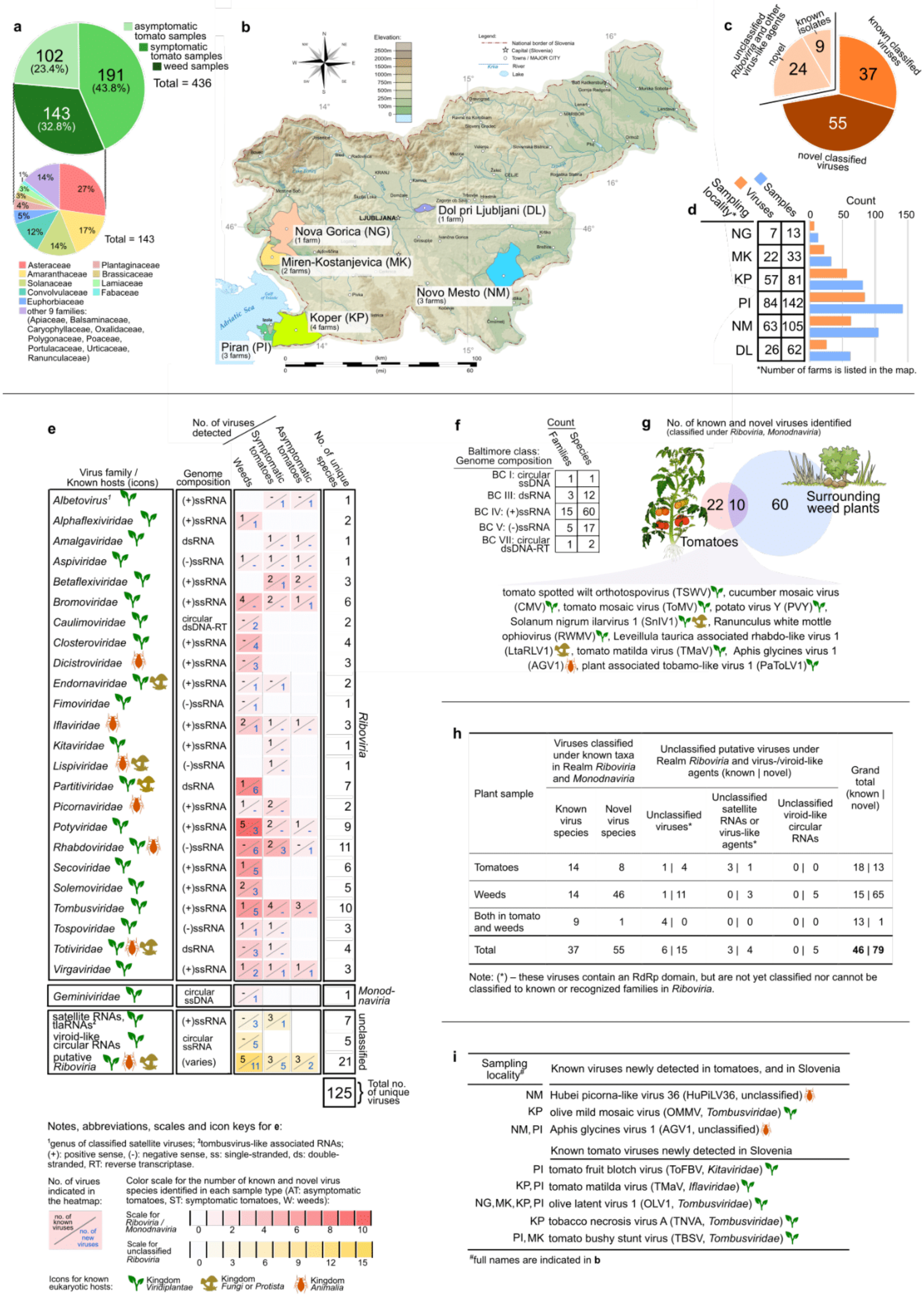
in phosphate buffer, was done on two leaves (second and third youngest), dusted with carborundum, as previously described [56]. The plants were kept in a controlled environment at 20-24°C, with 16 h daylight and 8 h darkness. Inoculated leaves were tested in pools for the presence of the target virus on 7th and 14th day post inoculation (dpi) in RT-PCR assays. Systemic leaves of inoculated plants were tested for the presence of the PTV1 using RT-PCR assays, wherein pooled newly grown (uninoculated) leaves at 14, 21, 28 and 35 dpi were used. TEM was done to confirm the presence of the virus particles in inoculated *N. clevelandii* plants. Tissue homogenates were applied to Formvar-coated, carbon-stabilized copper grids, and negatively stained with 1% uranyl acetate (SPI Supplies, PA, USA), before inspection in TEM. To associate the observed disease symptoms with the presence of PTV1, pool of five inoculated *N. clevelandii* plant showing virus disease-like symptoms and tested positive for PTV1 was collected at 21 dpi and analyzed using nanopore sequencing as described in section ' RNA extraction and sequencing' above.

## Results

### Overview of viruses detected in tomatoes and weeds and observed patterns of viral presence and diversity

Tomato (n=293), and weed (n=143, 59 species in 18 families) plant samples, were collected from six localities in Slovenia, wherein 14 farms were visited in 2019 and/or 2020 (Fig. 1a-b, for details see Supplementary Tables 1-3). Sequencing of pooled ribosomal (r)RNA-depleted total RNAs (*i.e.,* composite samples) from these samples, and subsequent bioinformatics analyses revealed 126 viruses (Fig. 1c), of which 37 are known and 55 are novel classified viruses that could be classified up to known species taxa (46 are exclusively from weeds). The remaining 33 viruses are either isolates of known viruses, which were not yet classified under established taxa in *Riboviria* (n=9), or unclassified putative novel *Riboviria,* satellite RNAs, and viroid-like circular RNAs (n=24, 19 are exclusively from weeds). Thus, the total of novel viruses discovered is 79, of which 65 were found exclusively in weed plants (Fig. 1h, for details see Supplementary Tables 4-6). Farms from the coastal region of SW Slovenia (Piran and Koper), where 51% of the samples were collected, have the highest count of virus species detected (*i.e.,* 57 viruses in Koper and 84 viruses in Piran) (Fig. 1d). The viruses were classified in 21 known plant virus taxa, and four other families that are known to be associated with other eukaryotic hosts (*Dicistroviridae, Iflaviridae, Lispiviridae,* and *Picornaviridae*) (Fig. 1e). Majority of the detected viruses were from 15 taxa of positive sense (+) single-stranded (ss) RNA viruses (n=60), followed by four families of negative sense (-) ssRNA viruses (n=17) (Fig. 1f). Ten viruses were found both in tomato and weed composite samples from several localities, eight of which are most likely plant-infecting. Some of the ten overlapping viruses are known to have wide host range, and are endemic in tomato (*i.e.,* tomato spotted wilt orthotospovirus (TSWV), cucumber mosaic virus (CMV), tomato mosaic virus (ToMV), and potato virus Y (PVY)) [15] (Fig. 1g). Viruses recently detected in tomato (*i.e.,* Solanum nigrum ilarvirus 1 (SnIV1), Ranunculus white mottle ophiovirus (RWMV), tomato matilda virus (TMaV)) [23,57–59], a known insect (Aphis glycines virus 1 (AGV1)) and a known fungal (Leveillula taurica associated rhabdo-like virus 1 (LtaRLV1)) virus, and a novel virus (plant associated tobamo-like virus 1 (PaToLV1)) were also detected in both sample types. Among the viruses detected both in tomatoes and weeds, there were several cases in which we could detect the same virus within the same location in both sample types: seven viruses (TSWV, CMV, ToMV, PaToLV1, LtaRLV1, PVY, and TMaV) with such pattern were observed.

Three known viruses were detected for the first time both in tomatoes and in Slovenia, and five others were detected for the first time in the country, (*i.e.*, were not reported before in local comprehensive records) [60] (Fig. 1i). Lastly, other known crop viruses were detected in composite weed samples, including two potyviruses (watermelon mosaic virus (WMV) and carrot thin leaf virus (CTLV)), ilarvirus (Prunus virus I (PrVI)), closterovirus (beet yellows virus), luteovirus (soybean dwarf virus), cucumovirus (peanut stunt virus), fabavirus (broad bean wilt virus 1), polerovirus (barley virus G), and potexvirus (white clover mosaic virus).



**d**

| Sampling locality* | Viruses | Samples |
|---|---|---|
| NG | 7 | 13 |
| MK | 22 | 33 |
| KP | 57 | 81 |
| PI | 84 | 142 |
| NM | 63 | 105 |
| DL | 26 | 62 |

*Number of farms is listed in the map.

**e**

No. of viruses detected

| Virus family / Known hosts (icons) | Genome composition | Weeds | Symptomatic tomatoes | Asymptomatic tomatoes | No. of unique species |
|---|---|---|---|---|---|
| *Albetovirus*[1] 🌱 | (+)ssRNA | | - / 1 | - / 1 | 1 |
| *Alphaflexiviridae* 🌱 | (+)ssRNA | 1 / 1 | | | 2 |
| *Amalgaviridae* 🌱 | dsRNA | | 1 / - | 1 / - | 1 |
| *Aspiviridae* 🌱 | (-)ssRNA | 1 / - | 1 / - | 1 / - | 1 |
| *Betaflexiviridae* 🌱 | (+)ssRNA | | 2 / 1 | 2 / - | 3 |
| *Bromoviridae* 🌱 | (+)ssRNA | 4 / - | 2 / - | 1 / 1 | 6 |
| *Caulimoviridae* 🌱 | circular dsDNA-RT | - / 2 | | | 2 |
| *Closteroviridae* 🌱 | (+)ssRNA | - / 4 | | | 4 |
| *Dicistroviridae* 🐞 | (+)ssRNA | - / 3 | | | 3 |
| *Endornaviridae* 🌱 🍄 | (+)ssRNA | - / 1 | - / 1 | | 2 |
| *Fimoviridae* 🌱 | (-)ssRNA | - / 1 | | | 1 |
| *Iflaviridae* 🐞 | (+)ssRNA | 2 / 1 | 1 / - | 1 / - | 3 |
| *Kitaviridae* 🌱 | (+)ssRNA | | 1 / - | | 1 |
| *Lispiviridae* 🐞 🍄 | (-)ssRNA | | 1 / - | | 1 |
| *Partitiviridae* 🌱 🍄 | dsRNA | 1 / 6 | | | 7 |
| *Picornaviridae* 🐞 | (+)ssRNA | 1 / - | 2 / - | | 2 |
| *Potyviridae* 🌱 | (+)ssRNA | 5 / 3 | 2 / - | 1 / - | 9 |
| *Rhabdoviridae* 🌱 🐞 | (-)ssRNA | - / 6 | 2 / 3 | - / 1 | 11 |
| *Secoviridae* 🌱 | (+)ssRNA | 1 / 5 | | | 6 |
| *Solemoviridae* 🌱 | (+)ssRNA | 2 / 3 | | | 5 |
| *Tombusviridae* 🌱 | (+)ssRNA | 1 / 5 | 4 / - | 3 / - | 10 |
| *Tospoviridae* 🌱 | (-)ssRNA | 1 / 1 | 1 / - | | 3 |
| *Totiviridae* 🌱 🐞 🍄 | dsRNA | - / 3 | 1 / - | | 4 |
| *Virgaviridae* 🌱 | (+)ssRNA | 1 / 2 | 1 / 1 | 1 / 1 | 3 |
| *Geminiviridae* 🌱 | circular ssDNA | - / 1 | | | 1 |
| satellite RNAs, tlaRNAs[2] 🌱 | (+)ssRNA | - / 3 | 3 / 1 | | 7 |
| viroid-like circular RNAs 🌱 | circular ssRNA | - / 5 | | | 5 |
| putative *Riboviria* 🌱 🐞 🍄 | (varies) | 5 / 11 | 3 / 5 | 3 / 2 | 21 |
| | | | | | 125 |

125 } Total no. of unique viruses

Notes, abbreviations, scales and icon keys for **e**:

[1]genus of classified satellite viruses; [2]tombusvirus-like associated RNAs; (+): positive sense, (-): negative sense, ss: single-stranded, ds: double-stranded, RT: reverse transcriptase.

No. of virues indicated in the heatmap: no. of known viruses / no. of new viruses

Color scale for the number of known and novel virus species identified in each sample type (AT: asymptomatic tomatoes, ST: symptomatic tomatoes, W: weeds):

Scale for *Riboviria* / *Monodnaviria*: 0 2 4 6 8 10

Scale for unclassified *Riboviria*: 0 3 6 9 12 15

Icons for known eukaryotic hosts: 🌱 Kingdom *Viridiplantae* 🍄 Kingdom *Fungi* or *Protista* 🐞 Kingdom *Animalia*

**f**

| Baltimore class: Genome composition | Count: Families | Count: Species |
|---|---|---|
| BC I: circular ssDNA | 1 | 1 |
| BC III: dsRNA | 3 | 12 |
| BC IV: (+)ssRNA | 15 | 60 |
| BC V: (-)ssRNA | 5 | 17 |
| BC VII: circular dsDNA-RT | 1 | 2 |

**g** No. of known and novel viruses identified (classified under *Riboviria, Monodnaviria*)

tomato spotted wilt orthotospovirus (TSWV)🌱, cucumber mosaic virus (CMV)🌱, tomato mosaic virus (ToMV)🌱, potato virus Y (PVY)🌱, Solanum nigrum ilarvirus 1 (SnIV1)🌱🍄, Ranunculus white mottle ophiovirus (RWMV)🌱, Leveillula taurica associated rhabdo-like virus 1 (LtaRLV1)🍄, tomato matilda virus (TMaV)🌱, Aphis glycines virus 1 (AGV1)🐞, plant associated tobamo-like virus 1 (PaToLV1)🌱

**h**

| Plant sample | Viruses classified under known taxa in Realm *Riboviria* and *Monodnaviria* | | Unclassified putative viruses under Realm *Riboviria* and virus-/viroid-like agents (known \| novel) | | | Grand total (known \| novel) |
|---|---|---|---|---|---|---|
| | Known virus species | Novel virus species | Unclassified viruses* | Unclassified satellite RNAs or virus-like agents* | Unclassified viroid-like circular RNAs | |
| Tomatoes | 14 | 8 | 1 \| 4 | 3 \| 1 | 0 \| 0 | 18 \| 13 |
| Weeds | 14 | 46 | 1 \| 11 | 0 \| 3 | 0 \| 5 | 15 \| 65 |
| Both in tomato and weeds | 9 | 1 | 4 \| 0 | 0 \| 0 | 0 \| 0 | 13 \| 1 |
| Total | 37 | 55 | 6 \| 15 | 3 \| 4 | 0 \| 5 | **46 \| 79** |

Note: (*) – these viruses contain an RdRp domain, but are not yet classified nor cannot be classified to known or recognized families in *Riboviria*.

**i**

| Sampling locality# | Known viruses newly detected in tomatoes, and in Slovenia |
|---|---|
| NM | Hubei picorna-like virus 36 (HuPiLV36, unclassified) 🐞 |
| KP | olive mild mosaic virus (OMMV, *Tombusviridae*) 🌱 |
| NM, PI | Aphis glycines virus 1 (AGV1, unclassified) 🐞 |
| | Known tomato viruses newly detected in Slovenia |
| PI | tomato fruit blotch virus (ToFBV, *Kitaviridae*) 🌱 |
| KP, PI | tomato matilda virus (TMaV, *Iflaviridae*) 🌱 |
| NG, MK, KP, PI | olive latent virus 1 (OLV1, *Tombusviridae*) 🌱 |
| KP | tobacco necrosis virus A (TNVA, *Tombusviridae*) 🌱 |
| PI, MK | tomato bushy stunt virus (TBSV, *Tombusviridae*) 🌱 |

#full names are indicated in **b**

**Figure 1**

**Figure 1 | Diversity and distribution of samples and viruses detected in tomatoes and weeds surrounding tomato farms. a** Pie chart showing proportion of sample count per sample type, and separately for weed samples, proportion of sample count per plant family. **b** Map showing the geographical locations where sampling was done. Farm codes are indicated for each locality. **c** Overall count of viruses, with (near) complete genomes, identified from this study, distributed as proportion of known, novel and unclassified *Riboviria* species. **d** Bar plot summarizing the number of samples collected, and viruses detected in each sampling locality. **e** Heatmap showing the diversity of identified viruses by genome composition, their distribution in each known virus taxa by sample type, and the known eukaryotic host (Kingdom) of each virus taxa. **f** Summary of count of identified viruses based on Baltimore class or genome composition. **g** Venn diagram showing the number of identified known and novel viruses found exclusively in tomato or weed composite samples, and the viruses found in both sample types. Credit: Images or icons used in the figure were from https://freesvg.com/, and are under Public Domain (CC0 license, https://creativecommons.org/licenses/publicdomain/). The map of Slovenia was derived from work of Andrei Nacu uploaded in Wikimedia Commons, the free media repository, under the Public Domain (CC0 license). The authors and publisher remain neutral with regard to jurisdictional claims in published maps.

To get general insights into the association of detected viruses with observed disease symptoms, we have compared the number and overlap of detected viruses in sampled symptomatic and asymptomatic tomatoes. Out of the 45 viruses detected in tomato composite samples, only four (8.9%) were exclusively detected in asymptomatic tomatoes, and 23 (51.1%) exclusively in symptomatic tomatoes (Fig. 2a). Eighteen (40.0%) viruses were detected in both types of tomato samples, of which, six (*i.e.,* southern tomato virus (STV), CMV, PVY, olive latent virus 1 (OLV1), TMaV, and ToMV) were detected in at least six composite samples. A total of seven new viruses, and eight known but still unclassified arthropod, fungal and oomycete viruses were detected in tomatoes. Using RT-PCR assays (for details, see Methods and Supplementary Table 7), we confirmed the presence of a subset of mostly novel viruses in weeds and tomatoes, and identified key hosts that could be potential transmission hubs, or alternate hosts (Fig. 2b, for details see Supplementary Table 9). Some examples include: SnIV1 detected in tomatoes and in another weed host, *Physalis* sp.*,* from a single farm*,* PaToLV1 detected in tomatoes and in *Convolvulus arvensis* also in a single farm*,* and TMaV detected in tomatoes and in three other weed species (*i.e., Chenopodium* sp., *Ranunculus repens,* and *Erigeron annuus*) that span five localities. RWMV was detected both in *Solanum nigrum,* and in four pools of tomato samples from three different localities. Twelve novel viruses (discussed in succeeding sections), including six rhabdoviruses and three tombusviruses, were detected in four Asteraceae species (*i.e., Picris echoides, Cichorium intybus, Taraxacum officinale,* and *Cirsium arvense*).

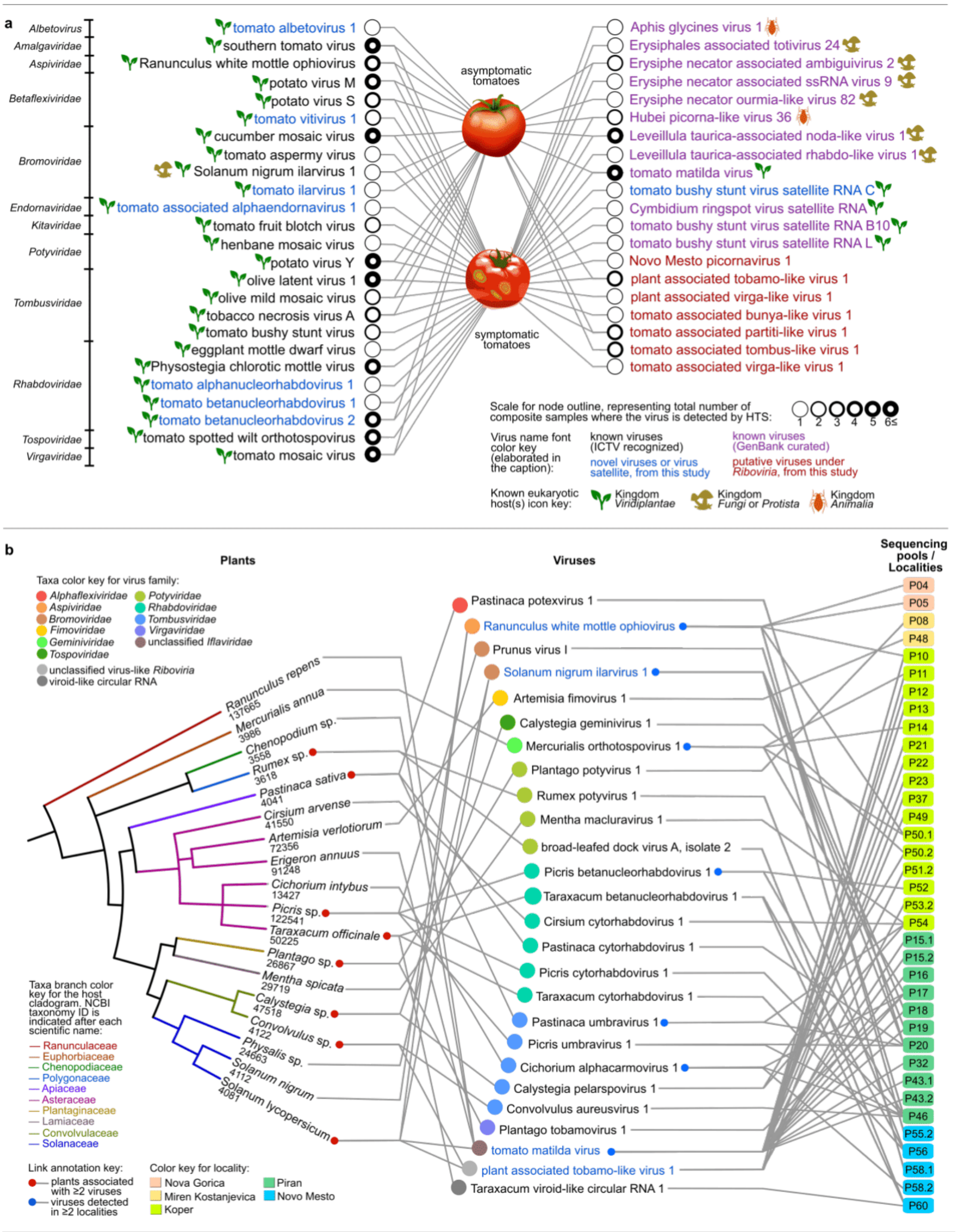


Figure 2

**Figure 2 | Connectivity and overlaps of viruses detected in different sample types. a** Bipartite network showing detection of viruses in composite symptomatic and asymptomatic tomato samples from the present study. The node represents the viruses, in which outline thickness is weighted based on the number of composite samples where the virus was detected by HTS. The lines connect viruses with a sample type in which they were detected. Virus names are color coded according to classification status: known viruses are either officially recognized ICTV species (black font), or viruses that are deposited and classified in GenBank, but not ICTV-recognized (purple). Novel viruses from this study, which are classified up to the species level, are in blue font, while putative viruses without any official classification yet are in red font. **b** Plant-virus-sample pool tripartite network, showing the connectivity of the subset of viruses detected in weeds with associated hosts. Shown in the network is the subset of novel viruses detected in weeds by HTS, which were further associated with specific host species (NCBI taxonomy IDs are shown) using RT-PCR assays or deduction from HTS data (for tomato, which was not pooled with other species). Virus names in blue font are those detected in both tomato and weed samples by HTS and RT-PCR. Credit: Images and icons used in the figure were from www.freesvg.com, and are under Public Domain (CC0 license, https://creativecommons.org/licenses/publicdomain/).

To gain further insights on the population genomic diversity of the most prevalent tomato viruses, we examined populations of 12 viruses (viruses for which we were able to assemble at least three full genomes). STV, ToMV, TMaV and TSWV showed the narrowest range of pairwise nucleotide identities, lowest nucleotide diversity and number of polymorphic sites, while Physostegia chlorotic mottle virus (PhCMoV), RWMV, and potato virus S (PVS) have a moderate level of diversity (Fig 3a, Supplementary Tables 11-22). PVY, CMV, potato virus M (PVM), tomato betanucleorhabdovirus 2 (TBRV2), and tomato vitivirus 1 (TomV1) showed wide range of pairwise nucleotide identities and high number of polymorphic sites (Fig 3a, Supplementary Tables 11-22). Sliding window analysis of nucleotide diversity for two novel tomato viruses found in Slovenia (TBRV2 and TomV1), did not pinpoint specific regions of their genomes that might be more variable than others (Fig. 3b-c). Divergent lineages detected for both TBRV2 and TomV1, resulted in a high genome-wide variability depicted as fluctuations of nucleotide diversity along the genome (Fig. 3b-c).

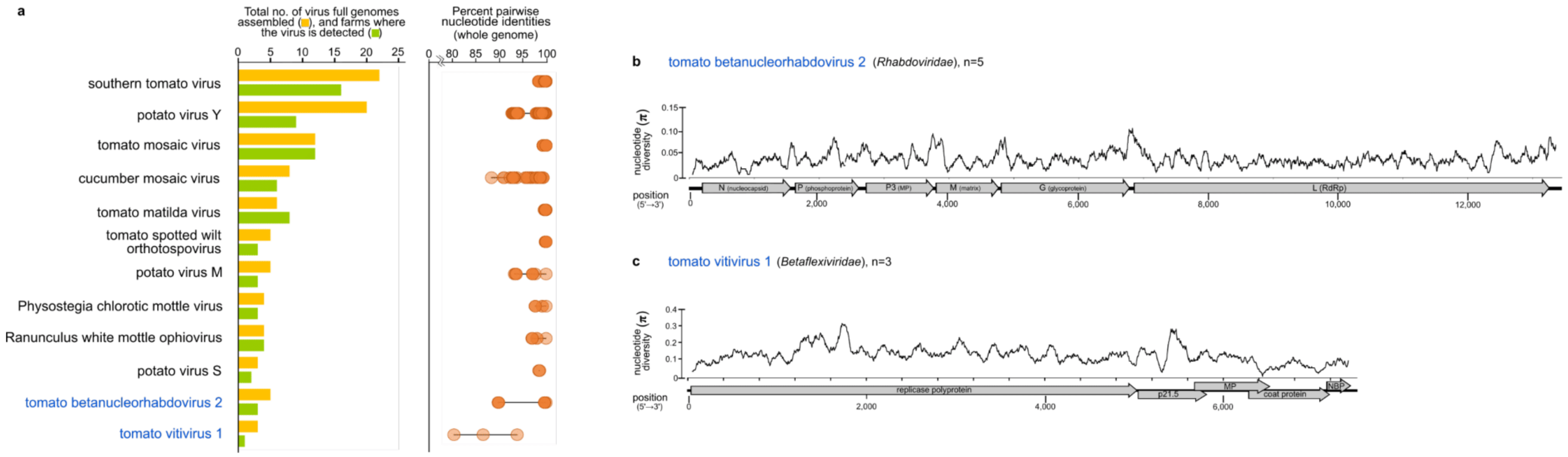


Figure 3

**Figure 3 | Molecular diversity and genome-wide variability of most frequently detected tomato viruses in this study. a** Pairwise nucleotide identities of populations of tomato viruses from Slovenia. Isolates of tomato viruses from weed samples, were included in the calculation of pairwise identities. **b, c** Genome-wide nucleotide diversity of novel viruses in tomatoes from Slovenia with at least three isolates. All open reading frames and protein domain cleavage sites are shown for each virus genome.

### (-)ssRNA viruses in tomatoes and weeds: discovery of novel orthotospovirus, an ophiovirus, and a divergent bunya-like virus

Several (-)ssRNA viruses were detected in both, tomatoes and weeds. A novel orthotospovirus, Mercurialis orthotospovirus 1 (MerV1), was detected in *Mercurialis annua* (Fig. 4a) in four composite samples from three localities. Pairwise comparison of RNA-dependent RNA polymerase (RdRp) amino acid (aa) sequences showed 72.4-76.0% identity of MerV1 to related *Tospoviridae* species. MerV1 has genome segments similar to plant orthotospoviruses (Fig. 4b,e). Phylogenetic analyses based on conserved RdRp aa sequences of orthotospoviruses revealed that MerV1 is related to viruses in phylogroup C (*i.e.,* a clade of phylogenetically-related orthotospoviruses) [61] (Fig. 4i).

A novel fimovirus, Artemisia fimovirus 1 (ArtV1) was detected in *Artemisia verlotiorum.* It is 30.2-46.1% identical to related *Fimoviridae* species based on RdRp aa comparison, and has genome organization similar to plant fimoviruses (Fig. 4a,c,f). Phylogenetic analyses with known fimoviruses revealed that ArtV1 is related to *Perilla mosaic virus,* making it the fourth member of the divergent phylogroup IV of *Fimoviridae* (*i.e.,* a clade of phylogenetically-related fimoviruses) [62,63] (Fig. 4i).

A novel bunya-like virus, closely related to *Fimoviridae* and *Tospoviridae,* was detected in seven symptomatic tomatoes using RT-PCR assays, thus named tomato associated bunya-like virus 1 (TaBLV1). Pairwise comparison of RdRp aa sequences showed that TaBLV1 is only 20.8-22.4% identical to closely related bunyaviruses, however, only L- and M-like genome segments were found for TaBLV1 (L, M and S segments are characteristic of plant-infecting orthotospoviruses) (Fig. 4a,g). TaBLV1 is more closely related to orthotospoviruses based on RdRp phylogenetic analyses (Fig. 4i).

We assembled for the first time, the full genome of RWMV, which was previously detected in tomatoes and peppers in Slovenia [57] (Fig. 4a,d,h). Using RT-PCR assays, RWMV was detected in three different localities, in eight tomatoes, and one *S. nigrum*, which is a newly identified associated host. All RWMV isolates form a single clade (100% bootstrap support (BS)), but Slovenian isolates cluster separately (98.9% BS) from the Australian and Italian subclade (96.6% BS) (Fig. 4j). For details of the pairwise comparisons, see Supplementary Table 23-25. Phylogenetic trees where the subtrees in Fig. 4 were derived depicting *Tospoviridae* and *Fimoviridae* families in one tree, and *Aspiviridae* with other related viruses in one tree, are shown in Supplementary Fig. 4-01 and 4-02, where the GenBank accession numbers of the sequences used in the analyses are also indicated.

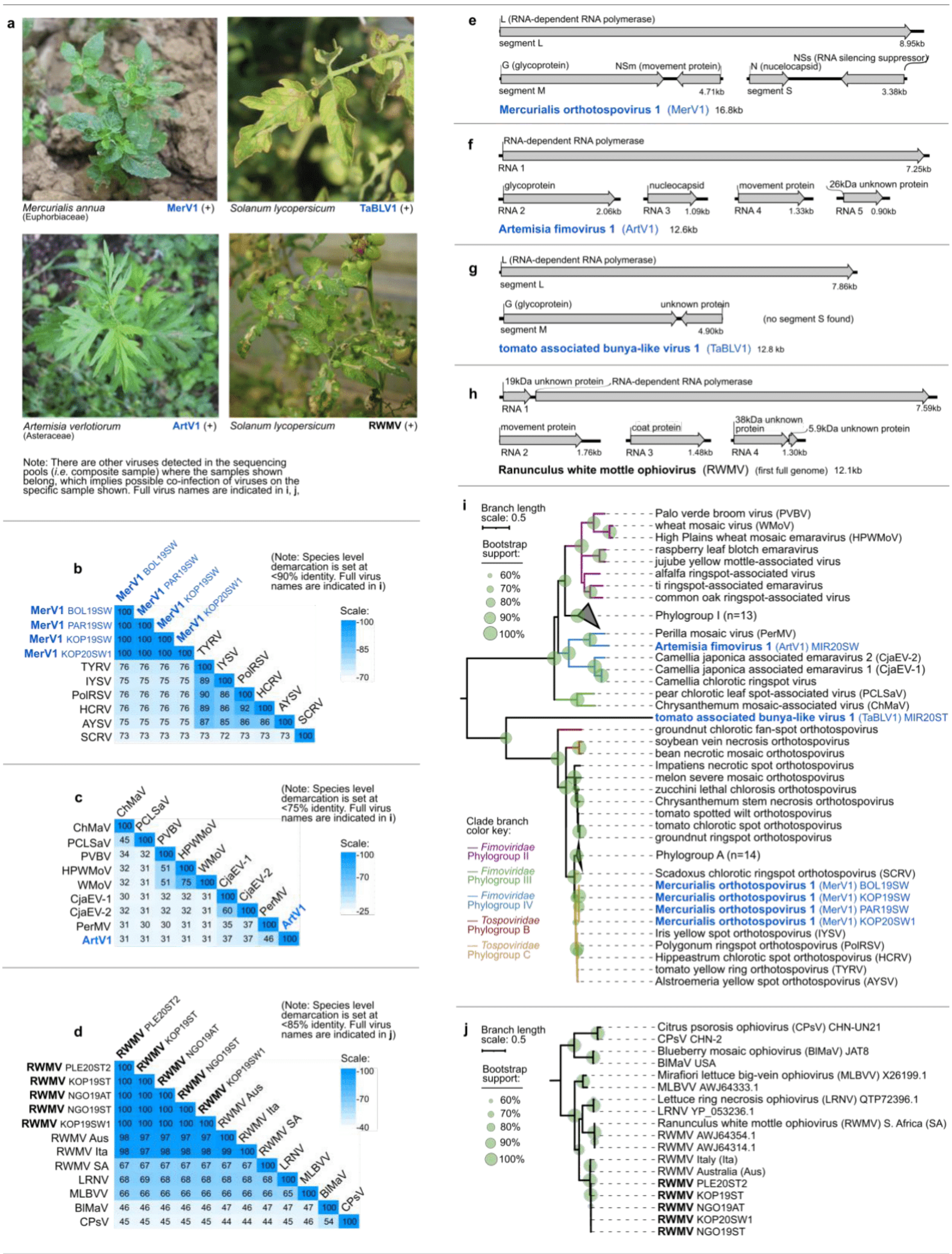


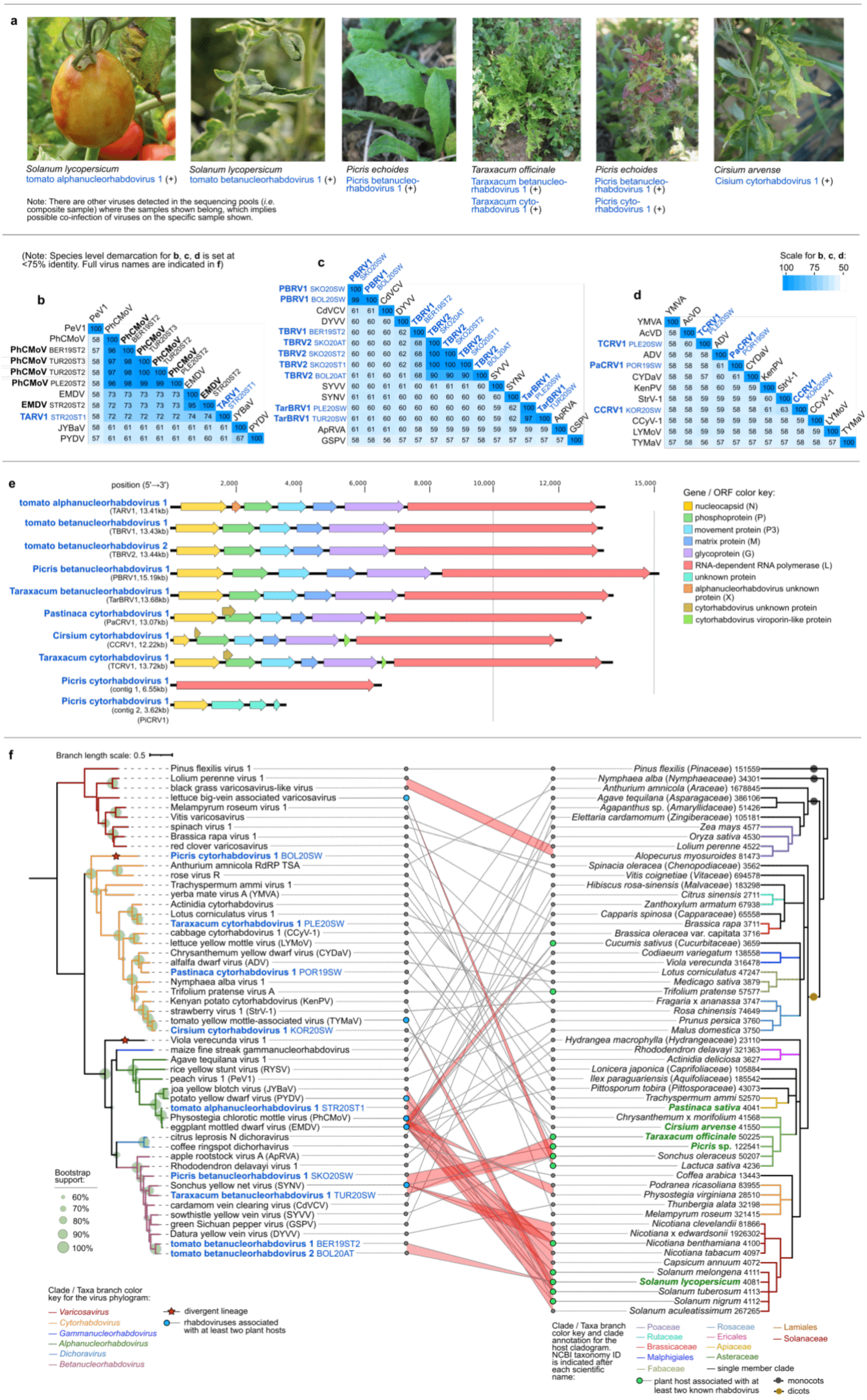
Figure 4

**Figure 4 | Characteristics of (-)ssRNA viruses under family *Tospoviridae, Fimoviridae*, and *Aspiviridae*, from the present study. a** Selected photographs showing associated symptoms in field samples that tested positive for the respective viruses in RT-PCR assays. **b-d** Heatmaps showing the pairwise identities of selected viruses based on alignment and comparison of full length RdRp amino acid sequences. **e-h** Genome organization of the viruses presented herewith showing the predicted open reading frames and protein products. **i-j** Maximum likelihood phylogenetic trees based on the conserved RNA-dependent RNA polymerase (RdRp) amino acid sequences of *Tospoviridae* and *Fimoviridae* also showing tomato associated bunya-like virus 1 (**i**), and *Aspivirdae* (**j**). Branch length scale represents amino acid substitution per site. Virus names and acronyms in blue bold font are the novel viruses, while those in black bold font are known viruses from the present study. Indicated after the name or acronym are the isolate IDs of the viruses. Full virus names of those abbreviated in the pairwise identity matrices (**b-d**) can be found in the genome organization and phylogenetic trees (**e-j**).

### Discovery of novel rhabdoviruses and their links to Solanaceae and Asteraceae hosts

In this study, nine novel rhabdoviruses were discovered in tomatoes and weeds. Using RT-PCR assays, tomato alphanucleorhabdovirus 1 (TARV1), tomato betanucleorhabdovirus 1 (TBRV1) and TBRV2 were confirmed in tomatoes. Five were detected in Asteraceae weeds: *P. echoides* (Picris betanucleorhabdovirus 1 (PBRV1), Picris cytorhabdovirus 1 (PiCRV1)), *T. officinale* (Taraxacum betanucleorhabdovirus 1 (TarBRV1) and Taraxacum cytorhabdovirus 1 (TCRV1)), *Cirsium arvense* (Cirsium cytorhabdovirus 1 (CCRV1)). One cytorhabdovirus was detected in *Pastinaca sativa* (Apiaceae) (Pastinaca cytorhabdovirus 1 (PaCRV1)). TarBRV1 and TCRV1 were found to be co-infecting a single *T. officinale* sample, and PBRV1 and PiCRV1 co-infecting one *P. echoides* sample (Fig. 5a). Viruses were distinguished based on pairwise comparison of full genome nucleotide (nt) sequences (Fig. 5b-d). All novel rhabdoviruses have genomes typical of their genus, except for the highly divergent PiCRV1, which might have a putative bipartite genome, or the two contigs were not assembled together in our analyses (Fig. 5e). PiCRV1 is only 29.1-33.5% identical to closely related cytorhabdoviruses, based on comparison of RdRp aa sequences (Supplementary Table 26-B).

Investigation of virus-host relationships was done by drawing links between rhabdovirus phylogram and plant host cladogram (Fig. 5f). This revealed that rhabdoviruses from certain clades are often associated with Solanaceae and Asteraceae plant hosts. In particular, a clade of closely related alphanucleorhabdoviruses, including one discovered from this study (potato yellow dwarf virus, joa yellow blotch virus, eggplant mottled dwarf virus, PhCMoV, TARV1), was associated with eight plant species from family Solanaceae, both experimentally and as natural hosts. A few associations of betanucleorhabdoviruses discovered in weeds (PBRV1, TarBV1), and in tomatoes (TBRV1, TBRV2) with solanaceous plants were also found. Two novel betanucleorhabdoviruses (PBRV1, TarBV1) from this study and one known virus (Sonchus yellow net virus) were associated with three Asteraceae plants. For details of the pairwise comparisons, see Supplementary Tables 26-28. An identical rhabdovirus phylogenetic is shown in Supplementary Fig. 4-03, where the GenBank accession numbers of the sequences used in the analyses are indicated.



Note: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown.

(Note: Species level demarcation for **b**, **c**, **d** is set at <75% identity. Full virus names are indicated in **f**)

**b**

| | PeV1 | PhCMoV | **PhCMoV** BER19ST2 | **PhCMoV** TUR20ST3 | **PhCMoV** TUR20ST2 | **PhCMoV** PLE20ST2 | EMDV | **EMDV** STR20ST2 | **TARV1** STR20ST1 | JYBaV | PYDV |
|---|---|---|---|---|---|---|---|---|---|---|---|
| PeV1 | 100 | | | | | | | | | | |
| PhCMoV | 58 | 100 | | | | | | | | | |
| **PhCMoV** BER19ST2 | 57 | 96 | 100 | | | | | | | | |
| **PhCMoV** TUR20ST3 | 58 | 97 | 98 | 100 | | | | | | | |
| **PhCMoV** TUR20ST2 | 58 | 97 | 98 | 100 | 100 | | | | | | |
| **PhCMoV** PLE20ST2 | 58 | 96 | 98 | 99 | 99 | 100 | | | | | |
| EMDV | 58 | 73 | 73 | 73 | 73 | 73 | 100 | | | | |
| **EMDV** STR20ST2 | 58 | 72 | 73 | 73 | 73 | 73 | 95 | 100 | | | |
| **TARV1** STR20ST1 | 58 | 72 | 72 | 72 | 72 | 72 | 74 | 74 | 100 | | |
| JYBaV | 58 | 61 | 61 | 61 | 61 | 61 | 61 | 61 | 61 | 100 | |
| PYDV | 57 | 61 | 61 | 61 | 61 | 61 | 61 | 60 | 61 | 67 | 100 |

**c**

| | **PBRV1** SKO20SW | **PBRV1** BOL20SW | CdVCV | DYVV | **TBRV1** BER19ST2 | **TBRV2** SKO20AT | **TBRV2** SKO20ST2 | **TBRV2** SKO20ST1 | **TBRV2** BOL20AT | SYVV | SYNV | **TarBRV1** PLE20SW | **TarBRV1** TUR20SW | ApRVA | GSPV |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **PBRV1** SKO20SW | 100 | | | | | | | | | | | | | | |
| **PBRV1** BOL20SW | 99 | 100 | | | | | | | | | | | | | |
| CdVCV | 61 | 61 | 100 | | | | | | | | | | | | |
| DYVV | 60 | 60 | 60 | 100 | | | | | | | | | | | |
| **TBRV1** BER19ST2 | 60 | 60 | 60 | 62 | 100 | | | | | | | | | | |
| **TBRV2** SKO20AT | 60 | 60 | 60 | 62 | 68 | 100 | | | | | | | | | |
| **TBRV2** SKO20ST2 | 60 | 60 | 60 | 62 | 68 | 100 | 100 | | | | | | | | |
| **TBRV2** SKO20ST1 | 60 | 60 | 60 | 62 | 68 | 100 | 100 | 100 | | | | | | | |
| **TBRV2** BOL20AT | 61 | 61 | 60 | 61 | 68 | 90 | 90 | 90 | 100 | | | | | | |
| SYVV | 60 | 60 | 61 | 61 | 60 | 61 | 61 | 61 | 60 | 100 | | | | | |
| SYNV | 61 | 61 | 61 | 60 | 60 | 60 | 60 | 60 | 60 | 60 | 100 | | | | |
| **TarBRV1** PLE20SW | 60 | 60 | 60 | 60 | 60 | 60 | 60 | 60 | 60 | 59 | 62 | 100 | | | |
| **TarBRV1** TUR20SW | 61 | 61 | 60 | 60 | 60 | 60 | 60 | 60 | 60 | 59 | 62 | 97 | 100 | | |
| ApRVA | 61 | 61 | 61 | 60 | 58 | 59 | 59 | 59 | 59 | 59 | 59 | 59 | 59 | 100 | |
| GSPV | 58 | 58 | 56 | 57 | 57 | 57 | 57 | 57 | 58 | 57 | 57 | 57 | 57 | 57 | 100 |

**d**

| | YMVA | AcVD | **TCRV1** PLE20SW | ADV | **PaCRV1** POR19SW | CYDaV | KenPV | StrV-1 | **CCRV1** KOR20SW | CCyV-1 | LYMoV | TYMaV |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YMVA | 100 | | | | | | | | | | | |
| AcVD | 58 | 100 | | | | | | | | | | |
| **TCRV1** PLE20SW | 58 | 60 | 100 | | | | | | | | | |
| ADV | 58 | 58 | 58 | 100 | | | | | | | | |
| **PaCRV1** POR19SW | 58 | 58 | 58 | 61 | 100 | | | | | | | |
| CYDaV | 58 | 58 | 57 | 60 | 61 | 100 | | | | | | |
| KenPV | 58 | 58 | 58 | 60 | 59 | 59 | 100 | | | | | |
| StrV-1 | 58 | 58 | 59 | 59 | 59 | 59 | 60 | 100 | | | | |
| **CCRV1** KOR20SW | 58 | 58 | 59 | 59 | 58 | 58 | 61 | 63 | 100 | | | |
| CCyV-1 | 58 | 58 | 58 | 59 | 59 | 59 | 58 | 58 | 59 | 100 | | |
| LYMoV | 58 | 58 | 59 | 59 | 58 | 58 | 58 | 58 | 58 | 59 | 100 | |
| TYMaV | 57 | 58 | 56 | 57 | 57 | 57 | 57 | 57 | 58 | 58 | 57 | 100 |

**Figure 5**

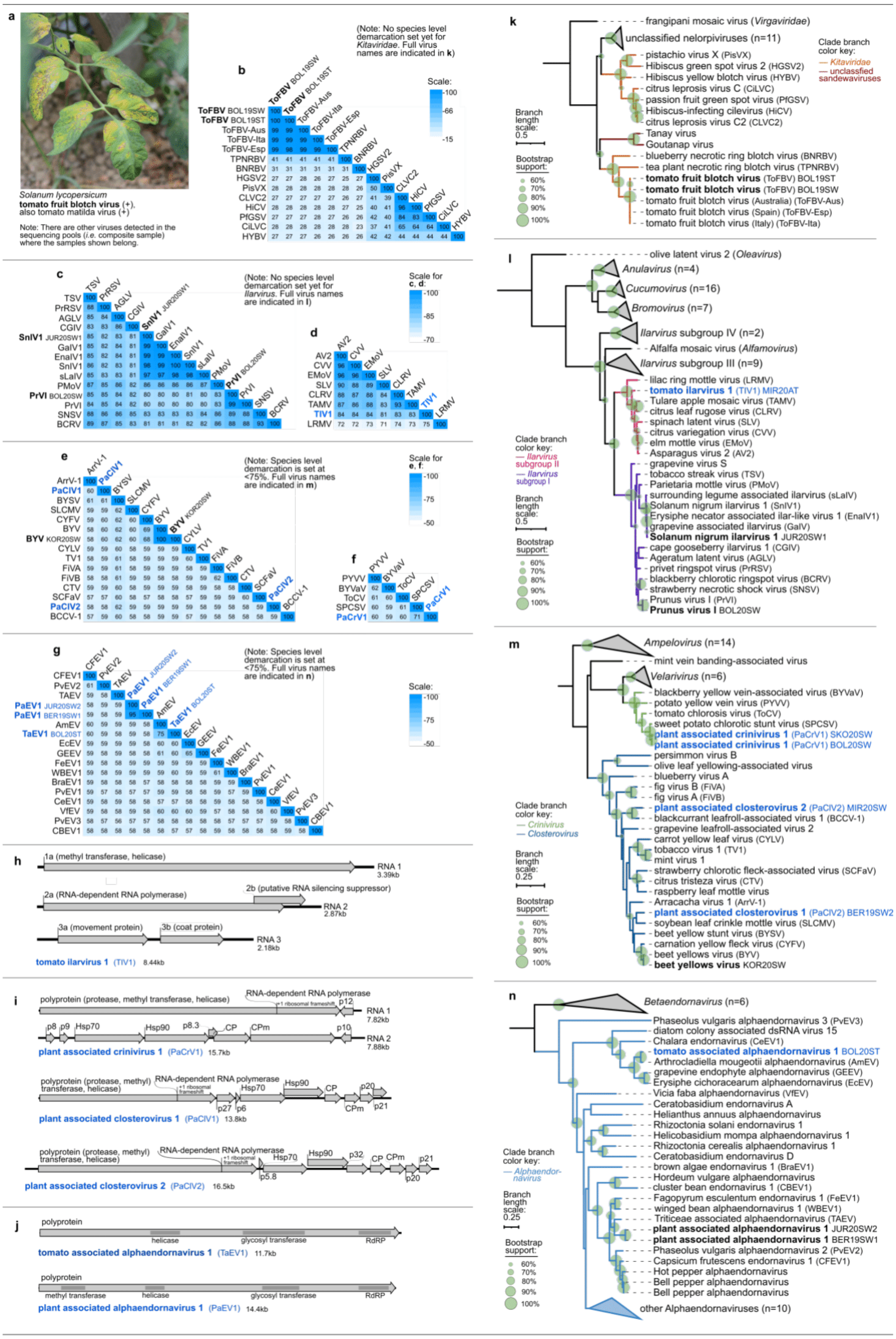
**Figure 5 | Characteristics of novel (-)ssRNA viruses classified in family *Rhabdoviridae* from the present study. a** Photographs of samples that tested positive for selected novel rhabdoviruses in RT-PCR assays. **b-d** Heatmaps showing the pairwise identities of species in genus *Alphanucleorhabdovirus* (**b**), *Betanucleorhabdovirus* (**c**), and *Cytorhabdovirus* (**d**), based on full genome length nucleotide sequences. Virus acronyms in blue bold font are the novel rhabdoviruses, while those in black bold font are known rhabdoviruses from the present study. Indicated after virus names and acronyms are the isolate IDs. **e** Genome organization of novel rhabdoviruses discovered in the present study. Genome lengths are shown to scale. Open reading frames (ORFs) and the proteins they code for are color coded accordingly. **f** Co-phylogenetic tree (tanglegram) showing the phylogenetic relationships of novel rhabdoviruses among known species (left tree), which are linked with associated plant host(s) indicated in GenBank, shown on the right tree. Numerous links of well-supported clade of viruses to taxonomically-related plants are highlighted in red. Maximum likelihood phylogenetic tree of rhabdoviruses was constructed **based** on the conserved amino acid sequence of the RdRp. Branch length scale represents amino acid substitution per site. The host cladogram was made in phyloT (www.phylot.biobyte.de). In the virus tree, viruses associated with at least two plant hosts are indicated by a blue circle. In the host tree, green circles are used to indicate plants that are associated with two or more rhabdoviruses, and the host species names in bold green font are those that have representative samples in the present study. The clades are separately color coded and annotated for each tree. Full virus names of those abbreviated in the pairwise identity matrices (**b-d**) can be found in the genome organization and phylogenetic trees (**e, f**).

### Detection of a kitavirus in tomatoes and other known and novel *Martellivirales* species

The recently described tomato fruit blotch virus (ToFBV, *Kitaviridae*) [28,64,65], was detected in two symptomatic tomato leaf samples from Slovenia (Fig. 6a). Infectivity and possible vector of ToFBV were not reported yet, and it is currently classified in the genus *Blunervirus.* Pairwise comparison of conserved RdRp aa sequences of blunerviruses (Fig. 6b), revealed high molecular divergence among members, with only 30.9-41.3% pairwise identity between species. Phylogenetic analyses using conserved RdRp aa sequences showed that all known ToFBV isolates from a single clade (100% BS) (Fig. 6k).

SnIV1, a recently described ilarvirus, was detected in *Physalis* sp., which is the sixth distinct source association with the virus, aside from three other plant species (*S. lycopersicum, S. nigrum*, and an unidentified legume plant) [23,29], and grapevines infected with a fungus (*Erysiphe necator*) and an oomycete (*Plasmopara viticola*) [66,67]. PrVI, recently discovered in sweet cherry [68], was detected in our study in *P. echoides*, co-infected with PiCRV1. Pairwise comparison of RdRp aa sequences of the isolates of SnIV1 and PrVI from this study showed that they are >98% identical to other isolates of each species (Fig. 6c). A novel subgroup II ilarvirus, tomato ilarvirus 1 (TIV1), was detected in an asymptomatic tomato sample, and is at most 83.3% identical to closely related ilarviruses based on RdRp aa sequence comparison (Fig. 6d,h).

Three new *Closteroviridae* species were detected in weeds through HTS (Fig. 6e,f,i).Two new alphaendornaviruses with their typical protein domains were also discovered, one of which is from a pool of symptomatic tomatoes (Fig. 6g,j). Novel ilarvirus, closterovirus and alphaendornavirus all form distinct phylogenetic clades with related viruses (>60% BS) (Fig. 6l-n). For details of the pairwise comparisons, see Supplementary Tables 29-33. Expanded versions of the collapsed phylogenetic trees in Fig. 6 are shown in Supplementary Fig. 4-04, 05, 06, and 07, where the GenBank accession numbers of the sequences used in the analyses are indicated. Details of InterPro domain search are in Supplementary Tables 43-44.



b

| | ToFBV BOL19SW | ToFBV BOL19ST | ToFBV-Aus | ToFBV-Ita | ToFBV-Esp | TPNRBV | BNRBV | HGSV2 | PisVX | CLVC2 | HiCV | PfGSV | CiLVC | HYBV |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **ToFBV** BOL19SW | 100 | | | | | | | | | | | | | |
| **ToFBV** BOL19ST | 100 | 100 | | | | | | | | | | | | |
| ToFBV-Aus | 99 | 99 | 100 | | | | | | | | | | | |
| ToFBV-Ita | 99 | 99 | 99 | 100 | | | | | | | | | | |
| ToFBV-Esp | 99 | 98 | 99 | 99 | 100 | | | | | | | | | |
| TPNRBV | 41 | 41 | 41 | 41 | 41 | 100 | | | | | | | | |
| BNRBV | 31 | 31 | 31 | 31 | 31 | 31 | 100 | | | | | | | |
| HGSV2 | 27 | 27 | 28 | 26 | 27 | 25 | 27 | 100 | | | | | | |
| PisVX | 28 | 28 | 28 | 28 | 28 | 28 | 26 | 50 | 100 | | | | | |
| CLVC2 | 27 | 27 | 27 | 27 | 27 | 26 | 27 | 41 | 39 | 100 | | | | |
| HiCV | 28 | 28 | 28 | 28 | 28 | 27 | 25 | 40 | 41 | 96 | 100 | | | |
| PfGSV | 27 | 27 | 27 | 28 | 27 | 26 | 26 | 42 | 40 | 84 | 83 | 100 | | |
| CiLVC | 28 | 28 | 28 | 28 | 28 | 28 | 23 | 37 | 41 | 65 | 64 | 64 | 100 | |
| HYBV | 27 | 27 | 27 | 26 | 26 | 26 | 26 | 42 | 42 | 44 | 44 | 44 | 44 | 100 |

c

| | TSV | PrRSV | AGLV | CGIV | SnIV1 JUR20SW1 | GaIV1 | EnaIV1 | SnIV1 | sLaIV | PMoV | PrVI BOL20SW | PrVI | SNSV | BCRV |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| TSV | 100 | | | | | | | | | | | | | |
| PrRSV | 88 | 100 | | | | | | | | | | | | |
| AGLV | 85 | 84 | 100 | | | | | | | | | | | |
| CGIV | 83 | 83 | 86 | 100 | | | | | | | | | | |
| **SnIV1** JUR20SW1 | 85 | 82 | 83 | 81 | 100 | | | | | | | | | |
| GaIV1 | 85 | 82 | 84 | 81 | 99 | 100 | | | | | | | | |
| EnaIV1 | 85 | 82 | 84 | 81 | 99 | 99 | 100 | | | | | | | |
| SnIV1 | 86 | 82 | 83 | 81 | 98 | 99 | 100 | 100 | | | | | | |
| sLaIV | 85 | 83 | 83 | 81 | 97 | 97 | 98 | 98 | 100 | | | | | |
| PMoV | 87 | 85 | 86 | 82 | 86 | 86 | 86 | 86 | 87 | 100 | | | | |
| **PrVI** BOL20SW | 85 | 85 | 84 | 82 | 80 | 80 | 80 | 81 | 80 | 83 | 100 | | | |
| PrVI | 84 | 85 | 84 | 82 | 80 | 80 | 80 | 80 | 80 | 83 | 99 | 100 | | |
| SNSV | 88 | 86 | 86 | 85 | 83 | 83 | 83 | 83 | 84 | 86 | 89 | 88 | 100 | |
| BCRV | 89 | 87 | 85 | 83 | 81 | 81 | 81 | 82 | 82 | 86 | 88 | 88 | 93 | 100 |

d

| | AV2 | CVV | EMoV | SLV | CLRV | TAMV | TIV1 | LRMV |
|---|---|---|---|---|---|---|---|---|
| AV2 | 100 | | | | | | | |
| CVV | 96 | 100 | | | | | | |
| EMoV | 96 | 96 | 100 | | | | | |
| SLV | 90 | 88 | 89 | 100 | | | | |
| CLRV | 88 | 87 | 88 | 84 | 100 | | | |
| TAMV | 87 | 86 | 88 | 83 | 93 | 100 | | |
| TIV1 | 84 | 84 | 84 | 81 | 83 | 83 | 100 | |
| LRMV | 72 | 72 | 73 | 71 | 74 | 73 | 75 | 100 |

e

| | ArrV-1 | PaClV1 | BYSV | SLCMV | CYFV | BYV | BYV KOR20SW | CYLV | TV1 | FiVA | FiVB | CTV | SCFaV | PaClV2 | BCCV-1 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ArrV-1 | 100 | | | | | | | | | | | | | | |
| PaClV1 | 60 | 100 | | | | | | | | | | | | | |
| BYSV | 61 | 61 | 100 | | | | | | | | | | | | |
| SLCMV | 59 | 59 | 62 | 100 | | | | | | | | | | | |
| CYFV | 59 | 60 | 62 | 60 | 100 | | | | | | | | | | |
| BYV | 58 | 60 | 62 | 60 | 69 | 100 | | | | | | | | | |
| **BYV** KOR20SW | 58 | 60 | 62 | 60 | 68 | 100 | 100 | | | | | | | | |
| CYLV | 59 | 59 | 60 | 58 | 59 | 59 | 59 | 100 | | | | | | | |
| TV1 | 58 | 59 | 61 | 58 | 59 | 59 | 59 | 60 | 100 | | | | | | |
| FiVA | 59 | 59 | 61 | 58 | 59 | 59 | 59 | 58 | 59 | 100 | | | | | |
| FiVB | 58 | 58 | 61 | 59 | 59 | 58 | 58 | 59 | 59 | 62 | 100 | | | | |
| CTV | 59 | 59 | 60 | 58 | 59 | 59 | 59 | 58 | 59 | 58 | 58 | 100 | | | |
| SCFaV | 57 | 57 | 60 | 58 | 57 | 58 | 58 | 57 | 59 | 59 | 59 | 60 | 100 | | |
| PaClV2 | 58 | 58 | 62 | 59 | 59 | 59 | 59 | 59 | 58 | 59 | 58 | 58 | 59 | 100 | |
| BCCV-1 | 57 | 59 | 60 | 58 | 58 | 59 | 59 | 57 | 59 | 58 | 58 | 58 | 58 | 59 | 100 |

f

| | PYVV | BYVaV | ToCV | SPCSV | PaCrV1 |
|---|---|---|---|---|---|
| PYVV | 100 | | | | |
| BYVaV | 62 | 100 | | | |
| ToCV | 61 | 60 | 100 | | |
| SPCSV | 60 | 59 | 61 | 100 | |
| PaCrV1 | 60 | 59 | 60 | 71 | 100 |

g

| | CFEV1 | PvEV2 | TAEV | PaEV1 JUR20SW2 | PaEV1 BER19SW1 | AmEV | TaEV1 BOL20ST | EcEV | GEEV | FeEV1 | WBEV1 | BraEV1 | PvEV1 | CeEV1 | VfEV | PvEV3 | CBEV1 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CFEV1 | 100 | | | | | | | | | | | | | | | | |
| PvEV2 | 61 | 100 | | | | | | | | | | | | | | | |
| TAEV | 59 | 58 | 100 | | | | | | | | | | | | | | |
| PaEV1 JUR20SW2 | 58 | 59 | 59 | 100 | | | | | | | | | | | | | |
| PaEV1 BER19SW1 | 59 | 58 | 59 | 95 | 100 | | | | | | | | | | | | |
| AmEV | 60 | 59 | 59 | 59 | 58 | 100 | | | | | | | | | | | |
| TaEV1 BOL20ST | 60 | 59 | 58 | 59 | 58 | 75 | 100 | | | | | | | | | | |
| EcEV | 59 | 59 | 59 | 59 | 58 | 60 | 60 | 100 | | | | | | | | | |
| GEEV | 59 | 58 | 59 | 58 | 58 | 61 | 60 | 65 | 100 | | | | | | | | |
| FeEV1 | 59 | 58 | 58 | 59 | 59 | 59 | 59 | 59 | 59 | 100 | | | | | | | |
| WBEV1 | 59 | 58 | 59 | 59 | 59 | 59 | 60 | 59 | 59 | 61 | 100 | | | | | | |
| BraEV1 | 59 | 58 | 58 | 58 | 57 | 58 | 58 | 58 | 58 | 59 | 59 | 100 | | | | | |
| PvEV1 | 59 | 57 | 58 | 57 | 57 | 59 | 59 | 58 | 58 | 59 | 57 | 59 | 100 | | | | |
| CeEV1 | 59 | 58 | 59 | 58 | 58 | 57 | 57 | 58 | 58 | 59 | 58 | 58 | 58 | 100 | | | |
| VfEV | 59 | 58 | 58 | 59 | 58 | 60 | 60 | 60 | 59 | 57 | 58 | 58 | 58 | 60 | 100 | | |
| PvEV3 | 58 | 57 | 56 | 57 | 57 | 58 | 58 | 58 | 58 | 58 | 57 | 57 | 57 | 59 | 58 | 100 | |
| CBEV1 | 58 | 58 | 58 | 58 | 58 | 58 | 57 | 57 | 58 | 59 | 58 | 58 | 58 | 58 | 59 | 58 | 100 |

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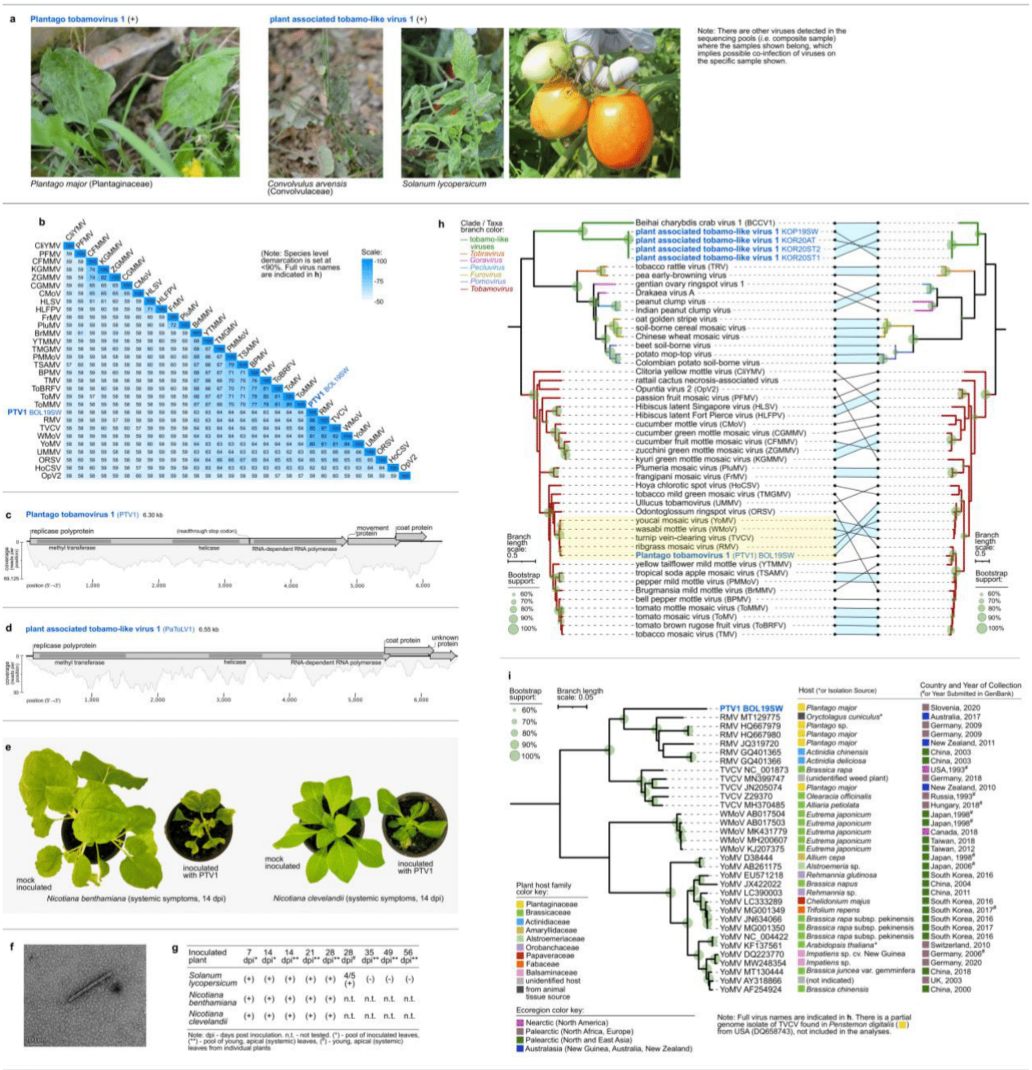
Figure 6

**Figure 6 | Characteristics of (+)ssRNA viruses in families *Kitaviridae*, *Bromoviridae*, *Closteroviridae*, and *Endornaviridae* from the present study. a** Photograph of one of the symptomatic tomato samples that tested positive for ToFBV in RT-PCR assays. **b-g** Heatmaps showing the pairwise identities to distinguish different *Kitaviridae* (**b**) and *Bromoviridae* (**c, d**) species based on alignment and comparison of RdRp amino acid sequences, members of *Closterovirus* genus (**e**) based on full genome nucleotide sequences, members of *Crinivirus* genus (**f**) based on full RNA1 segment nucleotide sequence, and members of *Alphaendornavirus* (**g**) based on full genome nucleotide sequences **h-j** Genomes of the novel viruses, with the predicted open reading frames, protein domains, and genome size. **k-n** Maximum likelihood phylogenetic trees constructed based on the conserved amino acid sequence of the RdRp of (**k**) *Kitaviridae*, (**l**) *Bromoviridae*, (**m**) *Closteroviridae*, and (**n**) *Endornaviridae*. Branch length scale represents amino acid substitution per site. Indicated after the acronym are the isolate IDs of the viruses. Virus names and acronyms in blue bold font are the novel viruses, while those in black bold font are known viruses from the present study. Full virus names of those abbreviated in the pairwise identity matrices (**b-g**) can be found in the genome organization and phylogenetic trees (**h-n**).

### Characteristics of a new tobamovirus, and a divergent tobamo-like virus species

A new tobamovirus, Plantago tobamovirus 1 (PTV1), was discovered in *Plantago major* (Fig. 7a), and percent pairwise identities based on whole genome nt sequences revealed that PVT1 is 80.4-85.7% identical to closely related tobamoviruses, which is below the current species demarcation at <90% (Fig. 7b). PTV1 has genome composition and organization typical of tobamoviruses (Fig. 7c). Maximum likelihood phylogenetic analyses using conserved methyl transferase-helicase aa sequences showed that PTV1 is closely related to ribgrass mosaic virus (RMV), turnip vein clearing virus (TVCV), youcai mosaic virus (YoMV), and wasabi mottle virus (WMoV) (Fig. 7h, highlighted in yellow). Phylogenetic analyses using full nt genome sequences of all known isolates from this tobamovirus clade including RMV, TVCV, YoMV, WMoV revealed relatedness but distinct divergence of PTV1 from the RMV clade (Fig. 7i). By superimposing information on host and country of origin (Fig. 7l), we found that aside from PTV1, *P. major* (Plantaginaceae) is a common host for RMV from Germany, and for RMV and TVCV in another eco-geographically distinct country, New Zealand [69,70]. Systemic infection with disease symptoms, which was confirmed by RT-PCR, was observed in *Nicotiana benthamiana* and *Nicotiana clevelandii* that were mechanically-inoculated with PTV1-infected *P. major* leaf tissues. Inoculated tomato plants remained asymptomatic, however, PTV1 was detected by RT-PCR in systemic leaves until 28 dpi but not at 35 dpi and beyond (Fig. 7e-g, Supplementary Fig. 5), which might be a consequence of either transient infection or cross-contamination during the experiment. Transmission electron microscopy of a *N. clevelandii* infected plant revealed PTV1 virions that are rigid rods, typical for tobamoviruses (Fig. 7f). HTS of the same plant confirmed the presence of PTV1 in systemic tissues (Supplementary Fig. 5).

A tobamo-like virus, PaToLV1, was detected in symptomatic tomatoes and in *Convolvulus arvensis* (Fig. 7a). Pairwise identity analysis using RdRp aa sequences showed that PaToLV1 is <31% identical to Plumeria mosaic virus (*Tobamovirus*), tobacco rattle virus (*Tobravirus*) and Beihai chrarybdis crab virus 1 (BCCV1, unclassified *Riboviria*) (Supplementary Table 35). PaToLV1 has genome structure similar to BCCV1, except for an additional unknown open reading frame (ORF) (Fig. 7d). Phylogenetic analyses based on the RdRp and CP aa sequences both revealed that PaToLV1 isolates form a monophyletic clade, which is clustered together with BCCV1 (Fig. 7h). For details of the pairwise comparisons, see Supplementary Table 34-35. Detailed version of the *Virgaviridae* phylogenetic trees in Fig. 7 are shown in Supplementary Fig. 4-08-A (methyl transferase, helicase-based) and Supplementary Fig. 4-08-B (coat protein-based), where the GenBank accession numbers of the sequences used in the analyses are indicated. Details of InterPro domain search for virus genomes are in Supplementary Tables 45-46.



| Inoculated plant | 7 dpi* | 14 dpi* | 14 dpi** | 21 dpi** | 28 dpi** | 28 dpi† | 35 dpi** | 49 dpi** | 56 dpi** |
|---|---|---|---|---|---|---|---|---|---|
| *Solanum lycopersicum* | (+) | (+) | (+) | (+) | (+) | 4/5 (+) | (-) | (-) | (-) |
| *Nicotiana benthamiana* | (+) | (+) | (+) | (+) | (+) | n.t. | n.t. | n.t. | n.t. |
| *Nicotiana clevelandii* | (+) | (+) | (+) | (+) | (+) | n.t. | n.t. | n.t. | n.t. |

Note: dpi - days post inoculation. n.t. - not tested. (*) - pool of inoculated leaves, (**) - pool of young, apical (systemic) leaves, (†) - young, apical (systemic) leaves from individual plants

Figure 7

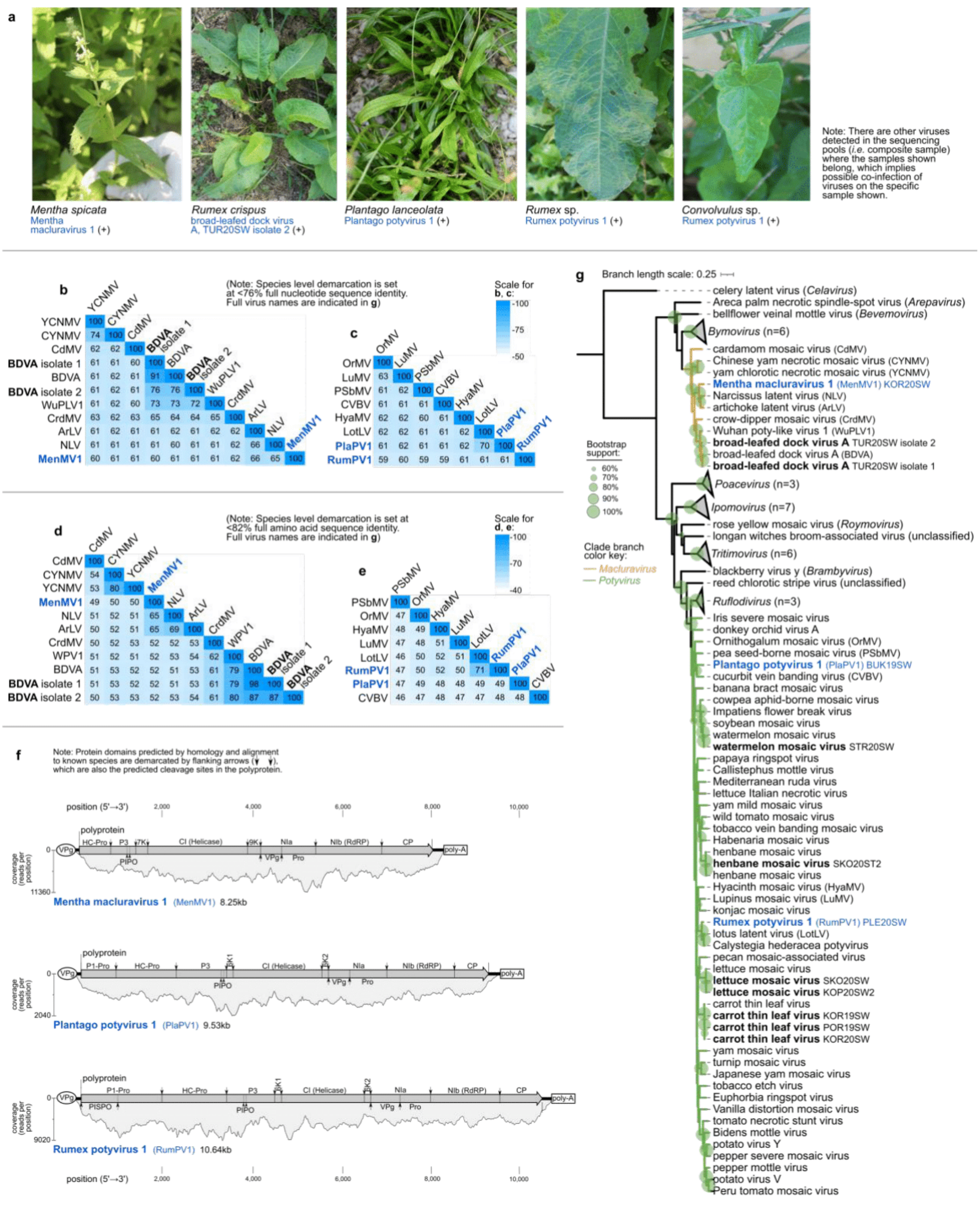
**Figure 7 | Characteristics of (+)ssRNA viruses in family *Virgaviridae* from the present study. a** Selected photographs of samples that tested positive in RT-PCR assays for the viruses presented herewith. **b** Heatmap of pairwise identities of *Tobamovirus* (*Virgaviridae*) species based on full genome nucleotide sequences. **c, d** Genome organization and read coverage of novel viruses showing the open reading frames, and the proteins they code for. **e** Photographs of the PTV1 inoculated symptomatic plants and mock inoculated control plants. **f**

Electronmicrograph showing particle morphology of PTV1. **g** RT-PCR assays of test plants inoculated with Plantago tobamovirus 1 (PTV1). **h** Maximum likelihood phylogenetic trees constructed based on the conserved amino acid sequence of methyl transferase-helicase (left) and coat protein (CP) (right). The phylogenetic congruence of the methyl transferase-helicase-based tree (left) is demonstrated by line connecting identical viruses to the CP-based tree (right). Congruent clades with >60% bootstrap support are highlighted (light blue). The clade of viruses closely related to PTV1 is highlighted in yellow. **i** Maximum likelihood phylogenetic tree, based on full genome nucleotide sequences, of all the isolates of a subgroup of tobamoviruses including PTV1. Virus names and acronyms in blue bold font are the novel viruses from the present study. Indicated after the acronym are the isolate IDs of the viruses. Branch length scale represents amino acid (**h**) or nucleotide substitution (**i**) per site. The hosts or isolation sources of the viruses as indicated in NCBI GenBank, and the countries and dates of collection are indicated. Full virus names of those abbreviated in (**b**) and (**i**) are indicated in (**c-d**) and (**h**).

### Characteristics of novel *Potyviridae* species, and crop-infecting potyviruses found in weeds

Aside from PVY, two known potyviruses (WMV and CTLV), previously detected in Slovenian crops and ornamentals [71,72], were detected in pools of weed plants from this study. Full genomes of these viruses were detected in composite samples from five different tomato farms, encompassing two localities in the Primorska region (SW Slovenia: Koper, Piran). Henbane mosaic virus, previously found in tomatoes from Slovenia[56], was detected in a composite sample of open field-grown symptomatic tomatoes. Three novel members of *Potyviridae* (Mentha macluravirus 1 (MenMV1), Plantago potyvirus 1 (PlaPV1) and Rumex potyvirus 1 (RumPV1)) were discovered in weeds showing virus disease-like symptoms (Fig. 8a). Pairwise comparison of full-length (nt, aa) polyprotein ORF distinguished the new species from the known ones based on molecular demarcation criteria for *Potyviridae* (<82% aa, <76% nt) [73] (Fig. 8b-e). The genome and polyprotein ORF of novel potyviruses were characterized, and all protein domains, typical of macluraviruses and potyviruses were found (Fig. 8f). Phylogenetic analyses based on conserved RdRp aa sequence placed MenMV1 in a clade with artichoke latent virus and Narcissus latent virus (100% BS) (Fig. 8g). PlaPV1 was placed in a clade with cucurbit vein banding virus (83.1% BS), and RumPV1 was placed in a clade with lotus latent virus and Calystegia hederacea virus (100% BS).

Two different lineages of broad-leafed dock virus A (BDVA), were also detected. A lineage with a considerably low pairwise identity compared with original isolate (86.6% aa, 76.0% nt) was found in *Rumex crispus*. For details of the pairwise comparisons, see Supplementary Tables 36-37. An expanded version of the collapsed *Potyviridae* phylogenetic tree in Fig. 8, is shown in Supplementary Fig. 4-09, where the GenBank accession numbers of the sequences used in the analyses are indicated. Details of protein domain and cleavage site search for virus genomes are in Supplementary Table 47.



**b**

| | YCNMV | CYNMV | CdMV | **BDVA** isolate 1 | BDVA | **BDVA** isolate 2 | WuPLV1 | CrdMV | ArLV | NLV | MenMV1 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| YCNMV | 100 | | | | | | | | | | |
| CYNMV | 74 | 100 | | | | | | | | | |
| CdMV | 62 | 62 | 100 | | | | | | | | |
| **BDVA** isolate 1 | 61 | 61 | 60 | 100 | | | | | | | |
| BDVA | 61 | 62 | 61 | 91 | 100 | | | | | | |
| **BDVA** isolate 2 | 61 | 62 | 61 | 76 | 76 | 100 | | | | | |
| WuPLV1 | 61 | 62 | 60 | 73 | 73 | 72 | 100 | | | | |
| CrdMV | 63 | 62 | 63 | 65 | 64 | 64 | 65 | 100 | | | |
| ArLV | 61 | 62 | 61 | 61 | 62 | 61 | 62 | 62 | 100 | | |
| NLV | 61 | 61 | 61 | 61 | 60 | 61 | 61 | 62 | 66 | 100 | |
| **MenMV1** | 60 | 61 | 61 | 60 | 61 | 61 | 61 | 62 | 66 | 65 | 100 |

**c**

| | OrMV | LuMV | PSbMV | CVBV | HyaMV | LotLV | PlaPV1 | RumPV1 |
|---|---|---|---|---|---|---|---|---|
| OrMV | 100 | | | | | | | |
| LuMV | 63 | 100 | | | | | | |
| PSbMV | 61 | 62 | 100 | | | | | |
| CVBV | 61 | 61 | 61 | 100 | | | | |
| HyaMV | 62 | 62 | 60 | 61 | 100 | | | |
| LotLV | 62 | 62 | 61 | 61 | 62 | 100 | | |
| **PlaPV1** | 61 | 62 | 61 | 61 | 62 | 70 | 100 | |
| **RumPV1** | 59 | 60 | 59 | 59 | 61 | 61 | 61 | 100 |

**d**

| | CdMV | CYNMV | YCNMV | MenMV1 | NLV | ArLV | CrdMV | WPV1 | BDVA | **BDVA** isolate 1 | **BDVA** isolate 2 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| CdMV | 100 | | | | | | | | | | |
| CYNMV | 54 | 100 | | | | | | | | | |
| YCNMV | 53 | 80 | 100 | | | | | | | | |
| **MenMV1** | 49 | 50 | 50 | 100 | | | | | | | |
| NLV | 51 | 52 | 51 | 65 | 100 | | | | | | |
| ArLV | 50 | 52 | 51 | 65 | 69 | 100 | | | | | |
| CrdMV | 50 | 52 | 53 | 52 | 52 | 53 | 100 | | | | |
| WPV1 | 51 | 52 | 51 | 52 | 53 | 54 | 62 | 100 | | | |
| BDVA | 51 | 53 | 52 | 52 | 51 | 53 | 61 | 79 | 100 | | |
| **BDVA** isolate 1 | 51 | 53 | 52 | 52 | 51 | 53 | 61 | 79 | 98 | 100 | |
| **BDVA** isolate 2 | 50 | 53 | 53 | 52 | 53 | 54 | 61 | 80 | 87 | 87 | 100 |

**e**

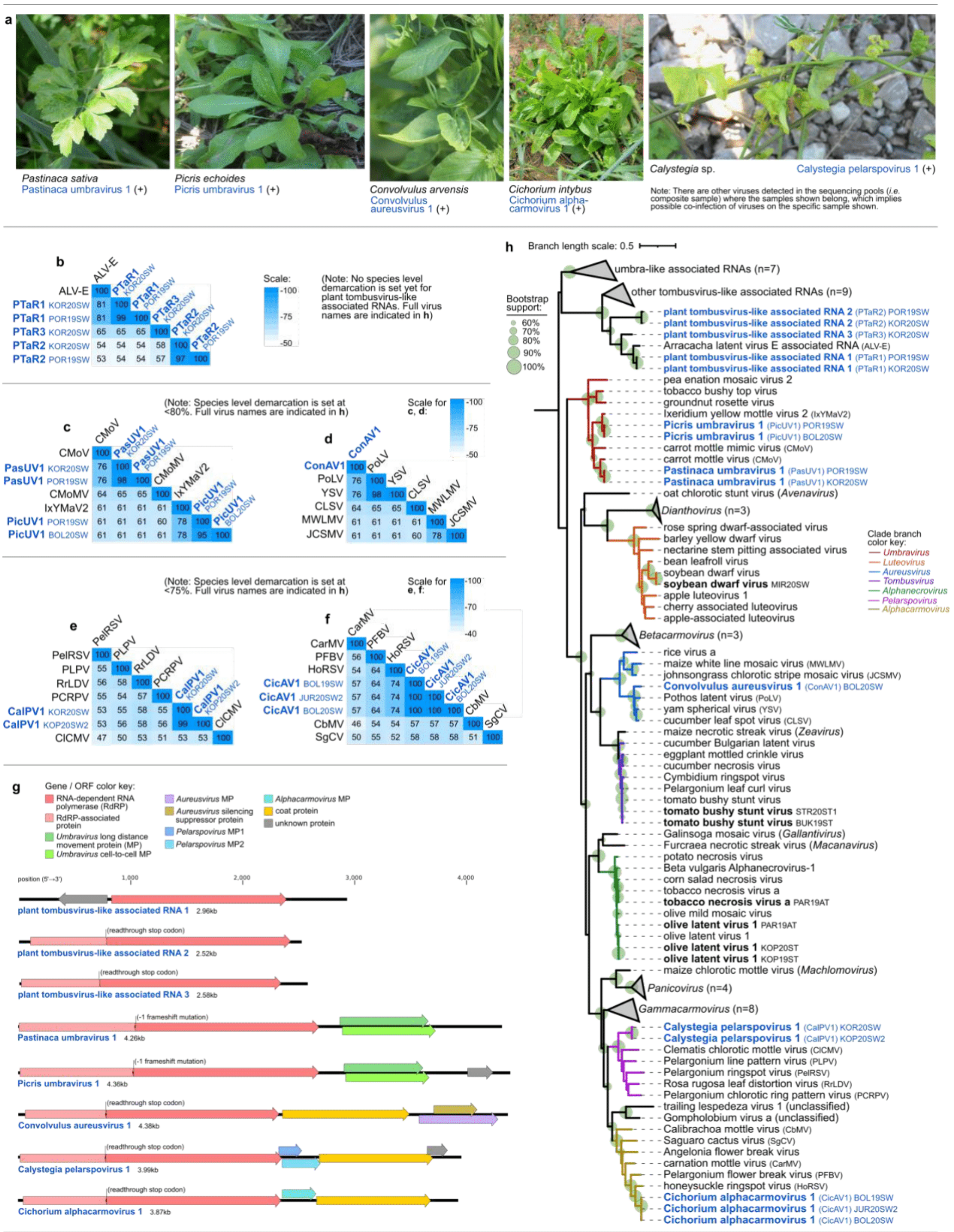
| | PSbMV | OrMV | HyaMV | LuMV | LotLV | RumPV1 | PlaPV1 | CVBV |
|---|---|---|---|---|---|---|---|---|
| PSbMV | 100 | | | | | | | |
| OrMV | 47 | 100 | | | | | | |
| HyaMV | 48 | 49 | 100 | | | | | |
| LuMV | 47 | 48 | 51 | 100 | | | | |
| LotLV | 46 | 50 | 52 | 51 | 100 | | | |
| **RumPV1** | 47 | 50 | 52 | 50 | 71 | 100 | | |
| **PlaPV1** | 47 | 49 | 48 | 48 | 49 | 49 | 100 | |
| CVBV | 46 | 47 | 48 | 47 | 47 | 48 | 48 | 100 |

**Figure 8**

**Figure 8 | Characteristics of (+)ssRNA viruses from family *Potyviridae* from the present study. a** Selected photographs of samples that tested positive in RT-PCR assays for the viruses presented herewith. **b-e** Heatmaps of the pairwise identities of *Macluravirus* and *Potyvirus* species based on alignment and comparison of full genome nucleotide sequences (**b-c**) and based on full polyprotein amino acid sequence (**d-e**). **f** Genome organization with predicted cistrons and read coverage for novel potyviruses from this study. **g** Maximum likelihood phylogenetic tree based on the alignment of conserved RdRp amino acid sequence of RefSeq species from the *Potyviridae* family. Branch length scale represents amino acid substitution per site. Virus names and acronyms in blue bold font are the novel viruses, while those in black bold font are known viruses from the present study. Indicated after the acronym are the isolate IDs of the viruses. Full virus names of those abbreviated in the pairwise identity matrices (**b-e**) can be found in the genome organization and phylogenetic trees (**f-g**).

### Known tomato tombusviruses, and discovery of new *Tombusviridae* species and tombusvirus-like associated RNAs in weeds

Genomes of three known members of *Tombusviridae* (tomato bushy stunt virus (TBSV), tobacco necrosis virus A (TNVA), olive latent virus 1 (OLV1)), and partial genome of olive mild mosaic virus (OMMV), were assembled from sequences derived from composite tomato samples. Five new viruses classified in four different *Tombusviridae* genera were discovered in weeds showing virus disease-like symptoms (Fig. 9a). These include two new umbraviruses (Pastinaca umbravirus 1 (PasUV1) and Picris umbravirus 1 (PicUV1)), one new aureusvirus (Convolvulus aureusvirus 1 (ConAV1)), one new pelarspovirus (Calystegia pelarspovirus 1 (CalPV1)), and one new alphacarmovirus (Cichorium alphacarmovirus 1 (CicAV1)). Three sequences, with similarity to self-replicating, coat-dependent RNA replicons, called tombusvirus-like associated RNAs [74], were also detected in composite weed samples. Pairwise comparisons of full genome nt or RdRp (replicase) aa sequences were done, whichever is appropriate for species demarcation (Fig. 9b-f). Genome organization typical for the genera was determined for the new *Tombusviridae* members. Novel unknown ORFs were detected in Picris umbravirus 1 and CalPV1 (Fig. 9g). Genome compositions and organizations of new tombusvirus-like associated RNAs were similar to those previously described [74], except for the two plant associated tombusvirus-like RNA 1 isolates, in which ambisense ORFs were detected. Phylogenetic analyses placed the novel tombusvirus-like associated RNAs in a clade with Arracacha latent virus E associated RNA, a member of subgroup III tombusvirus-like associated RNAs (78.7% BS) [74]. Novel tombusviruses were likewise placed in clades with known species of their respective genera (>60% BS) (Fig. 9h). For details of the pairwise comparisons, see Supplementary Tables 38-42. An expanded version of the collapsed *Tombusviridae* phylogenetic tree in Fig. 9, with providence virus (*Carmotetraviridae*) as outgroup, is shown in Supplementary Fig. 4-10, where the GenBank accession numbers of the sequences used in the analyses are also indicated.



| b | ALV-E | PTaR1 KOR20SW | PTaR1 POR19SW | PTaR3 KOR20SW | PTaR2 KOR20SW | PTaR2 POR19SW |
|---|---|---|---|---|---|---|
| ALV-E | 100 | | | | | |
| PTaR1 KOR20SW | 81 | 100 | | | | |
| PTaR1 POR19SW | 81 | 99 | 100 | | | |
| PTaR3 KOR20SW | 65 | 65 | 65 | 100 | | |
| PTaR2 KOR20SW | 54 | 54 | 54 | 58 | 100 | |
| PTaR2 POR19SW | 53 | 54 | 54 | 57 | 97 | 100 |

| c | CMoV | PasUV1 KOR20SW | PasUV1 POR19SW | CMoMV | IxYMaV2 | PicUV1 POR19SW | PicUV1 BOL20SW |
|---|---|---|---|---|---|---|---|
| CMoV | 100 | | | | | | |
| PasUV1 KOR20SW | 76 | 100 | | | | | |
| PasUV1 POR19SW | 76 | 98 | 100 | | | | |
| CMoMV | 64 | 65 | 65 | 100 | | | |
| IxYMaV2 | 61 | 61 | 61 | 61 | 100 | | |
| PicUV1 POR19SW | 61 | 61 | 61 | 60 | 78 | 100 | |
| PicUV1 BOL20SW | 61 | 61 | 61 | 61 | 78 | 95 | 100 |

| d | ConAV1 | PoLV | YSV | CLSV | MWLMV | JCSMV |
|---|---|---|---|---|---|---|
| ConAV1 | 100 | | | | | |
| PoLV | 76 | 100 | | | | |
| YSV | 76 | 98 | 100 | | | |
| CLSV | 64 | 65 | 65 | 100 | | |
| MWLMV | 61 | 61 | 61 | 61 | 100 | |
| JCSMV | 61 | 61 | 61 | 60 | 78 | 100 |

| e | PelRSV | PLPV | RrLDV | PCRPV | CalPV1 KOR20SW | CalPV1 KOP20SW2 | ClCMV |
|---|---|---|---|---|---|---|---|
| PelRSV | 100 | | | | | | |
| PLPV | 55 | 100 | | | | | |
| RrLDV | 56 | 58 | 100 | | | | |
| PCRPV | 55 | 54 | 57 | 100 | | | |
| CalPV1 KOR20SW | 53 | 55 | 58 | 55 | 100 | | |
| CalPV1 KOP20SW2 | 53 | 56 | 58 | 56 | 99 | 100 | |
| ClCMV | 47 | 50 | 53 | 51 | 53 | 53 | 100 |

| f | CarMV | PFBV | HoRSV | CicAV1 BOL19SW | CicAV1 JUR20SW2 | CicAV1 BOL20SW | CbMV | SgCV |
|---|---|---|---|---|---|---|---|---|
| CarMV | 100 | | | | | | | |
| PFBV | 56 | 100 | | | | | | |
| HoRSV | 54 | 64 | 100 | | | | | |
| CicAV1 BOL19SW | 57 | 64 | 74 | 100 | | | | |
| CicAV1 JUR20SW2 | 57 | 64 | 74 | 100 | 100 | | | |
| CicAV1 BOL20SW | 57 | 64 | 74 | 100 | 100 | 100 | | |
| CbMV | 46 | 54 | 54 | 57 | 57 | 57 | 100 | |
| SgCV | 50 | 55 | 52 | 58 | 58 | 58 | 51 | 100 |

Figure 9

**Figure 9 | Characteristics of (+)ssRNA viruses in family *Tombusviridae* from the present study. a** Selected photographs of samples that tested positive in RT-PCR assays for the viruses presented herewith. **b-f** Heatmaps of pairwise identities of plant tombusvirus-like associated RNAs based on alignment and comparison of RdRp amino acid sequences (**b**), *Umbravirus* species based on full genome nucleotide sequences (**c**), *Aureusvirus* species (**d**), *Pelarspovirus* species (**e**), and *Alphacarmovirus* species (**f**) based on RdRp amino acid sequences. **g** Genome organization of novel *Tombusviridae* species and tombusvirus-like associated RNAs from this study. Open reading frames (ORFs) and the proteins they code for are color coded accordingly. **h** Maximum likelihood phylogenetic tree based on the conserved amino acid sequence of RdRp. Virus names and acronyms in blue bold font are the novel viruses, while those in black bold font are known viruses from the present study. Indicated after the acronym are the isolate IDs of the viruses. Branch length scale represents amino acid substitution per site. Full virus names of those abbreviated in the pairwise matrices in (**b-f**) are in the phylogenetic tree (**h**).

### Discovery of other numerous viruses, satellite RNAs, and viroid-like circular RNAs

Aside from viruses mentioned above, a diverse set of 37 classified known and novel viruses, 21 putative virus-like *Riboviria* species (*i.e.,* cannot be classified in known virus taxa), and four known and new satellite RNAs were also detected (Supplementary Table 5). Genome organization of these viruses and phylogenetic trees including the viruses are shown in Supplementary Fig. 1 and 4. Aside from STV, other dsRNA viruses were discovered, including six new *Partitiviridae* members from weeds, two of which were detected in 2019 and 2020 at the same farm. Three new *Totiviridae* members were discovered, two of which are phylogenetically related to plant-associated members of the family. Circular DNA viruses were discovered, including two new caulimoviruses found in weeds, and partial genome of a new geminivirus (Calystegia geminivirus 1), from a symptomatic *Calystegia* sp. sample co-infected with CalPV1. To our knowledge, this could be one of the few geminiviruses in wild plants from Europe, since the majority of geminiviruses were found in Asia and the Americas [75]. Several other (+)ssRNA viruses were also discovered and classified under *Alphaflexiviridae* (n=1), *Dicistroviridae* (n=3), *Iflaviridae* (n=1), *Secoviridae* (n=5), and *Solemoviridae* (n=3). The new alphaflexivirus (Pastinaca potexvirus 1) was detected in a *P. sativa* sample co-infected with

PasUV1 and PaCRV1. One new satellite virus (tomato albetovirus 1) and new satellite RNA (TBSV satellite RNA C), associated with *Tombusviridae* species [76,77], were detected in tomatoes. Six putative virus-like sequences detected were previously associated with arthropod [4], fungi [66], or oomycete [67] hosts, while other 15 are highly divergent ones with unidentified hosts. Using a custom discovery pipeline based on SLS-PFOR2 [45], we assembled and screened 4249 circular RNAs, and identified 344 viroid-like candidates (Supplementary Table 6). Five viroid-like circular RNAs were preliminarily selected, based on predicted secondary structure, %GC content, and degree of branching. Genome circularity was confirmed for Taraxacum viroid-like circular RNA 1 (Supplementary Fig. 2), which was detected in a *T. officinale* sample co-infected with TarBV1.

## Discussion

Virus diversity in specific crops is relatively well-studied compared to weed plants or crop's wild relatives [20,21]. A few studies used HTS to uncover virus diversity and possible exchanges in the cultivated and wild compartments of agroecosystems [23,29]. Here, we detected 37 known and 55 novel viruses, which were classified in established virus taxa, and 33 unclassified *Riboviria* members. This indicates a highly understudied diversity of novel viruses in an agroecosystem, especially in weeds that might serve as reservoirs of viruses that could infect crops. This study represents the largest survey of viromes of diverse weed species within tomato agroecosystems or any cropping system. Forty-six novel viruses classified in known taxa, and additional 19 novel unclassified viruses, were detected in weeds, some of which are also present in tomatoes (*e.g.,* PaToLV1, LtaRLV1). Overall, the viromes were dominated by 60 (+)ssRNA viruses (under *Martellivirales, Potyviridae*, and *Tombusviridae*) and 17 (-)ssRNA viruses (under *Mononegavirales*). Another study looked at the exchanges of viruses between tomato and a wild relative, *S. nigrum,* in France*,* wherein PVY and SnIV1 were found to be present in both, cultivated and wild compartments [23]. Here we observed the same pattern, finding PVY and SnIV1 in tomato and a weed (*Physalis* sp.), and in addition, we identified new weed hosts of viruses found in tomatoes, such as RWMV in *S. nigrum*. We also detected in weed samples known viruses of other crops, which were previously detected in the country (*e.g.,* WMV, CTLV). The detection of crop-infecting viruses in weed plants implies the possible role of weeds as wild reservoirs and alternate hosts for such viruses [78].

In this study, around two-thirds (60/92) of the known and novel classified viruses detected were found exclusively in weeds surrounding tomato farms, 22 were found exclusively in tomatoes, and 10 viruses were found both in weed and tomato samples. The shared viruses include both generalist viruses (*i.e.*, viruses with known wide host range that includes wild plants) some of which are also important pathogens of tomatoes [15] (*e.g.,* TSWV, CMV, PVY). Overall, a small proportion of viruses was associated with plants from different families, which might suggest a wide host range for these viruses. Associated host plants were further confirmed using RT-PCR for 36 out of all 125 viruses detected, of which, only three (*i.e.,* TMaV, PaToLV, and Rumex potyvirus 1) were associated with at least two plants from different botanical families. Such small proportion of generalist viruses is consistent with previous hypotheses that most viruses evolved and settled as specialists that are only adapted to a few hosts (*i.e.,* have narrow host ranges), because of the fitness cost and evolutionary constraints associated to a generalist lifestyle [79]. This also implies presence of possible barriers for host-switching that could be established in the course of virus-host co-evolution [11]. Nevertheless, in this study, we collected just a portion of larger plant diversity and did not confirm plant infectivity of these viruses. Thus, post-discovery characterization and extending sampling and analysis to other crops and weeds, will help confirm these hypotheses.

Viruses infecting plants may not cause any disease symptoms, because of a rather neutral or beneficial interaction with its host, latent infection, host resistance, or modulation of environmental factors [10,80]. A previous study of tomato viruses in China focused only on symptomatic samples [25]. In our study, HTS and RT-PCR assays further revealed viruses that are shared between tomatoes and weeds, and those that were detected in both asymptomatic and symptomatic tomatoes. In tomatoes, 45 different viruses were detected, 18 of which were found in both asymptomatic and symptomatic tomatoes. This observation has an important implication when aiming to capture a significant breadth of virus diversity through sampling across ecosystem scales. This observation also gave important insights on possible symptom masking due to virus-tomato-environment interactions leading to latency, or due to host resistance or tolerance.

Monitoring virus diversity and evolutionary dynamics of economically important and widespread viruses could help anticipate emergence of new variants, thus preventing disease outbreaks [30]. Here, we investigated the molecular diversity of viruses based on full genome nucleotide identities, and variability among virus isolates based on genome-wide polymorphic sites and nucleotide diversity scanning. These were determined on the most prevalent viruses in tomatoes, wherein some were detected for the first time in Slovenian tomatoes and are present in several localities, such as TMaV. Low diversity was observed among the isolates of ToMV and the persistent STV, which is consistent with previous reports on their global diversity [81,82]. TSWV, in contrast to its considerable diversity at the global scale [83], showed low diversity in the samples analyzed here.. Sequenced genomes of PVY, CMV, PVM, PhCMoV, RWMV showed moderate levels of variability. PhCMoV is a recently detected, and widespread pathogen of tomato and other crops in Europe, where considerable level of diversity was observed among the isolates [84,85]. RWMV was recently detected in Slovenian peppers and tomatoes, where isolates showed moderate diversity as well [57]. Moreover, two new viruses (TBRV2, TomV1) associated with tomatoes, showed high level of variability, which might imply that these viruses are circulating in the area for a long time already and/or are undergoing diversifying evolution. Further diversity and evolution studies of viruses found in tomatoes in our virome survey, such as ToFBV, PhCMoV, TMaV, SnIV1, RWMV, TBRV2, and TomV1 would bring insightful information about the nature of the observed variations, *e.g.*, if they are the result of neutral processes or are subjected to different kind of selection pressures and/or possible ongoing adaptation to tomato.

We observed high diversity of novel viruses at higher taxonomical levels. The most illustrative example is detection of 11 rhabdoviruses, of which 9 are newly discovered species. Three new rhabdoviruses phylogenetically-related to plant rhabdoviruses were associated with tomato, which increases the count of known tomato rhabdoviruses from two to five. In weeds, six new rhabdoviruses were detected, primarily associated with Asteraceae species. Our observations added to the discoveries made in other studies, *e.g.,* a recent discovery of 27 new viruses that are phylogenetically-related to plant rhabdoviruses through homology searches in the transcriptome shotgun assembly database of NCBI [86]. Some rhabdoviruses are known to replicate in its arthropod vector as well [87], thus, further infectivity tests are needed to confirm their infectivity and pathogenicity in associated plant hosts.

Among the most economically important viruses of tomato, tobamoviruses are the most problematic in recent years, due to the emergence of ToBRFV [16]. We detected a novel tobamovirus (PTV1) in *Plantago major* surrounding a greenhouse farm in Slovenia. We demonstrated the systemic infection of PTV1 in various Solanaceae hosts, but more extensive biological and genetic characterization is needed to understand its biological characteristics. Nevertheless, such discovery calls for further research on risks associated with tobamoviruses as one of the major causes of disease outbreaks in tomato and other solanaceous crops [15]. A novel tobamo-like virus (PaToLV1) was also detected in tomatoes and in *Convolvulus arvensis*. A previous study showed the evolutionary relationship of the most similar known virus, BCCV1, to *Virgaviridae* and *Martellivirales* families [4], which could also be the case for PaToLV1.

Moreover, besides viruses, we also attempted to uncover new viroid-like agents in our dataset, with the aim to contribute to their possibly still undiscovered diversity [45]. We obtained five candidate viroids, wherein one was experimentally confirmed to be circular and structurally similar to members of *Avsunviroidae* due to the presence of a hammerhead ribozyme motif [88]. These results suggest that further research in this direction and development of new bioinformatics tools for viroid discovery within sequencing datasets could uncover even larger hidden diversity of these non-protein coding pathogenic agents.

Aside from studying virus diversity and evolution, understanding of host-virus co-evolutionary relationships is also essential in predicting possible virus emergence through host-switching [89]. We observed an association of a clade of closely related alphanucleorhabdoviruses with plant species from family Solanaceae. However, the general topology of tanglegram suggested discordant evolutionary historic events between plant rhabdoviruses and their hosts, which is similar to what was previously shown in animal/insect rhabdoviruses [89]. Likewise, we found frequent association of different but related viruses with a single plant host. This is the case of *Plantago major,* which was associated with PTV1, RMV, and TVCV isolates from four different countries from two very distinct eco-geographical regions. This subgroup was originally associated with brassica hosts [90] and recently, as reported in this study, with several Plantaginaceae and Actinidiaceae plants. This observation indicates a possibility of virus spread through introduction of plants, followed by diversifying evolution through a mix of confounding environmental and host-related factors [91].

## Conclusions

Viruses, viroids and other virus-like agents are well-studied in crops, but known to a much lesser extent in non-crop plants. Their phytosanitary implications and economic importance in crops such as tomato [15], resulted to an increased interest to discover novel species. Here, we presented an extensive viromics study, where we uncovered the vast diversity of viromes of plant species in defined agroecosystems linked with tomato production. Similar systematic surveys in various crop agroecosystems, which could also include fungal, oomycete, arthropod or nematode vectors and environmental media, such as soil and water should, in the future, provide more virome data from still undescribed compartments of agroecosystems. Collectively, this will help uncover of the fraction of unknown viruses in the global virosphere [92], and including their yet unknown ecological interactions and agroecosystem functions [8,9]. Overall, our study contributed valuable information that will, in future studies, help predict possible virus emergence in the wild-cultivated agroecological interface, a zone of possible virus spillovers and disease outbreaks [11,31,32].

## Supplementary information

**Additional File 1: Supplementary Table 1.** Individual plant samples, their species names, corresponding plant families and sampling locations. **Supplementary Table 2.** Composite samples used in high-throughput sequencing, their composition, year of collection, farm type and other associated information. **Supplementary Table 3.** Sequence read archive (SRA) metadata of the sequencing experiments, read counts, and other associated information.

**Additional File 2: Supplementary Table 4.** List summarizing all viruses detected in the composite samples. **Supplementary Table 5.** List of analyses done in the reconstruction and identification of individual virus genomes. **Supplementary Table 6.** List of circular RNAs assembled using a custom pipeline based on SLS-PFOR2, with filtering using BLASTn and BLASTx searches.

**Additional File 3: Supplementary Figure 1**. Genome organization of novel viruses, first full genomes of known viruses showing known and putative open reading frames and the protein they code for and predicted secondary structures of selected viroid-like circular RNAs detected in this study.

**Additional File 4: Supplementary Table 7.** RT-PCR primers and PCR conditions used in confirmation of associated plant hosts of selected viruses and putative viroids. **Supplementary Table 8.** RT-PCR thermocycling conditions used in the detection of selected viruses and putative viroids in associated plant hosts. **Supplementary Figure 2**. Orientation and annealing sites of the primers designed for the amplification of the circular genome of Taraxacum viroid-like circular RNA 1, and results of RT-PCR confirmation of the circular genome. **Supplementary Table 9.** List of confirmed associated plant hosts of selected viruses and putative viroids.

**Additional File 5: Supplementary Figure 3**. Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids.

**Additional File 6: Supplementary Table 10.** Model selection and other parameters used for phylogenetic analyses. **Supplementary Figure 4.** Phylogenetic trees up to the virus family or order level showing relationships of identified known and novel viruses in this study.

**Additional File 7 (Data Source): Supplementary Table 11-22.** Summary of all results from the DnaSP v. 6 analyses.

**Additional File 8 (Data Source): Supplementary Table 23-42.** Summary of all pairwise identity values from the SDT v. 1.2 analyses.

**Additional File 9 (Data Source): Supplementary Table 43-47.** Summary of all results from the protein domain prediction using InterPro scans, and homology alignments with known species of potyviruses to identify start and cleavage sites of proteins.

**Additional File 10: Supplementary Figure 5.** RT-PCR, TEM and nanopore sequencing results on the confirmation of infectivity of Plantago tobamovirus 1 in solanaceous hosts.

## Declarations

### Funding

This work mainly received funding from Horizon 2020 Marie Skłodowska-Curie Actions Innovative Training Network project "Innovative Network for Next Generation Training and Sequencing of Virome (INEXTVIR)" (GA 813542). It also received support from the Administration of the Republic of Slovenia for Food Safety, Veterinary Sector and Plant Protection and Slovenian Research Agency (ARRS) core (P4-0165, P4-0407), and project financing (projects L7-2632 and L4-3179, co-financed by the Ministry of Agriculture, Forestry and Food of the Republic of Slovenia, and BIA Laboratory and Process Equipment Co., Ltd.).

## Authors' contributions

M.R., D.K., and I.G.A. acquired funding. D.K., M.R., and M.P.S.R. formulated and designed the study. D.K. and M.R. supervised the study. M.P.S.R. did the laboratory and greenhouse work, the data analyses, and wrote the first draft of the manuscript. K.B. did the electron microscopy, and A.P. did a part of the nanopore sequencing of inoculated plants and data analyses. The rest of the authors significantly helped in sampling and sample processing. All authors contributed to editing the final manuscript.

## Acknowledgements

The authors would like to thank Zala Kogej, Živa Lengar, Meta Ješelnik, Lija Fajdiga, Miha Kitek, and Anja Cerovšek for their help in sampling and sample processing, Živa Ramšak and Henrik Krnec for helping in setting up bioinformatics programs used in viroid discovery, and Magda Tušek Žnidarič for guidance in the electron microscopy experiment. Finally, the authors would like to thank Benjamin Lee and Uri Neri for insightful discussions on viroid discovery, and the Plant Virus Ecology Journal Club led by Carolyn Malmstrom for the informative and stimulating discussions on virology that contributed useful insights to this study.

## Availability of data and material

Raw sequencing reads were submitted in the NCBI Sequence Read Archive (SRA), with the BioProject accession number PRJNA772045. All sample and sequencing metadata, and SRA accession numbers are in Supplementary Tables 1-3. All data related to virus genome assembly and identification, and their NCBI GenBank accession numbers are in Supplementary Tables 4-6. Description of other supplementary material are provided in the 'Supplementary information' section of this paper. High quality version of tables and figures and supplementary files are available in *Figshare* (link: https://doi.org/10.6084/m9.figshare.20200769).

**Competing interests**

The authors declare no competing interests.

**Ethics approval and consent to participate**

Not applicable.

**Consent for publication**

Not applicable.

## References

1. Hu B, Guo H, Zhou P, Shi Z-L. Characteristics of SARS-CoV-2 and COVID-19. Nat Rev Microbiol. 2021;19:141–54.
2. Sommers P, Chatterjee A, Varsani A, Trubl G. Integrating Viral Metagenomics into an Ecological Framework. Annu Rev Virol. Annual Reviews; 2021;8:133–58.
3. Maclot F, Candresse T, Filloux D, Malmstrom CM, Roumagnac P, van der Vlugt R, et al. Illuminating an ecological blackbox: using high throughput sequencing to characterize the plant virome across scales. Front Microbiol. 2020;11.
4. Shi M, Lin X-D, Tian J-H, Chen L-J, Chen X, Li C-X, et al. Redefining the invertebrate RNA virosphere. Nature. Nature Publishing Group; 2016;540:539–43.
5. Edgar RC, Taylor J, Lin V, Altman T, Barbera P, Meleshko D, et al. Petabase-scale sequence alignment catalyses viral discovery. Nature. 2022;602:142–7.
6. Neri U, Wolf YI, Roux S, Camargo AP, Lee B, Kazlauskas D, et al. A five-fold expansion of the global RNA virome reveals multiple new clades of RNA bacteriophages. bioRxiv. Cold Spring Harbor Laboratory; 2022;2022.02.15.480533.

7. Mifsud JCO, Gallagher R V., Holmes EC, Geoghegan JL. Transcriptome Mining Expands Knowledge of RNA Viruses across the Plant Kingdom. Simon AE, editor. J Virol. American Society for Microbiology 1752 N St., N.W., Washington, DC; 2022;

8. Schoelz JE, Stewart LR. The Role of Viruses in the Phytobiome. Annu Rev Virol. 2018;5:93–111.

9. Roossinck MJ. Viruses in the phytobiome. Curr Opin Virol. Elsevier B.V.; 2019;37:72–6.

10. Fraile A, García-Arenal F. Environment and evolution modulate plant virus pathogenesis. Curr Opin Virol. 2016;17:50–6.

11. Elena SF, Fraile A, García-Arenal F. Evolution and Emergence of Plant Viruses. Adv Virus Res. Elsevier; 2014. p. 161–91.

12. Anderson PK, Cunningham AA, Patel NG, Morales FJ, Epstein PR, Daszak P. Emerging infectious diseases of plants: pathogen pollution, climate change and agrotechnology drivers. Trends Ecol Evol. 2004;19:535–44.

13. Oerke EC. Crop losses to pests. J Agric Sci. Stockholm University Library; 2006;144:31–43.

14. FAO. World Food and Agriculture – Statistical Yearbook 2021. World Food Agric. – Stat. Yearb. 2021. FAO; 2021.

15. Rivarez MPS, Vučurović A, Mehle N, Ravnikar M, Kutnjak D. Global Advances in Tomato Virome Research: Current Status and the Impact of High-Throughput Sequencing. Front Microbiol. 2021;12.

16. Oladokun JO, Halabi MH, Barua P, Nath PD. Tomato brown rugose fruit disease: current distribution, knowledge and future prospects. Plant Pathol. 2019;68:1579–86.

17. Zaidi SS-E-A, Martin DP, Amin I, Farooq M, Mansoor S. Tomato leaf curl New Delhi virus : a widespread bipartite begomovirus in the territory of monopartite begomoviruses. Mol Plant Pathol. John Wiley & Sons, Ltd; 2017;18:901–11.

18. Lefeuvre P, Martin DP, Elena SF, Shepherd DN, Roumagnac P, Varsani A. Evolution and ecology of plant viruses. Nat Rev Microbiol. Springer US; 2019;17:632–44.

19. Olmos A, Boonham N, Candresse T, Gentit P, Giovani B, Kutnjak D, et al. High-throughput sequencing technologies for plant pest diagnosis: challenges and opportunities. EPPO Bull. 2018;48:219–24.

20. Hasiów-Jaroszewska B, Boezen D, Zwart MP. Metagenomic Studies of Viruses in Weeds and Wild Plants: A Powerful Approach to Characterise Variable Virus Communities. Viruses 2021 Vol 13 Page 1939. Multidisciplinary Digital Publishing Institute; 2021;13:1939.

21. Hančinský R, Mihálik D, Mrkvová M, Candresse T, Glasa M. Plant viruses infecting Solanaceae family members in the cultivated and wild environments: a review. Plants. Multidisciplinary Digital Publishing Institute; 2020;9:667.

22. García-Arenal F, Zerbini FM. Life on the Edge: Geminiviruses at the Interface Between Crops and Wild Plant Hosts. Annu Rev Virol. Annual Reviews; 2019;6:411–33.

23. Ma Y, Marais A, Lefebvre M, Faure C, Candresse T. Metagenomic analysis of virome cross-talk between cultivated Solanum lycopersicum and wild Solanum nigrum. Virology. Elsevier Inc.; 2020;540:38–44.

24. Bernardo P, Charles-Dominique T, Barakat M, Ortet P, Fernandez E, Filloux D, et al. Geometagenomics illuminates the impact of agriculture on the distribution and prevalence of plant viruses at the ecosystem scale. ISME J. 2018;12:173–84.

25. Xu C, Sun X, Taylor A, Jiao C, Xu Y, Cai X, et al. Diversity, Distribution, and Evolution of Tomato Viruses in China Uncovered by Small RNA Sequencing. Simon AE, editor. J Virol. American Society for Microbiology; 2017;91.

26. de Nazaré Almeida dos Reis L, Fonseca ME de N, Ribeiro SG, Naito FYB, Boiteux LS, Pereira-Carvalho R de C. Metagenomics of Neotropical Single-Stranded DNA Viruses in Tomato Cultivars with and without the Ty-1 Gene. Viruses. 2020;12:819.

27. Rego-Machado CM, Nakasu EYT, Blawid R, Nagata T, Inoue-Nagata AK. Complete genome sequence of a new bipartite begomovirus infecting tomato in Brazil. Arch Virol. 2019;164:2873–5.

28. Maachi A, Torre C, Sempere RN, Hernando Y, Aranda MA, Donaire L. Use of High-Throughput Sequencing and Two RNA Input Methods to Identify Viruses Infecting Tomato Crops. Microorganisms. 2021;9:1043.

29. Gaafar YZA, Herz K, Hartrick J, Fletcher J, Blouin AG, MacDiarmid R, et al. Investigating the Pea Virome in Germany—Old Friends and New Players in the Field(s). Front Microbiol. 2020;11:2605.

30. McLeish MJ, Fraile A, García-Arenal F. Population Genomics of Plant Viruses: The Ecology and Evolution of Virus Emergence. Phytopathology®. 2021;111:32–9.

31. Alexander HM, Mauck KE, Whitfield AE, Garrett KA, Malmstrom CM. Plant-virus interactions and the agro-ecological interface. Eur J Plant Pathol. 2014;138:529–47.

32. García-Arenal F, Zerbini FM. Life on the Edge: Geminiviruses at the Interface Between Crops and Wild Plant Hosts. Annu Rev Virol. Annual Reviews; 2019;6:411–33.

33. Pecman A, Adams I, Gutiérrez-Aguirre I, Fox A, Boonham N, Ravnikar M, et al. Systematic Comparison of Nanopore and Illumina Sequencing for the Detection of Plant Viruses and Viroids Using Total RNA Sequencing Approach. Front Microbiol. Frontiers; 2022;13:1424.

34. Pecman A, Kutnjak D, Gutiérrez-Aguirre I, Adams I, Fox A, Boonham N, et al. Next Generation Sequencing for Detection and Discovery of Plant Viruses and Viroids: Comparison of Two Approaches. Front Microbiol. 2017;8:1–10.

35. O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, et al. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res. 2016;44:D733–45.

36. Altschul S. Basic Local Alignment Search Tool. J Mol Biol. Elsevier BV; 1990;215:403–10.

37. Nurk S, Meleshko D, Korobeynikov A, Pevzner PA. MetaSPAdes: A new versatile metagenomic assembler. Genome Res. 2017;27:824–34.

38. De Coster W, D’Hert S, Schultz DT, Cruts M, Van Broeckhoven C. NanoPack: visualizing and processing long-read sequencing data. Berger B, editor. Bioinformatics. Oxford University Press; 2018;34:2666–9.

39. Vaser R, Sović I, Nagarajan N, Šikić M. Fast and accurate de novo genome assembly from long uncorrected reads. Genome Res. Cold Spring Harbor Laboratory Press; 2017;27:737–46.

40. Li H. Minimap2: pairwise alignment for nucleotide sequences. Birol I, editor. Bioinformatics. Oxford University Press; 2018;34:3094–100.

41. Lefkowitz EJ, Dempsey DM, Hendrickson RC, Orton RJ, Siddell SG, Smith DB. Virus taxonomy: The database of the International Committee on Taxonomy of Viruses (ICTV). Nucleic Acids Res. Oxford University Press; 2018;46:D708–17.

42. Blum M, Chang H-Y, Chuguransky S, Grego T, Kandasaamy S, Mitchell A, et al. The InterPro protein families and domains database: 20 years on. Nucleic Acids Res. 2021;49:D344–54.

43. Adams M, Antoniw J, Beaudoin F. Overview and analysis of the polyprotein cleavage sites in the family Potyviridae. Mol Plant Pathol. John Wiley & Sons, Ltd; 2005;6:471–87.

44. Muhire BM, Varsani A, Martin DP. SDT: A Virus Classification Tool Based on Pairwise Sequence Alignment and Identity Calculation. Kuhn JH, editor. PLoS ONE. 2014;9:e108277.

45. Zhang Z, Qi S, Tang N, Zhang X, Chen S, Zhu P, et al. Discovery of Replicating Circular RNAs by RNA-Seq and Computational Algorithms. Ding B, editor. PLoS Pathog. Public Library of Science; 2014;10:e1004553.

46. Gendron P, Lemieux S, Major F. Quantitative analysis of nucleic acid three-dimensional structures. J Mol Biol. 2001;308:919–36.

47. Untergasser A, Cutcutache I, Koressaar T, Ye J, Faircloth BC, Remm M, et al. Primer3—new capabilities and interfaces. Nucleic Acids Res. Oxford Academic; 2012;40:e115–e115.

48. Thompson JD, Higgins DG, Gibson TJ. CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Res. Oxford University Press; 1994;22:4673–80.

49. Katoh K, Standley DM. MAFFT multiple sequence alignment software version 7: Improvements in performance and usability. Mol Biol Evol. Oxford University Press; 2013;30:772–80.

50. Capella-Gutiérrez S, Silla-Martínez JM, Gabaldón T. trimAl: A tool for automated alignment trimming in large-scale phylogenetic analyses. Bioinformatics. Oxford University Press; 2009;25:1972–3.

51. Edgar RC. MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Res. 2004;32:1792–7.

52. Martin DP, Murrell B, Golden M, Khoosal A, Muhire B. RDP4: Detection and analysis of recombination patterns in virus genomes. Virus Evol. 2015;1.

53. Kumar S, Stecher G, Li M, Knyaz C, Tamura K. MEGA X: Molecular Evolutionary Genetics Analysis across Computing Platforms. Battistuzzi FU, editor. Mol Biol Evol. 2018;35:1547–9.

54. Letunic I, Bork P. Interactive Tree Of Life (iTOL) v5: an online tool for phylogenetic tree display and annotation. Nucleic Acids Res. 2021;49:W293–6.

55. Rozas J, Ferrer-Mata A, Sánchez-DelBarrio JC, Guirao-Rico S, Librado P, Ramos-Onsins SE, et al. DnaSP 6: DNA Sequence Polymorphism Analysis of Large Data Sets. Mol Biol Evol. 2017;34:3299–302.

56. Pecman A, Kutnjak D, Mehle N, Žnidarič MT, Gutiérrez-Aguirre I, Pirnat P, et al. High-throughput sequencing facilitates characterization of a "forgotten" plant virus: The case of a henbane mosaic virus infecting tomato. Front Microbiol. 2018;9:1–11.

57. Rivarez MPS, Kogej Z, Jakoš N, Pecman A, Seljak G, Vučurović A, et al. First Report of Ranunculus White Mottle Ophiovirus in Slovenia in Pepper with Yellow Leaf Curling Symptom and in Tomato. Plant Dis. 2022;

58. Saqib M, Wylie SJ, Jones MGK. Serendipitous identification of a new Iflavirus -like virus infecting tomato and its subsequent characterization. Plant Pathol. 2015;64:519–27.

59. Mahlanza T, Makwarela L, Roberts R, van der Merwe M. Occurrence of the Iflavirus-like Tomato Matilda Virus in Solanum Species in South Africa. Plant Dis. 2022;106:1766.

60. Kmetijski Institute Slovenia. Rastlinski Virusi In Njihovo Poimenovanje (in Slovenian). Plesko IM, editor. Ljiubljana, Slovenia; 2016.

61. Butković A, González R, Elena SF. Revisiting Orthotospovirus phylogeny using full-genome data and testing the contribution of selection, recombination and segment reassortment in the origin of members of new species. Arch Virol. 2021;166:491–9.

62. Fan X, Li C, Zhang Z, Ren F, Hu G, Shen H, et al. Identification and Characterization of a Novel Emaravirus From Grapevine Showing Chlorotic Mottling Symptoms. Front Microbiol. Frontiers; 2021;12:1437.

63. Kubota K, Usugi T, Tomitaka Y, Shimomoto Y, Takeuchi S, Kadono F, et al. Perilla Mosaic Virus Is a Highly Divergent Emaravirus Transmitted by Shevtchenkella sp. (Acari: Eriophyidae). Phytopathology®. Phytopathology; 2020;110:1352–61.

64. Ciuffo M, Kinoti WM, Tiberini A, Forgia M, Tomassoli L, Constable FE, et al. A new blunervirus infects tomato crops in Italy and Australia. Arch Virol. Springer; 2020;165:2379–84.

65. Nakasu EYT, Nagata T, Inoue-Nagata AK. First Report of Tomato Fruit Blotch Virus Infecting Tomatoes in Brazil. Plant Dis. Scientific Societies; 2022;

66. Chiapello M, Rodríguez-Romero J, Nerva L, Forgia M, Chitarra W, Ayllón MA, et al. Putative new plant viruses associated with Plasmopara viticola -infected grapevine samples. Ann Appl Biol. Blackwell Publishing Ltd; 2020;176:180–91.

67. Chiapello M, Rodriguez-Romero J, Ayllon M, Turina M. VIROPLANT: A report on the virome of obligatory biotrophs [Internet]. 2019 [cited 2022 May 20]. p. 106. Available from: https://ec.europa.eu/research/participants/documents/downloadPublic/K01rSjRoV0FVd0FRRm8vc1RrUHhlazdxOStqS3pyNWRJTzhUYWFEeFM5VjRmdGJybWdnbE5nPT0=/attachment/VFEyQTQ4M3ptUWZkVkZCb05IcXJuaTVTZmZYeXVTb0s=

68. Orfanidou CG, Xing F, Zhou J, Li S, Katis NI, Maliogka VI. Identification and Sequence Analysis of a Novel Ilarvirus Infecting Sweet Cherry. Plants. 2021;10:514.

69. Chavan RR, Cohen D, Blouin AG, Pearson MN. Characterization of the complete genome of ribgrass mosaic virus isolated from Plantago major L. from New Zealand and Actinidia spp. from China. Arch Virol. 2012;157:1253–60.

70. Chavan RR, Pearson MN. Molecular characterisation of a novel recombinant Ribgrass mosaic virus strain FSHS. Virol J 2016 131. BioMed Central; 2016;13:1–6.

71. Mehle N, Kutnjak D, Tušek Žnidarič M, Ravnikar M. First Report of Apium Virus Y and Carrot Thin Leaf Virus in Parsley in Slovenia. Plant Dis. 2019;103:592.

72. Vozelj N, Petrovic N, Pompe Novak M, Tusek M, Mavric I, Ravnikar M. The most frequent viruses on selected ornamental plants and vegetables in Slovenia. Zb Pred Ref 6 Slov Posvetovanje O Varstvu Rastl Zrece Slov 4-6 Marec 2003. Ljubljana, Slovenia: Plant Protection Society of Slovenia; Ljubljana Univ., Biotechnical Fac., Agronomy Dep.; 2003;498–504.

73. Adams MJ, Antoniw JF, Fauquet CM. Molecular criteria for genus and species discrimination within the family Potyviridae. Arch Virol. 2005;150:459–79.

74. Campbell AJ, Erickson A, Pellerin E, Salem N, Mo X, Falk BW, et al. Phylogenetic classification of a group of self-replicating RNAs that are common in co-infections with poleroviruses. Virus Res. Elsevier; 2020;276:197831.

75. Nawaz-ul-Rehman MS, Fauquet CM. Evolution of geminiviruses and their satellites. FEBS Lett. No longer published by Elsevier; 2009;583:1825–32.

76. Celix A, Rodriguez-Cerezo E, Garcia-Arenal F. New Satellite RNAs, but No DI RNAs, Are Found in Natural Populations of Tomato Bushy Stunt Tombusvirus. Virology. 1997;239:277–84.

77. Krupovic M. Plant Satellite Viruses (Albetovirus, Aumaivirus, Papanivirus, Virtovirus). Encycl Virol. Elsevier; 2021. p. 581–5.

78. Cooper I, Jones RAC. Wild Plants and Viruses: Under-Investigated Ecosystems. Adv. Virus Res. 2006. p. 1–47.

79. Elena SF, Agudelo-Romero P, Lalic J. The Evolution of Viruses in Multi-Host Fitness Landscapes. Open Virol J. 2009;3:1–6.

80. Takahashi H, Fukuhara T, Kitazawa H, Kormelink R. Virus Latency and the Impact on Plants. Front Microbiol. 2019;10.

81. Elvira-González L, Rubio L, Galipienso L. Geographically distant isolates of the persistent southern tomato virus (STV) show very low genetic diversity in the putative coat protein gene. Virus Genes 2020 565. 2020;56:668–72.

82. Rangel EA, Alfaro-Fernández A, Font-San-Ambrosio MI, Luis-Arteaga M, Rubio L. Genetic variability and evolutionary analyses of the coat protein gene of Tomato mosaic virus. Virus Genes. 2011;43:435–8.

83. Zhang Z, Wang D, Yu C, Wang Z, Dong J, Shi K, et al. Identification of three new isolates of Tomato spotted wilt virus from different hosts in China: molecular diversity, phylogenetic and recombination analyses. Virol J. 2016;13:8.

84. Temple C, Blouin AG, De Jonghe K, Foucart Y, Botermans M, Westenberg M, et al. Biological and genetic characterization of Physostegia chlorotic mottle virus in Europe based on host range, location, and time. Plant Dis. 2022;

85. Vučurović A, Kutnjak D, Mehle N, Stanković I, Pecman A, Bulajić A, et al. Detection of Four New Tomato Viruses in Serbia Using Post Hoc High-Throughput Sequencing Analysis of Samples From a Large-Scale Field Survey. Plant Dis. 2021;105:2325–32.

86. Bejerman N, Dietzgen RG, Debat H. Illuminating the Plant Rhabdovirus Landscape through Metatranscriptomics Data. Viruses. Multidisciplinary Digital Publishing Institute; 2021;13:1304.

87. Dietzgen RG, Bejerman NE, Goodin MM, Higgins CM, Huot OB, Kondo H, et al. Diversity and epidemiology of plant rhabdoviruses. Virus Res. 2020;281:197942.

88. Daròs J-A. Viroids: Small Noncoding Infectious RNAs with the Remarkable Ability of Autonomous Replication. Curr Res Top Plant Virol. Cham: Springer International Publishing; 2016. p. 295–322.

89. Geoghegan JL, Duchêne S, Holmes EC. Comparative analysis estimates the relative frequencies of co-divergence and cross-species transmission within viral families. Drosten C, editor. PLOS Pathog. 2017;13:e1006215.

90. Lartey RT, Voss TC, Melcher U. Tobamovirus evolution: gene overlaps, recombination, and taxonomic implications. Mol Biol Evol. 1996;13:1327–38.

91. Fraile A, García-Arenal F. Tobamoviruses as Models for the Study of Virus Evolution. In: Palukaitis P, Roossinck MJBT-A in VR, editors. Academic Press; 2018. p. 89–117.

92. Geoghegan JL, Holmes EC. Predicting virus emergence amid evolutionary noise. Open Biol. 2017;7:170189.

## 2.3 First Report of Ranunculus White Mottle Ophiovirus in Slovenia in Pepper with Yellow Leaf Curling Symptom and in Tomato

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Published in: *Plant Disease*, vol. 106 no. 7 (2022).
doi: 10.1094/PDIS-08-21-1624-PDN

Disease Note

Diseases Caused by Viruses

# First Report of Ranunculus White Mottle Ophiovirus in Slovenia in Pepper with Yellow Leaf Curling Symptom and in Tomato

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**Funding:** This study received funding from the Administration of the Republic of Slovenia for Food Safety, Veterinary Sector and Plant Protection, Slovenian Research Agency (ARRS) core financing (P4-0165), and the Horizon 2020 Marie Skłodowska-Curie Actions Innovative Training Network (H2020 MSCA-ITN) project “INEXTVIR” (GA 813542), under the management of the European Commission-Research Executive Agency. Plant Dis. 106:2003, 2022; published online as https://doi.org/10.1094/PDIS-08-21-1624-PDN. Accepted for publication 29 November 2021.

Pepper (*Capsicum annuum*) and tomato (*Solanum lycopersicum*) plants showing virus-like disease symptoms were collected in 2017, 2019, and 2020 in different parts of Slovenia. Total RNA was extracted from the leaf tissue of individual samples using an RNeasy Plant Mini kit (Qiagen) and pooled in four composite samples as follows: two pepper plants from 2017 (D2017), five pepper and four tomato plants from 2019 (D2019_P1), seven tomato plants (D2020_P1), and two pepper and four tomato plants (D2020_P3) from 2020. The pooled RNA samples were sequenced using Illumina platforms (details of the sequencing experiments are in the supplementary material). Reads were analyzed using CLC Genomics Workbench (v. 20.0, Qiagen) following the pipeline for plant virus discovery (Pecman et al. 2017). Reads and contigs mapping to Ranunculus white mottle ophiovirus (RWMV) (GenBank accession no. AY542957 or NC_043389) were detected in all pools. The longest contig (1,255 bp) was obtained from the 2019 composite sample, which mapped to the coat protein-coding RNA 3 segment of the RWMV genome (accession no. AY542957). Details of mapping, genome coverage, and other viruses detected in the pools are summarized in the supplementary material. To identify individual RWMV-infected plants from the pools, PCR primers were designed to target the coat protein gene. Two pepper samples from two

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different farms collected in 2017 and 2019 in southwest Slovenia and four tomato samples from two different farms collected in 2020 in central Slovenia tested positive for RWMV. To assess the diversity of RWMV isolates, amplicons were purified using QIAquick PCR purification kit (Qiagen) and sent for Sanger sequencing. Based on maximum likelihood phylogenetic analysis, Italian and Slovenian RWMV isolates form a monophyletic clade within the genus. Pairwise nucleotide identities of the Slovenian isolates (accession nos. MZ507604 to MZ507609) relative to the original Italian isolate coat protein (accession no. AY542957) range from 92 to 97%, indicating a moderate level of diversity among isolates. Since only RWMV, bell pepper alphaendornavirus (BPEV), and pepper cryptic virus 2 (PepCV2) were present in a pepper sample from 2017, and BPEV and PepCV2 infection in pepper are not known to be associated with any disease symptoms (Okada et al. 2011; Saritha et al. 2016), the symptoms observed on this plant might be associated with RWMV infection. We observed mottling with interveinal chlorosis or yellowing, slight to full curling of leaves from lamina inward, as well as necrotic and aborted flowers on this plant. We cannot easily associate observed symptoms with RWMV for RWMV-positive tomatoes, since several viruses were detected in the pools containing these samples. Nevertheless, the prominent symptoms in tomato plants were mottling with interveinal chlorosis and leaf curling, similar to those observed in pepper plants. RWMV was discovered and characterized in buttercups (*Ranunculus asiaticus*) and detected in anemones (*Anemone coronaria*) from Italy (Vaira et al. 1996, 1997, 2000, 2003). It was recently detected in pepper plants from Australia showing veinal yellowing (Gambley et al. 2019). Here, we detected RWMV for the first time in Slovenia and reported its first detection in tomato and pepper plants from Europe. These findings call for further studies on the effects of RWMV infection on tomato and pepper production and its monitoring in neighboring European countries.

*References*:

Gambley, C., et al. 2019. New Dis. Rep. 40:13.
Okada, R., et al. 2011. J. Gen. Virol. 92:2664.
Pecman, A., et al. 2017. Front. Microbiol. 8:1998.
Saritha, R. K., et al. 2016. Virusdisease. 27:327.
Vaira, A. M., et al. 1996. Acta Hortic. 432:36.
Vaira, A. M., et al. 1997. Arch. Virol. 142:2131.
Vaira, A. M., et al. 2000. Plant Dis. 84:1046.
Vaira, A. M., et al. 2003. Arch. Virol. 148:1037.

The author(s) declare no conflict of interest.

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*Keywords*: *Aspiviridae*, diagnostics, high-throughput sequencing, *Ophiovirus*, pepper, Ranunculus white mottle ophiovirus, Slovenia, tomato, virome, virus

# Chapter 3

# Discussion

**In the first publication**, “Global Advances in Tomato Virome Research: Current Status and the Impact of High-Throughput Sequencing”, we comprehensively collected all the information on viruses reported to infect or be associated with tomato from the literature and NCBI GenBank database. In addition, our study revealed that tomato is currently associated with 312 different virus species, which is significantly higher than the previous estimate of 136 viruses from more than a decade ago (Hanssen et al., 2010). These 312 viruses belong to 39 genera and 22 families. Among them are 220 species of DNA viruses, mostly from the family *Geminiviridae.* Nevertheless, a very diverse set of RNA viruses, comprising 84 species from 18 families, was also found. Eight viroids, from the *Pospiviridae* family, are known to infect tomato. Collectively, this set of tomato viruses is likely the largest recorded number of known viruses for any cultivated plant. Among these viruses, many known and several recently discovered viruses cause significant economic damage to tomato production in different parts of the world. This count was just recently updated through additional searches in the 1KP database and an updated GenBank database, bringing the current count to at least 485 different virus species (Wu et al., 2022), although this count still needs thorough curation and verification.

Additionally, we also assessed how HTS influenced tomato virus discovery and post-discovery characterization in the past decade (2011-2020) and provided insights into the epidemiology and ecology of tomato viruses. Specifically, we evaluated the extent of follow-up characterization studies (*i.e.,* based on genetic, biological or ecological properties) on newly discovered tomato viruses based on a published characterization framework and criteria (Massart et al., 2017). We found 45 novel virus species discovered in tomato in the recent decade (2011-2020), of which 14 were discovered using HTS. Through HTS, four viral families were, for the first time, associated with tomato, *i.e.*, *Iflaviridae* (Saqib et al., 2015), *Phenuiviridae* (Lecoq et al., 2019), *Kitaviridae* (Ciuffo et al., 2020) and *Genomoviridae* (de Nazaré Almeida dos Reis et al., 2020). Overall, we found out that the completeness of post-discovery characterization of these viruses highly depends on their economic and phytosanitary importance, and not solely on whether they were discovered by HTS or not. For instance, for tomato brown rugose fruit virus (ToBRFV), which is an emerging virus of significant economic importance (Oladokun et al., 2019; S. Zhang et al., 2022), almost all characterization criteria were fulfilled in less than four years after its discovery. Conversely, the extensive characterization of tomato necrotic stunt virus and tomato mottle mosaic virus, which were the first tomato-infecting viruses discovered using small RNA sequencing, required twice as much time as that of ToBRFV. With these findings, we addressed the first aim (see Section 1.3) and were able to assess the current body of knowledge on tomato viruses and how HTS influenced their discovery and characterization. We also confirmed that our first hypothesis (see Section 1.4) is true: the number of tomato viruses is underestimated and might represent one of the largest numbers of distinct viruses associated with a certain plant.

Overall, in this publication, we showed that HTS has accelerated the discovery of tomato viruses in the past decade (2011-2020). However, more efforts are needed to further understand the influence of these viruses on the health and phytobiome of tomato, and to dissect their ecological and epidemiological properties. We emphasized that beyond discovering and detecting viruses in tomato, HTS can enable an extended temporal and spatial scale exploration of viromes of crops, surrounding plants, wild plants, vectors, and environmental media (*e.g.*, soil and water), and can help determine possible exchanges among these parts of an ecosystem. We present a summary of information on economically important, endemic and possibly emerging viruses of tomato for a wider audience, thus disseminating basic important information for tomato virome research worldwide.

**In the second publication**, "In-depth study of tomato and weed viromes reveals undiscovered plant virus diversity in an agroecosystem", we build up on our global meta-analyses of tomato virome research from the first publication and performed further discovery and characterization research on viruses from tomato agroecosystems in Slovenia.

First, to address the second aim (see Section 1.3), we investigated the diversity of known and novel viruses, satellite RNAs, and viroid-like sequences in tomato, and weeds surrounding tomato growing areas in Slovenia. Specifically, we implemented a ribosomal RNA (rRNA)-depleted total RNA HTS approach to obtain virus sequences from tomato and weed plant metagenomes. Then, we implemented a bioinformatic pipeline to assemble, identify, and characterize genomes of known and novel viruses from metagenomic data. We distinguished viruses whether novel or known based on pairwise percent identities, genome organization, and other molecular or genomic demarcation criteria set by the ICTV. We also initiated efforts to develop an analysis pipeline for the assembly, identification and structural characterization of viroid-like circular RNAs from metagenomic data. A total of 293 tomato plants and 59 species (n=143, 18 families) of mostly broadleaf dicotyledonous weed plants from six localities in Slovenia were collected from 14 farms visited in 2019 and/or 2020. Our virome exploration from these plant samples revealed 125 viruses, of which 37 were known and 55 were novel viruses that could be classified up to known species taxa, and other 33 known or novel viruses not yet classified under established taxa in *Riboviria*, unclassified satellite RNAs, or viroid-like circular RNAs. Among the viruses detected, we were able to contribute new knowledge in the set of tomato viruses. We reported for the first time four known and 10 new species in tomato, and we also reported for the first time, members of *Vitivirus, Lispivirdae, Picornaviridae* and *Albetovirus* in tomato plants. Further inoculation assays are needed to confirm their infectivity in tomato and other plant species. With these results, we were able to show that previously established methods of HTS of rRNA-depleted total RNA (Pecman et al., 2017) from tissues of tomatoes and various species of weeds facilitated the efficient recovery of virus sequences from plant metagenomes. We also demonstrated that the use of bioinformatic analyses pipelines developed in-house (Pecman et al., 2017) for the assembly and identification of viral and viroid-like circular RNA genomes, enabled the precise detection and discovery of virus or viroid-like circular RNA reads, contigs and whole genomes from the metagenomic data. With these results, confirmed that our second hypothesis (see Section 1.4) is true: the diversity of viruses is largely unknown, even in well-studied tomato agroecosystems, and especially in weed plants within or surrounding tomato agroecosystems.

Second, to address the third aim (see Section 1.3), we examined the phylogenetic relationships and host associations of selected virus groups, genera, or families, identified in tomatoes and weeds. Specifically, we confirmed the presence of viruses in individual hosts using RT-PCR assays with virus-specific oligonucleotide primers. We discovered that certain viruses are present in both weeds and tomatoes. We then constructed phylogenetic trees and determined the phylogenetic placement of the novel viruses within known virus taxa. Furthermore, we determined associations between taxonomically-related plant hosts and clades, genera, or families of phylogenetically-related viruses. We demonstrated that 60 known and novel classified viruses were found exclusively in weeds, 22 were found exclusively in tomatoes, and 10 were found in both weed and tomato plants. The overlapping viruses have extremely wide host ranges and are important tomato pathogens (*e.g.,* tomato spotted wilt virus, cucumber mosaic virus, PVY). A study in France demonstrated the presence of PVY and SnIV1, which were found between cultivated (tomato) and wild (*S. nigrum*) habitats (Ma et al., 2020). The study also detected BBWV1 in *S. nigrum* but not in tomatoes. We observed a similar pattern, detecting SnIV1 in tomato and a related weed (*Physalis* sp.), and detecting BBWV1 only in pools of weed plants in three different locations but not in tomato plants. We also identified new weed hosts for tomato viruses, such as Ranunculus white mottle ophiovirus detected in *S. nigrum.* Known viruses of other crops were also detected in weeds, such as lettuce mosaic virus. These findings implied the presence of potential alternate hosts or wild reservoirs for such viruses (Cooper & Jones, 2006). Herein, we demonstrated that certain viruses are present in both tomatoes and weeds surrounding tomato-farming areas. We showed that this scenario for viruses infecting tomato and weed plant species within the same family, Solanaceae. Moreover, the highest diversity of novel detections was found with 11 rhabdoviruses, of which nine were newly discovered species that are phylogenetically-related to plant-infecting rhabdoviruses. In weeds alone, we detected six new rhabdoviruses associated with Asteraceae species. We further observed the link of a clade of closely related alphanucleorhabdoviruses with Solanaceae plant species, and the frequent association of *Plantago major* with different but phylogenetically-related tobamoviruses (Plantago tobamovirus 1, ribgrass mosaic virus, and turnip vein clearing virus). Herein, we observed that certain groups of evolutionarily-related viruses might be associated with specific groups of taxonomically-related plant hosts. Examining host-virus associations will enable generation of new hypotheses on their epidemiology, ecology and possible host adaptive evolution. With these results we confirmed that our third and fourth hypotheses (see Section 1.4) are true. We demonstrated that in an agroecosystem, there are overlaps in the presence of virus species, but not demonstrated overall in terms of viral isolates, in tomato (crop) and diverse weed plants within or surrounding the farming areas. We also confirmed that certain groups of evolutionarily-related viruses are associated with specific groups of taxonomically-related plant hosts, which indicates possible co-evolutionary links. More extensive sampling and wider co-phylogenetic analyses in the future will expand these findings and give a better picture of such virus-host relationships.

Third, to address the fourth aim (see Section 1.3), we characterized the pathobiology (*i.e.*, the infectivity and host range in Solanaceae species) of a novel tobamovirus, Plantago tobamovirus 1 (PTV1), which we discovered in *Plantago major* (*Plantaginaceae*). Tobamoviruses are known to have wide host ranges, exhibit persistence in the environment, and cause major disease outbreaks and pandemics in crops, such as tomato (Rivarez et al., 2021; E. Smith & Dombrovsky, 2020). Specifically, we examined the virion morphology of PTV1 using transmission electron microscopy (TEM) and determined its mechanical transmissibility and infectivity in selected herbaceous plant hosts within family Solanaceae. We demonstrated that PTV1 can systemically infect two Solanaceae hosts. We observed typical rod-shaped virions of tobamoviruses when apical, non-inoculated leaves of a PTV1-infected *Nicotiana clevelandii* was subjected to TEM. HTS of the same sample using nanopore sequencing revealed that PTV1 is the most abundant virus in the inoculated plant. Herein, we demonstrated that characterization of pathobiology of a novel virus (*e.g.,* those from economically important groups such as tobamoviruses) can provide information on virus infectivity and host range. With this result, we confirmed that our fifth hypothesis (see Section 1.4) is true: a novel virus from a family with a wide host range, that is found in weed plant(s) will be able to infect plants from a family different from its original weed host, at least in controlled experimental settings.

Fourth, to address the fifth aim (see Section 1.3), we determined the distribution, and genetic and genome-wide diversity of selected viruses to better understand their diversity and epidemiology. Specifically, we determined the genome-wide diversity of selected viruses identified in tomatoes and weeds in Slovenia. We determined that there is a variable level of diversities among isolates of tomato mosaic virus, southern tomato virus, tomato spotted wilt virus, potato virus Y, cucumber mosaic virus, potato virus M, Physostegia chlorotic mottle virus, and Ranunculus white mottle ophiovirus. Physostegia chlorotic mottle virus is a widespread pathogen of tomato and other crops in Europe (Temple et al., 2022; Vučurović et al., 2021), and Ranunculus white mottle ophiovirus was recently detected in peppers and tomatoes from Slovenia (Rivarez et al., 2022). Interestingly, two new tomato viruses (tomato betanucleorhabdovirus 2 and tomato vitivirus 1) showed high level of variability, due to the existence of one divergent strain or lineage for each species. Population genetic diversity of these viruses that circulate in crops and weeds should be further investigated to confirm if these viruses might have been either circulating for a long time already or are undergoing diversifying evolution. Herewith, we demonstrated that HTS data from virus-infected plants, across different years and locations, can be used to determine the occurrence and variability of previously undetected known and novel viruses. It is possible that these viruses might be already circulating in tomato and other economically-important crops, and remained undetected for several years, such as in the case of Ranunculus white mottle ophiovirus. With these results, we confirmed that our sixth hypothesis (see Section 1.4) is true: previously undetected viruses, which might be circulating in tomato and other economically-important crops and can be uncovered and studied in detail using HTS data.

Overall, in the second study, we uncovered the vast diversity of tomato viruses in Slovenia. Additionally, we pioneered the exploration of viruses of a very diverse set of weed plant species surrounding tomato agroecosystems. Our metagenomic exploration of viruses in the two types of flora in an agroecosystem is the largest simultaneous study of its kind conducted so far. We fully characterized the genomes of the 125 viruses, satellite viruses, and virus- or viroid-like sequences detected. We presented virus distribution, phylogenetic relationships among viruses, and possible links between viruses and plant hosts. We characterized the infectivity and other properties of a novel tobamovirus, which belongs to a group of viruses with high economic and phytosanitary importance in crops, including tomato. We looked deeper into some implications of these findings on virus ecology and epidemiology in tomato agroecosystem.

Nevertheless, we are aware that our sampling scope in terms of plant species richness, temporal and spatial scales are just small proportion of the overall status and dynamics in the agroecosystems we visited. Sequencing of total RNA extracts that are depleted of ribosomal RNAs, remain one of the most efficient strategy to recover viral sequences. However, we detected only a few plant DNA viruses. Thus, we hypothesize that adding DNA extraction and enrichment strategies to our experimental approach, would increase the chances of detecting DNA viruses. We are also aware that we sequenced pools of equimolar portions of each plant RNA extract for obvious practical reasons and budget constraints inherent to sequencing projects. This introduced bias toward sequencing of high coverage virus genomes and leaving out the low coverage ones. Sequencing of smaller size of pooled plants may have reduce this bias, but to what extent the pool size to be reduced to should be experimentally verified first. It would also be more efficient if we had pooled the RNAs by plant species and not by location, in this way it would have been easier to associate viruses with their hosts, which is more important than the location, for the purpose of this study.

In addition, looking deeper at isolates or strains should be more informative when investigating virus presence in both tomatoes and weeds. However, these strains should be well defined in the first place, *i.e.*, are they relevant in terms of pathobiology, geographic restriction, host preference, *etc.* In essence, since most of our virus detections are novel ones and only have one or two isolates, this is practically not doable (yet), and only so if more isolates are gathered. However, future studies should therefore investigate possible fluxes of known viruses with several isolates, present in tomatoes and weeds, which in the current study is very rare. More work is thus needed, especially a more systematic sampling should be done, possibly in more extensive time and space, in the same growing areas where these virus overlaps were detected. It is also worthwhile to note that inter-cropping, co-cultivation of tomatoes with other crops are common in these areas, so it has important implication for crops of the same family where there is higher chances of virus exchanges, as well as in weeds.

This study would then serve as baseline for future research that will either expand our sampling scope, or further characterize the numerous viruses we identified. This study could inspire similar systematic surveys in various crop agroecosystems, which could also include vectors (*e.g.,* fungal, oomycete, arthropod or nematode) and environmental media (*e.g.* soil and water). In the future, such studies could provide more virome data from still undescribed partitions of different agroecosystems.

**In the third publication**, "First report of Ranunculus white mottle ophiovirus in Slovenia in pepper with yellow leaf curling symptom and in tomato", we were able to determine the presence in different localities and the genetic diversity of Ranunculus white mottle ophiovirus (RWMV). Specifically, we determined the diversity of RWMV isolates from tomatoes and peppers from different localities in Slovenia, spanning three years of sampling (2017–2020). We also demonstrated that the isolates exhibited 92–97% pairwise identities, indicating a low to moderate level of genetic diversity with respect to the current threshold for species demarcation in *Aspiviridae* (<85%) (García et al., 2017). We reported the first full genome for RWMV its first detection in vegetable crops from Europe, since its discovery in nearby Italy more than two decades ago (Vaira et al., 2000), and its recent detection in Australia in 2019 (Gambley et al., 2019). Hence, we showed the use of HTS for proactive and unbiased monitoring of viruses in agroecosystems. It can enable the detection of novel viruses that might be already circulating, but have remained undetected, in tomato and other economically-important crops. With these results, addressed a part of the fifth aim (see Section 1.3) and determined the distribution and genetic diversity of selected viruses. We also confirmed that our sixth hypothesis (see Section 1.4) is true: there are previously undetected viruses, which might be circulating in tomato and other economically-important crops and can be uncovered using HTS data.

Overall, the studies presented in this dissertation will be relevant for the broader virology and plant pathology community in the field of virus discovery and in-depth studies of diversity, phylogenetic relationships, host associations, and further characterization. Specifically, our most relevant contributions are:

1. the most comprehensive and systematic review of all tomato viruses in the literature so far, highlighting the most economically important viruses, and demonstrating how HTS contributed to advancing tomato virus discovery and characterization,
2. the discovery of numerous novel viruses, satellite RNAs, and viroid-like sequences in tomato and weeds from tomato agroecosystems, and the further characterization of the infectivity of a novel tobamovirus in Solanaceae hosts,
3. the determination of patterns of presence and overlaps of viruses in symptomatic and asymptomatic tomato, and tomato and weed plants, and diversity analyses of the most prevalent viruses in tomatoes; such data are crucial for studying host ecology and host adaptation in viruses,
4. the expansion of the current knowledge on the genomic landscapes, phylogeny of detected viruses and their potential co-evolutionary links to their plant hosts such as the case of plant rhabdoviruses, and their geographic origin, such as the case for selected tobamoviruses, and
5. the detection of previously undetected known and novel viruses of tomato plants in Slovenia using HTS, which demonstrated that the use of HTS can improve the monitoring of viruses in crops, even before they emerge and cause disease outbreaks.

# Chapter 4

# Conclusions

This doctoral research comprehensively collected known and contributed new knowledge on viruses of tomato and the weed plants within and surrounding tomato agroecosystems. These information further enhanced our understanding of virus diversity, and portions of their ecology and epidemiology in such agroecosystems, that may serve as a model for similar studies in other crop plants.

First, we showed that the number of tomato viruses is underestimated and represent one of the largest numbers of distinct viruses associated with a certain plant. We showed that HTS accelerated the discovery and post-discovery characterization of novel tomato viruses, in the recent decade (2011–2020). This is evident for viruses that are of economic and phytosanitary importance, even for those not discovered through HTS. We synthesized information on economically important and possibly emerging tomato viruses for a wider audience, thus disseminating information for tomato virome research globally.

Second, we showed that there is still a vast undiscovered diversity of known and novel viruses, in tomatoes and various species of weed plants in tomato agroecosystems. We uncovered the vast diversity of 125 known and novel tomato viruses through the simultaneous and, by far, the largest exploration of viruses of a very diverse set of weed plant species surrounding an agroecosystem. Additionally, we showed that there are overlaps of presence of viruses in tomato and weed plants within or surrounding tomato farming areas, and that certain groups of evolutionarily-related viruses are associated with specific groups of taxonomically-related plant hosts. We showed that a novel virus of a family with a known wide host range that is found in weed plant(s) can infect plants of a botanical family different than its original weed host. This was for a novel Plantago tobamovirus 1, which belongs to a group of viruses of high economic and phytosanitary importance in crops, including tomato.

Third, we demonstrated that HTS could identify a previously undetected virus, Ranunculus white mottle ophiovirus, which is present in crop plants, including tomato. We reported the virus for the first time in vegetable crops from Europe, and that it is already present in Slovenian tomatoes and peppers for several years. With this, we demonstrated that previously undetected viruses circulating in tomato and other economically important crops and can be uncovered using HTS data. Hence, we demonstrated that HTS is suitable for proactive and unbiased monitoring of viruses in agroecosystems.

Our work has contributed to a comprehensive and deeper understanding of viruses in tomato and weed plants related to tomato production. Overall, we aimed to promote the importance and usefulness of HTS to uncover virus diversity in agroecosystems, monitor their distribution, uncover links to plant hosts, and understand portions of their biology, ecology and epidemiology. With the vast amount of data obtained through these plant viromic studies, useful contributions to illuminate the still undiscovered portion of the global virosphere can be made. More importantly, a deeper understanding of the properties and dynamics of viruses in agroecosystems can be obtained that will possibly aid in future studies in managing virus disease emergences.

# Appendix A

# Supplementary Materials of Publications

## A.1 Supplementary Material for Publication 2.1

Also available through the publisher's website:
https://www.frontiersin.org/articles/10.3389/fmicb.2021.671925/full#supplementary-material

**Steps made in collecting all tomato viruses** (Discussed in detail in the article):

1) Collect all the viruses containing "tomato" in their name from the latest master species list by the International Committee on Taxonomy of Viruses (ICTV) <https://talk.ictvonline.org/files/master-species-lists/m/msl/9601>.

2) To this list, add other viruses for which tomato is indicated as host in a curated list in Encyclopedia of Plant Viruses and Viroids <http://link.springer.com/10.1007/978-81-322-3912-3>.

3) Collect additional viruses (with tomato indicated as host) by mining complete genomes with supporting publications in GenBank and viral RefSeq in NCBI <https://www.ncbi.nlm.nih.gov/genbank/>, European Nucleotide Archive <https://www.ebi.ac.uk/ena/browser/home> and Virus-Host DB <https://www.genome.jp/virushostdb/>.

4) Additionally, tomato viruses with partial or unconfirmed full genomes, but with supporting publications and/or recognition by ICTV, were also included in the list.

**Table S1.** Meta-analysis of the extent of characterization of novel viruses discovered in tomato from 2011-2020.

Abbreviations and Legends used in **Table S1**:

| **Abbreviation** | |
|---|---|
| ssDNA | circular, positive sense, single stranded DNA (Group I) |
| (+)ssRNA | linear, positive/messenger sense, single stranded RNA (Group IV) |
| (-)ssRNA | linear, negative sense, single stranded RNA (Group V, wherein Tospoviridae and Phenuiviridae undergo ambisense transcription) |
| dsRNA | double stranded RNA (Group III) |
| total DNA-RCA | total DNA with rolling circle amplification |
| total RNA-RD | total RNA with rRNA depletion |
| sRNA | small RNA |
| N/A | not appplicable |
| | |
| **Legend:** | |
| 1 or Y | - means yes or affirmative |
| 0 or N | - means no or not affirmative |

**Table S1.** Meta-analysis of the extent of characterization of novel viruses discovered in tomato from 2011-2020.

| Family | Genus | Novel viruses discovered in tomato (2011-2020) | Acronym | Discovered through HTS? | extraction and library preparation approach | HTS (Illumina) platform used | year of first report | country of first report | ecoregion | primer design for detection | complete genome | gene diversity | genome diversity | survey at large scale | local survey | symptomatology | vector transmission | infectivity on original host | associated symptoms in field | co-infection with other viruses | infectivity on indicator hosts | natural host range | latent infection | total publications evaluated | years after first publication | number of criteria confirmed | First publications/reports (DOI) | Follow-up characterization studies / selected citing publications (DOI) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Alphasatellitidae* | unassigned | New alpha-satellite | - | Y | totDNA-RCA | HiSeq2500 | 2020 | Brazil | Neotropic | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | **1** | 0 | 4 | (dos Reis et al., 2020) | | | | |
| *Alphasatellitidae* | *Colecusatellite* | Tomato leaf curl Cameroon alphasatellite | ToLCCMA | N | N/A | N/A | 2011 | Cameroon | Afrotropic | 0 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **1** | 9 | 4 | (Leke et al., 2011) | | | | |
| *Bromoviridae* | *Ilarvirus* | Solanum nigrum ilarvirus 1 | SnIV1 | Y | dsRNA | HiSeq3000 | 2020 | France | Palearctic | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | **1** | 0 | 4 | (Ma et al., 2020) | | | | |
| *Bromoviridae* | *Ilarvirus* | Tomato necrotic streak virus | TomNSV | N | N/A | N/A | 2015 | USA | Nearctic | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | **2** | 5 | 10 | (Adkins et al., 2015) | (Badillo-Vargas et al., 2016) | | | |
| *Geminiviridae* | *Begomovirus* | New Begomovirus Species #1 | - | Y | totDNA-RCA | HiSeq2500 | 2020 | Brazil | Neotropic | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | **0** | 0 | 4 | (dos Reis et al., 2020) | | | | |
| *Geminiviridae* | *Begomovirus* | New Begomovirus Species #2 | - | Y | totDNA-RCA | HiSeq2500 | 2020 | Brazil | Neotropic | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | **0** | 0 | 4 | (dos Reis et al., 2020) | | | | |
| *Geminiviridae* | *Begomovirus* | New Begomovirus Species #3 | - | Y | totDNA-RCA | HiSeq2500 | 2020 | Brazil | Neotropic | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | **0** | 0 | 4 | (dos Reis et al., 2020) | | | | |
| *Geminiviridae* | *Begomovirus* | Pepper leafroll virus | PepLRV | N | N/A | N/A | 2014 | Peru | Neotropic | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | **2** | 6 | 11 | (Martínez-Ayala et al., 2014) | (Fiallo-Olivé et al., 2019) | | | |
| *Geminiviridae* | *Begomovirus* | Pepper yellow leaf curl Aceh virus | PepYLCAV | N | N/A | N/A | 2019 | Indonesia | Indo-Malay | 1 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | **1** | 1 | 6 | (Kesumawati et al., 2019) | | | | |
| *Geminiviridae* | *Begomovirus* | Tomato apical leaf curl virus | ToALCV | N | N/A | N/A | 2018 | Argentina | Neotropic | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | **1** | 2 | 8 | (Vaghi Medina et al., 2018) | | | | |
| *Geminiviridae* | *Begomovirus* | Tomato chlorotic leaf curl virus | ToCLCV | N | N/A | N/A | 2019 | Brazil | Neotropic | 0 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | **1** | 1 | 6 | (Quadros et al., 2019) | | | | |
| *Geminiviridae* | *Begomovirus* | Tomato chlorotic leaf distortion virus | TCLDV | N | N/A | N/A | 2011 | Venezuela | Neotropic | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | **1** | 9 | 7 | (Zambrano et al., 2011) | | | | |
| *Geminiviridae* | *Begomovirus* | Tomato dwarf leaf virus | ToDLV | N | N/A | N/A | 2012 | Argentina | Neotropic | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | **1** | 8 | 8 | (Vaghi Medina et al., 2012) | | | | |
| *Geminiviridae* | *Begomovirus* | Tomato interveinal chlorosis virus | ToICV | N | N/A | N/A | 2012 | Brazil | Neotropic | 0 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | **1** | 8 | 6 | (Albuquerque et al., 2012) | | | | |
| *Geminiviridae* | *Begomovirus* | Tomato interveinal chlorosis virus-2 | ToICV2 | Y | totDNA-RCA | HiSeq2000 | 2019 | Brazil | Neotropic | 1 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | **1** | 1 | 5 | (Rego-Machado et al., 2019) | | | | |
| *Geminiviridae* | *Begomovirus* | Tomato latent virus | TLV | N | N/A | N/A | 2016 | Cuba | Neotropic | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | **1** | 4 | 8 | (Fuentes et al., 2016) | | | | |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Burkina Faso virus | ToLCBFV | N | N/A | N/A | 2016 | Burkina Faso | Afrotropic | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | **1** | 4 | 6 | (Ouattara et al., 2017) | | | | |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Cameroon virus | ToLCCMV | N | N/A | N/A | 2011 | Cameroon | Afrotropic | 0 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **1** | 9 | 4 | (Leke et al., 2011) | | | | |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Kunene virus | ToLCKunV | N | N/A | N/A | 2020 | Namibia | Afrotropic | 0 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **1** | 0 | 4 | (Lett et al., 2020) | | | | |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Liwa virus | ToLCLV | N | N/A | N/A | 2014 | Oman | Palearctic | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 0 | 0 | **1** | 6 | 10 | (Khan et al., 2014) | | | | |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Mahé virus | ToLCMahV | N | N/A | N/A | 2018 | Seychelles | Afrotropic | 0 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **1** | 2 | 3 | (Scussel et al., 2018) | | | | |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Oman virus | ToLCOMV | N | N/A | N/A | 2011 | Oman | Palearctic | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 0 | 0 | **1** | 9 | 10 | (Idris et al., 2011) | | | | |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl purple vein virus | ToLCPVV | N | N/A | N/A | 2018 | Brazil | Neotropic | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 0 | 0 | **1** | 2 | 10 | (Macedo et al., 2018) | | | | |
| *Geminiviridae* | *Begomovirus* | Tomato leaf deformation virus | ToLDeV | N | N/A | N/A | 2011 | Peru | Neotropic | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 0 | 0 | **1** | 9 | 9 | (Márquez-Martín et al., 2011) | | | | |
| *Geminiviridae* | *Begomovirus* | Tomato mottle wrinkle virus | ToMoWV | N | N/A | N/A | 2015 | Argentina | Neotropic | 1 | 1 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | **1** | 5 | 7 | (Vaghi Medina et al., 2015) | | | | |
| *Geminiviridae* | *Begomovirus* | Tomato rugose yellow leaf curl virus | ToRYLCV | N | N/A | N/A | 2012 | Uruguay | Neotropic | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | **2** | 8 | 8 | (Márquez-Martín et al., 2012) | (Guerrero et al., 2013) | | | |
| *Geminiviridae* | *Begomovirus* | Tomato twisted leaf virus | ToTLV | N | N/A | N/A | 2019 | Venezuela | Neotropic | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 0 | 0 | **1** | 1 | 10 | (Romay et al., 2019) | | | | |
| *Geminiviridae* | *Begomovirus* | Tomato vein clearing leaf deformation virus | ToVCLDeV | N | N/A | N/A | 2020 | Argentina | Neotropic | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | **1** | 0 | 7 | (Vaghi Medina et al., 2020) | | | | |
| *Geminiviridae* | *Begomovirus* | Tomato wrinkled mosaic virus | ToWMV | N | N/A | N/A | 2018 | Venezuela | Neotropic | 0 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **1** | 2 | 4 | (Romay et al., 2018) | | | | |
| *Geminiviridae* | *Begomovirus* | Tomato yellow margin leaf curl virus | TYMLCV | N | N/A | N/A | 2013 | Venezuela | Neotropic | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | **1** | 7 | 8 | (Nava et al., 2013) | | | | |
| *Geminiviridae* | unassigned | Tomato associated geminivirus 1 | TaGV1 | Y | totDNA-RCA | HiSeq2500 | 2017 | Brazil | Neotropic | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | **1** | 3 | 8 | (Fontenele et al., 2017) | | | | |
| *Genomoviridae* | *Gemycircularvirus* | Plant-associated genomovirus 2 | - | Y | totDNA-RCA | HiSeq2500 | 2020 | Brazil | Neotropic | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | **0** | 0 | 4 | (dos Reis et al., 2020) | | | | |
| *Iflaviridae* | *Iflavirus* | Tomato matilda virus | TMaV | Y | total RNA | GAIIx | 2015 | Australia | Australasia | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | **1** | 5 | 4 | (Saqib et al., 2015) | | | | |
| *Kitaviridae* | *Blunervirus* | Tomato fruit blotch virus | ToFBV | Y | totRNA-RD | Illumina N/I | 2020 | Italy | Palearctic | 1 | 1 | 0 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **1** | 0 | 5 | (Ciuffo et al., 2020) | | | | |
| *Phenuiviridae* | *Tenuivirus* | Melon chlorotic spot virus | MeCSV | Y | sRNA | HiSeq | 2019 | France | Palearctic | 1 | 1 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | **1** | 1 | 9 | (Lecoq et al., 2019) | | | | |
| *Potyviridae* | *Potyvirus* | Tomato necrotic stunt virus | ToNSV | Y | sRNA | GA IIx | 2012 | Mexico | Nearctic | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | **3** | 8 | 11 | (Li et al., 2012) | (Li and Ling, 2014) | (Li et al., 2014) | | |
| *Rhabdoviridae* | *Cytorhabdovirus* | Tomato yellow mottle-associated virus | TYMaV | Y | sRNA | HiSeq2500 | 2017 | China | Indo-Malay | 1 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | **1** | 3 | 6 | (Xu et al., 2017) | | | | |
| *Tollecusatellitidae* | *Betasatellite* | Tomato leaf curl Hajipur betasatellite | ToLCHLB | N | N/A | N/A | 2013 | India | Indo-Malay | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 0 | 0 | 0 | **1** | 7 | 9 | (Kumar et al., 2013) | | | | |
| *Tollecusatellitidae* | *Betasatellite* | Tomato leaf curl Togo betasatellite | ToLCTGB | N | N/A | N/A | 2012 | Togo | Afrotropic | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 0 | 0 | **1** | 8 | 11 | (Kon and Gilbertson, 2012) | | | | |
| *Tospoviridae* | *Orthotospovirus* | Pepper necrotic spot virus | PNSV | N | N/A | N/A | 2012 | Peru | Neotropic | 1 | 0 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | 0 | 1 | 1 | 0 | **1** | 8 | 7 | (Torres et al., 2012) | | | | |
| *Tospoviridae* | *Orthotospovirus* | Tomato necrotic ringspot virus | TNRSV | N | N/A | N/A | 2011 | Thailand | Indo-Malay | 1 | 0 | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | **1** | 9 | 9 | (Seepiban et al., 2011) | | | | |
| *Tospoviridae* | *Orthotospovirus* | Tomato necrotic spot virus | TNSV | N | N/A | N/A | 2014 | China | Indo-Malay | 0 | 0 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | 1 | 1 | 0 | 0 | **1** | 6 | 6 | (Yin et al., 2014) | | | | |
| *Tymoviridae* | *Tymovirus* | Tomato blistering mosaic tymovirus | ToBMV | N | N/A | N/A | 2013 | Brazil | Neotropic | 1 | 1 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | **2** | 7 | 9 | (de Oliveira et al., 2013) | (Melo et al., 2014) | | | |
| *Virgaviridae* | *Tobamovirus* | Tomato brown rugose fruit virus | ToBRFV | N | N/A | N/A | 2016 | Jordan | Palearctic | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | **4** | 4 | 13 | (Salem et al., 2016) | (Luria et al., 2017) | (Levitzky et al., 2019) | (van de Vossenberg et al., 2020) | |
| *Virgaviridae* | *Tobamovirus* | Tomato mottle mosaic virus | ToMMV | Y | sRNA | HiSeq2000 | 2013 | Mexico | Nearctic | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | **4** | 7 | 11 | (Li et al., 2013) | (Li et al., 2017) | (Sui et al., 2016) | (Ambrós et al., 2016) | |

First Publications/Reports used in the meta-analyses:

Adkins, S., Baker, C. A., Badillo-Vargas, I. E., Frantz, G., Mellinger, H. C., Roe, N., et al. (2015). Necrotic streak disease of tomato in Florida caused by a new ilarvirus species related to Tulare apple mosaic virus. doi:10.5197/j.2044-0588.2015.031.016.

Albuquerque, L. C., Varsani, A., Fernandes, F. R., Pinheiro, B., Martin, D. P., de Tarso Oliveira Ferreira, P., et al. (2012). Further characterization of tomato-infecting begomoviruses in Brazil. Arch. Virol. 157, 747–752. doi:10.1007/s00705-011-1213-7.

Ciuffo, M., Kinoti, W. M., Tiberini, A., Forgia, M., Tomassoli, L., Constable, F. E., et al. (2020). A new blunervirus infects tomato crops in Italy and Australia. Arch. Virol. 165, 2379–2384. doi:10.1007/s00705-020-04760-x.

de Oliveira, V. C., Nagata, T., Guimarães, F. C., Ferreira, F. A., Kitajima, E. W., Nicolini, C., et al. (2013). Characterization of a novel tymovirus on tomato plants in Brazil. Virus Genes 46, 190–194. doi:10.1007/s11262-012-0830-x.

dos Reis, L. d. N. A., Fonseca, M. E. de N., Ribeiro, S. G., Naito, F. Y. B., Boiteux, L. S., and Pereira-Carvalho, R. de C. (2020). Metagenomics of Neotropical Single-Stranded DNA Viruses in Tomato Cultivars with and without the Ty-1 Gene. Viruses 12, 819. doi:10.3390/v12080819.

Fontenele, R. S., Lamas, N. S., Lacorte, C., Lacerda, A. L. M., Varsani, A., and Ribeiro, S. G. (2017). A novel geminivirus identified in tomato and cleome plants sampled in Brazil. Virus Res. 240, 175–179. doi:https://doi.org/10.1016/j.virusres.2017.08.007.

Fuentes, A., Carlos, N., Ruiz, Y., Callard, D., Sánchez, Y., Ochagavía, M. E., et al. (2016). Field Trial and Molecular Characterization of RNAi-Transgenic Tomato Plants That Exhibit Resistance to Tomato Yellow Leaf Curl Geminivirus. Mol. Plant-Microbe Interact. 29, 197–209. doi:10.1094/MPMI-08-15-0181-R.

Idris, A. M., Shahid, M. S., Briddon, R. W., Khan, A. J., Zhu, J. K., and Brown, J. K. (2011). An unusual alphasatellite associated with monopartite begomoviruses attenuates symptoms and reduces betasatellite accumulation. J. Gen. Virol. 92, 706–717. doi:10.1099/vir.0.025288-0.

Kesumawati, E., Okabe, S., Homma, K., Fujiwara, I., Zakaria, S., Kanzaki, S., et al. (2019). Pepper yellow leaf curl Aceh virus: a novel bipartite begomovirus isolated from chili pepper, tomato, and tobacco plants in Indonesia. Arch. Virol. 164, 2379–2383. doi:10.1007/s00705-019-04316-8.

Khan, A. J., Akhtar, S., Singh, A. K., Al-Shehi, A. A., Al-Matrushi, A. M., Ammara, U., et al. (2014). Recent evolution of a novel begomovirus causing tomato leaf curl disease in the Al-Batinah region of Oman. Arch. Virol. 159, 445–455. doi:10.1007/s00705-013-1853-x.

Kon, T., and Gilbertson, R. L. (2012). Two genetically related begomoviruses causing tomato leaf curl disease in Togo and Nigeria differ in virulence and host range but do not require a betasatellite for induction of disease symptoms. Arch. Virol. 157, 107–120. doi:10.1007/s00705-011-1139-0.

Kumar, J., Gunapati, S., Singh, S. P., Kumar, A., Lalit, A., Sharma, N. C., et al. (2013). A new betasatellite associated with cotton leaf curl Burewala virus infecting tomato in

India: influence on symptoms and viral accumulation. Arch. Virol. 158, 1349–1353. doi:10.1007/s00705-013-1613-y.

Lecoq, H., Wipf-Scheibel, C., Verdin, E., and Desbiez, C. (2019). Characterization of the first tenuivirus naturally infecting dicotyledonous plants. Arch. Virol. 164, 297–301. doi:10.1007/s00705-018-4057-6.

Leke, W. N., Kvarnheden, A., Ngane, E. B., Titanji, V. P. K., and Brown, J. K. (2011). Molecular characterization of a new begomovirus and divergent alphasatellite from tomato in Cameroon. Arch. Virol. 156, 925–928. doi:10.1007/s00705-011-0957-4.

Lett, J.-M., Ncho, J., Claverie, S., Hoareau, M., Lefeuvre, P., De Cauwer, V., et al. (2020). Tomato leaf curl Kunene virus: a novel tomato-infecting monopartite begomovirus from Namibia. Arch. Virol. 165, 1887–1889. doi:10.1007/s00705-020-04666-8.

Li, R., Gao, S., Fei, Z., and Ling, K.-S. (2013). Complete Genome Sequence of a New Tobamovirus Naturally Infecting Tomatoes in Mexico. Genome Announc. 1, e00794-13. doi:10.1128/genomeA.00794-13.

Li, R., Gao, S., Hernandez, A. G., Wechter, W. P., Fei, Z., and Ling, K.-S. (2012). Deep Sequencing of Small RNAs in Tomato for Virus and Viroid Identification and Strain Differentiation. PLoS One 7, e37127. doi:10.1371/journal.pone.0037127.

Ma, Y., Marais, A., Lefebvre, M., Faure, C., and Candresse, T. (2020). Metagenomic analysis of virome cross-talk between cultivated Solanum lycopersicum and wild Solanum nigrum. Virology 540, 38–44. doi:10.1016/j.virol.2019.11.009.

Macedo, M. A., Albuquerque, L. C., Maliano, M. R., Souza, J. O., Rojas, M. R., Inoue-Nagata, A. K., et al. (2018). Characterization of tomato leaf curl purple vein virus, a new monopartite New World begomovirus infecting tomato in Northeast Brazil. Arch. Virol. 163, 737–743. doi:10.1007/s00705-017-3662-0.

Márquez-Martín, B., Aragón-Caballero, L., Fiallo-Olivé, E., Navas-Castillo, J., and Moriones, E. (2011). Tomato leaf deformation virus, a novel begomovirus associated with a severe disease of tomato in Peru. Eur. J. Plant Pathol. 129, 1–7. doi:10.1007/s10658-010-9699-5.

Márquez-Martín, B., Maeso, D., Martínez-Ayala, A., Bernal, R., Teresa Federici, M., Vincelli, P., et al. (2012). Diverse population of a new bipartite begomovirus infecting tomato crops in Uruguay. Arch. Virol. 157, 1137–1142. doi:10.1007/s00705-012-1262-6.

Martínez-Ayala, A., Sánchez-Campos, S., Cáceres, F., Aragón-Caballero, L., Navas-Castillo, J., and Moriones, E. (2014). Characterisation and genetic diversity of pepper leafroll virus, a new bipartite begomovirus infecting pepper, bean and tomato in Peru. Ann. Appl. Biol. 164, 62–72. doi:10.1111/aab.12074.

Nava, A., Londoño, A., and Polston, J. E. (2013). Characterization and distribution of tomato yellow margin leaf curl virus, a begomovirus from Venezuela. Arch. Virol. 158, 399–406. doi:10.1007/s00705-012-1501-x.

Ouattara, A., Tiendrébéogo, F., Lefeuvre, P., Claverie, S., Hoareau, M., Traoré, E. V., et al. (2017). Tomato leaf curl Burkina Faso virus: a novel tomato-infecting monopartite begomovirus from Burkina Faso. Arch. Virol. 162, 1427–1429. doi:10.1007/s00705-017-3231-6.

Quadros, A. F. F., Silva, J. P., Xavier, C. A. D., Zerbini, F. M., and Boari, A. J. (2019). Two new begomoviruses infecting tomato and Hibiscus sp. in the Amazon region of Brazil. Arch. Virol. 164, 1897–1901. doi:10.1007/s00705-019-04245-6.

Rego-Machado, C. M., Nakasu, E. Y. T., Blawid, R., Nagata, T., and Inoue-Nagata, A. K. (2019). Complete genome sequence of a new bipartite begomovirus infecting tomato in Brazil. Arch. Virol. 164, 2873–2875. doi:10.1007/s00705-019-04380-0.

Romay, G., Chirinos, D. T., Geraud-Pouey, F., Gillis, A., Mahillon, J., and Bragard, C. (2018). Complete genome sequence of two tomato-infecting begomoviruses in Venezuela: evidence of a putative novel species and a novel recombinant strain. Arch. Virol. 163, 555–558. doi:10.1007/s00705-017-3611-y.

Romay, G., Geraud-Pouey, F., Chirinos, D., Mahillon, M., Gillis, A., Mahillon, J., et al. (2019). Tomato Twisted Leaf Virus: A Novel Indigenous New World Monopartite Begomovirus Infecting Tomato in Venezuela. Viruses 11, 327. doi:10.3390/v11040327.

Salem, N., Mansour, A., Ciuffo, M., Falk, B. W., and Turina, M. (2016). A new tobamovirus infecting tomato crops in Jordan. Arch. Virol. 161, 503–506. doi:10.1007/s00705-015-2677-7.

Saqib, M., Wylie, S. J., and Jones, M. G. K. (2015). Serendipitous identification of a new Iflavirus -like virus infecting tomato and its subsequent characterization. Plant Pathol. 64, 519–527. doi:10.1111/ppa.12293.

Scussel, S., Claverie, S., Hoareau, M., Moustache, R., Delatte, H., Lefeuvre, P., et al. (2018). Tomato leaf curl Mahé virus: a novel tomato-infecting monopartite begomovirus from the Seychelles. Arch. Virol. 163, 3451–3453. doi:10.1007/s00705-018-4007-3.

Seepiban, C., Gajanandana, O., Attathom, T., and Attathom, S. (2011). Tomato necrotic ringspot virus, a new tospovirus isolated in Thailand. Arch. Virol. 156, 263–274. doi:10.1007/s00705-010-0856-0.

Torres, R., Larenas, J., Fribourg, C., and Romero, J. (2012). Pepper necrotic spot virus, a new tospovirus infecting solanaceous crops in Peru. Arch. Virol. 157, 609–615. doi:10.1007/s00705-011-1217-3.

Vaghi Medina, C. G., Bornancini, V. A., and López Lambertini, P. M. (2020). Tomato vein clearing leaf deformation virus, a new begomovirus species infecting tomato in Argentina. Eur. J. Plant Pathol. 156, 285–290. doi:10.1007/s10658-019-01835-7.

Vaghi Medina, C. G., L. Lambertini, P. M., and Al, E. (2012). Tomato dwarf leaf virus, a New World begomovirus infecting tomato in Argentina. Arch. Virol. 157, 1975–1980. doi:10.1007/s00705-012-1355-2.

Vaghi Medina, C. G., Martin, D. P., and López Lambertini, P. M. (2015). Tomato mottle wrinkle virus, a recombinant begomovirus infecting tomato in Argentina. Arch. Virol. 160, 581–585. doi:10.1007/s00705-014-2216-y.

Vaghi Medina, C. G., Teppa, E., Bornancini, V. A., Flores, C. R., Marino-Buslje, C., and López Lambertini, P. M. (2018). Tomato Apical Leaf Curl Virus: A Novel, Monopartite Geminivirus Detected in Tomatoes in Argentina. Front. Microbiol. 8, 1–11. doi:10.3389/fmicb.2017.02665.

Xu, C., Sun, X., Taylor, A., Jiao, C., Xu, Y., Cai, X., et al. (2017). Diversity, Distribution, and Evolution of Tomato Viruses in China Uncovered by Small RNA Sequencing. J. Virol. 91. doi:10.1128/JVI.00173-17.

Yin, Y., Zheng, K., Dong, J., Fang, Q., Wu, S., Wang, L., et al. (2014). Identification of a new tospovirus causing necrotic ringspot on tomato in China. Virol. J. 11, 213. doi:10.1186/s12985-014-0213-0.

Zambrano, K., Geraud-Pouey, F., Chirinos, D., Romay, G., and Marys, E. (2011). Tomato chlorotic leaf distortion virus, a new bipartite begomovirus infecting Solanum lycopersicum and Capsicum chinense in Venezuela. Arch. Virol. 156, 2263–2266. doi:10.1007/s00705-011-1093-x.

Selected follow-up studies/citing publications used in the meta-analyses:

Ambrós, S., Martínez, F., Ivars, P., Hernández, C., De La Iglesia, F., and Elena, S. F. (2016). Molecular and biological characterization of an isolate of Tomato mottle mosaic virus (ToMMV) infecting tomato and other experimental hosts in a greenhouse in Valencia, Spain. bioRxiv. doi:10.1101/063255.

Badillo-Vargas, I. E., Baker, C. A., Turechek, W. W., Frantz, G., Mellinger, H. C., Funderburk, J. E., et al. (2016). Genomic and Biological Characterization of Tomato necrotic streak virus, a Novel Subgroup 2 Ilarvirus Infecting Tomato in Florida. Plant Dis. 100, 1046–1053. doi:10.1094/PDIS-12-15-1437-RE.

Fiallo-Olivé, E., Chirinos, D. T., Castro, R., and Navas-Castillo, J. (2019). A Novel Strain of Pepper Leafroll Virus Infecting Common Bean and Soybean in Ecuador. Plant Dis. 103, 167. doi:10.1094/PDIS-06-18-1076-PDN.

Guerrero, E. Ben, De Francesco, A., García, M. L., Balatti, P. A., and Bó, E. D. (2013). First Report of Tomato rugose yellow leaf curl virus Infecting Tomato in Argentina. Plant Dis. 97, 1662–1662. doi:10.1094/PDIS-01-13-0003-PDN.

Levitzky, N., Smith, E., Lachman, O., Luria, N., Mizrahi, Y., Bakelman, H., et al. (2019). The bumblebee Bombus terrestris carries a primary inoculum of Tomato brown rugose fruit virus contributing to disease spread in tomatoes. PLoS One 14, e0210871. Available at: https://doi.org/10.1371/journal.pone.0210871.

Li, R., Fei, Z., and Ling, K.-S. (2014). Molecular and biological properties of tomato necrotic stunt virus and development of a sensitive real-time RT-PCR assay. Arch. Virol. 159, 353–358. doi:10.1007/s00705-013-1830-4.

Li, R., and Ling, K. S. (2014). Development of reverse transcription loop-mediated isothermal amplification assay for rapid detection of an emerging potyvirus: Tomato necrotic stunt virus. J. Virol. Methods 200, 35–40. doi:10.1016/j.jviromet.2014.01.017.

Li, Y., Wang, Y., Hu, J., Xiao, L., Tan, G., Lan, P., et al. (2017). The complete genome sequence, occurrence and host range of Tomato mottle mosaic virus Chinese isolate. Virol. J. 14, 15. doi:10.1186/s12985-016-0676-2.

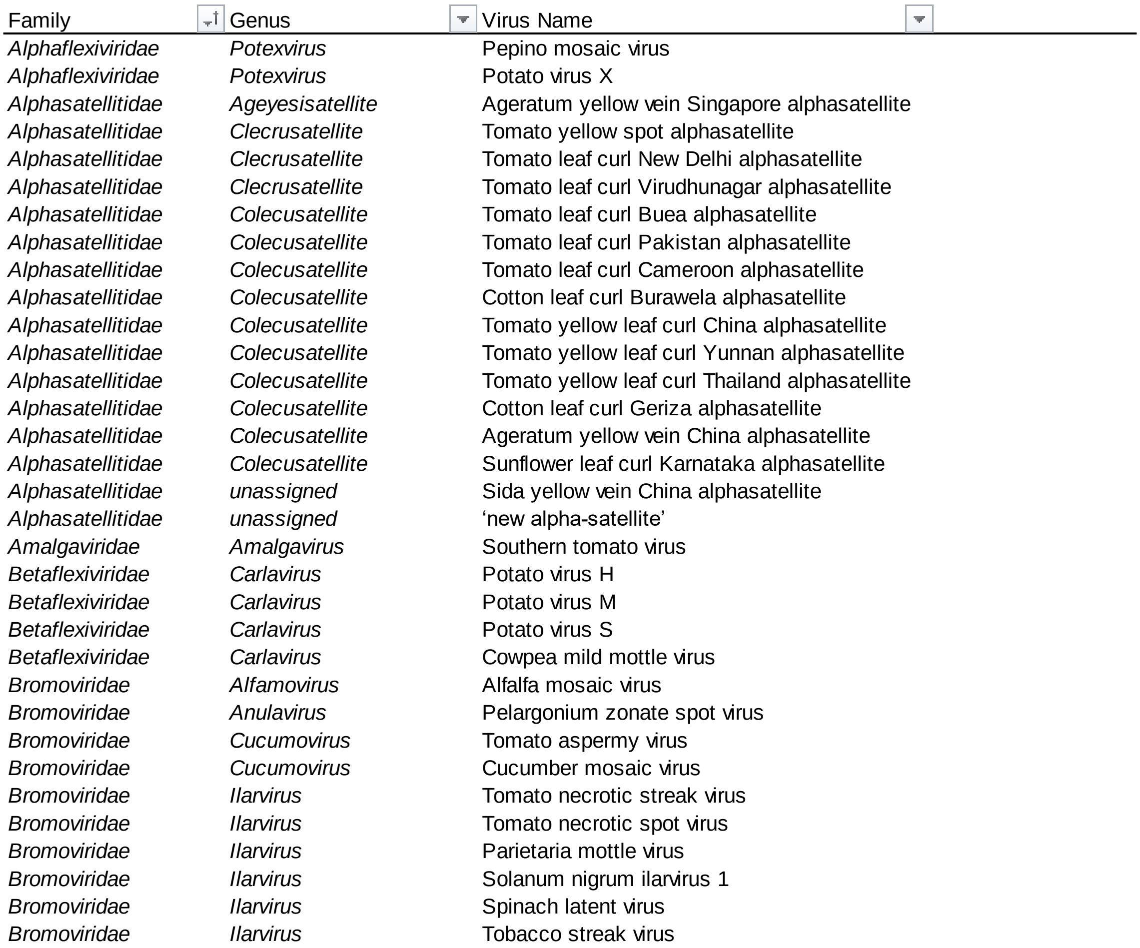
Luria, N., Smith, E., Reingold, V., Bekelman, I., Lapidot, M., Levin, I., et al. (2017). A New Israeli Tobamovirus Isolate Infects Tomato Plants Harboring Tm-22 Resistance Genes. PLoS One 12, e0170429. doi:10.1371/journal.pone.0170429.

Melo, F. L., Fernandes, J. E. A., Ribeiro, B. M., and Ribeiro, S. G. (2014). Complete Genome Sequence of a Tobacco-Infecting, Tomato-Blistering Mosaic Virus. Genome Announc. 2, 701–715. doi:10.1128/genomeA.00701-14.

Sui, X., Zheng, Y., Li, R., Padmanabhan, C., Tian, T., Groth-Helms, D., et al. (2016). Molecular and Biological Characterization of Tomato mottle mosaic virus and Development of RT-PCR Detection. Plant Dis. 101, 704–711. doi:10.1094/PDIS-10-16-1504-RE.

van de Vossenberg, B. T. L. H., Visser, M., Bruinsma, M., Koenraadt, H. M. S., Westenberg, M., and Botermans, M. (2020). Real-time tracking of Tomato brown rugose fruit virus (ToBRFV) outbreaks in the Netherlands using Nextstrain. PLoS One 15, e0234671. doi:10.1371/journal.pone.0234671.

**Table S2**. Summary list of all viruses with tomato indicated as host based on review of literature and different databases.



| Family | Genus | Virus Name |
|---|---|---|
| *Alphaflexiviridae* | *Potexvirus* | Pepino mosaic virus |
| *Alphaflexiviridae* | *Potexvirus* | Potato virus X |
| *Alphasatellitidae* | *Ageyesisatellite* | Ageratum yellow vein Singapore alphasatellite |
| *Alphasatellitidae* | *Clecrusatellite* | Tomato yellow spot alphasatellite |
| *Alphasatellitidae* | *Clecrusatellite* | Tomato leaf curl New Delhi alphasatellite |
| *Alphasatellitidae* | *Clecrusatellite* | Tomato leaf curl Virudhunagar alphasatellite |
| *Alphasatellitidae* | *Colecusatellite* | Tomato leaf curl Buea alphasatellite |
| *Alphasatellitidae* | *Colecusatellite* | Tomato leaf curl Pakistan alphasatellite |
| *Alphasatellitidae* | *Colecusatellite* | Tomato leaf curl Cameroon alphasatellite |
| *Alphasatellitidae* | *Colecusatellite* | Cotton leaf curl Burawela alphasatellite |
| *Alphasatellitidae* | *Colecusatellite* | Tomato yellow leaf curl China alphasatellite |
| *Alphasatellitidae* | *Colecusatellite* | Tomato yellow leaf curl Yunnan alphasatellite |
| *Alphasatellitidae* | *Colecusatellite* | Tomato yellow leaf curl Thailand alphasatellite |
| *Alphasatellitidae* | *Colecusatellite* | Cotton leaf curl Geriza alphasatellite |
| *Alphasatellitidae* | *Colecusatellite* | Ageratum yellow vein China alphasatellite |
| *Alphasatellitidae* | *Colecusatellite* | Sunflower leaf curl Karnataka alphasatellite |
| *Alphasatellitidae* | *unassigned* | Sida yellow vein China alphasatellite |
| *Alphasatellitidae* | *unassigned* | ‘new alpha-satellite’ |
| *Amalgaviridae* | *Amalgavirus* | Southern tomato virus |
| *Betaflexiviridae* | *Carlavirus* | Potato virus H |
| *Betaflexiviridae* | *Carlavirus* | Potato virus M |
| *Betaflexiviridae* | *Carlavirus* | Potato virus S |
| *Betaflexiviridae* | *Carlavirus* | Cowpea mild mottle virus |
| *Bromoviridae* | *Alfamovirus* | Alfalfa mosaic virus |
| *Bromoviridae* | *Anulavirus* | Pelargonium zonate spot virus |
| *Bromoviridae* | *Cucumovirus* | Tomato aspermy virus |
| *Bromoviridae* | *Cucumovirus* | Cucumber mosaic virus |
| *Bromoviridae* | *Ilarvirus* | Tomato necrotic streak virus |
| *Bromoviridae* | *Ilarvirus* | Tomato necrotic spot virus |
| *Bromoviridae* | *Ilarvirus* | Parietaria mottle virus |
| *Bromoviridae* | *Ilarvirus* | Solanum nigrum ilarvirus 1 |
| *Bromoviridae* | *Ilarvirus* | Spinach latent virus |
| *Bromoviridae* | *Ilarvirus* | Tobacco streak virus |

**Table S2** (continued rows)

| Family | Genus | Virus Name |
|---|---|---|
| *Closteroviridae* | *Crinivirus* | Lettuce chlorosis virus |
| *Closteroviridae* | *Crinivirus* | Potato yellow vein virus |
| *Closteroviridae* | *Crinivirus* | Tomato chlorosis virus |
| *Closteroviridae* | *Crinivirus* | Tomato infectious chlorosis virus |
| *Geminiviridae* | *Becurtovirus* | Beet curly top Iran virus |
| *Geminiviridae* | *Begomovirus* | Ageratum enation virus |
| *Geminiviridae* | *Begomovirus* | Ageratum yellow vein Hualian virus |
| *Geminiviridae* | *Begomovirus* | Ageratum yellow vein China virus |
| *Geminiviridae* | *Begomovirus* | Ageratum yellow vein virus |
| *Geminiviridae* | *Begomovirus* | Bean golden mosaic virus |
| *Geminiviridae* | *Begomovirus* | Chilli leaf curl virus |
| *Geminiviridae* | *Begomovirus* | Chino del tomate Amazonas virus |
| *Geminiviridae* | *Begomovirus* | Chino del tomate virus |
| *Geminiviridae* | *Begomovirus* | Cotton leaf curl Burewala virus |
| *Geminiviridae* | *Begomovirus* | Cotton leaf curl Geriza virus |
| *Geminiviridae* | *Begomovirus* | Cotton leaf curl Kokhran virus |
| *Geminiviridae* | *Begomovirus* | Cotton leaf curl Multan virus |
| *Geminiviridae* | *Begomovirus* | Croton yellow vein mosaic virus |
| *Geminiviridae* | *Begomovirus* | Eupatorium yellow vein virus |
| *Geminiviridae* | *Begomovirus* | Euphorbia yellow mosaic |
| *Geminiviridae* | *Begomovirus* | Honeysuckle yellow vein virus |
| *Geminiviridae* | *Begomovirus* | Lindernia anagallis yellow vein virus |
| *Geminiviridae* | *Begomovirus* | Malvastrum yellow vein virus |
| *Geminiviridae* | *Begomovirus* | Melon chlorotic leaf curl virus |
| *Geminiviridae* | *Begomovirus* | Merremia mosaic virus |
| *Geminiviridae* | *Begomovirus* | Mungbean yellow mosaic Indian virus |
| *Geminiviridae* | *Begomovirus* | Papaya leaf curl China virus |
| *Geminiviridae* | *Begomovirus* | Pedilanthus leaf curl virus |
| *Geminiviridae* | *Begomovirus* | Pepper golden mosaic virus |
| *Geminiviridae* | *Begomovirus* | Pepper huasteco yellow vein virus |
| *Geminiviridae* | *Begomovirus* | Pepper leafroll virus |
| *Geminiviridae* | *Begomovirus* | Pepper yellow leaf curl Aceh virus |
| *Geminiviridae* | *Begomovirus* | Pepper yellow leaf curl Indonesia virus |
| *Geminiviridae* | *Begomovirus* | Pepper yellow leaf curl Thailand virus |
| *Geminiviridae* | *Begomovirus* | Pepper yellow vein Mali virus |
| *Geminiviridae* | *Begomovirus* | Peru tomato mosaic virus |
| *Geminiviridae* | *Begomovirus* | Potato yellow mosaic Panama virus |
| *Geminiviridae* | *Begomovirus* | Potato yellow mosaic Trinidad virus |
| *Geminiviridae* | *Begomovirus* | Sida micrantha mosaic virus |
| *Geminiviridae* | *Begomovirus* | Tobacco curly shoot virus |
| *Geminiviridae* | *Begomovirus* | Tobacco leaf curl Japan virus |
| *Geminiviridae* | *Begomovirus* | Tobacco leaf curl Kochi virus |
| *Geminiviridae* | *Begomovirus* | Tobacco leaf curl Thailand virus |
| *Geminiviridae* | *Begomovirus* | Tobacco leaf curl virus |
| *Geminiviridae* | *Begomovirus* | Tomato bright yellow mosaic virus |
| *Geminiviridae* | *Begomovirus* | Tomato bright yellow mottle virus |
| *Geminiviridae* | *Begomovirus* | Tomato chino La Paz virus |
| *Geminiviridae* | *Begomovirus* | Tomato chlorotic leaf curl virus |
| *Geminiviridae* | *Begomovirus* | Tomato chlorotic leaf distortion virus |
| *Geminiviridae* | *Begomovirus* | Tomato chlorotic mottle Guyane virus |
| *Geminiviridae* | *Begomovirus* | Tomato chlorotic mottle virus |
| *Geminiviridae* | *Begomovirus* | Tomato common mosaic virus |
| *Geminiviridae* | *Begomovirus* | Tomato curly stunt virus |
| *Geminiviridae* | *Begomovirus* | Tomato dwarf leaf virus |
| *Geminiviridae* | *Begomovirus* | Tomato enation leaf curl virus |
| *Geminiviridae* | *Begomovirus* | Tomato golden leaf distortion virus |
| *Geminiviridae* | *Begomovirus* | Tomato golden leaf spot virus |
| *Geminiviridae* | *Begomovirus* | Tomato golden mosaic virus |
| *Geminiviridae* | *Begomovirus* | Tomato golden mottle virus |
| *Geminiviridae* | *Begomovirus* | Tomato golden vein virus |

**Table S2** (continued rows)

| Family | Genus | Virus Name |
|---|---|---|
| *Geminiviridae* | *Begomovirus* | Tomato interveinal chlorosis virus |
| *Geminiviridae* | *Begomovirus* | Tomato latent virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Anjouan virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Arusha virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Barka virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Bangalore virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Bangladesh virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Burkina Faso virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Cebu virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl China virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Comoros virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Cotabato virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Diana virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Gandhinagar virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Ghana virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Guangdong virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Guangxi virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Gujarat virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Hainan virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Hanoi virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Hsinchu virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Iran virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Japan virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Java virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Joydebpur virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Karnataka virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Karnataka virus 2 |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Karnataka virus 3 |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Kerala virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Kumasi virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Laos virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Liwa virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Madagascar virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Mahe virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Malaysia virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Mali virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Mayotte virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Mindanao virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Moheli virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Namakely virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl New Delhi virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl New Delhi virus 2 |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl New Delhi virus 4 |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl New Delhi virus 5 |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Nigeria virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Oman virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Palampur virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Patna virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Philippines virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Pune virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl purple vein virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Rajasthan virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Ranchi virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Seychelles virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Sinaloa virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Sri Lanka virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Sudan virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Sulawesi virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Taiwan virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Tanzania virus |

**Table S2** (continued rows)

| Family | Genus | Virus Name |
|---|---|---|
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Toliara virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Uganda virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Vietnam virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf deformation virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf distortion virus |
| *Geminiviridae* | *Begomovirus* | Tomato mild mosaic virus |
| *Geminiviridae* | *Begomovirus* | Tomato mild yellow leaf curl Aragua virus |
| *Geminiviridae* | *Begomovirus* | Tomato mosaic Havana virus |
| *Geminiviridae* | *Begomovirus* | Tomato mottle leaf curl virus |
| *Geminiviridae* | *Begomovirus* | Tomato mottle Taino virus |
| *Geminiviridae* | *Begomovirus* | Tomato mottle virus |
| *Geminiviridae* | *Begomovirus* | Tomato mottle wrinkle virus |
| *Geminiviridae* | *Begomovirus* | Tomato rugose mosaic virus |
| *Geminiviridae* | *Begomovirus* | Tomato rugose yellow leaf curl virus |
| *Geminiviridae* | *Begomovirus* | Tomato severe leaf curl Kalakada virus |
| *Geminiviridae* | *Begomovirus* | Tomato severe leaf curl virus |
| *Geminiviridae* | *Begomovirus* | Tomato severe rugose virus |
| *Geminiviridae* | *Begomovirus* | Tomato twisted leaf virus |
| *Geminiviridae* | *Begomovirus* | Tomato wrinkled mosaic virus |
| *Geminiviridae* | *Begomovirus* | Tomato yellow leaf curl Axarquia virus |
| *Geminiviridae* | *Begomovirus* | Tomato yellow leaf curl China virus |
| *Geminiviridae* | *Begomovirus* | Tomato yellow leaf curl Guangdong virus |
| *Geminiviridae* | *Begomovirus* | Tomato yellow leaf curl Indonesia virus |
| *Geminiviridae* | *Begomovirus* | Tomato yellow leaf curl Kanchanaburi virus |
| *Geminiviridae* | *Begomovirus* | Tomato yellow leaf curl Malaga virus |
| *Geminiviridae* | *Begomovirus* | Tomato yellow leaf curl Mali virus |
| *Geminiviridae* | *Begomovirus* | Tomato yellow leaf curl Sardinia virus |
| *Geminiviridae* | *Begomovirus* | Tomato yellow leaf curl Saudi virus |
| *Geminiviridae* | *Begomovirus* | Tomato yellow leaf curl Shuangbai virus |
| *Geminiviridae* | *Begomovirus* | Tomato yellow leaf curl Thailand virus |
| *Geminiviridae* | *Begomovirus* | Tomato yellow leaf curl Vietnam virus |
| *Geminiviridae* | *Begomovirus* | Tomato yellow leaf curl virus |
| *Geminiviridae* | *Begomovirus* | Tomato yellow leaf curl Yunnan virus |
| *Geminiviridae* | *Begomovirus* | Tomato yellow leaf distortion virus |
| *Geminiviridae* | *Begomovirus* | Tomato yellow margin leaf curl virus |
| *Geminiviridae* | *Begomovirus* | Tomato yellow mosaic virus |
| *Geminiviridae* | *Begomovirus* | Tomato yellow mottle virus |
| *Geminiviridae* | *Begomovirus* | Tomato yellow spot virus |
| *Geminiviridae* | *Begomovirus* | Tomato yellow vein streak virus |
| *Geminiviridae* | *Begomovirus* | Tomato interveinal chlorosis virus-2 |
| *Geminiviridae* | *Begomovirus* | Tomato vein clearing leaf deformation virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Kunene virus |
| *Geminiviridae* | *Begomovirus* | Tomato leaf curl Cameroon virus |
| *Geminiviridae* | *Begomovirus* | ‘new Begomovirus Species #1’ |
| *Geminiviridae* | *Begomovirus* | ‘new Begomovirus Species #2’ |
| *Geminiviridae* | *Begomovirus* | ‘new Begomovirus Species #3’ |
| *Geminiviridae* | *Capulavirus* | Euphorbia caput-medusae latent virus |
| *Geminiviridae* | *Curtovirus* | Beet curly top virus |
| *Geminiviridae* | *Mastrevirus* | Chickpea chlorotic dwarf virus-tomato |
| *Geminiviridae* | *Topocuvirus* | Tomato pseudo-curly top virus |
| *Geminiviridae* | *unassigned* | Tomato apical leaf curl virus |
| *Geminiviridae* | *unassigned* | ‘tomato associated geminivirus 1’ |
| *Genomoviridae* | *Genomovirus* | ‘plant-associated genomovirus 2’ |
| *Iflaviridae* | *Iflavirus* | Tomato matilda virus |
| *Kitaviridae* | *Blunervirus* | Tomato fruit blotch virus |
| *Luteoviridae* | *Polerovirus* | Turnip yellows virus |
| *Luteoviridae* | *Polerovirus* | Potato leafroll virus |
| *Nanoviridae* | *Nanovirus* | Milk vetch dwarf virus |
| *Phenuiviridae* | *Tenuivurus* | Melon chlorotic spot virus |

**Table S2** (continued rows)

| Family | Genus | Virus Name |
|---|---|---|
| *Pospiviroidae* | *Pospiviroid* | Tomato apical stunt viroid |
| *Pospiviroidae* | *Pospiviroid* | Tomato chlorotic dwarf viroid |
| *Pospiviroidae* | *Pospiviroid* | Tomato planta macho viroid |
| *Pospiviroidae* | *Pospiviroid* | Pepper chat fruit viroid |
| *Pospiviroidae* | *Pospiviroid* | Potato spindle tuber viroid |
| *Pospiviroidae* | *Pospiviroid* | Chrysanthemum stunt viroid |
| *Pospiviroidae* | *Pospiviroid* | Columnea latent viroid |
| *Pospiviroidae* | *Pospiviroid* | Citrus exocortis viroid |
| *Potyviridae* | *Ipomovirus* | Tomato mild mottle virus |
| *Potyviridae* | *Potyvirus* | Peru tomato mosaic virus |
| *Potyviridae* | *Potyvirus* | Tomato necrotic stunt virus |
| *Potyviridae* | *Potyvirus* | Tobacco etch virus |
| *Potyviridae* | *Potyvirus* | Mediterranean ruda virus |
| *Potyviridae* | *Potyvirus* | Wild potato mosaic virus |
| *Potyviridae* | *Potyvirus* | Wild tomato mosaic virus |
| *Potyviridae* | *Potyvirus* | Pepper mottle virus |
| *Potyviridae* | *Potyvirus* | Pepper veinal mottle virus |
| *Potyviridae* | *Potyvirus* | Pepper yellow mosaic virus |
| *Potyviridae* | *Potyvirus* | Tobacco vein banding mosaic virus |
| *Potyviridae* | *Potyvirus* | Potato virus A |
| *Potyviridae* | *Potyvirus* | Potato virus Y |
| *Potyviridae* | *Potyvirus* | Henbane mosaic virus |
| *Potyviridae* | *Potyvirus* | Chili veinal mottle virus |
| *Rhabdoviridae* | *Alphanucleorhabdovirus* | Physostegia chlorotic mottle virus |
| *Rhabdoviridae* | *Alphanucleorhabdovirus* | Eggplant mottled dwarf virus |
| *Rhabdoviridae* | *Cytorhabdovirus* | Tomato yellow mottle-associated virus |
| *Secoviridae* | *Cheravirus* | Cherry rasp leaf virus-tomato |
| *Secoviridae* | *Nepovirus* | Tomato black ring virus |
| *Secoviridae* | *Nepovirus* | Tomato ringspot virus |
| *Secoviridae* | *Nepovirus* | Tobacco ringspot virus |
| *Secoviridae* | *Torradovirus* | Tomato marchitez virus |
| *Secoviridae* | *Torradovirus* | Tomato necrotic dwarf virus |
| *Secoviridae* | *Torradovirus* | Tomato torrado virus |
| *Secoviridae* | *Torradovirus* | Tomato chocolate spot virus |
| *Secoviridae* | *Torradovirus* | Tomato chocolàte virus |
| *Tolecusatellitidae* | *Betasatellite* | Ageratum yellow vein betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Ageratum leaf curl Cameroon betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Chili leaf curl betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Cotton leaf curl Gezira betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Honeysuckle yellow vein betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tobacco leaf curl Japan betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tobacco leaf curl Yunnan betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato begomovirus satellite DNA beta |
| *Tolecusatellitidae* | *Betasatellite* | Tomato leaf curl Hajipur betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato leaf curl Bangalore betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato leaf curl Bangladesh betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato leaf curl betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato leaf curl China betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato leaf curl Gandhinagar betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato leaf curl Joydebpur betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato leaf curl Laguna betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato leaf curl Laos betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato leaf curl Malaysia betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato leaf curl Nepal betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato leaf curl Patna betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato leaf curl Philippine betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato leaf curl Sri Lanka betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato leaf curl Togo betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato leaf curl Yemen betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato leaf curl Yunnan betasatellite |

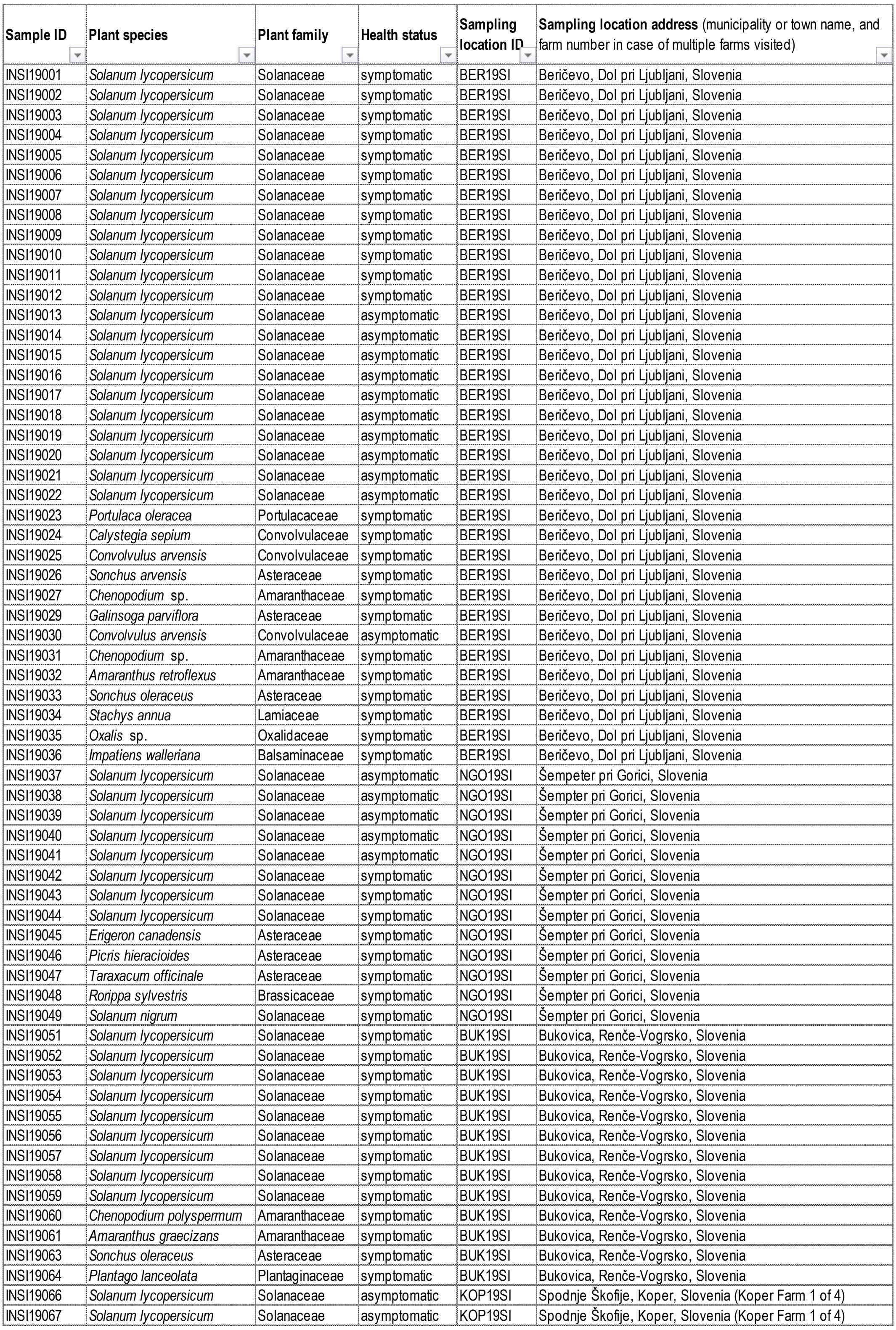
**Table S2** (continued rows)

| Family | Genus | Virus Name |
|---|---|---|
| *Tolecusatellitidae* | *Betasatellite* | Tomato yellow leaf curl China betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato yellow leaf curl Rajasthan betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato yellow leaf curl Shandong betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato yellow leaf curl Thailand betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato yellow leaf curl Vietnam betasatellite |
| *Tolecusatellitidae* | *Betasatellite* | Tomato yellow leaf curl Yunnan betasatellite |
| *Tolecusatellitidae* | *Deltasatellite* | Tomato leaf curl deltasatellite |
| *Tolecusatellitidae* | *Deltasatellite* | Tomato yellow leaf distortion deltasatellite 1 |
| *Tolecusatellitidae* | *Deltasatellite* | Tomato yellow leaf distortion deltasatellite 2 |
| *Tombusviridae* | *Alphanecrovirus* | Olive latent virus 1 |
| *Tombusviridae* | *Tombusvirus* | Tomato bushy stunt virus |
| *Tombusviridae* | *Tombusvirus* | Lettuce necrotic stunt virus |
| *Tospoviridae* | *Orthotospovirus* | Alstroemeria necrotic streak virus |
| *Tospoviridae* | *Orthotospovirus* | Capsicum chlorosis virus |
| *Tospoviridae* | *Orthotospovirus* | Groundnut ringspot virus |
| *Tospoviridae* | *Orthotospovirus* | Groundnut bud necrosis virus |
| *Tospoviridae* | *Orthotospovirus* | Impatiens necrotic spot virus |
| *Tospoviridae* | *Orthotospovirus* | Pepper chlorotic spot orthotospovirus |
| *Tospoviridae* | *Orthotospovirus* | Tomato chlorotic spot virus |
| *Tospoviridae* | *Orthotospovirus* | Tomato necrotic ring virus |
| *Tospoviridae* | *Orthotospovirus* | Tomato yellow ring virus |
| *Tospoviridae* | *Orthotospovirus* | Tomato spotted wilt virus |
| *Tospoviridae* | *Orthotospovirus* | Tomato zonate spot virus |
| *Tospoviridae* | *Orthotospovirus* | Watermelon bud necrosis virus |
| *Tospoviridae* | *Orthotospovirus* | Watermelon silver mottle virus |
| *Tospoviridae* | *Orthotospovirus* | Tomato necrotic spot virus |
| *Tospoviridae* | *Orthotospovirus* | Pepper necrotic spot virus |
| *Tospoviridae* | *Orthotospovirus* | Tomato necrotic ringspot virus |
| *Tymoviridae* | *Tymovirus* | Eggplant mosaic virus |
| *Tymoviridae* | *Tymovirus* | Tomato yellow blotch virus |
| *Tymoviridae* | *Tymovirus* | Tomato blistering mosaic virus |
| *Virgaviridae* | *Tobamovirus* | Pepper mild mottle virus |
| *Virgaviridae* | *Tobamovirus* | Tomato brown rugose fruit virus |
| *Virgaviridae* | *Tobamovirus* | Tobacco mild green mosaic virus |
| *Virgaviridae* | *Tobamovirus* | Tobacco mosaic virus |
| *Virgaviridae* | *Tobamovirus* | Tomato mosaic virus |
| *Virgaviridae* | *Tobamovirus* | Tomato mottle mosaic virus |
| *Virgaviridae* | *Tobravirus* | Tobacco rattle virus |
| *Virgaviridae* | *Tobravirus* | Pepper ringspot virus |

## A.2 Supplementary Material for Publication 2.2

Also available through *Figshare* doi: 10.6084/m9.figshare.20200769

**Supplementary Table 1.** Individual plant samples, their species name, plant family and sampling location of origin.



| **Sample ID** | **Plant species** | **Plant family** | **Health status** | **Sampling location ID** | **Sampling location address** (municipality or town name, and farm number in case of multiple farms visited) |
|---|---|---|---|---|---|
| INSI19001 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19002 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19003 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19004 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19005 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19006 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19007 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19008 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19009 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19010 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19011 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19012 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19013 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19014 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19015 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19016 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19017 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19018 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19019 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19020 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19021 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19022 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19023 | *Portulaca oleracea* | Portulacaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19024 | *Calystegia sepium* | Convolvulaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19025 | *Convolvulus arvensis* | Convolvulaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19026 | *Sonchus arvensis* | Asteraceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19027 | *Chenopodium* sp. | Amaranthaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19029 | *Galinsoga parviflora* | Asteraceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19030 | *Convolvulus arvensis* | Convolvulaceae | asymptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19031 | *Chenopodium* sp. | Amaranthaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19032 | *Amaranthus retroflexus* | Amaranthaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19033 | *Sonchus oleraceus* | Asteraceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19034 | *Stachys annua* | Lamiaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19035 | *Oxalis* sp. | Oxalidaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19036 | *Impatiens walleriana* | Balsaminaceae | symptomatic | BER19SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI19037 | *Solanum lycopersicum* | Solanaceae | asymptomatic | NGO19SI | Šempeter pri Gorici, Slovenia |
| INSI19038 | *Solanum lycopersicum* | Solanaceae | asymptomatic | NGO19SI | Šempter pri Gorici, Slovenia |
| INSI19039 | *Solanum lycopersicum* | Solanaceae | asymptomatic | NGO19SI | Šempter pri Gorici, Slovenia |
| INSI19040 | *Solanum lycopersicum* | Solanaceae | asymptomatic | NGO19SI | Šempter pri Gorici, Slovenia |
| INSI19041 | *Solanum lycopersicum* | Solanaceae | asymptomatic | NGO19SI | Šempter pri Gorici, Slovenia |
| INSI19042 | *Solanum lycopersicum* | Solanaceae | symptomatic | NGO19SI | Šempter pri Gorici, Slovenia |
| INSI19043 | *Solanum lycopersicum* | Solanaceae | symptomatic | NGO19SI | Šempter pri Gorici, Slovenia |
| INSI19044 | *Solanum lycopersicum* | Solanaceae | symptomatic | NGO19SI | Šempter pri Gorici, Slovenia |
| INSI19045 | *Erigeron canadensis* | Asteraceae | symptomatic | NGO19SI | Šempter pri Gorici, Slovenia |
| INSI19046 | *Picris hieracioides* | Asteraceae | symptomatic | NGO19SI | Šempter pri Gorici, Slovenia |
| INSI19047 | *Taraxacum officinale* | Asteraceae | symptomatic | NGO19SI | Šempter pri Gorici, Slovenia |
| INSI19048 | *Rorippa sylvestris* | Brassicaceae | symptomatic | NGO19SI | Šempter pri Gorici, Slovenia |
| INSI19049 | *Solanum nigrum* | Solanaceae | symptomatic | NGO19SI | Šempter pri Gorici, Slovenia |
| INSI19051 | *Solanum lycopersicum* | Solanaceae | symptomatic | BUK19SI | Bukovica, Renče-Vogrsko, Slovenia |
| INSI19052 | *Solanum lycopersicum* | Solanaceae | symptomatic | BUK19SI | Bukovica, Renče-Vogrsko, Slovenia |
| INSI19053 | *Solanum lycopersicum* | Solanaceae | symptomatic | BUK19SI | Bukovica, Renče-Vogrsko, Slovenia |
| INSI19054 | *Solanum lycopersicum* | Solanaceae | symptomatic | BUK19SI | Bukovica, Renče-Vogrsko, Slovenia |
| INSI19055 | *Solanum lycopersicum* | Solanaceae | symptomatic | BUK19SI | Bukovica, Renče-Vogrsko, Slovenia |
| INSI19056 | *Solanum lycopersicum* | Solanaceae | symptomatic | BUK19SI | Bukovica, Renče-Vogrsko, Slovenia |
| INSI19057 | *Solanum lycopersicum* | Solanaceae | symptomatic | BUK19SI | Bukovica, Renče-Vogrsko, Slovenia |
| INSI19058 | *Solanum lycopersicum* | Solanaceae | symptomatic | BUK19SI | Bukovica, Renče-Vogrsko, Slovenia |
| INSI19059 | *Solanum lycopersicum* | Solanaceae | symptomatic | BUK19SI | Bukovica, Renče-Vogrsko, Slovenia |
| INSI19060 | *Chenopodium polyspermum* | Amaranthaceae | symptomatic | BUK19SI | Bukovica, Renče-Vogrsko, Slovenia |
| INSI19061 | *Amaranthus graecizans* | Amaranthaceae | symptomatic | BUK19SI | Bukovica, Renče-Vogrsko, Slovenia |
| INSI19063 | *Sonchus oleraceus* | Asteraceae | symptomatic | BUK19SI | Bukovica, Renče-Vogrsko, Slovenia |
| INSI19064 | *Plantago lanceolata* | Plantaginaceae | symptomatic | BUK19SI | Bukovica, Renče-Vogrsko, Slovenia |
| INSI19066 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOP19SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI19067 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOP19SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |

**Supplementary Table 1**. (continued rows).

| Sample ID | Plant species | Plant family | Health status | Sampling location ID | **Sampling location address** (municipality or town name, and farm number in case of multiple farms visited) |
|---|---|---|---|---|---|
| INSI19068 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOP19SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI19069 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOP19SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI19070 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOP19SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI19071 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOP19SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI19072 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOP19SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI19073 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOP19SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI19074 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOP19SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI19075 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOP19SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI19077 | *Datura stramonium* | Solanaceae | asymptomatic | KOP19SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI19078 | *Solanum nigrum* | Solanaceae | symptomatic | KOP19SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI19080 | *Mercurialis annua* | Euphorbiaceae | symptomatic | KOP19SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI19082 | *Convolvulus arvensis* | Convolvulaceae | symptomatic | KOP19SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI19084 | *Solanum lycopersicum* | Solanaceae | asymptomatic | PAR19SI | Markova, Bertoki, Slovenia |
| INSI19085 | *Solanum lycopersicum* | Solanaceae | asymptomatic | PAR19SI | Markova, Bertoki, Slovenia |
| INSI19086 | *Solanum lycopersicum* | Solanaceae | asymptomatic | PAR19SI | Markova, Bertoki, Slovenia |
| INSI19087 | *Solanum lycopersicum* | Solanaceae | asymptomatic | PAR19SI | Markova, Bertoki, Slovenia |
| INSI19088 | *Solanum lycopersicum* | Solanaceae | asymptomatic | PAR19SI | Markova, Bertoki, Slovenia |
| INSI19089 | *Solanum lycopersicum* | Solanaceae | asymptomatic | PAR19SI | Markova, Bertoki, Slovenia |
| INSI19090 | *Solanum lycopersicum* | Solanaceae | asymptomatic | PAR19SI | Markova, Bertoki, Slovenia |
| INSI19091 | *Solanum lycopersicum* | Solanaceae | asymptomatic | PAR19SI | Markova, Bertoki, Slovenia |
| INSI19092 | *Solanum lycopersicum* | Solanaceae | asymptomatic | PAR19SI | Markova, Bertoki, Slovenia |
| INSI19093 | *Solanum lycopersicum* | Solanaceae | asymptomatic | PAR19SI | Markova, Bertoki, Slovenia |
| INSI19081 | *Solanum lycopersicum* | Solanaceae | symptomatic | PAR19SI | Markova, Bertoki, Slovenia |
| INSI19083 | *Solanum lycopersicum* | Solanaceae | symptomatic | PAR19SI | Markova, Bertoki, Slovenia |
| INSI19094 | *Solanum lycopersicum* | Solanaceae | symptomatic | PAR19SI | Markova, Bertoki, Slovenia |
| INSI19095 | *Solanum lycopersicum* | Solanaceae | symptomatic | PAR19SI | Markova, Bertoki, Slovenia |
| INSI19096 | *Convolvulus arvensis* | Convolvulaceae | symptomatic | PAR19SI | Markova, Bertoki, Slovenia |
| INSI19097 | *Amaranthus retroflexus* | Amaranthaceae | symptomatic | PAR19SI | Markova, Bertoki, Slovenia |
| INSI19098 | *Mercurialis annua* | Euphorbiaceae | symptomatic | PAR19SI | Markova, Bertoki, Slovenia |
| INSI19099 | *Chenopodium* sp. | Amaranthaceae | symptomatic | PAR19SI | Markova, Bertoki, Slovenia |
| INSI19103 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19104 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19105 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19106 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19107 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19108 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19109 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19110 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19111 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19112 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19113 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19100 | *Solanum lycopersicum* | Solanaceae | symptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19101 | *Solanum lycopersicum* | Solanaceae | symptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19102 | *Solanum lycopersicum* | Solanaceae | symptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19114 | *Solanum lycopersicum* | Solanaceae | symptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19115 | *Solanum lycopersicum* | Solanaceae | symptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19116 | *Solanum lycopersicum* | Solanaceae | symptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19117 | *Solanum lycopersicum* | Solanaceae | symptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19118 | *Solanum lycopersicum* | Solanaceae | symptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19119 | *Amaranthus retroflexus* | Amaranthaceae | symptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19120 | *Calystegia sepium* | Convolvulaceae | symptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19121 | *Mercurialis annua* | Euphorbiaceae | symptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19122 | *Solanum lycopersicum* | Solanaceae | symptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19123 | *Cichorium intybus* | Asteraceae | symptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19124 | *Plantago major* | Plantaginaceae | symptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19125 | *Pastinaca sativa* | Apiaceae | symptomatic | BOL19SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI19126 | *Solanum lycopersicum* | Solanaceae | symptomatic | POR19SI | Sečovlje, Piran, Slovenia (Piran Farm 2 of 3) |
| INSI19128 | *Solanum lycopersicum* | Solanaceae | symptomatic | POR19SI | Sečovlje, Piran, Slovenia (Piran Farm 2 of 3) |
| INSI19129 | *Solanum lycopersicum* | Solanaceae | symptomatic | POR19SI | Sečovlje, Piran, Slovenia (Piran Farm 2 of 3) |
| INSI19134 | *Solanum lycopersicum* | Solanaceae | symptomatic | POR19SI | Sečovlje, Piran, Slovenia (Piran Farm 2 of 3) |
| INSI19135 | *Solanum lycopersicum* | Solanaceae | symptomatic | POR19SI | Sečovlje, Piran, Slovenia (Piran Farm 2 of 3) |
| INSI19127 | *Solanum lycopersicum* | Solanaceae | asymptomatic | POR19SI | Sečovlje, Piran, Slovenia (Piran Farm 2 of 3) |
| INSI19130 | *Solanum lycopersicum* | Solanaceae | asymptomatic | POR19SI | Sečovlje, Piran, Slovenia (Piran Farm 2 of 3) |
| INSI19131 | *Solanum lycopersicum* | Solanaceae | asymptomatic | POR19SI | Sečovlje, Piran, Slovenia (Piran Farm 2 of 3) |
| INSI19132 | *Solanum lycopersicum* | Solanaceae | asymptomatic | POR19SI | Sečovlje, Piran, Slovenia (Piran Farm 2 of 3) |
| INSI19133 | *Solanum lycopersicum* | Solanaceae | asymptomatic | POR19SI | Sečovlje, Piran, Slovenia (Piran Farm 2 of 3) |
| INSI19136 | *Picris echioides* | Asteraceae | symptomatic | POR19SI | Sečovlje, Piran, Slovenia (Piran Farm 2 of 3) |
| INSI19137 | *Pastinaca sativa* | Apiaceae | symptomatic | POR19SI | Sečovlje, Piran, Slovenia (Piran Farm 2 of 3) |

**Supplementary Table 1**. (continued rows).

| **Sample ID** | **Plant species** | **Plant family** | **Health status** | **Sampling location ID** | **Sampling location address** (municipality or town name, and farm number in case of multiple farms visited) |
|---|---|---|---|---|---|
| INSI19138 | *Sorghum halepense* | Poaceae | symptomatic | POR19SI | Sečovlje, Piran, Slovenia (Piran Farm 2 of 3) |
| INSI19141 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOR19SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI19142 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOR19SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI19143 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOR19SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI19144 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOR19SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI19145 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOR19SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI19146 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOR19SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI19147 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOR19SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI19148 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOR19SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI19139 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR19SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI19149 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR19SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI19151 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR19SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI19152 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR19SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI19153 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR19SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI19154 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR19SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI19155 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR19SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI19140 | *Chenopodium* sp. | Amaranthaceae | symptomatic | KOR19SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI19150 | *Chenopodium* sp. | Amaranthaceae | symptomatic | KOR19SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI19156 | *Pastinaca sativa* | Apiaceae | symptomatic | KOR19SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI19157 | *Erigeron annuus* | Asteraceae | symptomatic | KOR19SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI19158 | *Ranunculus repens* | Ranunculaceae | symptomatic | KOR19SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| P29Pv-PK2 | *Phaseolus vulgaris* | Fabaceae | (internal or alien sequencing control for set of samples collected in 2019) | | |
| P30Pv-PK1 | *Phaseolus vulgaris* | Fabaceae | (internal or alien sequencing control for set of samples collected in 2019) | | |
| INSI20001 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20002 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20003 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20004 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20005 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20006 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20007 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20008 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20009 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20010 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20011 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20012 | *Solanum lycopersicum* | Solanaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20013 | *Taraxacum officinale* | Asteraceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20014 | *Solanum nigrum* | Solanaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20015 | *Capsella bursa-pastoris* | Brassicaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20016 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20017 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20018 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20019 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20020 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20021 | *Capsella bursa-pastoris* | Brassicaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20022 | *Solanum nigrum* | Solanaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20023 | *Solanum tuberosum* | Solanaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20024 | *Polygonum* sp. | Polygonaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20025 | *Veronica* sp. | Plantaginaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20027 | *Convolvulus arvensis* | Convolvulaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20028 | *Calystegia* sp. | Convolvulaceae | symptomatic | BER20SI | Beričevo, Dol pri Ljubljani, Slovenia |
| INSI20029 | *Solanum lycopersicum* | Solanaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20030 | *Solanum lycopersicum* | Solanaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20031 | *Solanum lycopersicum* | Solanaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20032 | *Solanum lycopersicum* | Solanaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20033 | *Solanum lycopersicum* | Solanaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20033F | *Solanum lycopersicum* | Solanaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20034 | *Solanum lycopersicum* | Solanaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20034F | *Solanum lycopersicum* | Solanaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20035 | *Solanum lycopersicum* | Solanaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20036 | *Solanum lycopersicum* | Solanaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20037 | *Solanum lycopersicum* | Solanaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20038 | *Solanum lycopersicum* | Solanaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20038F | *Solanum lycopersicum* | Solanaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20039 | *Solanum lycopersicum* | Solanaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20039F | *Solanum lycopersicum* | Solanaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20040 | *Solanum lycopersicum* | Solanaceae | asymptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20041 | *Solanum lycopersicum* | Solanaceae | asymptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20042 | *Solanum lycopersicum* | Solanaceae | asymptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20043 | *Solanum lycopersicum* | Solanaceae | asymptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |

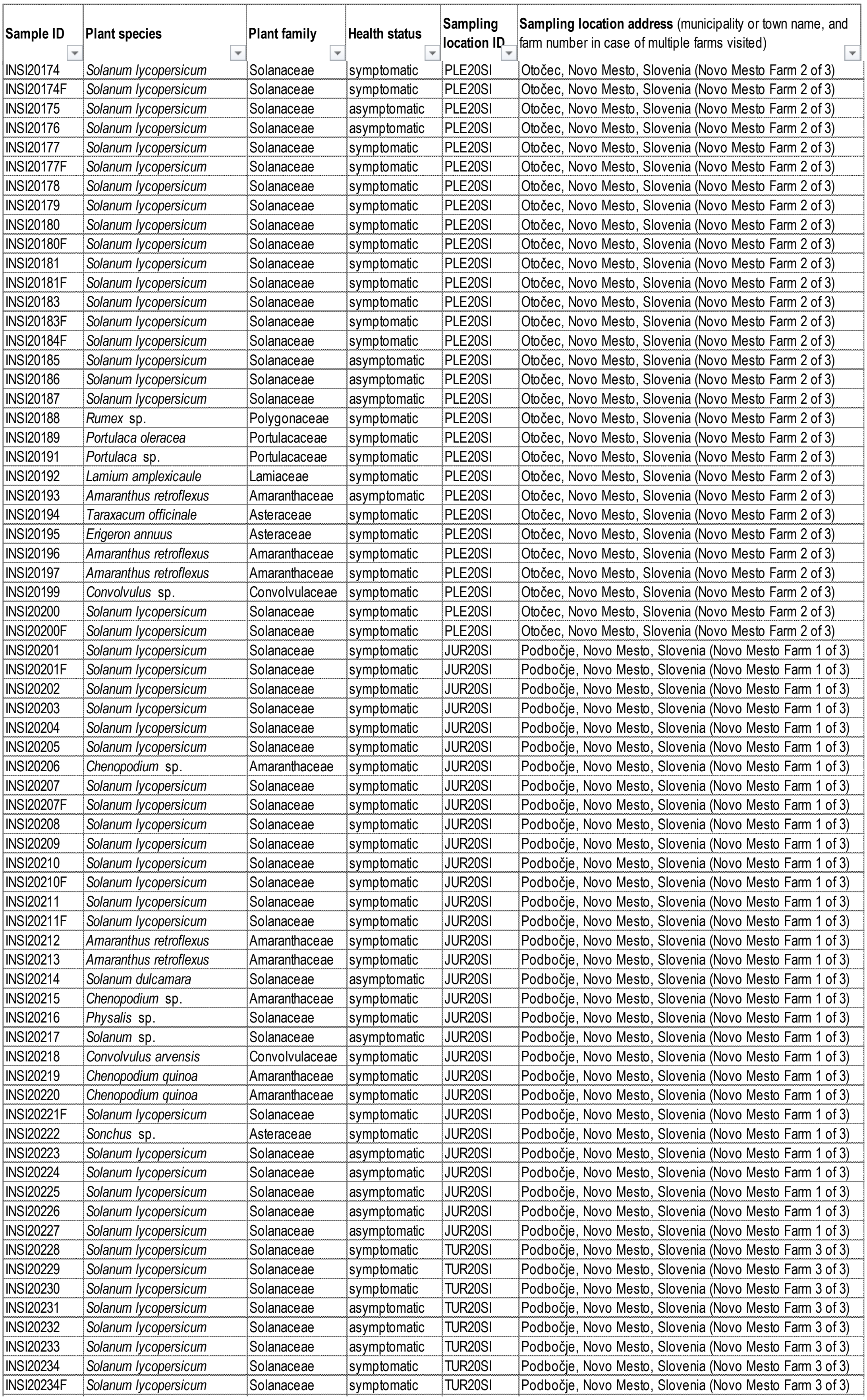
**Supplementary Table 1**. (continued rows).

| **Sample ID** | **Plant species** | **Plant family** | **Health status** | **Sampling location ID** | **Sampling location address** (municipality or town name, and farm number in case of multiple farms visited) |
|---|---|---|---|---|---|
| INSI20044 | *Solanum lycopersicum* | Solanaceae | asymptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20045 | *Mercurialis annua* | Euphorbiaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20046 | *Sonchus asper* | Asteraceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20047 | *Amaranthus retroflexus* | Amaranthaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20048 | *Solanum nigrum* | Solanaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20049 | *Veronica persicae* | Plantaginaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20051 | *Portulaca oleracea* | Portulacaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20052 | *Datura stramonium* | Solanaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20053 | *Solanum nigrum* | Solanaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20054 | *Datura stramonium* | Solanaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20055 | *Solanum lycopersicum* | Solanaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20056 | *Chenopodium album* | Amaranthaceae | symptomatic | STR20SI | Strunjan, Slovenia (Piran Farm 3 of 3) |
| INSI20057 | *Solanum lycopersicum* | Solanaceae | symptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20058 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20059 | *Solanum lycopersicum* | Solanaceae | symptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20060 | *Solanum lycopersicum* | Solanaceae | symptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20061 | *Solanum lycopersicum* | Solanaceae | symptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20062 | *Solanum lycopersicum* | Solanaceae | symptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20063 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20064 | *Solanum lycopersicum* | Solanaceae | symptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20066 | *Solanum lycopersicum* | Solanaceae | symptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20067 | *Solanum lycopersicum* | Solanaceae | symptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20068 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20069 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20070 | *Convolvulus arvensis* | Convolvulaceae | symptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20071 | *Solanum lycopersicum* | Solanaceae | asymptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20072 | *Convolvulus arvensis* | Convolvulaceae | symptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20073 | *Convolvulus arvensis* | Convolvulaceae | symptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20074 | *Cichorium intybus* | Asteraceae | symptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20075 | *Picris echioides* | Asteraceae | symptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20076 | *Clematis viticella* | Ranunculaceae | symptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20077 | *Cichorium intybus* | Asteraceae | symptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20078 | *Picris echioides* | Asteraceae | symptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20080 | *Picris echioides* | Asteraceae | symptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20081 | *Picris echioides* | Asteraceae | symptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20082 | *Picris echioides* | Asteraceae | symptomatic | BOL20SI | Lucija, Piran, Slovenia (Piran Farm 1 of 3) |
| INSI20083 | *Solanum lycopersicum* | Solanaceae | symptomatic | MIR20SI | Miren-Kostanjevica, Slovenia |
| INSI20084 | *Solanum lycopersicum* | Solanaceae | symptomatic | MIR20SI | Miren-Kostanjevica, Slovenia |
| INSI20084F | *Solanum lycopersicum* | Solanaceae | symptomatic | MIR20SI | Miren-Kostanjevica, Slovenia |
| INSI20085 | *Solanum lycopersicum* | Solanaceae | symptomatic | MIR20SI | Miren-Kostanjevica, Slovenia |
| INSI20086 | *Solanum lycopersicum* | Solanaceae | asymptomatic | MIR20SI | Miren-Kostanjevica, Slovenia |
| INSI20087 | *Solanum lycopersicum* | Solanaceae | asymptomatic | MIR20SI | Miren-Kostanjevica, Slovenia |
| INSI20088 | *Solanum lycopersicum* | Solanaceae | symptomatic | MIR20SI | Miren-Kostanjevica, Slovenia |
| INSI20088F | *Solanum lycopersicum* | Solanaceae | symptomatic | MIR20SI | Miren-Kostanjevica, Slovenia |
| INSI20089 | *Solanum lycopersicum* | Solanaceae | symptomatic | MIR20SI | Miren-Kostanjevica, Slovenia |
| INSI20090 | *Solanum lycopersicum* | Solanaceae | symptomatic | MIR20SI | Miren-Kostanjevica, Slovenia |
| INSI20091 | *Solanum lycopersicum* | Solanaceae | symptomatic | MIR20SI | Miren-Kostanjevica, Slovenia |
| INSI20092 | *Solanum lycopersicum* | Solanaceae | asymptomatic | MIR20SI | Miren-Kostanjevica, Slovenia |
| INSI20093 | *Solanum lycopersicum* | Solanaceae | asymptomatic | MIR20SI | Miren-Kostanjevica, Slovenia |
| INSI20094 | *Artemisia verlotiorum* | Asteraceae | symptomatic | MIR20SI | Miren-Kostanjevica, Slovenia |
| INSI20095 | *Parietaria judaica* | Urticaceae | symptomatic | MIR20SI | Miren-Kostanjevica, Slovenia |
| INSI20096 | *Solanum nigrum* | Solanaceae | asymptomatic | MIR20SI | Miren-Kostanjevica, Slovenia |
| INSI20097 | *Trifolium repens* | Fabaceae | symptomatic | MIR20SI | Miren-Kostanjevica, Slovenia |
| INSI20098 | *Salvia pratensis* | Lamiaceae | symptomatic | MIR20SI | Miren-Kostanjevica, Slovenia |
| INSI20099 | *Trifolium pratense* | Fabaceae | symptomatic | MIR20SI | Miren-Kostanjevica, Slovenia |
| INSI20100 | *Plantago major* | Plantaginaceae | symptomatic | MIR20SI | Miren-Kostanjevica, Slovenia |
| INSI20101 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20102 | *Solanum nigrum* | Solanaceae | asymptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20103 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20104 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20105 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20106 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20106F | *Solanum lycopersicum* | Solanaceae | symptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20107 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20108 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20109 | *Parietaria judaica* | Urticaceae | symptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20110 | *Convolvulus arvensis* | Convolvulaceae | symptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20111 | *Mercurialis annua* | Euphorbiaceae | symptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20112 | *Mercurialis annua* | Euphorbiaceae | symptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |

**Supplementary Table 1**. (continued rows).

| **Sample ID** | **Plant species** | **Plant family** | **Health status** | **Sampling location ID** | **Sampling location address** (municipality or town name, and farm number in case of multiple farms visited) |
|---|---|---|---|---|---|
| INSI20113 | *Taraxacum officinale* | Asteraceae | symptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20114 | *Sonchus oleraceus* | Asteraceae | symptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20115 | *Sonchus oleraceus* | Asteraceae | symptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20116 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20117 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20118 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20119 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20120 | *Portulaca oleracea* | Portulacaceae | symptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20121 | *Picris echioides* | Asteraceae | symptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20122 | *Calystegia sepium* | Convolvulaceae | symptomatic | KOP20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 1 of 4) |
| INSI20123 | *Solanum lycopersicum* | Solanaceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20124 | *Solanum lycopersicum* | Solanaceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20124F | *Solanum lycopersicum* | Solanaceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20125 | *Solanum lycopersicum* | Solanaceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20125F | *Solanum lycopersicum* | Solanaceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20126 | *Solanum lycopersicum* | Solanaceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20126F | *Solanum lycopersicum* | Solanaceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20127 | *Solanum lycopersicum* | Solanaceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20128 | *Solanum lycopersicum* | Solanaceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20129 | *Solanum lycopersicum* | Solanaceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20130 | *Solanum lycopersicum* | Solanaceae | asymptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20131 | *Solanum lycopersicum* | Solanaceae | asymptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20132 | *Solanum lycopersicum* | Solanaceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20133 | *Solanum lycopersicum* | Solanaceae | asymptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20134 | *Solanum lycopersicum* | Solanaceae | asymptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20135 | *Solanum lycopersicum* | Solanaceae | asymptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20136 | *Convolvulus arvensis* | Convolvulaceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20137 | *Artemisia vulgaris* | Asteraceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20138 | *Picris echioides* | Asteraceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20139 | *Cirsium arvense* | Asteraceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20140 | *Solanum nigrum* | Solanaceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20141 | *Sonchus asper* | Asteraceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20142 | *Solanum nigrum* | Solanaceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20143 | *Euphorbia helioscopia* | Euphorbiaceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20144 | *Taraxacum officinale* | Asteraceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20145 | *Sonchus asper* | Asteraceae | symptomatic | SKO20SI | Spodnje Škofije, Koper, Slovenia (Koper Farm 3 of 4) |
| INSI20146 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20146F | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20147 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20148 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20149 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20150 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20151 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20152 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20153F | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20154 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20154F | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20155 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20155F | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20156 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20156F | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20157 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20158 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20159 | *Solanum lycopersicum* | Solanaceae | asymptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20160 | *Chenopodium album* | Amaranthaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20161 | *Cirsium arvense* | Asteraceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20162 | *Chenopodium album* | Amaranthaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20163 | *Calystegia sepium* | Convolvulaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20164 | *Solanum nigrum* | Solanaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20165 | *Taraxacum officinale* | Asteraceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20166 | *Solanum lycopersicum* | Solanaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20167 | *Solanum nigrum* | Solanaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20168 | *Pastinaca sativa* | Apiaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20169 | *Mentha spicata* | Lamiaceae | symptomatic | KOR20SI | Črni Kal, Koper, Slovenia (Koper Farm 4 of 4) |
| INSI20170 | *Solanum lycopersicum* | Solanaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20170F | *Solanum lycopersicum* | Solanaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20171 | *Solanum lycopersicum* | Solanaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20172 | *Solanum lycopersicum* | Solanaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20173 | *Solanum lycopersicum* | Solanaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |

**Supplementary Table 1**. (continued rows).



| **Sample ID** | **Plant species** | **Plant family** | **Health status** | **Sampling location ID** | **Sampling location address** (municipality or town name, and farm number in case of multiple farms visited) |
|---|---|---|---|---|---|
| INSI20174 | *Solanum lycopersicum* | Solanaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20174F | *Solanum lycopersicum* | Solanaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20175 | *Solanum lycopersicum* | Solanaceae | asymptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20176 | *Solanum lycopersicum* | Solanaceae | asymptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20177 | *Solanum lycopersicum* | Solanaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20177F | *Solanum lycopersicum* | Solanaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20178 | *Solanum lycopersicum* | Solanaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20179 | *Solanum lycopersicum* | Solanaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20180 | *Solanum lycopersicum* | Solanaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20180F | *Solanum lycopersicum* | Solanaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20181 | *Solanum lycopersicum* | Solanaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20181F | *Solanum lycopersicum* | Solanaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20183 | *Solanum lycopersicum* | Solanaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20183F | *Solanum lycopersicum* | Solanaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20184F | *Solanum lycopersicum* | Solanaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20185 | *Solanum lycopersicum* | Solanaceae | asymptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20186 | *Solanum lycopersicum* | Solanaceae | asymptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20187 | *Solanum lycopersicum* | Solanaceae | asymptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20188 | *Rumex* sp. | Polygonaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20189 | *Portulaca oleracea* | Portulacaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20191 | *Portulaca* sp. | Portulacaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20192 | *Lamium amplexicaule* | Lamiaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20193 | *Amaranthus retroflexus* | Amaranthaceae | asymptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20194 | *Taraxacum officinale* | Asteraceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20195 | *Erigeron annuus* | Asteraceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20196 | *Amaranthus retroflexus* | Amaranthaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20197 | *Amaranthus retroflexus* | Amaranthaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20199 | *Convolvulus* sp. | Convolvulaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20200 | *Solanum lycopersicum* | Solanaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20200F | *Solanum lycopersicum* | Solanaceae | symptomatic | PLE20SI | Otočec, Novo Mesto, Slovenia (Novo Mesto Farm 2 of 3) |
| INSI20201 | *Solanum lycopersicum* | Solanaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20201F | *Solanum lycopersicum* | Solanaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20202 | *Solanum lycopersicum* | Solanaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20203 | *Solanum lycopersicum* | Solanaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20204 | *Solanum lycopersicum* | Solanaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20205 | *Solanum lycopersicum* | Solanaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20206 | *Chenopodium* sp. | Amaranthaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20207 | *Solanum lycopersicum* | Solanaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20207F | *Solanum lycopersicum* | Solanaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20208 | *Solanum lycopersicum* | Solanaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20209 | *Solanum lycopersicum* | Solanaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20210 | *Solanum lycopersicum* | Solanaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20210F | *Solanum lycopersicum* | Solanaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20211 | *Solanum lycopersicum* | Solanaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20211F | *Solanum lycopersicum* | Solanaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20212 | *Amaranthus retroflexus* | Amaranthaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20213 | *Amaranthus retroflexus* | Amaranthaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20214 | *Solanum dulcamara* | Solanaceae | asymptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20215 | *Chenopodium* sp. | Amaranthaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20216 | *Physalis* sp. | Solanaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20217 | *Solanum* sp. | Solanaceae | asymptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20218 | *Convolvulus arvensis* | Convolvulaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20219 | *Chenopodium quinoa* | Amaranthaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20220 | *Chenopodium quinoa* | Amaranthaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20221F | *Solanum lycopersicum* | Solanaceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20222 | *Sonchus* sp. | Asteraceae | symptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20223 | *Solanum lycopersicum* | Solanaceae | asymptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20224 | *Solanum lycopersicum* | Solanaceae | asymptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20225 | *Solanum lycopersicum* | Solanaceae | asymptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20226 | *Solanum lycopersicum* | Solanaceae | asymptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20227 | *Solanum lycopersicum* | Solanaceae | asymptomatic | JUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 1 of 3) |
| INSI20228 | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20229 | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20230 | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20231 | *Solanum lycopersicum* | Solanaceae | asymptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20232 | *Solanum lycopersicum* | Solanaceae | asymptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20233 | *Solanum lycopersicum* | Solanaceae | asymptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20234 | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20234F | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |

**Supplementary Table 1**. (continued rows).

| **Sample ID** | **Plant species** | **Plant family** | **Health status** | **Sampling location ID** | **Sampling location address** (municipality or town name, and farm number in case of multiple farms visited) |
|---|---|---|---|---|---|
| INSI20234F | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20235 | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20235F | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20236 | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20236F | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20237 | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20237F | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20238 | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20238F | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20239 | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20239F | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20240 | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20240F | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20241 | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20241F | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20242 | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20242F | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20243 | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20244 | *Galinsoga ciliata* | Asteraceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20245 | *Steleria media* | Caryophyllaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20246 | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20246F | *Solanum lycopersicum* | Solanaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20247 | *Taraxacum officinale* | Asteraceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20248 | *Plantago major* | Plantaginaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20249 | *Galinsoga ciliata* | Asteraceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20250 | *Capsella bursa-pastoris* | Brassicaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20251 | *Amaranthus retroflexus* | Amaranthaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20252 | *Taraxacum officinale* | Asteraceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20253 | *Rumex crispus* | Polygonaceae | symptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20254 | *Solanum nigrum* | Solanaceae | asymptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20255 | *Solanum lycopersicum* | Solanaceae | asymptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| INSI20256 | *Solanum lycopersicum* | Solanaceae | asymptomatic | TUR20SI | Podbočje, Novo Mesto, Slovenia (Novo Mesto Farm 3 of 3) |
| P61Pv-PK1 | *Phaseolus vulgaris* | Fabaceae | (internal or alien sequencing control for set of samples collected in 2020) | | |
| P62Pv-PK2 | *Phaseolus vulgaris* | Fabaceae | (internal or alien sequencing control for set of samples collected in 2020) | | |

**Supplementary Table 2.** Composite samples used in high-throughput sequencing, their composition, year of collection, farm type and other associated information.

| Sequencing pool number | Composite sample ID | Sampling location ID | Sample group | Year collected | Farm type | Cultural practice | Surroundings | No. of pooled samples |
|---|---|---|---|---|---|---|---|---|
| P1.1 | P1.1BER-ST | BER19SI | tomatoes | 2019 | greenhouse | conventional | agricultural | 6 |
| P1.2 | P1.2BER-ST | BER19SI | tomatoes | 2019 | greenhouse | conventional | agricultural | 6 |
| P02 | P02BER-AT | BER19SI | tomatoes | 2019 | greenhouse | conventional | agricultural | 10 |
| P3.1 | P3.1BER-SW | BER19SI | weeds | 2019 | greenhouse | conventional | agricultural | 6 |
| P3.2 | P3.2BER-SW | BER19SI | weeds | 2019 | greenhouse | conventional | agricultural | 7 |
| P04 | P04NGO-AT | NGO19SI | tomatoes | 2019 | greenhouse | conventional | urban | 5 |
| P05 | P05NGO-ST | NGO19SI | tomatoes | 2019 | greenhouse | conventional | urban | 3 |
| P06 | P06NGO-SW | NGO19SI | weeds | 2019 | greenhouse | conventional | urban | 5 |
| P07 | P07BUK-ST | BUK19SI | tomatoes | 2019 | greenhouse | conventional | agricultural | 9 |
| P08 | P08BUK-SW | BUK19SI | weeds | 2019 | greenhouse | conventional | agricultural | 4 |
| P09 | P09KOP-AT | KOP19SI | tomatoes | 2019 | greenhouse | conventional | agricultural | 5 |
| P10 | P10KOP-ST | KOP19SI | tomatoes | 2019 | greenhouse | conventional | agricultural | 5 |
| P11 | P11KOP-SW | KOP19SI | weeds | 2019 | greenhouse | conventional | agricultural | 4 |
| P12 | P12PAR-AT | PAR19SI | tomatoes | 2019 | greenhouse | conventional | agricultural | 10 |
| P13 | P13PAR-ST | PAR19SI | tomatoes | 2019 | greenhouse | conventional | agricultural | 4 |
| P14 | P14PAR-SW | PAR19SI | weeds | 2019 | greenhouse | conventional | agricultural | 4 |
| P15.1 | P15.1BOL-AT | BOL19SI | tomatoes | 2019 | greenhouse | organic | agricultural | 6 |
| P15.2 | P15.2BOL-AT | BOL19SI | tomatoes | 2019 | greenhouse | organic | agricultural | 5 |
| P16 | P16BOL-ST | BOL19SI | tomatoes | 2019 | greenhouse | organic | agricultural | 8 |
| P17 | P17BOL-SW | BOL19SI | weeds | 2019 | greenhouse | organic | agricultural | 7 |
| P18 | P18POR-ST | POR19SI | tomatoes | 2019 | greenhouse | conventional | agricultural | 5 |
| P19 | P19POR-AT | POR19SI | tomatoes | 2019 | greenhouse | conventional | agricultural | 5 |
| P20 | P20POR-SW | POR19SI | weeds | 2019 | greenhouse | conventional | agricultural | 3 |
| P21 | P21KOR-AT | KOR19SI | tomatoes | 2019 | open field | ecological | agricultural | 8 |
| P22 | P22KOR-ST | KOR19SI | tomatoes | 2019 | open field | ecological | agricultural | 7 |
| P23 | P23KOR-SW | KOR19SI | weeds | 2019 | open field | ecological | agricultural | 5 |
| P29 | P29Pv-PK2 | not applicable | not applicable | not applicable | not applicable | not applicable | not applicable | 1 |
| P30 | P30Pv-PK1 | not applicable | not applicable | not applicable | not applicable | not applicable | not applicable | 1 |
| P31 | P31BER20-AT | BER20SI | tomatoes | 2020 | greenhouse | conventional | rural, agricultural | 5 |
| P32 | P32STR20-AT | STR20SI | tomatoes | 2020 | open field | conventional | rural, agricultural | 5 |
| P33 | P33BOL20-AT | BOL20SI | tomatoes | 2020 | greenhouse | organic | rural, agricultural | 5 |
| P34 | P34MIR20-AT | MIR20SI | tomatoes | 2020 | greenhouse | conventional | semi-urban | 4 |
| P35 | P35KOP20-AT | KOP20SI | tomatoes | 2020 | greenhouse | conventional | semi-urban | 4 |
| P36 | P36SKO20-AT | SKO20SI | tomatoes | 2020 | open field | conventional | rural | 5 |
| P37 | P37KOR20-AT | KOR20SI | tomatoes | 2020 | open field | ecological | rural, agricultural | 5 |
| P3 | P38PLE20-AT | PLE20SI | tomatoes | 2020 | greenhouse | conventional | rural, agricultural | 5 |
| P39 | P39JUR20-AT | JUR20SI | tomatoes | 2020 | greenhouse | conventional | rural, agricultural | 5 |
| P40 | P40TUR20-AT | TUR20SI | tomatoes | 2020 | greenhouse | conventional | rural, agricultural | 5 |
| P41.1 | P41.1BER20-ST | BER19SI | tomatoes | 2020 | greenhouse | conventional | rural, agricultural | 7 |
| P41.2 | P41.2BER20-ST | BER19SI | tomatoes | 2020 | greenhouse | conventional | rural, agricultural | 5 |
| P42 | P42BER20-SW | BER19SI | weeds | 2020 | greenhouse | conventional | rural, agricultural | 10 |
| P43.1 | P43.1STR20-ST | STR20SI | tomatoes | 2020 | open field | conventional | rural, agricultural | 8 |
| P43.2 | P43.2STR20-ST | STR20SI | tomatoes | 2020 | open field | conventional | rural, agricultural | 8 |
| P44 | P44STR20-SW | STR20SI | weeds | 2020 | open field | conventional | rural, agricultural | 10 |
| P45 | P45BOL20-ST | BOL20SI | tomatoes | 2020 | greenhouse | organic | rural, agricultural | 8 |
| P46 | P46BOL20-SW | BOL20SI | weeds | 2020 | greenhouse | organic | rural, agricultural | 11 |
| P47 | P47MIR20-ST | MIR20SI | tomatoes | 2020 | greenhouse | conventional | semi-urban | 9 |
| P48 | P48MIR20-SW | MIR20SI | weeds | 2020 | greenhouse | conventional | semi-urban | 7 |
| P49 | P49KOP20-ST | KOP20SI | tomatoes | 2020 | greenhouse | conventional | semi-urban | 8 |
| P50.1 | P50.1KOP20-SW | KOP20SI | weeds | 2020 | greenhouse | conventional | semi-urban | 6 |
| P50.2 | P50.2KOP20-SW | KOP20SI | weeds | 2020 | greenhouse | conventional | semi-urban | 5 |
| P51.1 | P51.1SKO20-ST | SKO20SI | tomatoes | 2020 | open field | conventional | rural | 5 |
| P51.2 | P51.2SKO20-ST | SKO20SI | tomatoes | 2020 | open field | conventional | rural | 6 |
| P52 | P52SKO20-SW | SKO20SI | weeds | 2020 | open field | conventional | rural | 10 |
| P53.1 | P53.1KOR20-ST | KOR20SI | tomatoes | 2020 | open field | ecological | rural, agricultural | 7 |
| P53.2 | P53.2KOR20-ST | KOR20SI | tomatoes | 2020 | open field | ecological | rural, agricultural | 7 |
| P54 | P54KOR20-SW | KOR20SI | weeds | 2020 | open field | ecological | rural, agricultural | 9 |
| P55.1 | P55.1PLE20-ST | PLE20SI | tomatoes | 2020 | greenhouse | conventional | rural, agricultural | 7 |
| P55.2 | P55.2PLE20-ST | PLE20SI | tomatoes | 2020 | greenhouse | conventional | rural, agricultural | 6 |
| P55.3 | P55.3PLE20-ST | PLE20SI | tomatoes | 2020 | greenhouse | conventional | rural, agricultural | 7 |
| P56 | P56PLE20-SW | PLE20SI | bean | 2020 | greenhouse | conventional | rural, agricultural | 10 |
| P57.1 | P57.1JUR20-ST | JUR20SI | tomatoes | 2020 | greenhouse | conventional | rural, agricultural | 8 |
| P57.2 | P57.2JUR20-ST | JUR20SI | tomatoes | 2020 | greenhouse | conventional | rural, agricultural | 7 |
| P58.1 | P58.1JUR20-SW | JUR20SI | weeds | 2020 | greenhouse | conventional | rural, agricultural | 6 |
| P58.2 | P58.2JUR20-SW | JUR20SI | weeds | 2020 | greenhouse | conventional | rural, agricultural | 5 |
| P59.1 | P59.1TUR20-ST | TUR20SI | tomatoes | 2020 | greenhouse | conventional | rural, agricultural | 9 |
| P59.2 | P59.2TUR20-ST | TUR20SI | tomatoes | 2020 | greenhouse | conventional | rural, agricultural | 8 |
| P59.3 | P59.3TUR20-ST | TUR20SI | tomatoes | 2020 | greenhouse | conventional | rural, agricultural | 7 |
| P60 | P60TUR20-SW | TUR20SI | weeds | 2020 | greenhouse | conventional | rural, agricultural | 10 |
| P61 | P61Pv-PK1 | not applicable | not applicable | not applicable | not applicable | not applicable | not applicable | 1 |
| P62 | P62Pv-PK2 | not applicable | not applicable | not applicable | not applicable | not applicable | not applicable | 1 |

**Supplementary Table 2**. (continued columns).

| Sequencing pool number | ID of pooled samples |
|---|---|
| P1.1 | INSI19001, INSI19002, INSI19003,INSI19004, INSI19005, INSI19006 |
| P1.2 | INSI19007, INSI19008, INSI19009, INSI19010, INSI19011, INSI19012 |
| P02 | INSI19013, INSI19014, INSI19015, INSI19016, INSI19017, INSI19018, INSI19019, INSI19020, INSI19021, INSI19022 |
| P3.1 | INSI19023, INSI19024, INSI19025, INSI19027, INSI19028, INSI19029 |
| P3.2 | INSI19030, INSI19031, INSI19032, INSI19033, INSI19034, INSI19035, INSI19036 |
| P04 | INSI19037, INSI19038, INSI19039, INSI19040, INSI19041 |
| P05 | INSI19042, INSI19043, INSI19044 |
| P06 | INSI19045, INSI19046, INSI19047, INSI19048, INSI19049 |
| P07 | INSI19051, INSI19052, INSI19053, INSI19054, INSI19055, INSI19056, INSI19057, INSI19058, INSI19059 |
| P08 | INSI19060, INSI19061, INSI19063, INSI19064 |
| P09 | INSI19066, INSI19067, INSI19068, INSI19069, INSI19070 |
| P10 | INSI19071, INSI19072, INSI19073, INSI19074, INSI19075 |
| P11 | INSI19077, INSI19078, INSI19080, INSI19082 |
| P12 | INSI19084, INSI19085, INSI19086, INSI19087, INSI19088, INSI19089, INSI19090, INSI19091, INSI19092, INSI19093 |
| P13 | INSI19081, INSI19083, INSI19094, INSI19095 |
| P14 | INSI19096, INSI19097, INSI19098, INSI19099 |
| P15.1 | INSI19103, INSI19104, INSI19105, INSI19106, INSI19107, INSI19108 |
| P15.2 | INSI19109, INSI19110, INSI19111, INSI19112, INSI19113 |
| P16 | INSI19100, INSI19101, INSI19102, INSI19114, INSI19115, INSI19116, INSI19117, INSI19118 |
| P17 | INSI19119, INSI19120, INSI19121, INSI19122, INSI19123, INSI19124, INSI19125 |
| P18 | INSI19126, INSI19128, INSI19129, INSI19134, INSI19135 |
| P19 | INSI19127, INSI19130, INSI19131, INSI19132, INSI19133 |
| P20 | INSI19136, INSI19137, INSI19138 |
| P21 | INSI19141, INSI19142, INSI19143, INSI19144, INSI19145, INSI19146, INSI19147, INSI19148 |
| P22 | INSI19139, INSI19149, INSI19151, INSI19152, INSI19153, INSI19154, INSI19155 |
| P23 | INSI19140, INSI19150, INSI19156, INSI19157, INSI19158 |
| P29 | P29Pv-PK2 |
| P30 | P30Pv-PK1 |
| P31 | INSI20016, INSI20017, INSI20018, INSI20019, INSI20020 |
| P32 | INSI20040, INSI20041, INSI20042, INSI20043, INSI20044 |
| P33 | INSI20058, INSI20063, INSI20068, INSI20069, INSI20071 |
| P34 | INSI20086, INSI20087, INSI20092, INSI20093 |
| P35 | INSI20103, INSI20104, INSI20105, INSI20107 |
| P36 | INSI20130, INSI20131, INSI20133, INSI20134, INSI20135 |
| P37 | INSI20147, INSI20152, INSI20157, INSI20158, INSI20159 |
| P3 | INSI20175, INSI20176, INSI20185, INSI20186, INSI20187 |
| P39 | INSI20223, INSI20224, INSI20225, INSI20226, INSI20227 |
| P40 | INSI20231, INSI20232, INSI20233, INSI20255, INSI20256 |
| P41.1 | INSI20001, INSI20002, INSI20003, INSI20004, INSI20005, INSI20006, INSI20007 |
| P41.2 | INSI20008, INSI20009, INSI20010, INSI20011, INSI20012 |
| P42 | INSI20013, INSI20014, INSI20015, INSI20021, INSI20022, INSI20023, INSI20024, INSI20025, INSI20027, INSI20028 |
| P43.1 | INSI20029, INSI20030, INSI20031, INSI20032, INSI20033, INSI20033F, INSI20034, INSI20034F |
| P43.2 | INSI20035, INSI20036, INSI20037, INSI20038, INSI20038F, INSI20039, INSI20039F, INSI20055 |
| P44 | INSI20045, INSI20046, INSI20047, INSI20048, INSI20049, INSI20051, INSI20052, INSI20053, INSI20054, INSI20056 |
| P45 | INSI20057, INSI20059, INSI20060, INSI20061, INSI20062, INSI20064, INSI20066, INSI20067 |
| P46 | INSI20070, INSI20072, INSI20073, INSI20074, INSI20075, INSI20076, INSI20077, INSI20078, INSI20080, INSI20081, INSI20082 |
| P47 | INSI20083, INSI20084, INSI20084F, INSI20085, INSI20088, INSI20088F, INSI20089, INSI20090, INSI20091 |
| P48 | INSI20094, INSI20095, INSI20096, INSI20097, INSI20098, INSI20099, INSI20100 |
| P49 | INSI20101, INSI20106, INSI20106F, INSI20108, INSI20116, INSI20117, INSI20118, INSI20119 |
| P50.1 | INSI20102, INSI20109, INSI20110, INSI20111, INSI20112, INSI20113 |
| P50.2 | INSI20114, INSI20115, INSI20120, INSI20121, INSI20122 |
| P51.1 | INSI20123, INSI20124, INSI20124F, INSI20125, INSI20125F |
| P51.2 | INSI20126, INSI20126F, INSI20127, INSI20128, INSI20129, INSI20132 |
| P52 | INSI20136, INSI20137, INSI20138, INSI20139, INSI20140, INSI20141, INSI20142, INSI20143, INSI20144, INSI20145 |
| P53.1 | INSI20146, INSI20146F, INSI20148, INSI20149, INSI20150, INSI20151, INSI20153F |
| P53.2 | INSI20154, INSI20154F, INSI20155, INSI20155F, INSI20156, INSI20156F, INSI20166 |
| P54 | INSI20160, INSI20161, INSI20162, INSI20163, INSI20164, INSI20165, INSI20167, INSI20168, INSI20169 |
| P55.1 | INSI20170, INSI20170F, INSI20171, INSI20172, INSI20173, INSI20174, INSI20174F |
| P55.2 | INSI20177, INSI20177F, INSI20178, INSI20179, INSI20180, INSI20180F |
| P55.3 | INSI20181, INSI20181F, INSI20183, INSI20183F, INSI20184F, INSI20200, INSI20200F |
| P56 | INSI20188, INSI20189, INSI20191, INSI20192, INSI20193, INSI20194, INSI20195, INSI20196, INSI20197, INSI20199 |
| P57.1 | INSI20201, INSI20201F, INSI20202, INSI20203, INSI20204, INSI20205, INSI20207, INSI20207F |
| P57.2 | INSI20208, INSI20209, INSI20210, INSI20210F, INSI20211, INSI20211F, INSI20221F |
| P58.1 | INSI20206, INSI20212, INSI20213, INSI20214, INSI20215, INSI20216 |
| P58.2 | INSI20217, INSI20218, INSI20219, INSI20220, INSI20222 |
| P59.1 | INSI20228, INSI20229, INSI20230, INSI20234, INSI20234F, INSI20235, INSI20235F, INSI20236, INSI20236F |
| P59.2 | INSI20237, INSI20237F, INSI20238, INSI20238F, INSI20239, INSI20239F, INSI20240, INSI20240F |
| P59.3 | INSI20241, INSI20241F, INSI20242, INSI20242F, INSI20243, INSI20246, INSI20246F |
| P60 | INSI20244, INSI20245, INSI20247, INSI20248, INSI20249, INSI20250, INSI20251, INSI20252, INSI20253, INSI20254 |
| P61 | P61Pv-PK1 |
| P62 | P62Pv-PK2 |

**Supplementary Table 2**. (continued columns).

| Sequencing pool number | RNA extraction kit used (for individual samples) | RNA cleaning and concentration kit used (in preparting the composite samples) |
|---|---|---|
| P1.1 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P1.2 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P02 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P3.1 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P3.2 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P04 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P05 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P06 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P07 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P08 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P09 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P10 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P11 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P12 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P13 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P14 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P15.1 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P15.2 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P16 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P17 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P18 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P19 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P20 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P21 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P22 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P23 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1013) |
| P29 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | not applicable |
| P30 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | not applicable |
| P31 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P32 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P33 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P34 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P35 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P36 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P37 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P3 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P39 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P40 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P41.1 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P41.2 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P42 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P43.1 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P43.2 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P44 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P45 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P46 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P47 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P48 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P49 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P50.1 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P50.2 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P51.1 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P51.2 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P52 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P53.1 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P53.2 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P54 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P55.1 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P55.2 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P55.3 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P56 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P57.1 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P57.2 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P58.1 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P58.2 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P59.1 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P59.2 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P59.3 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P60 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | ZymoResearch RNA Clean and Concentrator (catalog no. R1014) |
| P61 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | not applicable |
| P62 | Qiagen Rneasy Plant Mini Kit (catalog no. 74904) | not applicable |

**Supplementary Table 3**. Sequence read archive (SRA) metadata of the sequencing experiments, read count and other associated information. Genome mapping was done on viral RefSeq version from July 2020.

| Bioproject accession | Biosample accession | Study | SRA accession | Composite sample / Library ID |
|---|---|---|---|---|
| PRJNA772045 | SAMN22357975 | SRP342893 | SRR16552271 | P1.1BER19-ST |
| PRJNA772045 | SAMN22357976 | SRP342893 | SRR16552270 | P1.2BER19-ST |
| PRJNA772045 | SAMN22357977 | SRP342893 | SRR16552235 | P02BER19-AT |
| PRJNA772045 | SAMN22357978 | SRP342893 | SRR16552224 | P3.1BER19-SW |
| PRJNA772045 | SAMN22357979 | SRP342893 | SRR16552261 | P3.2BER19-SW |
| PRJNA772045 | SAMN22357980 | SRP342893 | SRR16552250 | P04NGO19-AT |
| PRJNA772045 | SAMN22357981 | SRP342893 | SRR16552286 | P05NGO19-ST |
| PRJNA772045 | SAMN22357982 | SRP342893 | SRR16552275 | P06NGO19-SW |
| PRJNA772045 | SAMN22357983 | SRP342893 | SRR16552273 | P07BUK19-ST |
| PRJNA772045 | SAMN22357984 | SRP342893 | SRR16552272 | P08BUK19-SW |
| PRJNA772045 | SAMN22357985 | SRP342893 | SRR16552269 | P09KOP19-AT |
| PRJNA772045 | SAMN22357986 | SRP342893 | SRR16552244 | P10KOP19-ST |
| PRJNA772045 | SAMN22357987 | SRP342893 | SRR16552243 | P11KOP19-SW |
| PRJNA772045 | SAMN22357988 | SRP342893 | SRR16552242 | P12PAR19-AT |
| PRJNA772045 | SAMN22357989 | SRP342893 | SRR16552241 | P13PAR19-ST |
| PRJNA772045 | SAMN22357990 | SRP342893 | SRR16552240 | P14PAR19-SW |
| PRJNA772045 | SAMN22357991 | SRP342893 | SRR16552239 | P15.1BOL19-AT |
| PRJNA772045 | SAMN22357992 | SRP342893 | SRR16552238 | P15.2BOL19-AT |
| PRJNA772045 | SAMN22357993 | SRP342893 | SRR16552237 | P16BOL19-ST |
| PRJNA772045 | SAMN22357994 | SRP342893 | SRR16552236 | P17BOL19-SW |
| PRJNA772045 | SAMN22357995 | SRP342893 | SRR16552234 | P18POR19-ST |
| PRJNA772045 | SAMN22357996 | SRP342893 | SRR16552233 | P19POR19-AT |
| PRJNA772045 | SAMN22357997 | SRP342893 | SRR16552232 | P20POR19-SW |
| PRJNA772045 | SAMN22357998 | SRP342893 | SRR16552231 | P21KOR19-AT |
| PRJNA772045 | SAMN22357999 | SRP342893 | SRR16552230 | P22KOR19-ST |
| PRJNA772045 | SAMN22358000 | SRP342893 | SRR16552229 | P23KOR19-SW |
| PRJNA772045 | SAMN22358001 | SRP342893 | SRR16552228 | P29Pv19-PK2 |
| PRJNA772045 | SAMN22358002 | SRP342893 | SRR16552227 | P30Pv19-PK1 |
| PRJNA772045 | SAMN22358003 | SRP342893 | SRR16552226 | P31BER20-AT |
| PRJNA772045 | SAMN22358004 | SRP342893 | SRR16552225 | P41.1BER20-ST |
| PRJNA772045 | SAMN22358005 | SRP342893 | SRR16552223 | P41.2BER20-ST |
| PRJNA772045 | SAMN22358006 | SRP342893 | SRR16552222 | P42BER20-SW |
| PRJNA772045 | SAMN22358007 | SRP342893 | SRR16552221 | P32STR20-AT |
| PRJNA772045 | SAMN22358008 | SRP342893 | SRR16552268 | P43.1STR20-ST |
| PRJNA772045 | SAMN22358009 | SRP342893 | SRR16552267 | P43.2STR20-ST |
| PRJNA772045 | SAMN22358010 | SRP342893 | SRR16552266 | P44STR20-SW |
| PRJNA772045 | SAMN22358011 | SRP342893 | SRR16552265 | P33BOL20-AT |
| PRJNA772045 | SAMN22358012 | SRP342893 | SRR16552264 | P45BOL20-ST |
| PRJNA772045 | SAMN22358013 | SRP342893 | SRR16552263 | P46BOL20-SW |
| PRJNA772045 | SAMN22358014 | SRP342893 | SRR16552262 | P34MIR20-AT |
| PRJNA772045 | SAMN22358015 | SRP342893 | SRR16552260 | P47MIR20-ST |
| PRJNA772045 | SAMN22358016 | SRP342893 | SRR16552259 | P48MIR20-SW |
| PRJNA772045 | SAMN22358017 | SRP342893 | SRR16552258 | P35KOP20-AT |
| PRJNA772045 | SAMN22358018 | SRP342893 | SRR16552257 | P49KOP20-ST |
| PRJNA772045 | SAMN22358019 | SRP342893 | SRR16552256 | P50.1KOP20-SW |
| PRJNA772045 | SAMN22358020 | SRP342893 | SRR16552255 | P50.2KOP20-SW |
| PRJNA772045 | SAMN22358021 | SRP342893 | SRR16552254 | P36SKO20-AT |
| PRJNA772045 | SAMN22358022 | SRP342893 | SRR16552253 | P51.1SKO20-ST |
| PRJNA772045 | SAMN22358023 | SRP342893 | SRR16552252 | P51.2SKO20-ST |
| PRJNA772045 | SAMN22358024 | SRP342893 | SRR16552251 | P52SKO20-SW |
| PRJNA772045 | SAMN22358025 | SRP342893 | SRR16552249 | P37KOR20-AT |
| PRJNA772045 | SAMN22358026 | SRP342893 | SRR16552248 | P53.1KOR20-ST |
| PRJNA772045 | SAMN22358027 | SRP342893 | SRR16552247 | P53.2KOR20-ST |
| PRJNA772045 | SAMN22358028 | SRP342893 | SRR16552246 | P54KOR20-SW |
| PRJNA772045 | SAMN22358029 | SRP342893 | SRR16552245 | P38PLE20-AT |
| PRJNA772045 | SAMN22358030 | SRP342893 | SRR16552291 | P55.1PLE20-ST |
| PRJNA772045 | SAMN22358031 | SRP342893 | SRR16552290 | P55.2PLE20-ST |
| PRJNA772045 | SAMN22358032 | SRP342893 | SRR16552289 | P55.3PLE20-ST |
| PRJNA772045 | SAMN22358033 | SRP342893 | SRR16552288 | P56PLE20-SW |
| PRJNA772045 | SAMN22358034 | SRP342893 | SRR16552287 | P39JUR20-AT |
| PRJNA772045 | SAMN22358035 | SRP342893 | SRR16552285 | P57.1JUR20-ST |
| PRJNA772045 | SAMN22358036 | SRP342893 | SRR16552284 | P57.2JUR20-ST |
| PRJNA772045 | SAMN22358037 | SRP342893 | SRR16552283 | P58.1JUR20-SW |
| PRJNA772045 | SAMN22358038 | SRP342893 | SRR16552282 | P58.2JUR20-SW |
| PRJNA772045 | SAMN22358039 | SRP342893 | SRR16552281 | P40TUR20-AT |
| PRJNA772045 | SAMN22358040 | SRP342893 | SRR16552280 | P59.1TUR20-ST |
| PRJNA772045 | SAMN22358041 | SRP342893 | SRR16552279 | P59.2TUR20-ST |
| PRJNA772045 | SAMN22358042 | SRP342893 | SRR16552278 | P59.3TUR20-ST |
| PRJNA772045 | SAMN22358043 | SRP342893 | SRR16552277 | P60TUR20-SW |
| PRJNA772045 | SAMN22358044 | SRP342893 | SRR16552276 | P61Pv-PK1 |
| PRJNA772045 | SAMN22358045 | SRP342893 | SRR16552274 | P62Pv-PK2 |

**Supplementary Table 3**. (continued columns).

| Bioproject accession | Biosample accession | Title |
|---|---|---|
| PRJNA772045 | SAMN22357975 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Bericevo, Slovenia collected in 2019, 1st of 2 pools |
| PRJNA772045 | SAMN22357976 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Bericevo, Slovenia collected in 2019, 2nd of 2 pools |
| PRJNA772045 | SAMN22357977 | Sequencing of pooled rRNA-depleted total RNA extracts of asymptomatic tomato plants from Bericevo, Slovenia collected in 2019 |
| PRJNA772045 | SAMN22357978 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Bericevo, Slovenia collected in 2019, 1st of 2 pools |
| PRJNA772045 | SAMN22357979 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Bericevo, Slovenia collected in 2019, 2nd of 2 pools |
| PRJNA772045 | SAMN22357980 | Sequencing of pooled rRNA-depleted total RNA extracts of asymptomatic tomato plants from Nova Gorica, Slovenia collected in 2019 |
| PRJNA772045 | SAMN22357981 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Nova Gorica, Slovenia collected in 2019 |
| PRJNA772045 | SAMN22357982 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Nova Gorica, Slovenia collected in 2019 |
| PRJNA772045 | SAMN22357983 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Miren-Kostanjevica, Slovenia (Farm 1) collected in 2019 |
| PRJNA772045 | SAMN22357984 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Miren-Kostanjevica, Slovenia (Farm 1) collected in 2019 |
| PRJNA772045 | SAMN22357985 | Sequencing of pooled rRNA-depleted total RNA extracts of asymptomatic tomato plants from Koper, Slovenia (Farm 1) collected in 2019 |
| PRJNA772045 | SAMN22357986 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Koper, Slovenia (Farm 1) collected in 2019 |
| PRJNA772045 | SAMN22357987 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Koper, Slovenia (Farm 1) collected in 2019 |
| PRJNA772045 | SAMN22357988 | Sequencing of pooled rRNA-depleted total RNA extracts of asymptomatic tomato plants from Koper, Slovenia (Farm 2) collected in 2019 |
| PRJNA772045 | SAMN22357989 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Koper, Slovenia (Farm 2) collected in 2019 |
| PRJNA772045 | SAMN22357990 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Koper, Slovenia (Farm 2) collected in 2019 |
| PRJNA772045 | SAMN22357991 | Sequencing of pooled rRNA depleted total RNA extracts of asymptomatic tomato plants from Piran, Slovenia (Farm 1) collected in 2019, 1st of 2 pools |
| PRJNA772045 | SAMN22357992 | Sequencing of pooled rRNA-depleted total RNA extracts of asymptomatic tomato plants from Piran, Slovenia (Farm 1) collected in 2019, 2nd of 2 pools |
| PRJNA772045 | SAMN22357993 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Piran, Slovenia (Farm 1) collected in 2019 |
| PRJNA772045 | SAMN22357994 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Piran, Slovenia (Farm 1) collected in 2019 |
| PRJNA772045 | SAMN22357995 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Piran, Slovenia (Farm 2) collected in 2019 |
| PRJNA772045 | SAMN22357996 | Sequencing of pooled rRNA-depleted total RNA extracts of asymptomatic tomato plants from Piran, Slovenia (Farm 2) collected in 2019 |
| PRJNA772045 | SAMN22357997 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Piran, Slovenia (Farm 2) collected in 2019 |
| PRJNA772045 | SAMN22357998 | Sequencing of pooled rRNA-depleted total RNA extracts of asymptomatic tomato plants from Koper, Slovenia (Farm 4) collected in 2019 |
| PRJNA772045 | SAMN22357999 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Koper, Slovenia (Farm 4) collected in 2019 |
| PRJNA772045 | SAMN22358000 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Koper, Slovenia (Farm 4) collected in 2019 |
| PRJNA772045 | SAMN22358001 | Sequencing of rRNA-depleted total RNA extracts of Phaseolus vulgaris containing alphendornaviruses used as positive control for HTS, used with 2019 samples, 1st of 2 pools |
| PRJNA772045 | SAMN22358002 | Sequencing of rRNA-depleted total RNA extracts of Phaseolus vulgaris containing alphendornaviruses used as positive control for HTS, used with 2019 samples, 2nd of 2 pools |
| PRJNA772045 | SAMN22358003 | Sequencing of pooled rRNA-depleted total RNA extracts of asymptomatic tomato plants from Bericevo, Slovenia collected in 2020 |
| PRJNA772045 | SAMN22358004 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Bericevo, Slovenia collected in 2020, 1st of 2 pools |
| PRJNA772045 | SAMN22358005 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Bericevo, Slovenia collected in 2020, 2nd of 2 pools |
| PRJNA772045 | SAMN22358006 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Bericevo, Slovenia collected in 2020 |
| PRJNA772045 | SAMN22358007 | Sequencing of pooled rRNA-depleted total RNA extracts of asymptomatic tomato plants from Piran, Slovenia (Farm 3) collected in 2020 |
| PRJNA772045 | SAMN22358008 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Piran, Slovenia (Farm 3) collected in 2020, 1st of 2 pools |
| PRJNA772045 | SAMN22358009 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Piran, Slovenia (Farm 3) collected in 2020, 2nd of 2 pools |
| PRJNA772045 | SAMN22358010 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Piran, Slovenia (Farm 3) collected in 2020 |
| PRJNA772045 | SAMN22358011 | Sequencing of pooled rRNA-depleted total RNA extracts of asymptomatic tomato plants from Piran, Slovenia (Farm 1) collected in 2020 |
| PRJNA772045 | SAMN22358012 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Piran, Slovenia (Farm 1) collected in 2020 |
| PRJNA772045 | SAMN22358013 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Piran, Slovenia (Farm 1) collected in 2020 |
| PRJNA772045 | SAMN22358014 | Sequencing of pooled rRNA-depleted total RNA extracts of asymptomatic tomato plants from Miren-Kostanjevica, Slovenia collected in 2020 |
| PRJNA772045 | SAMN22358015 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Miren-Kostanjevica, Slovenia collected in 2020 |
| PRJNA772045 | SAMN22358016 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Miren-Kostanjevica, Slovenia collected in 2020 |
| PRJNA772045 | SAMN22358017 | Sequencing of pooled rRNA-depleted total RNA extracts of asymptomatic tomato plants from Koper, Slovenia (Farm 1) collected in 2020 |
| PRJNA772045 | SAMN22358018 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Koper, Slovenia (Farm 1) collected in 2020 |
| PRJNA772045 | SAMN22358019 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Koper, Slovenia (Farm 1) collected in 2020, 1st of 2 pools |
| PRJNA772045 | SAMN22358020 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Koper, Slovenia (Farm 1) collected in 2020, 2nd of 2 pools |
| PRJNA772045 | SAMN22358021 | Sequencing of pooled rRNA-depleted total RNA extracts of asymptomatic tomato plants from Koper, Slovenia (Farm 3) collected in 2020 |
| PRJNA772045 | SAMN22358022 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Koper, Slovenia (Farm 3) collected in 2020, 1st of 2 pools |
| PRJNA772045 | SAMN22358023 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Koper, Slovenia (Farm 3) collected in 2020, 2nd of 2 pools |
| PRJNA772045 | SAMN22358024 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Koper, Slovenia (Farm 3) collected in 2020 |
| PRJNA772045 | SAMN22358025 | Sequencing of pooled rRNA-depleted total RNA extracts of asymptomatic tomato plants from Koper, Slovenia (Farm 4) collected in 2020 |
| PRJNA772045 | SAMN22358026 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Koper, Slovenia (Farm 4) collected in 2020, 1st of 2 pools |
| PRJNA772045 | SAMN22358027 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Koper, Slovenia (Farm 4) collected in 2020, 2nd of 2 pools |
| PRJNA772045 | SAMN22358028 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Koper, Slovenia (Farm 4) collected in 2020 |
| PRJNA772045 | SAMN22358029 | Sequencing of pooled rRNA-depleted total RNA extracts of asymptomatic tomato plants from Novo Mesto, Slovenia (Farm 2) collected in 2020 |
| PRJNA772045 | SAMN22358030 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Novo Mesto, Slovenia (Farm 2) collected in 2020, 1st of 3 pools |
| PRJNA772045 | SAMN22358031 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Novo Mesto, Slovenia (Farm 2) collected in 2020, 2nd of 3 pools |
| PRJNA772045 | SAMN22358032 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Novo Mesto, Slovenia (Farm 2) collected in 2020, 3rd of 3 pools |
| PRJNA772045 | SAMN22358033 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Novo Mesto, Slovenia (Farm 2) collected in 2020 |
| PRJNA772045 | SAMN22358034 | Sequencing of pooled rRNA-depleted total RNA extracts of asymptomatic tomato plants from Novo Mesto, Slovenia (Farm 1) collected in 2020 |
| PRJNA772045 | SAMN22358035 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Novo Mesto, Slovenia (Farm 1) collected in 2020, 1st of 2 pools |
| PRJNA772045 | SAMN22358036 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Novo Mesto, Slovenia (Farm 1) collected in 2020, 2nd of 2 pools |
| PRJNA772045 | SAMN22358037 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Novo Mesto, Slovenia (Farm 1) collected in 2020, 1st of 2 pools |
| PRJNA772045 | SAMN22358038 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Novo Mesto, Slovenia (Farm 1) collected in 2020, 2nd of 2 pools |
| PRJNA772045 | SAMN22358039 | Sequencing of pooled rRNA-depleted total RNA extracts of asymptomatic tomato plants from Novo Mesto, Slovenia (Farm 3) collected in 2020 |
| PRJNA772045 | SAMN22358040 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Novo Mesto, Slovenia (Farm 3) collected in 2020, 1st of 3 pools |
| PRJNA772045 | SAMN22358041 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Novo Mesto, Slovenia (Farm 3) collected in 2020, 2nd of 3 pools |
| PRJNA772045 | SAMN22358042 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) tomato plants from Novo Mesto, Slovenia (Farm 3) collected in 2020, 3rd of 3 pools |
| PRJNA772045 | SAMN22358043 | Sequencing of pooled rRNA-depleted total RNA extracts of symptomatic (virus disease-like) weed plants from Novo Mesto, Slovenia (Farm 3) collected in 2020 |
| PRJNA772045 | SAMN22358044 | Sequencing of rRNA-depleted total RNA extracts of Phaseolus vulgaris containing alphendornaviruses used as positive control for HTS, used with 2020 samples, 1st of 2 pools |
| PRJNA772045 | SAMN22358045 | Sequencing of rRNA-depleted total RNA extracts of Phaseolus vulgaris containing alphendornaviruses used as positive control for HTS, used with 2020 samples, 2nd of 2 pools |

**Supplementary Table 3**. (continued columns).

| Bioproject accession | Biosample accession | Library strategy | Library source | Library selection | Library layout | Platform | Instrument model | Sequencing mode | Sequencing lane |
|---|---|---|---|---|---|---|---|---|---|
| PRJNA772045 | SAMN22357975 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22357976 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22357977 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22357978 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22357979 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22357980 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22357981 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22357982 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22357983 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22357984 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22357985 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22357986 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22357987 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22357988 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22357989 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22357990 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22357991 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22357992 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22357993 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22357994 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22357995 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22357996 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22357997 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22357998 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22357999 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358000 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358001 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358002 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358003 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358004 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358005 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358006 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358007 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358008 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358009 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358010 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358011 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358012 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358013 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358014 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358015 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358016 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358017 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358018 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358019 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358020 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358021 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358022 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358023 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358024 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358025 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358026 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358027 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358028 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358029 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358030 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358031 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358032 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358033 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358034 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358035 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358036 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358037 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358038 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358039 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358040 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358041 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358042 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |
| PRJNA772045 | SAMN22358043 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358044 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 1 |
| PRJNA772045 | SAMN22358045 | RNA-Seq | metagenomic | cDNA | paired | Illumina | HiSeq 2500 | 151bp PE reads (rapid run) | 2 |

**Supplementary Table 3**. (continued columns).

| Bioproject accession | Biosample accession | Design description |
|---|---|---|
| PRJNA772045 | SAMN22357975 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357976 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357977 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357978 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357979 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357980 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357981 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357982 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357983 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357984 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357985 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357986 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357987 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357988 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357989 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357990 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357991 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357992 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357993 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357994 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357995 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357996 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357997 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357998 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22357999 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358000 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358001 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358002 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358003 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358004 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358005 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358006 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358007 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358008 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358009 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358010 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358011 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358012 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358013 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358014 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358015 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358016 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358017 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358018 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358019 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358020 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358021 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358022 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358023 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358024 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358025 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358026 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358027 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358028 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358029 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358030 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358031 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358032 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358033 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358034 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358035 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358036 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358037 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358038 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358039 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358040 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358041 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358042 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358043 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358044 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |
| PRJNA772045 | SAMN22358045 | sequencing of pooled ribosomal-RNA depleted total RNA from plant samples, libraries prepared using TruSeq Stranded Total RNA LT Sample Prep Kit (Plant) (Illumina) (catalog no. 20020610) |

**Supplementary Table 3**. (continued columns).

| Bioproject accession | Biosample accession | Reads file type | Reference fasta file | Reference assembly | File name 1 | File name 2 |
|---|---|---|---|---|---|---|
| PRJNA772045 | SAMN22357975 | fastq | not applicable, performed de novo assembly | unaligned | P1-1BER-ST_1.fastq.gz | P1-1BER-ST_2.fastq.gz |
| PRJNA772045 | SAMN22357976 | fastq | not applicable, performed de novo assembly | unaligned | P1-2BER-ST_1.fastq.gz | P1-2BER-ST_2.fastq.gz |
| PRJNA772045 | SAMN22357977 | fastq | not applicable, performed de novo assembly | unaligned | P02BER-AT_1.fastq.gz | P02BER-AT_2.fastq.gz |
| PRJNA772045 | SAMN22357978 | fastq | not applicable, performed de novo assembly | unaligned | P3-1BER-SW_1.fastq.gz | P3-1BER-SW_2.fastq.gz |
| PRJNA772045 | SAMN22357979 | fastq | not applicable, performed de novo assembly | unaligned | P3-2BER-SW_1.fastq.gz | P3-2BER-SW_2.fastq.gz |
| PRJNA772045 | SAMN22357980 | fastq | not applicable, performed de novo assembly | unaligned | P04NGO-AT_1.fastq.gz | P04NGO-AT_2.fastq.gz |
| PRJNA772045 | SAMN22357981 | fastq | not applicable, performed de novo assembly | unaligned | P05NGO-ST_1.fastq.gz | P05NGO-ST_2.fastq.gz |
| PRJNA772045 | SAMN22357982 | fastq | not applicable, performed de novo assembly | unaligned | P06NGO-SW_1.fastq.gz | P06NGO-SW_2.fastq.gz |
| PRJNA772045 | SAMN22357983 | fastq | not applicable, performed de novo assembly | unaligned | P07BUK-ST_1.fastq.gz | P07BUK-ST_2.fastq.gz |
| PRJNA772045 | SAMN22357984 | fastq | not applicable, performed de novo assembly | unaligned | P08BUK-SW_1.fastq.gz | P08BUK-SW_2.fastq.gz |
| PRJNA772045 | SAMN22357985 | fastq | not applicable, performed de novo assembly | unaligned | P09KOP-AT_1.fastq.gz | P09KOP-AT_2.fastq.gz |
| PRJNA772045 | SAMN22357986 | fastq | not applicable, performed de novo assembly | unaligned | P10KOP-ST_1.fastq.gz | P10KOP-ST_2.fastq.gz |
| PRJNA772045 | SAMN22357987 | fastq | not applicable, performed de novo assembly | unaligned | P11KOP-SW_1.fastq.gz | P11KOP-SW_2.fastq.gz |
| PRJNA772045 | SAMN22357988 | fastq | not applicable, performed de novo assembly | unaligned | P12PAR-AT_1.fastq.gz | P12PAR-AT_2.fastq.gz |
| PRJNA772045 | SAMN22357989 | fastq | not applicable, performed de novo assembly | unaligned | P13PAR-ST_1.fastq.gz | P13PAR-ST_2.fastq.gz |
| PRJNA772045 | SAMN22357990 | fastq | not applicable, performed de novo assembly | unaligned | P14PAR-SW_1.fastq.gz | P14PAR-SW_2.fastq.gz |
| PRJNA772045 | SAMN22357991 | fastq | not applicable, performed de novo assembly | unaligned | P15-1BOL-AT_1.fastq.gz | P15-1BOL-AT_2.fastq.gz |
| PRJNA772045 | SAMN22357992 | fastq | not applicable, performed de novo assembly | unaligned | P15-2BOL-AT_1.fastq.gz | P15-2BOL-AT_2.fastq.gz |
| PRJNA772045 | SAMN22357993 | fastq | not applicable, performed de novo assembly | unaligned | P16BOL-ST_1.fastq.gz | P16BOL-ST_2.fastq.gz |
| PRJNA772045 | SAMN22357994 | fastq | not applicable, performed de novo assembly | unaligned | P17BOL-SW_1.fastq.gz | P17BOL-SW_2.fastq.gz |
| PRJNA772045 | SAMN22357995 | fastq | not applicable, performed de novo assembly | unaligned | P18POR-ST_1.fastq.gz | P18POR-ST_2.fastq.gz |
| PRJNA772045 | SAMN22357996 | fastq | not applicable, performed de novo assembly | unaligned | P19POR-AT_1.fastq.gz | P19POR-AT_2.fastq.gz |
| PRJNA772045 | SAMN22357997 | fastq | not applicable, performed de novo assembly | unaligned | P20POR-SW_1.fastq.gz | P20POR-SW_2.fastq.gz |
| PRJNA772045 | SAMN22357998 | fastq | not applicable, performed de novo assembly | unaligned | P21KOR-AT_1.fastq.gz | P21KOR-AT_2.fastq.gz |
| PRJNA772045 | SAMN22357999 | fastq | not applicable, performed de novo assembly | unaligned | P22KOR-ST_1.fastq.gz | P22KOR-ST_2.fastq.gz |
| PRJNA772045 | SAMN22358000 | fastq | not applicable, performed de novo assembly | unaligned | P23KOR-SW_1.fastq.gz | P23KOR-SW_2.fastq.gz |
| PRJNA772045 | SAMN22358001 | fastq | not applicable, performed de novo assembly | unaligned | P29Pv-PK2_1.fastq.gz | P29Pv-PK2_2.fastq.gz |
| PRJNA772045 | SAMN22358002 | fastq | not applicable, performed de novo assembly | unaligned | P30Pv-PK1_1.fastq.gz | P30Pv-PK1_2.fastq.gz |
| PRJNA772045 | SAMN22358003 | fastq | not applicable, performed de novo assembly | unaligned | P31BER20-AT_1.fastq.gz | P31BER20-AT_2.fastq.gz |
| PRJNA772045 | SAMN22358004 | fastq | not applicable, performed de novo assembly | unaligned | P41_1BER20-ST_1.fastq.gz | P41_1BER20-ST_2.fastq.gz |
| PRJNA772045 | SAMN22358005 | fastq | not applicable, performed de novo assembly | unaligned | P41_2BER20-ST_1.fastq.gz | P41_2BER20-ST_2.fastq.gz |
| PRJNA772045 | SAMN22358006 | fastq | not applicable, performed de novo assembly | unaligned | P42BER20-SW_1.fastq.gz | P42BER20-SW_2.fastq.gz |
| PRJNA772045 | SAMN22358007 | fastq | not applicable, performed de novo assembly | unaligned | P32STR20-AT_1.fastq.gz | P32STR20-AT_2.fastq.gz |
| PRJNA772045 | SAMN22358008 | fastq | not applicable, performed de novo assembly | unaligned | P43_1STR20-ST_1.fastq.gz | P43_1STR20-ST_2.fastq.gz |
| PRJNA772045 | SAMN22358009 | fastq | not applicable, performed de novo assembly | unaligned | P43_2STR20-ST_1.fastq.gz | P43_2STR20-ST_2.fastq.gz |
| PRJNA772045 | SAMN22358010 | fastq | not applicable, performed de novo assembly | unaligned | P44STR20-SW_1.fastq.gz | P44STR20-SW_2.fastq.gz |
| PRJNA772045 | SAMN22358011 | fastq | not applicable, performed de novo assembly | unaligned | P33BOL20-AT_1.fastq.gz | P33BOL20-AT_2.fastq.gz |
| PRJNA772045 | SAMN22358012 | fastq | not applicable, performed de novo assembly | unaligned | P45BOL20-ST_1.fastq.gz | P45BOL20-ST_2.fastq.gz |
| PRJNA772045 | SAMN22358013 | fastq | not applicable, performed de novo assembly | unaligned | P46BOL20-SW_1.fastq.gz | P46BOL20-SW_2.fastq.gz |
| PRJNA772045 | SAMN22358014 | fastq | not applicable, performed de novo assembly | unaligned | P34MIR20-AT_1.fastq.gz | P34MIR20-AT_2.fastq.gz |
| PRJNA772045 | SAMN22358015 | fastq | not applicable, performed de novo assembly | unaligned | P47MIR20-ST_1.fastq.gz | P47MIR20-ST_2.fastq.gz |
| PRJNA772045 | SAMN22358016 | fastq | not applicable, performed de novo assembly | unaligned | P48MIR20-SW_1.fastq.gz | P48MIR20-SW_2.fastq.gz |
| PRJNA772045 | SAMN22358017 | fastq | not applicable, performed de novo assembly | unaligned | P35KOP20-AT_1.fastq.gz | P35KOP20-AT_2.fastq.gz |
| PRJNA772045 | SAMN22358018 | fastq | not applicable, performed de novo assembly | unaligned | P49KOP20-ST_1.fastq.gz | P49KOP20-ST_2.fastq.gz |
| PRJNA772045 | SAMN22358019 | fastq | not applicable, performed de novo assembly | unaligned | P50_1KOP20-SW_1.fastq.gz | P50_1KOP20-SW_2.fastq.gz |
| PRJNA772045 | SAMN22358020 | fastq | not applicable, performed de novo assembly | unaligned | P50_2KOP20-SW_1.fastq.gz | P50_2KOP20-SW_2.fastq.gz |
| PRJNA772045 | SAMN22358021 | fastq | not applicable, performed de novo assembly | unaligned | P36SKO20-AT_1.fastq.gz | P36SKO20-AT_2.fastq.gz |
| PRJNA772045 | SAMN22358022 | fastq | not applicable, performed de novo assembly | unaligned | P51_1SKO20-ST_1.fastq.gz | P51_1SKO20-ST_2.fastq.gz |
| PRJNA772045 | SAMN22358023 | fastq | not applicable, performed de novo assembly | unaligned | P51_2SKO20-ST_1.fastq.gz | P51_2SKO20-ST_2.fastq.gz |
| PRJNA772045 | SAMN22358024 | fastq | not applicable, performed de novo assembly | unaligned | P52SKO20-SW_1.fastq.gz | P52SKO20-SW_2.fastq.gz |
| PRJNA772045 | SAMN22358025 | fastq | not applicable, performed de novo assembly | unaligned | P37KOR20-AT_1.fastq.gz | P37KOR20-AT_2.fastq.gz |
| PRJNA772045 | SAMN22358026 | fastq | not applicable, performed de novo assembly | unaligned | P53_1KOR20-ST_1.fastq.gz | P53_1KOR20-ST_2.fastq.gz |
| PRJNA772045 | SAMN22358027 | fastq | not applicable, performed de novo assembly | unaligned | P53_2KOR20-ST_1.fastq.gz | P53_2KOR20-ST_2.fastq.gz |
| PRJNA772045 | SAMN22358028 | fastq | not applicable, performed de novo assembly | unaligned | P54KOR20-SW_1.fastq.gz | P54KOR20-SW_2.fastq.gz |
| PRJNA772045 | SAMN22358029 | fastq | not applicable, performed de novo assembly | unaligned | P38PLE20-AT_1.fastq.gz | P38PLE20-AT_2.fastq.gz |
| PRJNA772045 | SAMN22358030 | fastq | not applicable, performed de novo assembly | unaligned | P55_1PLE20-ST_1.fastq.gz | P55_1PLE20-ST_2.fastq.gz |
| PRJNA772045 | SAMN22358031 | fastq | not applicable, performed de novo assembly | unaligned | P55_2PLE20-ST_1.fastq.gz | P55_2PLE20-ST_2.fastq.gz |
| PRJNA772045 | SAMN22358032 | fastq | not applicable, performed de novo assembly | unaligned | P55_3PLE20-ST_1.fastq.gz | P55_3PLE20-ST_2.fastq.gz |
| PRJNA772045 | SAMN22358033 | fastq | not applicable, performed de novo assembly | unaligned | P56PLE20-SW_1.fastq.gz | P56PLE20-SW_2.fastq.gz |
| PRJNA772045 | SAMN22358034 | fastq | not applicable, performed de novo assembly | unaligned | P39JUR20-AT_1.fastq.gz | P39JUR20-AT_2.fastq.gz |
| PRJNA772045 | SAMN22358035 | fastq | not applicable, performed de novo assembly | unaligned | P57_1JUR20-ST_1.fastq.gz | P57_1JUR20-ST_2.fastq.gz |
| PRJNA772045 | SAMN22358036 | fastq | not applicable, performed de novo assembly | unaligned | P57_2JUR20-ST_1.fastq.gz | P57_2JUR20-ST_2.fastq.gz |
| PRJNA772045 | SAMN22358037 | fastq | not applicable, performed de novo assembly | unaligned | P58_1JUR20-SW_1.fastq.gz | P58_1JUR20-SW_2.fastq.gz |
| PRJNA772045 | SAMN22358038 | fastq | not applicable, performed de novo assembly | unaligned | P58_2JUR20-SW_1.fastq.gz | P58_2JUR20-SW_2.fastq.gz |
| PRJNA772045 | SAMN22358039 | fastq | not applicable, performed de novo assembly | unaligned | P40TUR20-AT_1.fastq.gz | P40TUR20-AT_2.fastq.gz |
| PRJNA772045 | SAMN22358040 | fastq | not applicable, performed de novo assembly | unaligned | P59_1TUR20-ST_1.fastq.gz | P59_1TUR20-ST_2.fastq.gz |
| PRJNA772045 | SAMN22358041 | fastq | not applicable, performed de novo assembly | unaligned | P59_2TUR20-ST_1.fastq.gz | P59_2TUR20-ST_2.fastq.gz |
| PRJNA772045 | SAMN22358042 | fastq | not applicable, performed de novo assembly | unaligned | P59_3TUR20-ST_1.fastq.gz | P59_3TUR20-ST_2.fastq.gz |
| PRJNA772045 | SAMN22358043 | fastq | not applicable, performed de novo assembly | unaligned | P60TUR20-SW_1.fastq.gz | P60TUR20-SW_2.fastq.gz |
| PRJNA772045 | SAMN22358044 | fastq | not applicable, performed de novo assembly | unaligned | P61Pv-PK1_1.fastq.gz | P61Pv-PK1_2.fastq.gz |
| PRJNA772045 | SAMN22358045 | fastq | not applicable, performed de novo assembly | unaligned | P62Pv-PK2_1.fastq.gz | P62Pv-PK2_2.fastq.gz |

**Supplementary Table 3**. (continued columns).

| Bioproject accession | Biosample accession | Total bases | Raw read count | GC (%) | AT (%) | Q20 (%) | Read count after trimming and quality filtering | Percent of raw reads discarded | Number of quality controlled trimmed reads maped to viral RefSeq | Percent of of quality controlled trimmed reads maped to viral RefSeq |
|---|---|---|---|---|---|---|---|---|---|---|
| PRJNA772045 | SAMN22357975 | 3.04E+09 | 20,102,250 | 42.59 | 57.41 | 98.78 | 15,977,126 | 20.52% | 15,190,113 | 95.07% |
| PRJNA772045 | SAMN22357976 | 2.94E+09 | 19,464,840 | 42.30 | 57.70 | 98.94 | 15,212,226 | 21.85% | 14,871,276 | 97.76% |
| PRJNA772045 | SAMN22357977 | 3.72E+08 | 2,464,402 | 46.87 | 53.13 | 98.97 | 2,105,618 | 14.56% | 88,243 | 4.19% |
| PRJNA772045 | SAMN22357978 | 1.87E+09 | 12,381,000 | 44.65 | 55.35 | 99.17 | 9,900,018 | 20.04% | 1,665,639 | 16.82% |
| PRJNA772045 | SAMN22357979 | 1.69E+09 | 11,159,762 | 43.85 | 56.15 | 99.22 | 8,690,108 | 22.13% | 1,463,922 | 16.85% |
| PRJNA772045 | SAMN22357980 | 1.38E+09 | 9,119,326 | 45.57 | 54.43 | 99.27 | 7,633,846 | 16.29% | 413,643 | 5.42% |
| PRJNA772045 | SAMN22357981 | 2.27E+09 | 15,007,272 | 45.35 | 54.65 | 98.77 | 9,562,864 | 36.28% | 735,952 | 7.70% |
| PRJNA772045 | SAMN22357982 | 1.63E+09 | 10,780,132 | 45.06 | 54.94 | 99.32 | 8,391,776 | 22.16% | 1,479,569 | 17.63% |
| PRJNA772045 | SAMN22357983 | 2.68E+09 | 17,725,416 | 45.33 | 54.67 | 98.53 | 11,930,282 | 32.69% | 1,306,853 | 10.95% |
| PRJNA772045 | SAMN22357984 | 1.66E+09 | 11,025,476 | 43.72 | 56.28 | 99.30 | 8,382,226 | 23.97% | 1,854,829 | 22.13% |
| PRJNA772045 | SAMN22357985 | 1.30E+09 | 8,613,896 | 44.77 | 55.23 | 99.22 | 6,887,490 | 20.04% | 946,461 | 13.74% |
| PRJNA772045 | SAMN22357986 | 2.45E+09 | 16,252,934 | 46.40 | 53.60 | 98.63 | 10,534,437 | 35.18% | 957,098 | 9.09% |
| PRJNA772045 | SAMN22357987 | 1.46E+09 | 9,680,920 | 46.72 | 53.28 | 98.99 | 6,008,882 | 37.93% | 235,268 | 3.92% |
| PRJNA772045 | SAMN22357988 | 1.28E+09 | 8,450,008 | 45.32 | 54.68 | 99.21 | 6,805,972 | 19.46% | 459,399 | 6.75% |
| PRJNA772045 | SAMN22357989 | 2.55E+09 | 16,889,714 | 46.36 | 53.64 | 98.53 | 12,495,608 | 26.02% | 638,755 | 5.11% |
| PRJNA772045 | SAMN22357990 | 1.54E+09 | 10,230,502 | 46.17 | 53.83 | 98.82 | 6,281,082 | 38.60% | 839,391 | 13.36% |
| PRJNA772045 | SAMN22357991 | 1.75E+09 | 11,620,952 | 44.98 | 55.02 | 99.25 | 10,129,310 | 12.84% | 812,775 | 8.02% |
| PRJNA772045 | SAMN22357992 | 1.46E+09 | 9,644,616 | 45.03 | 54.97 | 99.25 | 8,130,829 | 15.70% | 661,456 | 8.14% |
| PRJNA772045 | SAMN22357993 | 3.22E+09 | 21,346,990 | 53.86 | 46.14 | 98.73 | 19,029,420 | 10.86% | 38,813 | 0.20% |
| PRJNA772045 | SAMN22357994 | 1.87E+09 | 12,362,218 | 46.72 | 53.28 | 99.13 | 9,230,820 | 25.33% | 2,616,894 | 28.35% |
| PRJNA772045 | SAMN22357995 | 2.18E+09 | 14,457,408 | 45.51 | 54.49 | 98.94 | 11,849,598 | 18.04% | 720,097 | 6.08% |
| PRJNA772045 | SAMN22357996 | 1.56E+09 | 10,325,900 | 45.22 | 54.78 | 99.23 | 6,743,412 | 34.69% | 862,219 | 12.79% |
| PRJNA772045 | SAMN22357997 | 1.72E+09 | 11,402,876 | 44.92 | 55.08 | 99.15 | 8,804,048 | 22.79% | 2,109,755 | 23.96% |
| PRJNA772045 | SAMN22357998 | 1.29E+09 | 8,575,304 | 45.68 | 54.32 | 99.03 | 5,762,644 | 32.80% | 539,687 | 9.37% |
| PRJNA772045 | SAMN22357999 | 3.15E+09 | 20,858,416 | 45.32 | 54.68 | 98.71 | 15,532,178 | 25.54% | 1,343,190 | 8.65% |
| PRJNA772045 | SAMN22358000 | 1.63E+09 | 10,799,652 | 43.75 | 56.25 | 99.21 | 8,802,666 | 18.49% | 1,065,551 | 12.10% |
| PRJNA772045 | SAMN22358001 | 2.82E+09 | 18,705,362 | 44.45 | 55.55 | 98.76 | 13,173,086 | 29.58% | – | – |
| PRJNA772045 | SAMN22358002 | 1.69E+09 | 11,206,262 | 43.14 | 56.86 | 99.17 | 8,937,238 | 20.25% | – | – |
| PRJNA772045 | SAMN22358003 | 2.22E+09 | 14,710,016 | 52.72 | 47.28 | 98.35 | 11,591,060 | 21.20% | 2,614 | 0.02% |
| PRJNA772045 | SAMN22358004 | 2.06E+09 | 15,512,122 | 43.25 | 56.75 | 98.67 | 13,482,850 | 13.08% | 10,650,072 | 78.99% |
| PRJNA772045 | SAMN22358005 | 2.38E+09 | 15,198,860 | 43.73 | 56.27 | 98.66 | 12,605,232 | 17.06% | 12,233,889 | 97.05% |
| PRJNA772045 | SAMN22358006 | 1.96E+09 | 12,903,738 | 44.14 | 55.86 | 98.53 | 9,330,024 | 27.70% | 2,264,788 | 24.27% |
| PRJNA772045 | SAMN22358007 | 1.90E+09 | 13,627,148 | 44.55 | 55.45 | 98.56 | 10,654,336 | 21.82% | 688,577 | 6.46% |
| PRJNA772045 | SAMN22358008 | 2.12E+09 | 15,368,822 | 44.32 | 55.68 | 98.60 | 12,247,590 | 20.31% | 1,518,641 | 12.40% |
| PRJNA772045 | SAMN22358009 | 2.04E+09 | 14,400,494 | 48.17 | 51.83 | 98.56 | 10,199,050 | 29.18% | 2,157,818 | 21.16% |
| PRJNA772045 | SAMN22358010 | 2.22E+09 | 13,915,426 | 45.01 | 54.99 | 98.52 | 9,208,088 | 33.83% | 5,624,799 | 61.09% |
| PRJNA772045 | SAMN22358011 | 2.02E+09 | 15,757,392 | 45.81 | 54.19 | 98.52 | 10,643,628 | 32.45% | 7,214 | 0.07% |
| PRJNA772045 | SAMN22358012 | 1.95E+09 | 16,431,398 | 45.77 | 54.23 | 97.93 | 11,343,340 | 30.97% | 14,280 | 0.13% |
| PRJNA772045 | SAMN22358013 | 2.34E+09 | 15,250,878 | 45.97 | 54.03 | 98.84 | 11,057,510 | 27.50% | 842,507 | 7.62% |
| PRJNA772045 | SAMN22358014 | 2.30E+09 | 13,004,858 | 42.02 | 57.98 | 99.03 | 8,521,224 | 34.48% | 8,487 | 0.10% |
| PRJNA772045 | SAMN22358015 | 1.95E+09 | 16,085,054 | 43.32 | 56.68 | 98.70 | 11,166,850 | 30.58% | 542,742 | 4.86% |
| PRJNA772045 | SAMN22358016 | 2.32E+09 | 13,027,650 | 44.42 | 55.58 | 98.73 | 10,032,414 | 22.99% | 582,197 | 5.80% |
| PRJNA772045 | SAMN22358017 | 2.17E+09 | 12,585,524 | 43.67 | 56.33 | 98.68 | 8,683,570 | 31.00% | 6,588 | 0.08% |
| PRJNA772045 | SAMN22358018 | 2.10E+09 | 16,674,042 | 46.14 | 53.86 | 98.50 | 12,472,146 | 25.20% | 10,826 | 0.09% |
| PRJNA772045 | SAMN22358019 | 2.48E+09 | 14,483,294 | 43.87 | 56.13 | 98.76 | 11,986,114 | 17.24% | 891,977 | 7.44% |
| PRJNA772045 | SAMN22358020 | 2.30E+09 | 12,677,400 | 45.21 | 54.79 | 98.56 | 11,228,498 | 11.43% | 1,089,349 | 9.70% |
| PRJNA772045 | SAMN22358021 | 2.43E+09 | 14,026,498 | 43.54 | 56.46 | 98.72 | 10,809,798 | 22.93% | 2,388,235 | 22.09% |
| PRJNA772045 | SAMN22358022 | 1.97E+09 | 16,989,660 | 43.70 | 56.30 | 98.55 | 13,648,750 | 19.66% | 5,099,363 | 37.36% |
| PRJNA772045 | SAMN22358023 | 2.52E+09 | 14,808,998 | 43.64 | 56.36 | 98.77 | 13,009,292 | 12.15% | 5,759,297 | 44.27% |
| PRJNA772045 | SAMN22358024 | 2.19E+09 | 13,300,190 | 42.13 | 57.87 | 98.70 | 10,782,856 | 18.93% | 1,147,132 | 10.64% |
| PRJNA772045 | SAMN22358025 | 1.91E+09 | 13,514,762 | 42.56 | 57.44 | 98.54 | 11,681,046 | 13.57% | 1,888,233 | 16.16% |
| PRJNA772045 | SAMN22358026 | 2.57E+09 | 14,444,148 | 44.95 | 55.05 | 98.63 | 12,026,412 | 16.74% | 4,184,115 | 34.79% |
| PRJNA772045 | SAMN22358027 | 2.24E+09 | 12,656,150 | 45.03 | 54.97 | 98.91 | 10,184,462 | 19.53% | 2,323,947 | 22.82% |
| PRJNA772045 | SAMN22358028 | 2.01E+09 | 14,453,848 | 43.07 | 56.93 | 98.36 | 11,300,292 | 21.82% | 773,240 | 6.84% |
| PRJNA772045 | SAMN22358029 | 2.18E+09 | 14,670,230 | 44.88 | 55.12 | 98.96 | 13,060,682 | 10.97% | 4,761,511 | 36.46% |
| PRJNA772045 | SAMN22358030 | 1.91E+09 | 8,036,376 | 44.97 | 55.03 | 98.82 | 5,987,696 | 25.49% | 4,786,888 | 79.95% |
| PRJNA772045 | SAMN22358031 | 2.18E+09 | 14,514,018 | 43.64 | 56.36 | 98.62 | 11,308,760 | 22.08% | 1,040,705 | 9.20% |
| PRJNA772045 | SAMN22358032 | 1.21E+09 | 14,373,190 | 47.06 | 52.94 | 98.83 | 10,696,138 | 25.58% | 3,353,345 | 31.35% |
| PRJNA772045 | SAMN22358033 | 2.19E+09 | 12,265,628 | 44.04 | 55.96 | 98.82 | 8,915,664 | 27.31% | 578,927 | 6.49% |
| PRJNA772045 | SAMN22358034 | 2.17E+09 | 13,409,018 | 43.40 | 56.60 | 98.58 | 10,613,368 | 20.85% | 25,952 | 0.24% |
| PRJNA772045 | SAMN22358035 | 1.85E+09 | 13,259,254 | 44.13 | 55.87 | 98.32 | 10,291,950 | 22.38% | 9,045,568 | 87.89% |
| PRJNA772045 | SAMN22358036 | 2.00E+09 | 16,262,482 | 41.84 | 58.16 | 98.69 | 13,544,006 | 16.72% | 12,595,303 | 93.00% |
| PRJNA772045 | SAMN22358037 | 2.46E+09 | 13,097,708 | 41.79 | 58.21 | 98.86 | 8,550,548 | 34.72% | 898,743 | 10.51% |
| PRJNA772045 | SAMN22358038 | 1.98E+09 | 12,735,572 | 44.44 | 55.56 | 98.54 | 8,875,980 | 30.31% | 550,638 | 6.20% |
| PRJNA772045 | SAMN22358039 | 1.92E+09 | 12,894,422 | 43.65 | 56.35 | 98.37 | 9,177,962 | 28.82% | 14,550 | 0.16% |
| PRJNA772045 | SAMN22358040 | 1.95E+09 | 12,930,854 | 43.44 | 56.56 | 98.80 | 10,895,156 | 15.74% | 2,556,525 | 23.46% |
| PRJNA772045 | SAMN22358041 | 2.04E+09 | 13,477,350 | 43.66 | 56.34 | 98.89 | 11,528,892 | 14.46% | 1,405,336 | 12.19% |
| PRJNA772045 | SAMN22358042 | 2.49E+09 | 16,493,456 | 43.58 | 56.42 | 98.90 | 13,843,698 | 16.07% | 2,360,297 | 17.05% |
| PRJNA772045 | SAMN22358043 | 1.99E+09 | 13,205,156 | 42.87 | 57.13 | 98.31 | 9,668,272 | 26.78% | 1,215,215 | 12.57% |
| PRJNA772045 | SAMN22358044 | 2.19E+09 | 14,535,248 | 42.83 | 57.17 | 98.69 | 12,181,720 | 16.19% | – | – |
| PRJNA772045 | SAMN22358045 | 1.69E+09 | 11,163,702 | 42.44 | 57.56 | 98.85 | 8,624,394 | 22.75% | – | – |

**Supplementary Table 4**. List summarizing all viruses detected in the composite samples.

Note: Only viruses with (near) complete or partial genomes, less than 20 kb were considered, because known plant viruses do not have genomes larger than 20 kb. Virus identification is based on percent genome / nucleotide similarity to known species and applicable demarcation criteria set by ICTV, as of 31st October 2021. Virus taxa and species names are based on the ICTV Master Species List (MSL) #36. In the table matrix, HTS-based detections are marked as A - detection with full genome, B - detection with partial genome, or C - probable sequencing cross-talk, contamination or low titer detection with a very small fraction of reads mapped to reference genome (<0.00001%).

(see next page)

**Note**: Virus names in yellow highlight are novel species, in red font are probable insect or fungal viral species, in green font are virus-like associated RNAs, satellite RNAs, putative viroids and viruses under Realm *Riboviria*; in blue font are viruses with unconfirmed weed host(s).

| | | | | Sampling location ID → | BER19 | | | | | NGO19 | | | BUK19 | | KOP19 | | | PAR19 | | | BOL19 | | | | POR19 | | | KOR19 | | | BER20 | | | | STR20 | | | | BOL20 | | | MIR20 | | | KOP20 | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | Number of plants in the composite sample → | 6 | 6 | 10 | 6 | 7 | 5 | 3 | 5 | 9 | 4 | 5 | 5 | 4 | 10 | 4 | 4 | 6 | 5 | 8 | 7 | 5 | 5 | 3 | 8 | 7 | 5 | 5 | 7 | 5 | 10 | 5 | 8 | 8 | 10 | 5 | 8 | 11 | 4 | 9 | 7 | 4 | 8 | 6 | 5 |
| | | | | Number of viruses detected (<20 kb genome only) → | 3 | 4 | 2 | 5 | 4 | 3 | 3 | 4 | 9 | 4 | 1 | 6 | 8 | 11 | 5 | 1 | 1 | 1 | 3 | 10 | 8 | 3 | 10 | 3 | 5 | 5 | 1 | 4 | 3 | 2 | 3 | 5 | 6 | 3 | 2 | 3 | 9 | 2 | 3 | 5 | 3 | 2 | 13 | 9 |
| Order | Family | Genus | Virus name (or tentative name for new species) | SRA accession number → Unique virus abbreviation ↓ | SRR16552271 | SRR16552270 | SRR16552235 | SRR16552224 | SRR16552261 | SRR16552250 | SRR16552286 | SRR16552275 | SRR16552273 | SRR16552272 | SRR16552269 | SRR16552244 | SRR16552243 | SRR16552242 | SRR16552241 | SRR16552240 | SRR16552239 | SRR16552238 | SRR16552237 | SRR16552236 | SRR16552234 | SRR16552233 | SRR16552232 | SRR16552231 | SRR16552230 | SRR16552229 | SRR16552226 | SRR16552225 | SRR16552223 | SRR16552222 | SRR16552221 | SRR16552268 | SRR16552267 | SRR16552266 | SRR16552265 | SRR16552264 | SRR16552263 | SRR16552262 | SRR16552260 | SRR16552259 | SRR16552258 | SRR16552257 | SRR16552256 | SRR16552255 |
| *Bunyavirales* | *Tospoviridae* | *Orthotospovirus* | tomato spotted wilt orthotospovirus | TSWV | | |C| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Bunyavirales* | *Tospoviridae* | *Orthotospovirus* | Mercurialis orthotospovirus 1 | MerV1 | | | | | | | | | | | | |A| | |A| | | |A| | | | | | | | | | | | | | | | | | | | | | |A| |
| *Bunyavirales* | unclassified | unclassified | tomato associated bunya-like virus 1 | TaBLV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | | |
| *Bunyavirales* | *Fimoviridae* | *Emaravirus* | Artemesia fimovirus 1 | ArtV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | |
| *Durnavirales* | *Amalgaviridae* | *Amalgavirus* | southern tomato virus | STV |B| |B| | |A|A| |B| | | | |A| | |B|A|B| |B|B| |A|A| |A|A| | |C|A|A| |B|A| |A|A| |A| | | |
| *Durnavirales* | *Partitiviridae* | *Deltapartitivirus* | plant associated deltapartitivirus 1 | PaDPV1 | | | |A| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Durnavirales* | *Partitiviridae* | *Deltapartitivirus* | plant associated deltapartitivirus 2 | PaDPV2 | | | | | | | | | | | | | | | | | | | |B| | | | | | | | | | | | | | | | | | | | | | |A| |
| *Durnavirales* | *Partitiviridae* | *Deltapartitivirus* | plant associated deltapartitivirus 3 | PaDPV3 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Durnavirales* | *Partitiviridae* | *Deltapartitivirus* | plant associated deltapartitivirus 4 | PaDPV4 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Durnavirales* | *Partitiviridae* | *Deltapartitivirus* | plant associated deltapartitivirus 5 | PaDPV5 | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | | | | | | | |A| | | | | | | |
| *Durnavirales* | *Partitiviridae* | *Deltapartitivirus* | plant associated deltapartitivirus 6 | PaDPV6 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Durnavirales* | *Partitiviridae* | *Gammapartitivirus* | Eysiphe necator associated partitivirus 2 | EnaPV2 | | | | | | | | | | | | |A| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Geplafuvirales* | *Geminiviridae* | unclassified | Calystegia geminivirus 1, partial genome | CGV1 | | | |C| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |B|
| *Ghabrivirales* | *Totiviridae* | unclassified | Erysiphales associated totivirus 24 | EaTV24 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | | |
| *Ghabrivirales* | *Totiviridae* | unclassified | Koper totivirus 1 | KTV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A|
| *Ghabrivirales* | *Totiviridae* | unclassified | Koper totivirus 2 | KTV2 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A|
| *Ghabrivirales* | *Totiviridae* | unclassified | Koper totivirus 3 | KTV3 | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | | | | | | | | | |
| *Martellivirales* | *Bromoviridae* | *Cucumovirus* | cucumber mosaic virus | CMV | | | |A| | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | |C| | | | | | | | | | |
| *Martellivirales* | *Bromoviridae* | *Cucumovirus* | peanut stunt virus | PSV | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | |
| *Martellivirales* | *Bromoviridae* | *Cucumovirus* | tomato aspermy virus | TAV | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Martellivirales* | *Bromoviridae* | *Ilarvirus* | Solanum nigrum ilarvirus 1 | SnIV1 | | | | | | | | | | | | | | | | | | | | |C|C|B| | | | | | | | | | | | | | | | | | | | | |
| *Martellivirales* | *Bromoviridae* | *Ilarvirus* | tomato ilarvirus 1 | TIV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | |
| *Martellivirales* | *Bromoviridae* | *Ilarvirus* | Prunus virus I | PrVI | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | |
| *Martellivirales* | *Closteroviridae* | *Closterovirus* | beet yellows virus | BYV | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Martellivirales* | *Closteroviridae* | *Closterovirus* | plant associated closterovirus 1 | PaClV1 | | | | |A| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Martellivirales* | *Closteroviridae* | *Closterovirus* | plant associated closterovirus 2 | PaClV2 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | |
| *Martellivirales* | *Closteroviridae* | *Crinivirus* | plant associated crinivirus 1 | PaCrV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | |
| *Martellivirales* | *Endornaviridae* | *Alphaendornavirus* | tomato associated alphaendornavirus 1 | TaAEV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | | |
| *Martellivirales* | *Endornaviridae* | *Alphaendornavirus* | plant associated alphaendornavirus 1 | PaAEV1 | | | |A| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Martellivirales* | *Kitaviridae* | *Blunervirus* | tomato fruit blotch virus | ToFBV | | | | | | | | | | | | | | | | | | |A|A| | | | | | | | | | | | | | | | | | | | | | | | |
| *Martellivirales* | *Virgaviridae* | *Tobamovirus* | tomato mosaic virus | ToMV |A|A|A|A|A| |C| | | | |B| | |B| | | | | | | | | | |A| |C|A|A|A| | |C| |C|C| | |C| | | | | |
| *Martellivirales* | unclassified | unclassified | plant associated tobamo-like virus 1 | PaTLV1 | | | | | | | | | | | | |A|C|C| | | | | | |C| | |C| | | | | |C| | | | | | | | | | | | | |
| *Martellivirales* | *Virgaviridae* | *Tobamovirus* | Plantago tobamovirus 1 | PTV1 | | | | | | | | | | | | |C| | | | | | |A| | | | | | | | | | | | | | | | | | | | | | | | |
| *Mononegavirales* | *Lispiviridae* | unclassified | Leveillula taurica associated rhabdo-like virus 1 | LtaRLV1 | | | | | |C|C| |A|B| | | |C| | | | | | |C| |C| | | | | | | | | | | |C| | | | | | | |C| | |
| *Mononegavirales* | *Rhabdoviridae* | *Alphanucleorhabdovirus* | eggplant mottled dwarf virus | EMDV | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | | |
| *Mononegavirales* | *Rhabdoviridae* | *Alphanucleorhabdovirus* | Physostegia chlorotic mottle virus | PhCMoV | |A| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Mononegavirales* | *Rhabdoviridae* | *Betanucleorhabdovirus* | tomato betanucleorhabdovirus 1 | TBRV1 | |A| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Mononegavirales* | *Rhabdoviridae* | *Cytorhabdovirus* | Pastinaca cytorhabdovirus 1 | PaCRV1 | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | | | | | | | | | | | | |
| *Mononegavirales* | *Rhabdoviridae* | *Betanucleorhabdovirus* | tomato betanucleorhabdovirus 2 | TBRV2 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | |A| | | | | | | | | |
| *Mononegavirales* | *Rhabdoviridae* | *Betanucleorhabdovirus* | Picris betanucleorhabdovirus 1 | PBRV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | |
| *Mononegavirales* | *Rhabdoviridae* | *Cytorhabdovirus* | Cirsium cytorhabdovirus 1 | CCRV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Mononegavirales* | *Rhabdoviridae* | *Betanucleorhabdovirus* | Taraxacum betanucleorhabdovirus 1 | TBRV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Mononegavirales* | *Rhabdoviridae* | *Cytorhabdovirus* | Picris cytorhabdovirus 1 | PiCRV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | |
| *Mononegavirales* | *Rhabdoviridae* | *Cytorhabdovirus* | Taraxacum cytorhabdovirus 1 | TCRV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Mononegavirales* | *Rhabdoviridae* | *Alphanucleorhabdovirus* | tomato alphanucleorhabdovirus 1 | TARV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | | | |
| *Ortervirales* | *Caulimoviridae* | *Caulimovirus* | plant associated caulimovirus 1 | PaCaV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A|
| *Ortervirales* | *Caulimoviridae* | *Soymovirus* | plant associated soymovirus 1 | PaSoV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |C| | | | | | |C| | | | | | |A|
| *Patatavirales* | *Potyviridae* | *Potyvirus* | potato virus Y | PVY |A|A| | | | | | | | | | | | | | | | | | | | | | | | | |A|A| |A|A|A| | | | | |A| | | | | |
| *Patatavirales* | *Potyviridae* | *Potyvirus* | carrot thin leaf virus | CTLV | | | | | | | | | | | | | | | | | | | | | | |A| | |A| | | | | | | | | | | | | | | | | | |
| *Patatavirales* | *Potyviridae* | *Potyvirus* | lettuce mosaic virus | LMV | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A|
| *Patatavirales* | *Potyviridae* | *Potyvirus* | Henbane mosaic virus | HMV | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Patatavirales* | *Potyviridae* | *Potyvirus* | watermelon mosaic virus | WMV | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | |
| *Patatavirales* | *Potyviridae* | *Macluravirus* | broad-leafed dock virus A | BLDVA | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Patatavirales* | *Potyviridae* | *Potyvirus* | Plantago potyvirus 1 | PlaPV1 | | | | | | | | | |A| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Patatavirales* | *Potyviridae* | *Potyvirus* | Rumex potyvirus 1 | RumPV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Patatavirales* | *Potyviridae* | *Macluravirus* | Mentha macluravirus 1 | MenMV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Patatavirales* | *Potyviridae* | *Macluravirus* | broad-leafed dock virus A, divergent strain | BLDVA-divergent | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Picornavirales* | *Dicistroviridae* | unclassified | Novo Mesto dicistrovirus 1 | NMDV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Picornavirales* | *Dicistroviridae* | unclassified | Novo Mesto dicistrovirus 2 | NMDV2 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Picornavirales* | *Dicistroviridae* | unclassified | Ljubljana dicistrovirus 1 | LDV1 | | | |C|A| | | | | | | | | | | | | | | | |C| | | | | | | |C| | | | | | | | | | | | | | |
| *Picornavirales* | *Iflaviridae* | *Iflavirus* | tomato matilda virus | TMaV | | | | | | | | | | | |B| |B|B| |C|C|B|B|A|A| |A|A|B| | | | |C|A|A| | | | | | | | |C| | |
| *Picornavirales* | *Iflaviridae* | *Iflavirus* | La Jolla virus | LJV | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| |
| *Picornavirales* | *Iflaviridae* | unclassified | Novo Mesto iflavirus 1 | NMIV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Picornavirales* | *Picornaviridae* | unclassified | Aphis glycines virus 1 | AGV1 | | | | |C| | | | | | | | | | | | | | | |A| | | |C| | | | | | | | | | | | | | | | | | | |
| *Picornavirales* | *Picornaviridae* | unclassified | Hubei picorna-like virus 36 | HuPiLV36 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Picornavirales* | *Secoviridae* | *Fabavirus* | broad bean wilt virus 1 | BBWV1 | | | | | | | |A| |A| | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | |
| *Picornavirales* | *Secoviridae* | *Waikavirus* | plant associated waikavirus 1 | PaWV1 | | | | |A| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Picornavirales* | *Secoviridae* | *Waikavirus* | plant associated waikavirus 2 | PaWV2 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Picornavirales* | *Secoviridae* | *Sequivirus* | plant associated sequivirus 1 | PaSV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Picornavirales* | *Secoviridae* | *Sequivirus* | plant associated sequivirus 2 | PaSV2 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Picornavirales* | *Secoviridae* | *Sequivirus* | plant associated sequivirus 3 | PaSV3 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Serpentovirales* | *Aspiviridae* | *Ophiovirus* | Ranunculus white mottle ophiovirus | RWMV | | | | | |A|A| | | | |A| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| |
| *Sobelivirales* | *Solemoviridae* | *Polerovirus* | Hubei polero-like virus 2 | HuPLV2 | | | |A| | | | | |A| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Sobelivirales* | *Solemoviridae* | *Polerovirus* | barley virus G | BVG | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | | | | | | | | | | | | |
| *Sobelivirales* | *Solemoviridae* | *Polerovirus* | plant associated polerovirus 1 | PaPoV1 | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | | | | | | | |A| | | | | | | |
| *Sobelivirales* | *Solemoviridae* | *Polerovirus* | plant associated polerovirus 2 | PaPoV2 | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | | | | | | | | | | | | | | | |
| *Sobelivirales* | *Solemoviridae* | *Polerovirus* | plant associated polerovirus 3 | PaPoV3 | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | | | | | | | | | | | | |
| *Tolivirales* | *Tombusviridae* | *Alphanecrovirus* | olive latent virus 1 | OLV1 | | | | | |B|B| |B| |B|B| |A| | | | | | |B| | | |B| | | | | | | | | | |C| |C|C| |B|A| | |
| *Tolivirales* | *Tombusviridae* | *Alphanecrovirus* | olive mild mosaic virus, partial genome | OMMV | | | | | | | | | | | |B| |B| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Tolivirales* | *Tombusviridae* | *Alphanecrovirus* | tobacco necrosis virus A | TNVA | | | | | | | | |B| | |B| |A| | | | | | | | | | | | | | | | | | | | | | | | | | | |B| | |
| *Tolivirales* | *Tombusviridae* | *Alphanecrovirus* | tomato bushy stunt virus | TBSV | | | | | | | | |A| | | | | | | | | | | | | | | | | | | | | | |A|C| | | | | | | | | | |
| *Tolivirales* | *Tombusviridae* | *Luteovirus* | soybean dwarf virus | SbDV | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | |
| *Tolivirales* | *Tombusviridae* | *Umbravirus* | Pastinaca umbravirus 1 | PasUV1 | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | | | | | | | | | | | | |
| *Tolivirales* | *Tombusviridae* | *Umbravirus* | Picris umbravirus 1 | PicUV1 | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | | | | | |A| | | | | | | |
| *Tolivirales* | *Tombusviridae* | *Aureusvirus* | Convolvulus aureusvirus 1 | ConAV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | |
| *Tolivirales* | *Tombusviridae* | *Pelarspovirus* | Calystegia pelarspovirus 1 | CalPV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A|
| *Tolivirales* | *Tombusviridae* | *Alphacarmovirus* | Cichorium alphacarmovirus 1 | CicAV1 | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | | | | | | | |A| | | | | | | |
| *Tymovirales* | *Alphaflexiviridae* | *Potexvirus* | white clover mosaic virus, near complete | WCMV | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| *Tymovirales* | *Alphaflexiviridae* | *Potexvirus* | Pastinaca potexvirus 1 | PasPV1 | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | | | | | | | | | | | | |
| *Tymovirales* | *Betaflexiviridae* | *Carlavirus* | potato virus M | PVM | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | | | | | | |
| *Tymovirales* | *Betaflexiviridae* | *Carlavirus* | potato virus S | PVS | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| |A| | | | | | | | | | | |
| *Tymovirales* | *Betaflexiviridae* | *Vitivirus* | tomato vitivirus 1 | TomV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| unclassified | unclassified | *Albetovirus* | tomato albetovirus 1 | TomAV1 | | | | | | | | |C| | |C| |A| | | | | | | | | | | | | | | | | | | | | | | | | | | |C| | |
| unclassified | unclassified | unclassified | Taraxacum viroid-like circular RNA 1 | TVCR1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| unclassified | unclassified | unclassified | plant associated viroid-like circular RNA 1 | PaVCR1 | | | | | | | |A| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| unclassified | unclassified | unclassified | plant associated viroid-like circular RNA 2 | PaVCR2 | | | | | | | |A| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| unclassified | unclassified | unclassified | plant associated viroid-like circular RNA 3 | PaVCR3 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A|
| unclassified | unclassified | unclassified | plant associated viroid-like circular RNA 4 | PaVCR4 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| unclassified | unclassified | satellite RNAs | plant tombusvirus-like associated RNA 1 | PTaR1 | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | | | | | | | | | | | | |
| unclassified | unclassified | satellite RNAs | plant tombusvirus-like associated RNA 2 | PTaR2 | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | | | | | | | | | | | | |
| unclassified | unclassified | satellite RNAs | plant tombusvirus-like associated RNA 3 | PTaR3 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| unclassified | unclassified | satellite RNAs | Cymbidium ringspot virus satellite RNA | CymRSV-satRNA | | | | | | | | |A| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| unclassified | unclassified | satellite RNAs | tomato bushy stunt virus satellite RNA C | TBSV-satRNA-C | | | | | | | | |A| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| unclassified | unclassified | satellite RNAs | tomato bushy stunt virus satellite B10 | TBSV-satRNA-B10 | | | | | | | | |B| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| unclassified | unclassified | satellite RNAs | tomato bushy stunt virus satellite RNA L | TBSV-satRNA-L | | | | | | | | |B| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Realm *Riboviria* | unclassified | unclassified | Erysiphe necator ourmia-like virus 82 | EnOLV82 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |B|A| | | |
| Realm *Riboviria* | unclassified | unclassified | plant associated botourmia-like virus 1 | PaBLV1 | | | | | | | | | | | | | | |C| | | | | | | | | | |A| | | | | | | | | | | | | | | | | | |
| Realm *Riboviria* | unclassified | unclassified | plant associated botourmia-like virus 2 | PaBLV2 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A|
| Realm *Riboviria* | unclassified | unclassified | Plasmopara viticola lesion associated monoambiguivirus 1 | PvLAMV1 | | | | | | | | | | | | |A| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Realm *Riboviria* | unclassified | unclassified | Leveillula taurica associated noda-like virus 1 | LtaNLV1 | | | | | | | | | | | | | |B| | | | | |B|A|A| |A|A| | | | | | | |A| | | | | | | | | | | |
| Realm *Riboviria* | unclassified | unclassified | Koper noda-like virus 1 | KNLV1 | | | | | | | | | | | | |A| | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| |
| Realm *Riboviria* | unclassified | unclassified | Koper noda-like virus 2 | KNLV2 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| |
| Realm *Riboviria* | unclassified | unclassified | Koper noda-like virus 3 | KNLV3 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| |
| Realm *Riboviria* | unclassified | unclassified | Koper noda-like virus 4 | KNLV4 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| |
| Realm *Riboviria* | unclassified | unclassified | Koper picorna-like virus 1 | KPLV1 | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | | | | | | | | | |
| Realm *Riboviria* | unclassified | unclassified | Novo Mesto picornavirus 1 | NMPV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Realm *Riboviria* | unclassified | unclassified | tomato associated partiti-like virus 1 | TaPLV1 | | | | | | | | | | | | | |B| | | | | | |A| | | | | | | | | | | | | | | | | | | | | | | |
| Realm *Riboviria* | unclassified | unclassified | tomato associated tombus-like virus 1 | TaTLV1 |C| | | | | |C|C| | | | | |A| | | | | | |A| | | | | | | | | | | | | | | | | | | | | | | |
| Realm *Riboviria* | unclassified | unclassified | Erysiphe necator associated ambiguivirus 2 | EnaAV2 | | | | | | | |A|C| | |C| |B|A| |C|C| | |C| | |C| | | | | | | | | | | | | | | | |C|C|B| |
| Realm *Riboviria* | unclassified | unclassified | plant associated tombus-like virus 1 | PaTLV1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| |
| Realm *Riboviria* | unclassified | unclassified | plant associated tombus-like virus 2 | PaTLV2 | | | | | | | |C| | | | | | |C| | | | | | | | | | | | | | |A| | | | | | | | | | | | | |
| Realm *Riboviria* | unclassified | unclassified | Sanxia tombus-like virus 7 | STLV7 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| | | | |
| Realm *Riboviria* | unclassified | unclassified | Erysiphe necator associated ssRNA virus 9 | EnaSRV9 | | | | | | | | | | | |C|A| |A|C| | | | | | | | | | | | | | | | | | | | | | | | |C|A| |
| Realm *Riboviria* | unclassified | unclassified | plant associated virga-like virus 1 | PaVLV1 | | | | | | | |C| | | |C|A|B|A|C| | | | | | | | | | | | | | | | | | | | | | | | |C|B| |
| Realm *Riboviria* | unclassified | unclassified | plant associated virga-like virus 2 | PaVLV2 | | | | | | | | | | | | |A| | | | | | | | | | | | | | | | | | | | | | | | | | | | |A| |
| Realm *Riboviria* | unclassified | unclassified | tomato associated virga-like virus 1 | TaVLV1 | | | | | | | | | | | | | | | | | | | | |A| | | | | | | | | | | | | | | | | | | | | | | |

## **Supplementary Table 4**. (continued columns).

**Note**: Virus names in **yellow highlight** are novel species, in **red font** are probable insect or fungal viral species, in **green font** are virus-like associated RNAs, satellite RNAs, putative viroids and viruses under Realm *Riboviria*; in **blue font** are viruses with unconfirmed weed host(s).

| | | | **Sampling location ID →** | | **SKO20** | | | | **KOR20** | | | | **PLE20** | | | | | **JUR20** | | | | | **TUR20** | | | | | **Total** | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | **Number of plants in the composite sample →** | | 5 | 5 | 6 | 10 | 5 | 7 | 7 | 9 | 5 | 7 | 6 | 7 | 10 | 5 | 8 | 7 | 6 | 5 | 5 | 9 | 8 | 7 | 10 | 436 | **plant samples** |
| | | | **Number of viruses detected** (<20 kb genome only) → | | 4 | 6 | 7 | 5 | 5 | 5 | 5 | 12 | 4 | 3 | 6 | 4 | 6 | 3 | 2 | 3 | 5 | 5 | 4 | 5 | 4 | 4 | 7 | 314 | **virus genomes (all isolates, full or partial)** |
| **Order** | **Family** | **Genus** | **Virus name** (or tentative name for new species) | **SRA accession number →** **Unique virus abbreviation ↓** | SRR16552254 | SRR16552253 | SRR16552252 | SRR16552251 | SRR16552249 | SRR16552248 | SRR16552247 | SRR16552246 | SRR16552245 | SRR16552291 | SRR16552290 | SRR16552289 | SRR16552288 | SRR16552287 | SRR16552285 | SRR16552284 | SRR16552283 | SRR16552282 | SRR16552281 | SRR16552280 | SRR16552279 | SRR16552278 | SRR16552277 | **Number of isolates** (full or partial genome) | **GenBank Accession Numbers** ( NOTE: Only isolates with full genomes, marked here with "A", were submitted in GenBank. Multiple GenBank accession numbers are listed successively → ) |
| *Bunyavirales* | *Tospoviridae* | *Orthotospovirus* | tomato spotted wilt orthotospovirus | TSWV | | | | | | | | | | | A | A | | | | | | | | A | A | A | A | 6 | |
| *Bunyavirales* | *Tospoviridae* | *Orthotospovirus* | Mercurialis orthotospovirus 1 | MerV1 | | | | | | | | | | | | | | | | | | | | | | | | 4 | |
| *Bunyavirales* | *unclassified* | unclassified | tomato associated bunya-like virus 1 | TaBLV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Bunyavirales* | *Fimoviridae* | *Emaravirus* | Artemesia fimovirus 1 | ArtV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Durnavirales* | *Amalgaviridae* | *Amalgavirus* | southern tomato virus | STV | A | A | A | | | | | | A | A | A | A | | | | A | | | B | A | A | A | | 34 | |
| *Durnavirales* | *Partitiviridae* | *Deltapartitivirus* | plant associated deltapartitivirus 1 | PaDPV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Durnavirales* | *Partitiviridae* | *Deltapartitivirus* | plant associated deltapartitivirus 2 | PaDPV2 | | | | | | | | | | | | | | | | | | | | | | | | 2 | |
| *Durnavirales* | *Partitiviridae* | *Deltapartitivirus* | plant associated deltapartitivirus 3 | PaDPV3 | | | | A | | | | | | | | | | | | | | | | | | | | 1 | |
| *Durnavirales* | *Partitiviridae* | *Deltapartitivirus* | plant associated deltapartitivirus 4 | PaDPV4 | | | | A | | | | | | | | | | | | | | | | | | | | 1 | |
| *Durnavirales* | *Partitiviridae* | *Deltapartitivirus* | plant associated deltapartitivirus 5 | PaDPV5 | | | | | | | | | | | | | | | | | | | | | | | | 2 | |
| *Durnavirales* | *Partitiviridae* | *Deltapartitivirus* | plant associated deltapartitivirus 6 | PaDPV6 | | | | | | | | | | | | | | | | | A | | | | | | | 1 | |
| *Durnavirales* | *Partitiviridae* | *Gammapartitivirus* | Eysiphe necator associated partitivirus 2 | EnaPV2 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Geplafuvirales* | *Geminiviridae* | unclassified | Calystegia geminivirus 1, partial genome | CGV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Ghabrivirales* | *Totiviridae* | unclassified | Erysiphales associated totivirus 24 | EaTV24 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Ghabrivirales* | *Totiviridae* | unclassified | Koper totivirus 1 | KTV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Ghabrivirales* | *Totiviridae* | unclassified | Koper totivirus 2 | KTV2 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Ghabrivirales* | *Totiviridae* | unclassified | Koper totivirus 3 | KTV3 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Martellivirales* | *Bromoviridae* | *Cucumovirus* | cucumber mosaic virus | CMV | A | A | A | | A | A | A | | C | A | | | | | | | | | | | | | | 9 | |
| *Martellivirales* | *Bromoviridae* | *Cucumovirus* | peanut stunt virus | PSV | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Martellivirales* | *Bromoviridae* | *Cucumovirus* | tomato aspermy virus | TAV | | | A | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Martellivirales* | *Bromoviridae* | *Ilarvirus* | Solanum nigrum ilarvirus 1 | SnIV1 | | | | | | | | | | | | | | | | | A | | | | | | | 2 | |
| *Martellivirales* | *Bromoviridae* | *Ilarvirus* | tomato ilarvirus 1 | TIV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Martellivirales* | *Bromoviridae* | *Ilarvirus* | Prunus virus I | PrVI | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Martellivirales* | *Closteroviridae* | *Closterovirus* | beet yellows virus | BYV | | | | | | | | A | | | | | | | | | | | | | | | | 1 | |
| *Martellivirales* | *Closteroviridae* | *Closterovirus* | plant associated closterovirus 1 | PaClV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Martellivirales* | *Closteroviridae* | *Closterovirus* | plant associated closterovirus 2 | PaClV2 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Martellivirales* | *Closteroviridae* | *Crinivirus* | plant associated crinivirus 1 | PaCrV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Martellivirales* | *Endornaviridae* | *Alphaendornavirus* | tomato associated alphaendornavirus 1 | TaAEV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Martellivirales* | *Endornaviridae* | *Alphaendornavirus* | plant associated alphaendornavirus 1 | PaAEV1 | | | | | | | | | | | | | | | | | | A | | | | | | 2 | |
| *Martellivirales* | *Kitaviridae* | *Blunervirus* | tomato fruit blotch virus | ToFBV | | | | | | | | | | | | | | | | | | | | | | | | 2 | |
| *Martellivirales* | *Virgaviridae* | *Tobamovirus* | tomato mosaic virus | ToMV | | | | | | A | | | | | | | | A | A | A | A | A | B | A | A | | | 20 | |
| *Martellivirales* | *unclassified* | unclassified | plant associated tobamo-like virus 1 | PaTLV1 | | | | | A | A | A | | | | | | | | | | | | | | | | | 4 | |
| *Martellivirales* | *Virgaviridae* | *Tobamovirus* | Plantago tobamovirus 1 | PTV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Mononegavirales* | *Lispivirdae* | unclassified | Leveillula taurica associated rhabdo-like virus 1 | LtaRLV1 | | | | | | | | | | | | | | | | | | C | C | | | | | 2 | |
| *Mononegavirales* | *Rhabdoviridae* | *Alphanucleorhabdovirus* | eggplant mottled dwarf virus | EMDV | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Mononegavirales* | *Rhabdoviridae* | *Alphanucleorhabdovirus* | Physostegia chlorotic mottle virus | PhCMoV | | | | | | | | | | | A | | | | | | | | | | A | A | | 4 | |
| *Mononegavirales* | *Rhabdoviridae* | *Betanucleorhabdovirus* | tomato betanucleorhabdovirus 1 | TBRV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Mononegavirales* | *Rhabdoviridae* | *Cytorhabdovirus* | Pastinaca cytorhabdovirus 1 | PaCRV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Mononegavirales* | *Rhabdoviridae* | *Betanucleorhabdovirus* | tomato betanucleorhabdovirus 2 | TBRV2 | A | A | A | | | | | | | | | | | | | | | | | | | | | 5 | |
| *Mononegavirales* | *Rhabdoviridae* | *Betanucleorhabdovirus* | Picris betanucleorhabdovirus 1 | PBRV1 | | | | A | | | | | | | | | | | | | | | | | | | | 2 | |
| *Mononegavirales* | *Rhabdoviridae* | *Cytorhabdovirus* | Cirsium cytorhabdovirus 1 | CCRV1 | | | | | | | | A | | | | | | | | | | | | | | | | 1 | |
| *Mononegavirales* | *Rhabdoviridae* | *Betanucleorhabdovirus* | Taraxacum betanucleorhabdovirus 1 | TBRV1 | | | | | | | | | | | | | A | | | | | | | | | | A | 2 | |
| *Mononegavirales* | *Rhabdoviridae* | *Cytorhabdovirus* | Picris cytorhabdovirus 1 | PiCRV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Mononegavirales* | *Rhabdoviridae* | *Cytorhabdovirus* | Taraxacum cytorhabdovirus 1 | TCRV1 | | | | | | | | | | | | | A | | | | | | | | | | | 1 | |
| *Mononegavirales* | *Rhabdoviridae* | *Alphanucleorhabdovirus* | tomato alphanucleorhabdovirus 1 | TARV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Ortervirales* | *Caulimoviridae* | *Caulimovirus* | plant associated caulimovirus 1 | PaCaV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Ortervirales* | *Caulimoviridae* | *Soymovirus* | plant associated soymovirus 1 | PaSoV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Patatavirales* | *Potyviridae* | *Potyvirus* | potato virus Y | PVY | A | A | A | A | A | A | A | | A | A | A | A | | A | A | A | | | | | | A | | 23 | |
| *Patatavirales* | *Potyviridae* | *Potyvirus* | carrot thin leaf virus | CTLV | | | | | | | | A | | | | | | | | | | | | | | | | 3 | |
| *Patatavirales* | *Potyviridae* | *Potyvirus* | lettuce mosaic virus | LMV | | | | A | | | | | | | | | | | | | | | | | | | | 2 | |
| *Patatavirales* | *Potyviridae* | *Potyvirus* | Henbane mosaic virus | HMV | | | A | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Patatavirales* | *Potyviridae* | *Potyvirus* | watermelon mosaic virus | WMV | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Patatavirales* | *Potyviridae* | *Macluravirus* | broad-leafed dock virus A | BLDVA | | | | | | | | | | | | | | | | | | | | | | | A | 1 | |
| *Patatavirales* | *Potyviridae* | *Potyvirus* | Plantago potyvirus 1 | PlaPV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Patatavirales* | *Potyviridae* | *Potyvirus* | Rumex potyvirus 1 | RumPV1 | | | | | | | | | | | | | A | | | | | | | | | | | 1 | |
| *Patatavirales* | *Potyviridae* | *Macluravirus* | Mentha macluravirus 1 | MenMV1 | | | | | | | | A | | | | | | | | | | | | | | | | 1 | |
| *Patatavirales* | *Potyviridae* | *Macluravirus* | broad-leafed dock virus A, divergent strain | BLDVA-divergent | | | | | | | | | | | | | C | | | | | | | | | | A | 1 | |
| *Picornavirales* | *Dicistroviridae* | unclassified | Novo Mesto dicistrovirus 1 | NMDV1 | | | | | | | | | | | | | | | | | A | | | | | | | 1 | |
| *Picornavirales* | *Dicistroviridae* | unclassified | Novo Mesto dicistrovirus 2 | NMDV2 | | | | | | | | | | | | | | | | | | A | | | | | | 1 | |
| *Picornavirales* | *Dicistroviridae* | unclassified | Ljubljana dicistrovirus 1 | LDV1 | | | | | | | | | | | | | C | | | | | | | | | | | 1 | |
| *Picornavirales* | *Iflaviridae* | *Iflavirus* | tomato matilda virus | TMaV | | | C | | | | | | | | | | | | | | | | | | | | | 12 | |
| *Picornavirales* | *Iflaviridae* | *Iflavirus* | La Jolla virus | LJV | | | | | | | | | | | | | | C | | | | | | | | | | 1 | |
| *Picornavirales* | *Iflaviridae* | unclassified | Novo Mesto iflavirus 1 | NMIV1 | | | | | | | | | | | | | | | | | | | | | | | A | 1 | |
| *Picornavirales* | *Picornaviridae* | unclassified | Aphis glycines virus 1 | AGV1 | | | | | | | | | | | | | A | | | | | | | | | | | 2 | |
| *Picornavirales* | *Picornaviridae* | unclassified | Hubei picorna-like virus 36 | HuPiLV36 | | | | | | | | | | | | | | A | | | | | | A | | | | 2 | |
| *Picornavirales* | *Secoviridae* | *Fabavirus* | broad bean wilt virus 1 | BBWV1 | | | | | | | | | | | | | | | | | | | | | | | | 3 | |
| *Picornavirales* | *Secoviridae* | *Waikavirus* | plant associated waikavirus 1 | PaWV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Picornavirales* | *Secoviridae* | *Waikavirus* | plant associated waikavirus 2 | PaWV2 | | | | | | | | A | | | | | | | | | | | | | | | | 1 | |
| *Picornavirales* | *Secoviridae* | *Sequivirus* | plant associated sequivirus 1 | PaSV1 | | | | | | | | A | | | | | | | | | | | | | | | | 1 | |
| *Picornavirales* | *Secoviridae* | *Sequivirus* | plant associated sequivirus 2 | PaSV2 | | | | | | | | | | | | | A | | | | | | | | | | | 1 | |
| *Picornavirales* | *Secoviridae* | *Sequivirus* | plant associated sequivirus 3 | PaSV3 | | | | | | | | | | | | | A | | | | | | | | | | | 1 | |
| *Serpentovirales* | *Aspiviridae* | *Ophiovirus* | Ranunculus white mottle ophiovirus | RWMV | | | | | | | | | | | A | | | | | | | | | | | | | 5 | |
| *Sobelivirales* | *Solemoviridae* | *Polerovirus* | Hubei polero-like virus 2 | HuPLV2 | | | | | | | | | | | | | | | | | | | | | | | | 2 | |
| *Sobelivirales* | *Solemoviridae* | *Polerovirus* | barley virus G | BVG | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Sobelivirales* | *Solemoviridae* | *Polerovirus* | plant associated polerovirus 1 | PaPoV1 | | | | | | | | | | | | | | | | | | | | | | | | 2 | |
| *Sobelivirales* | *Solemoviridae* | *Polerovirus* | plant associated polerovirus 2 | PaPoV2 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Sobelivirales* | *Solemoviridae* | *Polerovirus* | plant associated polerovirus 3 | PaPoV3 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Tolivirales* | *Tombusviridae* | *Alphanecrovirus* | olive latent virus 1 | OLV1 | | | | | | | | | | | | | | | | | | | B | | | | | 11 | |
| *Tolivirales* | *Tombusviridae* | *Alphanecrovirus* | olive mild mosaic virus, partial genome | OMMV | | | | | | | | | | | | | | | | | | | | | | | | 2 | |
| *Tolivirales* | *Tombusviridae* | *Alphanecrovirus* | tobacco necrosis virus A | TNVA | | | | | | | | | | | | | | | | | | | | | | | | 4 | |
| *Tolivirales* | *Tombusviridae* | *Alphanecrovirus* | tomato bushy stunt virus | TBSV | | | | | | | | | | | | | | | | | | | | | | | | 2 | |
| *Tolivirales* | *Tombusviridae* | *Luteovirus* | soybean dwarf virus | SbDV | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Tolivirales* | *Tombusviridae* | *Umbravirus* | Pastinaca umbravirus 1 | PasUV1 | | | | | | | | A | | | | | | | | | | | | | | | | 2 | |
| *Tolivirales* | *Tombusviridae* | *Umbravirus* | Picris umbravirus 1 | PicUV1 | | | | | | | | | | | | | | | | | | | | | | | | 2 | |
| *Tolivirales* | *Tombusviridae* | *Aureusvirus* | Convolvulus aureusvirus 1 | ConAV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Tolivirales* | *Tombusviridae* | *Pelarspovirus* | Calystegia pelarspovirus 1 | CalPV1 | | | | | | | | A | | | | | | | | | | | | | | | | 2 | |
| *Tolivirales* | *Tombusviridae* | *Alphacarmovirus* | Cichorium alphacarmovirus 1 | CicAV1 | | | | | | | | | | | | | | | | | | A | | | | | | 3 | |
| *Tymovirales* | *Alphaflexiviridae* | *Potexvirus* | white clover mosaic virus, near complete | WCMV | | | | | | | | | | | | | | | | | | | | | | | A | 1 | |
| *Tymovirales* | *Alphaflexiviridae* | *Potexvirus* | Pastinaca potexvirus 1 | PasPV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| *Tymovirales* | *Betaflexiviridae* | *Carlavirus* | potato virus M | PVM | | | | | A | A | A | | | | | A | | | | | | | | | | | | 5 | |
| *Tymovirales* | *Betaflexiviridae* | *Carlavirus* | potato virus S | PVS | | A | | | | | | | | | | | | | | | | | | | | | | 3 | |
| *Tymovirales* | *Betaflexiviridae* | *Vitivirus* | tomato vitivirus 1 | TomV1 | | A | A | | | | | | | | | | | | | | | | | | | | | 2 | |
| unclassified | unclassified | *Albetovirus* | tomato albetovirus 1 | TomAV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| unclassified | unclassified | unclassified | Taraxacum viroid-like circular RNA 1 | TVCR1 | | | | | | | | | | | | | | | | | | | | | | | A | 1 | |
| unclassified | unclassified | unclassified | plant associated viroid-like circular RNA 1 | PaVCR1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| unclassified | unclassified | unclassified | plant associated viroid-like circular RNA 2 | PaVCR2 | | | | | | | | | | | | | | | | | A | A | | | | | | 3 | |
| unclassified | unclassified | unclassified | plant associated viroid-like circular RNA 3 | PaVCR3 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| unclassified | unclassified | unclassified | plant associated viroid-like circular RNA 4 | PaVCR4 | | | | | | | | A | | | | | | | | | | | | | | | | 1 | |
| unclassified | unclassified | satellite RNAs | plant tombusvirus-like associated RNA 1 | PTaR1 | | | | | | | | A | | | | | | | | | | | | | | | | 2 | |
| unclassified | unclassified | satellite RNAs | plant tombusvirus-like associated RNA 2 | PTaR2 | | | | | | | | A | | | | | | | | | | | | | | | | 2 | |
| unclassified | unclassified | satellite RNAs | plant tombusvirus-like associated RNA 3 | PTaR3 | | | | | | | | A | | | | | | | | | | | | | | | | 1 | |
| unclassified | unclassified | satellite RNAs | Cymbidium ringspot virus satellite RNA | CymRSV-satRNA | | | | | | | | | C | | | | | | | | | | | | | C | | 1 | |
| unclassified | unclassified | satellite RNAs | tomato bushy stunt virus satellite RNA C | TBSV-satRNA-C | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| unclassified | unclassified | satellite RNAs | tomato bushy stunt virus satellite B10 | TBSV-satRNA-B10 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| unclassified | unclassified | satellite RNAs | tomato bushy stunt virus satellite RNA L | TBSV-satRNA-L | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| Realm *Riboviria* | unclassified | unclassified | Erysiphe necator ourmia-like virus 82 | EnOLV82 | | | | | | | | | | | | | | | | | | | | | | | | 2 | |
| Realm *Riboviria* | unclassified | unclassified | plant associated botourmia-like virus 1 | PaBLV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| Realm *Riboviria* | unclassified | unclassified | plant associated botourmia-like virus 2 | PaBLV2 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| Realm *Riboviria* | unclassified | unclassified | Plasmopara viticola lesion associated monoambiguivirus 1 | PvLAMV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| Realm *Riboviria* | unclassified | unclassified | Leveillula taurica associated noda-like virus 1 | LtaNLV1 | | | | | | | | | | | | | | | | | | | | | | | | 7 | |
| Realm *Riboviria* | unclassified | unclassified | Koper noda-like virus 1 | KNLV1 | | | | | | | | | | | | | | | | | | | | | | | | 2 | |
| Realm *Riboviria* | unclassified | unclassified | Koper noda-like virus 2 | KNLV2 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| Realm *Riboviria* | unclassified | unclassified | Koper noda-like virus 3 | KNLV3 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| Realm *Riboviria* | unclassified | unclassified | Koper noda-like virus 4 | KNLV4 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| Realm *Riboviria* | unclassified | unclassified | Koper picorna-like virus 1 | KPLV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| Realm *Riboviria* | unclassified | unclassified | Novo Mesto picornavirus 1 | NMPV1 | | | | | | | | | | | | | | | | | | | | A | | | | 1 | |
| Realm *Riboviria* | unclassified | unclassified | tomato associated partiti-like virus 1 | TaPLV1 | | | | | A | | A | | | | | | | | | | | | | | | | | 4 | |
| Realm *Riboviria* | unclassified | unclassified | tomato associated tombus-like virus 1 | TaTLV1 | | | | | | | | | A | | | | | | | | | | | | | | | 3 | |
| Realm *Riboviria* | unclassified | unclassified | Erysiphe necator associated ambiguivirus 2 | EnaAV2 | | | | | | | | | B | | B | | | | | | | | B | | C | C | | 7 | |
| Realm *Riboviria* | unclassified | unclassified | plant associated tombus-like virus 1 | PaTLV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| Realm *Riboviria* | unclassified | unclassified | plant associated tombus-like virus 2 | PaTLV2 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| Realm *Riboviria* | unclassified | unclassified | Sanxia tombus-like virus 7 | STLV7 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |
| Realm *Riboviria* | unclassified | unclassified | Erysiphe necator associated ssRNA virus 9 | EnaSRV9 | | | | | | | | | | | | | | | | | | | | | | | | 3 | |
| Realm *Riboviria* | unclassified | unclassified | plant associated virga-like virus 1 | PaVLV1 | | | | | | | | | | | | | | | | | | | | | | | | 4 | |
| Realm *Riboviria* | unclassified | unclassified | plant associated virga-like virus 2 | PaVLV2 | | | | | | | | | | | | | | | | | | | | | | | | 2 | |
| Realm *Riboviria* | unclassified | unclassified | tomato associated virga-like virus 1 | TaVLV1 | | | | | | | | | | | | | | | | | | | | | | | | 1 | |

**Supplementary Table 5**. List of analyses done in the reconstruction and identification of individual virus genomes. Only (near) complete or partial genomes, less than 20 kb, and with average mapping depth greater than 1.0 are listed.

Notes: [1]Virus identification is based on percent genome or nucleotide sequence similarity to known species and other applicable demarcation criteria set by ICTV, as of 31st October 2021. Virus and taxa and recognized species names and naming rules, are based on the information at the ICTV website (www.talk.ictvonline.org/) and Master Species List (MSL) #36. [2]All BLAST analyses were done using the nucleotide (nt) database version released on December 2020. Best hits have E-value less than 0.0001. [3]Genome mapping was done on viral RefSeq version from July 2020. [4]Mapping (95% nucleotide similarity and coverage was set) and assembly were done on CLC Genomics Workbench version 20.0, and assembly was also done using metaSPAdes (SPAdes version 3.14). [5]trimmed and quality-screened reads from the sequencing library. 6final consensus genome length / best hit genome length (in no. of nucleotides).

(see next page)

| SRA/Library ID | Virus name[1] (or tentative name for new species that are in **yellow highlight**; genome segment name is indicated if present) | Unique virus abbreviation | Best hit from BLASTn analysis[2] of mapping consensus[3] | | OR | Best hit from BLASTn analysis[2] of assembled contig[4] | | Remapping reads to final consensus genome sequence[4] and final BLASTn analysis for verification[2] | | | | | NBCI GenBank accession number of reconstructed viral genome | Remarks / Notes |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | Fraction of reads[5] mapped | Average mapping depth | Best hit in BLASTn[2] | | | | |
| | | | GenBank accession no. | Percent identity | | GenBank accession no. | Percent identity | | | GenBank accession no. | Genome covered[6] | Percent identity | | |
| **SRR16552271 / P1.1BER19-ST** | | | | | | | | | | | | | | |
| | potato virus Y | PVY | KX184817 | 99.69 | | - | - | 0.7087% | 1745.64 | KX184817 | 9709/9719 | 100.00 | OL472145 | full genome assembled |
| | tomato mosaic virus | ToMV | MN267904 | 99.00 | | - | - | 93.7180% | 351439.67 | MN267904 | 6384/6383 | 99.00 | OL472089 | full genome assembled |
| | southern tomato virus | STV | MN095716 | 96.00 | | - | - | 0.0003% | 2.45 | MN095716 | - | 96.00 | - | low read coverage, partial genome obtained (was not deposited) |
| **SRR16552270 / P1.2BER19-ST** | | | | | | | | | | | | | | |
| | potato virus Y | PVY | JF927761 | 99.80 | | - | - | 0.5200% | 1209.20 | JF927761 | - | 98.00 | - | reconstruction of consensus genome not possible due to presence of more than one viral strain |
| | tomato mosaic virus | ToMV | MN267904 | 99.42 | | - | - | 96.4897% | 8246.41 | MN267904 | 9684/9701 | 99.00 | OL472090 | full genome assembled |
| | Physostegia chlorotic mottle alphanucleorhabdovirus | PhCMoV | KY706238 | 96.00 | | - | - | 0.6600% | 1132.91 | KY706238 | 13318/13319 | 99.00 | MW366749 | full genome assembled |
| | tomato betanucleorhabdovirus 1 | TBRV1 | KM823531 | 66.80 | | - | - | 0.0106% | 17.83 | KM823531 | 13577/13188 | 66.80 | OL472119 | new species, full genome assembled |
| **SRR16552235 / P02BER19-AT** | | | | | | | | | | | | | | |
| | tomato mosaic virus | ToMV | MN267904 | 99.40 | | - | - | 0.8000% | 398.36 | MN267904 | 6364/6383 | 99.40 | OL472088 | full genome assembled |
| | southern tomato virus | STV | MN216389 | 100.00 | | - | - | 0.0069% | 6.41 | MN216389 | - | 100.00 | - | low read coverage, partial genome obtained (was not deposited) |
| **SRR16552224 / P3.1BER19-SW** | | | | | | | | | | | | | | |
| | cucumber mosaic virus, RNA1 | CMV | D00356 | 99.00 | | - | - | 0.1006% | 441.58 | D00356 | 3558/3557 | 98.70 | OL472030 | full genome assembled |
| | cucumber mosaic virus, RNA2 | CMV | AJ517801 | 99.00 | | - | - | 0.1017% | 490.83 | AJ517801 | 3052/3050 | 98.70 | OL472048 | full genome assembled |
| | cucumber mosaic virus, RNA3 | CMV | AJ517802 | 99.00 | | - | - | 0.2896% | 1935.45 | AJ517802 | 2216/2216 | 99.20 | OL472039 | full genome assembled |
| | tomato mosaic virus | ToMV | MN267904 | 97.74 | | - | - | 0.0141% | 32.92 | MN267904 | 6341/6383 | 99.40 | OL472091 | full genome assembled |
| | Hubei polero-like virus 2 | HuPLV2 | KX882844 | 98.00 | | - | - | 0.4138% | 1009.61 | KX882844 | 6083/6083 | 99.10 | OL472220 | full genome assembled |
| | plant associated alphaendornavirus 1 | PaAEV1 | MH182675 | 65.60 | | - | - | 0.0179% | 18.35 | MH182675 | 14445/14728 | 65.60 | OL472077 | new species, full genome assembled |
| | plant associated deltapartitivirus 1, RNA1 | PaDPV1 | - | - | | NC_038846 | 76.10 | 0.0091% | 79.00 | NC_038846 | 1555/1575 | 76.10 | OL472010 | new species, full genome assembled |
| | plant associated deltapartitivirus 1, RNA2a | PaDPV1 | - | - | | MK731958 | 70.31 | 0.0076% | 72.76 | MK731958 | 1544/1583 | 70.31 | OL472011 | new species, full genome assembled |
| | plant associated deltapartitivirus 1, RNA2b | PaDPV1 | - | - | | MK731957 | 64.88 | 0.0033% | 32.11 | MK731957 | 1510/1517 | 64.88 | OL472012 | new species, full genome assembled |
| **SRR16552261 / P3.2BER19-SW** | | | | | | | | | | | | | | |
| | tomato mosaic virus | ToMV | MN267904 | 99.30 | | - | - | 0.0190% | 38.68 | MN267904 | 6383/6383 | 99.40 | OL472092 | full genome assembled |
| | plant associated closterovirus 1 | PaClV1 | - | - | | LC480248 | 65.80 | 0.0296% | 29.22 | LC480248 | 13177/15597 | 65.80 | OL472072 | new species, full genome assembled |
| | plant associated waikavirus 1 | PaWV1 | - | - | | NC_040586 | 67.00 | 0.0247% | 29.23 | NC_040586 | 11022/12313 | 67.04 | OL472169 | new species, full genome assembled |
| | Ljubljana dicistrovirus 1 | LDV1 | - | - | | MH459180 | 67.00 | 0.0776% | 114.32 | MH459180 | 8841/8293 | 67.00 | OL472194 | new species, full genome assembled |
| **SRR16552250 / P04NGO19-AT** | | | | | | | | | | | | | | |
| | southern tomato virus | STV | MF422618 | 100.00 | | - | - | 0.0500% | 180.61 | MF422618 | 3414/3437 | 100.00 | OL471986 | full genome assembled |
| | olive latent virus 1 | OLV1 | MK376952 | 98.00 | | - | - | 0.0022% | 7.64 | MK376952 | - | 98.00 | - | low read coverage, partial genome obtained (was not deposited) |
| | Ranunculus white mottle ophiovirus, RNA1 | RWMV | NC_043389 | 91.20 | | - | - | 0.2140% | 201.00 | NC_043389 | 7622/4018 | 91.24 | OL472207 | first full sequence of genome segment assembled |
| | Ranunculus white mottle ophiovirus, RNA2 | RWMV | AF335430 | 90.10 | | - | - | | | AF335430 | 1787/263 | 90.08 | OL472208 | first full sequence of genome segment assembled |
| | Ranunculus white mottle ophiovirus, RNA3 | RWMV | AY542957 | 91.90 | | - | - | | | AY542957 | 1486/1063 | 91.94 | OL472209 | first full sequence of genome segment assembled |
| | Ranunculus white mottle ophiovirus, RNA4 | RWMV | KY769704 | 71.10 | | - | - | | | KY769704 | 1324/1381 | 71.11 | OL472210 | first full sequence of genome segment assembled |
| **SRR16552286 / P05NGO19-ST** | | | | | | | | | | | | | | |
| | southern tomato virus | STV | MF422618 | 100.00 | | - | - | 0.1073% | 434.84 | MF422618 | 3414/3437 | 100.00 | OL471987 | full genome assembled |
| | olive latent virus 1 | OLV1 | MK376952 | 97.70 | | - | - | 0.0040% | 15.20 | MK376952 | 3277/3699 | 98.00 | - | partial genome obtained (was not deposited) |
| | Ranunculus white mottle ophiovirus, RNA1 | RWMV | NC_043389 | 91.20 | | - | - | 0.1969% | 231.00 | NC_043389 | 7622/4018 | 91.24 | OL472211 | first full sequence of genome segment assembled |
| | Ranunculus white mottle ophiovirus, RNA2 | RWMV | AF335430 | 90.10 | | - | - | | | AF335430 | 1787/263 | 90.08 | OL472212 | first full sequence of genome segment assembled |
| | Ranunculus white mottle ophiovirus, RNA3 | RWMV | AY542957 | 91.90 | | - | - | | | AY542957 | 1486/1063 | 91.94 | OL472213 | first full sequence of genome segment assembled |
| | Ranunculus white mottle ophiovirus, RNA4 | RWMV | KY769704 | 71.10 | | - | - | | | KY769704 | 1324/1381 | 71.11 | OL472214 | first full sequence of genome segment assembled |
| **SRR16552275 / P06NGO19-SW** | | | | | | | | | | | | | | |
| | broad bean wilt virus 1, RNA1 | BBWV1 | - | - | | MN216350 | 88.30 | 1.7688% | 3820.85 | MN216350 | 5820/5771 | 88.27 | OL472172 | full genome assembled, probable divergent strain |
| | broad bean wilt virus 1, RNA2 | BBWV1 | - | - | | MN216379 | 88.70 | 2.1729% | 7952.26 | MN216379 | 3435/3303 | 88.68 | OL472173 | full genome assembled, probable divergent strain |
| | Erysiphe necator associated ambiguivirus 2 | EnaAV2 | - | - | | MN627469 | 97.90 | 0.0042% | 16.34 | MN627469 | 3198/3222 | 97.90 | OL472267 | full genome assembled |
| | plant associated viroid-like circular RNA 1 | PaVCR1 | not applicable | - | | not applicable | - | 0.0024% | 55.03 | not applicable | 556/ - | - | OL472257 | viroid-like circular RNA (putative new viroid species) |
| | plant associated viroid-like circular RNA 1 | PaVCR2 | not applicable | - | | not applicable | - | 0.0026% | 65.88 | not applicable | 491/ - | - | OL472258 | viroid-like circular RNA (putative new viroid species) |
| **SRR16552273 / P07BUK19-ST** | | | | | | | | | | | | | | |
| | southern tomato virus | STV | KT85253 | 99.70 | | - | - | 0.0046% | 23.56 | KT85253 | 3364/3437 | 99.60 | - | partial genome obtained (was not deposited) |
| | tomato bushy stunt virus | TBSV | M21958 | 94.00 | | - | - | 0.0075% | 2748.00 | M21958 | 4755/4776 | 94.00 | OL472233 | full genome assembled |
| | Leveillula taurica-associated rhabdo-like virus | LtaRLV1 | MN609860 | 99.80 | | - | - | 0.0196% | 24.94 | MN609860 | 13978/14003 | 99.80 | OL472123 | full genome assembled |
| | olive latent virus 1 | OLV1 | MK376952 | 97.00 | | - | - | 0.0032% | 15.26 | MK376952 | - | 98.00 | - | low read coverage, partial genome obtained (was not deposited) |
| | tomato bushy stunt virus satellite RNA L | TBSV-satRNA-L | FJ666076 | 90.70 | | - | - | 0.0001% | 3.14 | FJ666076 | 483/615 | 91.10 | OL472255 | partial genome obtained |
| | tomato bushy stunt virus satellite RNA B10 | TBSV-satRNA-B10 | AF022788 | 94.10 | | - | - | 0.0014% | 41.41 | AF022788 | 590/612 | 94.10 | OL472254 | partial genome obtained |
| | tomato bushy stunt virus satellite RNA C | TBSV-satRNA-C | AF022787 | 82.20 | | - | - | 0.0008% | 16.96 | AF022787 | 884/822 | 81.30 | OL472253 | new species, best hit covers only 55% of the genome |
| | Cymbidium ringspot virus satellite RNA | CymRSV-satRNA | D00720 | 94.81 | | - | - | 0.0008% | 25.30 | D00720 | 607/618 | 94.80 | OL472252 | full genome assembled |
| **SRR16552272 / P08BUK19-SW** | | | | | | | | | | | | | | |
| | broad bean wilt virus 1, RNA1 | BBWV1 | - | - | | MN216350 | 82.60 | 1.3066% | 2809.68 | MN216350 | 5836/5771 | 82.63 | OL472170 | full genome assembled, probable divergent strain |
| | broad bean wilt virus 1, RNA2 | BBWV1 | - | - | | MN216379 | 71.60 | 6.5586% | 23566.87 | MN216379 | 3386/3303 | 71.57 | OL472171 | full genome assembled, probable divergent strain |
| | Hubei polero-like virus 2 | HuPLV2 | - | - | | KX882844 | 97.40 | 0.5413% | 1117.07 | KX882844 | 6083/6083 | 97.40 | OL472221 | full genome assembled |
| | Plantago potyvirus 1 | PlaPV1 | - | - | | AF543212 | 73.60 | 0.9120% | 1199.42 | AF543212 | 9528/9797 | 73.60 | OL472140 | new species, full genome assembled |
| **SRR16552269 / P09KOP19-AT** | | | | | | | | | | | | | | |
| | olive latent virus 1 | OLV1 | MK376952 | 97.00 | | - | - | 0.0004% | 1.82 | MK376952 | - | 97.00 | - | partial genome obtained (was not deposited) |
| **SRR16552244 / P10KOP19-ST** | | | | | | | | | | | | | | |
| | olive latent virus 1 | OLV1 | MK376952 | 95.78 | | - | - | 0.0037% | 15.37 | MK376952 | - | 95.66 | - | partial genome obtained (was not deposited) |
| | tobacco necrosis virus A | TNVA | KX906928 | 92.98 | | - | - | 0.0037% | 15.84 | KX906928 | - | 89.35 | - | partial genome obtained (was not deposited) |
| | olive mild mosaic virus | OMMV | KX906929 | 92.63 | | - | - | 0.0043% | 18.14 | KX906929 | - | 94.10 | - | partial genome obtained (was not deposited) |
| | tomato mosaic virus | ToMV | MN267904 | 97.45 | | - | - | 0.0023% | 5.45 | MN267904 | - | 97.45 | - | partial genome obtained (was not deposited) |
| | tomato matilda virus | TMaV | MK517476 | 99.27 | | - | - | 0.0065% | 11.81 | MK517476 | - | 99.24 | - | partial genome obtained (was not deposited) |
| | Ranunculus white mottle ophiovirus, RNA1 | RWMV | NC_043389 | 91.20 | | - | - | 0.3633% | 470.00 | NC_043389 | 7622/4018 | 91.24 | OL472199 | first full sequence of genome segment assembled |
| | Ranunculus white mottle ophiovirus, RNA2 | RWMV | AF335430 | 90.10 | | - | - | | | AF335430 | 1787/263 | 90.08 | OL472200 | first full sequence of genome segment assembled |
| | Ranunculus white mottle ophiovirus, RNA3 | RWMV | AY542957 | 91.90 | | - | - | | | AY542957 | 1486/1063 | 91.94 | OL472201 | first full sequence of genome segment assembled |
| | Ranunculus white mottle ophiovirus, RNA4 | RWMV | KY769704 | 71.10 | | - | - | | | KY769704 | 1324/1381 | 71.11 | OL472202 | first full sequence of genome segment assembled |
| **SRR16552243 / P11KOP19-SW** | | | | | | | | | | | | | | |
| | Mercurialis orthotospovirus 1, L segment | MerV1 | - | - | | JN560178 | 72.44 | 3.7889% | 3780.22 | JN560178 | 9024/8877 | 72.44 | OL471967 | new species, full genome assembled |
| | Mercurialis orthotospovirus 1, M segment | MerV1 | - | - | | JN560177 | 70.77 | 2.6906% | 4620.18 | JN560177 | 5232/4786 | 70.77 | OL471968 | new species, full genome assembled |
| | Mercurialis orthotospovirus 1, S segment | MerV1 | - | - | | AY686718 | 65.94 | 3.8029% | 11629.66 | AY686718 | 2887/2734 | 65.94 | OL471969 | new species, full genome assembled |
| | plant associated tobamo-like virus 1 | PaToLV1 | - | - | | NC_032449 | 35.06 | 0.0105% | 15.00 | NC_032449 | 6434/6969 | 35.06 | OL472105 | new species, has virga-like domains, BLASTx hit is shown |
| | Erysiphe necator associated ssRNA virus 9 | EnaSRV9 | - | - | | MN627473 | 89.97 | 0.0106% | 14.29 | MN627473 | 3489/3506 | 89.97 | OL472271 | full genome assembled, possibly a divergent strain |
| | plant associated virga-like virus 1 | PaVLV1 | - | - | | MN035426 | 71.65 | 0.0196% | 48.65 | MN035426 | 3586/3685 | 71.65 | OL472274 | new species, partial genome obtained |
| | plant associated virga-like virus 2 | PaVLV2 | - | - | | QED42936 | 31.15 | 0.2176% | 538.75 | QED42936 | 3627/ - | 31.15 | OL472275 | new species, has virga-like domains, BLASTx hit is shown |
| | Eysiphe necator associated partitivirus 2, RNA1 | EnaPV2 | - | - | | MN605492 | 99.54 | 0.0592% | 175.42 | MN605492 | 1723/1735 | 99.54 | OL472008 | full genome assembled |
| | Eysiphe necator associated partitivirus 2, RNA2 | EnaPV2 | - | - | | MN605493 | 99.93 | | | MN605493 | 1534/1557 | 99.93 | OL472009 | full genome assembled |
| | Plasmopara viticola lesion associated monoambiguivirus 1 | PvLAMV1 | - | - | | MN556995 | 96.59 | 0.2726% | 396.98 | MN556995 | 6159/6099 | 96.59 | OL472280 | full genome assembled |
| | Koper noda-like virus 1 | KNLV1 | - | - | | MW648508 | 67.13 | 0.0336% | 94.01 | MW648508 | 3150/3115 | 67.13 | OL472281 | new species, best hit covers only 37% of genome |
| **SRR16552242 / P12PAR19-AT** | | | | | | | | | | | | | | |
| | Southern tomato virus | STV | MK948595 | 99.60 | | - | - | 0.0439% | 129.88 | MK948595 | 3436/3437 | 99.70 | OL471989 | full genome assembled |
| | tobacco necrosis virus A | TNVA | KX906928 | 97.10 | | - | - | 0.0448% | 124.06 | KX906928 | 3684/3684 | 97.10 | OL472227 | full genome assembled |
| | olive latent virus 1 | OLV1 | MK376952 | 97.00 | | - | - | 0.0229% | 63.43 | MK376952 | 3646/3669 | 96.20 | OL472228 | full genome assembled |
| | olive mild mosaic virus | OMMV | KY769774 | 91.00 | | - | - | 0.0093% | 25.35 | KY769774 | - | 91.00 | - | partial genome obtained (was not deposited) |
| | tomato albetovirus 1 | TomAV1 | - | - | | L06057 | 74.01 | 0.0024% | 19.35 | L06057 | 1261/1239 | 74.01 | OL472251 | new species, full genome assembled |
| | tomato associated tombus-like virus 1 | TaTLV1 | - | - | | MN609858 | 69.57 | 0.0303% | 89.37 | MN609858 | 3430/3314 | 69.57 | OL472264 | new species, full genome assembled |
| **SRR16552241 / P13PAR19-ST** | | | | | | | | | | | | | | |
| | tomato mosaic virus | ToMV | MN267904 | 92.70 | | - | - | 0.0004% | 1.31 | MN267904 | - | 92.70 | - | low read coverage, partial genome obtained (was not deposited) |
| | tomato matilda virus | TMaV | MK517476 | 99.00 | | - | - | 0.0030% | 6.50 | MK517476 | - | 99.00 | - | low read coverage, partial genome obtained (was not deposited) |
| | Erysiphe necator associated ambiguivirus 2 | EnaAV2 | - | - | | MN627469 | 90.27 | 0.0071% | 41.60 | MN627469 | 3198/3222 | 90.27 | OL472266 | full genome assembled |
| | Erysiphe necator associated ssRNA virus 9 | EnaSRV9 | - | - | | MN627473 | 89.97 | 0.0093% | 50.93 | MN627473 | 3372/3506 | 89.97 | OL472270 | full genome assembled, possibly a divergent strain |
| | plant associated virga-like virus 1 | PaVLV1 | - | - | | MN035426 | 71.65 | 0.0079% | 41.67 | MN035426 | 3572/3685 | 71.65 | OL472273 | new species, has virga-like domains |
| **SRR16552240 / P14PAR19-SW** | | | | | | | | | | | | | | |
| | Mercurialis orthotospovirus 1, L segment | MerV1 | - | - | | JN560178 | 72.47 | 0.0306% | 31.81 | JN560178 | 9055/8877 | 72.47 | OL471967 | new species, full genome assembled |
| | Mercurialis orthotospovirus 1, M segment | MerV1 | - | - | | JN560177 | 70.61 | 0.0712% | 142.00 | JN560177 | 4714/4786 | 70.61 | OL471968 | new species, full genome assembled |
| | Mercurialis orthotospovirus 1, S segment | MerV1 | - | - | | AY686718 | 65.93 | 0.0636% | 174.38 | AY686718 | 3407/2734 | 65.93 | OL471969 | new species, full genome assembled |
| **SRR16552239 / P15.1BOL19-AT** | | | | | | | | | | | | | | |
| | Southern tomato virus | STV | MF422618 | 99.00 | | - | - | 0.0145% | 64.21 | MF422618 | - | 100.00 | - | partial genome obtained (was not deposited) |
| **SRR16552238 / P15.2BOL19-AT** | | | | | | | | | | | | | | |
| | Southern tomato virus | STV | MF422618 | 99.00 | | - | - | 0.0222% | 78.51 | MF422618 | 3413/3437 | 99.00 | OL471983 | full genome assembled |
| **SRR16552237 / P16BOL19-ST** | | | | | | | | | | | | | | |
| | Southern tomato virus | STV | MF422618 | 99.50 | | - | - | 0.0007% | 5.51 | MF422618 | - | 99.50 | - | partial genome obtained (was not deposited) |
| | tomato matilda virus | TMaV | MK517476 | 99.00 | | - | - | 0.0006% | 2.04 | MK517476 | - | 99.00 | - | partial genome obtained (was not deposited) |
| | tomato fruit blotch virus, RNA1 | ToFBV | MT434819 | 98.10 | | - | - | 0.0028% | 13.74 | MT434819 | 5767/5778 | 98.10 | OL472087 | full genome assembled |
| | tomato fruit blotch virus, RNA2 | ToFBV | MT434820 | 98.80 | | - | - | 0.0010% | 7.97 | MT434820 | 3542/3610 | 98.80 | OL472080 | full genome assembled |
| | tomato fruit blotch virus, RNA3 | ToFBV | MT434821 | 94.50 | | - | - | 0.0020% | 20.08 | MT434821 | 2756/2761 | 94.50 | OL472081 | full genome assembled |
| | tomato fruit blotch virus, RNA4 | ToFBV | MT434822 | 95.60 | | - | - | 0.0009% | 13.54 | MT434822 | 1886/1900 | 95.60 | OL472082 | full genome assembled |

**Supplementary Table 5**. (continued rows).

| SRA/Library ID | Virus name[1] (or tentative name for new species that are in yellow highlight; genome segment name is indicated if present) | Unique virus abbreviation | Best hit from BLASTn analysis[2] of mapping consensus[3] | | OR | Best hit from BLASTn analysis[2] of assembled contig[4] | | Remapping reads to final consensus genome sequence[4] and final BLASTn analysis for verification[2] | | | | | NBCI GenBank accession number of reconstructed viral genome | Remarks / Notes |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | GenBank accession no. | Percent identity | | GenBank accession no. | Percent identity | Fraction of reads[5] mapped | Average mapping depth | Best hit in BLASTn[2] | | | | |
| | | | | | | | | | | GenBank accession no. | Genome covered[6] | Percent identity | | |
| **SRR16552236 / P17BOL19-SW** | | | | | | | | | | | | | | |
| | Mercurialis orthotospovirus 1, L segment | MerV1 | - | - | | JN560178 | 72.50 | 0.0088% | 13.47 | JN560178 | 8979/8877 | 72.50 | OL471973 | new species, full genome assembled |
| | Mercurialis orthotospovirus 1, M segment | MerV1 | - | - | | JN560177 | 71.92 | 0.0289% | 79.32 | JN560177 | 4758/4786 | 71.92 | OL471974 | new species, full genome assembled |
| | Mercurialis orthotospovirus 1, S segment | MerV1 | - | - | | AY686718 | 65.75 | 0.0236% | 89.29 | AY686718 | 3463/2734 | 65.75 | OL471975 | new species, full genome assembled |
| | Plantago tobamovirus 1 | PTV1 | - | - | | GQ401365 | 86.22 | 18.5267% | 174.38 | GQ401365 | 6295/6311 | 86.22 | OL472109 | new species, full genome assembled |
| | plant associated polerovirus 1 | PaPoV1 | - | - | | KT868949 | 76.87 | 0.1962% | 448.83 | KT868949 | 6025/6017 | 76.87 | OL472217 | new species, full genome assembled |
| | plant associated polerovirus 2 | PaPoV2 | - | - | | KR706247 | 73.27 | 0.0640% | 155.67 | KR706247 | 5669/5643 | 73.27 | OL472218 | new species, full genome assembled |
| | tomato fruit blotch virus, RNA1 | ToFBV | MT434819 | 98.15 | | - | - | 0.1904% | 450.19 | MT434819 | 5811/5811 | 98.15 | OL472083 | full genome assembled |
| | tomato fruit blotch virus, RNA2 | ToFBV | MT434820 | 98.72 | | - | - | 0.0574% | 217.18 | MT434820 | 3629/3643 | 98.72 | OL472084 | full genome assembled |
| | tomato fruit blotch virus, RNA3 | ToFBV | MT434821 | 99.37 | | - | - | 0.3069% | 1470.54 | MT434821 | 2872/2872 | 99.37 | OL472085 | full genome assembled |
| | tomato fruit blotch virus, RNA4 | ToFBV | MT434822 | 99.64 | | - | - | 0.1122% | 790.85 | MT434822 | 1945/1946 | 99.64 | OL472086 | full genome assembled |
| | Cichorium alphacarmovirus 1 | CicAV1 | - | - | | HQ677625 | 73.24 | 48.4527% | 167483.71 | HQ677625 | 3933/3933 | 73.24 | OL472224 | new species, full genome assembled |
| | plant associated deltapartitivirus 5, RNA1 | PaDPV5 | - | - | | MW546937 | 76.10 | 0.0109% | 50.22 | MW546937 | 1512/1583 | 76.10 | OL472019 | new species, full genome assembled |
| | plant associated deltapartitivirus 5, RNA2 | PaDPV5 | - | - | | MW546938 | 65.92 | | | MW546938 | 1471/1459 | 65.92 | OL472020 | new species, full genome assembled |
| **SRR16552234 / P18POR19-ST** | | | | | | | | | | | | | | |
| | Southern tomato virus | STV | MK610257 | 98.00 | | - | - | 0.0103% | 52.88 | MK610257 | - | 98.00 | - | partial genome obtained (was not deposited) |
| | olive latent virus 1 | OLV1 | DQ083996 | 95.60 | | - | - | 0.0019% | 9.03 | DQ083996 | - | 95.69 | - | partial genome obtained (was not deposited) |
| | tomato matilda virus | TMaV | MK517476 | 99.70 | | - | - | 0.8361% | 1718.93 | MK517476 | 8653/8653 | 99.71 | OL472166 | full genome assembled |
| | Aphis glycines virus 1 | AGV1 | - | - | | KM015260 | 97.33 | 0.1987% | 393.70 | KM015260 | 8983/8680 | 97.33 | OL472190 | full genome assembled |
| | Leveillula taurica-associated noda-like virus 1 | LtaNLV1 | - | - | | MN609862 | 99.64 | 0.1349% | 533.68 | MN609862 | 4483/4289 | 99.64 | OL472283 | 2 sequences (MN609862-63) map to the assembled contig |
| | tomato associated partiti-like virus 1 | TaPLV1 | - | - | | MZ443622 | 73.90 | 0.0017% | 51.66 | MZ443622 | 1500/1506 | 73.90 | OL472291 | new species, full genome assembled |
| | tomato associated tombus-like virus 1 | TaTLV1 | - | - | | MN609858 | 69.72 | 0.0100% | 20.06 | MN609858 | 3427/3314 | 69.72 | OL472265 | new species, full genome assembled |
| | tomato associated virga-like virus 1 | TaVLV1 | - | - | | no good hit | - | 0.1377% | 459.02 | no good hit | 5277/ - | - | OL472265 | new species, full genome assembled |
| **SRR16552233 / P19POR19-AT** | | | | | | | | | | | | | | |
| | Southern tomato virus | STV | MK610257 | 100.00 | | - | - | 0.0019% | 5.47 | MK610257 | - | 100.00 | - | partial genome obtained (was not deposited) |
| | tomato matilda virus | TMaV | MK517476 | 99.68 | | - | - | 0.0774% | 90.03 | MK517476 | 8656/8653 | 99.68 | OL472167 | full genome assembled |
| | Leveillula taurica-associated noda-like virus 1 | LtaNLV1 | - | - | | MN609862 | 99.36 | 0.0665% | 148.27 | MN609862 | 4483/4289 | 99.36 | OL472284 | 2 sequences (MN609862-63) map to the assembled contig |
| **SRR16552232 / P20POR19-SW** | | | | | | | | | | | | | | |
| | carrot thin leaf virus | CTLV | - | - | | MH170889 | 91.73 | 7.4399% | 10282.14 | MH170889 | 9534/9490 | 91.73 | OL472133 | full genome assembled |
| | barley virus G | BVG | - | - | | KT962089 | 97.99 | 0.3173% | 748.49 | KT962089 | 5584/5620 | 97.99 | OL472215 | full genome assembled |
| | Solanum nigrum ilarvirus 1, RNA1 | SnIV1 | MN216370 | 98.68 | | - | - | 0.0012% | 4.73 | MN216370 | - | 98.68 | - | low read coverage, partial genome obtained (was not deposited) |
| | Solanum nigrum ilarvirus 1, RNA2 | SnIV1 | MN216373 | 95.31 | | - | - | 0.0007% | 3.16 | MN216373 | - | 95.31 | - | low read coverage, partial genome obtained (was not deposited) |
| | Solanum nigrum ilarvirus 1, RNA3 | SnIV1 | MN216376 | 98.20 | | - | - | 0.0016% | 9.05 | MN216376 | - | 98.20 | - | low read coverage, partial genome obtained (was not deposited) |
| | plant associated polerovirus 3 | PaPoV3 | - | - | | GU327735 | 76.13 | 1.5439% | 3345.45 | GU327735 | 6009/5803 | 76.13 | OL472219 | new species, full genome assembled |
| | Pastinaca potexvirus 1 | PasPV1 | - | - | | LC460456 | 67.27 | 0.5653% | 1262.61 | LC460456 | 5896/5964 | 67.27 | OL472238 | new species, full genome assembled |
| | Pastinaca cytorhabdovirus 1 | PaCRV1 | - | - | | MH898500 | 67.04 | 0.0249% | 25.05 | MH898500 | 13072/14419 | 67.04 | OL472112 | new species, full genome assembled |
| | Pastinaca umbravirus 1 | PasUV1 | - | - | | LC434065 | 77.80 | 0.2817% | 849.71 | LC434065 | 4368/4193 | 77.80 | OL472236 | new species, full genome assembled |
| | Picris umbravirus 1 | PicUV1 | - | - | | KT946712 | 80.00 | 1.8046% | 5437.68 | KT946712 | 4357/4196 | 80.00 | OL472232 | new species, full genome assembled |
| | plant tombusvirus-like associated RNA 1 | PTaR1 | - | - | | MF136436 | 77.74 | 0.2362% | 1049.28 | MF136436 | 2962/1867 | 77.74 | OL472298 | new species, full genome assembled |
| | plant tombusvirus-like associated RNA 2 | PTaR2 | - | - | | KX883211 | 82.05 | 0.0049% | 25.46 | KX883211 | 2524/5082 | 82.05 | OL472297 | new species, full genome assembled |
| **SRR16552231 / P21KOR19-AT** | | | | | | | | | | | | | | |
| | Southern tomato virus | STV | MK948595 | 99.60 | | - | - | 0.0184% | 95.18 | MK948595 | 3408/3437 | 99.60 | OL471984 | full genome assembled |
| | tomato matilda virus | TMaV | MK517476 | 99.70 | | - | - | 0.0440% | 43.74 | MK517476 | 8657/8653 | 99.70 | OL472168 | full genome assembled |
| | Leveillula taurica-associated noda-like virus 1 | LtaNLV1 | - | - | | MN609862 | 99.39 | 0.0157% | 29.93 | MN609862 | 4430/4289 | 99.39 | OL472285 | 2 sequences (MN609862-63) map to the assembled contig |
| **SRR16552230 / P22KOR19-ST** | | | | | | | | | | | | | | |
| | Southern tomato virus | STV | MK948595 | 99.60 | | - | - | 0.0193% | 129.97 | MK948595 | 3412/3437 | 99.60 | OL471990 | full genome assembled |
| | tomato mosaic virus | ToMV | MN267904 | 99.37 | | - | - | 0.0096% | 35.20 | MN267904 | 6383/6383 | 99.37 | OL472101 | full genome assembled |
| | tomato matilda virus | TMaV | MK517476 | 99.73 | | - | - | 0.0193% | 99.25 | MK517476 | 8562/8653 | 99.73 | OL472177 | full genome assembled |
| | olive latent virus 1 | OLV1 | MK376952 | 100.00 | | - | - | 0.0009% | 6.54 | MK376952 | - | 100.00 | - | partial genome obtained (was not deposited) |
| | Leveillula taurica-associated noda-like virus 1 | LtaNLV1 | - | - | | MN609862 | 99.38 | 0.0058% | 29.93 | MN609862 | 4483/4289 | 99.38 | OL472286 | 2 sequences (MN609862-63) map to the assembled contig |
| **SRR16552229 / P23KOR19-SW** | | | | | | | | | | | | | | |
| | carrot thin leaf virus | CTLV | MH170889 | 92.00 | | - | - | 1.2444% | 1303.84 | MH170889 | 9471/9490 | 91.00 | OL472134 | full genome assembled |
| | Koper picorna-like virus 1 | KPLV1 | - | - | | MN714669 | 73.59 | 0.0038% | 9.81 | MN714669 | 5151/9979 | 73.59 | OL472294 | new species, full genome assembled |
| | Koper totivirus 3 | KTV3 | - | - | | MK279493 | 62.51 | 0.0055% | 14.63 | MK279493 | 4988/5174 | 62.51 | OL472029 | new species, full genome assembled |
| | plant associated botourmia-like virus 1 | PaBLV1 | - | - | | MN532659 | 73.49 | 0.0063% | 36.22 | MN532659 | 2300/2339 | 73.49 | OL472278 | new species, full genome assembled |
| **SRR16552228 / P29Pv19-PK2 / internal control** | | | | | | | | | | | | | | |
| | Phaseolus vulgaris alphaendornavirus 1 | PvAEV1 | NC_039217 | - | | - | - | 0.1532% | 214.50 | MK948542 | 13901/13981 | 99.68 | - | full genome assembled, not deposited (internal control) |
| | Phaseolus vulgaris alphaendornavirus 2 | PvAEV2 | NC_038422 | - | | - | - | 0.5200% | 685.33 | MF281671 | 14417/14780 | 98.91 | - | partial genome obtained, not deposited (internal control) |
| | Phaseolus vulgaris alphaendornavirus 3 | PvAEV3 | NC_040558 | - | | - | - | 0.0217% | 27.58 | NC_040558 | 8831/15205 | 88.05 | - | partial genome obtained, not deposited (internal control) |
| **SRR16552227 / P30Pv19-PK1 / internal control** | | | | | | | | | | | | | | |
| | Phaseolus vulgaris alphaendornavirus 1 | PvAEV1 | NC_039217 | - | | - | - | 0.1448% | 214.50 | MK948542 | 13900/13981 | 99.68 | - | full genome assembled, not deposited (internal control) |
| | Phaseolus vulgaris alphaendornavirus 2 | PvAEV2 | NC_038422 | - | | - | - | 0.4340% | 392.52 | MF281671 | 14168/14780 | 99.59 | - | partial genome obtained, not deposited (internal control) |
| | Phaseolus vulgaris alphaendornavirus 3 | PvAEV3 | NC_040558 | - | | - | - | 0.0185% | 16.33 | NC_040558 | 7633/15205 | 87.83 | - | partial genome obtained, not deposited (internal control) |
| **SRR16552226 / P31BER20-AT** | | | | | | | | | | | | | | |
| | Southern tomato virus | STV | MF422618 | 99.70 | | - | - | 0.0017% | 8.48 | MF422618 | 3438/3438 | 99.70 | - | full genome assembled (was not deposited) |
| **SRR16552221 / P32STR20-AT** | | | | | | | | | | | | | | |
| | potato virus Y | PVY | AB185833 | 96.08 | | - | - | 5.6002% | 9230.31 | AB185833 | 9688/9698 | 99.47 | OL472161 | full genome assembled |
| | potato virus S | PVS | MH937416 | 98.74 | | - | - | 1.3352% | 2515.60 | MH937416 | 8477/8485 | 98.74 | OL472247 | full genome assembled |
| | tomato betanucleorhabdovirus 2 | TBRV2 | - | - | | MF543022 | 67.02 | 0.0064% | 7.67 | MF543022 | 13414/14432 | 67.02 | OL472129 | new species, full genome assembled |
| **SRR16552265 / P33BOL20-AT** | | | | | | | | | | | | | | |
| | tomato betanucleorhabdovirus 2 | TBRV2 | - | - | | MH323437 | 67.40 | 0.2493% | 295.17 | MH323437 | 13436/13546 | 70.05 | OL472116 | new species, full genome assembled |
| | Southern tomato virus | STV | MK948545 | 100.00 | | - | - | 0.0032% | 14.75 | MK948545 | - | 100.00 | - | partial genome obtained (was not deposited) |
| **SRR16552262 / P34MIR20-AT** | | | | | | | | | | | | | | |
| | Southern tomato virus | STV | MF422618 | 100.00 | | - | - | 0.0042% | 11.41 | MF422618 | - | 100.00 | - | partial genome obtained (was not deposited) |
| | tomato ilarvirus 1, RNA 1 | TIV1 | - | - | | NC_039075 | 69.57 | 0.0441% | 212.82 | NC_039075 | 3392/3378 | 69.57 | OL472057 | new species, full genome assembled |
| | tomato ilarvirus 1, RNA 2 | TIV1 | - | - | | KY695013 | 74.03 | 0.0839% | 481.15 | KY695013 | 2866/2931 | 74.03 | OL472058 | new species, full genome assembled |
| | tomato ilarvirus 1, RNA 3 | TIV1 | - | - | | KY695014 | 67.27 | 0.1392% | 1048.57 | KY695014 | 2181/2296 | 67.27 | OL472059 | new species, full genome assembled |
| **SRR16552258 / P35KOP20-AT** | | | | | | | | | | | | | | |
| | Southern tomato virus | STV | MK610257 | 99.97 | | - | - | 0.0110% | 41.24 | MK610257 | 3414/3414 | 99.97 | OL471998 | full genome assembled |
| | olive latent virus 1 | OLV1 | MK376952 | 96.32 | | - | - | 0.0027% | 9.49 | MK376952 | - | 96.34 | - | full genome assembled (was not deposited, possible recombinant) |
| | Erysiphe necator ourmia-like virus 82 | EnOLV82 | MN611610 | 96.15 | | - | - | 0.0009% | 4.90 | MN611610 | 2627/2859 | 93.19 | OL472300 | full genome assembled |
| **SRR16552254 / P36SKO20-AT** | | | | | | | | | | | | | | |
| | Southern tomato virus | STV | MF422618 | 100.00 | | - | - | 0.0134% | 62.18 | MF422618 | - | 100.00 | - | full genome assembled |
| | potato virus Y | PVY | AB185833 | 97.77 | | - | - | 14.7054% | 24495.49 | AB185833 | 9698/9698 | 99.49 | OL472158 | full genome assembled |
| | cucumber mosaic virus, RNA1 | CMV | D00356 | 100.00 | | - | - | 2.6547% | 12692.24 | D00356 | 3357/3357 | 98.90 | OL472036 | full genome assembled |
| | cucumber mosaic virus, RNA2 | CMV | KC019300 | 96.98 | | - | - | 5.0193% | 12010.42 | KC019300 | 3048/3049 | 96.81 | OL472054 | full genome assembled |
| | cucumber mosaic virus, RNA3 | CMV | AJ517802 | 99.14 | | - | - | 2.6547% | 36466.12 | AJ517802 | 2215/2216 | 99.17 | OL472045 | full genome assembled |
| | tomato betanucleorhabdovirus 2 | TBRV2 | - | - | | MF543022 | 67.82 | 1.7041% | 2040.29 | MF543022 | 13453/14432 | 67.82 | OL472120 | new species, full genome assembled |
| **SRR16552249 / P37KOR20-AT** | | | | | | | | | | | | | | |
| | potato virus Y | PVY | AB185833 | 97.06 | | - | - | 5.6244% | 10169.76 | AB185833 | 9698/9698 | 99.44 | OL472151 | full genome assembled |
| | potato virus M | PVM | JX678982 | 97.02 | | - | - | 1.8675% | 3843.19 | JX678982 | 8523/8523 | 97.02 | OL472242 | full genome assembled |
| | cucumber mosaic virus, RNA1 | CMV | HE962478 | 94.62 | | - | - | 1.9706% | 10237.36 | HE962478 | 3359/3358 | 94.02 | OL472032 | full genome assembled |
| | cucumber mosaic virus, RNA2 | CMV | MG021461 | 96.28 | | - | - | 1.7648% | 10088.19 | MG021461 | 3055/3050 | 96.58 | OL472050 | full genome assembled |
| | cucumber mosaic virus, RNA3 | CMV | AJ517802 | 98.87 | | - | - | 3.8745% | 30600.28 | AJ517802 | 2216/2216 | 99.07 | OL472041 | full genome assembled |
| | plant associated tobamo-like virus 1 | PaToLV1 | - | - | | NC_032449 | 35.06 | 0.0045% | 11.98 | NC_032449 | 6552/6969 | 35.06 | OL472106 | new species, has virga-like domains (RdRP,CP), full genome |
| | tomato associated partiti-like virus 1 | TaPLV1 | - | - | | MZ443622 | 71.17 | 0.0007% | 8.32 | MZ443622 | 1494/1506 | 71.17 | OL472292 | new species, best hit has only 41% genome covered |
| **SRR16552245 / P38PLE20-AT** | | | | | | | | | | | | | | |
| | potato virus Y | PVY | MN216361 | 98.18 | | - | - | 41.6262% | 85069.36 | MN216361 | 9609/9609 | 99.85 | OL472154 | full genome assembled |
| | Southern tomato virus | STV | MK948545 | 99.82 | | - | - | 0.0210% | 119.29 | MK948545 | 3436/3436 | 99.82 | OL472006 | full genome assembled |
| | tomato associated tombus-like virus 1 | TaTLV1 | - | - | | MN609858 | 70.00 | 0.0030% | 16.98 | MN609858 | 3430/3314 | 70.00 | OL472263 | new species, full genome assembled |
| | Erysiphe necator associated ambiguivirus 2 | EnaAV2 | - | - | | MN627469 | 95.89 | 0.0008% | 4.99 | MN627469 | - | 95.89 | - | low read coverage, partial genome obtained (was not deposited) |
| **SRR16552287 / P39JUR20-AT** | | | | | | | | | | | | | | |
| | tomato mosaic virus | ToMV | MN267904 | 99.50 | | - | - | 0.0807% | 201.46 | MN267904 | 6383/6386 | 99.50 | OL472096 | full genome assembled |
| | potato virus Y | PVY | - | - | | KX184847 | 99.79 | 0.0444% | 72.91 | KX184847 | 9719/9719 | 99.79 | OL472148 | full genome assembled |
| | Hubei picorna-like virus 36 | HuPiLV36 | KX883970 | 99.06 | | - | - | 0.0171% | 27.34 | KX883970 | 9977/9856 | 99.06 | OL472187 | full genome assembled |
| **SRR16552281 / P40TUR20-AT** | | | | | | | | | | | | | | |
| | tomato mosaic virus | ToMV | MN267904 | 97.75 | | - | - | 0.0026% | 5.70 | MN267904 | - | 97.75 | - | low read coverage, partial genome obtained (was not deposited) |
| | olive latent virus 1 | OLV1 | MK376952 | 96.91 | | - | - | 0.0006% | 1.65 | MK376952 | - | 96.91 | - | low read coverage, partial genome obtained (was not deposited) |
| | Southern tomato virus | STV | MK610257 | 100.00 | | - | - | 0.0008% | 3.12 | MK610257 | - | 100.00 | - | low read coverage, partial genome obtained (was not deposited) |
| **SRR16552225 / P41.1BER20-ST** | | | | | | | | | | | | | | |
| | potato virus Y | PVY | JF927755 | 97.68 | | - | - | 4.2245% | 8824.20 | JF927755 | 9689/9697 | 99.30 | OL472146 | full genome assembled |
| | tomato mosaic virus | ToMV | MN267904 | 99.50 | | - | - | 0.0035% | 10.98 | MN267904 | 6383/6383 | 99.40 | OL472093 | full genome assembled |
| | Southern tomato virus | STV | KT438549 | 99.50 | | - | - | 0.0092% | 53.70 | KT438549 | 3411/3463 | 99.36 | OL471992 | full genome assembled |
| | cucumber mosaic virus, RNA1 | CMV | D00356 | 99.11 | | - | - | 29.3895% | 177136.45 | D00356 | 3357/3360 | 99.11 | OL472031 | full genome assembled |
| | cucumber mosaic virus, RNA2 | CMV | D00355 | 99.08 | | - | - | 20.9980% | 139195.19 | D00355 | 3045/3048 | 99.08 | OL472049 | full genome assembled |
| | cucumber mosaic virus, RNA3 | CMV | AJ517802 | 99.64 | | - | - | 24.1833% | 220717.27 | AJ517802 | 2215/2216 | 99.64 | OL472040 | full genome assembled |

**Supplementary Table 5**. (continued rows).

| SRA/Library ID | Virus name[1] (or tentative name for new species that are in yellow highlight; genome segment name is indicated if present) | Unique virus abbreviation | Best hit from BLASTn analysis[2] of mapping consensus[3] | | OR | Best hit from BLASTn analysis[2] of assembled contig[4] | | Remapping reads to final consensus genome sequence[4] and final BLASTn analysis for verification[2] | | | | | NBCI GenBank accession number of reconstructed viral genome | Remarks / Notes |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | Fraction of reads[5] mapped | Average mapping depth | Best hit in BLASTn[2] | | | | |
| | | | GenBank accession no. | Percent identity | | GenBank accession no. | Percent identity | | | GenBank accession no. | Genome covered[6] | Percent identity | | |
| **SRR16552223 / P41.2BER20-ST** | | | | | | | | | | | | | | |
| | potato virus Y | PVY | AB185833 | 96.16 | | - | - | 0.5191% | 1012.95 | AB185833 | 9687/9698 | 99.01 | OL472147 | full genome assembled |
| | potato virus M | PVM | JX678982 | 96.83 | | - | - | 0.4948% | 1098.02 | JX678982 | 8507/8523 | 96.83 | OL472246 | full genome assembled |
| | tomato mosaic virus | ToMV | MN267904 | 99.44 | | - | - | 31.4357% | 177136.45 | MN267904 | 6383/6383 | 99.40 | OL472094 | full genome assembled |
| **SRR16552222 / P42BER20-SW** | | | | | | | | | | | | | | |
| | tomato mosaic virus | ToMV | MN267904 | 99.44 | | - | - | 19.2552% | 21122.12 | MN267904 | 6381/6383 | 99.44 | OL472095 | full genome assembled |
| | plant associated tombus-like virus 2 | PaTLV2 | - | - | | MT317175 | 76.36 | 0.0099% | 41.43 | MT317175 | 3297/3360 | 76.36 | OL472269 | new species, full genome assembled |
| **SRR16552268 / P43.1STR20-ST** | | | | | | | | | | | | | | |
| | Southern tomato virus | STV | MK610257 | 100.00 | | - | - | 0.0099% | 52.82 | MK610257 | 3413/3414 | 100.00 | OL471996 | full genome assembled |
| | potato virus Y | PVY | KY847961 | 99.68 | | - | - | 12.6303% | 24095.87 | KY847961 | 9628/9630 | 99.68 | OL472162 | full genome assembled |
| | tomato bushy stunt virus | TBSV | M21958 | 94.97 | | - | - | 0.0094% | 36.06 | M21958 | 4778/4776 | 95.61 | OL472162 | full genome assembled |
| | tomato alphanucleorhabdovirus 1 | TARV1 | - | - | | KC905081 | 75.20 | 7.0251% | 9626.99 | KC905081 | 13406/13154 | 75.20 | OL472234 | new species, full genome assembled |
| | tomato matilda virus | TMaV | MK517476 | 99.75 | | - | - | 0.0054% | 11.54 | MK517476 | 8653/8653 | 99.79 | OL472174 | full genome assembled |
| **SRR16552267 / P43.2STR20-ST** | | | | | | | | | | | | | | |
| | Southern tomato virus | STV | KT852573 | 99.82 | | - | - | 0.0160% | 70.06 | KT852573 | 3438/3438 | 99.82 | OL472004 | full genome assembled |
| | eggplant mottle dwarf virus | EMDV | LN680656 | 94.63 | | - | - | 14.9232% | 17362.84 | LN680656 | 13097/13100 | 94.63 | OL472111 | full genome assembled |
| | potato virus Y | PVY | JF927760 | 99.27 | | - | - | 6.2712% | 9857.20 | JF927760 | 9690/9697 | 99.45 | OL472163 | full genome assembled |
| | potato virus S | PVS | MH937416 | 98.62 | | - | - | 0.3527% | 633.50 | MH937416 | 8485/8485 | 98.62 | OL472249 | full genome assembled |
| | tomato matilda virus | TMaV | MK517476 | 99.78 | | - | - | 0.0158% | 27.81 | MK517476 | 8653/8653 | 99.78 | OL472178 | full genome assembled |
| | Leveillula taurica-associated noda-like virus 1 | LtaNLV1 | - | - | | MN609862 | 99.38 | 0.0057% | 19.47 | MN609862 | 4483/4289 | 99.38 | OL472287 | 2 sequences (MN609862-63) map to the assembled contig |
| **SRR16552266 / P44STR20-SW** | | | | | | | | | | | | | | |
| | watermelon mosaic virus | WMV | MN914158 | 99.49 | | - | - | 14.5047% | 119818.52 | MN914158 | 10040/10040 | 99.47 | OL472139 | full genome assembled |
| | peanut stunt virus, RNA1 | PSV | LC380687 | 97.52 | | - | - | 14.1287% | 57575.88 | LC380687 | 3347/3354 | 97.10 | OL472066 | full genome assembled |
| | peanut stunt virus, RNA2 | PSV | LC380688 | 97.35 | | - | - | 10.4424% | 48511.80 | LC380688 | 2940/2943 | 97.15 | OL472067 | full genome assembled |
| | peanut stunt virus, RNA3 | PSV | LC380680 | 97.35 | | - | - | 22.2985% | 139685.41 | LC380680 | 2185/2185 | 98.81 | OL472068 | full genome assembled |
| | broad bean wilt virus 1, RNA1 | BBWV1 | MN216350 | 90.78 | | - | - | 0.0275% | 65.29 | MN216350 | 5766/5771 | 91.68 | OL472175 | full genome assembled |
| | broad bean wilt virus 1, RNA2 | BBWV1 | MN216379 | 88.91 | | - | - | 0.0227% | 92.84 | MN216379 | 3341/3303 | 88.67 | OL472176 | full genome assembled |
| **SRR16552264 / P45BOL20-ST** | | | | | | | | | | | | | | |
| | Southern tomato virus | STV | MF422618 | 100.00 | | - | - | 0.0275% | 134.33 | MF422618 | 3415/3438 | 100.00 | OL472007 | full genome assembled |
| | tomato associated alphaendornavirus 1 | TaAEV1 | - | - | | MH094752 | 75.83 | 0.0108% | 15.64 | MH094752 | 11692/11683 | 75.83 | OL472079 | new species, full genome assembled |
| | Erysiphales associated totivirus 24 | EaTV24 | MN628271 | 99.74 | | - | - | 0.0047% | 14.76 | MN628271 | 5400/5400 | 99.76 | OL472028 | full genome assembled |
| **SRR16552263 / P46BOL20-SW** | | | | | | | | | | | | | | |
| | plant associated polerovirus 1 | PaPoV1 | - | - | | KT868949 | 74.87 | 0.0042% | 11.41 | KT868949 | 6025/6017 | 74.35 | OL472216 | new species, full genome assembled |
| | Picris umbravirus 1 | PicUV1 | - | - | | KT946712 | 79.97 | 0.0904% | 337.69 | KT946712 | 4411/4196 | 79.97 | OL472231 | new species, full genome assembled |
| | Convolvulus aureusvirus 1 | ConAV1 | - | - | | MG967280 | 76.28 | 0.0299% | 73.22 | MG967280 | 4448/4512 | 76.28 | OL472230 | new species, full genome assembled |
| | Cichorium alphacarmovirus 1 | CicAV1 | - | - | | HQ677625 | 71.27 | 34.2071% | 143655.86 | HQ677625 | 3866/3965 | 71.27 | OL472222 | new species, full genome assembled |
| | Prunus virus I, RNA1 | PrVI | - | - | | MW579753 | 97.49 | 0.0258% | 1213.06 | MW579753 | 3444/3470 | 97.49 | OL472063 | full genome assembled |
| | Prunus virus I, RNA2 | PrVI | - | - | | MW579754 | 97.95 | 0.0416% | 156.76 | MW579754 | 2947/2876 | 97.95 | OL472064 | full genome assembled |
| | Prunus virus I, RNA3 | PrVI | - | - | | MW579755 | 95.11 | 0.0299% | 436.64 | MW579755 | 2222/2249 | 95.11 | OL472065 | full genome assembled |
| | Picris betanucleorhabdovirus 1 | PBRV1 | - | - | | BK014301 | 67.93 | 0.0112% | 12.02 | BK014301 | 15193/13719 | 67.93 | OL472130 | new species, full genome assembled |
| | Picris cytorhabdovirus 1, L segment | PiCRV1 | - | - | | MT952336 | 72.33 | 0.0434% | 110.00 | MT952336 | 6548/ - | 72.33 | OL472127 | new species, putatively bisegmented, best hit covered only 2% of genome |
| | Picris cytorhabdovirus 1, N segment | PiCRV1 | - | - | | CP048848 | 80.00 | 0.0345% | 156.95 | CP048848 | 3622/ - | 80.00 | OL472128 | new species, putatively bisegmented, best hit covered only 1% of genome |
| | plant associated crinivirus 1, RNA1 | PaCrV1 | - | - | | MW892835 | 70.88 | 0.0228% | 58.11 | MW892835 | 7823/8637 | 70.88 | OL472073 | new species, full genome assembled |
| | plant associated crinivirus 1, RNA2 | PaCrV1 | - | - | | KT069221 | 73.99 | 0.0516% | 120.07 | KT069221 | 7876/8210 | 73.99 | OL472074 | new species, full genome assembled |
| | plant associated deltapartitivirus 5, RNA1 | PaDPV5 | - | - | | MW546937 | 76.03 | 0.0100% | 52.35 | MW546937 | 1499/1583 | 76.03 | OL472021 | new species, full genome assembled |
| | plant associated deltapartitivirus 5, RNA2 | PaDPV5 | - | - | | MW546938 | 66.34 | | | MW546938 | 1503/1459 | 66.34 | OL472022 | new species, full genome assembled |
| **SRR16552260 / P47MIR20-ST** | | | | | | | | | | | | | | |
| | Southern tomato virus | STV | MF422618 | 100.00 | | - | - | 0.0135% | 64.14 | MF422618 | 3438/3438 | 100.00 | OL471999 | full genome assembled |
| | potato virus Y | PVY | KX184817 | 99.55 | | - | - | 5.7688% | 9848.89 | KX184817 | - | 99.55 | - | reconstruction of consensus genome not possible due to presence of more than one viral strain |
| | tomato associated bunya-like virus 1, segment L | TaBLV1 | - | - | | ATP79731 | 30.13 | 0.0144% | 18.79 | ATP79731 | 7864/8911 | 30.13 | OL471976 | no good hit in BLASTn, shown here is best hit in BLASTx |
| | tomato associated bunya-like virus 1, segment M | TaBLV1 | - | - | | QNT38480 | 23.86 | | | QNT38480 | 4910/4955 | 23.86 | OL471977 | no good hit in BLASTn, shown here is best hit in BLASTx |
| **SRR16552259 / P48MIR20-SW** | | | | | | | | | | | | | | |
| | Soybean dwarf virus | SbDV | JN674402 | 94.55 | | - | - | 0.0661% | 168.46 | JN674402 | 5860/5862 | 94.57 | OL472235 | full genome assembled |
| | Artemesia fimovirus 1, RNA1 | ArtV1 | - | - | | BBM96177 | 45.01 | 0.0361% | 42.98 | BBM96177 | 7249/ 7291 | 45.01 | OL471978 | new species, BLASTx hits to RNA1 of Perilla mosaic virus are shown |
| | Artemesia fimovirus 1, RNA2 | ArtV1 | - | - | | BBM96178 | 32.52 | | | BBM96178 | 2057/2092 | 32.52 | OL471979 | new species, BLASTx hits to RNA2 of Perilla mosaic virus are shown |
| | Artemesia fimovirus 1, RNA3 | ArtV1 | - | - | | BBM96179 | 39.56 | | | BBM96179 | 1088/1080 | 39.56 | OL471980 | new species, BLASTx hits to RNA3 of Perilla mosaic virus are shown |
| | Artemesia fimovirus 1, RNA4 | ArtV1 | - | - | | BBM96181 | 45.38 | | | BBM96181 | 1325/1294 | 45.38 | OL471981 | new species, BLASTx hits to RNA4 of Perilla mosaic virus are shown |
| | Artemesia fimovirus 1, RNA5 | ArtV1 | - | - | | BBM96182 | 36.31 | | | BBM96182 | 902/1066 | 36.31 | OL471982 | new species, BLASTx hits to RNA5 of Perilla mosaic virus are shown |
| | plant associated closterovirus 2 | PaClV2 | - | - | | MH460557 | 67.04 | 0.7318% | 663.59 | MH460557 | 16522/17313 | 67.43 | OL472075 | new species, full genome assembled |
| | Sanxia tombus-like virus 7 | STLV7 | KX883177 | 90.40 | | - | - | 0.0029% | 9.43 | KX883177 | 4558/4557 | 90.57 | OL472301 | full genome assembled |
| | Erysiphe necator ourmia-like virus 82 | EnOLV82 | MN611610 | 93.19 | | - | - | 0.0004% | 3.37 | MN611610 | - | 93.19 | - | partial genome obtained (was not deposited) |
| **SRR16552257 / P49KOP20-ST** | | | | | | | | | | | | | | |
| | olive latent virus 1 | OLV1 | MK376952 | 96.95 | | - | - | 0.0167% | 85.19 | MK376952 | 3669/3669 | 96.95 | OL472229 | full genome assembled |
| | tobacco necrosis virus A | TNVA | KX906928 | 96.68 | | - | - | 0.0097% | 49.67 | KX906928 | 3686/3686 | 90.43 | - | full genome but probable recombinant (was not deposited) |
| **SRR16552256 / P50.1KOP20-SW** | | | | | | | | | | | | | | |
| | Ranunculus white mottle ophiovirus, RNA1 | RWMV | - | - | | NC_043389 | 90.90 | 0.0065% | 9.58 | NC_043389 | 7677/4018 | 90.90 | OL472203 | first full sequence of genome segment assembled |
| | Ranunculus white mottle ophiovirus, RNA2 | RWMV | - | - | | AF355430 | 88.21 | | | AF355430 | 1839/263 | 88.97 | OL472204 | first full sequence of genome segment assembled |
| | Ranunculus white mottle ophiovirus, RNA3 | RWMV | - | - | | AY542957 | 92.63 | | | AY542957 | 1476/1063 | 91.88 | OL472205 | first full sequence of genome segment assembled |
| | Ranunculus white mottle ophiovirus, RNA4 | RWMV | - | - | | KY769704 | 71.10 | | | KY769704 | 1315/1315 | 71.10 | OL472206 | first full sequence of genome segment assembled |
| | Mercurialis orthotospovirus 1, L segment | MerV1 | - | - | | JN560178 | 72.47 | 9.9625% | 10050.06 | JN560178 | 9055/8877 | 72.47 | OL471964 | new species, full genome assembled |
| | Mercurialis orthotospovirus 1, M segment | MerV1 | - | - | | JN560177 | 70.61 | | | JN560177 | 4714/4786 | 70.61 | OL471965 | new species, full genome assembled |
| | Mercurialis orthotospovirus 1, S segment | MerV1 | - | - | | AY686718 | 65.93 | | | AY686718 | 3407/2734 | 65.93 | OL471966 | new species, full genome assembled |
| | La Jolla virus | LJV | - | - | | KP714073 | 98.69 | 0.0153% | 26.75 | KP714073 | 10253/9722 | 98.69 | OL472185 | full genome assembled |
| | Erysiphe necator associated ssRNA virus 9 | EnaSRV9 | - | - | | MN627473 | 89.93 | 0.0012% | 6.24 | MN627473 | 3456/3506 | 89.93 | OL472272 | full genome assembled, possibly a divergent strain |
| | Koper noda-like virus 1 | KNLV1 | - | - | | MW648508 | 67.24 | 0.0091% | 51.98 | MW648508 | 3147/3147 | 67.24 | OL472282 | new species, only 37% of genome covered by best hit |
| | Koper noda-like virus 2 | KNLV2 | - | - | | MT482496 | 69.61 | 0.0019% | 10.31 | MT482496 | 3195/3195 | 69.61 | OL472288 | new species, only 16% of genome covered by best hit |
| | Koper noda-like virus 3 | KNLV3 | - | - | | MK533155 | 64.75 | 0.0039% | 20.17 | MK533155 | 3482/3482 | 64.75 | OL472289 | new species, only 65% of genome covered by best hit |
| | Koper noda-like virus 4 | KNLV4 | - | - | | KX883237 | 68.24 | 0.0037% | 19.02 | KX883237 | 3459/3459 | 68.24 | OL472290 | new species, only 4% of genome covered by best hit |
| | plant associated tombus-like virus 1 | PaTLV1 | - | - | | MT317175 | 76.36 | 0.0017% | 8.97 | MT317175 | 3297/3360 | 76.36 | OL472268 | new species, full genome assembled |
| | plant associated virga-like virus 2 | PaVLV2 | - | - | | QED42936 | 31.15 | 0.0012% | 6.09 | QED42936 | 3561/ - | 31.15 | OL472276 | new species, has virga-like domains, BLASTx hit is shown |
| | plant associated deltapartitivirus 2, RNA1 | PaDPV2 | - | - | | MH898486 | 66.77 | 0.0288% | 171.96 | MH898486 | 1566/1590 | 66.77 | OL472013 | new species, full genome assembled |
| | plant associated deltapartitivirus 2, RNA2 | PaDPV2 | - | - | | MT159330 | 64.10 | | | MT159330 | 1443/1410 | 64.10 | OL472014 | new species, full genome assembled |
| **SRR16552256 / P50.2KOP20-SW** | | | | | | | | | | | | | | |
| | lettuce mosaic virus | LMV | - | - | | KJ161185 | 92.65 | 2.3264% | 3899.38 | KJ161185 | 10065/10065 | 92.65 | OL472136 | full genome assembled |
| | Koper totivirus 1 | KTV1 | - | - | | MN428836 | 69.00 | 0.0171% | 48.51 | MN428836 | 5240/4999 | 69.00 | OL472026 | new species, full genome assembled |
| | Koper totivirus 2 | KTV2 | - | - | | KX882939 | 70.49 | 0.0145% | 51.05 | KX882939 | 4794/4958 | 70.49 | OL472027 | new species, full genome assembled |
| | plant associated caulimovirus 1 | PaCaV1 | - | - | | MH898523 | 68.12 | 2.2229% | 3882.70 | MH898523 | 9644/8026 | 68.12 | OL472131 | new species, full genome assembled |
| | plant associated soymovirus 1 | PaSoV1 | - | - | | X15828 | 68.91 | 0.4420% | 779.22 | X15828 | 9571/8178 | 68.91 | OL472132 | new species, full genome assembled |
| | Calystegia pelarspovirus 1 | CalPV1 | - | - | | MH231181 | 68.89 | 0.0741% | 305.57 | MH231181 | 3952/3867 | 68.89 | OL472225 | new species, full genome assembled |
| | plant associated botourmia-like virus 2 | PaBLV2 | - | - | | MN611580 | 70.17 | 0.0026% | 17.47 | MN611580 | 2227/2257 | 70.17 | OL472279 | new species, full genome assembled |
| | Calystegia geminivirus 1, partial genome | CGV1 | - | - | | AF224760 | 73.85 | 0.0003% | 4.47 | AF224760 | 1208/2632 | 73.85 | OL472025 | new species, partial DNA-A (rep-encoding) genome assembled |
| | plant associated viroid-like circular RNA 3 | PaVCR3 | not applicable | - | | not applicable | - | 0.0025% | 73.29 | not applicable | 580/ - | - | OL472259 | viroid-like circular RNA (putative new viroid species) |
| **SRR16552253 / P51.1SKO20-ST** | | | | | | | | | | | | | | |
| | Southern tomato virus | STV | MF422618 | 100.00 | | - | - | 0.0107% | 63.04 | MF422618 | 3438/3438 | 100.00 | OL472001 | full genome assembled |
| | potato virus Y | PVY | MN216357 | 99.05 | | - | - | 2.3761% | 5040.00 | MN216357 | 9525/9649 | 99.80 | OL472159 | full genome assembled |
| | potato virus S | PVS | MH937416 | 98.62 | | - | - | 1.7858% | 4306.63 | MH937416 | 8485/8485 | 98.62 | OL472248 | full genome assembled |
| | cucumber mosaic virus, RNA1 | CMV | D00356 | 99.40 | | - | - | 8.5781% | 52083.05 | D00356 | 3357/3357 | 98.89 | OL472037 | full genome assembled |
| | cucumber mosaic virus, RNA2 | CMV | HE793684 | 99.14 | | - | - | 4.2257% | 28138.61 | HE793684 | 3048/3050 | 98.85 | OL472055 | full genome assembled |
| | cucumber mosaic virus, RNA3 | CMV | AJ517802 | 98.60 | | - | - | 22.0708% | 204713.16 | AJ517802 | 2203/2216 | 98.46 | OL472046 | full genome assembled |
| | tomato vitivirus 1 | TomV1 | - | - | | NC_043088 | 70.28 | 2.7331% | 7418.50 | MT454065 | 7501/7565 | 70.28 | OL472239 | new species, full genome assembled |
| | tomato betanucleorhabdovirus 2 | TBRV2 | - | - | | MF543022 | 67.14 | 0.0107% | 523.78 | MF543022 | 13423/14432 | 67.14 | OL472114 | new species, full genome assembled |
| **SRR16552252 / P51.2SKO20-ST** | | | | | | | | | | | | | | |
| | Southern tomato virus | STV | MF422618 | 99.97 | | - | - | 0.0209% | 118.46 | MF422618 | 3438/3438 | 100.00 | OL471993 | full genome assembled |
| | potato virus Y | PVY | AB185833 | 96.78 | | - | - | 6.9756% | 14070.72 | AB185833 | 9699/9698 | 96.78 | OL472160 | full genome assembled |
| | tomato aspermy virus, RNA1 | TAV | LC380669 | 99.59 | | - | - | 12.2690% | 70227.26 | LC380669 | 3412/3414 | 99.41 | OL472069 | full genome assembled |
| | tomato aspermy virus, RNA2 | TAV | KF432414 | 98.39 | | - | - | 8.5030% | 53640.10 | KF432414 | 3070/3096 | 99.29 | OL472070 | full genome assembled |
| | tomato aspermy virus, RNA3 | TAV | AJ277268 | 98.91 | | - | - | 11.6600% | 95556.45 | AJ277268 | 2385/2386 | 99.03 | OL472071 | full genome assembled |
| | cucumber mosaic virus, RNA1 | CMV | D00356 | 98.33 | | - | - | 2.5361% | 14681.51 | D00356 | 3357/3357 | 96.65 | OL472038 | full genome assembled |
| | cucumber mosaic virus, RNA2 | CMV | KC019300 | 95.22 | | - | - | 1.8205% | 11652.00 | KC019300 | 3007/3049 | 96.85 | OL472056 | full genome assembled |
| | cucumber mosaic virus, RNA3 | CMV | AJ517802 | 96.91 | | - | - | 3.8116% | 33588.51 | AJ517802 | 2201/2216 | 99.18 | OL472047 | full genome assembled |
| | Henbane mosaic virus | HMV | MH779472 | 99.06 | | - | - | 0.7538% | 1456.09 | MH779472 | 10155/10127 | 99.06 | OL472138 | full genome assembled |
| | tomato vitivirus 1 | TomV1 | - | - | | NC_043088 | 72.79 | 0.7931% | 2027.14 | NC_043088 | 7501/7565 | 72.79 | OL472241 | new species, full genome assembled |
| | tomato betanucleorhabdovirus 2 | TBRV2 | - | - | | MF543022 | 67.02 | 1.0702% | 1555.31 | MF543022 | 13453/14432 | 67.02 | OL472113 | new species, full genome assembled |

## **Supplementary Table 5**. (continued rows).

| SRA/Library ID | Virus name[1] (or tentative name for new species that are in yellow highlight; genome segment name is indicated if present) | Unique virus abbreviation | Best hit from BLASTn analysis[2] of mapping consensus[3] |  | OR | Best hit from BLASTn analysis[2] of assembled contig[4] |  | Remapping reads to final consensus genome sequence[4] and final BLASTn analysis for verification[2] |  |  |  |  | NBCI GenBank accession number of reconstructed viral genome | Remarks / Notes |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  |  |  | GenBank accession no. | Percent identity |  | GenBank accession no. | Percent identity | Fraction of reads[5] mapped | Average mapping depth | Best hit in BLASTn[2] GenBank accession no. | Genome covered[6] | Percent identity |  |  |
| **SRR16552251 / P52SKO20-SW** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | potato virus Y | PVY | AJ890347 | 97.97 |  | - | - | 2.3643% | 3946.54 | AJ890347 | 9677/9701 | 99.18 | OL472165 | full genome assembled |
|  | lettuce mosaic virus | LMV | - | - |  | KJ161185 | 85.25 | 1.1995% | 1924.08 | KJ161185 | 10079/10065 | 85.25 | OL472137 | full genome assembled, divergent strain |
|  | Picris betanucleorhabdovirus 1 | PBRV1 | - | - |  | OU015520 | 67.04 | 0.0573% | 61.09 | OU015520 | 15193/13719 | 67.04 | OL472117 | new species, full genome assembled |
|  | plant associated deltapartitivirus 3, RNA1 | PaDPV3 | - | - |  | NC_040483 | 68.35 | 0.0060% | 30.08 | NC_040483 | 1581/1569 | 68.35 | OL472015 | new species, full genome assembled |
|  | plant associated deltapartitivirus 3, RNA2 | PaDPV3 | - | - |  | MT159292 | 73.20 |  |  | MT159292 | 1602/1418 | 73.20 | OL472016 | new species, full genome assembled |
|  | plant associated deltapartitivirus 4, RNA1 | PaDPV4 | - | - |  | MW546937 | 75.79 | 0.0014% | 7.59 | MW546937 | 1499/1583 | 75.79 | OL472017 | new species, full genome assembled |
|  | plant associated deltapartitivirus 4, RNA2 | PaDPV4 | - | - |  | MW546938 | 67.49 |  |  | MW546938 | 1468/1459 | 67.49 | OL472018 | new species, full genome assembled |
| **SRR16552248 / P53.1KOR20-ST** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | potato virus Y | PVY | AB185833 | 97.59 |  | - | - | 4.6472% | 8651.54 | AB185833 | 9698/9698 | 99.38 | OL472152 | full genome assembled |
|  | potato virus M | PVM | JX678982 | 97.19 |  | - | - | 0.0082% | 17.46 | JX678982 | 8523/8523 | 97.19 | OL472243 | full genome assembled |
|  | tomato mosaic virus | ToMV | MN267904 | 99.42 |  | - | - | 0.0243% | 68.07 | MN267904 | 6383/6383 | 99.42 | OL472102 | full genome assembled |
|  | cucumber mosaic virus, RNA1 | CMV | HE793684 | 99.08 |  | - | - | 7.3644% | 39461.92 | HE793684 | 3359/3360 | 98.54 | OL472033 | full genome assembled |
|  | cucumber mosaic virus, RNA2 | CMV | HF572915 | 98.49 |  | - | - | 5.8783% | 34691.12 | HF572915 | 3046/3046 | 97.93 | OL472051 | full genome assembled |
|  | cucumber mosaic virus, RNA3 | CMV | AJ517802 | 98.51 |  | - | - | 15.8069% | 129494.19 | AJ517802 | 2201/2216 | 98.51 | OL472042 | full genome assembled |
|  | plant associated tobamo-like virus 1 | PaToLV1 | - | - |  | NC_032449 | 35.06 | 0.0050% | 13.68 | NC_032449 | 6552/6969 | 35.06 | OL472107 | new species, has virga-like domains (RdRP, CP), full genome |
| **SRR16552247 / P53.2KOR20-ST** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | potato virus Y | PVY | AB185833 | 96.11 |  | - | - | 3.8621% | 6080.61 | AB185833 | 9698/9698 | 99.46 | OL472153 | full genome assembled |
|  | potato virus M | PVM | JX678982 | 97.19 |  | - | - | 5.1725% | 9268.55 | JX678982 | 8523/8523 | 97.19 | OL472245 | full genome assembled |
|  | cucumber mosaic virus, RNA1 | CMV | D00356 | 91.35 |  | - | - | 4.0621% | 18381.11 | D00356 | 3358/3357 | 92.10 | OL472034 | full genome assembled |
|  | cucumber mosaic virus, RNA2 | CMV | D00355 | 91.53 |  | - | - | 1.7048% | 8470.45 | D00355 | 3048/3050 | 94.71 | OL472052 | full genome assembled |
|  | cucumber mosaic virus, RNA3 | CMV | AJ517802 | 89.03 |  | - | - | 3.4026% | 23276.95 | AJ517802 | 2211/2216 | 91.70 | OL472043 | full genome assembled |
|  | tomato associated partiti-like virus 1 | TaPLV1 | - | - |  | MZ443622 | 71.17 | 0.0007% | 7.38 | MZ443622 | 1496/1506 | 71.17 | OL472293 | new species, best hit has only 41% genome covered |
|  | plant associated tobamo-like virus 1 | PaToLV1 | - | - |  | NC_032449 | 35.06 | 0.0067% | 15.56 | NC_032449 | 6552/6969 | 35.06 | OL472108 | new species, has virga-like domains (RdRP, CP), full genome |
| **SRR16552246 / P54KOR20-SW** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | beet yellows virus | BYV | AF190581 | 97.72 |  | - | - | 3.1094% | 3407.77 | AF190581 | 15469/15468 | 97.72 | OL472076 | full genome assembled |
|  | carrot thin leaf virus | CTLV | MH170889 | 91.46 |  | - | - | 0.3981% | 710.56 | MH170889 | 9490/9490 | 91.46 | OL472135 | full genome assembled |
|  | Pastinaca umbravirus 1 | PasUV1 | - | - |  | LC434065 | 78.33 | 0.0147% | 57.04 | LC434065 | 4354/4193 | 78.33 | OL472237 | new species, full genome assembled |
|  | Calystegia pelarspovirus 1 | CalPV1 | - | - |  | MH231181 | 69.49 | 0.5793% | 2452.04 | MH231181 | 4006/3867 | 69.49 | OL472226 | new species, full genome assembled |
|  | plant associated waikavirus 2 | PaWV2 | - | - |  | KT238881 | 69.00 | 0.1458% | 213.32 | KT238881 | 11512/11649 | 69.00 | OL472179 | new species, full genome assembled |
|  | plant associated sequivirus 1 | PaSV1 | - | - |  | NC_038320 | 68.27 | 0.1177% | 100.09 | NC_038320 | 9988/9905 | 68.27 | OL472180 | new species, full genome assembled |
|  | Mentha macluravirus 1 | MenMV1 | - | - |  | KP405232 | 67.44 | 3.0165% | 6199.99 | KP405232 | 8250/~8287 | 67.44 | OL472141 | new species, full genome assembled |
|  | Cirsium cytorhabdovirus 1 | CCRV1 | - | - |  | KY075646 | 69.04 | 0.0139% | 22.26 | KY075646 | 12216/13389 | 69.04 | OL472122 | new species, full genome assembled |
|  | plant associated viroid-like circular RNA 4 | PaVCR4 | not applicable | - |  | not applicable | - | 0.0175% | 1081.50 | not applicable | 274/ - | - | OL472260 | viroid-like circular RNA (putative new viroid species) |
|  | plant tombusvirus-like associated RNA 1 | PTaR1 | - | - |  | MF136436 | 77.44 | 0.0180% | 103.15 | MF136436 | 2903/1867 | 77.44 | OL472296 | new species, full genome assembled |
|  | plant tombusvirus-like associated RNA 2 | PTaR2 | - | - |  | KX883211 | 79.07 | 0.0031% | 20.58 | KX883211 | 2505/5082 | 79.07 | OL472295 | new species, only 3% of genome covered by best hit |
|  | plant tombusvirus-like associated RNA 3 | PTaR3 | - | - |  | MF136436 | 72.04 | 0.0173% | 116.79 | MF136436 | 2515/1867 | 72.04 | OL472299 | new species, full genome assembled |
| **SRR16552291 / P55.1PLE20-ST** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | potato virus Y | PVY | MN216361 | 98.98 |  | - | - | 0.9470% | 2012.44 | MN216361 | 9609/9609 | 99.82 | OL472155 | full genome assembled |
|  | Southern tomato virus | STV | MK948545 | 99.82 |  | - | - | 0.0024% | 14.32 | MK948545 | 3436/3436 | 99.82 | OL471997 | full genome assembled |
|  | cucumber mosaic virus, RNA1 | CMV | D00356 | 99.37 |  | - | - | 9.6260% | 58233.96 | D00356 | 3361/3357 | 98.63 | OL472035 | full genome assembled |
|  | cucumber mosaic virus, RNA2 | CMV | AJ517801 | 99.15 |  | - | - | 7.6703% | 51002.24 | AJ517801 | 3055/3052 | 98.95 | OL472053 | full genome assembled |
|  | cucumber mosaic virus, RNA3 | CMV | AJ517802 | 99.19 |  | - | - | 18.7449% | 172075.53 | AJ517802 | 2217/2216 | 99.19 | OL472044 | full genome assembled |
| **SRR16552290 / P55.2PLE20-ST** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | Southern tomato virus | STV | KT852573 | 99.97 |  | - | - | 0.0441% | 215.41 | KT852573 | 3438/3438 | 99.97 | OL472005 | full genome assembled |
|  | potato virus Y | PVY | DQ008213 | 99.62 |  | - | - | 5.4331% | 9517.27 | DQ008213 | 9666/9666 | 99.63 | OL472156 | full genome assembled |
|  | tomato spotted wilt virus, segment L | TSWV | KP008130 | 97.98 |  | - | - | 0.5646% | 1074.24 | KP008130 | 8913/8914 | 97.98 | OL471946 | full genome assembled |
|  | tomato spotted wilt virus, segment M | TSWV | KU179608 | 96.47 |  | - | - | 0.5083% | 1805.31 | KU179608 | 4766/4767 | 98.38 | OL471947 | full genome assembled |
|  | tomato spotted wilt virus, segment S | TSWV | DQ376178 | 99.01 |  | - | - | 0.4960% | 2864.77 | DQ376178 | 2929/2927 | 99.62 | OL471948 | full genome assembled |
|  | Physostegia chlorotic mottle alphanucleorhabdovirus | PhCMoV | - | - |  | MK948541 | 99.00 | 23.1530% | 29434.37 | MK948541 | 13303/13320 | 96.35 | OL472115 | full genome assembled |
|  | Ranunculus white mottle ophiovirus, RNA1 | RWMV | - | - |  | NC_043389 | 91.24 | 3.0891% | 4266.95 | NC_043389 | 7622/4018 | 91.24 | OL472195 | first full sequence of genome segment assembled |
|  | Ranunculus white mottle ophiovirus, RNA2 | RWMV | - | - |  | AF335430 | 88.00 |  |  | AF335430 | 1787/263 | 88.17 | OL472196 | first full sequence of genome segment assembled |
|  | Ranunculus white mottle ophiovirus, RNA3 | RWMV | - | - |  | AY542957 | 92.33 |  |  | AY542957 | 1486/1063 | 92.33 | OL472197 | first full sequence of genome segment assembled |
|  | Ranunculus white mottle ophiovirus, RNA4 | RWMV | - | - |  | KY769704 | 70.85 |  |  | KY769704 | 1324/1381 | 71.85 | OL472198 | first full sequence of genome segment assembled |
| **SRR16552289 / P55.3PLE20-ST** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | Southern tomato virus | STV | KT852573 | 99.97 |  | - | - | 0.0940% | 434.68 | KT852573 | 3437/3438 | 99.97 | OL471994 | full genome assembled |
|  | potato virus Y | PVY | MN216361 | 98.05 |  | - | - | 17.1494% | 28313.32 | MN216361 | 9666/9666 | 98.93 | OL472157 | full genome assembled |
|  | potato virus M | PVM | EU604672 | 93.55 |  | - | - | 2.6925% | 5039.69 | EU604672 | 8523/8523 | 93.55 | OL472244 | full genome assembled |
|  | tomato spotted wilt virus, segment L | TSWV | KP008130 | 97.98 |  | - | - | 6.4013% | 11486.88 | KP008130 | 8913/8914 | 97.98 | OL471949 | full genome assembled |
|  | tomato spotted wilt virus, segment M | TSWV | KU179608 | 96.39 |  | - | - | 4.1578% | 13938.59 | KU179608 | 4766/4767 | 96.39 | OL471950 | full genome assembled |
|  | tomato spotted wilt virus, segment S | TSWV | DQ376178 | 99.04 |  | - | - | 4.1320% | 22488.38 | DQ376178 | 2927/2927 | 99.62 | OL471951 | full genome assembled |
| **SRR16552288 / P56PLE20-SW** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | Aphis glycines virus 1 | AGV1 | - | - |  | KM015260 | 97.30 | 0.0076% | 11.31 | KM015260 | 8986/8680 | 98.97 | OL472191 | full genome assembled |
|  | Rumex potyvirus 1 | RumPV1 | - | - |  | MK778804 | 71.15 | 3.9703% | 5105.66 | MK778804 | 10368/10068 | 71.15 | OL472144 | new species, full genome assembled |
|  | Taraxacum betanucleorhabdovirus 1 | TBRV1 | - | - |  | OU015520 | 66.38 | 0.0557% | 53.93 | OU015520 | 13736/14421 | 66.38 | OL472118 | new species, full genome assembled |
|  | Taraxacum cytorhabdovirus 1 | TCRV1 | - | - |  | KM817650 | 65.25 | 0.0125% | 12.09 | KM817650 | 13781/13490 | 65.25 | OL472125 | new species, full genome assembled |
|  | plant associated sequivirus 2 | PaSV2 | - | - |  | MT559284 | 76.28 | 0.4589% | 614.67 | MT559284 | 9940/9795 | 76.28 | OL472182 | new species, full genome assembled |
|  | plant associated sequivirus 3 | PaSV3 | - | - |  | MT559283 | 75.59 | 0.4012% | 523.38 | MT559283 | 10227/9786 | 75.59 | OL472184 | new species, full genome assembled |
| **SRR16552285 / P57.1JUR20-ST** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | potato virus Y | PVY | MN216361 | 98.26 |  | - | - | 0.2516% | 402.50 | MN216361 | 9609/9609 | 99.63 | OL472149 | full genome assembled |
|  | tomato mosaic virus | ToMV | MN267904 | 99.50 |  | - | - | 85.9657% | 206944.04 | MN267904 | 6383/6386 | 99.50 | OL472097 | full genome assembled |
| **SRR16552284 / P57.2JUR20-ST** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | Southern tomato virus | STV | LC487710 | 99.88 |  | - | - | 0.0212% | 124.39 | LC487710 | 3438/3438 | 99.88 | OL471995 | full genome assembled |
|  | potato virus Y | PVY | JF927751 | 99.50 |  | - | - | 0.6062% | 1270.24 | JF927751 | 9697/9697 | 99.45 | OL472150 | full genome assembled |
|  | tomato mosaic virus | ToMV | MN267904 | 99.50 |  | - | - | 90.9592% | 289236.20 | MN267904 | 6381/6386 | 99.50 | OL472098 | full genome assembled |
| **SRR16552283 / P58.1JUR20-SW** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | tomato mosaic virus | ToMV | MN267904 | 99.50 |  | - | - | 1.6374% | 3263.75 | MN267904 | 6370/6383 | 99.50 | OL472099 | full genome assembled |
|  | Solanum nigrum ilarvirus 1, RNA1 | SnIV1 | MN216370 | 96.60 |  | - | - | 5.7116% | 20573.99 | MN216370 | 3521/3445 | 96.60 | OL472060 | full genome assembled |
|  | Solanum nigrum ilarvirus 1, RNA2 | SnIV1 | MN216373 | 96.73 |  | - | - | 1.6923% | 7551.14 | MN216373 | 2842/2757 | 96.73 | OL472061 | full genome assembled |
|  | Solanum nigrum ilarvirus 1, RNA3 | SnIV1 | MN216376 | 98.02 |  | - | - | 8.9289% | 49833.09 | MN216376 | 2277/2242 | 98.02 | OL472062 | full genome assembled |
|  | plant associated deltapartitivirus 6, RNA1 | PaDPV6 | - | - |  | KX525268 | 83.90 | 0.1732% | 707.56 | KX525268 | 1593/1586 | 83.90 | OL472023 | new species, full genome assembled |
|  | plant associated deltapartitivirus 6, RNA2 | PaDPV6 | - | - |  | KY923704 | 72.36 |  |  | KY923704 | 1512/1525 | 72.36 | OL472024 | new species, full genome assembled |
|  | Novo Mesto dicistrovirus 1 | NMDV1 | - | - |  | KX884398 | 67.63 | 0.0585% | 74.11 | KX884398 | 10055/9785 | 67.63 | OL472188 | new species, full genome assembled |
|  | plant associated viroid-like circular RNA 3 | PaVCR3 | not applicable | - |  | not applicable | - | 0.0135% | 352.00 | not applicable | 580/ - | - | OL472262 | viroid-like circular RNA (putative new viroid species) |
| **SRR16552282 / P58.2JUR20-SW** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | tomato mosaic virus | ToMV | MN267904 | 99.01 |  | - | - | 0.0045% | 9.28 | MN267904 | 6345/6383 | 99.01 | OL472100 | full genome assembled |
|  | Plant associated alphaendornavirus 1 | PaAEV1 | - | - |  | LC500285 | 65.45 | 0.0983% | 77.77 | LC500285 | 14528/14878 | 65.45 | OL472078 | new species, full genome assembled |
|  | Cichorium alphacarmovirus 1 | CicAV1 | - | - |  | HQ677625 | 71.22 | 0.0038% | 13.00 | HQ677625 | 3895/3956 | 71.22 | OL472223 | new species, full genome assembled |
|  | Novo Mesto dicistrovirus 2 | NMDV2 | - | - |  | MT745591 | 80.82 | 0.0422% | 43.76 | MT745591 | 8897/8446 | 80.82 | OL472189 | new species, but only 45% genome covered by best hit |
|  | plant associated viroid-like circular RNA 3 | PaVCR3 | not applicable | - |  | not applicable | - | 0.0016% | 43.45 | not applicable | 580/ - | - | OL472261 | viroid-like circular RNA (putative new viroid species) |
| **SRR16552280 / P59.1TUR20-ST** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | Southern tomato virus | STV | MF422618 | 100.00 |  | - | - | 0.1741% | 824.26 | MF422618 | 3438/3438 | 100.00 | OL472003 | full genome assembled |
|  | tomato mosaic virus | ToMV | MN267904 | 99.48 |  | - | - | 0.0120% | 30.62 | MN267904 | 6345/6383 | 99.01 | OL472103 | full genome assembled |
|  | tomato spotted wilt virus, segment L | TSWV | KP008130 | 97.99 |  | - | - | 9.3851% | 17240.41 | KP008130 | 8913/8914 | 97.99 | OL471952 | full genome assembled |
|  | tomato spotted wilt virus, segment M | TSWV | KU179608 | 96.07 |  | - | - | 7.7732% | 26697.40 | KU179608 | 4766/4767 | 98.32 | OL471953 | full genome assembled |
|  | tomato spotted wilt virus, segment S | TSWV | DQ376178 | 98.94 |  | - | - | 6.1946% | 34624.29 | DQ376178 | 2926/2927 | 99.56 | OL471954 | full genome assembled |
|  | Hubei picorna-like virus 36 | HuPiLV36 | - | - |  | KX883970 | 99.22 | 0.1305% | 214.72 | KX883970 | 9951/9856 | 99.22 | OL472186 | full genome assembled |
|  | Novo Mesto picornavirus 1 | NMPV1 | - | - |  | MH614316 | 71.28 | 0.0210% | 33.59 | MH614316 | 10189/- | 71.28 | OL472193 | new species, but best hit covers only 10% of the genome |
| **SRR16552279 / P59.2TUR20-ST** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | Southern tomato virus | STV | MF422618 | 100.00 |  | - | - | 0.1646% | 824.26 | MF422618 | 3438/3438 | 100.00 | OL472000 | full genome assembled |
|  | tomato mosaic virus | ToMV | MN267904 | 99.43 |  | - | - | 0.0067% | 18.05 | MN267904 | 6383/6383 | 99.43 | OL472104 | full genome assembled |
|  | Physostegia chlorotic mottle alphanucleorhabdovirus | PhCMoV | - | - |  | KX636164 | 96.42 | 41.9384% | 54539.21 | KX636164 | 13313/13320 | 96.49 | OL472124 | full genome assembled |
|  | tomato spotted wilt virus, segment L | TSWV | D10066 | 100.00 |  | - | - | 2.7554% | 5355.46 | D10066 | 8813/8897 | 97.99 | OL471955 | full genome assembled |
|  | tomato spotted wilt virus, segment M | TSWV | KU179608 | 96.27 |  | - | - | 3.0355% | 11030.08 | KU179608 | 4766/4767 | 98.41 | OL471956 | full genome assembled |
|  | tomato spotted wilt virus, segment S | TSWV | DQ376178 | 98.91 |  | - | - | 2.2612% | 13373.55 | DQ376178 | 2925/2927 | 99.52 | OL471957 | full genome assembled |
| **SRR16552278 / P59.3TUR20-ST** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | Southern tomato virus | STV | MF422618 | 100.00 |  | - | - | 0.0598% | 359.49 | MF422618 | 3438/3438 | 100.00 | OL472002 | full genome assembled |
|  | potato virus Y | PVY | - | - |  | AB185833 | 98.47 | 9.2900% | 19495.54 | AB185833 | 9726/9698 | 98.47 | OL472164 | full genome assembled, NTN strain |
|  | Physostegia chlorotic mottle alphanucleorhabdovirus | PhCMoV | - | - |  | KX636164 | 96.48 | 43.8871% | 68474.03 | KX636164 | 13313/13320 | 96.49 | OL472110 | full genome assembled |
|  | tomato spotted wilt virus, segment L | TSWV | KP008130 | 97.98 |  | - | - | 1.9117% | 4459.18 | KP008130 | 8913/8914 | 97.98 | OL471958 | full genome assembled |
|  | tomato spotted wilt virus, segment M | TSWV | KU179608 | 96.16 |  | - | - | 1.5082% | 6575.65 | KU179608 | 4766/4767 | 98.41 | OL471959 | full genome assembled |
|  | tomato spotted wilt virus, segment S | TSWV | DQ376178 | 98.87 |  | - | - | 1.4441% | 10244.53 | DQ376178 | 2926/2627 | 99.49 | OL471960 | full genome assembled |
| **SRR16552277 / P60TUR20-SW** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | white clover mosaic virus | WCMV | MN399741 | 96.37 |  | - | - | 0.0049% | 12.27 | MN399741 | 5774/5774 | 96.39 | OL472250 | full genome assembled |
|  | tomato spotted wilt virus, segment L | TSWV | KP008130 | 97.98 |  | - | - | 1.3634% | 2204.07 | KP008130 | 8913/8914 | 97.99 | OL471961 | full genome assembled |
|  | tomato spotted wilt virus, segment M | TSWV | KU179608 | 96.37 |  | - | - | 0.7429% | 2235.94 | KU179608 | 4766/4767 | 98.41 | OL471962 | full genome assembled |
|  | tomato spotted wilt virus, segment S | TSWV | DQ376178 | 98.94 |  | - | - | 1.5398% | 7540.49 | DQ376178 | 2925/2927 | 99.52 | OL471963 | full genome assembled |

## **Supplementary Table 5**. (continued rows).

| SRA/Library ID | **Virus name**[1] (or tentative name for new species that are in **yellow highlight**; genome segment name is indicated if present) | **Unique virus abbreviation** | **Best hit from BLASTn analysis[2] of mapping consensus[3]** | | **OR** | **Best hit from BLASTn analysis[2] of assembled contig[4]** | | **Remapping reads to final consensus genome sequence[4] and final BLASTn analysis for verification[2]** | | | | | **NBCI GenBank accession number of reconstructed viral genome** | **Remarks / Notes** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | Fraction of reads[5] mapped | Average mapping depth | **Best hit in BLASTn[2]** | | | | |
| | | | GenBank accession no. | Percent identity | | GenBank accession no. | Percent identity | | | GenBank accession no. | Genome covered[6] | Percent identity | | |
| | broad-leafed dock virus A | BLDVA | - | - | | NC_038560 | 91.00 | 0.0601% | 105.72 | NC_038560 | 8170/8174 | 91.00 | OL472142 | full genome assembled |
| | Taraxacum viroid-like circular RNA 1 | TVCR1 | not applicable | - | | not applicable | - | 0.0027% | 86.14 | not applicable | 447/ - | - | OL472256 | viroid-like circular RNA (putative new viroid species) |
| | broad-leafed dock virus A, divergent isolate | BLDVA-divergent | - | - | | NC_038560 | 75.69 | 0.1074% | 170.71 | NC_038560 | 9047/8174 | 75.69 | OL472143 | divergent isolate, full genome assembled |
| | Taraxacum betanucleorhabdovirus 1 | TBRV1 | - | - | | OU015520 | 66.38 | 0.1728% | 180.41 | OU015520 | 13680/14424 | 66.38 | OL472121 | new species, full genome assembled |
| | Novo Mesto iflavirus 1 | NMIV1 | - | - | | MK729664 | 76.74 | 0.0150% | 24.55 | MK729664 | 8849/8868 | 76.74 | OL472192 | new species, full genome assembled |
| **SRR16552276 / P61Pv-PK1 / internal control** | | | | | | | | | | | | | | |
| | Phaseolus vulgaris alphaendornavirus 1 | PvAEV1 | NC_039217 | - | | - | - | 0.1956% | 254.20 | MK948542 | 13903/13981 | 99.68 | - | full genome assembled |
| | Phaseolus vulgaris alphaendornavirus 2 | PvAEV2 | NC_038422 | - | | - | - | 0.5667% | 698.89 | MF281671 | 14240/14780 | 99.50 | - | full genome assembled |
| | Phaseolus vulgaris alphaendornavirus 3 | PvAEV3 | NC_040558 | - | | - | - | 0.0237% | 28.43 | NC_040558 | 7881/15205 | 88.90 | - | full genome assembled |
| **SRR16552274 / P62Pv-PK2 / internal control** | | | | | | | | | | | | | | |
| | Phaseolus vulgaris alphaendornavirus 1 | PvAEV1 | NC_039217 | - | | - | - | 0.1683% | 154.27 | MK948542 | 13901/13981 | 99.61 | - | full genome assembled |
| | Phaseolus vulgaris alphaendornavirus 2 | PvAEV2 | NC_038422 | - | | - | - | 0.4657% | 405.61 | MF281671 | 14224/14780 | 99.58 | - | full genome assembled |
| | Phaseolus vulgaris alphaendornavirus 3 | PvAEV3 | NC_040558 | - | | - | - | 0.0187% | 15.83 | NC_040558 | 7707/15205 | 88.41 | - | full genome assembled |
| | cucumber mosaic virus, RNA1-3 | CMV | - | - | | - | - | 0.0009% | - | - | - | - | - | possible sequencing crosstalk |

**Supplementary Table 6**. List of circular RNAs assembled using a custom pipeline based on SLS-PFOR2, with filtering using BLASTn and BLASTx searches using the nt and nr databases from December 2020. Shown here are 344 contigs, out of the original 4249 contigs, that do not have any significant hits to the GenBank database (nucleotide (nt) database version released on December 2020).

Notes: [1]First characters before '_' in the Contig ID corresponds to the shortened sequencing library (or pool) number indicated in Supplementary Table 2. Putative viroid-like circular RNAs indicated in Supplementary Table 5 are in blue font. [2]Assignation of (+) and (-) strands orientation is random, both strands are rotationally identical.

(see next page)

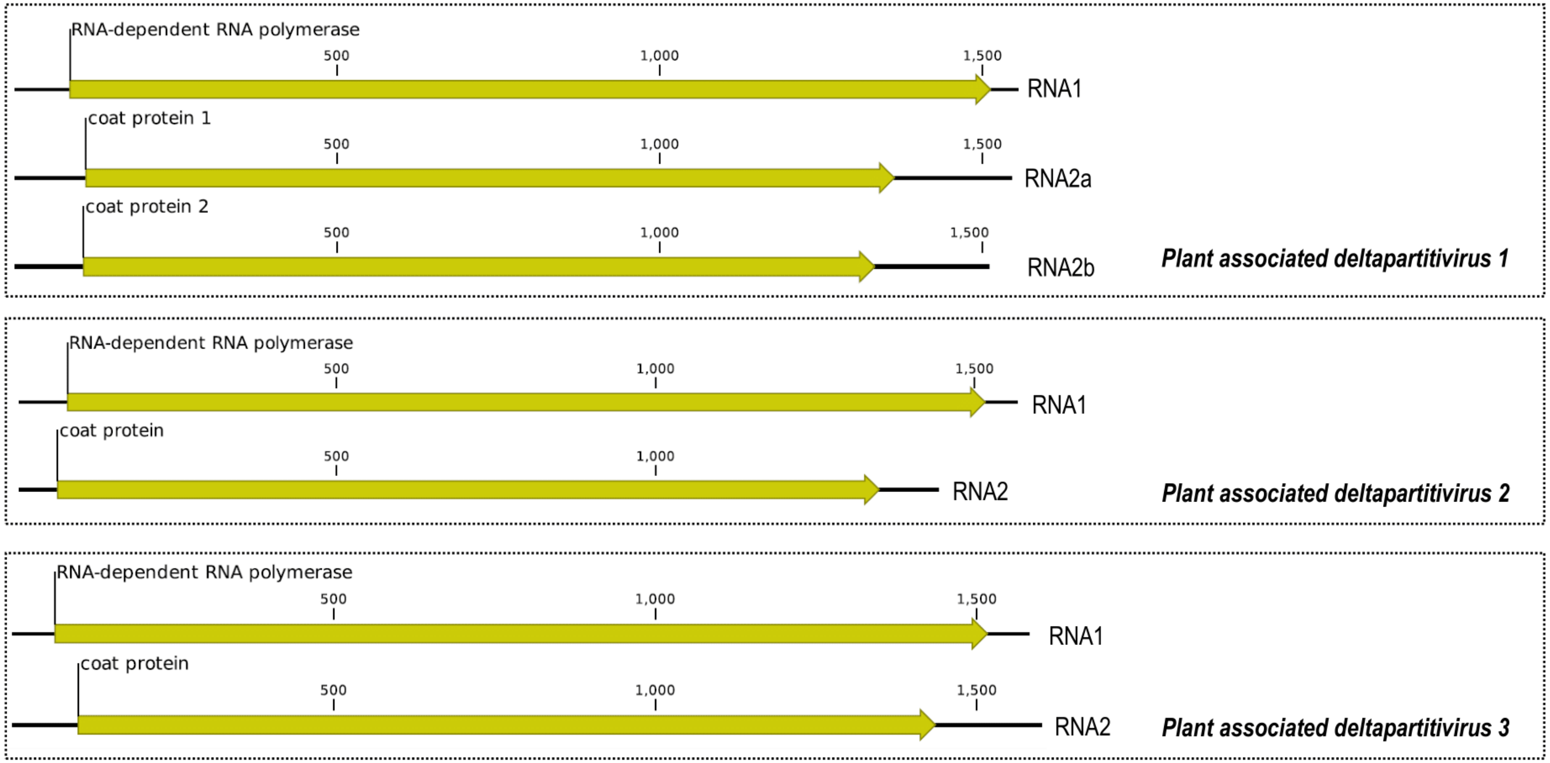
| Contig ID[1] | Name of putative viroid-like circular RNA | Assigned strand[2] | Length (bases) | %GC content | Linear sequence |
|---|---|---|---|---|---|
| P06_Contig-1008 | plant associated viroid-like circular RNA 2 | (-) strand | 491 | 62.3 | ACAGGGCTGTCGGCCTATCTACGGTGTCGTCATGGGACGCCCCTCCTCCTTTTCACGGACTGGGGACCGTCCAGCTGAAGCTGGGTGGAGTTAGCGTTAACCTCGCCTCGGTGTAAACCGAGCCGGTCTCAAGCCCGGGTTAAGAGGGAGAGGCGTTGGTGTTGACG |
| P06_Contig-131 | plant associated viroid-like circular RNA 2 | (+) strand | 491 | 62.3 | TAACTCCACCCAGCTTCAGCTGGACGGTCCCCAGTCCGTGAAAAGGAGGAGGGGCGTCCCATGACGACACCGTAGATAGGCCGACAGCCCTGTCAACATCAGATCAACCTGACGGTGCGCCATGGGGTAAGGAAGTAGTGCATCGGCTTCGGCTTTTATGCGCTCCCG |
| P06_Contig-16 | plant associated viroid-like circular RNA 1 | (+) strand | 541 | 52.7 | CTTGTGACCGGCGCGAGGCGGCCCTCCGTAAACGGAGGCCGTAACAACACGGCTGCATTTGGACTAGTGGTTCCCTCCTTCCCATCATCTCCAGAGGGCTTCCTGCTTGGACGGATAAAGGTCACACTCACATCACTATCTATAGTGGATGCAAGCCACGCAACGATTA |
| P06_Contig-4077 | *not applicable* | *not applicable* | 231 | 27.7 | TATATAATATAGACAAAATTTAAAATTTTAATGATAGATCTAATGATAAAAAATATTGTGTCAGCCGGGGAAGCAGGAAAAGGGAATTAAGTGATTCGCCTTTTTTATTCTATCTTTGAAAGGTTGAAAAATACTATATGTTCGTAATCTACTAATCTAATTAAGTTCATTTTTCA |
| P06_Contig-4110 | plant associated viroid-like circular RNA 1 | (-) strand | 541 | 52.7 | CGCGCCGGTCACAAGCCCGGGACACTTCTTAGGAAGTGATGCAGAGTGGGACCTTCTAAAAGACAAAACGTCTAATAGCTTAAGTCCACCATGCCTTTACGGACAGGTGTGGTGACGCGACAATAGCTTAGCTGCTATAGACGCTAGTCGTTCCTCTCATCCTTCATCAG |
| P06_Contig-653 | *not applicable* | *not applicable* | 319 | 48.6 | GGAGGTGACCCGTAGTAGCAATCGGTAGTCGGTATTTACGTAATGACCCCCTGGCCATATGGTAGCATATGGTCTGCGAAGGACGGAGGTGATTGGCTCGGGTGGGAGGTGCTGGTTTCGGTAGTGAATCATGTCTGCTTGATAGATTTCGTAGAAAATGCTTTGTATTT |
| P07_Contig-1 | *not applicable* | *not applicable* | 766 | 27.9 | CAACACCATTTTATGTCTCCTCTCCTTATCTTATATTCATCGATAAGGATGGCACACCTTATCCCTAAGTTACGGTGTCATTTTGCCGAGTTCCTTAATGATTGTTAGCTCAAACGCCTTCGTATTCTCTACTAGCTTACTTGTGGTAGTTTTTAGGTACGGTTTTAGTATAT |
| P07_Contig-16 | *not applicable* | *not applicable* | 441 | 32.2 | TAATAAACTTATTATATTAACTCTCATTCCTGCAAGTTGCTGGTTCAGCCGTTAGGCCATTGACCAAGATTCCTCACTGCTGTACTAGACGTATTGGGGTTTTTTCAGACCCAGTGTGGCCAATAGACCTCTCAGTCCTGACTACGGACACAAGCTAAATATGCCATTACC |
| P08_Contig-1504 | *not applicable* | *not applicable* | 342 | 48.8 | AAAAAATATGGCCTACTCAAAGGCTTTACTCCTTGGTTTCCTCTTAGCGATAACTCTACTCATTTCTTCTGAGGTGTCAGCTCGTATGCTTGCTGAGACTACTCAAAACACTCCGTCCGAGGAGGAGGCCAAGTATTACCATGGCGGTGGTGGCTATTACCATGGAGGAG |
| P08_Contig-3034 | *not applicable* | *not applicable* | 210 | 51.9 | CATGGAAGCCCACAAGTCCATGGCAGCCAACACGGCCATGGAAGCCCACAGATGCATGGCAACCCACACGGAAATGGCCATGGGAGTCCACATGCTCTTGGGAAACCACAGGGCTATGGAAATTCACATGGCTATGGTAATCCCCACGGCTATGAAAACTCATTCAACC |
| P08_Contig-40 | *not applicable* | *not applicable* | 315 | 26.7 | AAAAAACATTTCTTACTGTAGAAATAAAAGAAATAAAAAATAGATGGAAAAAATTGCGTCCAATAGGATTTGAACCTATACCAAAGGTTTAGAAGACCTCTGTCCTATCCATTAGACAATGGACGCCATTCATTCCGATTTTTCGTATTCTTGTGTTTGATTGAACACAAAAAT |
| P08_Contig-437 | *not applicable* | *not applicable* | 293 | 57.3 | TGACATCGGTTGCGGTTGCGTTGCCTCTGTGCACTGAGTCGCGTGTATTGCCTTGGTGATGTGCTCTTACTCACATCTGACCACAGACGTGTATGCTCCTCGTGGGTGTGCACCGAGGACGGTGTGTGTGGACTCTCGTGTGCCCCCGACGGTGCTCGACCTTTGTTG |
| P08_Contig-450 | *not applicable* | *not applicable* | 434 | 33.2 | TTGGTTTAGATTGGTCATCGAATCCGAATATTAACTATTCGGAGTCGTTATTTGACGAAGAAGTCTTGTACGATGTGTGATTAAATAAAAAAGGATGTTCTATAGAACGATTCCCCCTTTTTAGTTGATTTTATTCAACGATTGACCAAACGAAAATATTAATAAATAATAAATT |
| P08_Contig-4656 | *not applicable* | *not applicable* | 206 | 26.7 | AAAATAGTTGACGGCTTCATGCATATTACTCGATTGATTAACATAAGAGTTTGAAATAACTTCTACTTACAAAAAAGGATTTATTTAAAAATAGGAATCCTTTATGATATAAAATAGATATATTACCACTTGGTTTTTTTAAACGGAGCCTGGATACTTCATTTTTTGAGTCCA |
| P09_Contig-16 | *not applicable* | *not applicable* | 212 | 45.8 | GTGAAAAGAAGCGGCCTATCATACTGAACAACTTTTGTTTTGGAACCATTTCTGTATCTCCAATAGTTTAGGTGGGCTCCTGGTGGTACACCTGGTGGTCTACATCTATACTCCAGACCCTCGAATGGTGATAAAAAGTAGCCTATGTCCGTTCTCGGTATGCTAGCAATC |
| P10_Contig-16 | *not applicable* | *not applicable* | 494 | 59.1 | GTTGGGATATCGGAGTAGCAATCTCCGGCGTAAAGGCGCACCGAACCTTTACGTCAGGGATTTGCTCGCCTTAGCGCATAATCTCCCTGACCCCAACGTCTTCGCAACGTTGTCCATCACGCCACTCCCTCTTTATCCGGGCTTGTGACCGGTCGGGTTCCCCAATGA |
| P10_Contig-43 | *not applicable* | *not applicable* | 494 | 59.1 | TATTGCCTATCCGTATTGCTTGCAAACTCCCTAACATCTGCGCCCTCCTCCTTTATCCGGACTGGGGACCGGCACCTTCCCGTGAGGGAAGGGGTGGAGTTACGCTAACCTCGCTCGGGTACCCTTCATTGGGGAACCCGACCGGTCACAAGCCCGGATAAAGAGGGA |
| P11_Contig-1 | *not applicable* | *not applicable* | 752 | 32.0 | GCTCTTTGCCTCCCCCCCCGCTGTGTAATATTCGTTTTTTCCTTTAAAGTCCTGCCAGGGGGTAAAATTATTTTTCCCCTATTTTTTAAAGCATCCTTGAGAAAGAAACCTTAGGCTCCCCTTGCCTCCTATTGATAGGGCACACACCGAAGGTTTCCGCAAAGGCAAACA |
| P11_Contig-165 | *not applicable* | *not applicable* | 512 | 53.3 | GGAGTCCGCGAGGAGCCCGAAGGCTCCCAGCGCGTTCCATCATCGAGTTGAACCTGGGCGGACACGAGAAACAACTCTTAGGAACGCTATTCCGCTAATGCACATTCCGTCATCGAGTTGCTCCGGGGCGGCTTATGCCCAAAGCAACCCTTAGAAATATGCAACGGAG |
| P11_Contig-2004 | *not applicable* | *not applicable* | 201 | 39.3 | AGTTTAAATTCTAATACCCTAGCTACGCAGGGGTAGAATACATTAGTTATATTGCCCTAGCAACCAGCTCTAAAGTATAGAGTCCTGCCTTACCTTTCATAGGGCAAAACAGAATGATTCATTTTTCAACACGAAAACAGCAGGTCATTAGTACCGTACTAGTCCCCCCCG |
| P11_Contig-277 | *not applicable* | *not applicable* | 504 | 25.2 | ATAAATATCTCAGAGTTTTTTAGTCTTTTTTGAAATTAACTCAATTAAACCCCAATAAATACTAATAATTGTATTATTATTAGGTAGGGACAAATCCTATCCCTAGCGTAGCTTTTCAAAAATCCAAGACCTTTCCTTAATGCATCTTGTGATCATATGCCCCGCTTACGCGA |
| P11_Contig-2980 | *not applicable* | *not applicable* | 272 | 46.0 | TCTTACCGGGGGGGGTTACCTCCCGTTGTTATTCTGGCCTAGGCGTAGCGCGTCCTGGGTGCCACTCTATGTGGAATTCCGGTATCACTTCGTCCAGGAGTGATTCGTAGCTTATTCTTCGCGCTTTGTAAACTCAGCGATTATTTTTAGCTCGAAATGTAGTAGTAGTT |
| P11_Contig-764 | *not applicable* | *not applicable* | 205 | 32.2 | AATATTTACAATATTTGTTGCTAGATTTACACCTTGTTTTATTTGTCTGGTTCCGTCTTGCATTATTCGCTTACCCCACTGGTGTTATTAATTCGCCTATTCAAGCCGGAACCCTTTTTTTTTTCCGTAAACTACAGGATAAAATCCCTCATATATTCATTAAAAAGTAAATGT |
| P11_Contig-88 | *not applicable* | *not applicable* | 512 | 52.9 | CTCGATGATGGAACGCGCTGGGAGCCTTCGGGCTCCTCGCGGACTCTGGTTACTGAGCAAACGACGATTCGGGCACAGTGGAAGTAAAAAGACACGCCGGTCGAATCCTAGCAAGCGAGGTAACCGGATTTGCTGACGGTGTCGGTTGGCGGGCTTTGGCTTTTGCCA |
| P11_Contig-947 | *not applicable* | *not applicable* | 204 | 28.9 | AGGTAGTCCGGTACAAGTAACTGATTTAGAAACAAATACTAAAGTAATTTATGATACAGCAAATAAAGCCGCCCAAAGTTTACTTTGTAGTACTTCTACGGTTAATTCGTACAGAAGTAAAAAATATATTTTTTTATAAAAAATATACAATATTTAATTGTATCTGTAACCAGG |
| P13_Contig-5 | *not applicable* | *not applicable* | 208 | 46.6 | GTGAATTGCAGTCAAACGGTGTCTTCTAACTACCTCCTAGGCATGGGGCGCATTTATAGGATAAGTAAGTGCTATCTGTCAGTATATGGTGAACTGTCTGTGGAAGCTTCAGGAAGCTTTGGTCCCGCAACGACGATAAACTGCCGCAAGGAAATCCGCAAATATAAATCT |
| P14_Contig-101 | *not applicable* | *not applicable* | 202 | 21.8 | AAGTATTAATAGTATAAAAAATTAAAATAACAAAACCAAGAAAAAATTATTATTCAATTAGTAAATTATAAAAAAACAAAAGTAGTGGAGAGAATTGGAGGAGAGAGAATATGAAATTAATAAAATATAATTTATGTTGGGTCCACTAAGTGAGAGAAATTAATTAAATATTGTAAA |
| P14_Contig-1047 | *not applicable* | *not applicable* | 205 | 13.2 | AAAATTTGTTAATTATTTAAAATATTTTTGCAACAATAAATTTTTTAATTAATTTTCTCTTTTAAATTCGAGAAATTTTACCCATAAAATTTTTTTTAATAAACTCTGATACACAAGATACAATAAATAAAAATTTACTTTTAAATGAATTTTTTTTTCATATATTTCAAATTTATTTTA |
| P14_Contig-161 | *not applicable* | *not applicable* | 353 | 47.0 | AGTGGCTGAGAATATACCTTCATTCAACAGATTTTTGGTTGCATGCTCTGGGTCTGGAATCTTTGCTCTTCTCTTTTGCATTTCCGCTGCCTGCGTTCTTTCTTCGTGTCCGTTCGTATCGCAAAGCGGGTCGACGCCAGCTATAGCTATAATGGTTGAAAAGAGGGGG |
| P14_Contig-281 | *not applicable* | *not applicable* | 509 | 52.1 | TGGTCCCTTCTTCCGTTGTTTTGCCCCTCCGTTGCATATTTCCAAGGGTTGTTTCGGGCATAAGCCGCCCGGAGCAACTCGATGACGGAATGTGCATTAGCGGAATAGCGTTCCTAAGAGTTGTTTCTCGTGTCCGCCCAGGTTCAACTCAATGATGGAACGCGCTGGG |
| P14_Contig-931 | *not applicable* | *not applicable* | 298 | 29.2 | GGAAAAAATAGAAGTTACTAAATAAATTGAAAATGAATTTCAATTTGTAAATGAAATTAGAAATGAAATAAAAAAAGGAACACAACGATTTCTAAACTATATTTCAAATTGAAGTAATTTCAGTATAGAATTCCCGTCCTAGATCTTCATTTTCGATTCTACCCACACCCCTCTAT |
| P17_Contig-193 | *not applicable* | *not applicable* | 512 | 53.3 | TGCGAGATGTGCGTGAGTGGTCCCTTCTTCCGTTGTTTTGCCCCTCCGTTGCATATTTCCAAGGGTTGCTTTGGGCATAAGCCGCCCCGGAGCATCTCGATGACGGAATGTGCATTAGCGGAATAGCGTTCCTAAGAGTTGTTTCTCGTGTCCGCCCAGGTTCAACTCA |
| P17_Contig-38 | *not applicable* | *not applicable* | 244 | 51.2 | AGCATCATGACGTAATTGTTCGCGGCCTGGAGTCGTGTTCGCTGTCGATGCTATCTCTTTGTTGGTTATGAACGGATGCGGGACTTTTTCGGTGACAATCGTTGCTGACCTCCGCTTGTGGTTCTTAGAGCTTGTTGTGGTCGTTGGTGGCCTTTGTCCAAGGGTTGCTG |
| P17_Contig-49 | *not applicable* | *not applicable* | 512 | 53.1 | AATAACGGAAGAAGGGACCACTCACGCACATCTCGCATTGCGCACGTCGCTTACGTTAACCATTAATTAGCAAGACCCCAGCTCAGAAAAACTGTGCACAATAGGCCACACCAATTTAGGTCTTCGCTAGAAACGGCCGCGTCGATAAGTACGAAAAGAACACAAAACAAA |
| P17_Contig-81 | *not applicable* | *not applicable* | 244 | 52.0 | CAACCCTTGGACAAAGGCCACCAACGACCACAACAAGCTCTAAGATCCACAAGCGGAGGTCAGCAACGATTGTCACCGAAAAAGTCCCGCATCCGTTCATAACCAACAAAGAGATAGCATCGACAGCGAACACGACTCCAGGCCGCGAACAATTACGTCATGATGCTAAC |
| P18_Contig-11 | *not applicable* | *not applicable* | 744 | 57.0 | AGGAGTTCAACCAAATCGAGTCTGGTCTGGTGTTGGAGGGTGACTTGGTTTACGAGTCGCAAAACAACAAGCAGCACTACGCCGGTTTGTTGCCAAAGATGGTGCGCGTCAACATGTCCATGCCAGTGATGGGCAAGACCGTGAACGTGATCGAGATCACTCTGCGCCA |
| P18_Contig-20 | *not applicable* | *not applicable* | 327 | 63.6 | CCGTATCCTCCAGCCGAGGCTCCGTATCCAGAGTTTCCTGATGAGGCTCCGCCGTAGCCGCCTTGGTTTCCACCTTGAGCGCCGTAGCCTGACGATTGTTGTTGTTGGCCGTAGCCTGACTCTTGTTGAGCGGCAGCTCCGCCGTATCCACCGGCTGAGGCTCCGTTT |
| P18_Contig-3 | *not applicable* | *not applicable* | 351 | 63.2 | TCGTCAGGTAACTCAGGATACGGAGCTATGAGCTCTGGTAACTCCGGTTACGGTGCCTCGTCGGGCGCTGCCGCCGGTGGATACGGAGCCGGAAACGGAGCTTCAGCTGGTGGATACGGATCAGGCAACCAGGGTGGACACGGTGGCGCCGGAAAGGCCAGCTACAA |
| P18_Contig-30 | *not applicable* | *not applicable* | 650 | 40.8 | AAAAAAAAAACCCCCCGGGCCCCCCCCCCCTAAGGAAGGAAAAAAAAAAAAAAGAAAGAAAAACATTTTTCCATTAAGGAATAAAATATTCTTGGTTTATTTAACTCGGCAACAACTACGGACTGTTTAACAAAAACAACGCTCGTGTTATTTCGAGCAAACCCTGCCCGG |
| P18_Contig-39 | *not applicable* | *not applicable* | 277 | 39.7 | TTGCTCTGTTATCCCTTAGGTAGCTTATTATTTGTGTTATTATTTTTTTAATTCTCAAAATTTAAGTGAGTGTATTCCCCAAACAATACCTTTGGTAATAGCTCTGAGGGTCTTCTCGTCTTAGGGTAAAGTCTGTAATTTTTTAGACTTTGATTTCATTATTTGGCTTATCAA |
| P18_Contig-5 | *not applicable* | *not applicable* | 753 | 37.3 | ACCGAAGGAGTACTATCTATTTAAAACCTATTTACCCAATGTTCCGCTACCCCATAAATAATACTTAAATAACCTTTAAGTATAGTAAACTAGGATTATACCTAATATAATTATTATGGACAAGGTGTCGGTGTTTTGTTTTAGATCCGTTAAATTTTCGGTGCTTTCAACTTTT |
| P20_Contig-100 | *not applicable* | *not applicable* | 246 | 61.8 | TAGCCATGGCCGTAACCTCCAAAGACCCCATGTCCACCGTGTCCGCTATGCCCATGAGAAAGCTTGTGTGCTCCATACGCAGCTGCTGCGGCAGCGGCACCTCCAGCTAGAACTGTGCCCATCCCCATGTGTCCACCACCATGGCTGCCCCCATAACCCTGGTGAGAT |
| P20_Contig-1001 | *not applicable* | *not applicable* | 226 | 46.9 | TTGGCCGCGGTGTGGAGTTGTGTTTGATGACAGCCGGGATACAACAAGCTGGTAATAAAACAACGGATGAACTCTCTGAGAGACCGAATGAGTGTTTATATGCAGCACAGCGTGTAGAAGAAAATGATCCTAATCAATCTTCCAACTTTCGGAGTTGAGATGGGGGAGTT |
| P20_Contig-1062 | *not applicable* | *not applicable* | 273 | 61.2 | GCATGGGTACCCTCAACCTGGTGGCTACCCACCGCAGGGTGGCTATCCCCCTGCAGGTTACCCCGGCTCATCTCACCAGGGTCATGGGGGCAGCCATGGTGGTGGACACATGGGGATGGGCACAGTTCTAGCTGGAGGTGCTGCTGCCGCAGCAGCTGCTTATGGAG |
| P20_Contig-128 | *not applicable* | *not applicable* | 244 | 50.8 | AACCGAATAAGGGCTAAGACCGGGGGCAAACGTTCCCAACACTCTTGGCTTAACCTTCCAGCAACCCTTGGACAAAGGCCACCAACGACCACAACAATCTCTAAGACCCACAAGCGGAGGTCAGCAACGATTGTCACCGAAAAGTCCCGCATCCGTTCATAACCAACAA |
| P20_Contig-1540 | *not applicable* | *not applicable* | 221 | 36.2 | TATATATATATATATACATACATACACAACAAAGTACATTCTTGCGGTTGGACTAACATCAACTGGCTATGTCGGTAAAACCTTTAAATATTGTTGTTATTATTATTATTACGAAGAGGAGGCTGTGATGATATATAATTTAATTCTAGTCGGAGCAAACCCAAATGGGCTTGG |
| P20_Contig-1839 | *not applicable* | *not applicable* | 226 | 46.9 | CAGCCAAAAGCCTACACAGACCGGTTCCCCGTATCCAAACTCCCCCCATCTCAACTCCGAAAGTTGGAAGATTGATTAGGATCATTTTCTTCTACACGCTGTGCTGCATATAAACACTCATTCGGTCTCTCAGAGAGTTCATCCGTTGTTTTATTACCAGCTTGTTGTATC |
| P20_Contig-194 | *not applicable* | *not applicable* | 468 | 30.6 | AATAAAGAAGAAGGAAGGAAAGATAAATAGAAGTTATTAACTTGAAATCCAATTATGAAAACTTTCGCTGCAATCAATATACTAAAAAAATTTCTAAACTTTATTTCAAATTCAAATCACAGTATTTCATTTACATTTAAGTACCTTGTTTGTATAAGAGTCTTGTCGTAGATCTA |
| P20_Contig-2057 | *not applicable* | *not applicable* | 291 | 40.9 | ATGAGAACACGACAATGACTCGTCGAGCCCCCAACATGCATCGGATAAGGAATGTCTTTTAAATGCTCTAGTCGAACTAAATCGTTAAAAGAGCAAAAGAAATACATTAGCCAGCCGCATGCCAAGGCTCTAAAATCATTGTGGAGTTTTCTTAGTGTCCCACCATAATATT |
| P20_Contig-2557 | *not applicable* | *not applicable* | 744 | 41.8 | GCTACAATGAAAGTGATATTGATCTGAGTGAAAGCTATGATTCAGACAACAGCAGTGACAATAACGATAGATCAGATCTCTTGAGTCGAAGTGAAACTGCCAGTCAAGTACCGGAAAACAACGAAGACAACGAAATATCTTTTACTACGCCTACGACTACTACTTCAAAGCC |
| P20_Contig-304 | *not applicable* | *not applicable* | 244 | 52.0 | GTTGGTGGCCTTTGTCCAAGGGTTGGTGGACGGTGAAGCCAAGAGTGTTGGGAACGTTTGCCCCCGGTCTTAGCCCTTATTCGGTTCTCATCAAACGGGGTTAGCATCATGACGTAATTGTTCGCGGCCTGGAGTCGTGTTCGCTGTCGATGCTATCTCTTTGTTGGTT |
| P20_Contig-326 | *not applicable* | *not applicable* | 391 | 35.5 | AGCCTAGCCTCGTTCTTCTTTAGATCCCTTGTTTCACTCCGATAGTATCCTAGATTGCGTCAATGCAGAGGAAATGATTGCATTTTCATACTATTCAATTTTACATAAGTGAACTGAGAAACCATAATTATGGTTTCTCAGTTCACTTATGTAAAATTGAATAGTATGAAAATG |
| P20_Contig-327 | *not applicable* | *not applicable* | 744 | 41.8 | TTTCACTTCGACTCAAGAGATCTGATCTATCGTTATTGTCACTGCTGTTGTCTGAATCATAGCTTTCACTCAGATCAATATCACTTTCATTGTAGCCATCGTTGCCACCAGAGCTATCATCACTCGAAATGGTTGTTAAAGAGTCATCATTGTTGTTGCCATCACTACTAGA |
| P20_Contig-363 | *not applicable* | *not applicable* | 298 | 40.9 | AATAAGTTGGGCTTGTTGTCTACTCGAGTGTATCGATAAACCAGTCATCTCAACATTCCAAATTCCTATGTTTCTAGCCAGCAGCCTATTACGTAAACAGCTTTGTCAACGTTGACATATACATTGGAAAATGAATCCTTTGGCCAGGTTCAGTAAAGAGAAATCGCAGGAT |
| P20_Contig-372 | *not applicable* | *not applicable* | 247 | 45.3 | TCAATTATACTGCTGGGCGTAACATACCTTCAAGTCAGTCTTCTTTGCTGTGGGCAGCAGGGCTTCTCTTGATGTAATGCCGTCTCATTGTCAAATTGGTTGTCTTTGAATGGACTCTCGTGAGCAGCAGGTTTAGTGGTGCTCTCTTCCTTTTGCCTTAGTATTGCACAT |
| P20_Contig-4413 | *not applicable* | *not applicable* | 222 | 44.6 | ATGAAGAGTATGCAAGTGAGTAGAATGCCACCATAGGTACTATTAATGAGGAGAGATAGCCTACCTTCGGCCTACCGCTATCGGTTGAGCTATAAAAGAAAAGGCATTTCCTCTCCTTTCCAGTCGAGCAAGTAAACTCCCTCATGCTTGCTTTGTGGTGCCTAGTCCAAA |
| P20_Contig-6332 | *not applicable* | *not applicable* | 247 | 45.3 | CTGACTTGAAGGTATGTTACGCCCAGCAGTATAATTGATCAAGGGCCTCCCAGTGATGAGAAGGAAGATATTGGAGTTCACAACAACGGTCGAGTTTCAGAACTTCAGTAGACAATGTGCAATACTAAGGCAAAAGGAAGAGAGCACCACTAAACCTGCTGCTCACGAGAG |
| P20_Contig-663 | *not applicable* | *not applicable* | 228 | 44.7 | TCTTCTGCGGGCACTCCTTGAGCTTCGTTTGTCTCTCCAGTTAAGGTTACACTTTCACCACCATACGGTAAGTTAGCAGGTACATCAGCATCCACTGCATCTTCATATCTTCGTGTTCTTCCGTGGGCACTTCTGAAGCATCAGCTTCTGCATCAATACTATCTTGATGA |
| P20_Contig-68 | *not applicable* | *not applicable* | 231 | 69.3 | GGCGGCCGTCTACGCCGACAAGTACTCCCTCAGCGGCTGCGGCTACGGCTACGGCGGCTACGGCGGCGAGCAGGAGCACTTCAAGAGGGAGGAGAAGCAGCACAAGCAAAAGGAACGCCTCGGCGAGTTCGGCGCCCTCGCCGGCGGCGCCTTCGCACTGTACGAG |
| P20_Contig-726 | *not applicable* | *not applicable* | 229 | 40.2 | TAGAGCATTTAAAAGACATTCCTTATCCGATGCATGTTGTGGGCTCGACGAGTCATTGTCGTGTTCTCATTGTGACCTACCTTATTTTGGCCCAAAGCAAAACCTTTTTTTAAAATGCCCGATCTAGCACGGGCACAACATGCCCGTGCTAGCAACAACTTTTTACGATTT |
| P23_Contig-10304 | *not applicable* | *not applicable* | 223 | 48.0 | TAGGCTATAATATATAAGGGGGAATACCGCTTTCAATTTCAAAGAGCTCTATTTCCGCTACAAAATGAATCCGTTTAAATAAGCCTTCCTCCCAGTACCAACTGATAATTGGACAGGGAAGTTGTAAATCCGTGAGAACTTCGGCTAGAAGAGAGGGGTCTAGCGCGCCCG |
| P23_Contig-1078 | *not applicable* | *not applicable* | 244 | 45.1 | TTCAACGGGGTGGCGATCATCTCTCCCCGGAATATTCATCATGATGGCACCTACCTCATCATGGTAACAATTACCTCACCGGGGTAACTCAATGTTCAACATGGTGTCGATCAACTTACCATGGACGCATTCAACTTGGTGGCAACACCTCACCAAGGACAATTGCCTTTC |
| P23_Contig-11287 | *not applicable* | *not applicable* | 220 | 48.2 | GGCTTGACGAGGACGTCAAAAGTTTAAGTGGAGGAATTTGTAACACCTCAGTCCCACATCGAGTAGATTGATTCGTCGAGTTGCCGGAGGTAGGAACACGAAAGCTGATGGTATTATCCCATAATGGACAGAGGTCCGGAGGTGGGGACACGAAACCAACCGGTATTATC |
| P23_Contig-1159 | *not applicable* | *not applicable* | 278 | 40.6 | CACAATCAACCAATTATTTGATTGCTCCAAAATGTGGCAGGGGCTTCCAGTCTTGTCTTGTTTAATTCTCTGATTTGTGAGGAGGGTCTTAATCAAATCTGACGATTGCCTCCCCAACTTAGATAGGTTATGAAAGTATGTAGTTAACCCTTTCTTATCAGAAATTCATTTAA |
| P23_Contig-118 | *not applicable* | *not applicable* | 339 | 45.4 | CCCGGTGAGGTAATCTTAGCCATGAAGAGGTAGGTACTCTCATGTTGAATGCATCCGGGGTGATTTGATCACCACCCCGTTGAAGTAAAAAGTTATCCCGGTGAGATAACTAGTAATGAGGAGGATGTTGCCCTCATGTGAAATGTAAGACCTAATGAAAGGCATTTGTCC |
| P23_Contig-13897 | *not applicable* | *not applicable* | 204 | 36.8 | TTTCTAATAGAGTCGTTAGTTCCGCAGCTCTTGGAGAGTTTTTCATTTGAAATGTTTTTGTATGTTTCTAGAGTCAAGGGAGAATGCCGTTTTCAAAAGGTATCCCTCTTCTGTTTCGATTTATGCTGCTTTTCTAGTTGAAGCTGCCTGGAGATTCAAATCATTTTCATTCT |
| P23_Contig-145 | *not applicable* | *not applicable* | 747 | 30.1 | CCTCTACCATAGCATCAGTAGCGCCATCTGTTAGTAGTTTTAAAGAGGTATGAAAAGCCTTGGCTAAAAGACTCGTATTTTTTTTAATGTAGATTTTTACATTTAATGTTAGGAAGAATGTTCTTGTGTTTGTGACGGTTTTTATTTAATGATTTATAATTTGGGGAGTTTAA |
| P23_Contig-2046 | *not applicable* | *not applicable* | 220 | 48.6 | ACTCGATGTGGGACTGAGGTGTTACAAATTCCTCCACTTAAACTTTTGACGTCCTCGTCAAGCCTGAACGAATATCCTATAGGTTCCAAGATCGTTCCTCCCTAGCCATTGTGGGATAATACCACCAGCCTTCGTGTCCCCACCTCCGGACCTCTGTCCATTATGGGATA |
| P23_Contig-2180 | *not applicable* | *not applicable* | 278 | 41.0 | TACTTTCATAACCTATATAAGTTGGGGAGGCAATCATCAGACCCGATTAAGACCCCACTCACAAATCAGAGAATTAAACAAGACAAGACTGGAAGCCCCTGCCACATTTTGGAGCAATCAAATAATTGGTTGATTGTGGGGTTGTGAAGGAGGAGGGCTCGCACTACCTGT |
| P23_Contig-2209 | *not applicable* | *not applicable* | 229 | 37.6 | GGTGCAGGGTTAGGTAGTCGACCTTTGGAACTGGTGAAAAATTGTTTGAAAAAAAGAAGCTGCAAATTTTGCAAAGATTATACACCTCCGGTCTTACTATGATTATCATCAGGAACTCACAAATAACAGAAGTTTGCTGATAACGAATGTGAGTTCTCAGTTTTTAATGAGCT |
| P23_Contig-240 | *not applicable* | *not applicable* | 653 | 40.4 | CAATCTACCTTTACATCAATTGTCCATCTTTAACTTAAATAATACCCCAACTTTTTTGATATTCCAAAGTTTTGGTGGAGAAGTTTGTTAGGGACGCCTAATAGCCCAATTTACTACTACCTTGCTAATCATCAACCCACGCGGTCAAACTTTCCTTAAAAATTACGATCGTT |
| P23_Contig-3220 | *not applicable* | *not applicable* | 262 | 35.5 | TACTATATGAGATGAATAGAGGGTATCGCATATTTGGTTCAGTCAACAGGATTGTAGTTGGTTGTGATCAAGGAACCATCATGGGAGAAGTTATAAATGCTTAAAGTTAAAGATTCTGTGTATGTCTTCATCATCAGTCCTGGTGGAAAAGCTACTCAGCTATATTAATGCTT |
| P23_Contig-33 | *not applicable* | *not applicable* | 766 | 42.2 | TTCTGTGAGATTCACCTTTACTTGATGATCGACCTTGTGCCTTTTGACATTCTGTTTGTACATTATCAGCAACCATTTGATTGGCCACCTCAATGGTTTTAACCTTGCCTTTGCTTTTTAGGTCTTCTGACAAGTGGCTTTGCTGCTGCAAATAAGAAGAAGATTTTGAACT |
| P23_Contig-34000 | *not applicable* | *not applicable* | 229 | 37.6 | GACTCAGAATATAGTTGTTTCGGATGCATTTCCTGCACTTTATTAACTCTCACACATTGATGGTTCTGAGTTGCAGGAAGGGAATGTCCGTCCTGTTTTTTGGTCCATTTTGTTGGCTGACATTGATGGTTCGGGAAAATACCTTTCATTAGAAAGAAATTACAACGCAGTT |
| P23_Contig-3924 | *not applicable* | *not applicable* | 311 | 41.2 | ATAATGATCATATATGGTTCCAAACGTCATTATATGACCCTAATATGTATCCCTAGGGTCTCAAGACTTTTCGCCACCGGGCCCCGTAACCTCAAAATTCCTCAAAAAGCGTGGATTATAGCCTTCAATTTTGGAATTTTTTCGCCCGGAAATAAAAATTGCCGAGATGTTT |
| P23_Contig-448 | *not applicable* | *not applicable* | 771 | 46.7 | TTCCTTCGGCAGCAGGTTCAACTTCCAGCCCATATACTGGCAATGTATTGCACTCTGCGACATCTTTCTGTTCCTCAACACCTTGTCCATCTTGCACAAATACAGGACCAACAGCTTCATCGGTGTGTAACAGAGGCATGTCATTTGTCACAAACACTGGCAACTCAGACC |
| P23_Contig-455 | *not applicable* | *not applicable* | 324 | 47.5 | TTCTATTAGCCTAAGCGTCTTCGCTAACTCGCTCGCCTACTATACAATACATTAAGTAGGGTAGGCTAACTCAGCCGCTTACTTCTACTAATGTAGGGCTAAGTAGCCGCCTTTTGAATTGAATCTTAAGTAGTCTATCAGTGTGCGAAGCGGCTTTGCCCCTTTTCAGTA |
| P23_Contig-4886 | *not applicable* | *not applicable* | 375 | 38.7 | AACTTTCACATGCATATTTTTGATTAGGTCAACAACCCATTTCGTGATAGGTGCAGGAGTCCGATGGACATGGCACCACATCCAAAAAATAGGTCTAGCAGATTCATTTCTATTGGTTTATTGCTCCCTGCGTCTTTGTGAATATCATCACTTTCACTTTAGATGGTCGAATT |
| P23_Contig-508 | *not applicable* | *not applicable* | 252 | 48.0 | ACCTCCGACCTCCGATCTCCCGAGGGTGATAGAAAATGGATGACCTCTTGAAGGACCACTCTACCTCTGTACGGCTACCCGAATTGTCTAAGGACAACTGGCTTGAGTGGAAGGACCTTATATACGACATACTGGAATCAAAGGACCTCCTCTCAACGATTAAACCTGGA |
| P23_Contig-5451 | *not applicable* | *not applicable* | 244 | 50.8 | TCGGTTCTCATCAAACGGGGTTAGCATCATGACGTAATTGTTCGCGGCCTGGAGTCGTGTTCGCTGTCGATGCTATCTTTTTGTTGGTTATGAACCGATGCGGGACTTTTTCGGTGACAATCGTTGCTGACCTCCGCTTGTGGTTCTTAGAGCTTGTTGTGGTCGTTGGT |
| P23_Contig-646 | *not applicable* | *not applicable* | 578 | 46.2 | AAAAGCCAGAGGTATTCACACTAACGTAGAAACCGGATACTTCCCTCCGACCGACGGGTACCAACTCCAATGAAGGTATCGGAGGAAAAAGCACGGTAGAAGAACAGTGGAAATAAAGCTGAAACTAAAACCTAGCTGATAGTAGTGGAATAGGTGTCACGGTATGGGTTA |
| P23_Contig-6685 | *not applicable* | *not applicable* | 296 | 34.5 | TAATTATAGTCAAATTCGTTTAAACTCTCGGGCTGAGTGACGTCCCTGCTCATAACTGTAAGTCTGTAACTATATCTCCAGTTGAATTATGCCATATGGACCCTTTTATCTGTTTTATACTTGTGTATCTGTATCAGTGACTTGCAATTGACCACGGAGAAACTGAACATTGC |
| P23_Contig-730 | *not applicable* | *not applicable* | 261 | 57.5 | TGAGGACAAGAACACCGACCCCGCTGTGTACCCAGGTCACGATGGCCACACCACCTACCCCGTCCCACCGAAGGAGACCCCGTACTACCCAGGCAAACCTTCAGCAACTTACCAGTTGACCACGACCCTGAGCACTTACTACACTCAGCCTAACGGACAGCCAACATA |
| P23_Contig-7699 | *not applicable* | *not applicable* | 262 | 35.5 | TCTCCCATGATGGTTCCTTGATCACAACCAACTACAATCCTGTTGACTGAACCAAATATGCGATACCCTCTATTCATCTCATATAGTAGTGTTGGAACATTATTCGATATCTTCTATGACTGTCACACATGTCACAGACTTATTCTTACAAAACACAACAATCAAAATACAAA |
| P23_Contig-805 | *not applicable* | *not applicable* | 244 | 50.0 | ACCACAACAAGCTCTAAGAACCACAAGCGGAGGTCAGCAACGATTGTCACCGAAAAAGTCCCGCATCGGTTCATAACCAACAAAAAGATAGCATCGACAGTGAACACGACTCCAGGCCGCGAACAATTACGTCATGATGGTAACCCCGTTTGATGAGAACCGAATAAGGG |
| P23_Contig-93 | *not applicable* | *not applicable* | 213 | 48.4 | AGAAACGAGTAGGAAAGAAGGCAGTTGCTTCAAAGGAGGTTGCACCCCCACCAAAAGATGAGTCGGAAGATGATGAAGCTGCTAGTGACTCGGATGCAGAGCCCCAAAAACGAACAGAAAAGAAAGCCTTTGATGCAGAGGAGGATGTTAAAGCTCCACCAAAAGATGACT |
| P23_Contig-944 | *not applicable* | *not applicable* | 714 | 40.2 | GTAGTTCCAGTCACTAACAATTCTCGATTCTCTTGACTCACGTAGTTCTGACTTAAGGCAGATAGCAATTCTCGATTCTCTAACTCACGTCGTTCGGATTAAGGAAAAAATTGTACTTTTGACCAAAAAAGAGTTAATTCCAAAGGTTGTACATACTCCAAGATTGCAGTAAA |
| P23_Contig-979 | *not applicable* | *not applicable* | 296 | 21.6 | TTATCGTGGGTTATCGATTTATAAACAGGTTCCTCTAATTAGATAAATGCCGCCAGGATATAAAGGTTGAAATTCCTTAATTTTTAATATACAAGGGTATCTAATCCTTTTTTATATCAAAATTTTTGCTTATTTTGTTTATTATTTGAAATAAATTTTTTAAATTATATTTATAT |
| P3-1_Contig-1135 | *not applicable* | *not applicable* | 762 | 45.7 | GTGGGTTGCTACTGTTAGGCTCGGTTAACGGGTAAAATGGACTTAGATGATTAAGTTGCATGAAACCTAGCTCTAAACATGGGTTATGAGTAAACTGAGACTACTGGAGTTGGACCTAACCTTAGGGAACCTTAGTGAATCCTCTTGAGTGGTTTTAGACGGCTGGAACAA |
| P3-1_Contig-1186 | *not applicable* | *not applicable* | 274 | 45.3 | GATTGTTTCTTCAATCGAGCGTCATTCTAGGGTTTGTTGAGATTTGGGGCTTTTACGGTCTGATCCTTTTGTTTAGATCTGTTATAGATCTGGTGTTGGATCGTGTAGCAGTGAAGGTTCTTGACAGACTCTGTGTTAGGGTTTTCAGTCTAAACCCTAAGAGAAGTGTTCT |
| P3-1_Contig-1949 | *not applicable* | *not applicable* | 216 | 60.6 | GCCGGCGATCCTATAGGGGCAGAGGCTCCCGGAACATAGCCGGACGGTGAAGATGCCGGCGACCCTTTTGCCGGAGAGGTTCCCGGAGAATTGCCGTACGGTGATGATGTGGGCGAACCATTTGGCGCGAAAGCTCCTGGAGCATTTCCGGACGGTGAGCTTGCCGG |
| P3-1_Contig-2062 | *not applicable* | *not applicable* | 439 | 42.8 | AGAGGGTTATTCCTACACCGCCATGGCTGCAACTCCTGTTGCCCCGCCAAGATACGGGTCAGGTCACTCCATACCGGATGAATGTAGAAAAACCTTCATCATCATCACAGCCTACATAAACAGCATTCATAATAATAATAGCAACAACAACGACAACAGCATGAACAGGAA |
| P3-1_Contig-2628 | *not applicable* | *not applicable* | 222 | 30.2 | TCATTTCGTTCCTCCATGGAGAACCCTTTATTCTAAGTCACAAGATAAGAATTCACTATCTTTCTTTGATTACAGGATTAAGATTCATTTATATCTATATAATATTTCTATATATTTAGATTTATAGCTATGAAATCGCGGCTTGATAAAAATTTTCATTTCGTTGCATCCAAGA |
| P3-1_Contig-28 | *not applicable* | *not applicable* | 408 | 36.8 | TTTACTACCAGATTGATTAATTGCTTGGTTGTGTTTTATCAACTCCTTGGTTAAGACTTGGCTGAACACTAGAACTGGGATGCATCTTGAACACTGGCCAAGCTTCGTTGATAGGGTCTTGTTCTAAAACAGCTTAATCTGGTCAGTCTTGTAGTTTACTTGATTTGTTGGT |
| P3-1_Contig-4263 | *not applicable* | *not applicable* | 262 | 47.3 | CAAAATGTAATCAAGCCGACCAATGCCACAGATTAGGTATGCACACAGTAACCCACTAGATGATCAAGGCAAAACAGCCAAGAACACAACTGAAAAGGTAAGAACGCGTAGAAGTTGCTGCTCAAGCAGACATCCAACCACCCGAAACAAACCAAACACCACTCATGCAC |
| P3-1_Contig-717 | *not applicable* | *not applicable* | 224 | 37.9 | TTTTTTTAAAAAAATAATGTCGTATGCAAAAGTTATGGAATTTTTAAATTGGTGGGGAAATTGGCATGTGCCTTGCATGTGGAGAGAGAAAGTCAACAAATGTGTTTTCCCCTTTATACCCTTTCCCTTTTGGTCCCCACTTGACACATGTCATGCTCAGAATCCTTCCTAC |
| P3-2_Contig-1269 | *not applicable* | *not applicable* | 262 | 50.0 | CTCTTATTCTAGACTGCGGGCAAGGCAATTGCATTGGTCTCTGTGCGTTCCAATCCTGCTTTCTTTGGTCTGGGTGATCACGAGCAAAGGCAATCACAGAGACCTTCACACGTTCCTATTCCACAAGTCACAAATGCATCAATAGTCTTCTATTGTGACAGCAGGCAAGGC |
| P3-2_Contig-14 | *not applicable* | *not applicable* | 565 | 52.4 | CTGAAGCACAAGGCGTGAGGGCCTTAAACCTCTTTAACCCCAAGTCGCTAGTGGTAACCCTAGTGCAAACCCCGAAGGCAAGAACGGTCGCCCCTGCGGCGTGCCGTCCCCTTCTCTGGCAGGACTTCGGTTCTCGCGCATTTATACCTTTGCCTTGACCGGCAGAGT |
| P3-2_Contig-1530 | *not applicable* | *not applicable* | 331 | 37.5 | TTATTTGGTAAAACTACGTTGCTCGTCTTCCATTTTTAGTCCAAAAAGTGGATAGCTTTTCTAGACGGAGGGTACTAGTTTACTATCTACAGGAACAACATCTACTGGTTTTCTTGCTAATGCATACAGAACGCAAAGGAAACCCTTAACGTGATGGCCTTAATTTATGCAAT |
| P3-2_Contig-154 | *not applicable* | *not applicable* | 368 | 51.6 | GATGACGAACAATCGACCGGGTGGATCGCGGGACGTGTATGGTGGGCTTTGGTTTGACGAAGGGTTGTTAATGCCCTTCTGATTGGCTGTTAGGCGACAGGAATGTGCAGCTGGTTCTGCAATGGCCCTCGCCCGCGGCGGAACTGGTGTAATCGGTATCGGAACGCAC |
| P3-2_Contig-1640 | *not applicable* | *not applicable* | 259 | 55.6 | TTACTAACGATCGTTTTTCTGCTTCTTCCACACTTGGACCGCGGGCAAAGGCCATTGCAGAACCAGCTGCACATTCCTGTCGCCTAACAGCCAATCAGAAGGGCATTAACAACCCTTCGTCAAACCAAAGCCCACCATACACGTCCCGCGATCCACCCGGTCGATTGTT |
| P3-2_Contig-371 | *not applicable* | *not applicable* | 290 | 32.8 | ACGGGTTCACAAAAGATTAAGGGGTCAAACTTACTTACTTTTACTTTTACGATAAAAAGGACAGTTTTAGGCTTAGCCGGTTTTTGGCTTAGCAGCCTTTTTGGATGTAAAGATAAGAGTAAACTGAGAATGATTACCTAAATGAGTAAGGTAAAATAATATAATTTTTACTTA |
| P3-2_Contig-515 | *not applicable* | *not applicable* | 232 | 33.6 | AGAGAGTCAATACTTAAAGTAGGAATAAAATTGATTTCACTAAACATAGTTAGTAAATCGAGGCATACTTTTTAATTTAAGTATCCTTATTTTCCTGTCTTTTCAACTCATTTCTATCTAATCCATTTTTTTGGGCTCGGCTATTCATCTAGCCGAGCCCTTCGCCTTTATGAC |
| P3-2_Contig-608 | *not applicable* | *not applicable* | 759 | 41.8 | TTTTTCTTGTTTTCCTACAATTTTTAAGATCATTTTCTTTTCTAGCTATAACACGATTGGTGTTCCATCCTTTGTTGATAATAAGAATTGTTTGTCTTGTTCTCTTGTTGATAGATCTAAGAAAACTCATACACGAATAGGCCTTGTCCATCCTGGTTTGTTTCCAGCTAGGTC |
| P3-2_Contig-784 | *not applicable* | *not applicable* | 321 | 46.1 | GAAGAAAGCGATTCTGAAGAAGAGGTTAAGGCTGCCCCTGCTAAGAAACCTGCAGCAGCTGCTGCTGCAACCAAGAAGGCTGATTCTGATGATGAAAGCTCTGAAGAGGAGAGTTCATCTGATGATGAGGAACCTCAGAAGAAGAAGAGTAAGCCAACTGAGACAAAAGCT |
| P3-2_Contig-838 | *not applicable* | *not applicable* | 753 | 39.2 | TTAATTGTGTCATCCAAAAGGGTCTTAGGTTTTACATGACCTGTTTTTGTGCTACACACTGAATGATGTGTGAGGTGGGGTCTAAATAGCATTCAAGTAGCTTGGTGATGTGGTGTGCGGAGATAGCTAACTTAATGATAGAAGATTAGATCCTGTTATGATTAGATTATGGA |
| P3-2_Contig-987 | *not applicable* | *not applicable* | 514 | 53.3 | TCAGACATGGGCTTCTTGAGTGTTGCGCCCCGGCTCAACTTACTCCTCCGAAGAGTTTCTGATTTCCGTTGTTTCACACCAGTCCACCCACGTCCTCGGCTAAGGGCGCTGCATAACTTGTCATGCTGCAAGCAGCAGAGGACCGCAGCACAGCAGGCTGGCTAGGTAA |
| P37_Contig-189 | *not applicable* | *not applicable* | 332 | 35.8 | TCTTTTTCGTTACTCGTGTCAGCATTCTCGCTTGGGATATACTGGACTAGCGCTAAATAGCGCTCAAACTACGTTGTAGTTATCTTTAAACTTATGTACGTCGACTAGTTATTATTTACTAATAGTAGTGCTTTTTTCTTCCTAGTACAATACTTTTATATTTCCTTTGTTTCT |
| P37_Contig-724 | *not applicable* | *not applicable* | 308 | 44.5 | TTGGCTACAGTGAAATACCACTACTCTCATAGTTTCTTTACTTACACGGTTAAAGGGAAGTTGGGATAGTGTCTCTCTCACTTGGGTTTACCTCAGGGTTCGGGAAGGCCTCCTATCCTTAAATTCTAGAGCAAAGTGTGGGTACTTTCATCAATGCTCAAGACCCTATGA |
| P38_Contig-38 | *not applicable* | *not applicable* | 217 | 35.5 | TATCTTATTGCAAAGTGCTTTGTTTTAATTAAACAGTCGTACAACGCCATTTTATGTCTCCTCTCCTTATCTTATATTCATCGATAAGGATGGCACACCTTATCCCTAAGTTACGGTGTCATTTTGCCGAGTTCCTTAATGATTGTTAACTCAAACGCCTTTGTATACTCTAC |
| P40_Contig-32 | *not applicable* | *not applicable* | 217 | 28.1 | CTTACTGCGTCTTGCGGTCTTTATGCCCTGCTTACGCAACTGATAGACGTGTATGTCAAACAGTAAAGCAAGATTAAGCCATTAAACTTTTAAAGTAAAATAATAATCATTTTCTTAATATCAAAAGCATATTAAGAAAATAAACTAAAACACTACTGTCACTTTATAAACATT |
| P42_Contig-1275 | *not applicable* | *not applicable* | 238 | 44.1 | TTCTTTCCCCAGTGTTCCTGGCATATATGGTTTTTAGACCACAATAAGTTCTTCAACAGCTACAGTTTGACCCGCAACTGCAGTTTGATCCGCAGCTGCAGTTGTCGCACTCCTGGTTGTAGTTCTTCTCGCAACTGCAAGAGTCACCGCATTTGCAGGAGGAGCCACAT |
| P42_Contig-1579 | *not applicable* | *not applicable* | 210 | 49.5 | GCATGGACCTGGTATTGGGGGAATGTTAGCTGGAGGGGCTGCAGGTGCGGCACTTGCTTATGGTGCTACTCATTTGTTACATGGAGGTTCTCATCACGGAGGTGGTCATTATGGAGGACATGTTGGTCATTATGGACATGGTGGTCATCATGGTCATGGCAAGTTCAAGC |
| P42_Contig-1912 | *not applicable* | *not applicable* | 283 | 44.2 | AGTGCAGAATCTTTTATTCGAATGACTATTCGGTTCCCGTTGTGTGCGATGACTTGGCATTCATATGGTCTTCTAAGCAGACGAACTAGTATTCAAGCTTGAGCCAGCATCGGTCCATCAGGTTTTGTCTGGCGCGTGTGGGAGTTATTGGTTTCGGTGGCGAATCATGTC |
| P42_Contig-262 | *not applicable* | *not applicable* | 511 | 52.4 | GTTGTTTTGCCCCTCGTTGCATATTTCCAAGGGTTGCTTTGGGCATAAGCCGCCCCGGAGCATCTCGATGACGGAATGTGCATTAGCGGAATAGCGTTCCTAAGAGTTGTTTCTCGTGTCCGCCCAGGTTCAACTCAATGATGGAACGCGCTGGGAGCCTTTGGGCTCC |
| P42_Contig-280 | *not applicable* | *not applicable* | 281 | 43.1 | GTTGATTGTCTGCTTGTGCAGGAACTGCCATGCGTTCTTACCTCTTCAATTGTCCCTTACGATGATTATATGGTGAAAACCACGAATATTTTTTGTACAAAACATTTTTAAACAATCATTTGGTGGGTTCATGATTTCGTATCGTGTGGTGCATTCTGGGGGTTGTTCTGTCT |
| P42_Contig-317 | *not applicable* | *not applicable* | 574 | 31.9 | TGAATTGTCTTCTTATGACTCATCAATCAGATAGATTCGTTTTTTGAAAGAACTGTTCAAGGAAAAAGCAACCCCCTCGCCCAGTACCAGTTCATCCTCAGACCTGCCCCCCCTCTTCTTCCATCAACTAAATGGATTCTGAGATCTTGTTCATGAGATTAAGAAAAAGAAC |
| P42_Contig-424 | *not applicable* | *not applicable* | 512 | 52.7 | TAACCGGAGTCCGCGAGGAGCCCGAAGGCTCCCAGCACGTTCCATCATCGAGTTGAACCTGGGCGGACGCGAGAAACAACCCTTAGGAACGCTATTCCGCTAATGCACATTCCGTCATCGAGTTGCTCCGGGGCGGCTTATGCCCAAAGCAACCCTTAGAAATATGCAA |
| P42_Contig-482 | *not applicable* | *not applicable* | 284 | 50.4 | ACCATATGAATGCCAGGTCATCGCACACAACGGGAACCACATAGTCATTGTGTGAATCCATGCAATCCACTGGTGTACGAGTACAAAGCATTTTCCACGAAATCTATCAAGCAGACATGATTCACTACCGAAACCAGCACCTCCCACCCGAGCCAATCACCTCCGTCCTT |
| P42_Contig-491 | *not applicable* | *not applicable* | 406 | 30.5 | CAAGATGAATTTCTATGTTAAGTAGAGTTCGTCGATGTATATCTATCGGATGTGGCTTCATGTACCAAATATTTTTATATCGACGCAGCCGGTATTTTTATTTTGGTTACCACGGTGTAGTGGAGAATGGATGCAAAAAAGAGACTTTGATTTCCAATCTTGTATTTTTTATT |
| P42_Contig-512 | *not applicable* | *not applicable* | 226 | 34.5 | ATATCTTAAAAAGAAAAATAGGATAACTCCCCTTTTCCTGGGCGGGTCAACAAAGTCATGAAATATTTCGATTTACTTTTTCTATAAAAAAATGGATTTACCTGGACTAATACATGATTTTCTTTTAGTTTTTCTGGGATTCGGTCTTCTAGTAGGAGGTCTGGGAGTGGTATT |
| P42_Contig-608 | *not applicable* | *not applicable* | 319 | 30.1 | TATTTTGTTGTGAACCGAGTAATTCATAGAATTGTTTATATCTAAAATAATAACATCTCCTTCCTTTATATGATCCCCTATAGTTATATACATACAAATAAATAGATTGACTGGAATTTCAGACATCGGCCCGACGATGATCCTTTTTTCAAAAGAGCGCAAATTTTTTTACGTT |
| P42_Contig-707 | *not applicable* | *not applicable* | 281 | 43.1 | GCCTACCAGACAACTACCCCCTCGGCAACATGCGTGAGAAAGCAATCATAAGACAGAACAACCCCCAGAATGCACCACACGATACGAAATCATGAACCCACCAAATGATTGTTTAAAAATGTTTTGTACAAAAAATATTCGTGGTTTTCACCATATAATCATCGTAAGGGAC |
| P42_Contig-807 | *not applicable* | *not applicable* | 321 | 46.7 | AGTGCTGAAAGCATATAGGCACGAAGTTTACTTTAAAATATTCTTAAATATACGTCAGAGAATACTACGAAAAATGGGGGGGGCTGGGGTGTTCATTAATAAATATTTCCCAGCGATCGATAAAAAAACTAGTTCCCTCGATTTATCCCCCCTTCCTTCGGCGGGGGGGATT |
| P43-2_Contig-43 | *not applicable* | *not applicable* | 213 | 31.9 | TGGAAATGTTATTTGCCTGTTTCAGGGTGCCTTTGTGCCAATTCTGTAGTGTTTTTTTAGATGTCCCAGTTAATGCATTCAGATCCAAAGCATCTACTTTCAAAAATAAATTGAAAAACTTTGTATCTGTGCCATACTTCTAAAATTGACTCAATACCACACTTACATTTTTA |

**Supplementary Table 6**. (continued rows).

| Contig ID[1] | Name of putative viroid-like circular RNA | Assigned strand[2] | Length (bases) | %GC content | Linear sequence |
|---|---|---|---|---|---|
| P43-2_Contig-60 | *not applicable* | *not applicable* | 213 | 32.4 | TCAATTTTAGAAGTATGGCACAGTTACAAAGTTTTTCAATTTATTTTTGAAAGTAGATGCTTTGGATCTGAATGCATTAACTGGGACATCTAAAAAAAACACTACAGAATTGGCACAAAGGCACCCTGAAACAGGCAAATAACATTTCCAAGTATGAACTAATTTTCATTGCTT |
| P44_Contig-12 | *not applicable* | *not applicable* | 686 | 55.8 | ATAAAATTGACTCGATGGCGGATTTCTTTGACTTGTGTGTCTGGGCTTTTGTACGTGCGGTGCATGAGTGGCGCTTGGCTTGTGGCGATTTGTTGGTTCCCTGCTCCGGCAGCGACAACATCTCTCCCTAGCCTTTTCATTTTGTGGCCGATGATGTCAATCGTCGGCC |
| P44_Contig-296 | *not applicable* | *not applicable* | 226 | 52.2 | CGACCGGAGTAGACCCTTAAACGAGTGGACGGGTCAACAAGGCTTGCTAGGCAAGAATTATGGCATGCCTAGCATGCCATAACGCTTGCCTAGCAAGCCTTGTTGACCCGTCCACTCGTTTAAGGGTCTACTCCGGTCGGAACGGATCAACAAGGCTTGCTAAGCAAGC |
| P44_Contig-44 | *not applicable* | *not applicable* | 733 | 29.7 | TGAATTTTTCTTAAATTTCCACGAATGGACTCTTATCAAAATTCAATTAGATAAGTTTTATAAGTATAATGGGGAACAGCGGATCCCTTTTGTTTCAATATTTCATTTCAAAATTCAAAGAAGTTTTCATCCCATCGAACTCTTTCGAGCATCTATCCACCAGCCAATCAATTC |
| P44_Contig-570 | *not applicable* | *not applicable* | 268 | 35.4 | AAAAAAAAGAGAGCCTAGCCCCTCATAGGATCCCCTATCTGTACATATATAAAAATGTCTGCACGTATATAACAAGCTTTGCATTTCTTTCAGGCATCCGCTACAGTCTCAATTTATTTTCAAATAGCCCATTTACTTAATATCTTATATTTACGCCTGCGCCTAAGAACCTT |
| P44_Contig-646 | *not applicable* | *not applicable* | 287 | 57.5 | GCTTGTGACTTGGTCGAGTACACCGAATGGGCCGCAGCCATGGGGTCGGGCTCCTGTGCGAACCGGTTGGCCTTGTGCCATCTTAGAAGTAGCACTTCCAAACGCGTGACATGCATTTCGCTCAGGGTGGTGGAGGCCCAAAGCGTTCGGATTTGCCGATGGGGATG |
| P44_Contig-89 | *not applicable* | *not applicable* | 348 | 39.9 | CCCATACAGAGGATAGGCTGGTTCGCTTAAAGAGAATCTTTTCTATGATCAGATCCAATCATGTTGTACATGAACAGGCTCCGTAAGATCCAGTCGAATGTGTGATTTTGCATAATATAATCTAGATTATATTATGCAAAATCACACATTCGACTGGATCTTACGGAGCCTG |
| P44_Contig-91 | *not applicable* | *not applicable* | 568 | 51.2 | CCAACCACCTATGGCCGTTCAGCTTAACCAAGATTGAGTTCCTAGCATGTATAGAACAACCTTTAGGTGTGGCTAGCCGTTGGGGGTGGGCAAACGAGCAGGTGGTGGGATAATCGGTTTTTTGCTGCTCGGGATCTCAATGCTCGTGTGCTCACGGCCCTTTAGCCTA |
| P44_Contig-93 | *not applicable* | *not applicable* | 686 | 56.0 | TGACATCATCGGCCACAAAATGAAAAGGCTAGGGAGAGATGTTGTCGCTGCCGGAGCAGGGAACCAACAAATCGCCACAAGCCAAGCGCCACTCATGCACCGCACGTACAAAAGCCCAGACACACAAGTCAAAGAAATCCGCCATCGAGTCAATTTTATGACCCAACTCG |
| P44_Contig-95 | *not applicable* | *not applicable* | 568 | 51.2 | AGCCACACCTAAAGGTTGTTCTATACATGCTAGGAACTCAATCTTGGTTAAGCTGAACGGCCATAGGTGGTTGGGTGGATGATGTGTTGTGTTTGAGGTTGGGCTTGATAGTGGTCAACACACAAGGATCAAGATCACAAGCAGCAAAAATCCGATAATCCCACAAGCTGC |
| P45_Contig-62 | *not applicable* | *not applicable* | 472 | 28.4 | TTTACTCCATTTCTTTATGTTGTCACATATAATCTCCTCATCATTTTATCCTTTAGGTTTAATTTAGAGACCGATTAACTTTCCCATAAGCTTAAGGCGAGGGGCTATCCCTTTTTCGTTACTCATGTCAGCATTATCACTTGGGTTATCATATATTTATTATTAAAAACAATA |
| P45_Contig-7 | *not applicable* | *not applicable* | 344 | 33.4 | GTACTATCTATTTAAAACCTATTTACCCAATGTTCCGCTACCCCATAAATAATACTTAAATAACCTTTAAGTATAGTAAACTAGGATTATACCTAATATAATTATTATGGACAAGGTGTCGGTGTTTTGTTTTAGATCCGTTATATCTTCGGCGCTTTTAACTAATTAGGTTAA |
| P46_Contig-1109 | *not applicable* | *not applicable* | 412 | 46.8 | CTTCGAATGGAATCTTAGCCCGCCTCACTTGACTGAGCATAAGCGAAGTCAAGGGATTTCCTTCTAACTAGTGGCTGAGAGTAAGCAAGCTACCTTCATTCAACAGATTTGTGGTTGAGTCAGCTCCGAGATGAGAAGGCGTCACATTCCCCTTCCACCTTCGCCTTTGA |
| P46_Contig-1196 | *not applicable* | *not applicable* | 214 | 37.9 | GTATGAGTTGATACCATCATTATCCGTAGGTAGAAACAGCCGGGGTGTGAATATATATATTTGTATATATGGATGCATGAGCCGGCATGTATGTTTGTGAAGTAAATAAAAACGGCCCCGACTCCATGTCCGAATAAAGTGGTAATAAGTCCTACAGGATCCGTGGGTTCAT |
| P46_Contig-1773 | *not applicable* | *not applicable* | 270 | 38.1 | GAAATCGTGATGAGAGTACCAATGAATCACTTCAACAAATCGAACGGTGTCACCCTCTTCAACTTGCACGATGTTCTTCACTTTCCTTCTCTTCAAACGTCTTCTTCTTCAAATCTGCTCTAGGTCTTCAATCTACTTGAAGCTTCAACTCCCAAGGATCGGATTAGCTCTT |
| P46_Contig-1815 | *not applicable* | *not applicable* | 349 | 50.4 | GGCCACTGCGCCACATGCAGTAAACCCCGATCACGGCAGGGTAGCATGTGGTTTGGCCCGATGATGGGGATCGATTGTTTTGATAAAATTTTTAGGCCACGTTGAAATTCGATTCAAAACATGAAATATCCGGAGGGCTCAGGTTGAGCTAGTGGGTGAATAGCTCGGAA |
| P46_Contig-227 | *not applicable* | *not applicable* | 768 | 35.3 | TTTTTTTATTTTGTAATTCTCTTCAATGCTTTTCAGTCTTCGTTGTTTTTCGGTTGCTGTGGTCCATCAACAAGTGTTTTAAGACGATTTTTTTGGAGCAACCATTCTATTCTAGAAGAGCAATGTATTTATTTTGCATGTGATCATCTTCAAGGAGAGCCAGAGCATGGGTT |
| P46_Contig-2778 | *not applicable* | *not applicable* | 266 | 39.8 | GGGCCAAGCTAAGGTTGGTCACTATGAAAACACGACAATGACTCGTCGAGCCCACAACATGCATCGGATAAGGGACGTCTTTTTAATGCTCTAGTCGAACTAAATCGTTAAAAGAGCAAAAGAAATACATTACCCAGCCGCATGCCAAGGCTCTAAAATCATTGTGGAGTT |
| P46_Contig-286 | *not applicable* | *not applicable* | 512 | 54.1 | CGTTGCATATTTCCAAGGGTTGCTTTGGGCATAAGCCGCCCCGGAGCATCTCGATGACGGAATGTGCATTAGCGGAATAGCGTTCCTAAGAGTTGTTTCTCGTGTCCGCCCAGGTTCAACTCAATGATGGAACGCGCTGGGAGCCTTTGGGCTCCTCGCGGACTCCGGT |
| P46_Contig-29 | *not applicable* | *not applicable* | 717 | 49.0 | TCTAAATCAGTCCCGAATCATTACCATTGCCCAAGCCCCGCTAGCAATCGGTAGTGCAGAGAATCAGTCGCTAAATCACGATCAAAATCACTACCAATGCCCAAGCCCCAGCTAGCAATTGGTAGTGATGAGATCAGTCGCTTTAATGAACTTGTTCGCGTATCGTTCGGT |
| P46_Contig-3866 | *not applicable* | *not applicable* | 354 | 37.6 | GTAAAGTAACTCGTGACCATGGGTGCACCCGCAAGGGTGAGAGGTGCCGGATCTTGGACTGTATCCGTTACTTTACCAAGGGGTCGCCACTGGTGAATTAAAAGGGAACTAAAAAGGGTTTAGTTAAATAGGGTCTTTAATCTGTAATGAAATTGTATGTGAGTTCCTCAC |
| P46_Contig-3877 | *not applicable* | *not applicable* | 200 | 38.5 | TCTAGACAAGTACGGAGTGTTGTGGAAAAGGGCGGAAGGATCTAGAAGACTCTAGCAAGGGGCTGCCCAGAAGGTTCTAGTTTTGCATCTAACTTAATAGTTTCTAGAATATGTCATGTAGTGTTATCTAGAAAATACCATGTAAAGTATATAGAAAGTATCATAGGAAAAG |
| P46_Contig-425 | *not applicable* | *not applicable* | 228 | 36.8 | AAGATCTTATCTGTCACCAAAGCATGTCAGCCATAAGGAAACACTGCCAGCACAAGTTGAGATAAAAAATTATAAAATTTTATGACAACGTAAAGCTAATGCATATTTGGCACAACGCAACTGATGAACTAAGAACGTACTTGTAACCACACCAAGGACCTAGATCTGAAAAG |
| P46_Contig-433 | *not applicable* | *not applicable* | 511 | 53.0 | TAACCGGAGTCCGCGAGGAGCCCGAAGGCTCCCAGCGCGTTCCATCATTGAGTTGAACCTGGGCGGACGCGAGAAACAACTCTTAGGAACGCTATTCCGCTAATGCACATTCCGTCATCGAGATGCTCCGGGGCGGCTTATGCCCAAAGCAACCCTTAGAAATATGCAA |
| P46_Contig-439 | *not applicable* | *not applicable* | 752 | 42.3 | AGTAAGCCATCATGGCTGTTAATATATACGAAAGACGGGAAGTATTCGAGTTTACTCAGGTACTCTTTATTGTTGCAATTGAGAAGAACTCCATATTGAAGACTCAGACACCAATCATGACTTTGAAATATACCAGAGAAAACACGAGCCTAGCCTGCAGATAATCAACCTT |
| P46_Contig-744 | *not applicable* | *not applicable* | 276 | 34.8 | CTAGTTAGTGAAATAGAGTCTAACGTGTGATTTCCGCCGAACATAAAGGAAAAGGTTCTTAGGTCTGTAGAAACGTGATATATGGATATTTGAATTTTAGCAATTGAAAAATAGATCAGGATCCGCCGGATGACTTAAATTTTAAAATGAAGTCGGCGGATCTATATGTAATAT |
| P46_Contig-790 | *not applicable* | *not applicable* | 409 | 38.9 | AACACCACCCTTTGGTGCCACCCCCTTGGTGTATCAAGGTCACGCGTTCCCTACGTGCCAAGATGAGGTTTCCCCTTTACTCTTTATTAGACACAACCATTATTAAAGTAAACCCTATTACTTTCCCACATACACAGTAAGCATAGCAATTCACACACATACCCAAAATAAT |
| P47_Contig-110 | *not applicable* | *not applicable* | 213 | 32.4 | TCAATTTTAGAAGTATGGCACAGATACAAAGTTTTTCAATTTATTTTTGAAAGTAGATGCTTTGGATCTGAATGCATTAACTGGGACATCTAAAAAAAACACTACAGAATTGGCACAAAGGCACCCTGAAACAGGCAAATAACATTTCCAAGTATGAACTAATTTTCATTGCTT |
| P47_Contig-82 | *not applicable* | *not applicable* | 213 | 31.9 | TGGAAATGTTATTTGCCTGTTTCAGGGTGCCTTTGTGCCAATTCTGTAGTGTTTTTTTTAGATGTCCCAGTTAATGCATTCAGATCCAAAGCATCTACTTTCAAAAATAAATTGAAAAACTTTGTATCTGTGCCATACTTCTAAAATTGACTCAATACCACACTTACATTTTTA |
| P48_Contig-10965 | *not applicable* | *not applicable* | 210 | 39.5 | TTAGGGACAATGGCCAACTCAAATATCATCTCGTGAAGGCACTAGATTTCCAGCCAACTAATAACACCCACATAAGCAAACTCATGAACATGGCAATTGCCAACCAATTACCAGCTCTAACATAACTGATGAACAATAAGCCATGTACCCAGGAAAGCATGACAGTTTCAAA |
| P48_Contig-1194 | *not applicable* | *not applicable* | 557 | 41.5 | AGACAGACCAAAGGAGAAATAGCCCAGACGCATACTCCAGACATAGAACACCTCAACATAATGCTACCGAAACAGCCACATCCATAATTGCATGAACATAAAGAGGAGAGCTACTATGACAACCATTTGCCACATAACACAGACGCCATGTATTTCAAAGCCAACCTGATT |
| P48_Contig-1198 | *not applicable* | *not applicable* | 220 | 32.7 | TATGAAGGTTTAAATTGAGATTTAAAGCTTTTAGAATGAATACCGGCCTTTTTTTGGACCAATATAAAGTTATAAAGGTGTAAATATAGTTTTTAAATAATTCTCAAAAAGTTAGACCCATTATTGGAGCAACGGAAACTTCGTCCAAACTACTTTGACCAAAACTGCCCAACT |
| P48_Contig-12185 | *not applicable* | *not applicable* | 231 | 28.6 | TATTTTCGAAGACCTCATATCATTTTCCGAGTGTTCGAGGCTTCTATTATTTATGTATGATTTTTTTTATCGTCCCCTTGTTTCGAATGGGTTTATAATTTATTAATTTCTAATAAATTCAAATTAGTGTTTTGTAACCCGACCAAGTTAAGAACTCAATTCGTTTATCCTTTCCT |
| P48_Contig-14867 | *not applicable* | *not applicable* | 229 | 51.1 | TTTCTTCTAGAGTACGGGAAACCGGCGTCACAATTACTGCTGCTCTCCTCGTGCTCGTCGGACTCGTTCGAAGATAACTCGGTGATTCCGCTCGAACCCGAGGAGGAGGAACTTGGCACGAGATTTAAATCAGCTCTTCTCTTCGTCGTCATGAAATCATAGAACACCGG |
| P48_Contig-1710 | *not applicable* | *not applicable* | 352 | 32.7 | AATCGTATGTCCTTTGTTACAACAATAATGACAAACAATATGAGGATTACTTTTCTTGTGATCCTTTTCAACAAATTTATACTTTTTATTTCTCGGTTTAAAAGATTTGTTGAATTTAGATGGATCAACCGCAAAAGTAATCTCCGGCTTGGATGGTTCTTTTAACTTCTCTTG |
| P48_Contig-19 | *not applicable* | *not applicable* | 589 | 40.4 | GAAAAAACTTGAAGAGAAGTACAAAAGAACTTGAGAAGACCCCCTGTAACTTCATAAGGAACAAGAAGACAGAACCAACAGAATGAACCCATCACCTACATCTATATTACAACGAAAAGCTGGTGAAAGAGATCAAAGGGAACAGACATCAAACCAGTACAGCCTTCAGGTC |
| P48_Contig-2 | *not applicable* | *not applicable* | 740 | 37.0 | AGAAAGAGACAGTGATTTCATTAAAAGTGTTTGCCATAAAAAGCAAAAATACAATAGCTGCGCCTGCGGCAAGGAATAGCACATGAATGCCTATTTCCGCGGCCCCTAAATGAAGATTAACATGAAGATTAGTTCCAACGATACACCATATAGGTAGCAAATATAAGAATTTA |
| P48_Contig-2199 | *not applicable* | *not applicable* | 430 | 29.1 | AAAAAGGAACGAAAAAAGTATAAGTTGATAATTCAAAATCAAATTATGAAAGATTTTGTTCCAATTAATTTAATTAATATAGTACAGTAATAATTCACTAATACAATGATTTCGAACTATATTTCGAATCACAGTACAGTATTTCATTTTTCATTTTAATATCTTGTATGATATTCT |
| P48_Contig-2443 | *not applicable* | *not applicable* | 201 | 58.7 | TTGCTCTGGCAAGTATCAGGGCTGCACCATGCCTCCCCAGTGCCGCAGTGGCCCCAGATACTGCAGCAAAGATTTCCGGGGCACGGACGGATTCGCGAGCACCTAAATGACTGCCCGAACTTGCCATCTATGGCGGATTTGGCCAACTCCTTTCCAGATGTGCCCTCC |
| P48_Contig-296 | *not applicable* | *not applicable* | 217 | 32.3 | AATGGAATCTTTCAACTAAAGCAATGAGATGCTTAAATGGAATTCTTTTAGTTCTAATAAATCAGGAGGAATTTAATGACAGGACATGAATTCAAGTCCTGGATTTTAGAATTGAGAGAGATATTGAGAGAGATCAAGTTATTTATATTATTCCGTAGAATAATACGGATCCAA |
| P48_Contig-3001 | *not applicable* | *not applicable* | 489 | 57.1 | GAATTTTCCATGACCCATGTGACCACCACCATGTGCATAGCCGCCATGAGCGTAGCCACCTTGTGGATAGCCACCCGGTGGATAATGGCCCTGAGCACCATGGGAGCCGTGGGAGATATGGTGAGCACCATAAGCAGTGGCAGCAGCAGCTGCACCCCCAGCAAGCAT |
| P48_Contig-3205 | *not applicable* | *not applicable* | 209 | 44.0 | TAACTATGCATTGGACGAGATCGAGGAGGTCAAATGAGCGCTTTAGATTTTCAGTGTAAATTGTAATTGTGTTATTTTATATTTCAGTCCCTGTGGTTGTTCTTCCCAGGAATGTGTATCATACTCTGATCTCTCTCGCTCTCTCTCTCTCTCTTATCTTTCTCCTTCTTTC |
| P48_Contig-3656 | *not applicable* | *not applicable* | 307 | 49.2 | ATCAAGTCACCTAAAGAAACGAGTCCCTCCACCTTAACAACCGCGTACGAGTGAGTCAAACTAGCAGACGCAAGCGACATATCGCCACGTTTGCAAAGTGATGGATTCAAATCACTAACGAGGCATGAGAGACCGGTCCGGACACGGGCATATCGGTAAGCAATTACAGG |
| P48_Contig-4757 | *not applicable* | *not applicable* | 438 | 48.4 | AAGCGATGATGACCCGAAGAGACCCAAATCGTGAAAGAGTTAGGCGAGAGCGTCGGCAAGTGTGGTCGCTTGTGGGAAACGTTGCTGAATGGAATTCGAAATCCTGTAATTGCTTACCGATATGCCCGTGTCCGGACCGGTCTCTCATGCCTCGTTAGTGATTTGAATCC |
| P48_Contig-5254 | *not applicable* | *not applicable* | 244 | 38.1 | CGCAAATGACCATTAATTTTTACTCGAGACTAAACGTTCAATTTTTACGCGAGGAATATGCTAAATGTTATGAAGCGCAAATAAAACTGTCATAGAAATAGCCGTTATCAAATTAATCCTTCAACGCGATCGGATAGATCGCAACGCGATCAGATAGACCGCAGATAAACATT |
| P48_Contig-5342 | *not applicable* | *not applicable* | 264 | 40.5 | CTATCCGATCGCGTTACGGTCTATCCGATCACGTTGATGGTTTAAGTGACAATATTTATGTATGTGACAATGTTTATCTGCGGTCTATCTGATCGCGTTGCGATCTATCCGATCGCGTTGAAGGATTAATTTGATAACGGCTATTTCTATGACAGTTTTATTTGCGCTTCA |
| P48_Contig-593 | *not applicable* | *not applicable* | 218 | 48.2 | TTGGGCATAGAAAGAATGATGCTCACCTTTTTCCGTTAATGACGCTACTCGGTAAATGATGTTGCCCTTGAGTTGAGTTGCTTGGTTGGCCAGATAGTCGTGGCTGTCCCTTCTCGGTAAACTCTCATTTGCATAGACGGGCTTGCCTTGCTTATGCTTTTGGGATGAGG |
| P48_Contig-711 | *not applicable* | *not applicable* | 583 | 39.5 | ATTGGGTTTGTTAACGGGTGCGCCTTATATGAGTTTTGGTAACGGTATTCAGGTTCTTTTTGTGTCACCCTCTATTCCAACTTATAGTTTATTTCGACTTAAAGGTATTTGTTATGGTGGATGCATGTGGTTATTGTGCTCTGTAGGTGGGATAAAGTATAACTAGATAGTAG |
| P48_Contig-9556 | *not applicable* | *not applicable* | 398 | 33.4 | TCAAAAAGGGGGAGAATGTAAGTGCACCAGTTCATCCTCATGTTTTAATAATTGTCAAAACACATGAAAATAGGTTGAACATATTTTGGCAAACTTTACAAATGACTTGACAACAAAGAACTATTTTCAAAACCTTGAAAAACTGACTTTTTGGTGTTTTGTATCGATACATAC |
| P49_Contig-133 | *not applicable* | *not applicable* | 213 | 32.4 | AGGCAAATAACATTTCCAAGTATGAACTAATTTTCATTGCTTCACCACCAATAACAATAAAAATGTAAGTGTGGTATTGAGTCAATTTTAGAAGTATGGCACAGTTACAAAGTTTTTCAATTTATTTTTGAAAGTAGATGCTTTGGATCTGAATGCATTAACTGGGACATCTAA |
| P49_Contig-41 | *not applicable* | *not applicable* | 213 | 32.4 | ATTCTGTAGTGTTTTTTTTAGATGTCCCAGTTAATGCATTCAGATCCAAAGCATCTACTTTCAAAAATAAATTGAAAAACTTTGTAACTGTGCCATACTTCTAAAATTGACTCAATACCACACTTACATTTTTATTGTTATTGGTGGTGAAGCAATGAAAATTAGTTCATACTTG |
| P49_Contig-91 | *not applicable* | *not applicable* | 326 | 25.8 | ATATATGTATAAAGATAAATAAAAGAACTAGGCAAAATCAAACTTCAACTGTTTAACAAAAACATAACTCAATGAATATTAATAATGAGCAATTTCTGCTCAATGAGCAATTAAATAGCCGCAGTATATTAACTGTGCTAAGGTAGCATAATAATTAGTTTTTTAATTAAAAAACT |
| P50-1_Contig-1102 | *not applicable* | *not applicable* | 214 | 30.4 | TAAAATTCCTCCTTCTTTGGATTTTTTATTCAATGATTAGTTGTTAATTAAAAAAACAGAAGTTTAGAAGTTTTGACTCTGATCTATGTAATATTGTCAAACTAAAACAAAAGGAGCCGATTAATACCAAGGCTTCCCTGAGAAGATTTTTAGACCACTACAGATTACAGAGAAA |
| P50-1_Contig-11245 | *not applicable* | *not applicable* | 288 | 51.0 | AAACTATAACAAAGGATCAAAATACTTGAAAAATGGGACGTTTTCTAGCTAGTTTCTGTTGCTTGTGTTATTTCCATTGCTGTTAATGTGGCTATTGGCGGAACTGCCGTTAGCCCCACCAATAATCGAGGTGATGGCCGCGGCGAGAGCTGCTGTGAAGTTGGGATCGGC |
| P50-1_Contig-1435 | *not applicable* | *not applicable* | 350 | 23.7 | AAAAAAAAAAGAAAAAGAAAGGGAAATTTTTGGAGTAAATACTGATGAACTTAAAAAAAACGATTTTAATTTTTTGAGATACTAAAATAAATAGAATAAGGTTCTATTAGTCTTTCTATTAGTCTAGAAAAAATGGGTATGATATTGGATCGATAGAAATTTAGAAAATATTATAGT |
| P50-1_Contig-14645 | *not applicable* | *not applicable* | 231 | 28.6 | TATTTTCGAAGACCTCATATCATTTTCCGAGTGTTCGAGGCTTCTATTATTTATGTATGATTTTTTTTATCGTCCCCTTGTTTCGAATGGGTTTATAATTTATTAATTTCTAATAAATTCAAATTAGTGTTTTGTAACCCGACCAAGTTAAGAACTCAATTCGTTTATCCTTTCCT |
| P50-1_Contig-1595 | *not applicable* | *not applicable* | 426 | 40.8 | TCAGAACTCGAAGTTGGTGCAGATGACAGTGTCTGAGTCTGCTCTTGTGGTGTCTCCGCTGAATACTCTTTAATTTCTTCTTGTCCTTCTGACATAGACTCTAAAATGGATTCAGAATCTTCTTTCTTGTCTTCATTTTCAACTGAAGTCCTTATTGCGTCCTGTGCTTCGT |
| P50-1_Contig-1800 | *not applicable* | *not applicable* | 261 | 35.2 | TGATCAATTGATTGAAGCAGATATCGTTAGTTGTTTCGATAATATAAAGCACGATAGTCTTTTGGATAGCATAAATCAATATCAAAAATTACCAGTTCGCTCAGGTAATTTTTGCTTTCCTTACAACATCTATCTTAGATAAAGATTGAAAAAACAACTCAACAAGAGGAGAAA |
| P50-1_Contig-2820 | *not applicable* | *not applicable* | 306 | 38.2 | TCGTTGATTAGGTCAAATTTATTCAAAATCAAACCGTGTCTTGTTGACTAGATCAAAATGACGCAGGACTCACCGTGTCTCGTTGATCAAGTCAAAATTATTCAGTACCCACAGTGTCACGTTGTTTAGTTCAAAATTATTCTGAACACACCATGTCTAGTTGATTAGGTCAT |
| P50-1_Contig-3249 | *not applicable* | *not applicable* | 234 | 52.1 | TCACAGTTTGGTTTACCGGACTGTGAAATCCGAAGTGCTCAATGACCCTAGCCATCATTTGGCTCGGCGAGGGTGCGCCTAACTACCCGAGTGTGCCTTGCACTAAATTGCCCACTCGACAGGTAGGATTTTGGGAAGCCCCATGTGCATGAGGCCTAGGCCTTGTGTA |
| P50-1_Contig-3293 | *not applicable* | *not applicable* | 349 | 38.7 | GACACGGTGTTATCCTAAGAAACTTTAAGTTAATCAACGAGACGCGGTGAGTTCTGACTTTGAGCTAATCTACGAGACACGGCGTGTTCAGAGTAATTATGACCTAATCAACTAGACATGGTGTGTTCAGAATAATTTTGAACTAAACAACGTGACACTGTGGGTACTGAAT |
| P50-1_Contig-3501 | *not applicable* | *not applicable* | 208 | 46.6 | TTGCGGCAGTTTATCGTCGTTGCGGGACCAAAGCTTCCTGAAGCTTCCACAGACAGTTCACCATATACTGACAGATAGCACTTACTTATCCTATAAATGCGCCCCATGCCTAGGAGGTAGTTAGAAGACACCGTTTGACTGCAATTCACAACCGGTGCCACCGAACTAAT |
| P50-1_Contig-3626 | *not applicable* | *not applicable* | 278 | 45.7 | GGCGTTTGAATTTTTGAGAACCTCGGATCGGGGAATTGTGAGAATTCGTCTCCGGGGAAATGATTTCAATACCTGGCCCGCGCGGATTGGGGAACTGTAAGGATGGTCTCTAGGTAAAACCTTTCCCTCTCGGGTCTGTGGCGCTTGATGTTTCATCGTGCAGTTAAATC |
| P50-1_Contig-3660 | *not applicable* | *not applicable* | 538 | 36.4 | TATATATCCTTAAATCCAGTATTTAAGATATCATAGTTATTAGTGATTGGTTTACAAAACGTATAATGTAGGTGTATTGAAGAAAGAAGACGAACTGTTAGGTTCGTTCTTTCATTAATTCCATTTGCGTTATAGTGAGCCTTATAATCGAACTAGTATGACTAGTGGTGCCCC |
| P50-1_Contig-3749 | *not applicable* | *not applicable* | 776 | 39.4 | TGGTACTTCAAAGAGAATTTTATAGAAAAAACAAAAAACAATGTATGTAATAAGCGACATCCCAACATTAATCAACAGGTAGACAGGCACTATGCAAAAATATACATTCTTCGAGGGGAGCGTATAAAAGACGGACTGATAACAGTAGCTGTAGAAACTAATAAATTAAATTAT |
| P50-1_Contig-3976 | *not applicable* | *not applicable* | 248 | 29.4 | CAACAATATGTGGTTCGCGAATATTGCTTTTTATTTATTCGTTGTTCTCTTTTTTTTTTTCGTGAATACTATCTATAATATTTTTACCTGATCTGATCCTCAGTTTCTATTCCGACGTTAATAATAGAGAAAACCTTTCTAATATTATATATTATAGTTCAAGTACTACTACATG |
| P50-1_Contig-3980 | *not applicable* | *not applicable* | 507 | 39.8 | AGATATTATTGGCCTATGATTCCAGGTTCTTCCTCTCGTATGCTGGTCTAAGCGGTTCAGGTTCTTTTTCTAGGCTATTCTTTTATTTGGGCACGTCGGCTTGGCCGGATGATAGCCTAGAGACGATAAGTTATGATTAGGTTTTATTTATTGAGGAGATAGCTGTCAGCGA |
| P50-1_Contig-4746 | *not applicable* | *not applicable* | 512 | 52.7 | AAAAAGACACGCCGGTCGAATCCTAGCAAGCGAGGTAACCGGATTTGTTGACGGTGTCGGTTGGCGGGCTTTGGCTTTTGCCAACCGATTTGAGGCGCGTTCGCGTGCTAGCGGCAGCTAATGTGGGTTTTGTTGTGTGTTCTCTTTGCACTTATCGACGCAGGCGTTT |
| P50-1_Contig-510 | *not applicable* | *not applicable* | 278 | 45.0 | GCCACAGACCCGAGAGGGAAAGGTTTACCTAGAGACCATCCTTACAGTTCCCCAATCCGCGCGGGCCAGGTATTGAAATCATTTCCCCAGAGACGAATTCTCACAATTCCCCGATCCGAGGTTCTCAAAAATTCAAACGCAACGGGCCAGGTAGTGTAAAAAAATCTCT |
| P50-1_Contig-5168 | *not applicable* | *not applicable* | 200 | 44.5 | ATCGATGCGAGTTGTTGATTTATGCCCTTGGTTTACCTTAGATCGGCCGACCCTGTCTTGTTTGGCATGGATCTGTTGAACAGCGTGTCAGATCTACATCTTTTGCTTGCCAGGGCTAAGGAGAAGGTTTCTTGAGGATTTTTAGCGTTCTTTGATGCTCATGATCCGGTT |
| P50-1_Contig-5369 | *not applicable* | *not applicable* | 208 | 46.6 | TCAGGAAGCTTTGGTCCCGCAACGACGATAAACTGCCGCAAGGAAATCCGCAAATATAAATCTGCGATGAGTGTCTTGCATTAGTTCGGTGGCACCGGTTGTGAATTGCAGTCAAACGGTGTCTTCTAACTACCTCCTAGGCATGGGGCGCATTTATAGGATAAGTAAGT |
| P50-1_Contig-6376 | *not applicable* | *not applicable* | 262 | 32.4 | TTTGGGCATGAAATAGTTTGAACTCAGAAATGATGAAATCATTTACGACTTTTATTAATGAAGGCATGTTGATCATTCGTAAAGACAATCCAATTGCATCACTGTTTAATATGTTCAGAACATATGAAGCAAAGGTTTTGAAAGTAAATTTGGTTTGATTAGACGTGCTGGGTA |
| P50-2_Contig-11765 | *not applicable* | *not applicable* | 236 | 54.7 | AATGTGGGCTGGGCCTCTGGTGCGCACCGGGCTATGGTCTATCACCGTTGGGCCTCTGAGTCACCGTGATTTACCCCTCACATCCTTTGCGGGGCTGTTAGGGTGTCGGTATTACACCTTTTGGAGTAATATATTTAGATGCCCGTCACGGGTAGCTCAGTGGTCGAGC |
| P50-2_Contig-13 | *not applicable* | *not applicable* | 268 | 25.0 | AAAGAAGTTCATGCGTTACTAATTGCTAATTAAATGAAATCCTAATTTGCTATACATATTAAAGTTTTTGGATCCATTGCACTCTTTTTTTACCTGAAAGAGTAATTCGAAACTAAAACTATTTGAAATCATTACAGTAAACAGATTTTCAATACAAATTAAGTTGGGATTTTCAT |
| P50-2_Contig-1352 | *not applicable* | *not applicable* | 625 | 37.4 | AATTTTTGACTAGGAATCTTCTTGCTGTGGCAGATCGATAGGGTTATTGGTCAATATGTGCGTGAAATCAATATTAGATATTATTATCCAAGCGGGTCATGACGACAATTCCAGGTTCTTCTTGTATGTTCTCATCTTCGATGATGGCTATATTTCGATAGCAAAGCTATATT |
| P50-2_Contig-2067 | *not applicable* | *not applicable* | 225 | 43.6 | GTCCCTCGGCTGATTTTTATTAAGTTAAGGGGGCCTTAGGCCTTATTCCCTATTGTATTTGTATTTGTATTGTGTAGTGCTTTTTTATTTTCTAAAGGTGGCCGACCCTCGGCAACTATTATTTCTAGTTTATTTATGAATAAAGGTGGCCATAGGCCCCTATGGTCCATTGGTGCCC |
| P50-2_Contig-2115 | *not applicable* | *not applicable* | 236 | 54.7 | GGCATCTAAATATATTACTCCAAAAGGTGTAATACCGACACCCTAACAGCCCCGCAAAGGATGTGAGGGGTAAATCACGGTGACTCAGAGGCCCAACGGTGATAGACCATAGCCCGGTGCGCACCAGAGGCCCAGCCCACATTAAAGCTGTAACCTCCACACGGTCGCT |
| P50-2_Contig-2942 | *not applicable* | *not applicable* | 220 | 37.7 | TTATGAGAACTTTTGATTGAGGTGATGCTATCTTCTTCCACTCATTTATCAAGTTTTGCCCGAGTATTAGAGTTTTGATTGATGAATGTTGACCTGCATTTGTTCTACAATTCCCGAGCTTCCGATTGAGGTGATATCTTCTACTCAGTTGTCAAGTTTGCCCGAGGAGTAT |
| P50-2_Contig-339 | plant associated viroid-like circular RNA 3 | (+) strand | 580 | 39.8 | TCTGTATGCCTGACTAGCTGACGAGATCAAAGTAGATCGAAACAGATTGGCATTACAGTTATGGTTATGTGGTTAAACCACCATAATCCAAAATACATAATGTCGCACAAGGCTATTCAGAATGAATATTATACATTTTGAAAGGCTTCACCTAATTGACTCTTTCGTTAGAA |
| P50-2_Contig-3505 | plant associated viroid-like circular RNA 3 | (-) strand | 580 | 40.0 | TTTCGATCTACTTTGATCTCGTCAGCTAGTCAGGCATACAGACTAGTACAGATAGGTGATATATGTTGGTTTATACCACCTTTCCAAATAAAGTATATGGTCTCACCTGCCTGTTATGGAATGTTTACAAACTTCCAAGGCCTTCCTTAACGTCGATCACGATGGACCCGTT |
| P50-2_Contig-3680 | *not applicable* | *not applicable* | 244 | 40.2 | TATAAATAGCCCTACGGTTTATTTCGTTTCTCACAACACGAAACACACAAACACACACACTAGACATATATATACACTTAGGCACTCATAAGCCTCTGAGAGGGCACGATAGGAGTCTGAGAAGCTTCGGCAAGGCTAGCAGTAAGTCAGGTGAGTAACACTAACCTTCTTA |
| P50-2_Contig-3933 | *not applicable* | *not applicable* | 355 | 36.3 | ACTTCATTCATGAGCCACCCAAAATCAATTTTCACATAGACATTCCAATAACTAGACTTATTACCAAGTAGGGAAAACTTAATTACTTCTCAAAGCTCTCTAGAAAAACATCTTCATCTCACAAGGAGAAGACATAAACTTGGCAACTTAAACACTGTTGACAGGCAATAATGT |
| P50-2_Contig-480 | *not applicable* | *not applicable* | 205 | 50.2 | TGTGACTTTAAGACCCAACCCCAAAGGTGTCAGGGTCGAACCTCACAAGGGAATACTTATTGGCCTTTCAATGTGTGAGTCAGTCAGCTATGGGCAACCTAAGCTGGTTTACCTCCTTGTGGTCCTTTGCCGGCTAGGGTCACCCGATATCAGAAGTGTGAGACCTTACA |
| P50-2_Contig-4989 | *not applicable* | *not applicable* | 220 | 50.9 | TAGGTTGCCCATAGCTGACTGACTCACACATTGAAAGGCCAATAAGTATTCCCTTGTGAGGTTCGACCCTGACACCTTTGGGGTTGGGTCTTAAAGTCACATGTTCGACCAGTCAAACTGGGGGATTTTCCCCCCTTGTAAGGTCTCACACTTCTGATGTCAGAAAGAAGT |
| P50-2_Contig-517 | *not applicable* | *not applicable* | 455 | 27.7 | CTGGACTACTTTATGTGGTTTTTTGTTATGGGTTATATTTGTCTAAGTTACGTTGGTTTTCTTTGTAAGGTTTATGTATTTTTCGAAATGTATGTTTGGTTTGTAATTTCAAAAAAATTCTCAATTACTAAGCTCAGTTTGGGTCTAAAAAAATGATATTCTTTTGCTTGGTAAA |
| P50-2_Contig-551 | *not applicable* | *not applicable* | 340 | 38.2 | GGAGAGGAAAACAGAACACCAAATCATCACAGCCTCTCGTCAGTCGTCACAGTTTTCATATATATATATAATACTCCCTCCGTATAATGAATTCCATAGTTAAAGGCGCAGATTCAAAGCTCAGAAAGAAGAGCAGAGGATGAAGCTTGAGCTTTTGCAAACGGAAAACTGCTA |
| P50-2_Contig-5582 | *not applicable* | *not applicable* | 377 | 32.6 | TTGAAAAAACTGTTCAAGGACCAAGCGATACCCCCTCTCAATATCAATACCACGGATCTTCAGACCTATTCCCATTCTTATTCCAGTAACTAATGTTATTCTTAGATCGTGTTCGTAAGATTAAGAAAAATTCTTCTAATTTCTATGTATACTAATTATATTCATTAGAAGTCT |
| P50-2_Contig-564 | *not applicable* | *not applicable* | 210 | 50.0 | GGCTTCCATGGCTAATTGAATTCTCATAGCCATGGATTTTTGGGCTTCCATTGCCATGTGGGCTCCCATGGCCTTGTGGGCTTCCATGGTTGATTGAGTTTTCATAGCCGTGGGAATTACCGTAGCCATGTGAATTTCCATAGCCTTGTGGTTTCCCAAGAGCATGTGGA |
| P50-2_Contig-587 | *not applicable* | *not applicable* | 386 | 41.7 | GCTCTAAATTCATGGTCGGGTTCTCATAGTGGCCACAACAACACAATGACTCGTCGAGTCCCCAACATGCATCTGATAAGGGACGTCTTTTTAATGCTCTAGTCGAACTAAATCGTTAAAAGAGCAAAAGAAATACATTAGCCAGCCGCATGCCAAGGCTCTAAAATCATT |
| P50-2_Contig-6442 | *not applicable* | *not applicable* | 251 | 32.7 | TATAATAGTTCAAATCAACATTTTATATTTTTAAAATAACTTCAACATCATAATTATATATGCATAATGTTATACCAAATCAGAAACGGCCAGGTCAGTCAAGTCGGGAGGCAGGACGATTTCGGTTTATAACCTTTCTCAAGTCCAGCAACCAAGCCGATCATGCTTTCCTA |
| P50-2_Contig-6677 | *not applicable* | *not applicable* | 204 | 50.5 | CTCTCAAGTTACCAACAACTACAGCGCTTTACAACTACACCTCGCAAATCTAATGCAACAACAGAATCAGCAAAGTACACAAGATTGCGAGGTTGTTGAAAGAAAATCCGAGGAGAGAAGAAACCCGAGAGAGAAGAAACCACCGTGCCGAGACAGTTTTTGGAGTTGGTACC |
| P50-2_Contig-711 | *not applicable* | *not applicable* | 342 | 42.7 | AAGTAGCTACTAACGTGAATGGCGAGGAACTCACGATTTCCTTACAATCAATATTACAAGTGGCTAACACATTACACCTAATTTCATCGGTAGTCACTCACTGGTACTATAACGGATACAGCCCGAGAGTCTCTCCCTACCGGCCCTCTAACACCATATAGATGTTCACCC |
| P50-2_Contig-8145 | *not applicable* | *not applicable* | 302 | 39.4 | AAAACCAGCAAGAATCGCCTCCCTCGGTATTTAAATGCAAGCAGTAGCCCAGATCCTGCATCACAACACACAAATTGTCAAGTAGAACCATTATAAAATAGGATAATCAATAGGCCAGGGGAAGCAAGCTAAGTTCTTATTGTAGGAAAAGGACAATAGTGTTACTTTCTTA |
| P50-2_Contig-8494 | *not applicable* | *not applicable* | 282 | 31.6 | ATAATTTACACTAATATATTTTATATATCTTTTGAGAGGATTTTTTTATTAGAAGTGGTGTACAGGTGAGTAAAGGATATTTTGGCTACCTTAAAGTGAGGTTAATAAATGCCTTATGGTTTTTAATCTGCCTGATGAGATCTAATATAAGATCTTTGCCTATGCGCAAACTTC |
| P50-2_Contig-8497 | *not applicable* | *not applicable* | 270 | 53.0 | CACCATCATCATCACGCCTCTCGTAGCTAGGCTTGCGATAACCTTCACTCTCCTCAGTCTCGTAGCTTGAACGACCATAGCTAGGTTTTCTTCACCATAGCTTGGCTTCCGACCATATCCACCCGATCCATATTCCGATTCGGATTCGGTACGACGCCCATAACCAGAT |
| P51-1_Contig-166 | *not applicable* | *not applicable* | 213 | 31.9 | AGGCAAATAACATTTCCAAGTATGAACTAATTTTCATTGCTTCACCACTAATAACAATAAAAATGTAAGTGTGGTATTGAGTCAATTTTAGAAGTATGGCACAGATACAAAGTTTTTCAATTTATTTTTGAAAGTAGATGCTTTGGATCTGAATGCATTAACTGGGACATCTAA |
| P51-1_Contig-52 | *not applicable* | *not applicable* | 213 | 31.9 | ATTCTGTAGTGTTTTTTTTAGATGTCCCAGTTAATGCATTCAGATCCAAAGCATCTACTTTCAAAAATAAATTGAAAAACTTTGTATCTGTGCCATACTTCTAAAATTGACTCAATACCACACTTACATTTTTATTGTTATTAGTGGTGAAGCAATGAAAATTAGTTCATACTTG |
| P51-2_Contig-347 | *not applicable* | *not applicable* | 213 | 32.4 | TGGAAATGTTATTTGCCTGTTTCAGGGTGCCTTTGTGCCAATTCTGTAGTGTTTTTTTTAGATGTCCCAGTTAATGCATTCAGATCCAAAGCATCTACTTTCAAAAATAAATTGAAAAACTTTGTATCTGTGCCATACTTCTAAAATTGACTCAATACCACACTTACATTTTTA |
| P51-2_Contig-698 | *not applicable* | *not applicable* | 213 | 32.4 | AAAACACTACAGAATTGGCACAAAGGCACCCTGAAACAGGCAAATAACATTTCCAAGTATGAACTAATTTTCATTGCTTCACCACCAATAACAATAAAAATGTAAGTGTGGTATTGAGTCAATTTTAGAAGTATGGCACAGTTACAAAGTTTTTCAATTTATTTTTGAAAGTAG |
| P52_Contig-1398 | *not applicable* | *not applicable* | 337 | 43.3 | GTGCCATGTTTGAGGTTTCACCATTCCTTTATTACACCATATTCATATGTAAACAACCCACATTATCAAGCATAGCAAGCATACACACATTCAACATCAAGAGCATACATACACACTACAAGCAACATTACAAGTAACTACTAACGTGAATGGCAGGGAACTCACGATTTCAT |
| P52_Contig-1551 | *not applicable* | *not applicable* | 274 | 46.0 | AGCGCTTACCAAGTCATATTACCTTACGGGAGGACATGACAAGTACCAAAAATCTTACCCGGTAAGAGCGAAGACAAGAAAAACAAGGACCAAGAGTCTTACCCGGGTAAGCAATTACGACGGATCTTACCCCGGTAAGCGCTTACCGGGGTAAGATCCGTCGTAATTGCT |
| P52_Contig-2314 | *not applicable* | *not applicable* | 471 | 31.8 | TGAAGTTTTCTTTTTATCGGAATCGGAAAGAAATAGAACAAAAATGGGCAAAAGGAAATATAAGAAAGATGGCGAGAAAGAATAAAGTATAAAATAATAAAATATAGGATACTATAACAGTTTAATGCACATATAAGAATACGTAAAAATATTTATTTTTAGAAATCTCATGAACA |
| P52_Contig-2391 | *not applicable* | *not applicable* | 512 | 53.1 | AAAAAGACACGCCGGTCGAATCCTAGCAAGCGATGTAACCGGATTTGCTGACGGTGTCGGAGGGCGGGCTTTGGCTTTTGCCAACCGATTTGAGGCGCGTTCGCGTGCTAGCGGCAGCTAATGTGGGTTTTGTTGTGTGTTCTCTTTGCACTTATCGATGCGGGCGTTT |
| P52_Contig-2465 | *not applicable* | *not applicable* | 207 | 43.5 | AAAATAAATAAAATACTGGTCTGAGACTGTTAAGATGCCCTGCGCCACATCAGCATCTGATTCGGGATTAGTGTAAAAATGGTACTTGATATATATGTATATAACGGTGGATGGAGGGGTCACGAGGTTCAGATGTTACCACGTCAACCTCTGGATGGAGACGTCACGAGCT |
| P52_Contig-2468 | *not applicable* | *not applicable* | 282 | 35.5 | AAATTGGGATTTACAAATTTCAGCAAAATCACCTCCTTTACTCACTCTGAGAGTTCAAATTCAAAATTAACACACCCAAAATTCGAATTTATAAAATTTCACTCTGATTCGCAATGACAATCTTGACTAATCTAATTGCAGCAGCAACGAGGAAGGAACGTTTTTCAGTTGGAC |
| P52_Contig-247 | *not applicable* | *not applicable* | 681 | 32.3 | ATTTATTTGTGTATAAGCATCCATTCGACAATTTAGTGAAATATCGATCTGATATAGGTCAACATAGATATTCAGTAATGGTATGGATCATACATGATATATACTTAACTTATCCATCTAGATATATAGCCTTTCTAGATGAATAAAGAGTTTATGTTATAAAAGTTTATGTTGA |
| P52_Contig-467 | *not applicable* | *not applicable* | 269 | 37.5 | TATGAAAAAACCCTCCCAATCTATACAGACAAATTAATCCACACAGACAACTTTATTCATACAGGACTTAATGGAAAACCAACCAAACAACCCCTTAATGAGCTTAATGGGACTCGCAACTTATTTGGTCAGCTATACATGACTATTTGGTAGTGGCTTAATGATATAGAAAAT |
| P52_Contig-5322 | *not applicable* | *not applicable* | 337 | 43.0 | GGTGAAACCTCAAACATGGCACGTAGAGGACTCGTGACCATGGGGCCCCTTCTGGGGTGAGCATCTATATGGTGTTAGAGGGCCGGTAGGGAGAGACTCTCGGGCTGTATCCGTTATAGTACCAGGGAGTGACTACCGATGAAATTATGTGTATAATGTGTTAACCTGCT |
| P52_Contig-560 | *not applicable* | *not applicable* | 221 | 24.4 | TTAATGCCATTTTATATGAGCGAATGTGCCCATACTTGTTCATCATTAGAGGACACTATTCGTAATAATTTCCCTTATTTTTTCTAACTTTCTTTATAAATTTTTCTAATTTATGAATAAAATATGATTAGGATAAAGTACAATATTATAAAGATAATAAAGGCTTTGTTACGTT |
| P52_Contig-625 | *not applicable* | *not applicable* | 320 | 50.0 | CAACAATTAGCCACCCCTTGGCAACAAGGCCATGAGAGCAACCAAAAGCCAAAACAACCCCCAAAATGCACCAAACGATACGAAAGAACAAACAGAACTAATGTGCATCACGCCCCGATCCTTGGCACAAGCAATGCTAGCCAGGCTTATGCAACTGGTTATGCTTTAGAT |
| P52_Contig-803 | *not applicable* | *not applicable* | 782 | 37.9 | GATGGTGGTAAACGTCTAGGGTAATAATTGAATTTTTGACTAGGAATCTTCTTGCTGTGGCAGATCGATAGGGTTATTGGTCAATATGTGCGTGAAATCAATATTAGATATTATTATCCAAGCGGGTCATGACGACAATTCCAGGTTCTTCTTCTTGTATGTTCTCATCTTCG |
| P52_Contig-99 | *not applicable* | *not applicable* | 411 | 45.7 | CATTCATTGTCGAAACATTGCTTCGTAGTAGCATTTGAAGGCTGCAATGCAGTTCGGAGGGTGGAGTCATCCCTACGTAGTGCGTTTATATATACTTTCCCTCAGTTTGTATAAATACTTGCACAGGCGGTGCTGGTGTTGCCTCTTTGCCCGTAGCATATAAGATCGTGG |
| P53-2_Contig-1 | *not applicable* | *not applicable* | 397 | 51.1 | CGTTTTGCTTTCCGACCCTTCGTCGTCCGAAGACGTCAAACTACACTCTCAATCGCTAGTGCTGAGTTGGTAGTATTGCTAAACTGCCTGAAGTCCCTAAACGTGTTTGCGCGGGGAACGGGTTGTCCAGCCAGCTTACGGCTAAAAGGTCAGTCGTGTCTTTCACGCC |
| P54_Contig-1214 | *not applicable* | *not applicable* | 222 | 30.6 | TAAATATAAGAAAAAAAAAAAATTGACTGGATTCTTTTTTCTGGAGTTGAAACTATCGAGTGCAAAAAATTCAGTTCTTACAAATAAATACTCAATACCCAAGTAGGCTTATAAAATAGATCGTGATATGATCAATTGCTTTCTGGGTCGTCTCAGGCTTTACGATTACTATGTT |
| P54_Contig-1568 | *not applicable* | *not applicable* | 734 | 38.6 | GCAAAACCATGAATCTCAAATTTCCTGTCATCAGCTGGGCCAAACAGATACGTTTGCTATATGATTTATTTCAGCAAGAAAAAAGGAGAAAAGCCCGACAAACCACAACTCTTCAGTGTCGCCAACAAAGAACCACCAAACGCCGACCTCTGAAAATTGAGGAGCAAAAGAT |
| P54_Contig-1733 | *not applicable* | *not applicable* | 244 | 51.6 | TGGACAAAGGCCACCAACGACCACAACAAGCTCTAAGAACCACAAGCGGAGGTCAGCAACGATTGTCACCGAAAAAGTCCCGCATCGGTTCATAACCAACAAAAAGATAGCATCGACAGCGAACACGACTCCAGGCCGCGAACAATTACGTCATGATGCTAACCCCGTTT |
| P54_Contig-180 | *not applicable* | *not applicable* | 761 | 38.5 | TCCCAAAGCAAAGCAAAGAGCTCACACCCAGAACAATTCCAATAATAATCTAGATCACTTGCACAAAGCTGCAGATCCAATGAACAGATATAAACGAAGAAAGAAAATTAATAGTACCGGGGACTATATAGAGACTGAAAACCATCTTTCTTGTCCATCAATTCCAGTTTGCA |
| P54_Contig-2005 | *not applicable* | *not applicable* | 343 | 44.0 | CCTTAACAGTAGAGAGAGCTCTTTCTCACCAGTGAGGGCTAAACAGAGTTCATCATCTACGAGATTGTCTCATCGTCATCTACGAGATTCGAGTTAGTCCGTTGTTGTTCTCTCTTTTAGTCGTATGTATTCTTTTTCTCTTTTAGCCTATGTTCATTTCTATAGTAAGCAA |
| P54_Contig-2409 | *not applicable* | *not applicable* | 483 | 38.7 | TTCTGTCCATGAACTCATTTGATATAAACATTTTCTATGATGTTTTAAGATAAGCTAGAGCCGAACCCGTAAGCATTTCTTCACGTTTTTGATTCGGGCCTTTTATCGAACAGTTGGCGTGCACGTTTTGTTCAGCATTTTCGAACCCTTTCCCGACTCTATCTCATTTCGA |
| P54_Contig-2942 | *not applicable* | *not applicable* | 220 | 37.7 | TTATGAGAACTTTTGATTGAGGTGATGCTATCTTCTTCCACTCATTTATCAAGTTTTGCCCGAGTATTAGAGTTTTGATTGATGAATGTTGACCTGCATTTGTTCTACAATTCCCGAGCTTCCGATTGAGGTGATATCTTCTACTCAGTTGTCAAGTTTGCCCGAGGAGTAT |
| P54_Contig-3019 | *not applicable* | *not applicable* | 255 | 46.7 | CGATTACAAGCTTGAAGTTCGGGTAATCCACAGTCTGCTGATTCGGCAAAGCCATTCGCTTTCTGCTTTACTGATTGAAAGACAAACAGAATCTGAGGAGAGAGAAAGAGAGGAGAGAGAAGAGAGAGAGAGAGAGGGATACATTCATCATACATCGATTCAAAACCCTAACCCTA |
| P54_Contig-3125 | *not applicable* | *not applicable* | 265 | 40.0 | AGTCTGTGTGTGATTAGATTGTGTTTTGTGTGTAGGTTCTGTTGCTGTCAAGCACCATGTCCAGGCCATTTGCTGGTTTTTCTATAATTTCTATGATCGTCTTTTGTTTTAGCATTAATGTTTCTTATGGTAGTTGTCTTGGGCTAAACTATGTTCCCCTTGCTATTTGAAAC |

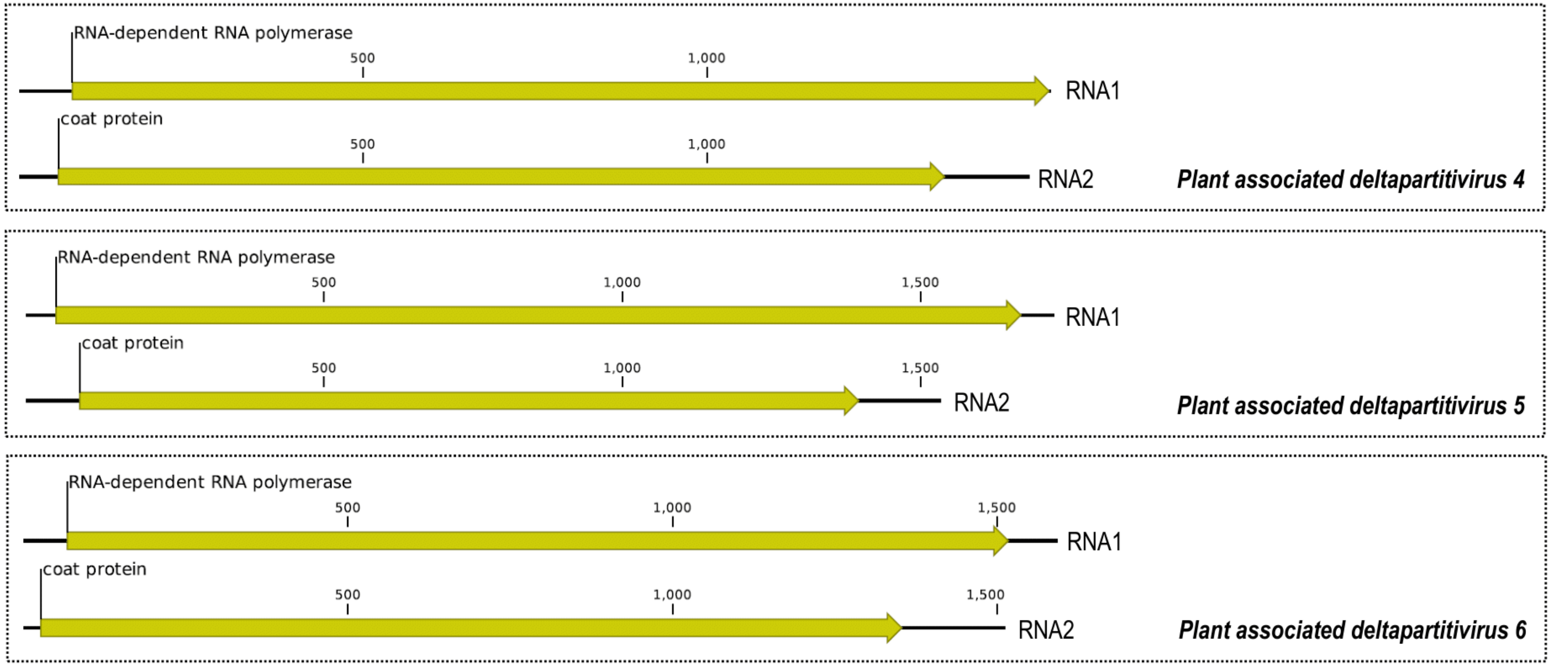
**Supplementary Table 6**. (continued rows).

| Contig ID[1] | Name of putative viroid-like circular RNA | Assigned strand[2] | Length (bases) | %GC content | Linear sequence |
|---|---|---|---|---|---|
| P54_Contig-3295 | *not applicable* | *not applicable* | 220 | 39.1 | GTAGGAGTGATCTTTCTGTTTTGAAGGACTAACATGTTCTAGAGTTGATCTTTATTTATACATCACTTTTGTACTAGAATTTTCAATATTTGGGCCTGTCTTTGTCATCTGCCGGATCAGATCAGTGTGACTATTACAATCCTGTAGTCCTATGTAGTTCTATAACCACTGAT |
| P54_Contig-3590 | *not applicable* | *not applicable* | 231 | 42.0 | AAAAGACGATCATAGAAATTATAGAAAAACCAGCAAATGGCCTGGACATGGTGCTTGACAGCAACAGAACCTACACACAAAACACAATCTAATCACACACAGACTTGCACAAAGAAAATGGAGATATCAAAGATTAGGCAAAATAGCGGGCAGGGAAGAAAACACGTGTGCC |
| P54_Contig-375 | *not applicable* | *not applicable* | 740 | 39.6 | ACAGAGAAAGAGCCGTACCAATTCAAATAGAAACACAAGCGACCAGATTTGTAGAAGTTTCAGACTTAAGAAGCACCCCACGAGGATTAGATGCAACTGCCCACCAAATATCATGATGAAGGATAGTAGATATTGAAAATAACCTTGATTTACTTCGCCTGCAGAAAACCG |
| P54_Contig-4353 | *not applicable* | *not applicable* | 254 | 46.1 | GAAAGGTGGAAAGCGGTGCTGCGTAATGGCTAGAGTCACGATTATTTCAACTAAATCTGCAAGTCCCTCTGACAAGGGCCCTCTTCCCAGAGACGGTTCTAGGCCGGTGGCAGATCTTGGTTAATGGAATATCGATTACTGGCTTTAGTCGCGGATAGAGTCAGATTGCT |
| P54_Contig-45 | *not applicable* | *not applicable* | 389 | 46.0 | TGGGTTCTGGTAGGCAAGATACCTTTTGTCAGGCAATCCAGTAGATCCTTCTTTCATCGAGTCACAGGCAAGCAGACTAAGAATCAGGTATGGAAGGAAGTGAAGGTGAAGCAGACTTTCTTTCTCGGTCCTAATCAACAAGGGCAGCATGGATATAGTTGCTCGTAGTAG |
| P54_Contig-467 | *not applicable* | *not applicable* | 314 | 43.3 | CTAAGCGTCTTCGCTAACTCGCTCGCCTACTATACAATACATTAAGTAGGGTAGGCTAACTCAGCCGCTTACTTATACTAATGTAGGGCTAAGTAGCCGCCTTTTGAATTGAATCTTAAGTAGTCTATCAGTGGTGCAAAGCTAATTCTTTTCAGTAGGGGGCGAAAGGTT |
| P54_Contig-5055 | *not applicable* | *not applicable* | 301 | 38.2 | AATATAAAGCAATCCCTCCAATCGGAATCGAAAGCAGTACAATTGCTGCGCTTACGCCTTTTATTGGCATTCAAGCAAGAGCTCCGAGCCTATCAGCAAAGATAAAAGGTTTTCTTTTAAAGCTATGGAGTGAATTCATAATTCAAGAGGAAAGGATTCGTTGTTAGGAAAG |
| P54_Contig-5090 | *not applicable* | *not applicable* | 220 | 39.1 | CCACAAGCAGGCATTTTACAAGCATTATCAGTGGTTATAGAACTACATAGGACTACAGGATTGTAATAGTCACACTGATCTGATCCGGCAGATGACAAAGACAGGCCCAAATATTGAAAATTCTAGTACAAAAGTGATGTATAAATAAAGATCAACTCTAGAACATGTTAGTC |
| P54_Contig-729 | *not applicable* | *not applicable* | 222 | 38.3 | TCTTTGATTACGATTAAAAGAGAACCAAAACACATTTTTTTGTACTATCGCAGTCTCGACCAAAATTGTTTCGGCGCCGGATTTTCAGGACAACCCTGAAGACCTTTTTTAAGTCCGTTATAGAAAAAAACAATGAATTTGCAGCGATATCTCATTTCTTGGAAGCTACTATA |
| P54_Contig-7327 | plant associated viroid-like circular RNA 4 | (+) strand | 274 | 63.9 | TTAGGGAATAAGAATGCAGGCGCTTGTTCGTCGGCCCCCTATGTTAATGTCCGGCCTCGCGCCTAATGCGTCACGTCGGGAGCTGTAAGCGTTGGTTGTGTGCTAGTGTCGGCCTCTAGCCGGGGAGAGCTGCAACGCAGGAGCGTCGGCAGCCCCGATTGTCCCGA |
| P54_Contig-7860 | plant associated viroid-like circular RNA 4 | (-) strand | 274 | 64.2 | GCCGGCAGCGGGAGCGGTGAGGTCGGGACAATCGGGGCTGCCGCCGCTCCTGCGTTGCAGCTCTCCCCGGCTAGAGGCCGACACTAGCACACAACCAACGCTTACAGCTCCCGACGTGACGCATTAGGCGCGAGGCCGGACATTAACATAGGGGGCCGACGAACAA |
| P54_Contig-964 | *not applicable* | *not applicable* | 363 | 33.9 | TTAAATACCATAAGCTTAAGGCGAGGGGCTATCCCTTTTTCGTTACTCATGCCAGCATTCTCACTTGGGATATACTGGACTAGCGCTATTTAGCGCTCAAACTACGTTGTAATTATCTTAAAACTTATGTACATCAACTCCTAGCTATTATTTACTAATAGTAGTGCTTTTT |
| P55-3_Contig-167 | *not applicable* | *not applicable* | 213 | 32.4 | TGGAAATGTTATTTGCCTGTTTCAGGGTGCCTTTGTGCCAATTCTGTAGTGTTTTTTTTAGATGTCCCAGTTAATGCATTCAGATCCAAAGCATCTACTTTCAAAAATAAATTGAAAAACTTTGTATCTGTGCCATACTTCTAAAATTGACTCAATACCACACTTACATTTTTA |
| P55-3_Contig-225 | *not applicable* | *not applicable* | 213 | 32.4 | TCAATTTTAGAAGTATGGCACAGATACAAAGTTTTTCAATTTATTTTTGAAAGTAGATGCTTTGGATCTGAATGCATTAACTGGGACATCTAAAAAAAACACTACAGAATTGGCACAAAGGCACCCTGAAACAGGCAAATAACATTTCCAAGTATGAACTAATTTTCATTGCTT |
| P55-3_Contig-40 | *not applicable* | *not applicable* | 256 | 30.1 | TTGGTTAGATCCATTAAATTAACGTAAACCCTTGCTTTATTTAATAATACATAGAGTACTTTTCCAATAATTATTGGAAAAGTACTCTATGTATTATTAAATAAAGCAAGGGTTTACGTTAATTTAATGGATCTAACCAAAGTCTCACGACATTAACTAAAGACAGCCGTGCAAC |
| P56_Contig-1040 | *not applicable* | *not applicable* | 355 | 53.0 | TACTAAGTCACGTCCTTCCGTGGCCCGCAACCTTTCTTTAGGCCTCAAGCGTATCTCAACCGAAGGGACCATCGACACGAATCAGCCCGCGTACTGAACCACGTCAAGAAAACCCGTCATGCCGCCTGAGCGGGTAGCCGGAGATCACGAGACGCAACCTTTCACACC |
| P56_Contig-10402 | *not applicable* | *not applicable* | 225 | 64.4 | CCGCCGCAGAGAAAACAGAGGAAGTGACCCCGCCGGAAACAGAACCATCCAAGGAGGCAGAAAAGGAGGAGGAGAAATCCGCGCCACCGCCCACGGCGGATCCCACGGCGGAGCCGGCGGTGGTTGTGGAGAACATCGACGAAAAGACCGTCCCACCGGCGGAGGAA |
| P56_Contig-1052 | *not applicable* | *not applicable* | 248 | 37.5 | AACAATTGAAGGATCAAATCGACGAAAATTGACAAGTAGGGACCAAATTGACGATCATGCAACAATTGAGGGACCAAAATAGCGATTATCCATAGTTTTTTGTTTTTGGTTATCAGAGCCATTTTCTTAGTCACAGATCTATGTTTATGAAGTGAAATTGATGTTGGAAATGA |
| P56_Contig-1170 | *not applicable* | *not applicable* | 210 | 46.7 | TCTCCTCCCCCACCATCTCCTCCCTATTCCCCCCCCTATATATACTCATCTCCACCTCCACCACCATATCATTACATATCTCCACCTCCACCTAAAAAGTCAAATCCACCTCCTTATTATTATAAGTCACCTCCACCACCACCAATGCATTCTCCACCACCTCCACCAAC |
| P56_Contig-1276 | *not applicable* | *not applicable* | 482 | 35.1 | TATAAAGACAAAAATGCCCCTGCTTAATTGAATTGAAGGAGGGCAATTTTGTCCATAAAGCCCTATCTTTTCTTCCCAAGTCCATGGGAATTCAAATACCGGAGATGTGAGATTTGAATTCTCATGAAATGAGGGAATTGCAATTCCCTCATTTCATGAGAATTCAAATCTCA |
| P56_Contig-1539 | *not applicable* | *not applicable* | 206 | 50.5 | GGCATGGACCTGGTATTGGGGAATGTTAGCTGGAGGGGCTGCAGGTGCGGCACTTGCTTATGGTGCTACTCATTTGTTACATGGAGGTTCTCATCACGGAGGTGGTCATTATGGAGGACATGTTGGTCATTATGGACACGGTGGTCATGGCAAGTTCAAGCACGGGAA |
| P56_Contig-1566 | *not applicable* | *not applicable* | 215 | 36.3 | GTTAGCATTTAGAATCGAAATGCCAACTTGAAATGCTGGTCAGGGCAGAATCTCAAAAAACAGCATTTGGGATCAAAATACTGTTGCGAAATGCTATTTACCAAACACCAATTTTAGCCGCTGACTGCTAACTTCTAATTGCCAAACAAGTCCAAAAGTTTAGCTGATAGTT |
| P56_Contig-157 | *not applicable* | *not applicable* | 462 | 37.0 | AACCCACGGCAGTTGGTTTCTTTATCCAGATTTAATTGTTAGACTTAACATGGAATGAAATAAAGGGAGAAAATCTAAGGAAAACATTACCTCAAAACATACATAGAAATAAACACCTTGTAGGTCAAAATCAAATAGGACATCTACTGTTCCTTCATGTAAGTTGGCCATTA |
| P56_Contig-2 | *not applicable* | *not applicable* | 771 | 33.7 | CATGTAACAAGAGATCAAAGCCTAAACTTCTCTTCTTCCTCCTCCTCCTCCTCTTCTTCTTCTTCTTCTTTTTTTTTTTTTTTTTCTTTTTTTCTTTTAGTGTCTTCTTTATTATATATCCCCTATCCCTCATATGAATCTAAAACTCCACCAGAGTCTATCGTTCCGCGGATTG |
| P56_Contig-2771 | *not applicable* | *not applicable* | 225 | 36.0 | GGGTTATTGGTTCATGTGTGCAAGAAATTAAGATCGGTTATTATGTTCATGACGAAAATTCCAGGTTGCTTTCTTCTTGTATGTTCTTATCTTCTATCATGGTTATATCTCGACAGCTATATGTTATGGCAGATACATCAGGTTATTGGTTGATAGGTGGGCTAAGTTACGAC |
| P56_Contig-3439 | *not applicable* | *not applicable* | 205 | 37.6 | TGGAAGATCGTCACAACTTTTATTCTCAGGCATTTTTCATAGCTTCAATGCTTTACATTTAATGGCCTTCCATGTCCTCCCTTTTCCTTGACAAATTAGGGATTTTCGGAGCTCTTGATTTTAGGGTTTATGGGTTCTTGCTTGATTGAGATTGCAAAACCCACAATCTTCC |
| P56_Contig-3793 | *not applicable* | *not applicable* | 241 | 40.7 | TTATAAGTAGGGCGAGAGAAAGTCCATATATTCTATTTGCGTTGGTCTTTCCAACGGAAACTAAGCACTTTTTTCTTGACTCCGGCGCTCCAATGAACAAGAGTTCTCCGCCTTACTCTATTTAGAATAGTGGTCGATACCTCGGGAGGGAGTTAGATTCGTAACAAGATG |
| P56_Contig-3962 | *not applicable* | *not applicable* | 205 | 37.6 | GACACTTTGGAAGATTGTGGGTTTTGCAATCTCAATCAAGCAAGAACCCATAAACCCTAAAATCAAGAGCTCCGAAAATCCCTAATTTGTCAAGGAAAAGGGAGGACATGGAAGGCCATTAAATGTAAAGCATTGAAGCTATGAAAAATGCCTGAGAATAAAAGTTGTGACG |
| P56_Contig-400 | *not applicable* | *not applicable* | 206 | 41.3 | GGAAGTGTAAAACTGACGCGGATTGCAAGTTTTGTGTGCCAACAGCTGGTTGCGAGAAAATTATTCTCCCCGGTCTTTGTGCGTAGTGATCTCATTTCCCACTCGTCAGCACCTCTGATCTGATCTGCTTGTGTAATATATGTATGTTAAGTAGTTGCTTGGGAATATATC |
| P56_Contig-511 | *not applicable* | *not applicable* | 452 | 33.2 | GATCGTACTACAATCACTCTCTTTGTTGGTTTGGAATTTTGTAGCTTCATTCTCTTTAACCTCAATGGAACTCATTTGCTTCAACGCTTCATCATCCTTTTTTCCTTGACTAATATTTACTTCCGCATTTAAATCCTGATTCACACCATCGACAGTGGTTGTTCCACTATTAT |
| P56_Contig-6069 | *not applicable* | *not applicable* | 302 | 39.4 | AAAACCAGCAAGAATCGCCTCCCTCGGTATTTAAATGCAAGCAGTAGCCCAGATCCTGCATCACAACACACAAATTGTCAAGTAGAACCATTATAAAATAGGATAATCAATAGGCCAGGGGAAGCAAGCTAAGTTCTTATTGTAGGAAAAGGACAATAGTGTTACTTTCTTA |
| P56_Contig-7136 | *not applicable* | *not applicable* | 246 | 40.7 | AACTTAAATCAAGAAACTCAAGCTTTGGAAGTAGTCTTGTTGGAAGGTTCTTGGTCTCATTATAGTTGAGGAAACTAGTGATGAGATTGTTACGCAAATCCAGCTCCTCCAGATCTTTCATGGCCTCCAAATCATCAACTTTAATTTGCCCATTCAAGCCAACGTTGGATAA |
| P56_Contig-786 | *not applicable* | *not applicable* | 273 | 46.9 | AAAAAACAACAACCCCTACATAAGGGGGTATACTCCAACCCCATTCAAAAAATGAATGAATTCACAGACCTGCCCATAAAGCAGGGCCCTCTCCCCGTTTAAAAACAAATCCAAGCAATCATATTGGCTTATTGCCGGATTATCCACCGGGCTCTGAGTAACCGCGATTAC |
| P56_Contig-892 | *not applicable* | *not applicable* | 719 | 55.6 | GGACTTGCTTGGGCGTGCTTGCCGGAGATTGCCGAGTTGGGTCATAAAATTGACTCGATGGCGGATTTCTTTGACTTGTGTGTCTGGGCTTTTGTACGTGCGGTGCATGAGTGGCGCTTGGCTTGTGGCGATTTGTTGGTTCCCTGCTCCGGCAGCGACAACATCTCTC |
| P56_Contig-921 | *not applicable* | *not applicable* | 359 | 35.7 | TAACCATCCAATCGGTACAACTTGATGAGCAGATGGCCAGCTTTTAACAACCAGCAATATAGCCCTACAAACACAATAAATAATCTAACCACTCTTGATTGTGATACCAAAAAAACCCAAATTGAAAAAACAACAGAAATACAGCAACCAACTATCAAGTAAATCAAACTCCA |
| P58-1_Contig-109 | *not applicable* | *not applicable* | 396 | 29.3 | AAAAAAGATCGAATTTCCTATTTTTTGATTGTTTATTGAATATCGTATGGAATTTAAATTTAAGTAAAAAAAAGGAAACTTGAAATGAAAGTTTCTTTCACACATGCAGTCTCCATCCCATTGTCGGAACATAAATACGGGATGCATAGATATAGAGATAGTTGGTACATGAAAC |
| P58-1_Contig-1482 | *not applicable* | *not applicable* | 316 | 50.9 | AGGTAGCAGAAGAAGCTTTAGCAGAAGCCCCGGCAACTGAGACAAAAGATGAAGCCTCAGAAAAAACCGAGGCCCCAGCAGTAGAAACCGAGCCAGAGCCAGAGGCAGAACCCGAGGTAGAGACCAAGGAAGTTGAGGCTGCACCAGCAGTTGAAGAAGAGAAGGCAGC |
| P58-1_Contig-1681 | *not applicable* | *not applicable* | 230 | 40.4 | GTATTCACACTTCTAGCCTAAAGGGATCAAGTGTGAGGAGGTGTGTTAAAGTATATAACATATCTTGGGGCCTCAATCATGAGATTAAACTTTTGGCTGAGTTGGTTCTTTGAAATAGTATTAGAAGCTAGTGTGACAAGAGATCGCGGGTTTAAATCTCAACCATATCTTC |
| P58-1_Contig-1734 | *not applicable* | *not applicable* | 205 | 37.6 | ATTAAATGTAAAGCATTGAAGCTATGAAAAATGCCTGAGAATAAAAGTTGTGACGATCTTCCATCCCAAATTTGTCTTTTAAGTCAATGACACTTTGGAAGATTGTGGGTTTTGCAATCTCAATCAAGCAAGAACCCATAAACCCTAAAATCAAGAGCTCCGAAAATCCCTAA |
| P58-1_Contig-1818 | *not applicable* | *not applicable* | 342 | 48.2 | AAAAAATATGGCCTACTCAAAGGCTTTACTCCTTGGTTTCCTCTTAGCGATAACTCTACTCATTTCTTCTGAGGTGTCAGCTCGTATGCTTGCTGAGACTACTCAAAACACTCCGTCCGAGGAGGAGGCCAAGTATTACCATGGCGGTGGTGGCTATTACCATGGAGGAG |
| P58-1_Contig-1846 | *not applicable* | *not applicable* | 240 | 50.8 | GCACCGGGTGGTGGAGGATACTGTCCCTGTGGATATCCGTGATGACCACCAGAATGATGACCAGCAGAATGACCAGCTATACCACCCACAAGACTGGAAATGATTCCCTTGTCAGAACCATCCGAACCTTGTGGAGGATATCCTTGTTGTTGAGGATAATCAGCAGGCG |
| P58-1_Contig-2033 | *not applicable* | *not applicable* | 201 | 38.3 | ACAGAAACTCAGAGATCATAAAGACGTAGAGCACAAAGATATAAAAGAAACGGATCCTGGTTACCGTCAAGATAGCTATCGAAATAAGAATCTTGGCAATGTGAGAAAAACATGGTTTTTGTTTCATGATGATCAGCGGTCTGAAGAAACTATGCCAGGAAAAGAGAAGGTTT |
| P58-1_Contig-254 | *not applicable* | *not applicable* | 621 | 34.5 | TCTCTTTGTTGGTTTGGATTGTAGTAGCTTCATTCTCCTTAACCTCAATGGAACTCATTTGCTTCAACGCTTCATCATCCTTTTCTCCTTGACTGATATTTACTTCCACATTTAAATCCTGATTCACACCATCGACAGTGGTTGTTCCACTATTATTTGCTTCAACAATGTCC |
| P58-1_Contig-34 | *not applicable* | *not applicable* | 384 | 34.6 | GTTGATGATAAGGTGTTGCTTGGTGTTTCACCAACTAGAGAAGTAATGAGATTCTGGAAGAAGGGTAAATAAGTCTGAGGTTCGTGGGACCCTACGAGATTTTTGAGAGCATTGGTGATAATGATGAACTTGGATAATTTTGTCACATAATATGAGAGTTCGTGAAGATAAAG |
| P58-1_Contig-340 | *not applicable* | *not applicable* | 215 | 30.2 | TTTTTTCTTGAAGGAATTTTTTATGATCATTATCAACTAAATCATTTTCTTTATTCTATAGAATCCCTAGAATTCATTAAAACAAAAAGGGCCTGGCGAGGTATTGATCAGGCCAGGCCGTGGGAATCCAAAAAGAGTCCCCTTCGGGCGAAGAAGTATTTAATTAAATATTC |
| P58-1_Contig-355 | *not applicable* | *not applicable* | 438 | 42.9 | TTCCAGCAAAGAAAAAAGGCTGAATCAAGTGATGACAGCAGCGATGATAGCTCTGATGAAGATGATGCTCCCAAGAAGGCGTCTGCTCCAGCTACGAAAAAGGAAGTGGAATCTAGTGATAGCTCGTCTGATGAAAGTGAATCTGAGGATGATTCTTCTTCTGATGACGAAC |
| P58-1_Contig-397 | *not applicable* | *not applicable* | 265 | 29.4 | AAAGTTTTTGATCGGAATAGTAATCAAACCGGTAGACCCCTTAACTATTAAGGGGTTAATAGAACGAATCACACTTTTACCACTAAACTATACCCGCTACAGTTGGATTATTGTATCGAAATAAAACTTTTGTCGAACACTGAAATTGGATGTAATCAAGATAGGATTCGAAAA |
| P58-1_Contig-4155 | *not applicable* | *not applicable* | 350 | 43.1 | TGTGAGCTCTCAAGGTGCTGTGAAGGTTTTCGGGCCATGCGGTACGAAAGACGCTATGGCCCAAGGGAAGGAAGGTGGTAGCATAGACCCTCACCCCGAGCCGTGAGCCAAGAATCATCAGCTGTGAGCCGTGAGACCCCCCGCCCCTTACGATTATGGCTTTTAAGG |
| P58-1_Contig-446 | *not applicable* | *not applicable* | 491 | 62.5 | GTTAACGCTAACTCCACCCAGCTTCTGCTGGACGGTCCCCAGTCCGTGTAAAGGAGGAGGGGCGTCCCATGACGACACTGTAGATAGGCCGACAGCCCTGTCAACATCAGATCAACCTGACAGTGCGCCATGGGGTAAGGAAGTAGTGCGTCGGCTTCGGCTTTTATG |
| P58-1_Contig-451 | *not applicable* | *not applicable* | 679 | 48.7 | AAAGGATGGAGTCTTGAAGGTGACAAAAGGGTGCTTGGTGCACTTGAAGGGAGTGATGGGCAACATTGGCCATGTGTTGCTAAAGAGTAGAGACTTACACCATGTCGAGAGGGGTGCAAGACTCAAGTCACCAAGGAGAGTGACATTTGATGATGGTGGCCACAATGAAA |
| P58-1_Contig-511 | *not applicable* | *not applicable* | 345 | 51.6 | TCCTCCTCAAGGTTATCCACCAGAAGCATACCCAAAAGAAGCATACCCACCAGCCGGGTATCCTACACAAGGCTACCCACCCCCACAAGGAGGTTATGGATACCCTCCACAAGGAGGATACCCGCCTGCTGATTATCCTCAACAACAAGGATATCCTCCACAAGGTTCG |
| P58-1_Contig-585 | *not applicable* | *not applicable* | 216 | 26.9 | ATTTTTTCCTTCTTTAGAAGGAATATGTCCCTAGTACATACATATATAATATATATGTGTGGATGATATTTGTGTAGAGTCGGACCCGATACTTTACTTCAAACTTCAAGTGAATTCCAATTTAATTCTTTATTTATTTTAGTCAATTCATTCAAGAAATTTTAATTTGACCCCT |
| P58-1_Contig-680 | *not applicable* | *not applicable* | 282 | 45.7 | GGTGGAGACTTGTAGATATAAGGAGGAGGATGAGACTTAGGAGGAGGCGGGGATGTATAGTGACAAGTTGGAGGAGGAGGAGAAGAATACTTATAAGGAGGCATATGAGGTGGAGGAGTTGACTTGTAGTAATATTCAGGTGGCGGTGGAGATTTATAAATATAAGTTGTA |
| P58-1_Contig-7226 | *not applicable* | *not applicable* | 205 | 37.6 | CATAGCTTCAATGCTTTACATTTAATGGCCTTCCATGTCCTCCCTTTTCCTTGACAAATTAGGGATTTTCGGAGCTCTTGATTTTAGGGTTTATGGGTTCTTGCTTGATTGAGATTGCAAAACCCACAATCTTCCAAAGTGTCATTGACTTAAAAGACAAATTTGGGATGGA |
| P58-1_Contig-808 | *not applicable* | *not applicable* | 491 | 62.5 | ACAGGGCTGTCGGCCTATCTACAGTGTCGTCATGGGACGCCCCTCCTCCTTTACACGGACTGGGGACCGTCCAGCAGAAGCTGGGTGGAGTTAGCGTTAACCTCGCCTCGGTGCAAACCGAGCCGGTCTCAAGCCCGGGTAAAGAGGGAGAGGCGTTGGTGTTGACG |
| P58-1_Contig-830 | *not applicable* | *not applicable* | 306 | 43.5 | TGGTTTCCACCAATCTTACCAATATCGACACCCCCAGATTTCTCCTTTTTGTTTCCAAATTTAACATCTCCATTTTTCTGTATGCCTGATCCATTTGAGTTTCCTCCCGAGTTGAAGGAACTTCCAGGAGGGATGACTGCCACTGGGTAATTGTTGTAAGGTGGTGCAGGA |
| P58-1_Contig-8729 | *not applicable* | *not applicable* | 201 | 38.3 | TAGTTTCTTCAGACCGCTGATCATCATGAAACAAAAACCATGTTTTTCTCACATTGCCAAGATTCTTATTTCGATAGCTATCTTGACGGTAACCAGGATCCGTTTCTTTTATATCTTTGTGCTCTACGTCTTTATGATCTCTGAGTTTCTGTCGTTCAGCAGATACATTTGAG |
| P58-1_Contig-965 | *not applicable* | *not applicable* | 537 | 42.3 | AAGTGGTGCCATAATGATGCCTGATGGTATTGCGCTCCATTGCAATTTCACAGCTAAACCAGCCAATCAGGATTCCGATTCTTCCATTAAGCTCTTCTTTGGCGAGATGCTCATTGGTCCAAACGATGTTCATATAGTCACTTATTGTGATATATTAAATGGTAAATCTCAT |
| P58-2_Contig-1085 | *not applicable* | *not applicable* | 793 | 32.5 | AATGAATATTTGGTTTAGATTGGTCATCGAATCCGAATATTAACTATTCGGAGTCGTTATTTGACGAAGAAGTCCTGTACGATGTGTGATTAAATAAAAAAGGATGTTCTATAGAACGATTCCCCCTTTTTAGTTGATTTTATTCAACGATTGACCAAACGAAAATATTAATAA |
| P58-2_Contig-1131 | *not applicable* | *not applicable* | 204 | 31.9 | AAAAAGGCACTCAACACAAGGGCATGCTCGAGCATCATTAAAAAACTCCTTATCAATCTTGACTTGTTTCAATAAGAAAAAAATTCAACCGATTCGATTGACTAGTATCTAACAATCTAACAAATATGTAACAACAAAATCTAGTGGTAATATATTGACTTCACGCTAAAGGCT |
| P58-2_Contig-1464 | *not applicable* | *not applicable* | 760 | 40.5 | TATATTAATAAATGCTGATTGTCATTATCAATGATAGACAAACAAGCCGGATTTATTAAACCCCTTAATTGTAGGTTTATAAACCGAATGTTAAGCCCAAGGGTCTTTCCTTATGATAGGGTAACTGGTGCAGTTACCCACCCTCATACGATTCAAAGACCGGGCTTATGCTG |
| P58-2_Contig-1487 | *not applicable* | *not applicable* | 391 | 34.3 | AACAAACGAATCAAAATCTCTTATCTGCTGATATAAATCACCCAAATTTTCCCCAGTAGAACAGAATAAGGGGATTGTTGATACTTGGTTGATTCTAAACATCTATTCTGGGGATTTTGTAAAAGATTGGAAATCTTTCAATCTAAAATTCAAAGAAAGATTATATTATAATGGT |
| P58-2_Contig-1679 | *not applicable* | *not applicable* | 491 | 62.9 | ACAGGGCTGTCGGCCTATCTACAGTGTCGTCATGGGACGCCCCTCCTCCTTTACACGGACTGGGGACCGTCCAGCAGAAGCTGGGTGGAGTTAGCGTTAACCTCGCCTCGGTGCAAACCGAGCCGGTCTCAAGCCCGGGTAAAGAGGGAGAGGCGTTGGTGTTGACG |
| P58-2_Contig-225 | *not applicable* | *not applicable* | 265 | 30.2 | CGATTGAATAAATGGATCGAACCTTATGGTTCAAATTCTGAGGAAAGAAAGAACAACGAGTTTATTTTCATAATTTGAATGATTTCCCGGTCTAATTAGACGTTAAAAAAATATTAGTGCCCAATACGGGAAGGCTTTCTCCCAGGAATTTATTCTTGATTTTTTAATGAATCC |
| P58-2_Contig-2259 | *not applicable* | *not applicable* | 344 | 37.5 | GGGTCTCACCACAGCCGTCGCTGCACTTATAGAACTGGAGCTGCAAAGGATAGAACGGCAGAGCACAAGAATTTTTTTTTATATCTATAGCCTAGATAAAAAATTATTTTTTATAATAGCTATATCTAAGCGTATTTTTATTTTCGAAAATAAAAATACGCTTAGATATAGCTA |
| P58-2_Contig-2811 | *not applicable* | *not applicable* | 239 | 37.2 | TAGTTCAGATTGTAGAGCTTCCAGCTGGAAGGTTTCAGATACTTTGCTTGGACAGCATATGGTTTGATTAATCATGTTTACCCTATAAATTTTTATTCCTTTGGGAATTTGTCTTTTTCTGTGAAGAGTTCTGTTTCCCAATTATTTTTCTGTCTGACTTGATGATCAGATTG |
| P58-2_Contig-282 | *not applicable* | *not applicable* | 439 | 43.1 | AGAGAGGGCCTTCACCCCGAGGGAGCCGCCCACTTTAGATAAAAAATACCAAAGAAAGAGCATGCCCCCGTTTTCAGGCAAATAATATAGAACATAAGCATAAGAGTTAGGACTAATATCAATTTCATGTAAACTTTGGTGAACTTCCCTCGAACCTGACTGAACCGACTT |
| P58-2_Contig-3038 | *not applicable* | *not applicable* | 455 | 36.9 | ATCCATCAAGTTGCAAAGACCACACCGCAAAAACTCATGCACCTTCATGTTGATACTGATTTTGTATAAGAAACAACGTAGGCCATCACATCATATGGAAGACTCCGACTCTTGACAAGAAATGACAACCCCATTGATTCAGATGGTTGTGAAAAAGAAATAACATTCAATTC |
| P58-2_Contig-3138 | *not applicable* | *not applicable* | 225 | 28.0 | ATTGAATATCGTATGGAATTCAAATTAAGTAAAAAATAGAAAATTCTCTGTATCTTTCTTCGATCCGTGAAAGTGAAACGATATATTCTGACATTTCCGATTGATCGGAAGGAAAAAACTAACTATAAATAGACAAAACTAAACATATATTTATTCGAGAATAATCTCGAAAGA |
| P58-2_Contig-3259 | *not applicable* | *not applicable* | 370 | 33.5 | TTTATTTCGTCCTTTATTTATTTTCATTTCTTTGGACTCCGCAAGAATTTGTCGATATTTCCGATTAAATCTTTGTATTCCTAGTTATTCCATAGGAATAAATTGGCGAGTCTCTTCTGCCTAGAAGGGAGAAAACTTTGTGGTTATTTCAAATCACAACCTAAAAAAGCCATC |
| P58-2_Contig-39 | *not applicable* | *not applicable* | 226 | 49.1 | ATCGCCAACCCAGATCGTCTTATTATCTTCGCTCGAAGTCTGAATCTGATTACCTTTTTGTGATTGTTGTTGATACTGCTGTGCTTGCTGTTGTTGATAATGATAAGGCATGTAGTGTGGCGGTGGTTGTTGGTACATCATCGCTGGATGATGCATCGCCATTGACGCAGC |
| P58-2_Contig-4776 | *not applicable* | *not applicable* | 229 | 27.1 | AATAAAAAAAATAAAGACAAGGAATTCTCGTTTTGACACTCTAGAAAACCCAAAAATAAAAAAAATTTTTAAAAAAAAAAAATGCTAAAAAATAGGAATCAAAAGCGTCCATAGTCTAATGGATAGGACAGAGGTCTTCTAAACCTTTGGTATAGGTTCAAATCCTATTGGACGC |
| P58-2_Contig-4895 | *not applicable* | *not applicable* | 210 | 51.9 | TGTGGAGGGTACCCTTGAGGAGGATACCCTTGCTGGGGAGGATACTGTCCCGGTGGATATCCGTGATGACCACCAGAATGATGACCGCCAGAATGATGACCAGCTATACCACCCACAAGACTGGAAATGATTCCCTTGTCAGAACCATCCGAACCTTGTTGTGGAGGAT |
| P58-2_Contig-5245 | *not applicable* | *not applicable* | 405 | 32.1 | TTTGAATTACTATATTTTTTATTTCCAATATGAATCTCGGTATCTATTGAAAGAATCAAATCAATGAAGGAAAAGCGATAGATATAGGCATATTCAAAAAATCACGTAGTAATCTTTTTTAACATTCCCAAGAAGTAATTGAGTAAACCATTGACAGTAGTTCCACGGGCATCG |
| P58-2_Contig-675 | *not applicable* | *not applicable* | 352 | 32.7 | GAAGAAGTGGACTCTAGAGGTCCTAATCAATCGAGTTTAAGGAATCAATTTGTTTCAATTTTGTTATAGATCGTTCTGCAACACGTTTTTAGCTATTTAAAATATCTTCTCCAAATTCCATTGGGATTGACTGGAATAATTTATTAGAAGAATTCTACTCTGTCAATCAAACAG |
| P58-2_Contig-793 | *not applicable* | *not applicable* | 276 | 34.8 | CTAGTTAGTGAAATAGAGTCTAACGTGTGATTTCCGCCGAACATAAAGGAAAAGGTTCTTAGGTCTGTAGAAACGTGATATATGGATATTTGAATTTTAGCAATTGAAAAATAGATCAGGATCCGCCGGATGACTTAAATTTTAAAATGAAGTCGGCGGATCTATATGTAATAT |
| P58-2_Contig-925 | *not applicable* | *not applicable* | 491 | 62.9 | GTTAACGCTAACTCCACCCAGCTTCTGCTGGACGGTCCCCAGTCCGTGTAAAGGAGGAGGGGCGTCCCATGACGACACTGTAGATAGGCCGACAGCCCTGTCAACATCAGATCAACCTGACAGTGCGCCATGGGGTAAGGAAGTAGTGCGTCGGCTTCGGCTTTTATG |
| P59-1_Contig-6 | *not applicable* | *not applicable* | 733 | 32.7 | TATCTAGGTACGGTTGTCAAATGTAAAGTTTTTATACGCTTTTTAAGCGACCAGTACATCACATTACATGACGTACTATTACATTTAATGGTCTTTTTCCAGAACATTATGTACTCAAAATATCACAATGTTGTTAGACATATCTAAAGATTTTCTCATCGTTTAATCCTTTAG |
| P59-1_Contig-93 | *not applicable* | *not applicable* | 260 | 29.6 | ATAATGACATGTTTGCTTCTTTATTTTTTTTTTTACTCCATATTGGAGATAAAAAAAAAAAGCTAGGGAAAACAAAGCTCTAACCACTGATATATTAAATAAGTAAAACGGGCAATAACCTGTTTGAATATAAGGGGAACCTTCCTCTAAGCCTTAATATAATATACAAGTAATA |
| P59-2_Contig-89 | *not applicable* | *not applicable* | 246 | 43.9 | AGAAAAGCTTGAAGAACCATTGGTTGGAGAGACGACCGAAGAACCGACAATTGAGGAGAAACCTGAAAAAACAGCAACTGAAGAAACACCTAAGGAACCATCATTTGAAGAGAAACATGACGAACCAACCGTTGAAGAGGAGAAACCTGAAGAATCAAAATTTGAGGAGAAA |
| P59-3_Contig-116 | *not applicable* | *not applicable* | 215 | 33.0 | TTATTTACTATTTATATCTTTGTTAGACCTGACCGTTGATTGTTACGATCATAAATATTGGTCGCCTTTTTCCAGAACACTGTTTACTCACACATCACAACGTGCTGATTTTTTTTTTACACGAAGCTAGTCTTTAAATTTTCAATGTTGTTAGACATACCTGAAGATTTTTCT |
| P59-3_Contig-25 | *not applicable* | *not applicable* | 759 | 34.3 | TTATATGCTTTTCCAGAACATTTTACTCCATTTCTTTATGTTGTCACATATAATCTCCTCATCATTTTATCCTTTAGGTTAAATTTAGAGACCGAATCACTTTACCATAAGCTTAAGGCGAGGGGCTATCCCTTTTTCGTTACTCATGTCAGCATTCTCACTTGGGGTCATCT |
| P60_Contig-1006 | *not applicable* | *not applicable* | 458 | 39.5 | TTAAGATCGGTTATTATGTTCATGACGAAAATTCCAGGTTGCTTTTTTCTTGTATGTTCTTATCTACTATCATGGTTATATCTCGACAGCTATATGTTATGGCAGATACATCAGGTTATTGGTTGATCGGTTGGCTAAGTTATCACAAGATGGTTAACCAAGGAGTTACTGAT |
| P60_Contig-113 | *not applicable* | *not applicable* | 780 | 46.4 | ACTACTAGCGGCTACTTAGCAATATCCTCCTCATATGTGAGGCTCCGTCACCGCCCACAAAAGAATTGCAAACCCATTTCCATTCACGCATCCCACAAATGATTCGAATCCAAAGGGGTGACAGTTGCATGGCAAGGTAGATGGACGAGTTCACAAAGCAGTGCTTCTCC |
| P60_Contig-1436 | *not applicable* | *not applicable* | 305 | 39.3 | TTATCTGGCCTTGTGGATACAACATAATGTTCATTTGTAGCAGGGCTATGTCCCCTTATAGTTTACACTTACAGGTTTCTACAATTTTTTCTCTTTTTGTTGTGTCATAATTTCTCTTTACACTCCTAATTAGAAGGCATGGGTGGTACTTAATATTTGTTTCCCGCATGTAG |
| P60_Contig-1537 | Taraxacum viroid-like circular RNA 1 | (+) strand | 447 | 46.1 | GATACACATCTCTCGACGGCTAGTTTTCCGACCAGGCTGTCGACTTCAAGAAGTGGATTACCCTTCCTACAGGGTTTATCTCCTCTTGAAGGAGCTCCTCTTAGAGAGGGGGTCTAAAGGTTTTTCCGAAACCTTTATCGGCTAGTCTTTTTCGGTAACTAGTTAACCGTA |
| P60_Contig-234 | *not applicable* | *not applicable* | 531 | 50.8 | TGATACGTGTGTCAACTGGTTTCGCCCTGCCATGGGCTCATCAGGGAGGCGGCACTAGCCCCCGACCAGTTGTGTCGTACCCACATGGTACGGATAGACAAAACCTTCTGAGCTAGCTCGGCTCCCCACTGAGTGAGCATAGCAGGTGAAACAGTGACACGTCTTCGG |
| P60_Contig-2553 | *not applicable* | *not applicable* | 225 | 28.9 | TGAATTTTTCTACGAAGAGTACTGAACAAAAGTTGGTTTGTTCATCCACAACTGGAAAAAGATCGATTGGGTCCATTGAAATGAAATATGTTTTTGCTTTGATATTATACTTTAAACGATCCCAAATAATGGGCTTATAGTAATGATTGTCTTTTGATGAAGCAATCAGTCAGT |
| P60_Contig-308 | *not applicable* | *not applicable* | 773 | 52.3 | TGACGAGGACGTACCAGAGAGTTGGATAGTTGCGCGGCGAGTTGAGTCCTTTCTCCTGGAACGAGGATGTTCCGATTTCATCAAGTCCGAGAGGGTGTTACGGCTCAGATATTTCGCCGTAACCATGAAGGCCGAAGACCGAAGACGTGTCACTGTTTCACCTGCTATG |
| P60_Contig-396 | *not applicable* | *not applicable* | 245 | 52.2 | ACGATTCAAGAGGGATGATAGTTGCATGGCCTTGGCAGCGATCGTTTCGAAAGCGCCGCCCACAGTTCCCGTATATCGCGGCAAGCGTAGGGACTAAGGAAAAGTGGACGAGGATACAAGGTCCTACACGCCGGCTACTCGGTTCAAGCCGCCTCAGCACTTACATCG |
| P60_Contig-4789 | *not applicable* | *not applicable* | 248 | 55.2 | TCGAAAGACCTCTGAAGCGGTTGAGGGGCAGCTTTCCGAAAGGATAGCAGGTAGGCCGCGCATGCTAACTAAAGAACCAAAACCACACCTCTGGGCGCCCGGGCCGACCGACCGGCTACGGGATCGTATTTTTTTCCTTTGCCTATAAAAGAGGGAGAGAGATATCT |
| P60_Contig-4864 | Taraxacum viroid-like circular RNA 1 | (-) strand | 447 | 46.1 | CTATACTCTACTGAAAGGTAGAGATGTAGGTCAGTTCTAAGACTCAAACCAGATTAGATCTGGGGAGGCTCGCTTAGACTCTACAAATTGTGTTGGAACCAGTCTCCGATTAAGGAAGAGGTTCTTAACCGTTTCGTTCTTTCGAACTCATCAGGGTAGACACACATCTAC |
| P60_Contig-578 | *not applicable* | *not applicable* | 368 | 37.5 | TGAGATCTTATGTCCCAGAAATAAGAGGATTTTAGTTTCGTCTATGTAGGTTTGACCAGTGCCAAATACAGTGGTGCAGGGTTTTATGACCATTCTGCTGGTTATTCTTTGATTTGTATAATCTCTTCAACTTTAAACAATACTGGATATTCATCTTTCAATGTGACACGAAC |
| P60_Contig-789 | *not applicable* | *not applicable* | 282 | 38.7 | GTTTAATGGTTTTAGGTTCATCCTCTGGTTATCGTTTCGCAAGCCATCTGTTATGGTCAATCTGTCACGGTTTCAGCTCGTATCGTCTGCGTTATGTGATTCGGATTCGAAAGCTGTTTATAACGATATGGAACGATGAGTATGATTTCGAAATTTGTTTCCATAGATCAGA |
| P60_Contig-809 | *not applicable* | *not applicable* | 367 | 44.7 | TACCCCCTCGGCAACATGCGTGAGAAAGCAATCATAAGACAGAACAACCCCCAGAATGCACCACACGATACGAAATCATGAACCCACCAAATGATTGTTTAAAAATGTTTTGTACAAAAAATATTCGTGGTTTTCACCATATAATCATCGTAAGGGACAGGGAAACCCTTGA |
| P60_Contig-8442 | *not applicable* | *not applicable* | 275 | 48.0 | ACAGCATTACCACACGCGGGGAATTCAACACGAGAAACAGTCTTTTCGCCATCAACAGCATATGCCGCTGAAGCCAAACAATGAGAACACATCAATTGCCAACAGTTTCCTACAATGAAAGGATCCCGCCAACCTACATGAAAGTTATGCCGCTCACACGCTCTGAAGA |
| P60_Contig-931 | *not applicable* | *not applicable* | 273 | 42.5 | GTTGCTGCGGTTACTATGGAAGGTGTAGGTGCTGCGCTACCGCGGCCGAGGCCACCGCTGAAGCTTCAAAGGCAACTCAGCCACAGAACTGATCAATTCGATTTGATCACTGCTTTGTTGTCCGAACCAAACTTGGTTTGGGCTTTTTACTTTCAGAAATAGTGCATATA |



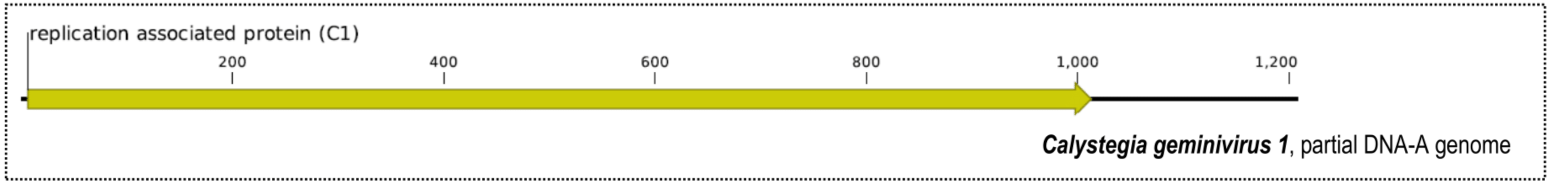
**Supplementary Figure 1-01.** Genomes of new virus species discovered under family *Partitiviridae,* order *Durnavirales.*

**Supplementary Figure 1.** Genome organization of novel viruses or first full genomes of known viruses, showing known and putative open reading frames and the protein it codes for, and predicted secondary structures of selected viroid-like circular RNAs detected in this study. **Note**: Genome length in number of bases are shown with a scale. For full information on genome length, protein domains, *etc.,* please refer to Supplementary Table 5, and the corresponding accession in GenBank.

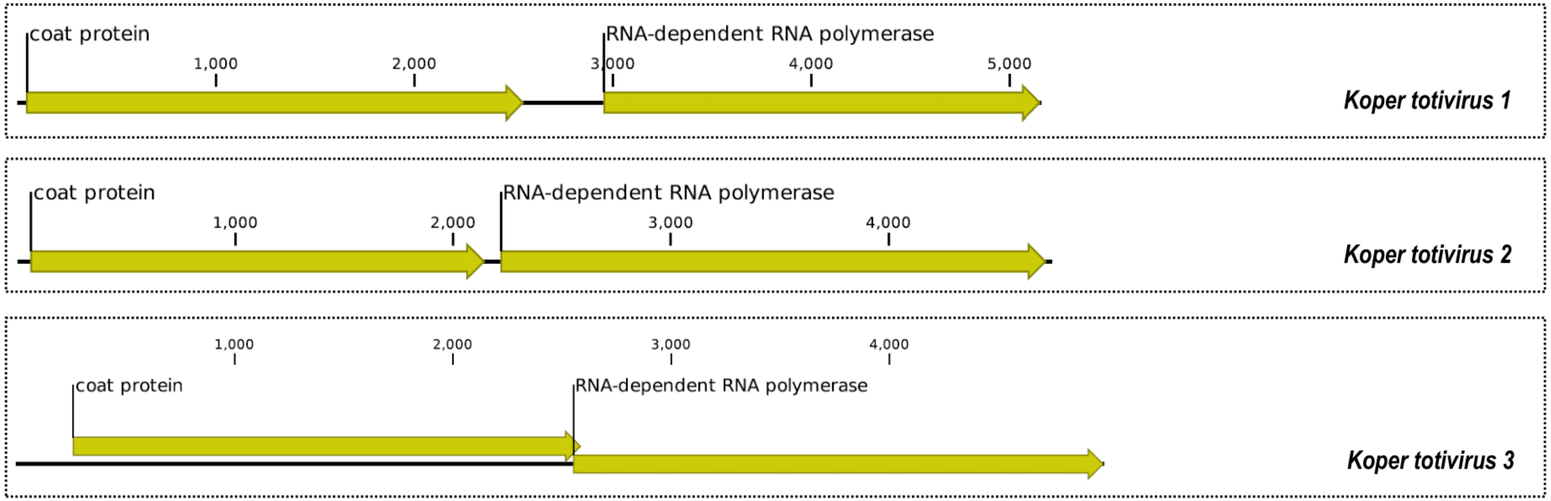


**Supplementary Figure 1-01** (continued)**.** Genomes of new virus species discovered under family *Partitiviridae,* order *Durnavirales.*

**Supplementary Figure 1** (continued)**.** Genome organization of novel viruses or first full genomes of known viruses, showing known and putative open reading frames and the protein it codes for, and predicted secondary structures of selected viroid-like circular RNAs detected in this study. **Note**: Genome length in number of bases are shown with a scale. For full information on genome length, protein domains, *etc.,* please refer to Supplementary Table 5, and the corresponding accession in GenBank.

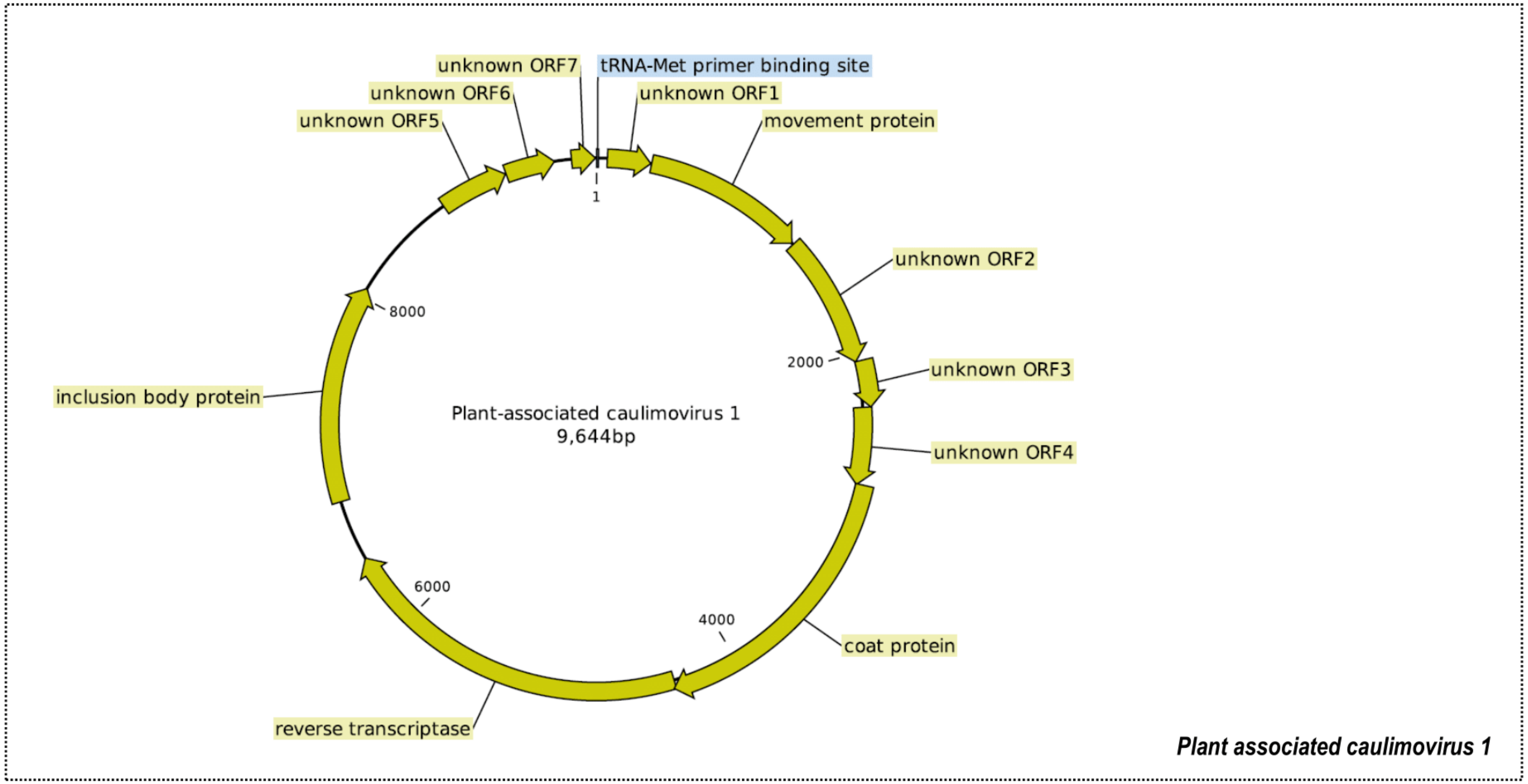


**Supplementary Figure 1-02.** Genomes of new virus species discovered under *Geminiviridae* (order *Geplafuvirales*).



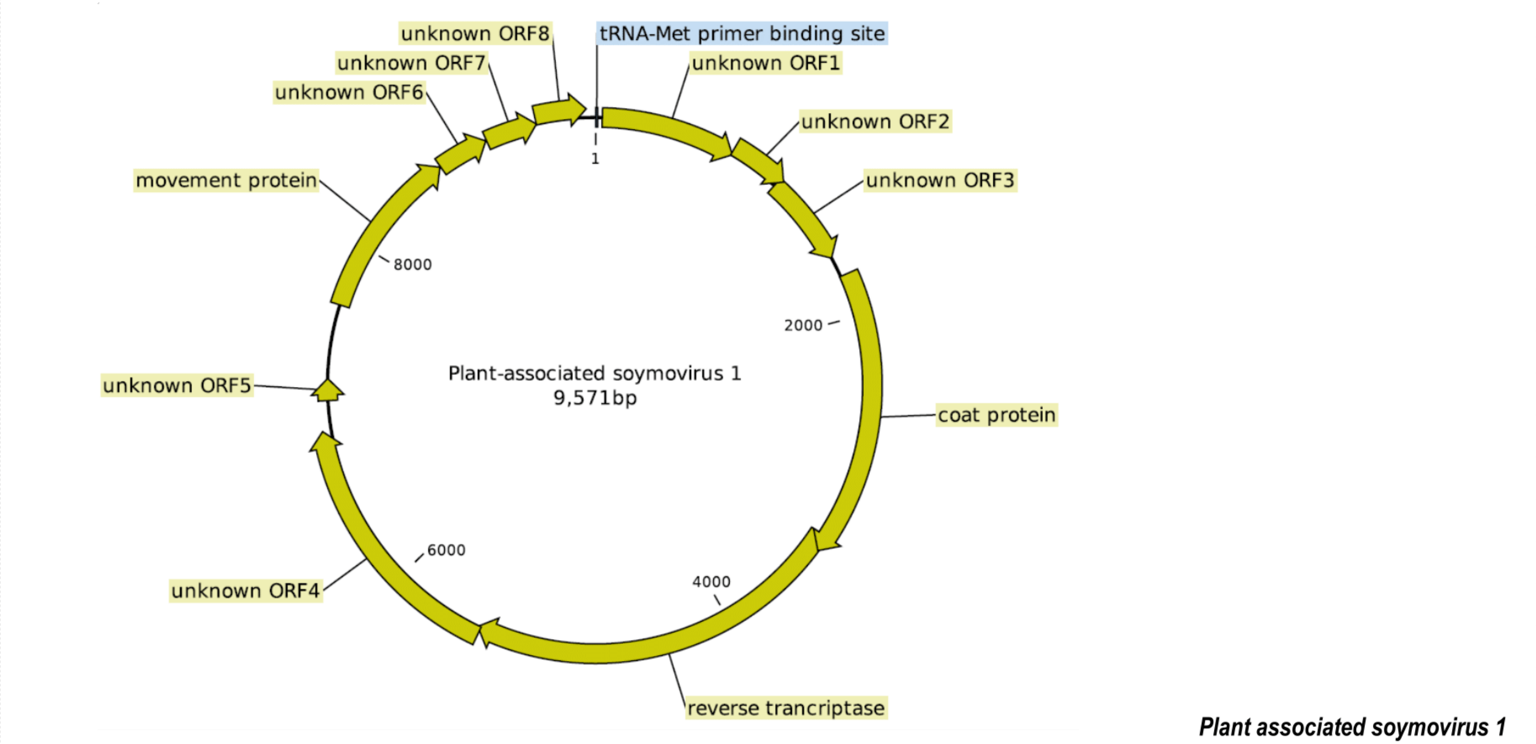
**Supplementary Figure 1-03.** Genomes of new virus species discovered under *Totiviridae* (order *Ghabrivirales*).

**Supplementary Figure 1** (continued)**.** Genome organization of novel viruses or first full genomes of known viruses, showing known and putative open reading frames and the protein it codes for, and predicted secondary structures of selected viroid-like circular RNAs detected in this study. **Note**: Genome length in number of bases are shown with a scale. For full information on genome length, protein domains, *etc.*, please refer to Supplementary Table 5, and the corresponding accession in GenBank.



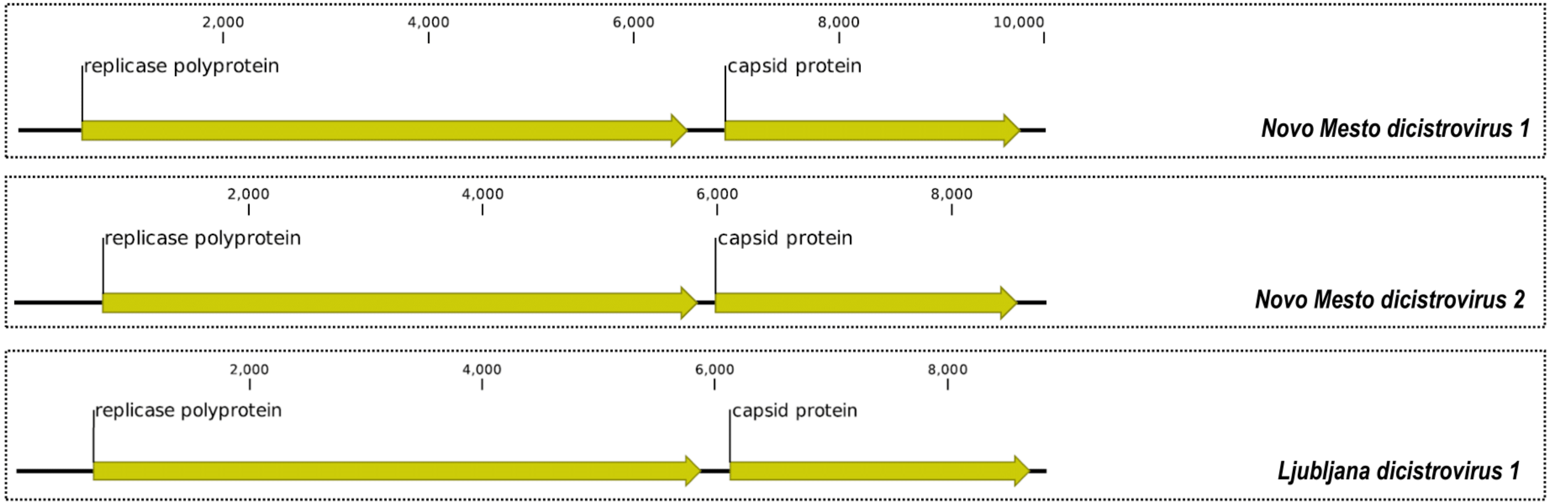
**Supplementary Figure 1-04.** Genomes of new virus species discovered under family *Caulimoviridae* (order *Ortelivirales*).

**Supplementary Figure 1** (continued)**.** Genome organization of novel viruses or first full genomes of known viruses, showing known and putative open reading frames and the protein it codes for, and predicted secondary structures of selected viroid-like circular RNAs detected in this study. **Note**: Genome length in number of bases are shown with a scale. For full information on genome length, protein domains, *etc.,* please refer to Supplementary Table 5, and the corresponding accession in GenBank.

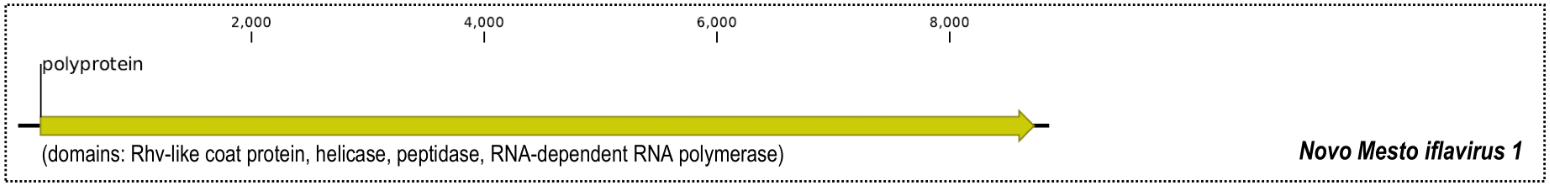


**Supplementary Figure 1-04** (continued)**.** Genomes of new virus species discovered under family *Caulimoviridae* (order *Ortelivirales*).

**Supplementary Figure 1** (continued)**.** Genome organization of novel viruses or first full genomes of known viruses, showing known and putative open reading frames and the protein it codes for, and predicted secondary structures of selected viroid-like circular RNAs detected in this study. **Note**: Genome length in number of bases are shown with a scale. For full information on genome length, protein domains, *etc.,* please refer to Supplementary Table 5, and the corresponding accession in GenBank.

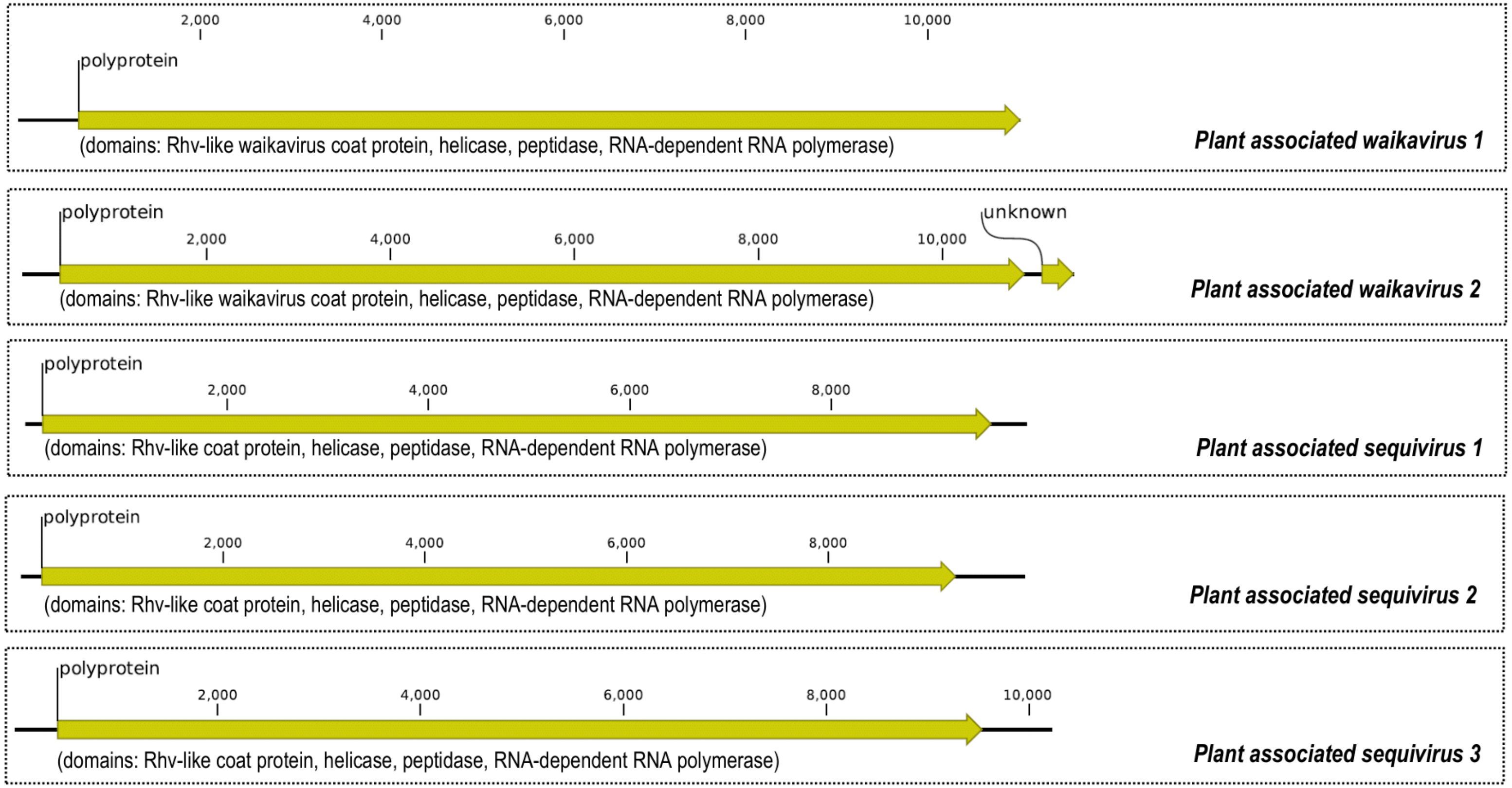


**Supplementary Figure 1-05.** Genomes of new virus species discovered under family *Dicistroviridae* (order *Picornavirales*).



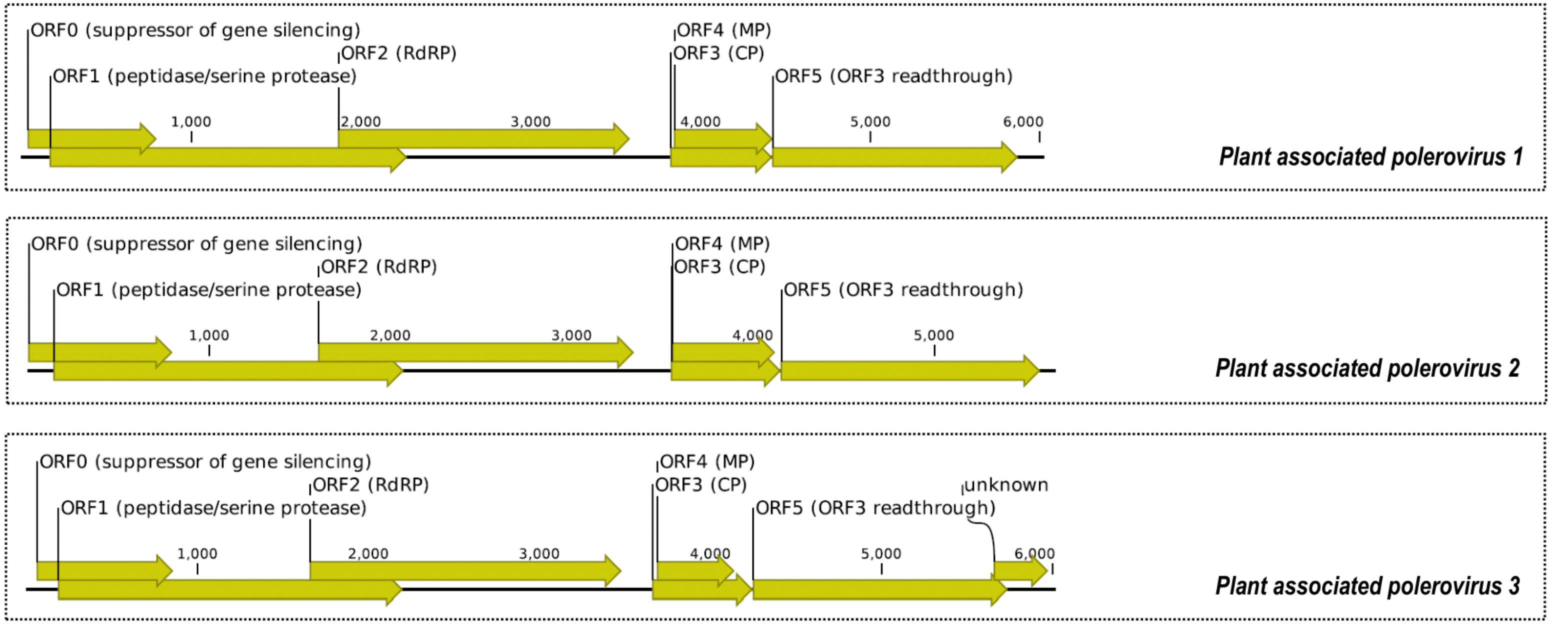
**Supplementary Figure 1-06.** Genomes of new virus species discovered under family *Iflaviridae* (order *Picornavirales*).

**Supplementary Figure 1** (continued)**.** Genome organization of novel viruses or first full genomes of known viruses, showing known and putative open reading frames and the protein it codes for, and predicted secondary structures of selected viroid-like circular RNAs detected in this study. **Note**: Genome length in number of bases are shown with a scale. For full information on genome length, protein domains, *etc.,* please refer to Supplementary Table 5, and the corresponding accession in GenBank.



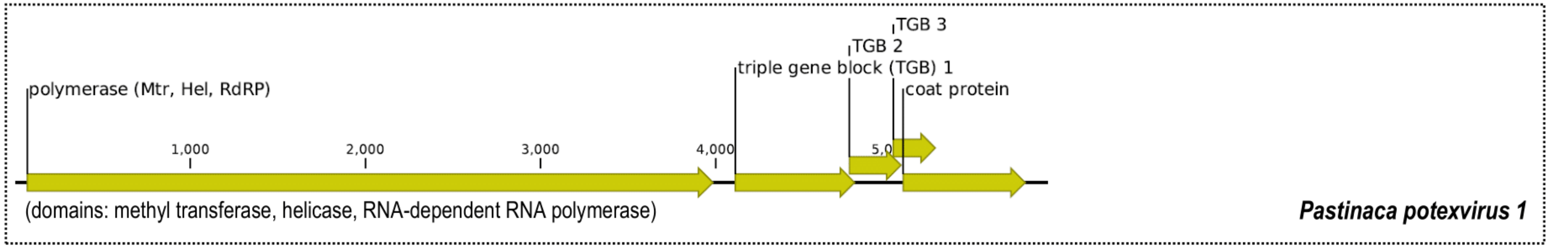
**Supplementary Figure 1-07.** Genomes of new virus species discovered under family *Secoviridae* (order *Picornavirales*).

**Supplementary Figure 1** (continued)**.** Genome organization of novel viruses or first full genomes of known viruses, showing known and putative open reading frames and the protein it codes for, and predicted secondary structures of selected viroid-like circular RNAs detected in this study. **Note**: Genome length in number of bases are shown with a scale. For full information on genome length, protein domains, *etc.,* please refer to Supplementary Table 5, and the corresponding accession in GenBank.

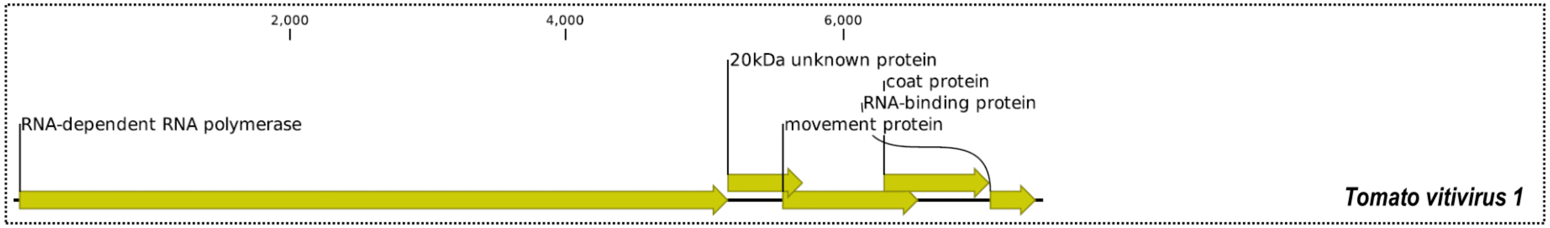


**Supplementary Figure 1-08.** Genomes of new virus species discovered under genus *Polerovirus,* family *Solemoviridae* (order *Sobelivirales*). **Note:** RdRP - RNA-dependent RNA polymerase, MP - movement protein, CP - coat protein.

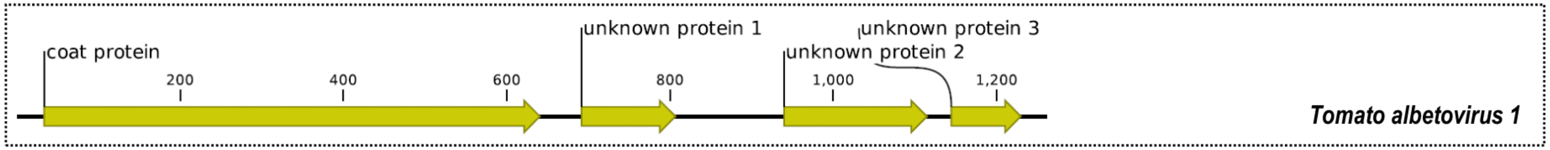
**Supplementary Figure 1** (continued)**.** Genome organization of novel viruses or first full genomes of known viruses, showing known and putative open reading frames and the protein it codes for, and predicted secondary structures of selected viroid-like circular RNAs detected in this study. **Note**: Genome length in number of bases are shown with a scale. For full information on genome length, protein domains, *etc.,* please refer to Supplementary Table 5, and the corresponding accession in GenBank.



**Supplementary Figure 1-09.** Genome of new virus species discovered under genus *Potexvirus,* family *Alphaflexiviridae* (order *Tymovirales*).

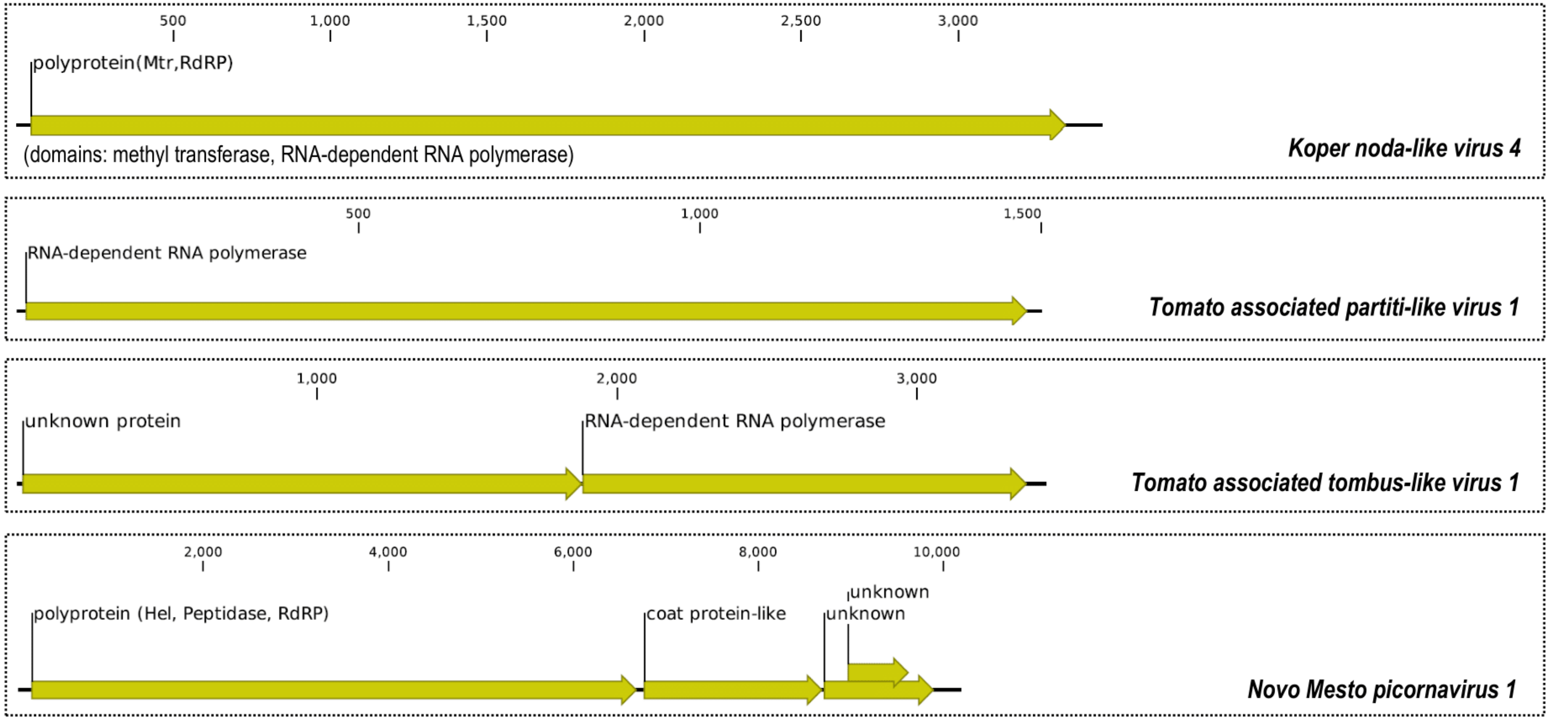


**Supplementary Figure 1-10.** Genome of new virus species discovered under genus *Vitivirus,* family *Betaflexiviridae* (order *Tymovirales*).



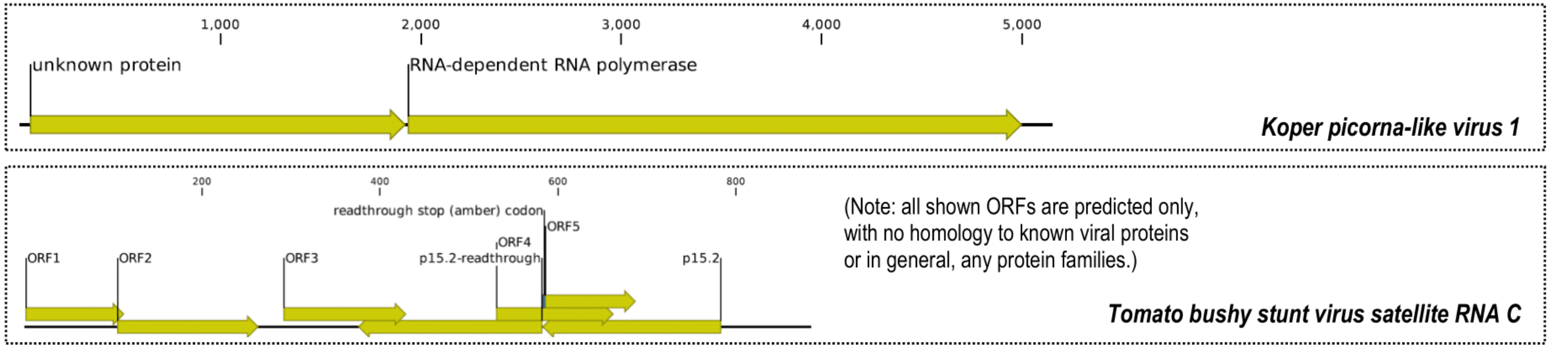
**Supplementary Figure 1-11.** Genome of new virus species discovered under genus *Albetovirus,* under unclassified satellite viruses.

**Supplementary Figure 1** (continued)**.** Genome organization of novel viruses or first full genomes of known viruses, showing known and putative open reading frames and the protein it codes for, and predicted secondary structures of selected viroid-like circular RNAs detected in this study. **Note**: Genome length in number of bases are shown with a scale. For full information on genome length, protein domains, *etc.,* please refer to Supplementary Table 5, and the corresponding accession in GenBank.



**Supplementary Figure 1-12** (continued)**.** Genome of new but unclassified virus species discovered under Realm *Riboviria.*

**Supplementary Figure 1** (continued)**.** Genome organization of novel viruses or first full genomes of known viruses, showing known and putative open reading frames and the protein it codes for, and predicted secondary structures of selected viroid-like circular RNAs detected in this study. **Note**: Genome length in number of bases are shown with a scale. For full information on genome length, protein domains, *etc.*, please refer to Supplementary Table 5, and the corresponding accession in GenBank.



***Koper picorna-like virus 1***

(Note: all shown ORFs are predicted only, with no homology to known viral proteins or in general, any protein families.)

***Tomato bushy stunt virus satellite RNA C***

**Supplementary Figure 1-12** (continued)**.** Genome of new but unclassified virus species discovered under Realm *Riboviria.*

**Supplementary Figure 1** (continued)**.** Genome organization of novel viruses or first full genomes of known viruses, showing known and putative open reading frames and the protein it codes for, and predicted secondary structures of selected viroid-like circular RNAs detected in this study. **Note**: Genome length in number of bases are shown with a scale. For full information on genome length, protein domains, *etc.,* please refer to Supplementary Table 5, and the corresponding accession in GenBank.

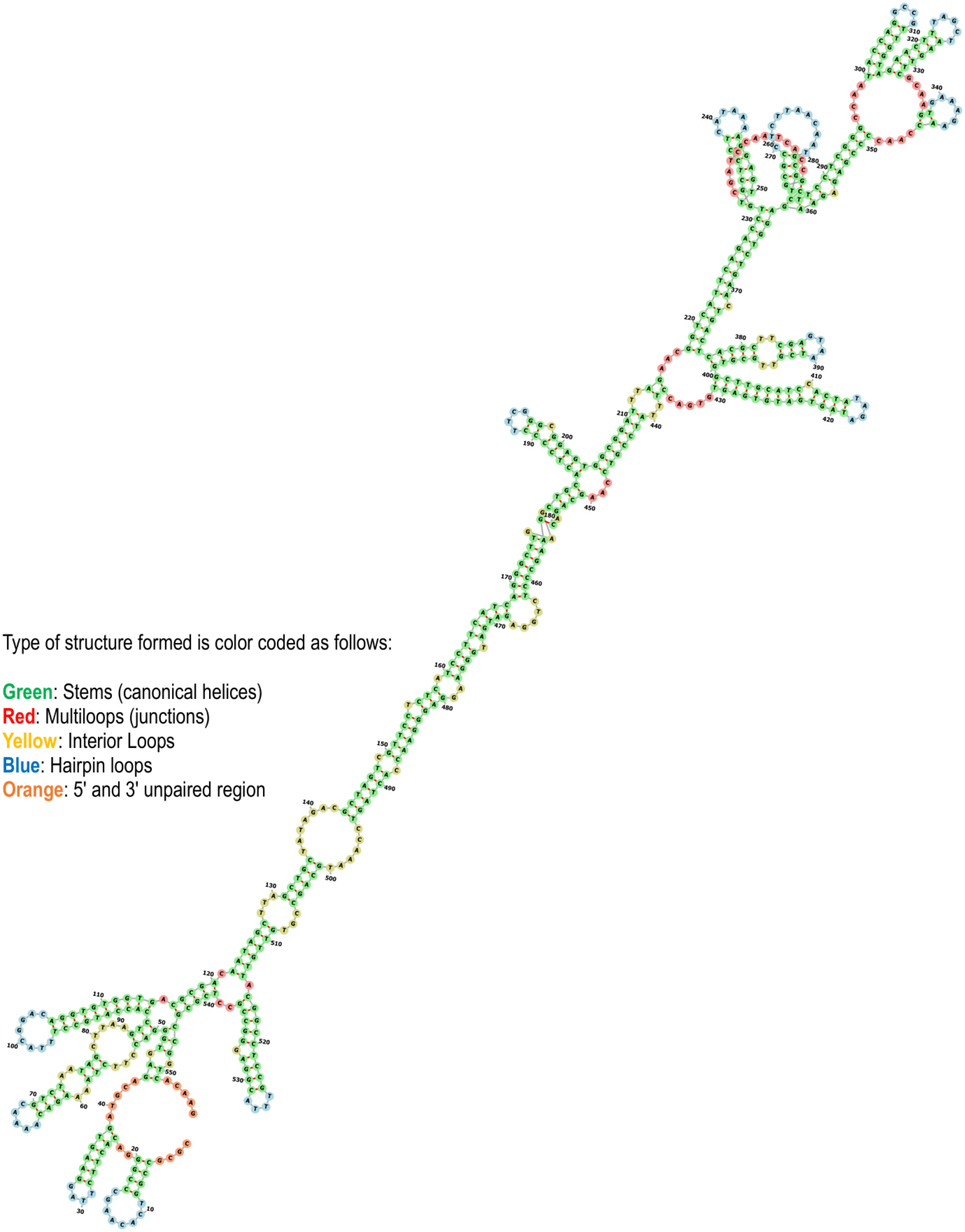
Type of structure formed is color coded as follows:

**Green**: Stems (canonical helices)
**Red**: Multiloops (junctions)
**Yellow**: Interior Loops
**Blue**: Hairpin loops
**Orange**: 5' and 3' unpaired region

***Taraxacum viroid-like circular RNA 1***
dG = -194.35, at 37°C with 1 M NaCl concentration

**Supplementary Figure 1-13**. Predicted secondary structures of selected viroid-like circular RNAs detected in this study.

**Supplementary Figure 1** (continued)**.** Genome organization of novel viruses, or first full genomes of known viruses showing known and putative open reading frames and the protein it codes for, and predicted secondary stuctures of viroid-like circular RNAs detected in this study. **Note**: Genome length in number of bases are shown with a scale. For full information on genome length, protein domains, etc., please refer to Supplementary Table 5 (of the Supplementary Information), and the corresponding accession in GenBank.



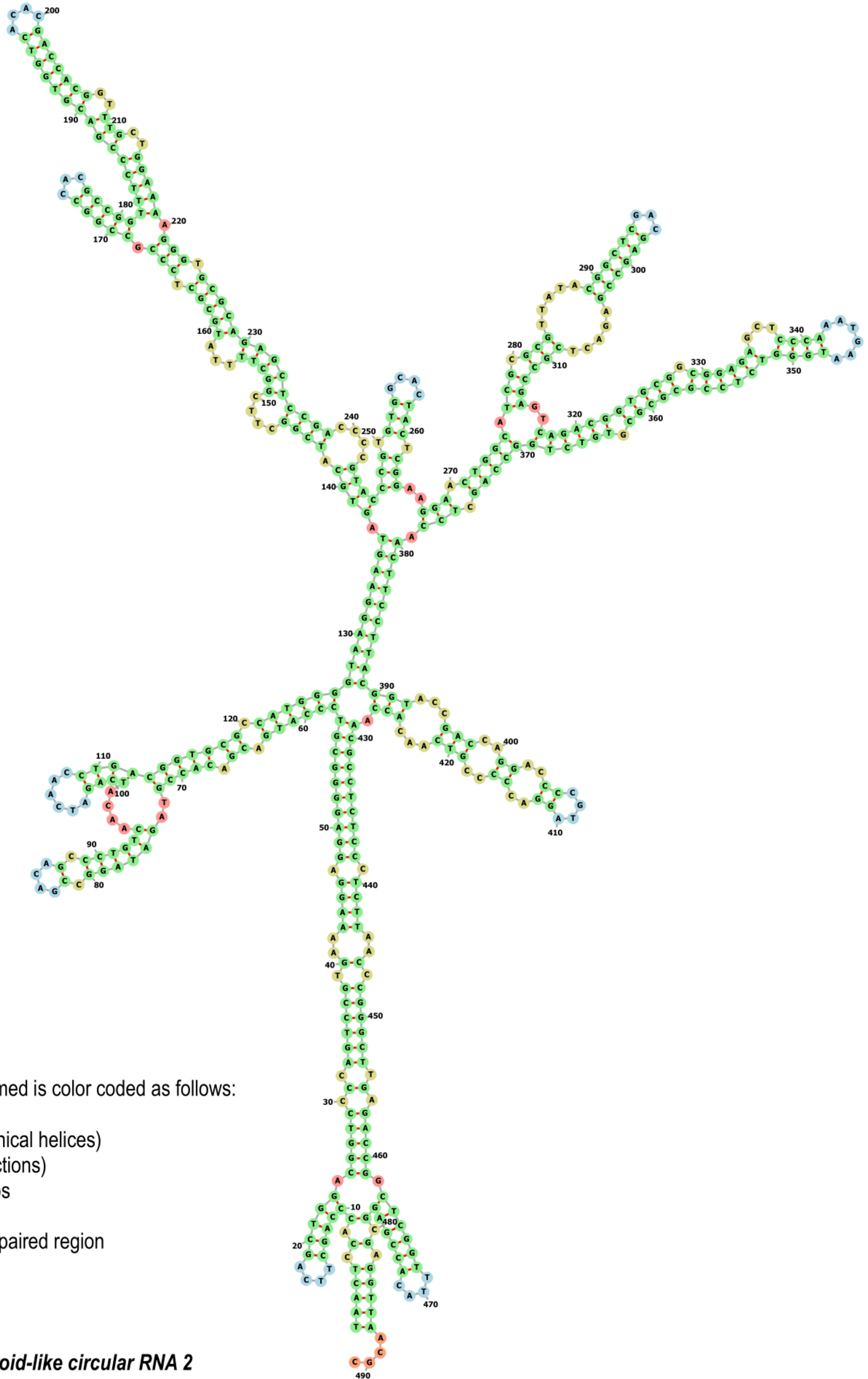
Type of structure formed is color coded as follows:

**Green**: Stems (canonical helices)
**Red**: Multiloops (junctions)
**Yellow**: Interior Loops
**Blue**: Hairpin loops
**Orange**: 5' and 3' unpaired region

***Plant associated viroid-like circular RNA 1*** dG = -181.90, at 37°C with 1 M NaCl concentration

**Supplementary Figure 1-13** (continued). Predicted secondary structures of selected viroid-like circular RNAs detected in this study.

**Supplementary Figure 1** (continued**).** Genome organization of novel viruses, or first full genomes of known viruses showing known and putative open reading frames and the protein it codes for, and predicted secondary stuctures of viroid-like circular RNAs detected in this study. **Note**: Genome length in number of bases are shown with a scale. For full information on genome length, protein domains, etc., please refer to Supplementary Table 5 (of the Supplementary Information), and the corresponding accession in GenBank.



Type of structure formed is color coded as follows:

**Green**: Stems (canonical helices)
**Red**: Multiloops (junctions)
**Yellow**: Interior Loops
**Blue**: Hairpin loops
**Orange**: 5' and 3' unpaired region

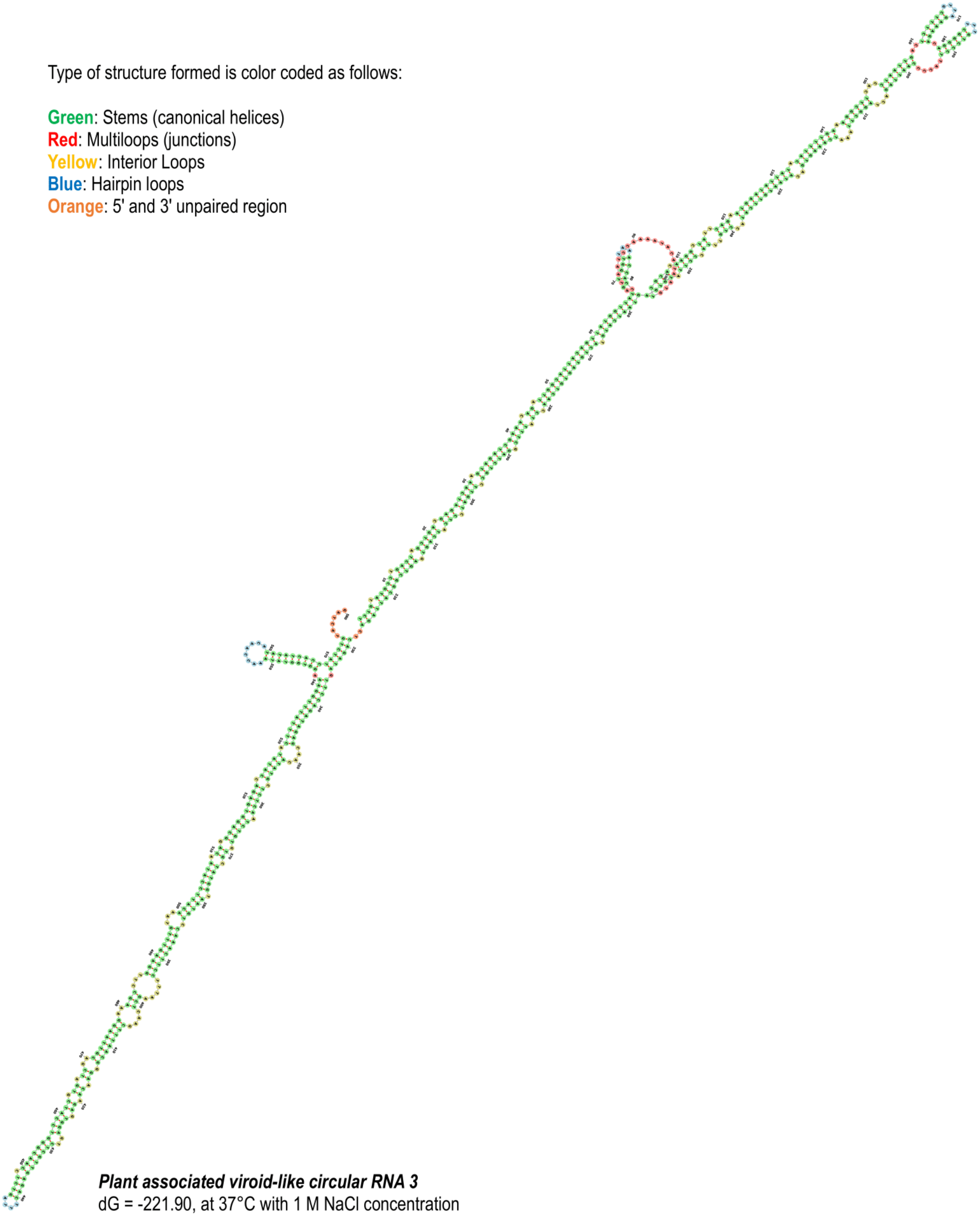
***Plant associated viroid-like circular RNA 2***
dG = -247.60, at 37°C with 1 M NaCl concentration

**Supplementary Figure 1-13** (continued). Predicted secondary structures of selected viroid-like circular RNAs detected in this study.

**Supplementary Figure 1** (continued)**.** Genome organization of novel viruses, or first full genomes of known viruses showing known and putative open reading frames and the protein it codes for, and predicted secondary stuctures of viroid-like circular RNAs detected in this study. **Note**: Genome length in number of bases are shown with a scale. For full information on genome length, protein domains, etc., please refer to Supplementary Table 5 (of the Supplementary Information), and the corresponding accession in GenBank.

Type of structure formed is color coded as follows:

**Green**: Stems (canonical helices)
**Red**: Multiloops (junctions)
**Yellow**: Interior Loops
**Blue**: Hairpin loops
**Orange**: 5' and 3' unpaired region



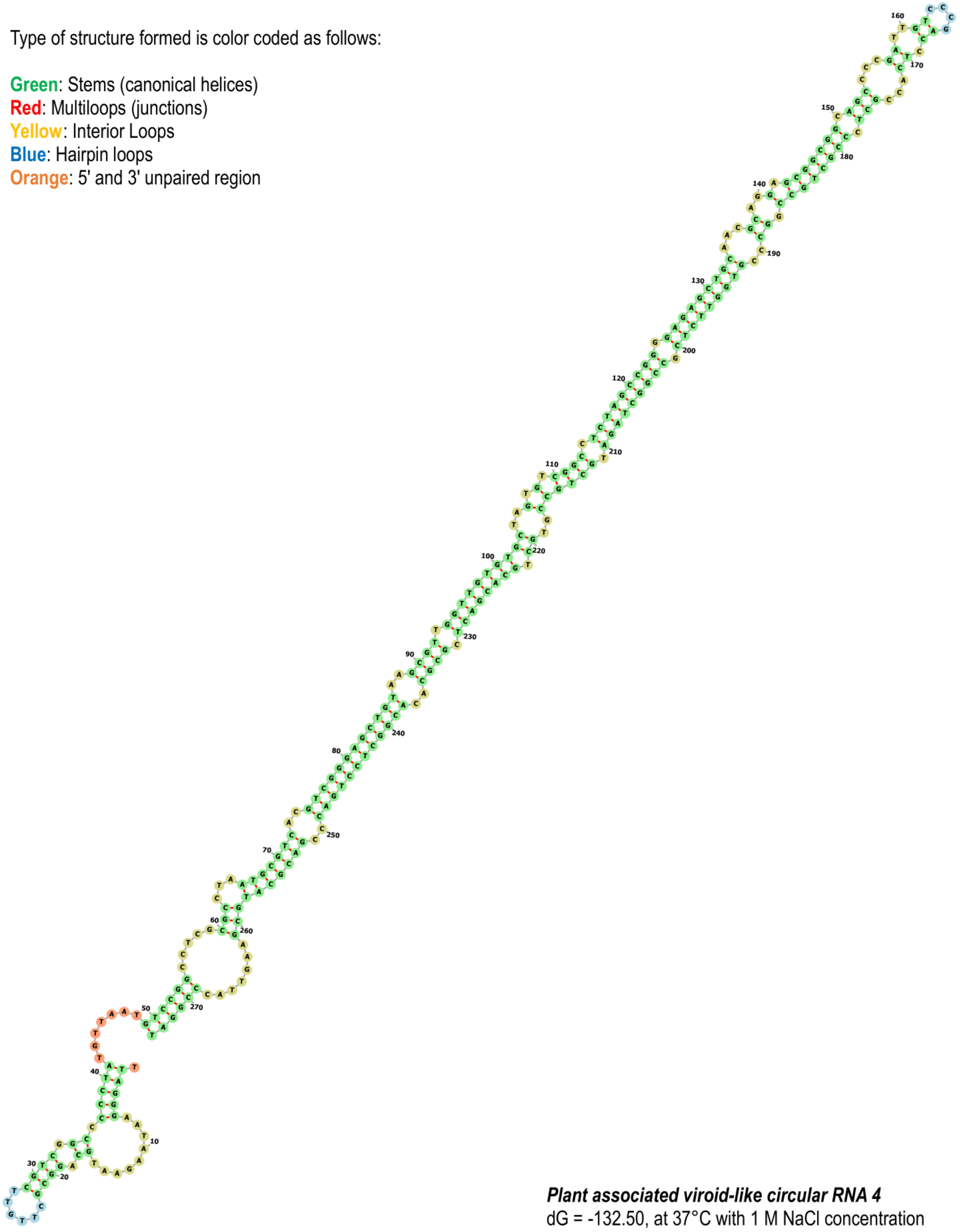
***Plant associated viroid-like circular RNA 3***
dG = -221.90, at 37°C with 1 M NaCl concentration

**Supplementary Figure 1-13** (continued). Predicted secondary structures of selected viroid-like circular RNAs detected in this study.

**Supplementary Figure 1** (continued)**.** Genome organization of novel viruses, or first full genomes of known viruses showing known and putative open reading frames and the protein it codes for, and predicted secondary stuctures of viroid-like circular RNAs detected in this study. **Note**: Genome length in number of bases are shown with a scale. For full information on genome length, protein domains, etc., please refer to Supplementary Table 5 (of the Supplementary Information), and the corresponding accession in GenBank.

Type of structure formed is color coded as follows:

**Green**: Stems (canonical helices)
**Red**: Multiloops (junctions)
**Yellow**: Interior Loops
**Blue**: Hairpin loops
**Orange**: 5' and 3' unpaired region



***Plant associated viroid-like circular RNA 4***
dG = -132.50, at 37°C with 1 M NaCl concentration

**Supplementary Figure 1-13** (continued). Predicted secondary structures of selected viroid-like circular RNAs detected in this study.

**Supplementary Figure 1** (continued)**.** Genome organization of novel viruses, or first full genomes of known viruses showing known and putative open reading frames and the protein it codes for, and predicted secondary stuctures of viroid-like circular RNAs detected in this study. **Note**: Genome length in number of bases are shown with a scale. For full information on genome length, protein domains, etc., please refer to Supplementary Table 5 (of the Supplementary Information), and the corresponding accession in GenBank.

**Supplementary Table 7.** RT-PCR primers and PCR conditions used in confirmation of associated plant hosts of selected viruses and a putative viroid. Note: GenBank accession numbers of the species indicated above are in Supplementary Table 5.

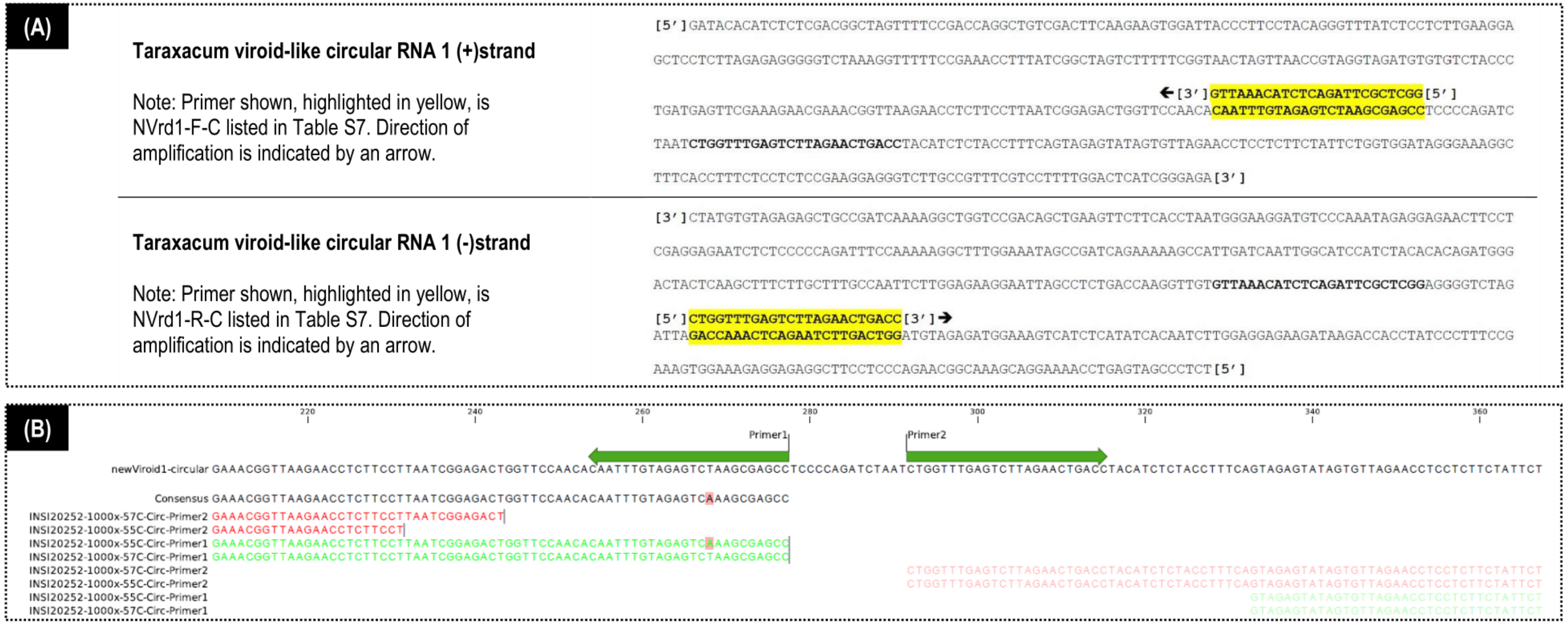
| No. | Target virus name | Primer ID | Strand | Sequence (5'→3') | Length (bases) | Target genome region (start, end position / gene(s)) | | | Annealing tempera-ture. (°C) | Amplicon size (bases) |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | Start | End | Gene | | |
| 01 | Artemesia fimovirus 1 | NFimo1-F<br>NFimo1-R | forward<br>reverse | ACATGGAAGTGACAGGTTCTCC<br>ATAGTTGACGCCTACCCATTGC | 22<br>22 | 5889 | 6435 | RdRP | 57 | 547 |
| 02 | Calystegia geminivirus 1 | NGemi1-F<br>NGemi1-R | forward<br>reverse | CAGAACCTCAACCTTCCATTCC<br>CCAATCAGCTCTTTCCAGTGC | 22<br>21 | 248 | 817 | replicase | 57 | 570 |
| 03 | Plantago potyvirus 1 | NPoty1-F<br>NPoty1-R | forward<br>reverse | AGGCTAGAGATCGCAAACTTGG<br>CAACTTTATCCGTGCTCTGTGG | 22<br>22 | 5687 | 6550 | polyprotein | 57 | 864 |
| 04 | Mentha macluravirus 1 | NPoty2-F<br>NPoty2-R | forward<br>reverse | ACATACGGCTCAGCTTTCTTCC<br>GGCACAGAGAACTTCAACATCG | 22<br>22 | 2474 | 3306 | polyprotein | 57 | 833 |
| 05 | Rumex potyvirus 1 | NPoty3-F<br>NPoty3-R | forward<br>reverse | GTTGACCTAACCCCTCACAACC<br>CACTACTGGTAGCCCACACTGC | 22<br>22 | 7098 | 7733 | polyprotein | 57 | 636 |
| 06 | broad-leafed dock virus A, isolate 2 | NPoty4-F<br>NPoty4-R | forward<br>reverse | GGATGAGGAATATGGAGCTTGG<br>TACTAGGCGGTGGAAGAAAACC | 22<br>22 | 7502 | 8178 | polyprotein | 57 | 677 |
| 07 | Pastinaca umbravirus 1 | NTomb1-F<br>NTomb1-R | forward<br>reverse | GCGAGACTGTCTGTACCACTGC<br>CAGTCGTACCCCCTCTAACTGG | 22<br>22 | 2504 | 3354 | RdRP-MP | 57 | 851 |
| 08 | Picris umbravirus 1 | NTomb2-F<br>NTomb2-R | forward<br>reverse | TCGTGCTGTATAGGGTTCATGG<br>CAAACTCCCCAAATGGACTACC | 22<br>22 | 1846 | 2839 | RdRP | 57 | 994 |
| 09 | Convolvulus aureusvirus 1 | NTomb3-F<br>NTomb3-R | forward<br>reverse | GAAAGTCAGCCGAATTGTAGGG<br>CAATCCAAGTTGGTCCTTCTCC | 22<br>22 | 1088 | 1814 | RdRP | 57 | 727 |
| 10 | Calystegia pelarspovirus 1 | NTomb4-F<br>NTomb4-R | forward<br>reverse | GCCGAATGAGGGTATGTTTAGG<br>GTTCCGCTGTTCTTCAACTGG | 22<br>21 | 1019 | 1594 | RdRP | 57 | 576 |
| 11 | Cichorium alphacarmovirus 1 | NTomb6-F<br>NTomb6-R | forward<br>reverse | GGAGAAACATGAGGAACGAACC<br>AGAAAACCCTTTCCAGGAGACC | 22<br>22 | 322 | 989 | RdRP | 57 | 668 |
| 12 | Pastinaca potexvirus 1 | NAflex1-F<br>NAflex1-R | forward<br>reverse | CACAGTGGATGAGGATGTAGCC<br>TTCGTAAGCTGAGCTGAGTTGG | 22<br>22 | 3565 | 4542 | polypro-tein-TGB | 57 | 978 |
| 13 | plant associated tobamo-like virus 1 | NVirga1-F<br>NVirga1-R | forward<br>reverse | CTTCACCTGTCTCAGTGAGGAC<br>TATGAGTTGCGATGGGTAGACG | 22<br>22 | 115 | 522 | replicase | 55 | 408 |
| 14 | Plantago tobamovirus 1 | NVirga2-F<br>NVirga2-R | forward<br>reverse | AACGCACTATCCGAGCTATCTG<br>TACAGCCACCCTAAACCATGTC | 22<br>22 | 1720 | 2421 | replicase | 55 | 702 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| 15 | Mercurialis orthotospovirus 1 | NTospo1-F | forward | TAGAGCCGAAGATGTTGTGGAC | 22 | 1661 | 2291 | L gene (RdRP) | 55 | 631 |
| | | NTospo1-R | reverse | GTCAGCGACCATTAAGCCTTTG | 22 | | | | | |
| 16 | tomato associated bunya-like virus 1 | NTospo2-F | forward | CGAAAGGAGGCGATAGTGATGC | 22 | 7109 | 7615 | L gene (RdRP) | 56 | 507 |
| | | NTospo2-R | reverse | CTGCGTCATCCCTACCTGATAC | 22 | | | | | |
| 17 | tomato vitivirus 1 | NBflexi1-F | forward | TCTTTCCCCTCTTGATCTGTGC | 22 | 1057 | 1540 | movement protein | 55 | 484 |
| | | NBflexi1-R | reverse | GTGAACCCTGAATTGGTTGAGC | 22 | | | | | |
| 18 | Prunus virus I | NBromo1-F | forward | AAGTTTCGAGACCTTTGCGTTG | 22 | 826 | 1699 | movement protein | 55 | 874 |
| | | NBromo1-R | reverse | CTCAAACACACTTCCGCTTCAG | 22 | | | | | |
| 19 | tomato ilarvirus 1 | NBromo2-F | forward | ACATGGCGTTAGATGGTAGGTC | 22 | 945 | 1824 | movement protein | 55 | 880 |
| | | NBromo2-R | reverse | AAATTCGCAGACAAGGTTCGTG | 22 | | | | | |
| 20 | Ranunculus white mottle ophiovirus | RWMV-F | forward | TGTGTGTTCATCTCTCTTCTGC | 22 | 804 | 1296 | coat protein | 54 | 493 |
| | | RWMV-R | reverse | ACAGGGAAGTGAATCACACCTA | 22 | | | | | |
| 21 | tomato betanucleorhabdovirus 1 | NRhabdo1-F | forward | GACGGTAGGTTACAATCTCC | 20 | 12078 | 12589 | L gene (RdRP) | 55 | 512 |
| | | NRhabdo1-R | reverse | TGATAGGGCTAGGATATGGG | 20 | | | | | |
| 22 | Pastinaca cytorhabdovirus 1 | NRhab3-F | forward | GAGGAAAAAGTCTGTCATGGAC | 22 | 1395 | 1925 | L gene (RdRP) | 52 | 531 |
| | | NRhab3-R | reverse | GCAAGGTAATAATAGCACTCGG | 22 | | | | | |
| 23 | tomato betanucleorhabdovirus 2 | NRhab4-F | forward | TTCCTGTTCATTATCACAATGC | 22 | 4279 | 4874 | L gene (RdRP) | 51 | 596 |
| | | NRhab4-R | reverse | GTTAGTTGACCAAGAGTACCAG | 22 | | | | | |
| 24 | Picris betanucleorhabdovirus 1 | NRhab5-F | forward | ATTGTTACACGATATTGCTGGG | 22 | 3300 | 3816 | L gene (RdRP) | 52 | 517 |
| | | NRhab5-R | reverse | TTCCTCATATCTCCACCTCAAC | 22 | | | | | |
| 25 | Cirsium cytorhabdovirus 1 | NRhab6-F | forward | TTTAGTTAGATCATTCACGGCG | 22 | 2204 | 2742 | L gene (RdRP) | 52 | 539 |
| | | NRhab6-R | reverse | TGAGGTCCCTTGATAATCGATC | 22 | | | | | |
| 26 | Taraxacum betanucleorhabdovirus 1 | NRhab7-F | forward | ATAGTTCGGACAGATCAAGGAG | 22 | 5196 | 5757 | L gene (RdRP) | 52 | 562 |
| | | NRhab7-R | reverse | ATCTCAAATGTTTGCCACTCTC | 22 | | | | | |
| 27 | Picris cytorhabdovirus 1 | NRhab8-F | forward | TCGACCAAAAGATAACAACGAC | 22 | 5798 | 6389 | L gene (RdRP) | 52 | 592 |
| | | NRhab8-R | reverse | CTTTGAAAATCACTAGTCCGGG | 22 | | | | | |
| 28 | Taraxacum cytorhabdovirus 1 | NRhab9-F | forward | CTGTATGTGGTGAAGTCAATGG | 22 | 2799 | 3347 | L gene (RdRP) | 52 | 549 |
| | | NRhab9-R | reverse | TCTCATTCTTTTCGCTTCTTCG | 22 | | | | | |
| 29 | tomato alphanucleorhabdovirus 1 | NRhab10-F | forward | GATTGTATTTCCCACTACGGACAAC | 25 | 3182 | 4230 | L gene (RdRP) | 55 | 1049 |
| | | NRhab10-R | reverse | CATACCATCATCACATAGTGTTGGC | 25 | | | | | |
| 30 | Leveillula taurica associated rhabdo-like virus 1 | NRhab2-F | forward | CCACATTATGACACAAGACCAG | 22 | 330 | 844 | L gene (RdRP) | 52 | 515 |
| | | NRhab2-R | reverse | TAAGCTTTGTTACCTAACGCAC | 22 | | | | | |
| 31 | eggplant mottled dwarf alphanucleorhabdovirus | EMDV-F | forward | TACTCATTACACAAAGAGAAGC | 22 | 143 | 699 | L gene (RdRP) | 51 | 557 |
| | | EMDV-R | reverse | CGGTATAGTTATACTAGCAGCA | 22 | | | | | |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| 32 | Physostegia chlorotic mottle alphanucleorhabdovirus | PhCMoV-F | forward | ATAGTGACATTCTGTTTGACCG | 22 | 2810 | 3463 | L gene (RdRP) | 52 | 654 |
| | | PhCMoV-R | reverse | CCCATACTACCCATTATTCTGC | 22 | | | | | |
| 33 | tomato fruit blotch virus | ToFBV-R3-F | forward | GTGGTTATTATGGATATACCTGCG | 24 | 654 | 1371 | coat protein | 52 | 718 |
| | | ToFBV-R3-R | reverse | GAGAGAACACAAAACAAGAAGC | 22 | | | | | |
| 34 | Solanum nigrum ilarvirus 1 | SnIV-R3-F | forward | GTATGAAAACTTCAACCTCTCC | 22 | 1248 | 1916 | coat protein | 52 | 669 |
| | | SnIV-R3-R | reverse | ATATAGCTACCCAGAAATCAGC | 22 | | | | | |
| 35 | tomato matilda virus | TMaV-F | forward | ACTAGCCGTTATATTTAGTGGG | 22 | 5293 | 5900 | polyprotein | 52 | 608 |
| | | TMaV-R | reverse | CTACTATACTGAGAACTCCTTTCC | 24 | | | | | |
| 36 | Taraxacum viroid-like circular RNA 1 | NVrd1-F-LP | forward | TCGGCTAGTCTTTTTCGGTAAC | 22 | 138 | 392 | not applicable | 55 | 255 |
| | | NVrd1-R-LP | reverse | AGGTGAAAGCCTTTCCCTATCC | 22 | | | | | |
| | (Note: LP - linear amplification, C - circular amplification) | NVrd1-F-C | primer 1 | GGCTCGCTTAGACTCTACAAATTG | 24 | 277<br>(+) strand | 291<br>(-) strand | not applicable | 55 | 433 |
| | | NVrd1-R-C | primer 2 | CTGGTTTGAGTCTTAGAACTGACC | 24 | | | | | |

**Supplementary Table 8.** RT-PCR thermocycling conditions used in the detection of selected viruses and putative viroids in associated plant hosts.

| | | |
|---|---|---|
| Reverse transcription step (2 sub-steps): | 30 min at 50ºC<br>15 min at 95ºC | |
| PCR step (3 sub-steps): | 0.5 min at 94ºC<br>0.5 min at annealing temperature (ºC) in **Table S7**<br>1.0 min at 72ºC | 35 cycles |
| Extension step: | 10 min at 72ºC | |



**(A)**

**Taraxacum viroid-like circular RNA 1 (+)strand**

Note: Primer shown, highlighted in yellow, is NVrd1-F-C listed in Table S7. Direction of amplification is indicated by an arrow.

```
[5′]GATACACATCTCTCGACGGCTAGTTTTCCGACCAGGCTGTCGACTTCAAGAAGTGGATTACCCTTCCTACAGGGTTTATCTCCTCTTGAAGGA

GCTCCTCTTAGAGAGGGGGTCTAAAGGTTTTTCCGAAACCTTTATCGGCTAGTCTTTTTCGGTAACTAGTTAACCGTAGGTAGATGTGTGTCTACCC

                                                                      ← [3′]GTTAAACATCTCAGATTCGCTCGG[5′]
TGATGAGTTCGAAAGAACGAAACGGTTAAGAACCTCTTCCTTAATCGGAGACTGGTTCCAACACAATTTGTAGAGTCTAAGCGAGCCTCCCCAGATC

TAATCTGGTTTGAGTCTTAGAACTGACCTACATCTCTACCTTTCAGTAGAGTATAGTGTTAGAACCTCCTCTTCTATTCTGGTGGATAGGGAAAGGC

TTTCACCTTTCTCCTCTCCGAAGGAGGGTCTTGCCGTTTCGTCCTTTTGGACTCATCGGGAGA[3′]
```

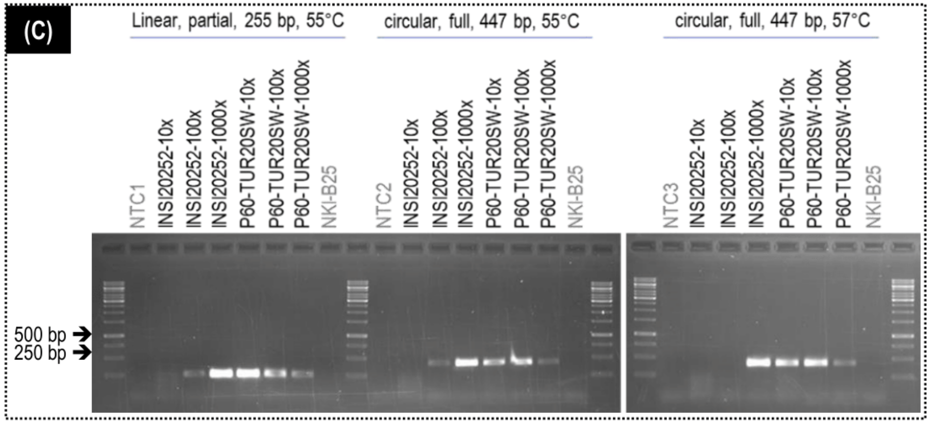
**Taraxacum viroid-like circular RNA 1 (-)strand**

Note: Primer shown, highlighted in yellow, is NVrd1-R-C listed in Table S7. Direction of amplification is indicated by an arrow.

```
[3′]CTATGTGTAGAGAGCTGCCGATCAAAAGGCTGGTCCGACAGCTGAAGTTCTTCACCTAATGGGAAGGATGTCCCAAATAGAGGAGAACTTCCT

CGAGGAGAATCTCTCCCCCAGATTTCCAAAAAGGCTTTGGAAATAGCCGATCAGAAAAAGCCATTGATCAATTGGCATCCATCTACACACAGATGGG

ACTACTCAAGCTTTCTTGCTTTGCCAATTCTTGGAGAAGGAATTAGCCTCTGACCAAGGTTGTGTTAAACATCTCAGATTCGCTCGGAGGGGTCTAG

[5′]CTGGTTTGAGTCTTAGAACTGACC[3′]→
ATTAGACCAAACTCAGAATCTTGACTGGATGTAGAGATGGAAAGTCATCTCATATCACAATCTTGGAGGAGAAGATAAGACCACCTATCCCTTTCCG

AAAGTGGAAAGAGGAGAGGCTTCCTCCCAGAACGGCAAAGCAGGAAAACCTGAGTAGCCCTCT[5′]
```

**(B)**

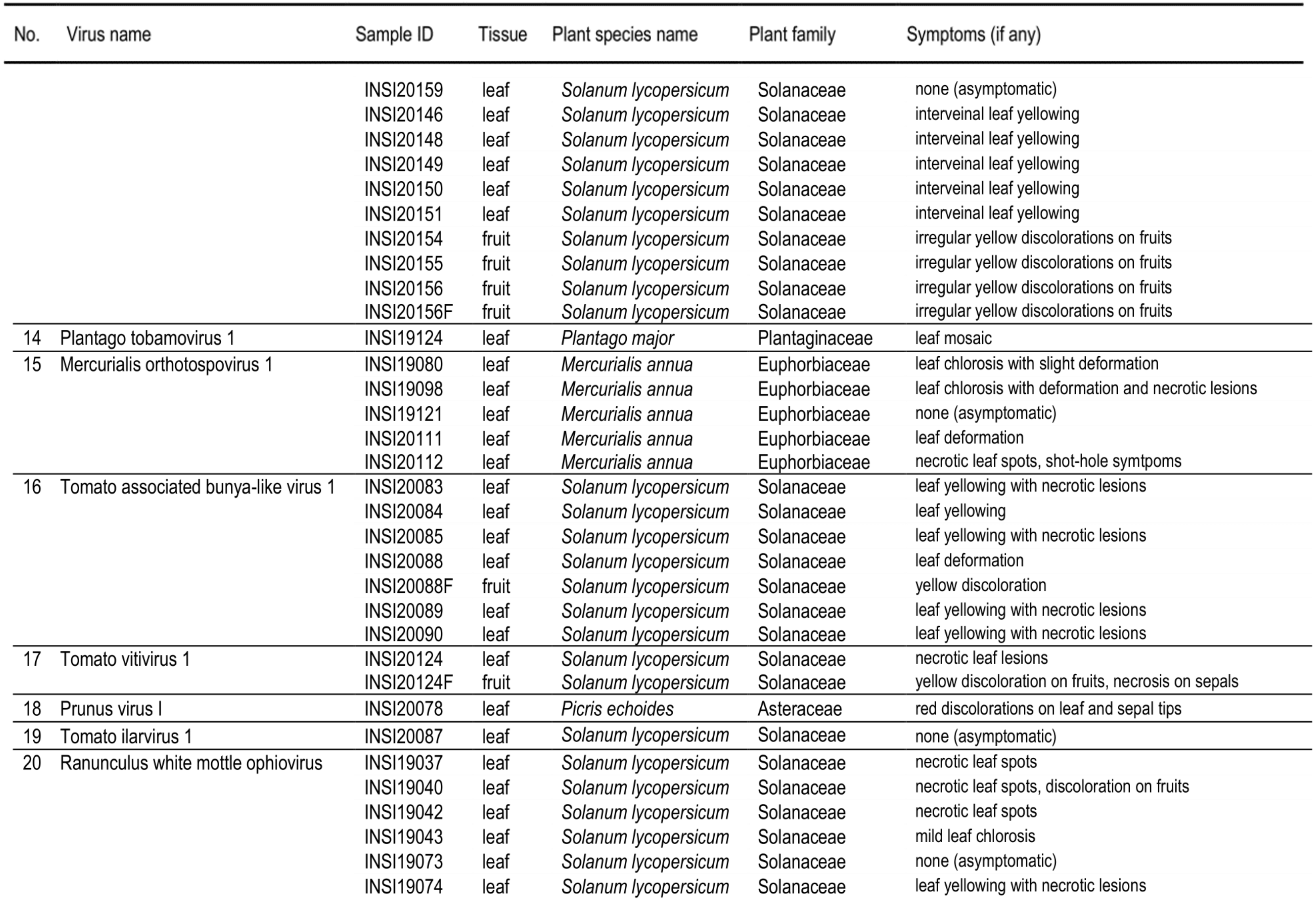
```
newViroid1-circular GAAACGGTTAAGAACCTCTTCCTTAATCGGAGACTGGTTCCAACACAATTTGTAGAGTCTAAGCGAGCCTCCCCAGATCTAATCTGGTTTGAGTCTTAGAACTGACCTACATCTCTACCTTTCAGTAGAGTATAGTGTTAGAACCTCCTCTTCTATTCT

          Consensus GAAACGGTTAAGAACCTCTTCCTTAATCGGAGACTGGTTCCAACACAATTTGTAGAGTCAAAGCGAGCC
INSI20252-1000x-57C-Circ-Primer2 GAAACGGTTAAGAACCTCTTCCTTAATCGGAGACT
INSI20252-1000x-55C-Circ-Primer2 GAAACGGTTAAGAACCTCTTCCT
INSI20252-1000x-55C-Circ-Primer1 GAAACGGTTAAGAACCTCTTCCTTAATCGGAGACTGGTTCCAACACAATTTGTAGAGTCAAAGCGAGCC
INSI20252-1000x-57C-Circ-Primer1 GAAACGGTTAAGAACCTCTTCCTTAATCGGAGACTGGTTCCAACACAATTTGTAGAGTCTAAGCGAGCC
INSI20252-1000x-57C-Circ-Primer2                                                                               CTGGTTTGAGTCTTAGAACTGACCTACATCTCTACCTTTCAGTAGAGTATAGTGTTAGAACCTCCTCTTCTATTCT
INSI20252-1000x-55C-Circ-Primer2                                                                               CTGGTTTGAGTCTTAGAACTGACCTACATCTCTACCTTTCAGTAGAGTATAGTGTTAGAACCTCCTCTTCTATTCT
INSI20252-1000x-55C-Circ-Primer1                                                                                                                       GTAGAGTATAGTGTTAGAACCTCCTCTTCTATTCT
INSI20252-1000x-57C-Circ-Primer1                                                                                                                       GTAGAGTATAGTGTTAGAACCTCCTCTTCTATTCT
```



**Supplementary Figure 2.** Primer design and RT-PCR tests for Taraxacum viroid-like circular RNA 1. (A) Orientation and annealing sites of the primers designed to amplify the circular genome of Taraxacum viroid-like circular RNA 1. (B-C) Reassembly of selected sequenced amplicons form the RT-PCR tests (B) in samples with increasing dilution factors shown in (C). Abutting primers are shown in green arrows, demarcating the 14 nucleotide gap between them (B). Note: In (C): NTC1, NTC2 – non-template controls; NKI-B25 - negative control of isolation in the RNA extraction, INSI20252 - *Taraxacum officinale* sample, P60-TUR20SW - sequenced composite sample where INSI20252 belong.

**Supplementary Table 9.** List of confirmed associated plant hosts of selected viruses. For information related to the individual plant samples and the composite samples, please refer to Supplementary Table 1 and 2. Note: In most of the cases infection of multiple viruses in individual plants with cannot be excluded, except if stated otherwise.

| No. | Virus name | Sample ID | Tissue | Plant species name | Plant family | Symptoms (if any) |
|---|---|---|---|---|---|---|
| 01 | Artemesia fimovirus 1 | INSI20094 | leaf | *Artemisia verlotiorum* | Asteraceae | mild leaf yellowing |
| 02 | Calystegia geminivirus 1 | INSI20122 | leaf | *Calystegia* sp. | Convolvulaceae | leaf yellowing with crumpling deformation |
| 03 | Plantago potyvirus 1 | INSI19064 | leaf | *Plantago lanceolata* | Plantaginaceae | interveinal leaf yellowing with deformation |
| 04 | Mentha macluravirus 1 | INSI20169 | leaf | *Mentha spicata* | Lamiaceae | mild leaf yellowing with a few necrotic spots |
| 05 | Rumex potyvirus 1 | INSI20188 | leaf | *Rumex* sp. | Polygonaceae | ring-like chlorotic lesions and red spots on leaves |
| | | INSI20199 | leaf | *Convolvulus* sp. | Convolvulaceae | leaf chlorosis |
| 06 | Broad-leafed dock virus A, isolate 2 | INSI20253 | leaf | *Rumex crispus* | Polygonaceae | leaf chlorosis with mottling |
| 07 | Pastinaca umbravirus 1 | INSI19137 | leaf | *Pastinaca sativa* | Apiaceae | necrotic spots, mosaic on leaves |
| | | INSI19156 | leaf | *Pastinaca sativa* | Apiaceae | irregular leaf chlorosis |
| | | INSI20168 | leaf | *Pastinaca sativa* | Apiaceae | irregular leaf chlorosis |
| 08 | Picris umbravirus 1 | INSI19136 | leaf | *Picris echoides* | Asteraceae | necrotic leaf lesions |
| | | INSI20082 | leaf | *Picris echoides* | Asteraceae | chlorotic leaf spots |
| 09 | Convolvulus aureusvirus 1 | INSI20072 | leaf | *Convolvulus arvensis* | Convolvulaceae | necrotic leaf lesions |
| | | INSI20073 | leaf | *Convolvulus arvensis* | Convolvulaceae | leaf curling with mild yellowing |
| 10 | Calystegia pelarspovirus 1 | INSI20122 | leaf | *Calystegia* sp. | Convolvulaceae | leaf yellowing with crumpling deformation |
| | | INSI20163 | leaf | *Calystegia* sp. | Convolvulaceae | necrotic leaf lesions with yellow halo |
| 11 | Cichorium alphacarmovirus 1 | INSI19123 | leaf | *Cichorium intybus* | Asteraceae | leaf mosaic, leaf dwarfing and deformation |
| | | INSI20074 | leaf | *Cichorium intybus* | Asteraceae | necrotic leaf lesions |
| | | INSI20075 | leaf | *Picris echoides* | Asteraceae | leaf mosaic |
| | | INSI20078 | leaf | *Picris echoides* | Asteraceae | redness of leaves, necrosis on flowers |
| | | INSI20082 | leaf | *Picris echoides* | Asteraceae | chlorotic leaf spots |
| 12 | Pastinaca potexvirus 1 | INSI19137 | leaf | *Pastinaca sativa* | Apiaceae | necrotic spots, mosaic on leaves |
| 13 | Plant associated tobamo-like virus 1 | INSI19082 | leaf | *Convolvulus arvensis* | Convolvulaceae | with powdery mildew colonization / infection |
| | | INSI20147 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI20152 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI20157 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI20158 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |



| No. | Virus name | Sample ID | Tissue | Plant species name | Plant family | Symptoms (if any) |
|---|---|---|---|---|---|---|
| | | INSI20159 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI20146 | leaf | *Solanum lycopersicum* | Solanaceae | interveinal leaf yellowing |
| | | INSI20148 | leaf | *Solanum lycopersicum* | Solanaceae | interveinal leaf yellowing |
| | | INSI20149 | leaf | *Solanum lycopersicum* | Solanaceae | interveinal leaf yellowing |
| | | INSI20150 | leaf | *Solanum lycopersicum* | Solanaceae | interveinal leaf yellowing |
| | | INSI20151 | leaf | *Solanum lycopersicum* | Solanaceae | interveinal leaf yellowing |
| | | INSI20154 | fruit | *Solanum lycopersicum* | Solanaceae | irregular yellow discolorations on fruits |
| | | INSI20155 | fruit | *Solanum lycopersicum* | Solanaceae | irregular yellow discolorations on fruits |
| | | INSI20156 | fruit | *Solanum lycopersicum* | Solanaceae | irregular yellow discolorations on fruits |
| | | INSI20156F | fruit | *Solanum lycopersicum* | Solanaceae | irregular yellow discolorations on fruits |
| 14 | Plantago tobamovirus 1 | INSI19124 | leaf | *Plantago major* | Plantaginaceae | leaf mosaic |
| 15 | Mercurialis orthotospovirus 1 | INSI19080 | leaf | *Mercurialis annua* | Euphorbiaceae | leaf chlorosis with slight deformation |
| | | INSI19098 | leaf | *Mercurialis annua* | Euphorbiaceae | leaf chlorosis with deformation and necrotic lesions |
| | | INSI19121 | leaf | *Mercurialis annua* | Euphorbiaceae | none (asymptomatic) |
| | | INSI20111 | leaf | *Mercurialis annua* | Euphorbiaceae | leaf deformation |
| | | INSI20112 | leaf | *Mercurialis annua* | Euphorbiaceae | necrotic leaf spots, shot-hole symtpoms |
| 16 | Tomato associated bunya-like virus 1 | INSI20083 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing with necrotic lesions |
| | | INSI20084 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing |
| | | INSI20085 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing with necrotic lesions |
| | | INSI20088 | leaf | *Solanum lycopersicum* | Solanaceae | leaf deformation |
| | | INSI20088F | fruit | *Solanum lycopersicum* | Solanaceae | yellow discoloration |
| | | INSI20089 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing with necrotic lesions |
| | | INSI20090 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing with necrotic lesions |
| 17 | Tomato vitivirus 1 | INSI20124 | leaf | *Solanum lycopersicum* | Solanaceae | necrotic leaf lesions |
| | | INSI20124F | fruit | *Solanum lycopersicum* | Solanaceae | yellow discoloration on fruits, necrosis on sepals |
| 18 | Prunus virus I | INSI20078 | leaf | *Picris echoides* | Asteraceae | red discolorations on leaf and sepal tips |
| 19 | Tomato ilarvirus 1 | INSI20087 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| 20 | Ranunculus white mottle ophiovirus | INSI19037 | leaf | *Solanum lycopersicum* | Solanaceae | necrotic leaf spots |
| | | INSI19040 | leaf | *Solanum lycopersicum* | Solanaceae | necrotic leaf spots, discoloration on fruits |
| | | INSI19042 | leaf | *Solanum lycopersicum* | Solanaceae | necrotic leaf spots |
| | | INSI19043 | leaf | *Solanum lycopersicum* | Solanaceae | mild leaf chlorosis |
| | | INSI19073 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19074 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing with necrotic lesions |

| No. | Virus name | Sample ID | Tissue | Plant species name | Plant family | Symptoms (if any) |
|---|---|---|---|---|---|---|
| | | INSI19074 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing with necrotic lesions |
| | | INSI19102 | leaf | *Solanum nigrum* | Solanaceae | none (asymptomatic) |
| | | INSI20177 | leaf | *Solanum lycopersicum* | Solanaceae | leaf folding |
| | | INSI20177F | fruit | *Solanum lycopersicum* | Solanaceae | fruit deformation, cracking |
| 21 | Tomato betanucleorhabdovirus 1 | INSI19008 | leaf | *Solanum lycopersicum* | Solanaceae | leaf folding |
| 22 | Pastinaca cytorhabdovirus 1 | INSI19137 | leaf | *Pastinaca sativa* | Apiaceae | necrotic spots, mosaic on leaves |
| 23 | Tomato betanucleorhabdovirus 2 | INSI20041 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI20068 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI20123 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing and deformation, uneven fruit ripening |
| | | INSI20132 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing and deformation |
| | | INSI20133 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| 24 | Picris betanucleorhabdovirus 1 | INSI20078 | leaf | *Picris echoides* | Asteraceae | red discolorations on leaf and sepal tips |
| | | INSI20080 | leaf | *Picris echoides* | Asteraceae | red discolorations on leaf and sepal tips |
| | | INSI20138 | leaf | *Picris echoides* | Asteraceae | cholorotic and necrotic spots |
| 25 | Cirsium cytorhabdovirus 1 | INSI20161 | leaf | *Cirsium arvense* | Asteraceae | leaf yellowing (near leaf lamina) |
| 26 | Taraxacum betanucleorhabdovirus 1 | INSI20194 | leaf | *Taraxacum officinale* | Asteraceae | systemic leaf chlorosis |
| | | INSI20252 | leaf | *Taraxacum officinale* | Asteraceae | interveinal leaf chlorosis |
| 27 | Picris cytorhabdovirus 1 | INSI20080 | leaf | *Picris echoides* | Asteraceae | red discolorations on leaf and sepal tips |
| | | INSI20081 | leaf | *Picris echoides* | Asteraceae | leaf mosaic |
| | | INSI20082 | leaf | *Picris echoides* | Asteraceae | red lesions on leaves and midribs |
| 28 | Taraxacum cytorhabdovirus 1 | INSI20194 | leaf | *Taraxacum officinale* | Asteraceae | systemic leaf chlorosis |
| 29 | Tomato alphanucleorhabdovirus 1 | INSI20029 | leaf | *Solanum lycopersicum* | Solanaceae | fruit mottling, showing large irregular shape yellow dents |
| | | INSI20030 | leaf | *Solanum lycopersicum* | Solanaceae | fruit mottling, showing large irregular shape yellow dents |
| | | INSI20030F | fruit | *Solanum lycopersicum* | Solanaceae | fruit mottling, showing large irregular shape yellow dents |
| 30 | Leveillula taurica associated rhabdo-like virus 1 | INSI19051 | leaf | *Solanum lycopersicum* | Solanaceae | leaves with powdery mildew colonization, necrotic spots |
| | | INSI19053 | leaf | *Solanum lycopersicum* | Solanaceae | leaves with powdery mildew colonization, necrotic spots |
| | | INSI19054 | leaf | *Solanum lycopersicum* | Solanaceae | leaves with powdery mildew colonization, necrotic spots |
| | | INSI19055 | leaf | *Solanum lycopersicum* | Solanaceae | leaves with powdery mildew colonization, necrotic spots |
| | | INSI19056 | leaf | *Solanum lycopersicum* | Solanaceae | leaves with powdery mildew colonization, necrotic spots |
| | | INSI19058 | leaf | *Solanum lycopersicum* | Solanaceae | leaves with powdery mildew colonization, necrotic spots |
| 31 | Eggplant mottled dwarf alphanucleorhabdovirus | INSI20038 | leaf | *Solanum lycopersicum* | Solanaceae | necrotic spots on leaves |
| | | INSI20038F | fruit | *Solanum lycopersicum* | Solanaceae | fruit mottling, showing circular yellow dents |
| | | INSI20039 | leaf | *Solanum lycopersicum* | Solanaceae | necrotic spots on leaves |

| No. | Virus name | Sample ID | Tissue | Plant species name | Plant family | Symptoms (if any) |
|---|---|---|---|---|---|---|
| | | INSI20039F | fruit | *Solanum lycopersicum* | Solanaceae | fruit mottling, showing circular yellow dents |
| 32 | Physostegia chlorotic mottle alphanucleorhabdovirus | INSI19009 | leaf | *Solanum lycopersicum* | Solanaceae | fruit and leaf mottling and yellowing, leaf folding |
| | | INSI20177 | leaf | *Solanum lycopersicum* | Solanaceae | leaf folding |
| | | INSI20177F | fruit | *Solanum lycopersicum* | Solanaceae | fruit deformation, cracking |
| | | INSI20239F | fruit | *Solanum lycopersicum* | Solanaceae | fruit and leaf mottling and yellowing |
| | | INSI20242F | fruit | *Solanum lycopersicum* | Solanaceae | fruit and leaf mottling and yellowing |
| 33 | Tomato fruit blotch virus | INSI19101 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing with necrotic lesions |
| | | INSI19122 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing with necrotic lesions |
| 34 | Solanum nigrum ilarvirus 1 | INSI19127 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19133 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19134 | leaf | *Solanum lycopersicum* | Solanaceae | mild yellowing and leaf twisting and deformations |
| | | INSI20216 | leaf | *Physalis* sp. | Solanaceae | uneven leaf yellowing |
| 35 | Tomato matilda virus | INSI19073 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19085 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19086 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19087 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19088 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19089 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19091 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19092 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19093 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19081 | leaf | *Solanum lycopersicum* | Solanaceae | corky symptoms on fruits, leaf yellwoing |
| | | INSI19094 | leaf | *Solanum lycopersicum* | Solanaceae | yellow spots on leaves |
| | | INSI19103 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19104 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19106 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19108 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19110 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19111 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19112 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19113 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19100 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing with necrotic lesions |
| | | INSI19101 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing with necrotic lesions |
| | | INSI19114 | leaf | *Solanum lycopersicum* | Solanaceae | necrotic leaf lesions |

| No. | Virus name | Sample ID | Tissue | Plant species name | Plant family | Symptoms (if any) |
|---|---|---|---|---|---|---|
| | | INSI19115 | leaf | *Solanum lycopersicum* | Solanaceae | leaf chlorosis with necrotic lesions |
| | | INSI19116 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing with necrotic lesions |
| | | INSI19117 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing with necrotic lesions |
| | | INSI19122 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing with necrotic lesions |
| | | INSI19126 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing with necrotic lesions |
| | | INSI19128 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing with necrotic lesions |
| | | INSI19129 | leaf | *Solanum lycopersicum* | Solanaceae | yellow spots on leaves |
| | | INSI19134 | leaf | *Solanum lycopersicum* | Solanaceae | mild yellowing and leaf twisting and deformations |
| | | INSI19135 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing with necrotic lesions |
| | | INSI19127 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19130 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19131 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19132 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19133 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19141 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19142 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19143 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19144 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19147 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19148 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19139 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing with necrotic lesions |
| | | INSI19149 | leaf | *Solanum lycopersicum* | Solanaceae | leaf yellowing |
| | | INSI19151 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI19154 | leaf | *Solanum lycopersicum* | Solanaceae | leaf mottling, dwarfing and twisting |
| | | INSI19155 | leaf | *Solanum lycopersicum* | Solanaceae | leaf mottling, dwarfing and twisting |
| | | INSI19140 | leaf | *Chenopodium* sp. | Chenopodiaceae | yellow spots on leaves |
| | | INSI19150 | leaf | *Chenopodium* sp. | Chenopodiaceae | yellow spots on leaves |
| | | INSI19157 | leaf | *Erigeron annuus* | Asteraceae | necrotic lesions on leaves |
| | | INSI19158 | leaf | *Ranunculus repens* | Ranunculaceae | leaf mosaic |
| | | INSI20040 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI20041 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI20042 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI20043 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |

| No. | Virus name | Sample ID | Tissue | Plant species name | Plant family | Symptoms (if any) |
|---|---|---|---|---|---|---|
| | | INSI20044 | leaf | *Solanum lycopersicum* | Solanaceae | none (asymptomatic) |
| | | INSI20030 | leaf | *Solanum lycopersicum* | Solanaceae | necrotic leaf spots |
| | | INSI20031 | leaf | *Solanum lycopersicum* | Solanaceae | necrotic leaf spots |
| | | INSI20033 | leaf | *Solanum lycopersicum* | Solanaceae | necrotic leaf spots |
| | | INSI20035 | leaf | *Solanum lycopersicum* | Solanaceae | purpling of leaf lamina |
| | | INSI20036 | leaf | *Solanum lycopersicum* | Solanaceae | interveinal leaf yellowing |
| | | INSI20037 | leaf | *Solanum lycopersicum* | Solanaceae | necrotic leaf spots, necrosis on leaf lamina |
| | | INSI20038 | leaf | *Solanum lycopersicum* | Solanaceae | necrotic leaf spots, necrosis on leaf lamina |
| | | INSI20055 | leaf | *Solanum lycopersicum* | Solanaceae | purpling of leaf lamina |
| | | INSI20108 | leaf | *Solanum lycopersicum* | Solanaceae | leaf deformation |
| | | INSI20126 | leaf | *Solanum lycopersicum* | Solanaceae | necrotic leaf spots |
| | | INSI20127 | leaf | *Solanum lycopersicum* | Solanaceae | necrotic leaf spots, necrosis on leaf lamina |
| | | INSI20128 | leaf | *Solanum lycopersicum* | Solanaceae | necrotic leaf spots, necrosis on leaf lamina |
| | | INSI20129 | leaf | *Solanum lycopersicum* | Solanaceae | necrotic leaf spots, necrosis on leaf lamina |
| | | INSI20132 | leaf | *Solanum lycopersicum* | Solanaceae | leaf deformation and dwarfing |
| 36 | Taraxacum viroid-like circular RNA 1 | INSI20252 | leaf | *Taraxacum officinale* | Asteraceae | interveinal leaf chlorosis |

**Supplementary Figure 3-01.** Artermisia fimovirus 1. The confirmed associated plant host(s) shown is/are *Artemisia verlotiorum* (Asteraceae).

**Supplementary Figure 3.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-02.** Calystegia geminivirus 1 and Calystegia pelarspovirus 1. The confirmed associated plant host(s) shown is/are *Calystegia sp.* (Convolvulaceae).

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-03.** Plantago potyvirus 1. The confirmed associated plant host(s) shown is/are *Plantago lanceolata* (Plantaginaceae).

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-04.** Mentha macluravirus 1. The confirmed associated plant host(s) shown is/are *Mentha spicata* (Lamiaceae).

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-05.** Rumex potyvirus 1. The confirmed associated plant host(s) shown is/are *Rumex* sp. (Polygonaceae) (INSI20188) and *Convolvulus* sp. (Convolvulaceae) (INSI20199).

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-06.** Broad-leafed dock virus A, isolate 2. The confirmed associated plant host(s) shown is/are *Rumex crispus* (Polygonaceae).

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-07.** Pastinaca umbravirus 1. The confirmed associated plant host(s) shown is/are *Pastinaca sativa* (Apiaceae). Sample INSI19137 is also the confirmed associated plant host of Pastinaca potexvirus 1 and Pastinaca cytorhabdovirus 1.

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-08.** Picris umbravirus 1. The confirmed associated plant host(s) shown is/are *Picris echoides* (Asteraceae). The sample shown is also confirmed associated host of Cichorium alphacarmovirus 1 and Picris cytorhabdovirus 1.

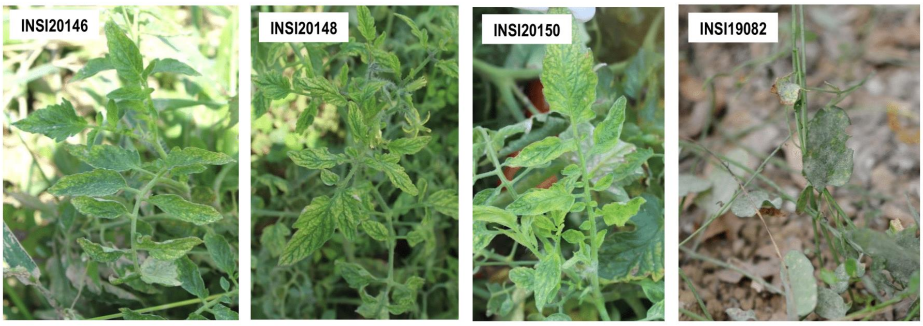
**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-09.** Convolvulus aureusvirus 1. The confirmed associated plant host(s) shown is/are *Convolvulus arvensis* (Convolvulaceae).

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-10.** Cichorium alphacarmovirus 1. The confirmed associated plant host(s) shown is/are *Calystegia* sp. (Convolvulaceae).

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

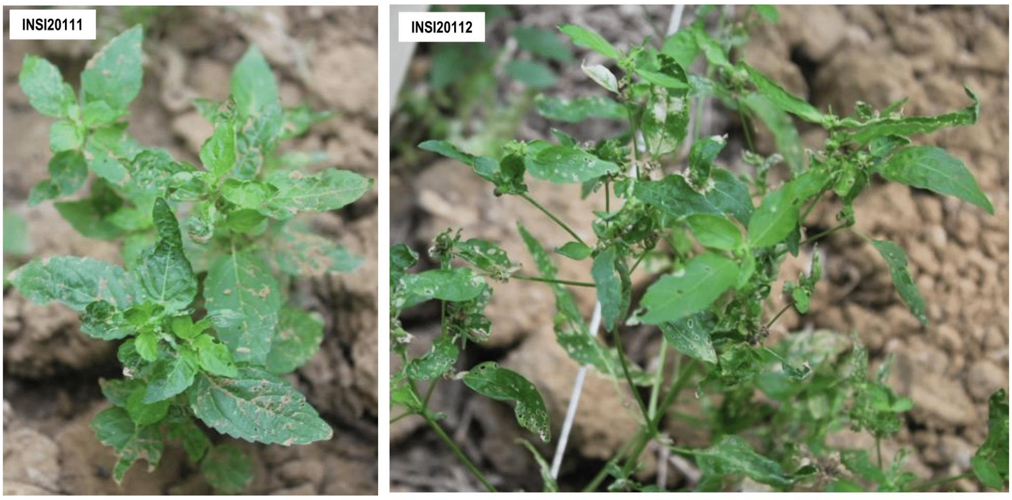


**Supplementary FigureS3-11.** Plant associated tobamo-like virus 1. The confirmed associated plant host(s) shown is/are *Solanum lycopersicum* (Solanaceae) (INSI20146, INSI20148, INSI20150) and *Convolvulus arvensis* (Convolvulaceae) (INSI19082).

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-12.** Plantago tobamovirus 1. The confirmed associated plant host shown is *Plantago major* (Plantaginaceae).

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.



**Supplementary Figure 3-13.** Mercurialis orthotospovirus 1. The confirmed associated plant hosts shown are *Mercurialis annua*.

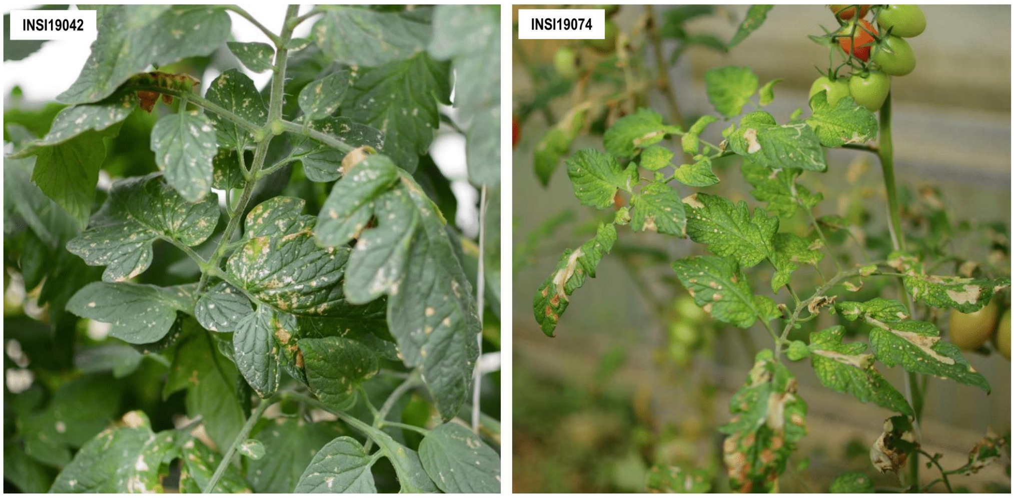
**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-14.** Tomato associated bunya-like virus 1. The confirmed associated plant host shown is *Solanum lycopersicum*.

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-15.** Tomato vitivirus 1. The confirmed associated plant host(s) shown is/are *Solanum lycopersicum* (Solanaceae).

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

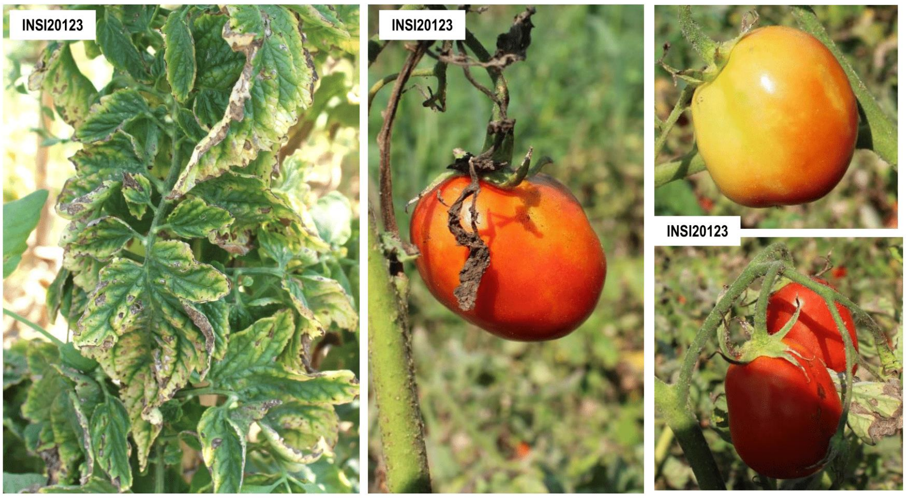


**Supplementary Figure 3-16.** Ranunculus white mottle ophiovirus. The confirmed associated plant hosts shown are tomatoes (*Solanum lycopersicum*).

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-17.** Tomato betanucleorhabdovirus 1. The confirmed associated plant host shown is tomato (*Solanum lycopersicum*).

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.



**Supplementary Figure 3-18.** Tomato betanucleorhabdovirus 2. The confirmed associated plant host shown is tomato (*Solanum lycopersicum*).

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-19.** Picris betanucleorhabdovirus 1. The confirmed associated plant host shown is *Picris echoides* (Asteraceae). The sample shown is also confirmed associated host of Cichorium alphacarmovirus 1 and Prunus virus I.

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-20.** Cirsium cytorhabdovirus 1. The confirmed associated plant host shown is *Cirsium arvense* (Asteraceae).

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-21.** Taraxacum betanucleorhabdovirus 1. The confirmed associated plant host shown is *Taraxacum officinale* (Asteraceae). Sample INSI20194 is also confirmed associated host of Taraxacum cytorhabdovirus 1, while sample INSI20252 is also confirmed associated host of Taraxacum viroid-like circular RNA 1.

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-22.** Tomato alphanucleorhabdovirus 1. The confirmed associated plant host shown is tomato (*Solanum lycopersicum*).

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-23.** Leveillula taurica associated rhabdo-like virus 1. The confirmed associated plant host shown is *Solanum lycopersicum* (Solanaceae).

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-24.** Eggplant mottled dwarf alphanucleorhabdovirus. The confirmed associated plant host shown is *Solanum lycopersicum* (Solanaceae).

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-25.** Physostegia chlorotic mottle alphanucleorhabdovirus. All confirmed associated plant hosts shown are tomatoes (*Solanum lycopersicum*).
**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-26.** Tomato fruit blotch virus and Tomato matilda virus co-infected samples.
The confirmed associated plant host shown is *Solanum lycopersicum* (Solanaceae).

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Figure 3-27.** Solanum nigrum ilarvirus 1. The confirmed associated plant host shown is *Physalis* sp. (Solanaceae).

**Supplementary Figure 3** (continued)**.** Representative field photos of confirmed associated plant hosts of selected viruses and putative viroids. **Note**: There are other viruses detected in the sequencing pools (*i.e.* composite sample) where the samples shown belong, which implies possible co-infection of viruses on the specific sample shown. Thus, it is difficult to associate the symptom phenotype with the detection of a single specific virus. Complete information on the individual samples can be found in Supplementary Table 1 and the description of symptoms of the associated plant hosts are summarized in Supplementary Table 9.

**Supplementary Table 10.** Model selection and other parameters used for maximum likelihood phylogenetic analyses. Note: aa – amino acid, nt – nucleotide.

| Virus family / families (or virus order) | Gene analyzed (amino acid sequence, or *DNA sequence, as indicated) | Number of sequences in the dataset | Alignment and trimming programs used | Number of positions in final alignment | Substitution model selected* | Number of parameters tested |
|---|---|---|---|---|---|---|
| *Tospoviridae* and *Fimoviridae* (*Bunyavirales*) | RNA-dependent RNA polymerase (RdRP) | 65 | ClustalW, MAFFT (after manual trimming), trimAl | 376 aa | LG+G+I+F | 164 |
| *Partitiviridae* (*Durnavirales*) | RNA-dependent RNA polymerase (RdRP) | 57 | ClustalW, MAFFT (after manual trimming), trimAl | 326 aa | LG+G+I | 233 |
| *Geminiviridae* (*Geplafuvirales*) | replicase (C1 gene in DNA-A) | 109 | ClustalW, MAFFT (after manual trimming), trimAl | 289 aa | LG+G | 484 |
| *Totiviridae* (*Ghabrivirales*) | RNA-dependent RNA polymerase (RdRP) | 27 | ClustalW, MAFFT (after manual trimming), trimAl | 363 aa | LG+G+I | 155 |
| *Bromoviridae* (*Martellivirales*) | RNA-dependent RNA polymerase (RdRP) | 63 | ClustalW, MAFFT (after manual trimming), trimAl | 327 aa | LG+G+I | 125 |
| *Closteroviridae* (*Martellivirales*) | RNA-dependent RNA polymerase (RdRP) | 48 | ClustalW, MAFFT (after manual trimming), trimAl | 219 aa | LG+G+I | 97 |
| *Endornaviridae* (*Martellivirales*) | RNA-dependent RNA polymerase (RdRP) | 45 | ClustalW, MAFFT (after manual trimming), trimAl | 278 aa | LG+G+I | 89 |
| *Kitaviridae* (*Martellivirales*) | RNA-dependent RNA polymerase (RdRP) | 29 | ClustalW, MAFFT (after manual trimming), trimAl | 583 aa | LG+G+I+F | 76 |
| *Virgaviridae* (*Martellivirales*) | replicase (methyl transferase, helicase) | 67 | ClustalW, MAFFT (after manual trimming), trimAl | 542 aa | LG+G+I | 133 |
| | coat protein (CP) | 51 | ClustalW, MAFFT (after manual trimming), trimAl | 68 aa | LG+G | 100 |
| Subgroup 3 *Tobamovirus* (*Virgaviridae)* | full genome nucleotide sequence | 41 | MUSCLE (and manual trimming of ends) | 6233 nt | GTR+G+I | 89 |
| *Rhabdoviridae* (*Mononegavirales*) | RNA-dependent RNA polymerase (RdRP) | 75 | ClustalW, MAFFT (after manual trimming), trimAl | 604 aa | LG+G+I+F | 170 |
| *Caulimoviridae* (*Ortelivirales*) | reverse transcriptase (RT) | 57 | ClustalW, MAFFT (after manual trimming), trimAl | 220 aa | LG+G | 112 |
| *Potyviridae* (*Patatavirales*) | RNA-dependent RNA polymerase (RdRP) | 98 | ClustalW, MAFFT (after manual trimming), trimAl | 470 aa | LG+G+I | 195 |

| | | | | | | |
|---|---|---|---|---|---|---|
| *Virgaviridae* (*Martellivirales*) | (08-A) Supplementary Figure 4-08-A | Mtr, Hel | 48 | ClustalW, MAFFT (after manual trimming), trimAl | 542 aa | LG+G+I |
| | Figure 7h [b,(08-A)] (left tree) | | | | | |
| | (08-B) Supplementary Figure 4-08-B | CP | 48 | ClustalW, MAFFT (after manual trimming), trimAl | 68 aa | LG+G |
| | Figure 7h [b,(08-B)] (right tree) | | | | | |
| | Figure 7i | full genome nt sequence | 41 | MUSCLE (and manual trimming of ends) | 6233 nt | GTR+G+I |
| *Potyviridae* (*Patatavirales*) | (09) Supplementary Figure 4-09 | RdRp | 93 | ClustalW, MAFFT (after manual trimming), trimAl | 470 aa | LG+G+I |
| | Figure 8g [b,(09)] | | | | | |
| *Tombusviridae* (*Tolivirales*) | (10) Supplementary Figure 4-10 | RdRp | 108 | ClustalW, MAFFT (after manual trimming), trimAl | 291 aa | LG+G+I |
| | Figure 9h [b,(10)] | | | | | |
| *Partitiviridae* (*Durnavirales*) | (11) Supplementary Figure 4-11 | RdRp | 57 | ClustalW, MAFFT (after manual trimming), trimAl | 326 aa | LG+G+I |
| *Geminiviridae* (*Geplafuvirales*) | (12) Supplementary Figure 4-12 | replicase (C1 gene) | 109 | ClustalW, MAFFT (after manual trimming), trimAl | 289 aa | LG+G |
| *Totiviridae* (*Ghabrivirales*) | (13) Supplementary Figure 4-13 | RdRp | 71 | ClustalW, MAFFT (after manual trimming), trimAl | 363 aa | LG+G+I |
| *Caulimoviridae* (*Ortelivirales*) | (14) Supplementary Figure 4-14 | RT | 57 | ClustalW, MAFFT (after manual trimming), trimAl | 220 aa | LG+G |
| *Iflaviridae* (*Picornavirales*) | (15) Supplementary Figure 4-15 | RdRp | 29 | ClustalW, MAFFT (after manual trimming), trimAl | 460 aa | LG+G+I |
| *Dicistroviridae* and *Iflaviridae* (*Picornavirales*) | (16) Supplementary Figure 4-16 | RdRp | 61 | ClustalW, MAFFT (after manual trimming), trimAl | 307 aa | LG+G |

| | | | | | | |
|---|---|---|---|---|---|---|
| *Secoviridae* (*Picornavirales*) | (17) Supplementary Figure 4-17 | RdRp | 63 | ClustalW, MAFFT (after manual trimming), trimAl | 364 aa | LG+G |
| *Solemoviridae* (*Sobelivirales*) | (18) Supplementary Figure 4-18 | RdRp | 47 | ClustalW, MAFFT (after manual trimming), trimAl | 191 aa | LG+G |
| *Tymovirales* | (19) Supplementary Figure 4-19 | RdRp | 75 | ClustalW, MAFFT (after manual trimming), trimAl | 293 aa | LG+G+I |
| Satellite viruses (*Albetovirus, Aumaivirus*) | (20) Supplementary Figure 4-20 | CP | 10 | ClustalW, MAFFT (after manual trimming), trimAl | 109 aa | LG+G |

**Details of multiple sequence alignments and phylogenetic tree construction:**

Representative viral RefSeq genomes of ICTV-recognized species, which were translated to amino acid sequences, and selected best hit in BLASTp searches (E-val<$10^{-4}$) of the viruses of interest, were gathered for the phylogenetic analyses. When applicable, outgroup virus sequences were chosen based on known phylogenetic relationships to the closest related taxa (*i.e.* species of a closely related family), and with reference to phylogenetic trees published in peer-reviewed articles. Multiple sequence alignments were initially done using ClustalW (Thompson et al., 1994), and after manual trimming of unaligned ends, MAFFT alignment was implemented (Katoh and Standley, 2013). Thereafter, further trimming of the alignments with trimAl (Capella-Gutiérrez et al., 2009) was performed. Highly divergent sequences (*i.e.* <30%) based on overall pairwise amino acid similarity, examined in SDT v. 1.2 (Muhire et al., 2014), were removed from the final alignment prior to further analyses. In the case of tobamoviruses, a nucleotide-based phylogenetic analyses was done on full genomes. Genomes of different isolates of turnip vein-clearing virus, ribgrass mosaic virus, wasabi mosaic virus, youcai mosaic virus and Plantago tobamovirus 1, were gathered from GenBank and viral RefSeq database and aligned using MUSCLE (Edgar, 2004). The unaligned ends were trimmed, then checked for possible recombinants before proceeding with the phylogenetic analyses with the alignments free of recombinants. Substitution model selection was done on the final alignments, with either amino acid or nucleotide alignments. The best model was chosen, based on the lowest Bayesian Information Criteria (BIC) value (Schwarz, 1978). Selected amino acid substitution models indicated in the table above are as follows: Le_Gascuel_2008 model (Le and Gascuel, 2008) with discrete Gamma distribution with 5 rate categories (LG+G), which may also assume that a certain fraction of sites are evolutionarily invariable (LG+G+I) and may account for amino acid frequencies (LG+G+I+F). For the tobamovirus dataset, a General Time Reversible (GTR) model was selected, with discrete gamma distribution (+G) and evolutionarily invariable sites (+I). The final phylogenetic trees after the analyses have the highest log likelihood value inferred with 1000 bootstrap replicates (Felsenstein, 1985). In the succeeding phylogenetic trees shown in **Supplementary Figure 4**, the percentage of replicate trees in which the associated taxa clustered together in the bootstrap test is shown next to the branches, with only >0.6 (>60%) support shown. The trees are drawn to scale for easier visualization, with branch lengths (scale bar is shown) measured in the number of amino acid (or nucleotide) substitutions per site. ClustalW alignment, manual trimming and pairwise similarity analysis were done in CLC Genomics Workbench v. 20.0 (Qiagen). MAFFT was executed in EMBL-EBI website (www.ebi.ac.uk/Tools/msa/mafft/), and trimAI was downloaded from (www.trimal.cgenomics.org), and was executed in command line, with 'automated1' option. Substitution model testing and phylogenetic tree construction were done in MEGA X (Kumar et al., 2018), and the final phylogenetic trees were annotated in Interactive Tree of Life (iToL) (Letunic and Bork, 2021).

**References for substitution models, online tools and programs used in the phylogenetic analyses:**

Capella-Gutiérrez, S., Silla-Martínez, J. M., and Gabaldón, T. (2009). trimAl: A tool for automated alignment trimming in large-scale phylogenetic analyses. *Bioinformatics* 25, 1972–1973. doi:10.1093/bioinformatics/btp348.

Edgar, R. C. (2004). MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res.* 32, 1792–1797. doi:10.1093/nar/gkh340.

Felsenstein, J. (1985). Confidence Limits on Phylogenies: An Approach Using the Bootstrap. *Evolution (N. Y).* 39, 783. doi:10.2307/2408678.

Katoh, K., and Standley, D. M. (2013). MAFFT multiple sequence alignment software version 7: Improvements in performance and usability. *Mol. Biol. Evol.* 30, 772–780. doi:10.1093/molbev/mst010.

Kumar, S., Stecher, G., Li, M., Knyaz, C., and Tamura, K. (2018). MEGA X: Molecular Evolutionary Genetics Analysis across Computing Platforms. *Mol. Biol. Evol.* 35, 1547–1549. doi:10.1093/molbev/msy096.

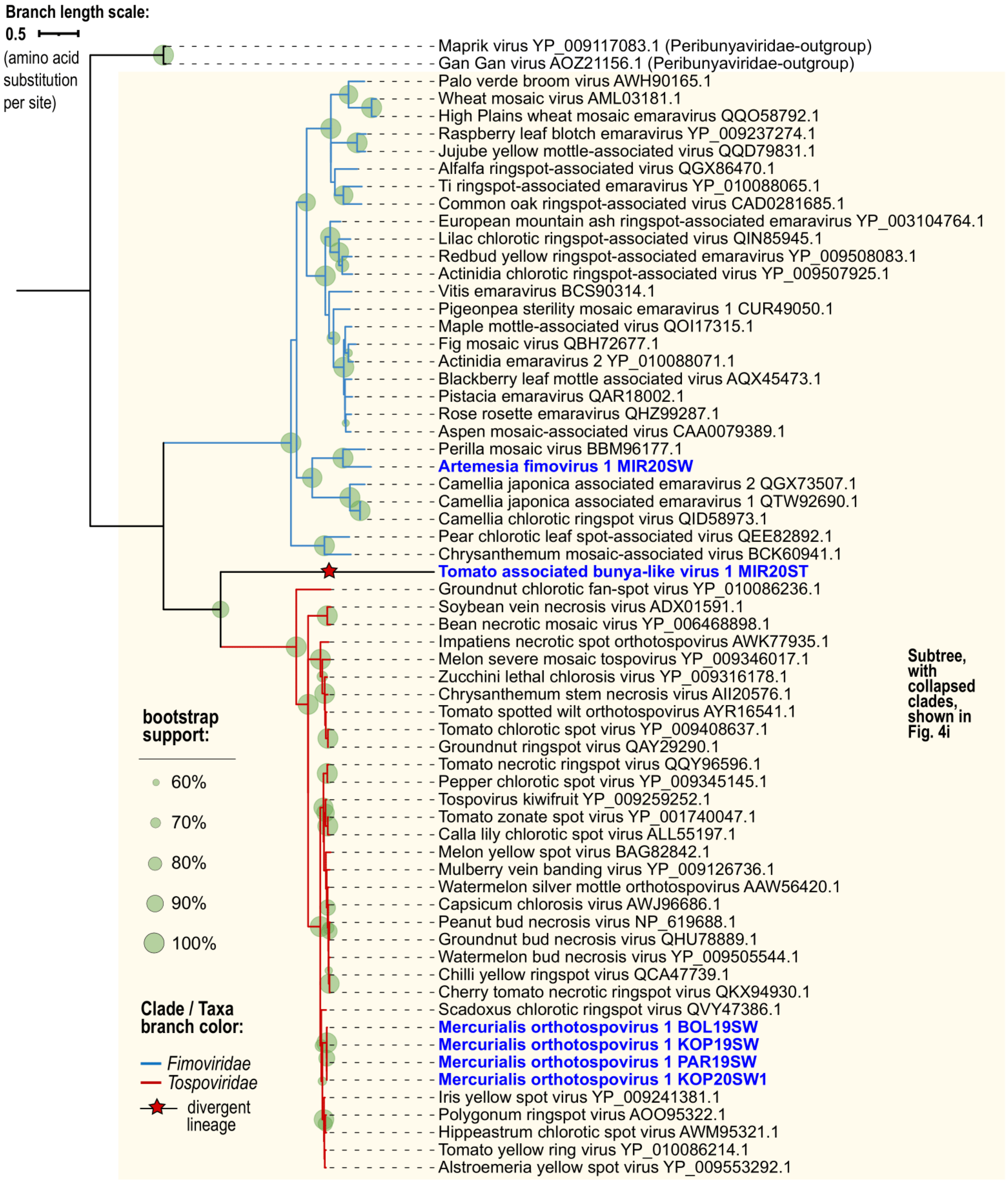
Le, S. Q., and Gascuel, O. (2008). An improved general amino acid replacement matrix. *Mol. Biol. Evol.* 25, 1307–1320. doi:10.1093/molbev/msn067.

Letunic, I., and Bork, P. (2021). Interactive Tree Of Life (iTOL) v5: an online tool for phylogenetic tree display and annotation. *Nucleic Acids Res.* 49, W293–W296. doi:10.1093/nar/gkab301.

Muhire, B. M., Varsani, A., and Martin, D. P. (2014). SDT: A Virus Classification Tool Based on Pairwise Sequence Alignment and Identity Calculation. *PLoS One* 9, e108277. doi:10.1371/journal.pone.0108277.

Schwarz, G. (1978). Estimating the Dimension of a Model. *Ann. Stat.* 6. doi:10.1214/aos/1176344136.

Thompson, J. D., Higgins, D. G., and Gibson, T. J. (1994). CLUSTAL W: Improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res.* 22, 4673–4680. doi:10.1093/nar/22.22.4673.

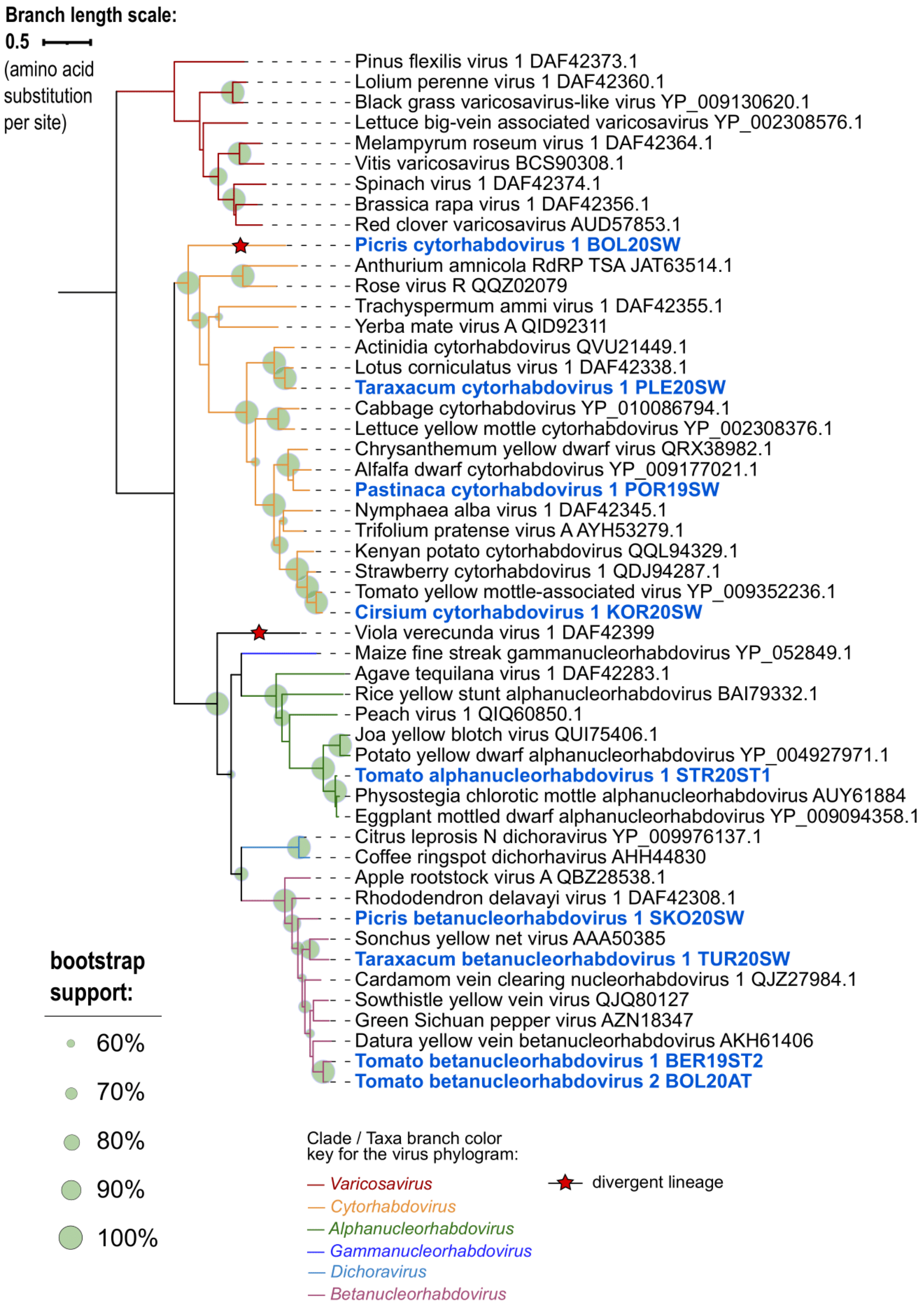


**Supplementary Figure 4-01.** Maximum likelihood phylogenetic tree based on the alignment of conserved RNA-dependent RNA polymerase amino acid sequence of virus species under *Tospoviridae* and *Fimoviridae* (*Bunyavirales*).

**Supplementary Figure 4.** Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font) virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.

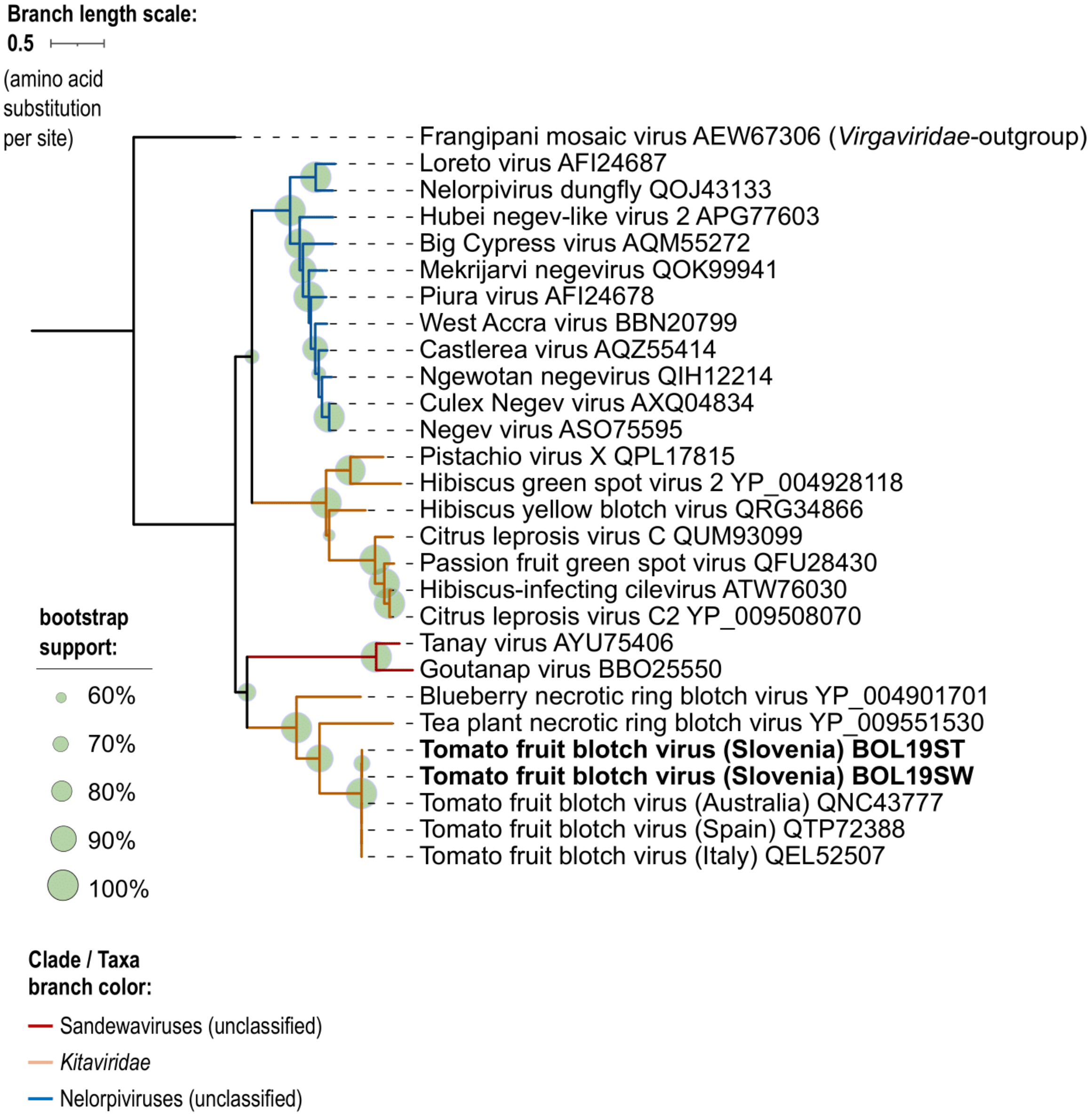
**Supplementary Figure 4-02.** Maximum likelihood phylogenetic tree based on the alignment of conserved RNA-dependent RNA polymerase amino acid sequence of virus species under family *Aspiviridae* (*Serpentovirales*).

**Supplementary Figure 4.** Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font) virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.



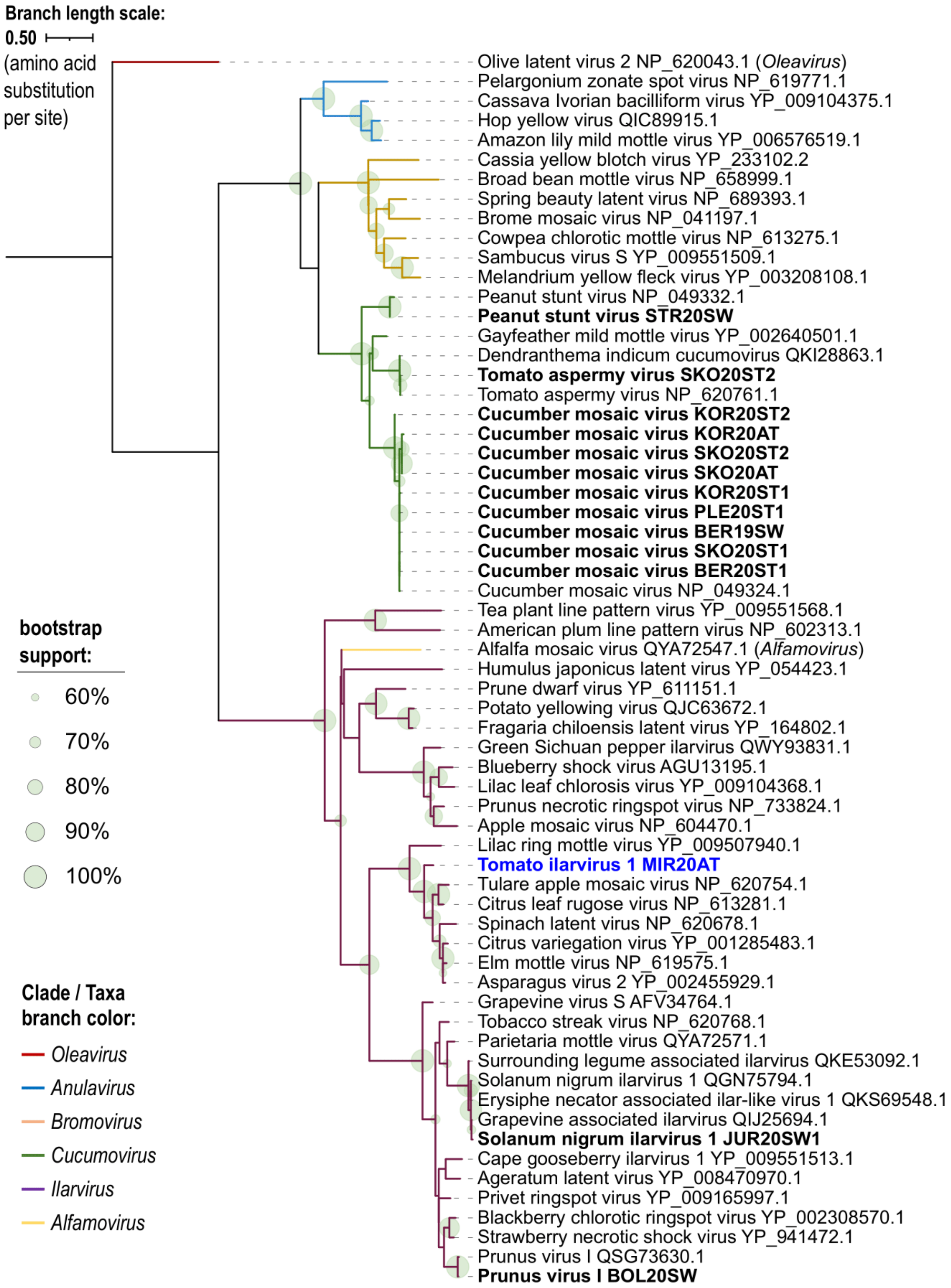
**Supplementary Figure 4-03.** Maximum likelihood phylogenetic tree based on the alignment of conserved RNA-dependent RNA polymerase amino acid sequence of virus species under family *Rhabdoviridae* (*Mononegavirales*).

**Supplementary Figure 4.** Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font) virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.



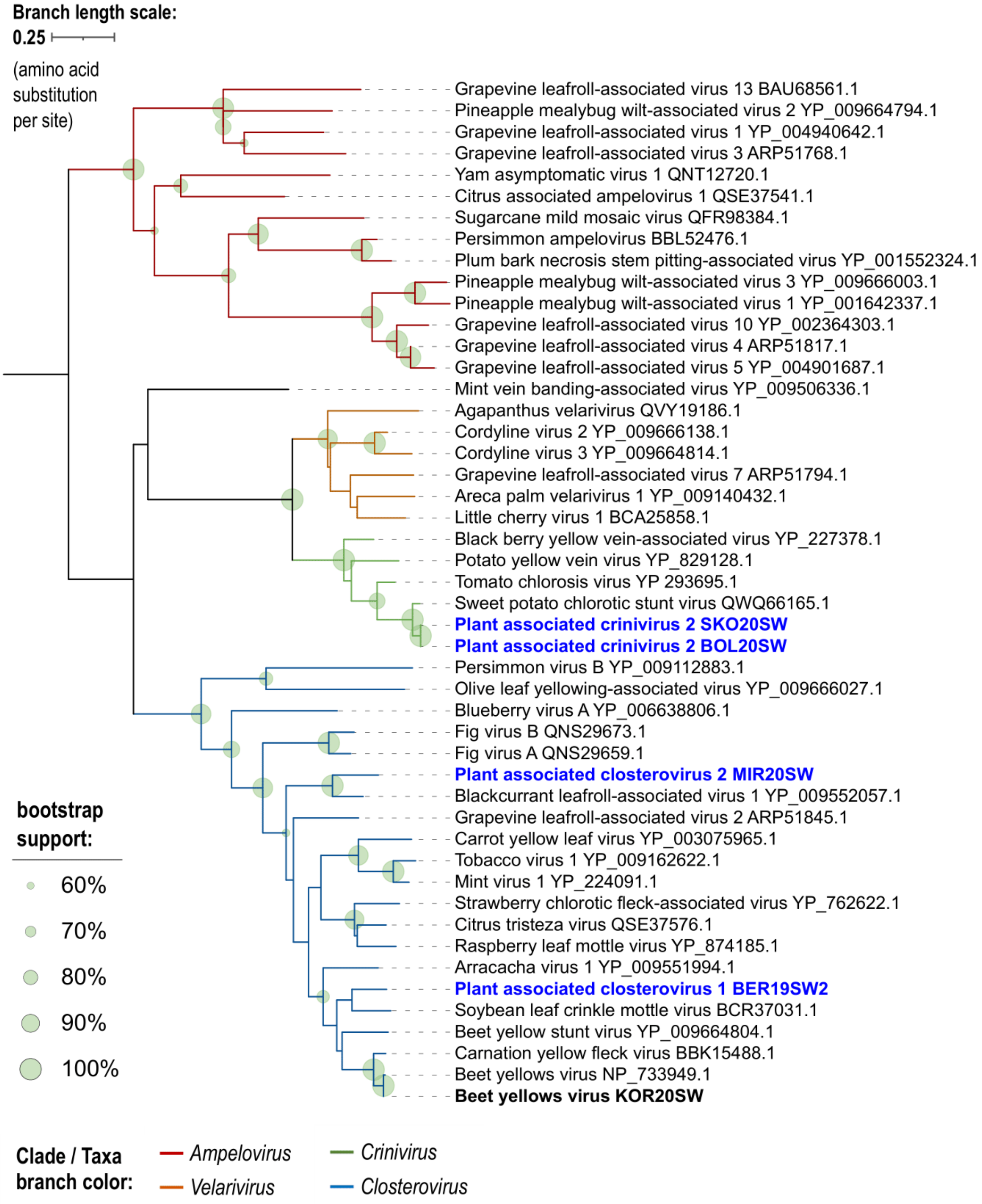
**Supplementary Figure 4-04.** Maximum likelihood phylogenetic tree based on the alignment of conserved RNA-dependent RNA polymerase amino acid sequence of virus species under family *Kitaviridae* (*Martellivirales*).

**Supplementary Figure 4.** Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font) virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.



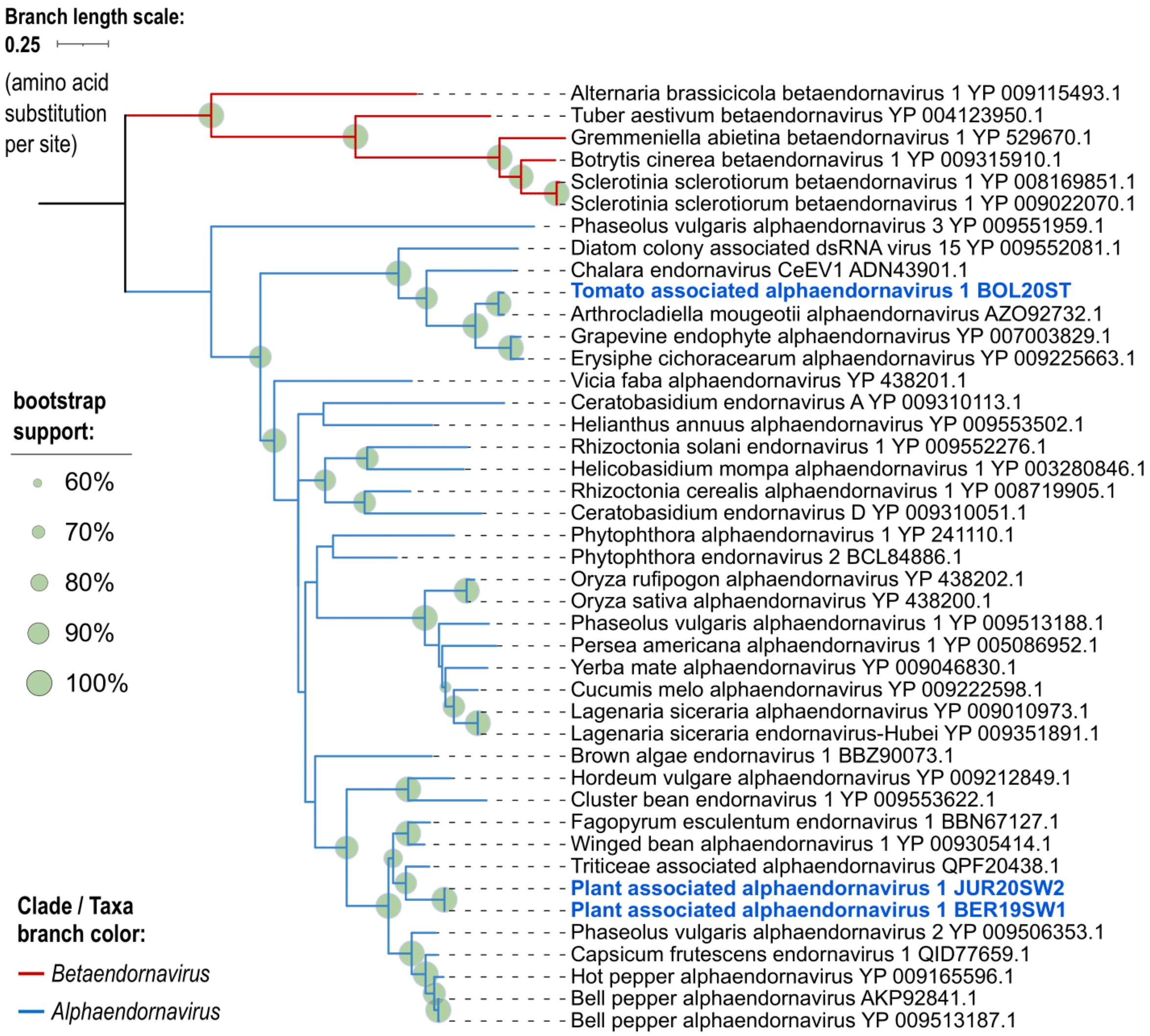
**Supplementary Figure 4-05.** Maximum likelihood phylogenetic tree based on the alignment of conserved RNA-dependent RNA polymerase amino acid sequence of virus species under family *Bromoviridae* (*Martellivirales*).

**Supplementary Figure 4.** Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font) virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.



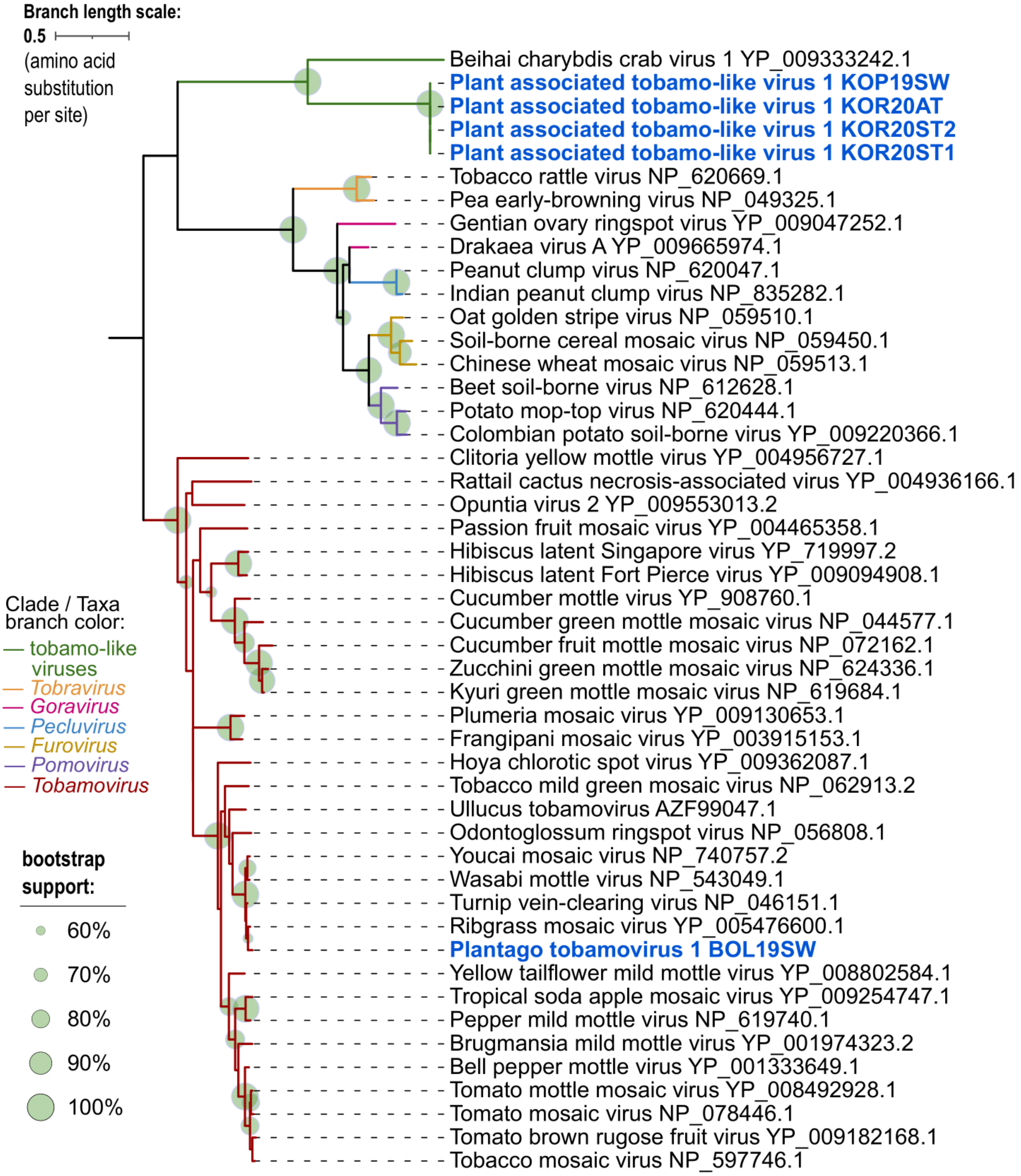
**Supplementary Figure 4-06.** Maximum likelihood phylogenetic tree based on the alignment of conserved RNA-dependent RNA polymerase amino acid sequence of virus species under family *Closteroviridae* (*Martellivirales*).

**Supplementary Figure 4.** Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font) virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.



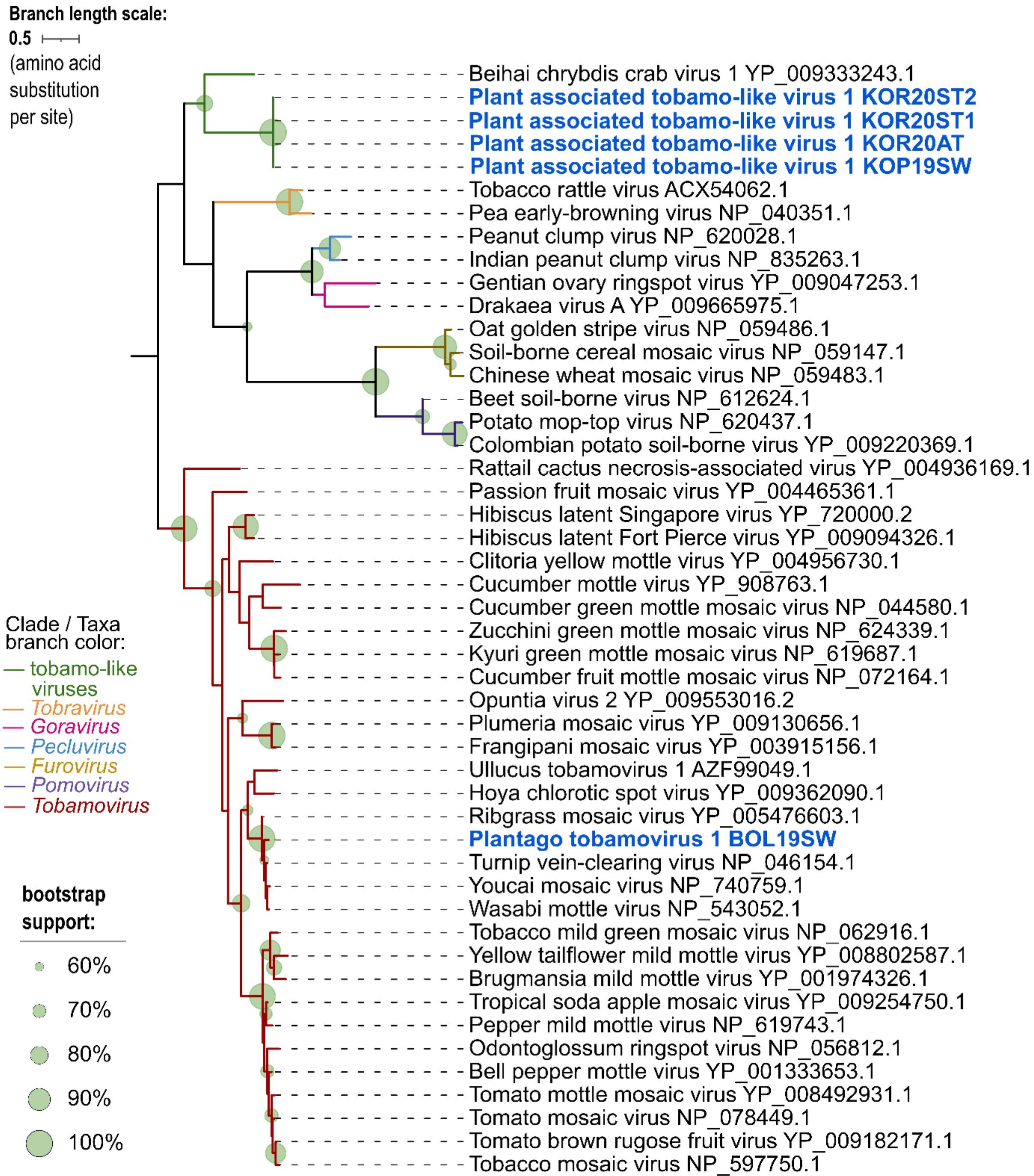
**Supplementary Figure 4-07.** Maximum likelihood phylogenetic tree based on the alignment of conserved RNA-dependent RNA polymerase amino acid sequence of virus species under family *Endornaviridae* (*Martellivirales*).

**Supplementary Figure 4.** Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font) virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.



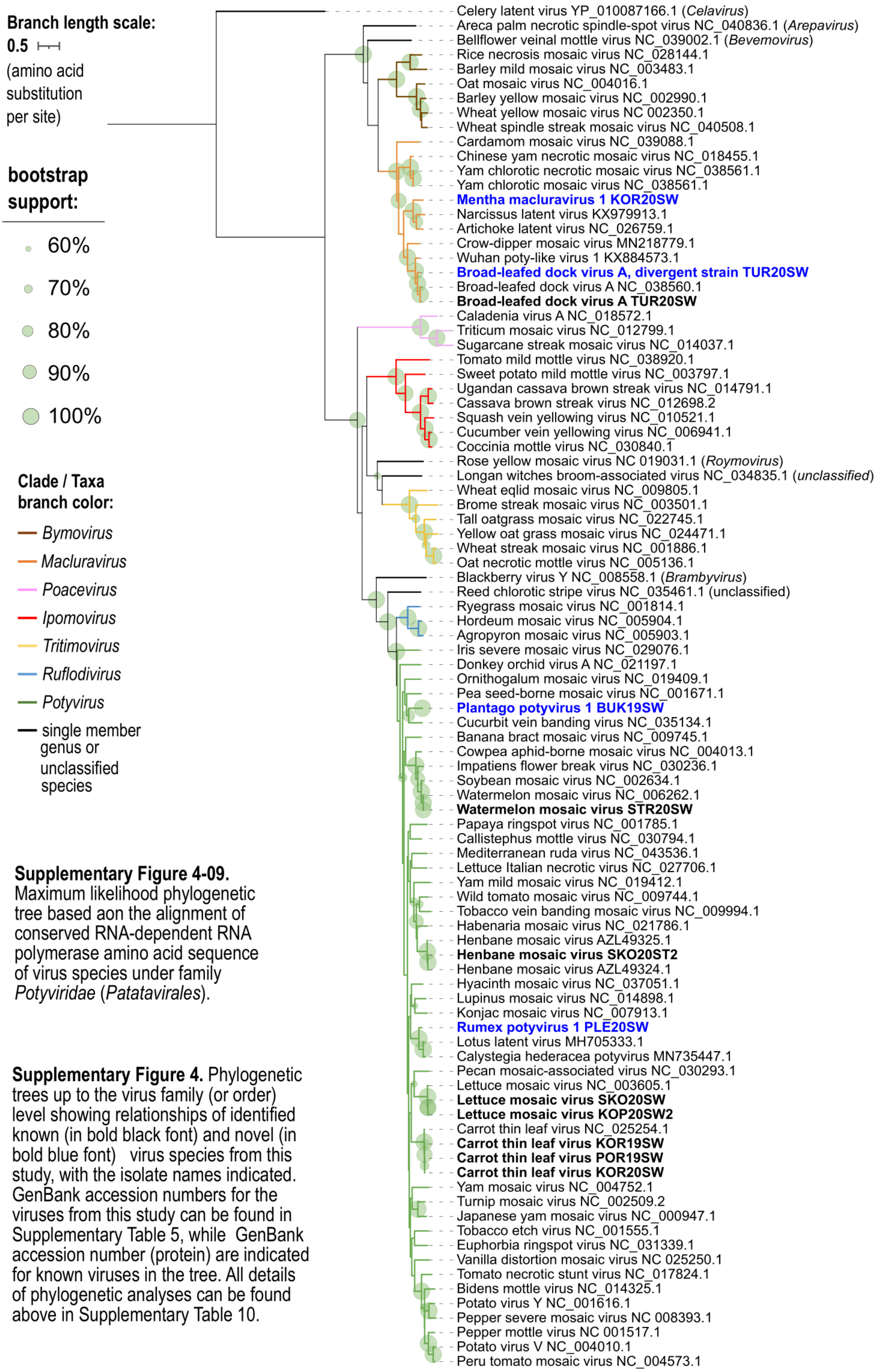
**Supplementary Figure 4-08-A.** Maximum likelihood phylogenetic tree based on the alignment of conserved methyl transferase-helicase amino acid sequence of virus species under family *Virgaviridae* (*Martellivirales*).

**Supplementary Figure 4.** Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font) virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.



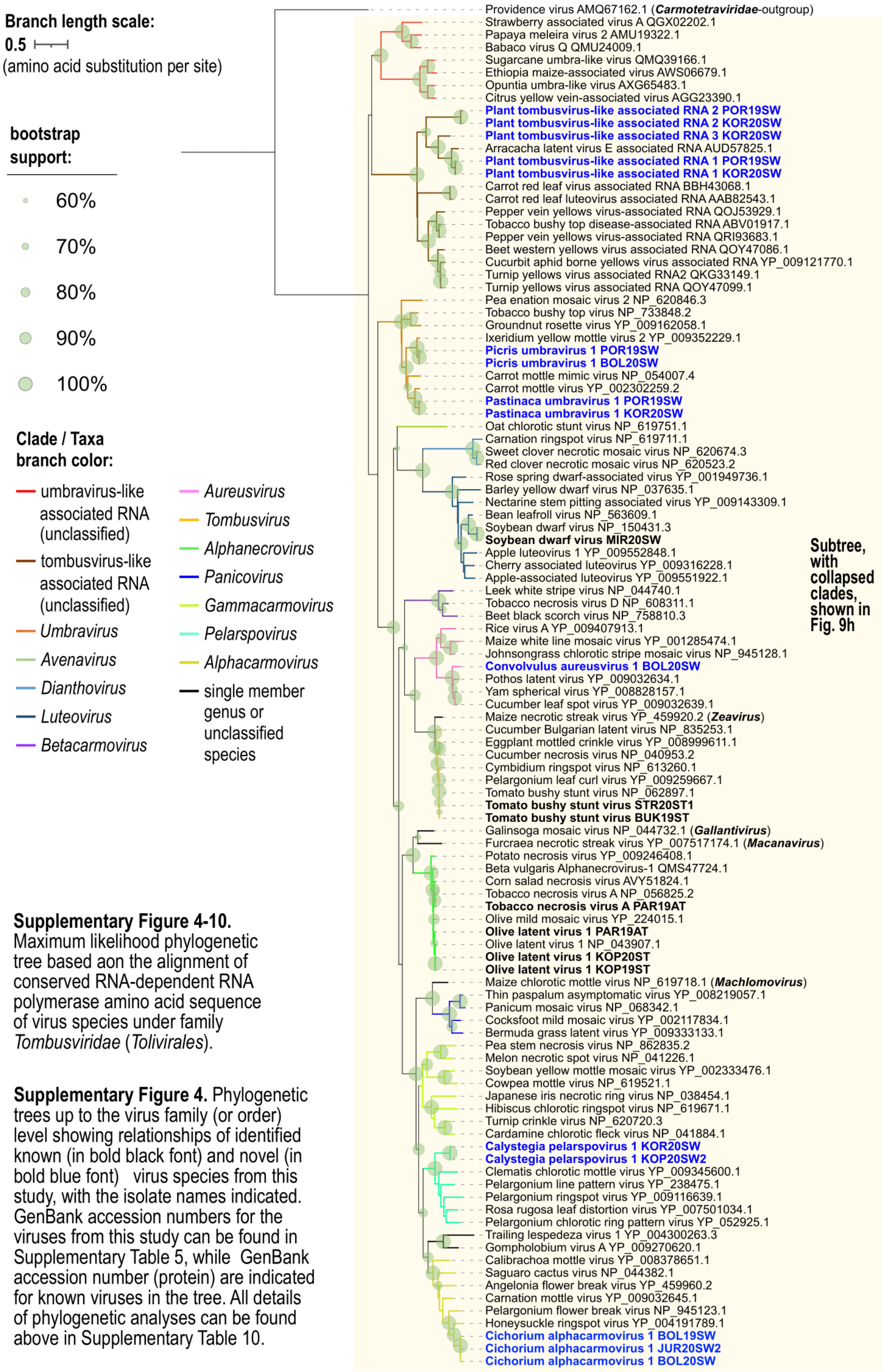
**Supplementary Figure 4-08-B.** Maximum likelihood phylogenetic tree based on the alignment of conserved coat protein amino acid sequence of virus species under family *Virgaviridae* (*Martellivirales*).

**Supplementary Figure 4.** Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font) virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.



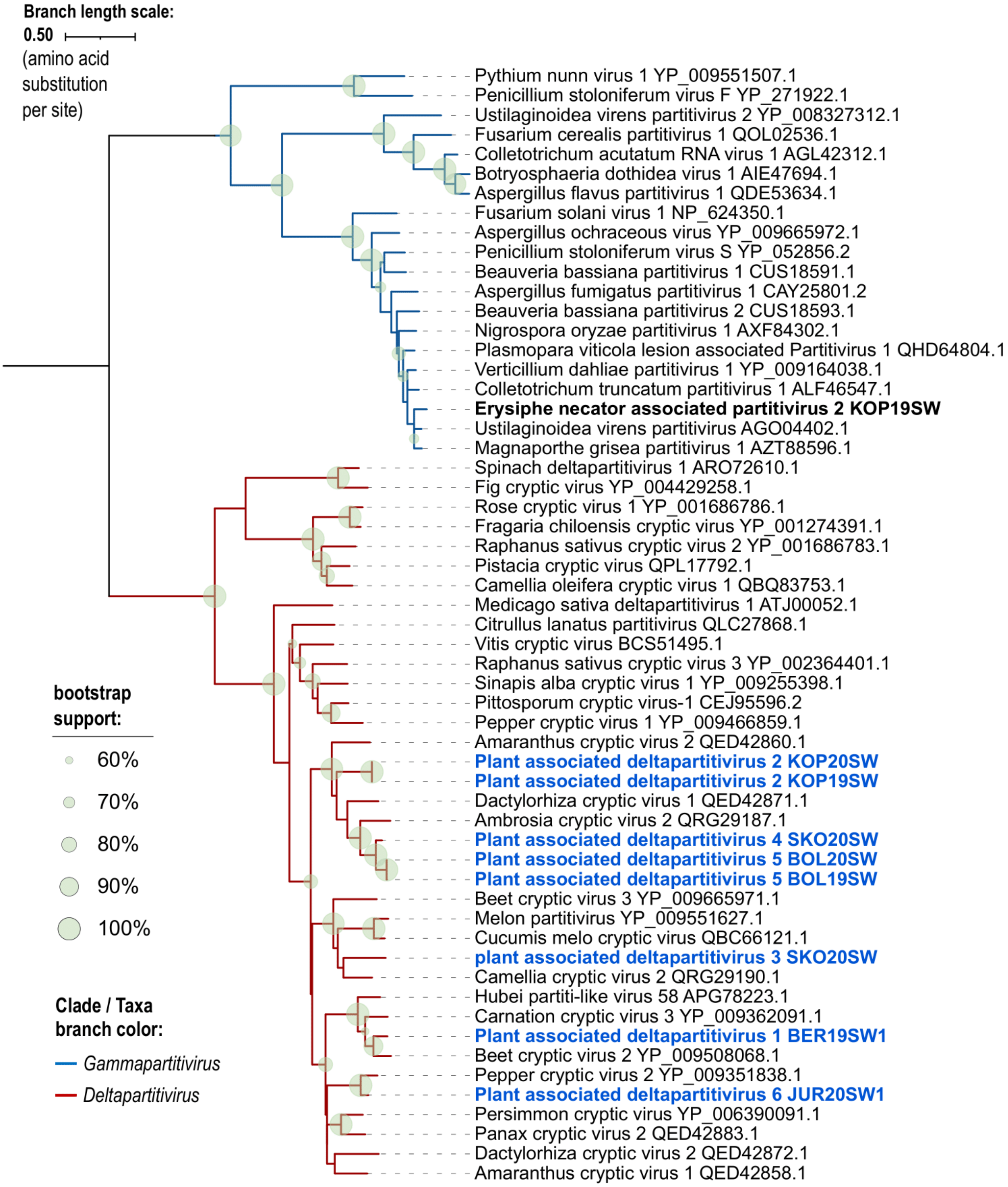
**Supplementary Figure 4-09.** Maximum likelihood phylogenetic tree based aon the alignment of conserved RNA-dependent RNA polymerase amino acid sequence of virus species under family *Potyviridae* (*Patatavirales*).

**Supplementary Figure 4.** Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font) virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.



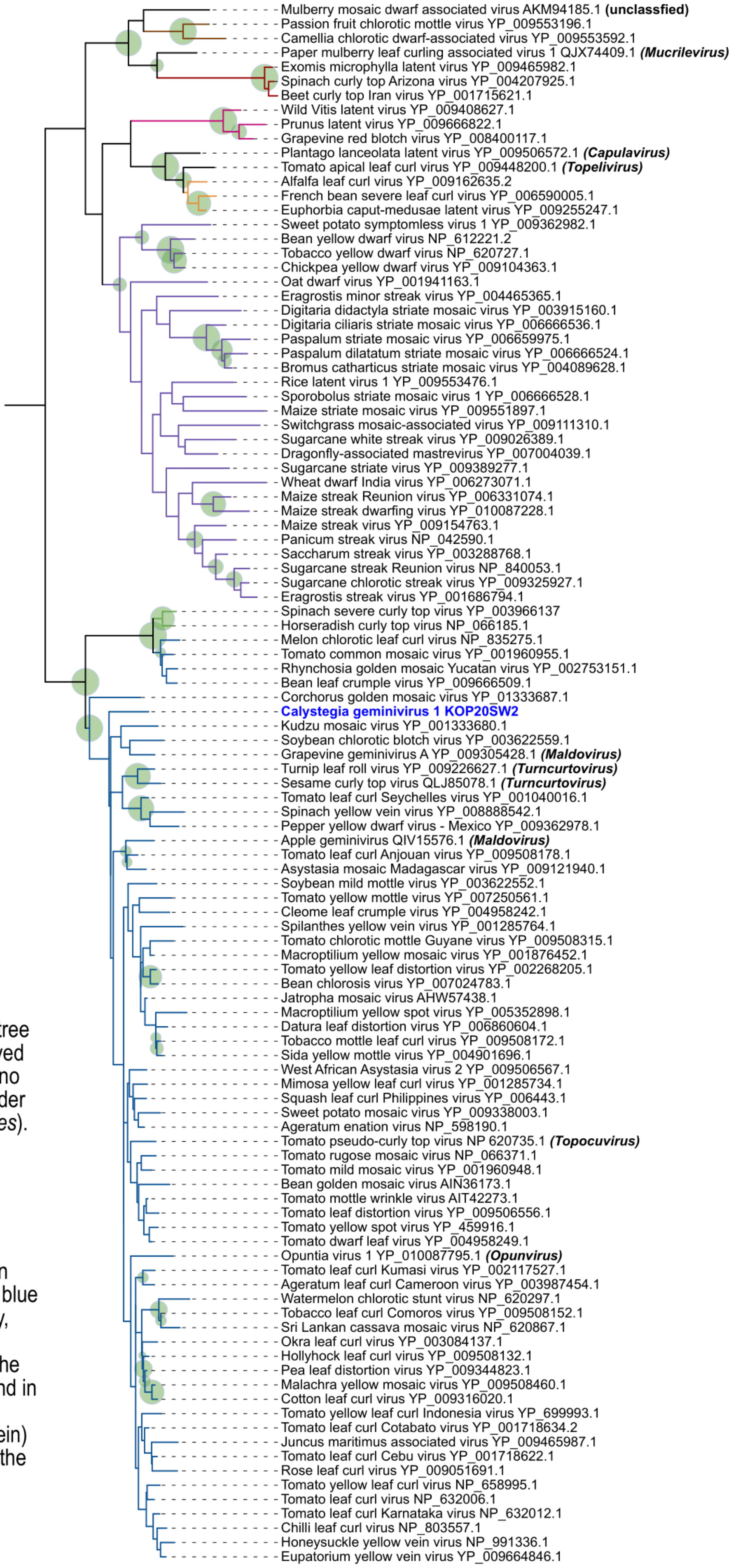
**Supplementary Figure 4-10.** Maximum likelihood phylogenetic tree based aon the alignment of conserved RNA-dependent RNA polymerase amino acid sequence of virus species under family *Tombusviridae* (*Tolivirales*).

**Supplementary Figure 4.** Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font)  virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while  GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.



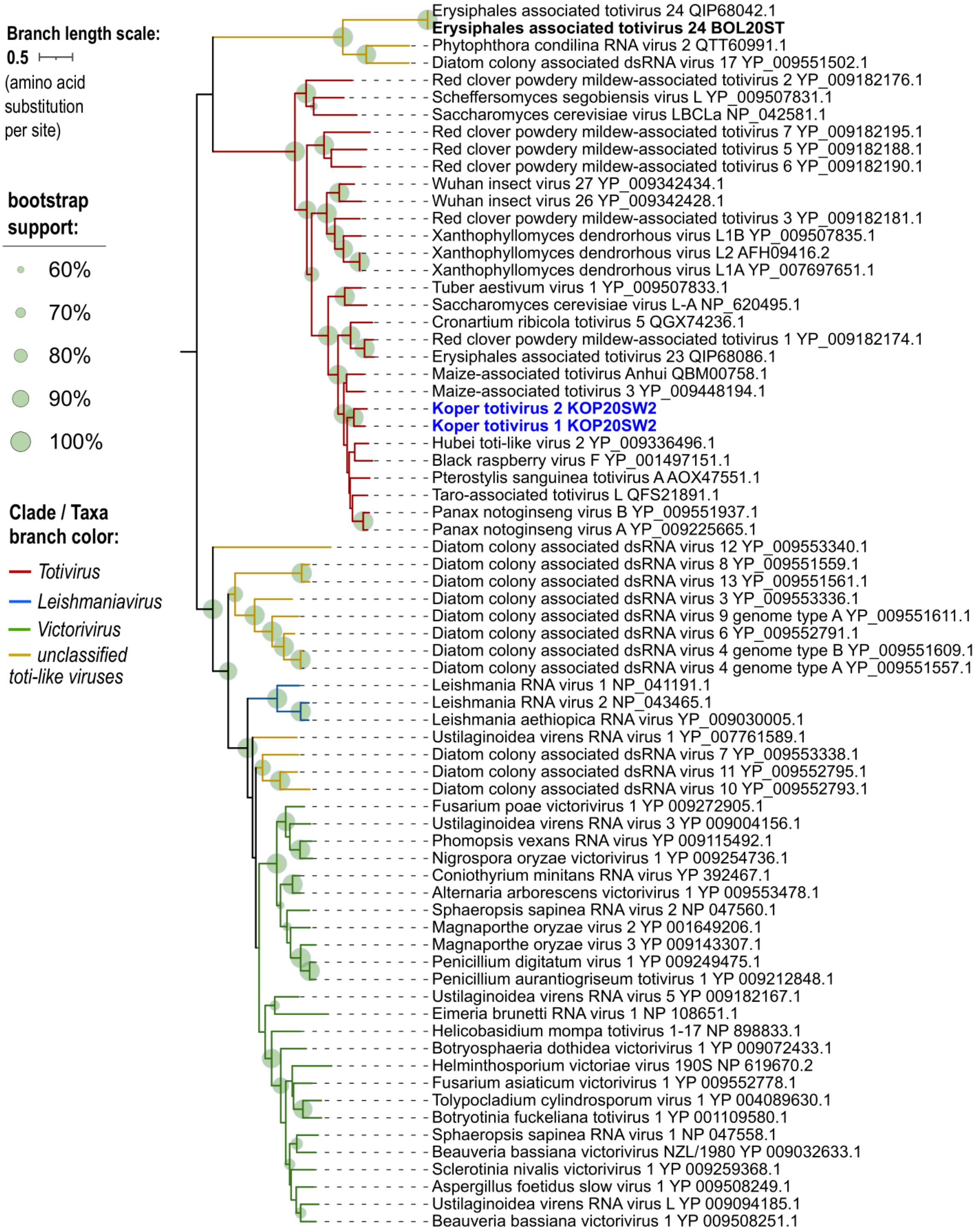
**Supplementary Figure 4-11.** Maximum likelihood phylogenetic tree based on the alignment of conserved RNA-dependent RNA polymerase amino acid sequence of virus species under family *Partitiviridae* (*Durnavirales*).

**Supplementary Figure 4.** Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font) virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.



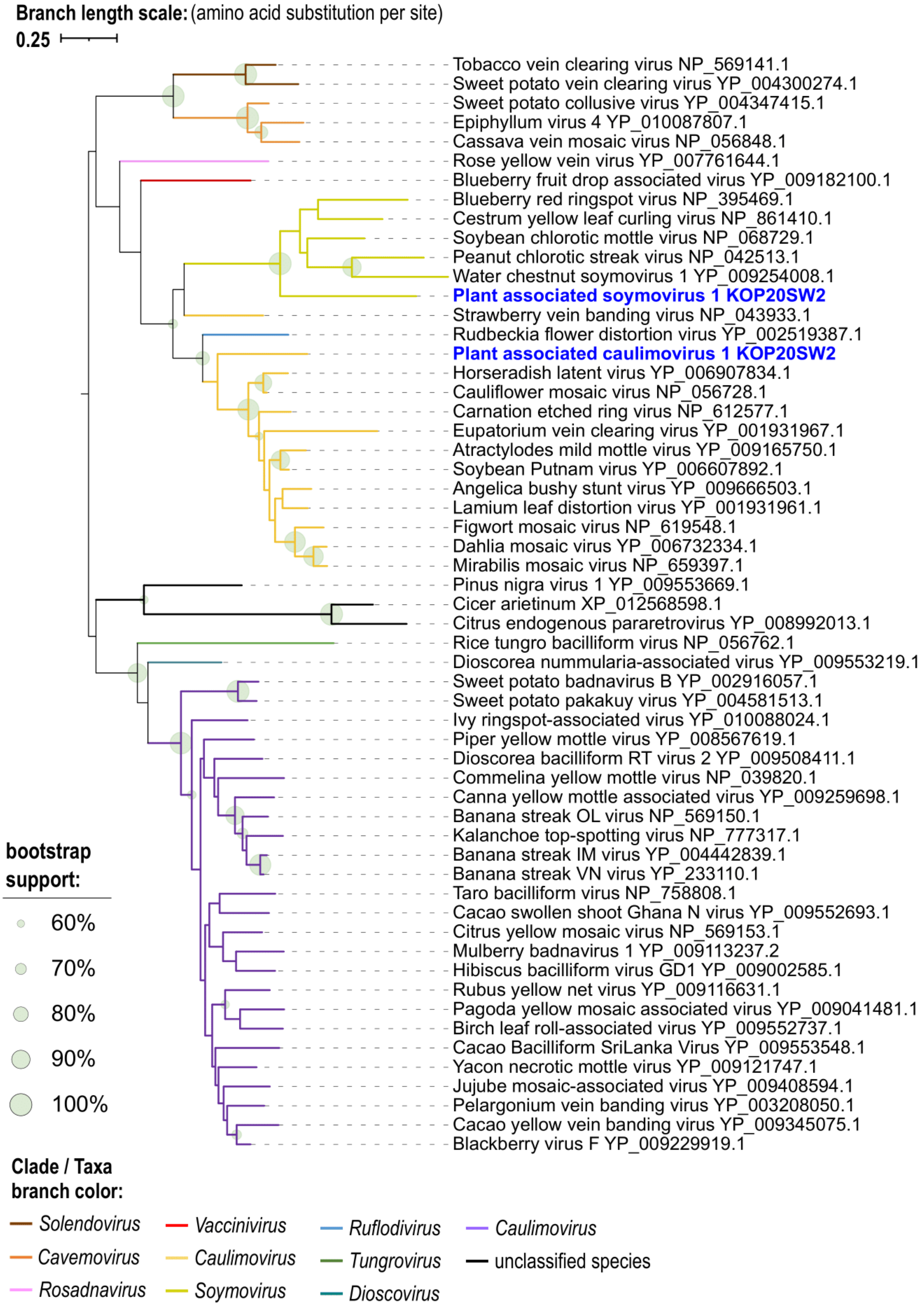
**Supplementary Figure 4-12.**
Maximum likelihood phylogenetic tree based on the alignment of conserved replicase (C1 gene in DNA-A) amino acid sequence of virus species under family *Geminiviridae* (*Geplafuvirales*).

**Supplementary Figure 4.**
Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font) virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.



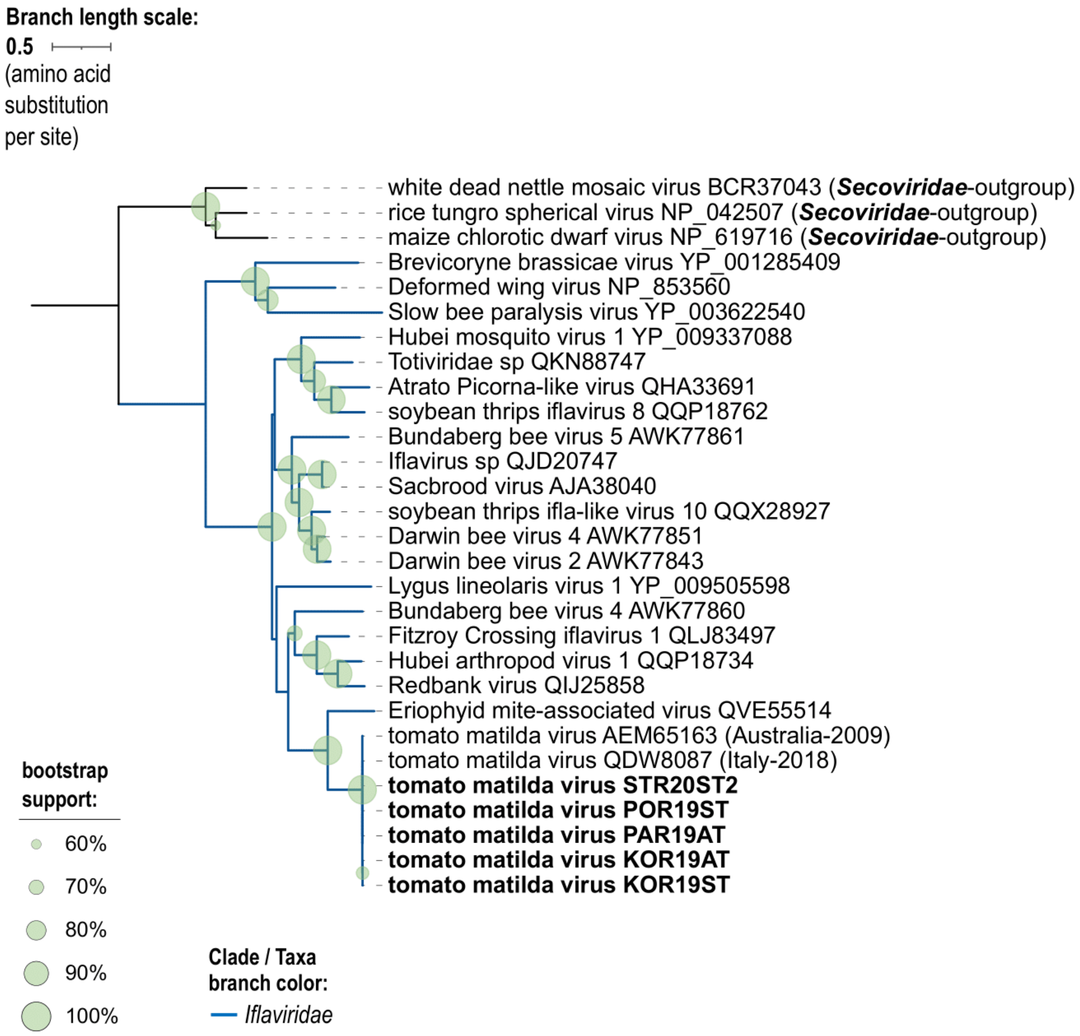
**Supplementary Figure 4-13.** Maximum likelihood phylogenetic tree based on the alignment of conserved RNA-dependent RNA polymerase amino acid sequence of virus species under family *Totiviridae* (*Ghabrivirales*).

**Supplementary Figure 4.** Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font) virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.



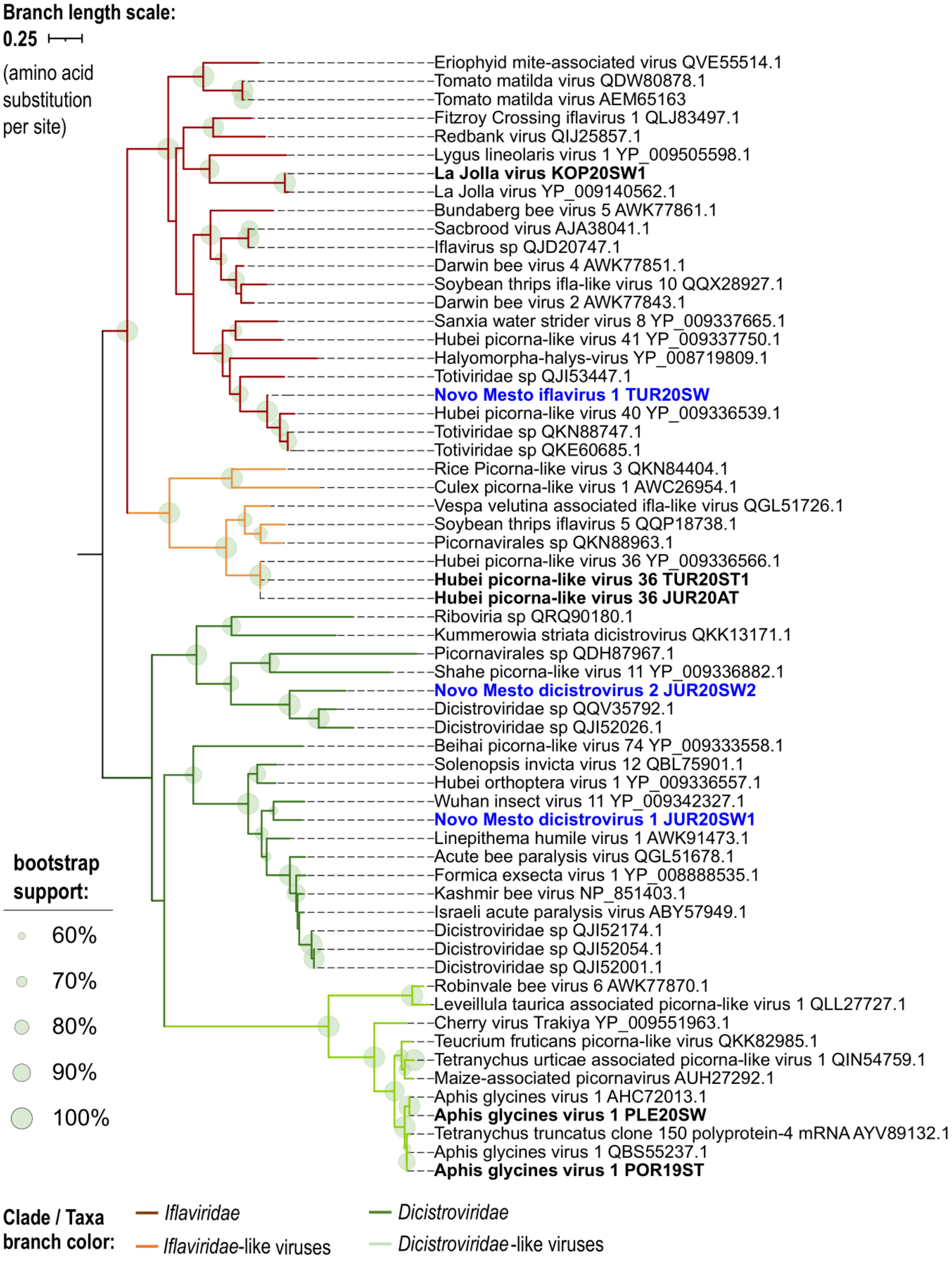
**Supplementary Figure 4-14.** Maximum likelihood phylogenetic tree based on the alignment of conserved reverse transcriptase (RT) amino acid sequence of virus species under family *Caulimoviridae* (*Ortelivirales*).

**Supplementary Figure 4.** Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font) virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.



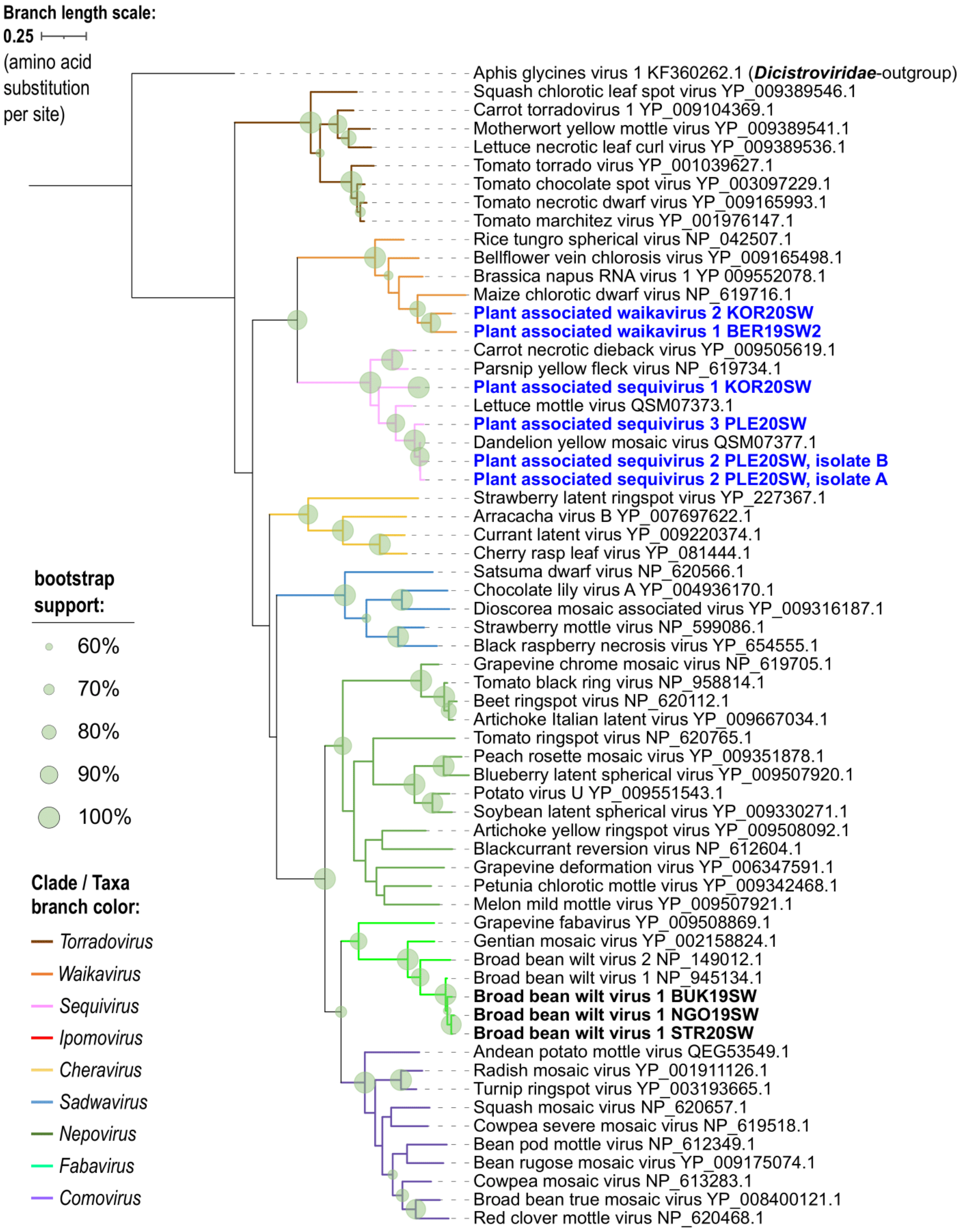
**Supplementary Figure 4-15.** Maximum likelihood phylogenetic tree based on the alignment of conserved RNA-dependent RNA polymerase amino acid sequence of virus species under *Iflaviridae* (*Picornavirales*), highlighting isolates of Tomato matilda virus from this study.

**Supplementary Figure 4.** Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font)  virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.



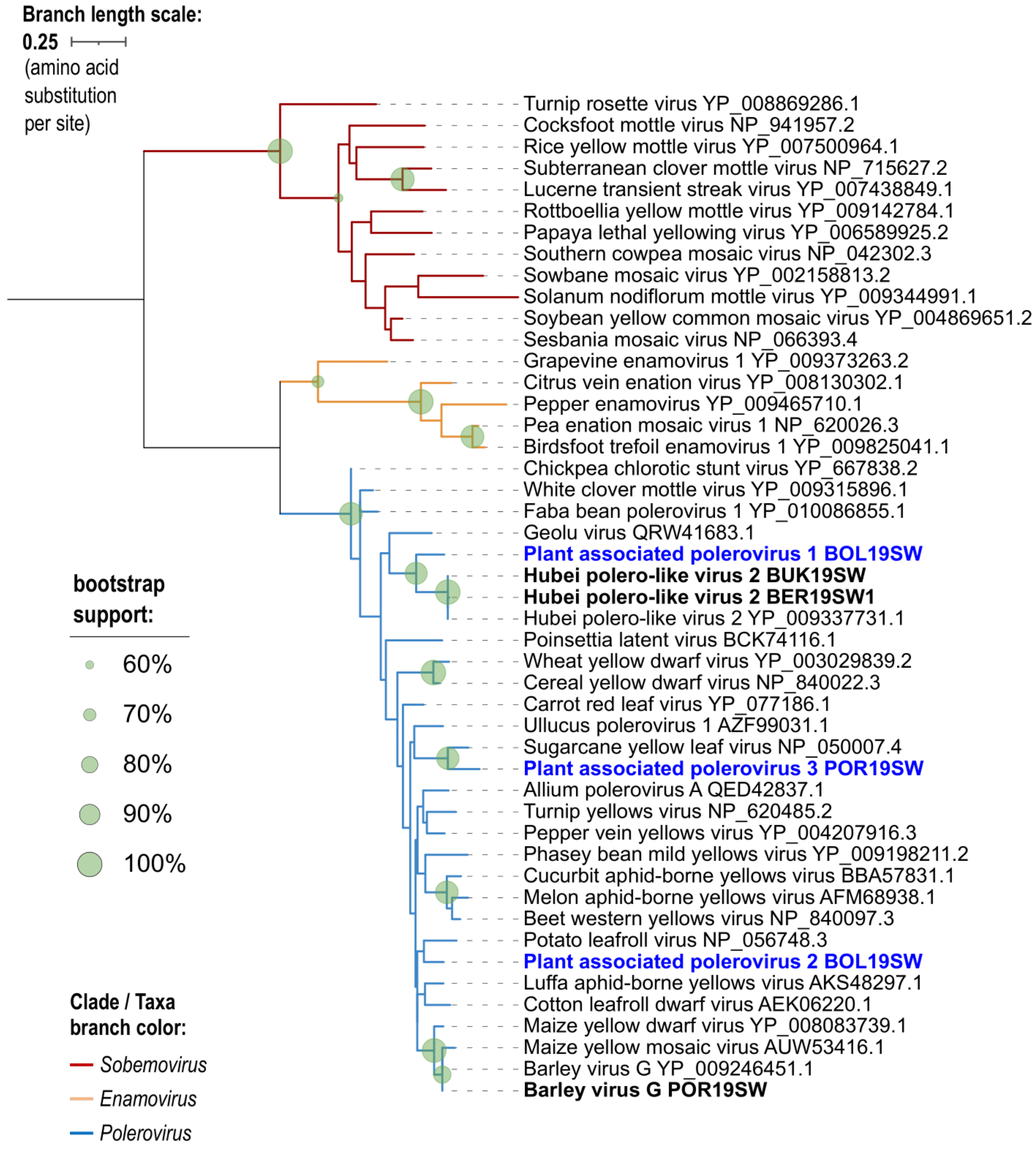
**Supplementary Figure 4-16.** Maximum likelihood phylogenetic tree based on the alignment of conserved RNA-dependent RNA polymerase amino acid sequence of virus and virus-like species classifiable under family *Dicistroviridae* and *Iflaviridae* (*Picornavirales*).

**Supplementary Figure 4.** Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font) virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.



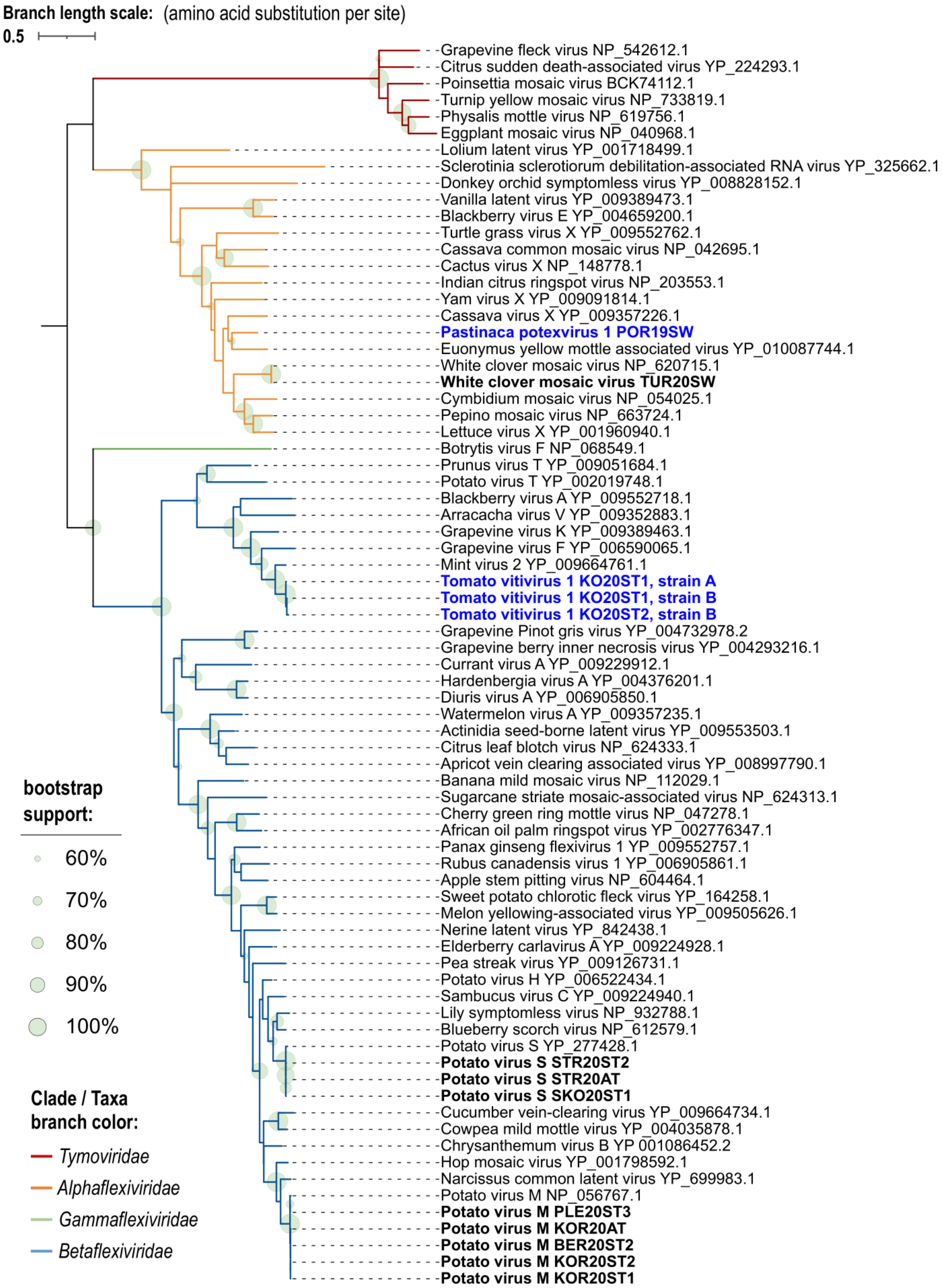
**Supplementary Figure 4-17.** Maximum likelihood phylogenetic tree based on the alignment of conserved RNA-dependent RNA polymerase amino acid sequence of virus species under family *Secoviridae* (*Picornavirales*).

**Supplementary Figure 4.** Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font) virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.



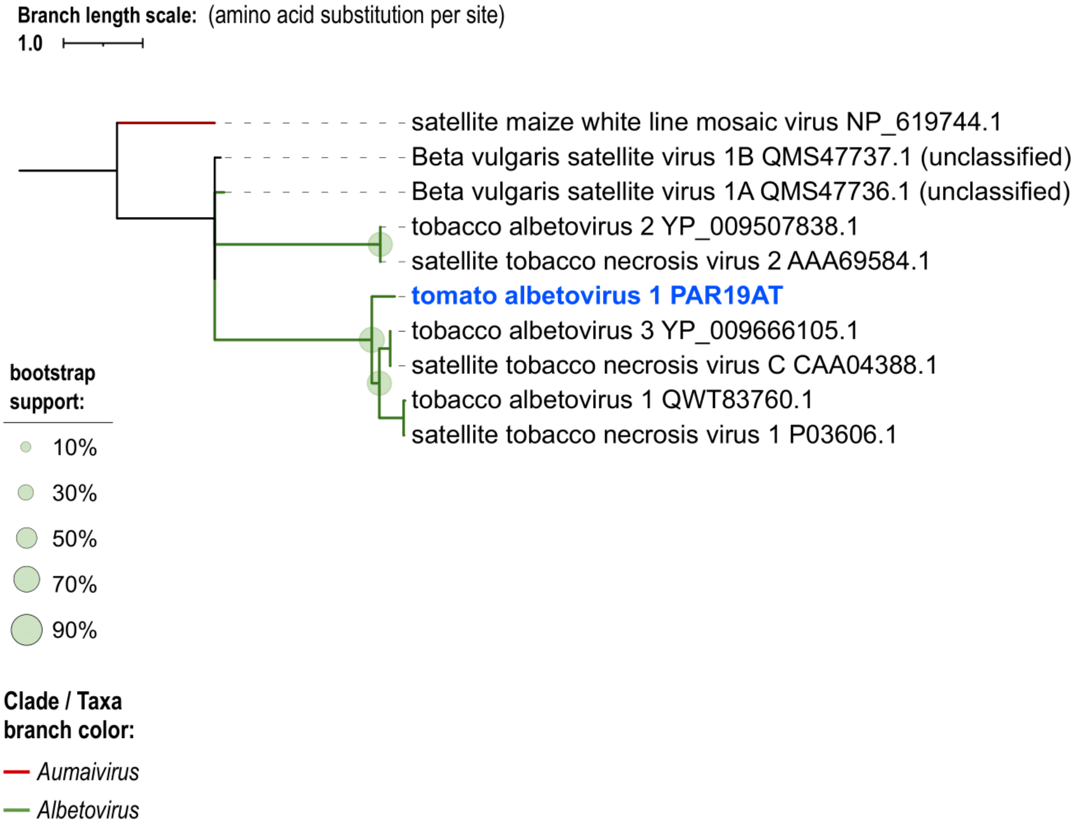
**Supplementary Figure 4-18.** Maximum likelihood phylogenetic tree based on the alignment of conserved RNA-dependent RNA polymerase amino acid sequence of virus species under family *Solemoviridae* (*Sobelivirales*).

**Supplementary Figure 4.** Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font) virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.



**Supplementary Figure 4-19.** Maximum likelihood phylogenetic tree based on the alignment of conserved RNA-dependent RNA polymerase amino acid sequence of virus species under order *Tymovirales*.

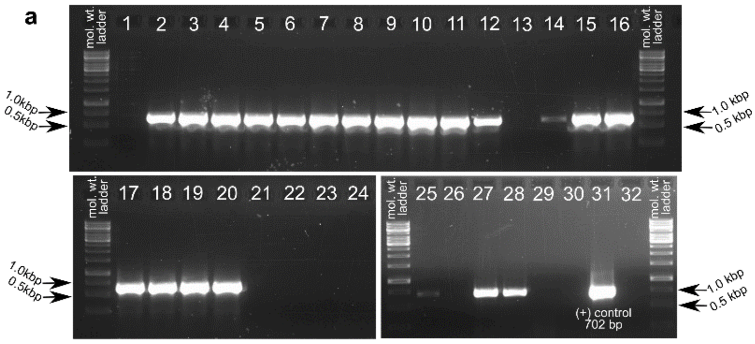
**Supplementary Figure 4.** Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font) virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.



**Supplementary Figure 4-20.** Maximum likelihood phylogenetic tree based on the alignment of conserved coat protein amino acid sequence of satellite virus species with emphasis on genus *Albetovirus*.

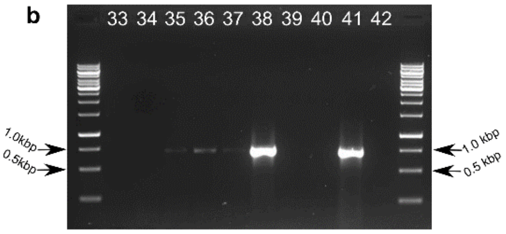
**Supplementary Figure 4.** Phylogenetic trees up to the virus family (or order) level showing relationships of identified known (in bold black font) and novel (in bold blue font) virus species from this study, with the isolate names indicated. GenBank accession numbers for the viruses from this study can be found in Supplementary Table 5, while GenBank accession number (protein) are indicated for known viruses in the tree. All details of phylogenetic analyses can be found above in Supplementary Table 10.

**a**



Note: kbp - kilo base pairs

**b**



Note: kbp - kilo base pairs

Samples tested in the RT-PCR assay shown in **a**:

Assay controls in **a**:

1 - non-template control 1
13 - blank 1
21 - negative control of RNA isolation 1
22 - negative control of RNA isolation 2
23 - non-template control 1
24 - blank 2
31 - positive control (PTV1 RNA)
32 - negative control of RNA isolation 3

| Inoculated plant | 7dpi pool of inoculated leaves | 14 dpi pool of inoculated leaves | 14 dpi pool of young apical (systemic) leaves | 21 dpi pool of young apical (systemic) leaves | 28 dpi pool of young apical (systemic) leaves | 35 dpi pool of young apical (systemic) leaves |
|---|---|---|---|---|---|---|
| *Solanum lycopersicum* | $2^{asym}$ | $8^{asym}$ | $14^{asym}$ | $25^{a,asym}$<br>$26^{b,asym}$ | $27^{a,asym}$<br>$28^{b,asym}$ | $29^{a,asym}$<br>$30^{b,asym}$ |
| *Nicotiana benthamiana* | $3^{sym}$ | $9^{sym}$ | $15^{sym}$ | $17^{sym}$ | $19^{sym}$ | not tested |
| *Nicotiana clevelandii* | $4^{sym}$ | $10^{sym}$ | $16^{sym}$ | $18^{sym}$ | $20^{sym,HTS(+)}$ | not tested |

Note: dpi - days post inoculation, $^{a}$10x diluted RNA, $^{b}$100x diluted RNA, $^{asym}$asymptomatic, $^{sym}$symptomatic, $^{HTS(+)}$was used in HTS where presence of PTV1 was confirmed. Other inoculated plants tested: 7dpi/14dpi pool of inoculated leaves: *Nicotiana tabacum* (lane 5/lane11), *Nicotiana glutinosa* (lane 6/lane12), *Chenopodium quinoa* (lane 7/-);

Samples tested in the RT-PCR assay shown in **b**:

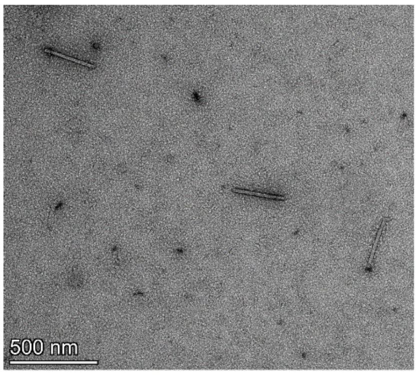
Assay controls in **b**:

33 - non-template control
41 - positive control (PTV1 RNA)
42 - negative control of RNA isolation

| Inoculated plant | 28 dpi young apical (systemic) leaves from individual plants | | | | | 49 dpi pool of young apical (systemic) leaves | 56 dpi pool of young apical (systemic) leaves |
|---|---|---|---|---|---|---|---|
| | plant 1 | plant 2 | plant 3 | plant 4 | plant 5 | | |
| *Solanum lycopersicum* | $34^{asym}$ | $35^{asym}$ | $36^{asym}$ | $37^{asym}$ | $38^{asym}$ | $39^{asym}$ | $40^{asym}$ |

Note: RNA extracts used in this assay (**b**) were diluted 1:200, except for the positive control. dpi - days post inoculation. $^{asym}$asymptomatic. $^{sym}$symptomatic.

**c**



**d**

| Test plant / collection dpi / individual or pooled? | No. of quality-controlled (QC) reads | No. of reads mapping to PTV1 genome | Percentage of QC reads mapping to PTV1 genome |
|---|---|---|---|
| *Solanum lycopersicum* / 28 dpi / individual plant$^{a}$ | 157191 | 0 | 0.00% |
| *Solanum lycopersicum* / 28 dpi / individual plant$^{b}$ | 160438 | 0 | 0.00% |
| *Nicotiana clevelandii* / 21 dpi / pooled plants$^{c}$ | 159570 | 14216 | 8.91% |

Note: $^{a}$lane 35 in (**b**). $^{b}$lane 37 in (**b**). $^{c}$lane 18 in (**a**).

**Supplementary Figure 5.** RT-PCR, TEM and nanopore sequencing results on the confirmation of infectivity of Plantago tobamovirus 1 (PTV1) on Solanaceae hosts. **a, b** RT-PCR assays for the detection of PTV1 in inoculated and young apical (systemic) leaves at different time points. **c** Transmission electron micrograph showing three virions of PTV1 from crude preparations of infected *Nicotiana clevelandii* tissues. **d** Number and proportion of long reads mapping to PTV1 genome, derived from selected inoculated plants.

**Data source supplementary materials are available through *Figshare* doi:** 10.6084/m9.figshare.20200769

**Supplementary Table 11-22**. Summary of all results from the DnaSP v. 6 analyses.

**Supplementary Table 23-42**. Summary of all pairwise identity values from the SDT v. 1.2 analyses

**Supplementary Table 43-47**. Summary of all results from the protein domain prediction using InterPro scans and homology alignments with known species of potyviruses to identify start and cleavage sites of proteins.

# A.3 Supplementary Material for Publication 2.3

## First Report of Ranunculus white mottle ophiovirus in Slovenia in Pepper with yellow leaf curling symptom and in Tomato

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[§]These authors contributed equally to this work. *Corresponding author: D. Kutnjak (denis.kutnjak@nib.si)

### SUPPLEMENTARY MATERIAL

**Supplementary Table 1.** Summary of high throughput sequencing (HTS) kits and platforms used, viruses detected in pools and information on detection of Ranunculus white mottle ophiovirus (RWMV) in each sequencing pool.

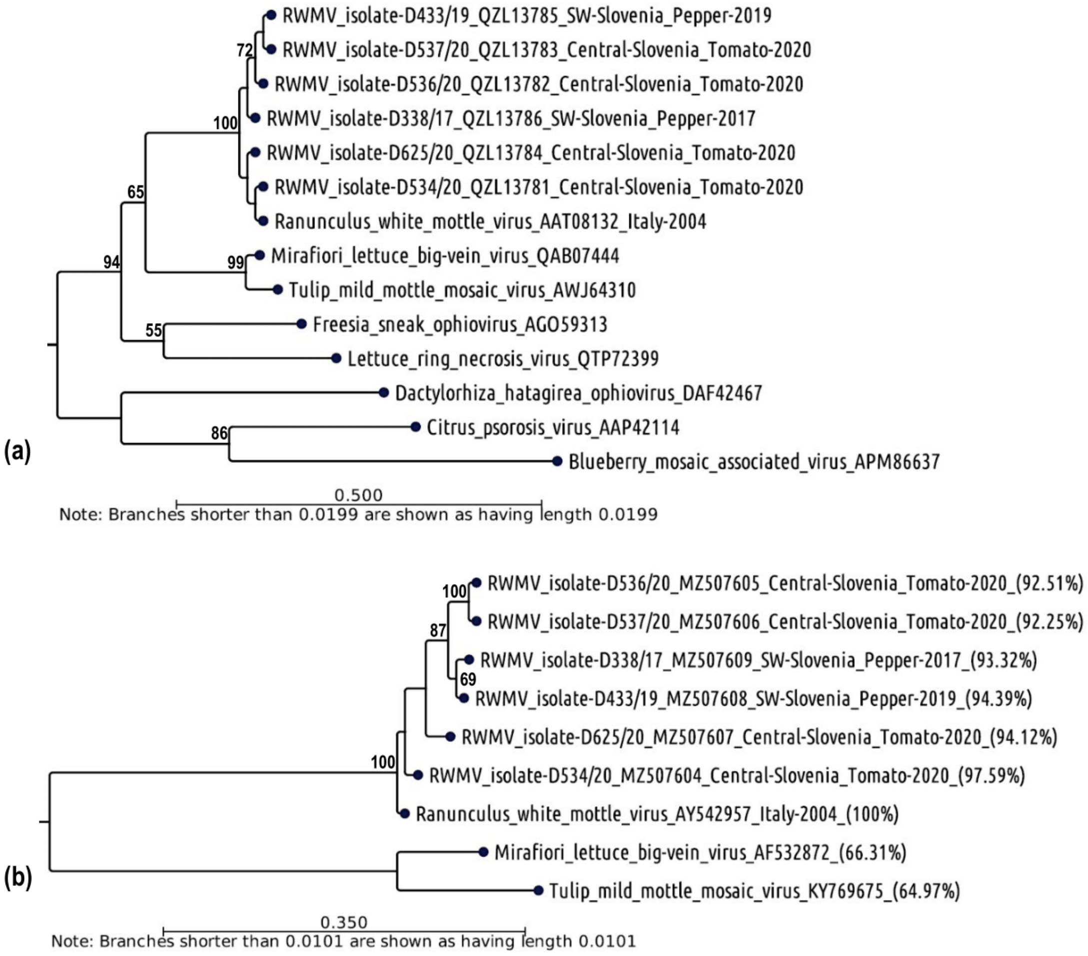
| **HTS pool ID** / Sequencing kits, sequencing approach and platform used | Number of reads* and length | Reads of other viruses detected in the pool, aside from RWMV, using HTS | Reads mapped to RWMV**, no. of contigs assembled (longest contig length in bp), % of reference covered, and the average read coverage depth for the reference (ref.) used | Laboratory identification codes of RWMV positive samples / GenBank accession numbers of sequenced coat protein amplicons from each sample |
|---|---|---|---|---|
| **D2017** / small RNA sequencing (TailorMix miRNA libraries (Seqmatic, LLC)) in Illumina NextSeq | 1,439,218<br>(21-24 bp) | BPEV, PepCV2 | ref. = AY542957:<br>646 reads, 13 contigs (509 bp),<br>% reference covered = 47.88%<br>average read coverage = 12.65 | D338/17 (pepper) / MZ507609 |
| | | | ref. = NC_043389:<br>222 reads, 1 contig (564 bp)<br>% reference covered = 14.04%<br>average read coverage = 0.97 | |
| **D2019_P1** / ribosomal RNA-depleted total RNA sequencing (Strand-specific cDNA libraries (Seqmatic, LLC)) in Illumina HiSeq | 14,240,153<br>(<150 bp, paired-end) | CMV, BPEV, TMaV, TNVA | ref. = AY542957:<br>27 reads, 1 contig (1255 bp),<br>% reference covered = 96.14%<br>average read coverage = 3.77 | D433/19 (pepper) / MZ507608 |
| | | | ref. = NC_043389:<br>4 reads, 2 contigs (268 bp)<br>% reference covered = 12.20%<br>average read coverage = 0.15 | |
| **D2020_P1** / ribosomal RNA-depleted total RNA sequencing (Nextera XT libraries (Illumina)) in Illumina MiSeq | 2,472,511<br>(<250 bp, paired-end) | CMV, PVY, STV, OLV1 | ref. = AY542957:<br>1 read, 1 contig (251 bp)<br>% reference covered = 23.61%<br>average read coverage = 0.24 | D534/20 (tomato) / MZ507604 and<br>D625/20 (tomato) / MZ507607 |
| | | | ref. = NC_043389:<br>1 read, 1 contig (251 bp)<br>% reference covered = 6.25%<br>average read coverage = 0.89 | |
| **D2020_P3** / ribosomal RNA-depleted total RNA sequencing (Nextera XT libraries (Illumina)) in Illumina MiSeq | 2,448,828<br>(<250 bp, paired-end) | CMV, PVY, BPEV, BBWV1, STV, OLV1, SnIV1 | ref. = AY542957: 0 reads; | D536/20 (tomato) / MZ507605 and<br>D537/20 (tomato) / MZ507606 |
| | | | ref. = NC_043389:<br>2 reads, 1 contig (282 bp)<br>% reference covered = 7.02%<br>average read coverage = 0.12 | |

**Note:** *number of adapter-trimmed and quality-filtered (≥95% probability score) reads; **number of adapter-trimmed and quality-filtered reads mapping to RWMV sequences in GenBank (reference (ref.) = AY542957 (coat protein gene, partial cds) and NC_043389 (putative RNA-dependent RNA polymerase, partial cds)). Mapping was done in CLC Genomics Workbench (v. 20.0, Qiagen), with parameters: no reference masking, match score=1, mismatch cost=2, with linear gap cost (insertion cost=3, deletion cost=3), and executed as random mapping with ≥90% similarity and read length fraction. **Virus acronyms:** BBWV1 - broad bean wilt virus 1, BPEV - bell pepper alphaendornavirus, CMV - cucumber mosaic virus, OLV1 - olive latent virus 1, PepCV2 - pepper cryptic virus 2, PVY - potato virus Y, SnIV1 - Solanum nigrum ilarvirus 1, STV - southern tomato virus, TMaV - tomato matilda virus, TNVA - tobacco necrosis virus A.

**Supplementary Table 2.** Primers and thermocycling conditions used for confirming Ranunculus white mottle ophiovirus in individual plant samples. Target region and amplicon size are also indicated.

| | | |
|---|---|---|
| **Forward primer:** | `5′-TGTGTGTTCATCTCTCTTCTGC-3′` | |
| **Reverse primer:** | `5′-ACAGGGAAGTGAATCACACCTA-3′` | |
| **RT-PCR kit used** | QIAGEN OneStep RT-PCR Kit | |
| **RT-PCR program used:** | | |
| Reverse transcription step (1 cycle): | 30 min at 50ºC | |
| | 15 min at 95ºC | |
| PCR step (35 cycles): | 0.5 min at 94ºC | 35 cycles |
| | 0.5 min at 55ºC | |
| | 1.0 min at 72ºC | |
| Extension step (1 cycle): | 10 min at 72ºC | |
| **Target region:** | around the 800-1300 region of RNA 3 segment coding for coat protein | |
| **Product size**: | 493 bp | |

**Supplementary Figure 1.** Photos from the field of pepper and tomato samples that tested positive for Ranunculus white mottle ophiovirus (RWMV) using RT-PCR. (a), (b) The pepper sample was collected in July 2017 and showed virus disease-like symptoms, such as interveinal chlorosis or yellowing, while midrib and veins remain green. Symptoms in mature leaves or flowers include mottling and chlorosis, coupled with slight to almost full curling of leaves from lamina inward, as well as necrotic and aborted flowers. Aside from RWMV, bell pepper alphaendornavirus and pepper cryptic virus 2 are the only viruses detected in the sequencing pool where the plant sample shown here belongs. However, these viruses are not known to be associated with any disease symptoms. (c), (d) and (e) show tomato samples that tested positive for RWMV, that show the interveinal yellowing symptoms. There are other viruses detected in the tomato samples that may contribute to the symptoms shown. Thus, it is difficult to associate observed symptoms in tomato to single RWMV infection.



**Supplementary Figure 2.** Maximum likelihood phylogenetic trees based on the alignment of (a) conserved 124 amino acids sequence segment of the coat protein, and (b) the corresponding conserved 374 nucleotide segment of RNA 3 coding for the coat protein, of Ranunculus white mottle ophiovirus isolates from Slovenia and other known ophioviruses (*Aspiviridae*) used as outgroup (NCBI accession numbers are indicated). Alignments were done using ClustalW (Thompson et al., 1994), and after trimming, MAFFT alignment (Katoh and Standley, 2013) and further trimming of the alignments with trimAl (Capella-Gutiérrez et al., 2009) were performed. The final phylogenetic trees shown have the highest log likelihood value inferred with 1000 bootstrap replicates (Felsenstein, 1985), and are based on Le_Gascuel_2008 model (Le and Gascuel, 2008) with discrete Gamma distribution for (a) and Hasegawa-Kishino-Yano model (Hasegawa et al., 1985) with discrete Gamma distribution for (b). The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (>50% support) is shown next to the branches. The trees are drawn to scale for easier visualization, with branch lengths measured in the number of amino acid substitutions per site in (a) or nucleotide substitutions per site in (b). Pairwise similarity of aligned and trimmed nucleotide sequences relative to the Italian isolate AY542957 are shown in each tree node in (b). ClustalW alignment, manual trimming and pairwise similarity analysis were done in CLC Genomics Workbench (Qiagen). MAFFT was executed in EMBL-EBI website (www.ebi.ac.uk/Tools/msa/mafft/), and trimAl was downloaded from <www.trimal.cgenomics.org> and was executed in command line, with 'automated1' option. Best model testing, substitution matrix estimation and phylogenetic tree construction were done in MEGA X (Kumar et al., 2018), and the final phylogenetic tree was edited in CLC Genomics Workbench (Qiagen).

**References for the tools used in phylogenetic analyses:**

Capella-Gutiérrez, S., Silla-Martínez, J. M., and Gabaldón, T. (2009). trimAl: A tool for automated alignment trimming in large-scale phylogenetic analyses. *Bioinformatics* 25, 1972–1973. doi:10.1093/bioinformatics/btp348.

Felsenstein, J. (1985). Confidence Limits on Phylogenies: An Approach Using the Bootstrap. *Evolution (N. Y).* 39, 783. doi:10.2307/2408678.

Hasegawa, M., Kishino, H., and Yano, T. aki (1985). Dating of the human-ape splitting by a molecular clock of mitochondrial DNA. *J. Mol. Evol.* 22, 160–174. doi:10.1007/BF02101694.

Katoh, K., and Standley, D. M. (2013). MAFFT multiple sequence alignment software version 7: Improvements in performance and usability. *Mol. Biol. Evol.* 30, 772–780. doi:10.1093/molbev/mst010.

Kumar, S., Stecher, G., Li, M., Knyaz, C., and Tamura, K. (2018). MEGA X: Molecular Evolutionary Genetics Analysis across Computing Platforms. *Mol. Biol. Evol.* 35, 1547–1549. doi:10.1093/molbev/msy096.

Le, S. Q., and Gascuel, O. (2008). An improved general amino acid replacement matrix. *Mol. Biol. Evol.* 25, 1307–1320. doi:10.1093/molbev/msn067.

Thompson, J. D., Higgins, D. G., and Gibson, T. J. (1994). CLUSTALW: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res.* 22, 4673–4680. doi:10.1093/nar/22.22.4673.

# Appendix B

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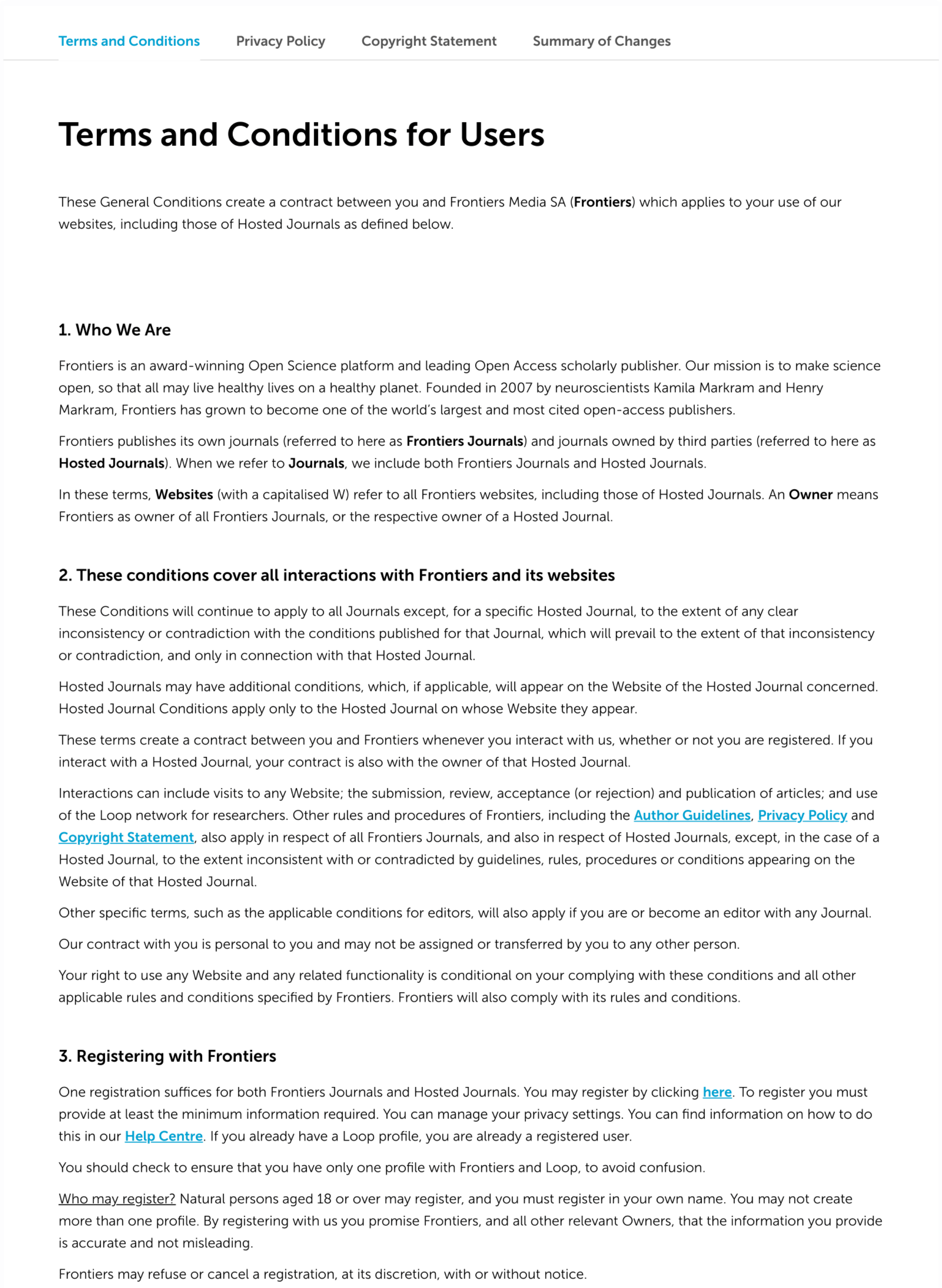

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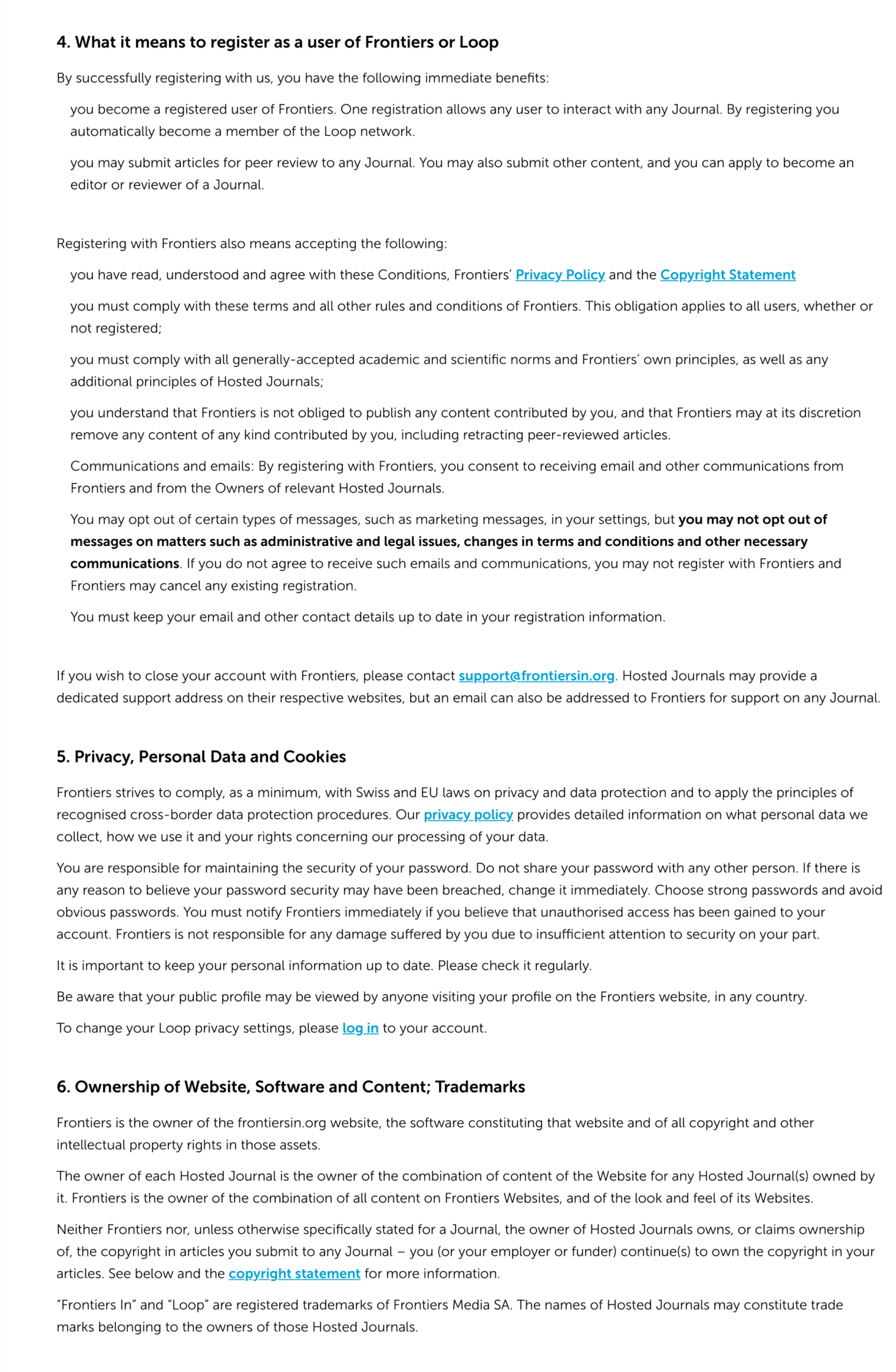

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By successfully registering with us, you have the following immediate benefits:

- you become a registered user of Frontiers. One registration allows any user to interact with any Journal. By registering you automatically become a member of the Loop network.
- you may submit articles for peer review to any Journal. You may also submit other content, and you can apply to become an editor or reviewer of a Journal.

Registering with Frontiers also means accepting the following:

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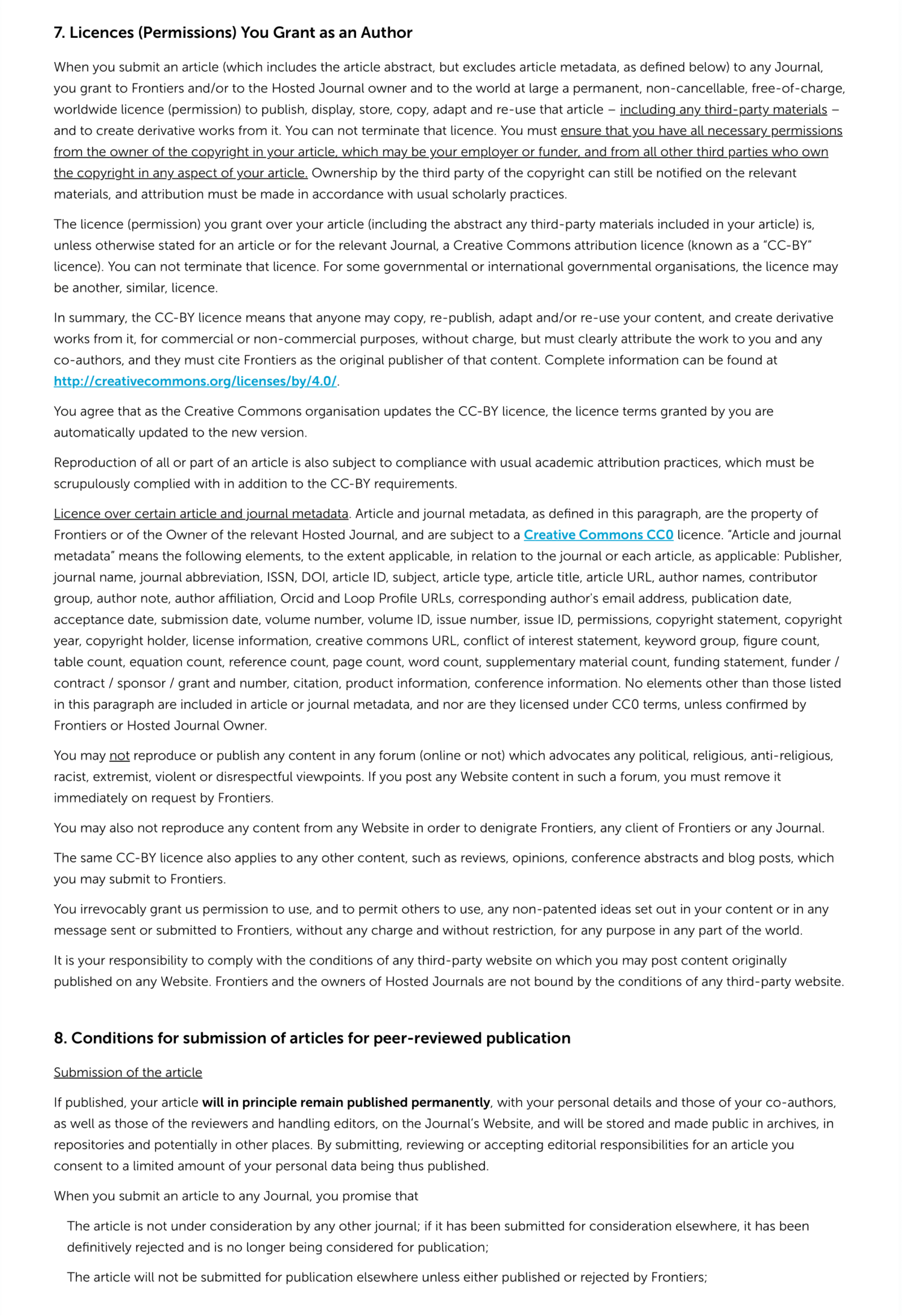

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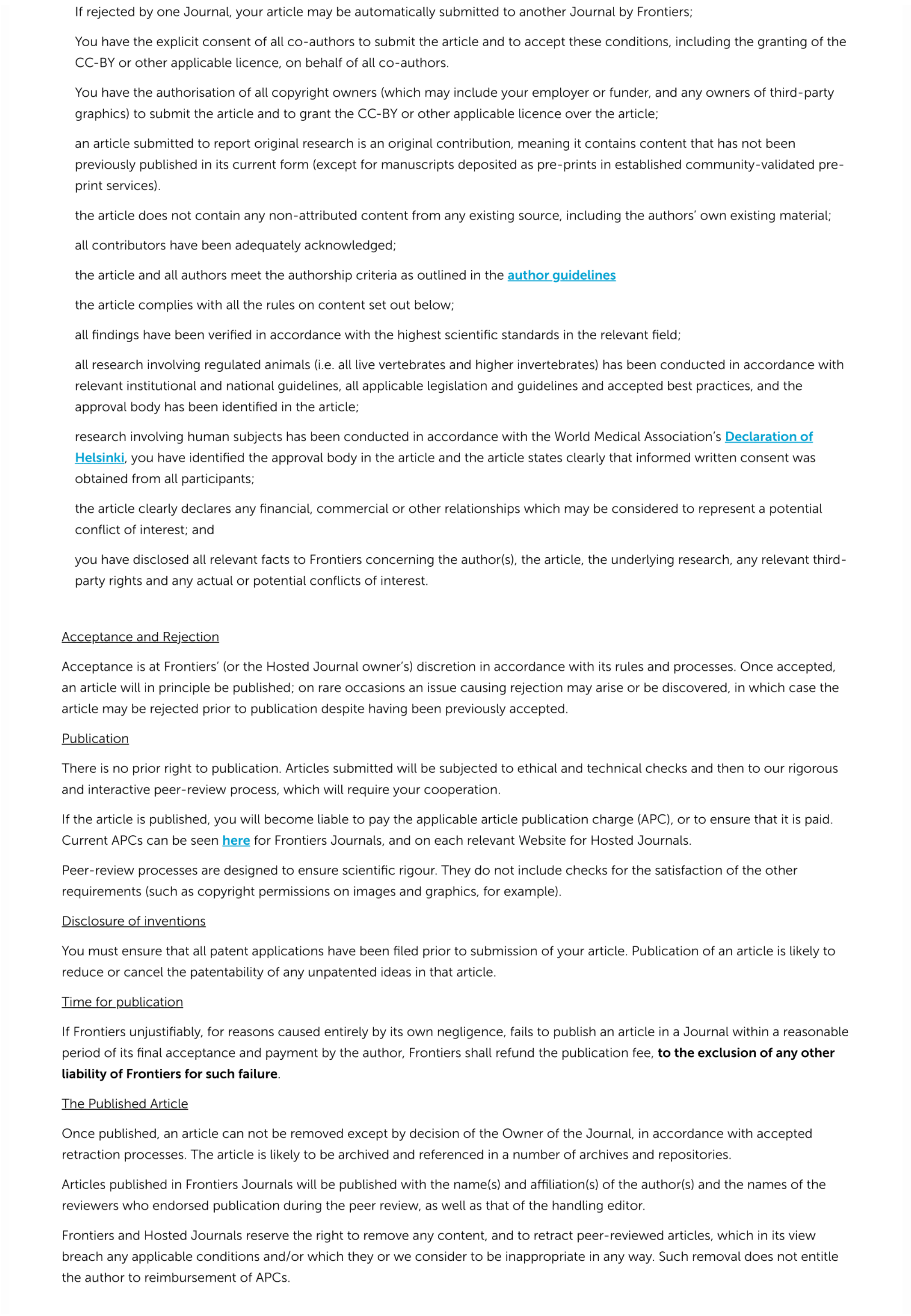

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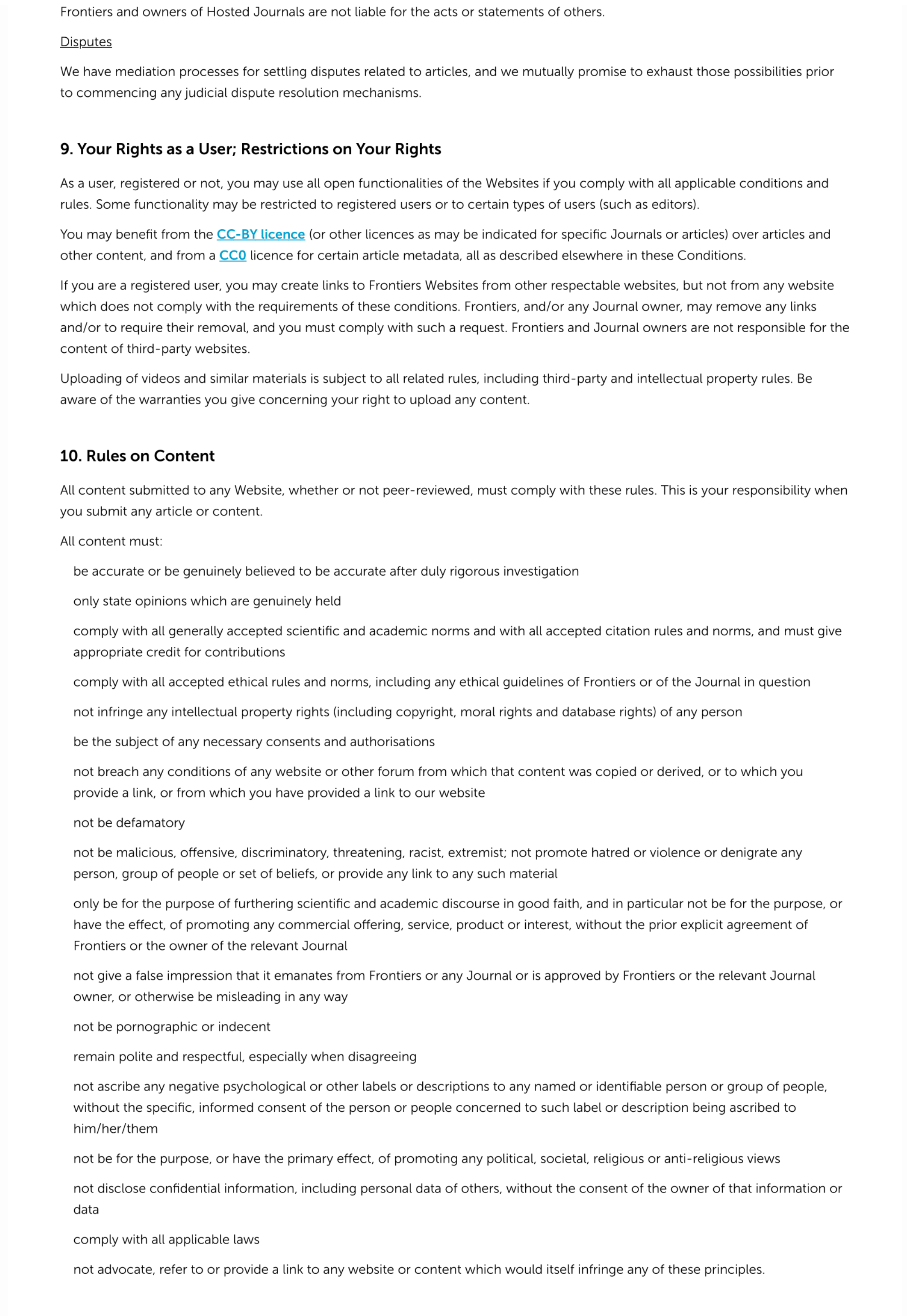

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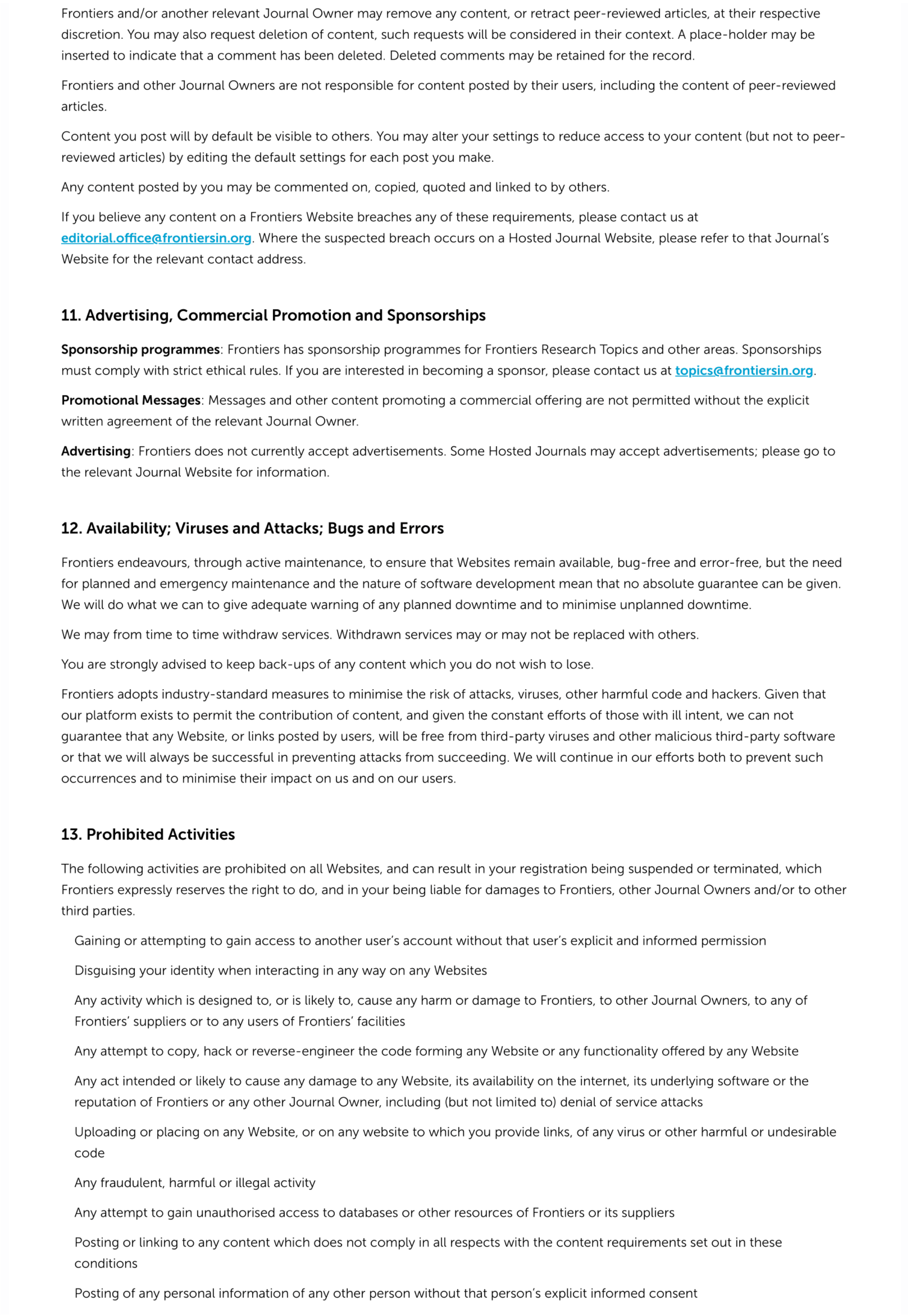

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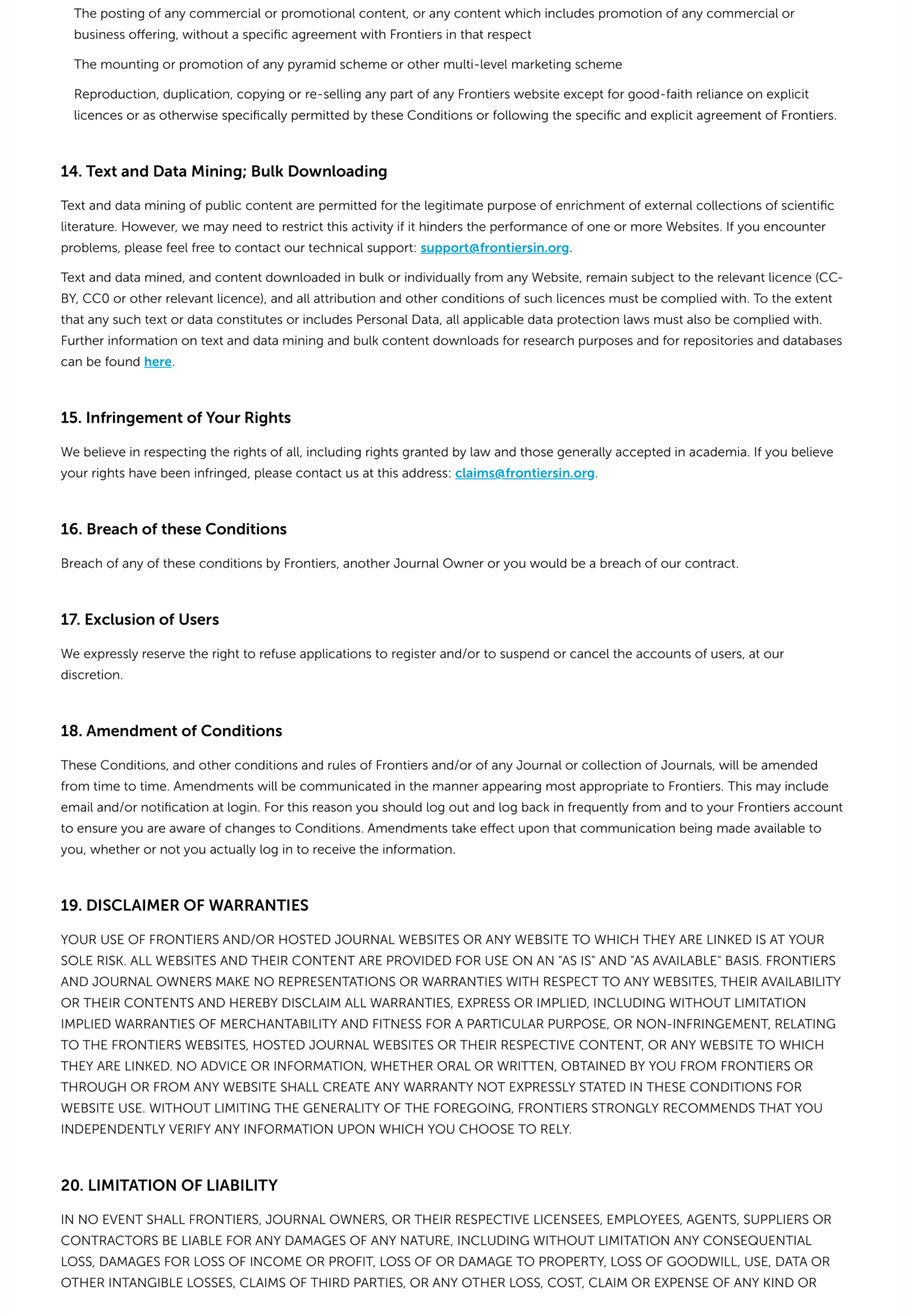

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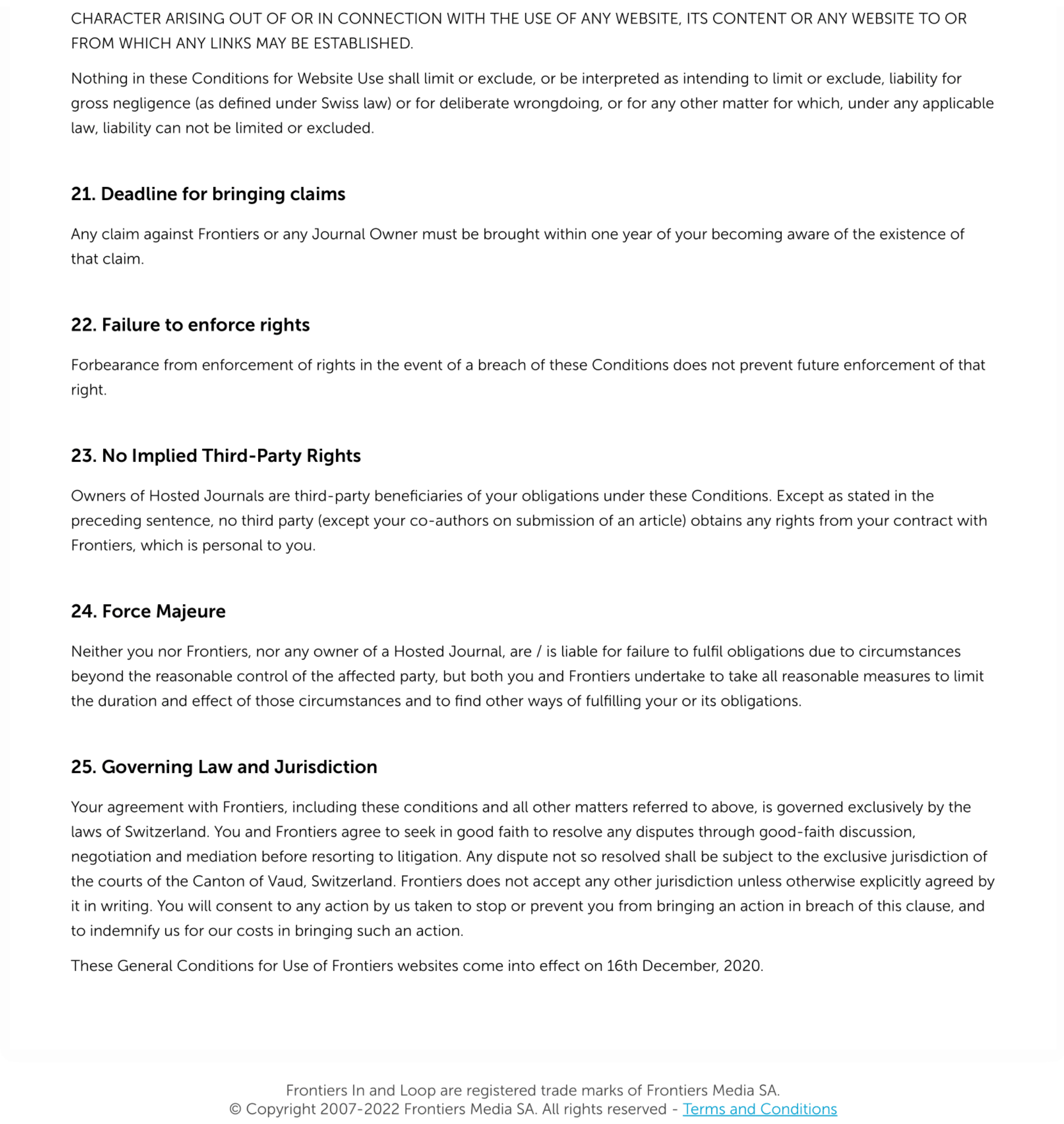

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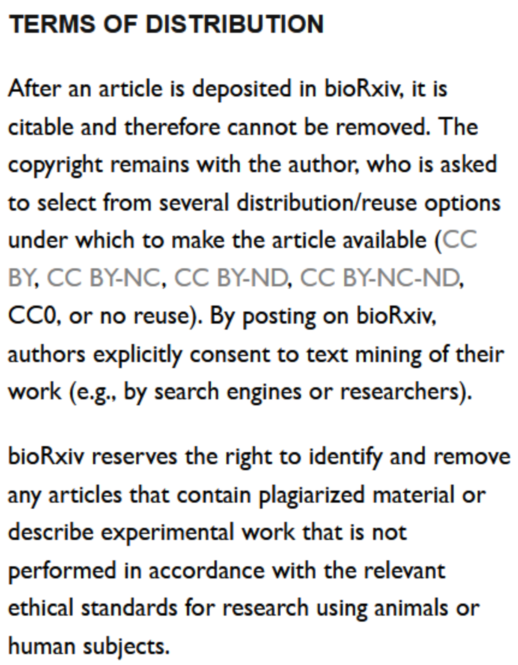

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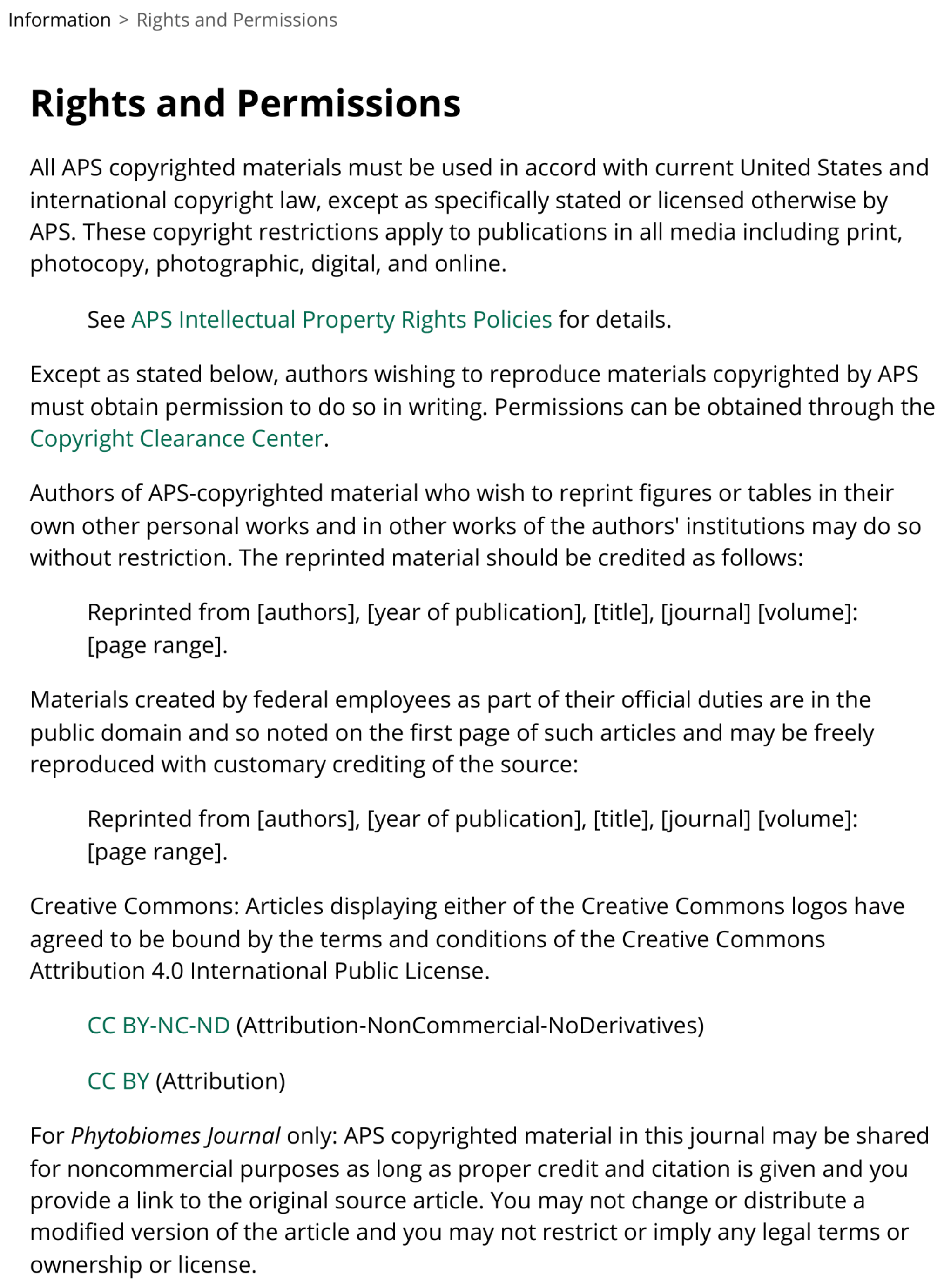

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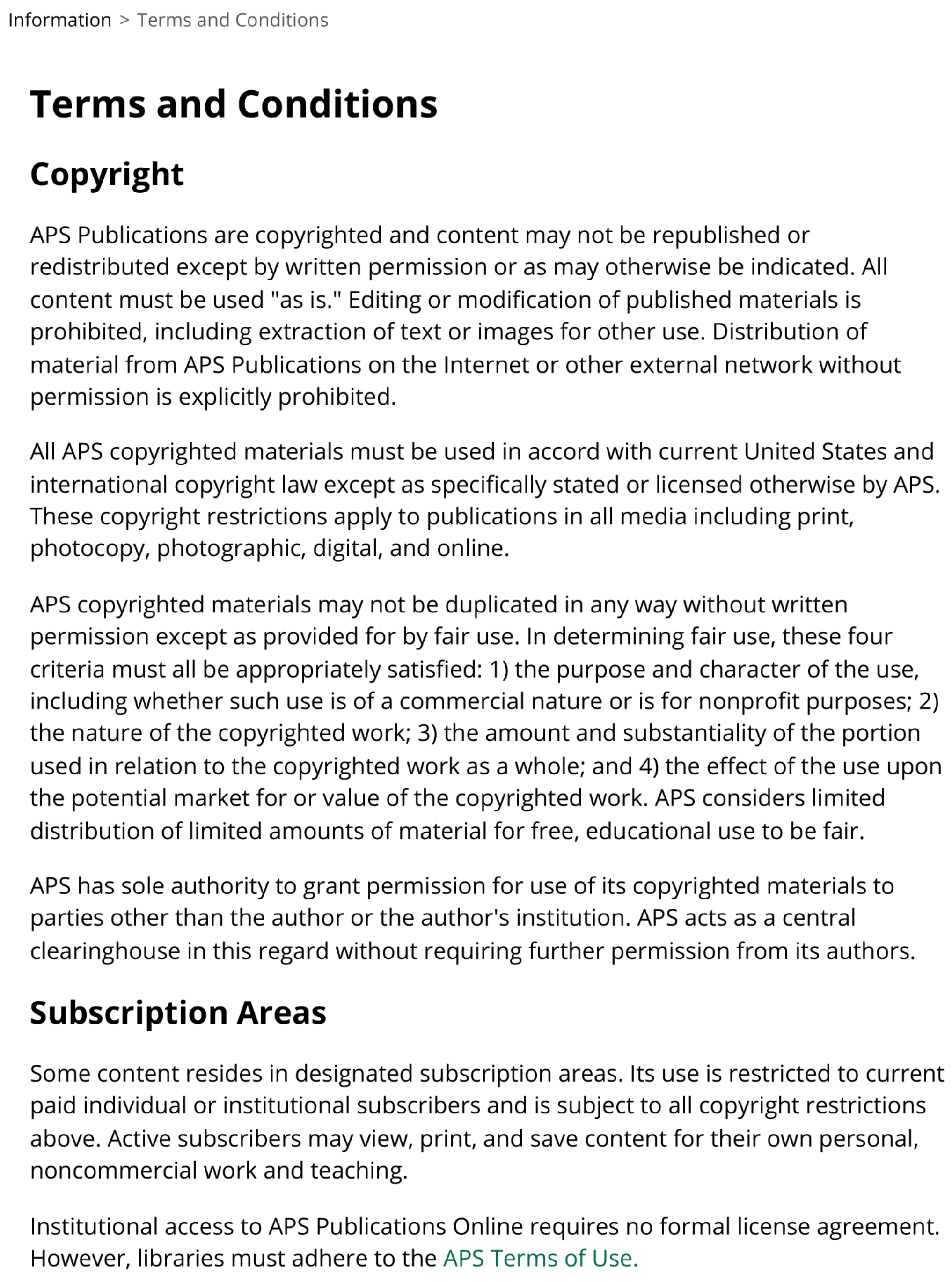

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# References

Alcalá-Briseño, R. I., Casarrubias-Castillo, K., López-Ley, D., Garrett, K. A., & Silva-Rosales, L. (2020). Network Analysis of the Papaya Orchard Virome from Two Agroecological Regions of Chiapas, Mexico. *MSystems*, *5*(1). https://doi.org/10.1128/msystems.00423-19

Alexander, H. M., Mauck, K. E., Whitfield, A. E., Garrett, K. A., & Malmstrom, C. M. (2014). Plant-virus interactions and the agro-ecological interface. *European Journal of Plant Pathology*, *138*(3), 529–547. https://doi.org/10.1007/s10658-013-0317-1

Alleyne, A. T., Cummins, C., Rowe, K., James, M., Gutiérrez, D. L., & Fuentes, S. (2019). Sequencing and assembly of small RNAs reveal the presence of several begomoviruses, potyviruses, badnaviruses and mastreviruses in the sweet potato leaf virome in Barbados. *Journal of Plant Pathology*, *101*(2), 339–347. https://doi.org/10.1007/s42161-018-00214-1

Anderson, P. K., Cunningham, A. A., Patel, N. G., Morales, F. J., Epstein, P. R., & Daszak, P. (2004). Emerging infectious diseases of plants: Pathogen pollution, climate change and agrotechnology drivers. *Trends in Ecology & Evolution*, *19*(10), 535–544. https://doi.org/10.1016/j.tree.2004.07.021

Bačnik, K., Kutnjak, D., Pecman, A., Mehle, N., Tušek Žnidarič, M., Gutiérrez Aguirre, I., & Ravnikar, M. (2020). Viromics and infectivity analysis reveal the release of infective plant viruses from wastewater into the environment. *Water Research*, *177*, 115628. https://doi.org/10.1016/j.watres.2020.115628

Beijerinck, M. (1898). Ueber ein Contagium vivum fluidum als Ursache der Fleckenkrankheit der Tabaksblätter (Eng. Translation: Concerning a contagium vivum fluidum as cause of the spot disease of tobacco leaves. Published as Phytopath Classics 7 (1942): 33–54). *Verh Kon Akad Wetensch*, *65*, 3–21.

Benson, D. A., Clark, K., Karsch-Mizrachi, I., Lipman, D. J., Ostell, J., & Sayers, E. W. (2015). GenBank. *Nucleic Acids Research*, *43*(D1), D30–D35. https://doi.org/10.1093/NAR/GKU1216

Bernardo, P., Charles-Dominique, T., Barakat, M., Ortet, P., Fernandez, E., Filloux, D., Hartnady, P., Rebelo, T. A., Cousins, S. R., Mesleard, F., Cohez, D., Yavercovski, N., Varsani, A., Harkins, G. W., Peterschmitt, M., Malmstrom, C. M., Martin, D. P., & Roumagnac, P. (2018). Geometagenomics illuminates the impact of agriculture on the distribution and prevalence of plant viruses at the ecosystem scale. *The ISME Journal*, *12*(1), 173–184. https://doi.org/10.1038/ismej.2017.155

Bertran, A. (2022). *Next-Generation Sequencing.* https://docs.google.com/presentation/d/e/2PACX-

1vTzEQ65KsEQPVoU85ezzzYtLRM7lmukkTuJbmsJLmGKmcIbg3VzdbJjMKqr3J-2ECkCEs65NxXq_VJ1/pub?start=false&loop=false&delayms=3000&slide=id.g12f6843f869_0_11

Call, L., Nayfach, S., & Kyrpides, N. C. (2021). Illuminating the Virosphere Through Global Metagenomics. *Annual Review of Biomedical Data Science*. https://doi.org/10.1146/annurev-biodatasci-012221

Carlson, C. J., Albery, G. F., Merow, C., Trisos, C. H., Zipfel, C. M., Eskew, E. A., Olival, K. J., Ross, N., & Bansal, S. (2022). Climate change increases cross-species viral transmission risk. *Nature*, 1–1. https://doi.org/10.1038/s41586-022-04788-w

Carpino, C., Elvira-González, L., Rubio, L., Peri, E., Davino, S., & Galipienso, L. (2019). A comparative study of viral infectivity, accumulation and symptoms induced by broad bean wilt virus 1 isolates. *Journal of Plant Pathology*, *101*(2), 275–281. https://doi.org/10.1007/s42161-018-00198-y

Carroll, D., Daszak, P., Wolfe, N. D., Gao, G. F., Morel, C. M., Morzaria, S., Pablos-Méndez, A., Tomori, O., & Mazet, J. A. K. (2018). The Global Virome Project. *Science*, *359*(6378), 872–874. https://doi.org/10.1126/science.aap7463

Chiapello, M., Bosco, L., Ciuffo, M., Ottati, S., Salem, N., Rosa, C., Tavella, L., & Turina, M. (2021). Complexity and Local Specificity of the Virome Associated with Tospovirus-Transmitting Thrips Species. *Journal of Virology*, *95*(21). https://doi.org/10.1128/JVI.00597-21

Ciuffo, M., Kinoti, W. M., Tiberini, A., Forgia, M., Tomassoli, L., Constable, F. E., & Turina, M. (2020). A new blunervirus infects tomato crops in Italy and Australia. *Archives of Virology*, *165*(10), 2379–2384. https://doi.org/10.1007/s00705-020-04760-x

Cooper, I., & Jones, R. A. C. (2006). Wild Plants and Viruses: Under-Investigated Ecosystems. In *Advances in Virus Research* (Vol. 67, pp. 1–47). https://doi.org/10.1016/S0065-3527(06)67001-2

Creager, A. N. H., Scholthof, K. B. G., Citovsky, V., & Scholthof, H. B. (1999). Tobacco Mosaic Virus: Pioneering Research for a Century. *The Plant Cell*, *11*(3), 301–308. https://doi.org/10.1105/TPC.11.3.301

de Nazaré Almeida dos Reis, L., Fonseca, M. E. de N., Ribeiro, S. G., Naito, F. Y. B., Boiteux, L. S., & Pereira-Carvalho, R. de C. (2020). Metagenomics of Neotropical Single-Stranded DNA Viruses in Tomato Cultivars with and without the Ty-1 Gene. *Viruses*, *12*(8), 819. https://doi.org/10.3390/v12080819

Donaire, L., Wang, Y., Gonzalez-Ibeas, D., Mayer, K. F., Aranda, M. A., & Llave, C. (2009). Deep-sequencing of plant viral small RNAs reveals effective and widespread targeting of viral genomes. *Virology*, *392*(2), 203–214. https://doi.org/10.1016/j.virol.2009.07.005

Edgar, R. C., Taylor, J., Lin, V., Altman, T., Barbera, P., Meleshko, D., Lohr, D., Novakovsky, G., Buchfink, B., Al-Shayeb, B., Banfield, J. F., de la Peña, M., Korobeynikov, A., Chikhi, R., & Babaian, A. (2022). Petabase-scale sequence alignment catalyses viral discovery. *Nature*, *602*(7895), 142–147. https://doi.org/10.1038/s41586-021-04332-2

Elena, S. F., Agudelo-Romero, P., & Lalic, J. (2009). The Evolution of Viruses in Multi-Host Fitness Landscapes. *The Open Virology Journal*, *3*(1), 1–6. https://doi.org/10.2174/1874357900903010001

Elena, S. F., Fraile, A., & García-Arenal, F. (2014). Evolution and Emergence of Plant Viruses. In *Advances in Virus Research* (Vol. 88, pp. 161–191). Elsevier. https://doi.org/10.1016/B978-0-12-800098-4.00003-9

FAO. (2021). World Food and Agriculture – Statistical Yearbook 2021. In *World Food and Agriculture – Statistical Yearbook 2021*. FAO. https://doi.org/10.4060/cb4477en

Fetters, A. M., Cantalupo, P. G., Wei, N., Robles, M. T. S., Stanley, A., Stephens, J. D., Pipas, J. M., & Ashman, T.-L. (2022). The pollen virome of wild plants and its association with variation in floral traits and land use. *Nature Communications*, *13*(1), 523. https://doi.org/10.1038/s41467-022-28143-9

Fontenele, R. S., Lamas, N. S., Lacorte, C., Lacerda, A. L. M., Varsani, A., & Ribeiro, S. G. (2017). A novel geminivirus identified in tomato and cleome plants sampled in Brazil. *Virus Research*, *240*, 175–179. https://doi.org/10.1016/j.virusres.2017.08.007

Fowkes, A. R., McGreig, S., Pufal, H., Duffy, S., Howard, B., Adams, I. P., Macarthur, R., Weekes, R., & Fox, A. (2021). Integrating High throughput Sequencing into Survey Design Reveals Turnip Yellows Virus and Soybean Dwarf Virus in Pea (Pisum Sativum) in the United Kingdom. *Viruses 2021, Vol. 13, Page 2530*, *13*(12), 2530. https://doi.org/10.3390/V13122530

Fraile, A., & García-Arenal, F. (2016). Environment and evolution modulate plant virus pathogenesis. *Current Opinion in Virology*, *17*, 50–56. https://doi.org/10.1016/j.coviro.2016.01.008

Gaafar, Y. Z. A., Herz, K., Hartrick, J., Fletcher, J., Blouin, A. G., MacDiarmid, R., & Ziebell, H. (2020). Investigating the Pea Virome in Germany—Old Friends and New Players in the Field(s). *Frontiers in Microbiology*, *11*, 2605. https://doi.org/10.3389/fmicb.2020.583242

Gambley, C., Persley, D., & Thomas, J. E. (2019). First record of Ranunculus white mottle virus from Australia. *New Disease Reports*, *40*(1), 13–13. https://doi.org/10.5197/j.2044-0588.2019.040.013

García, M. L., Bó, E. D., da Graça, J. V., Gago-Zachert, S., Hammond, J., Moreno, P., Natsuaki, T., Pallás, V., Navarro, J. A., Reyes, C. A., Luna, G. R., Sasaya, T., Tzanetakis, I. E., Vaira, A. M., Verbeek, M., & ICTV Report ConsortiumYR 2017. (2017). ICTV Virus Taxonomy Profile: Ophioviridae. *Journal of General Virology*, *98*(6), 1161–1162. https://doi.org/10.1099/jgv.0.000836

García-Arenal, F., & Zerbini, F. M. (2019). Life on the Edge: Geminiviruses at the Interface Between Crops and Wild Plant Hosts. *Annual Review of Virology*, *6*(1), 411–433. https://doi.org/10.1146/annurev-virology-092818-015536

Garrett, K. A., Alcalá-Briseño, R. I., Andersen, K. F., Buddenhagen, C. E., Choudhury, R. A., Fulton, J. C., Hernandez Nopsa, J. F., Poudel, R., & Xing, Y. (2018). Network analysis: A systems framework to address grand challenges in plant pathology. *Annual Review of Phytopathology*, *56*(1), 559–580. https://doi.org/10.1146/annurev-phyto-080516-035326

Geoghegan, J. L., & Holmes, E. C. (2017). Predicting virus emergence amid evolutionary noise. *Open Biology*, *7*(10), 170189. https://doi.org/10.1098/rsob.170189

Gorbalenya, A. E., Krupovic, M., Mushegian, A., Kropinski, A. M., Siddell, S. G., Varsani, A., Adams, M. J., Davison, A. J., Dutilh, B. E., Harrach, B., Harrison, R. L., Junglen, S., King, A. M. Q., Knowles, N. J., Lefkowitz, E. J., Nibert, M. L., Rubino, L., Sabanadzovic, S., Sanfaçon, H., … Kuhn, J. H. (2020). The new scope of virus taxonomy: Partitioning the virosphere into 15 hierarchical ranks. *Nature Microbiology 2020 5:5*, *5*(5), 668–674. https://doi.org/10.1038/s41564-020-0709-x

Gregory, A. C., Zayed, A. A., Conceição-Neto, N., Temperton, B., Bolduc, B., Alberti, A., Ardyna, M., Arkhipova, K., Carmichael, M., Cruaud, C., Dimier, C., Domínguez-Huerta, G., Ferland, J., Kandels, S., Liu, Y., Marec, C., Pesant, S., Picheral, M., Pisarev, S., … Roux, S. (2019). Marine DNA Viral Macro- and Microdiversity from Pole to Pole. *Cell*, *177*(5), 1109-1123.e14. https://doi.org/10.1016/J.CELL.2019.03.040

Hančinský, R., Mihálik, D., Mrkvová, M., Candresse, T., & Glasa, M. (2020). Plant viruses infecting Solanaceae family members in the cultivated and wild environments: A review. *Plants*, *9*(5), 667. https://doi.org/10.3390/plants9050667

Hanssen, I. M., Lapidot, M., & Thomma, B. P. H. J. (2010). Emerging viral diseases of tomato crops. *Molecular Plant-Microbe Interactions®*, *23*(5), 539–548. https://doi.org/10.1094/MPMI-23-5-0539

Hasiów-Jaroszewska, B., Boezen, D., & Zwart, M. P. (2021). Metagenomic Studies of Viruses in Weeds and Wild Plants: A Powerful Approach to Characterise Variable Virus Communities. *Viruses 2021, Vol. 13, Page 1939*, *13*(10), 1939. https://doi.org/10.3390/V13101939

Hou, W., Li, S., & Massart, S. (2020). Is there a “biological desert” with the discovery of new plant viruses? A retrospective analysis for new fruit tree viruses. *Frontiers in Microbiology*, *11*, 2953. https://doi.org/10.3389/fmicb.2020.592816

Huang, H.-J., Ye, Z.-X., Wang, X., Yan, X.-T., Zhang, Y., He, Y.-J., Qi, Y.-H., Zhang, X.-D., Zhuo, J.-C., Lu, G., Lu, J.-B., Mao, Q.-Z., Sun, Z.-T., Yan, F., Chen, J.-P., Zhang, C.-X., & Li, J.-M. (2021). Diversity and infectivity of the RNA virome among different cryptic species of an agriculturally important insect vector: Whitefly Bemisia tabaci. *Npj Biofilms and Microbiomes 2021 7:1*, *7*(1), 1–15. https://doi.org/10.1038/s41522-021-00216-5

ICTV. (2022). *ICTV Master Species List 2021.v1*. https://talk.ictvonline.org/files/master-species-lists/m/msl/13425

Islam, W., Noman, A., Naveed, H., Alamri, S. A., Hashem, M., Huang, Z., & Chen, H. Y. H. (2020). Plant-insect vector-virus interactions under environmental change. *Science of The Total Environment*, *701*, 135044. https://doi.org/10.1016/j.scitotenv.2019.135044

Ivanovsky, D. (1892). Über Die Mosaikkrankheit Der Tabakspflanze. *Bull. Acad. Imper. Sci. St. Petersburg*, *35*, 67–70.

Jones, R. A. C. (2009). Plant virus emergence and evolution: Origins, new encounter scenarios, factors driving emergence, effects of changing world conditions, and prospects for control. *Virus Research*, *141*(2), 113–130. https://doi.org/10.1016/j.virusres.2008.07.028

Jones, R. A. C. (2016). Future Scenarios for Plant Virus Pathogens as Climate Change Progresses. In *Advances in Virus Research* (Vol. 95, pp. 87–147). Academic Press Inc. https://doi.org/10.1016/bs.aivir.2016.02.004

Jones, R. A. C. (2018). Plant and Insect Viruses in Managed and Natural Environments: Novel and Neglected Transmission Pathways. In *Advances in Virus Research* (Vol. 101, pp. 149–187). Academic Press Inc. https://doi.org/10.1016/bs.aivir.2018.02.006

Jones, R. A. C. (2021). Global Plant Virus Disease Pandemics and Epidemics. *Plants*, *10*(2), 233. https://doi.org/10.3390/plants10020233

Katsarou, K., Bardani, E., Kallemi, P., & Kalantidis, K. (2019). Viral detection: Past, present, and future. *BioEssays*, *41*(10), 1900049. https://doi.org/10.1002/bies.201900049

Koonin, E. V., Dolja, V. V., Krupovic, M., & Kuhn, J. H. (2021). Viruses Defined by the Position of the Virosphere within the Replicator Space. *Microbiology and Molecular Biology Reviews*. https://doi.org/10.1128/MMBR.00193-20

Kreuze, J. F., Perez, A., Untiveros, M., Quispe, D., Fuentes, S., Barker, I., & Simon, R. (2009). Complete viral genome sequence and discovery of novel viruses by deep sequencing of small RNAs: A generic method for diagnosis, discovery and sequencing of viruses. *Virology*, *388*(1), 1–7. https://doi.org/10.1016/j.virol.2009.03.024

Kuhn, J. H., Wolf, Y. I., Krupovic, M., Zhang, Y. Z., Maes, P., Dolja, V. V., & Koonin, E. V. (2019). Classify viruses—The gain is worth the pain. *Nature 2021 566:7744*, *566*(7744), 318–320. https://doi.org/10.1038/d41586-019-00599-8

Lecoq, H. (2001). Découverte du premier virus, le virus de la mosaïque du tabac: 1892 ou 1898 ? *Comptes Rendus de l'Académie des Sciences - Series III - Sciences de la Vie*, *324*(10), 929–933. https://doi.org/10.1016/S0764-4469(01)01368-3

Lecoq, H., Wipf-Scheibel, C., Verdin, E., & Desbiez, C. (2019). Characterization of the first tenuivirus naturally infecting dicotyledonous plants. *Archives of Virology*, *164*(1), 297–301. https://doi.org/10.1007/s00705-018-4057-6

Lee, B. D., Neri, U., Roux, S., Wolf, Y. I., Camargo, A. P., Krupovic, M., Simmonds, P., Kyrpides, N., Gophna, U., Dolja, V. V., & Koonin, E. V. (2022). *A vast world of viroid-like circular RNAs revealed by mining metatranscriptomes* (p. 2022.07.19.500677). bioRxiv. https://doi.org/10.1101/2022.07.19.500677

Leebens-Mack, J. H., Barker, M. S., Carpenter, E. J., Deyholos, M. K., Gitzendanner, M. A., Graham, S. W., Grosse, I., Li, Z., Melkonian, M., Mirarab, S., Porsch, M., Quint, M., Rensing, S. A., Soltis, D. E., Soltis, P. S., Stevenson, D. W., Ullrich, K. K., Wickett, N. J., DeGironimo, L., … Wong, G. K. S. (2019). One thousand plant transcriptomes and the phylogenomics of green plants. *Nature*, *574*(7780), 679–685. https://doi.org/10.1038/s41586-019-1693-2

Lefeuvre, P., Martin, D. P., Elena, S. F., Shepherd, D. N., Roumagnac, P., & Varsani, A. (2019). Evolution and ecology of plant viruses. *Nature Reviews Microbiology*, *17*(10), 632–644. https://doi.org/10.1038/s41579-019-0232-3

Lefkowitz, E. J., Dempsey, D. M., Hendrickson, R. C., Orton, R. J., Siddell, S. G., & Smith, D. B. (2018). Virus taxonomy: The database of the International Committee on Taxonomy of Viruses (ICTV). *Nucleic Acids Research*, *46*(D1), D708–D717. https://doi.org/10.1093/nar/gkx932

Li, N., Huang, Y., Li, W., & Xu, S. (2022). Virome Analysis Reveals Diverse and Divergent RNA Viruses in Wild Insect Pollinators in Beijing, China. *Viruses*, *14*(2), 227. https://doi.org/10.3390/v14020227

Li, R., Gao, S., Hernandez, A. G., Wechter, W. P., Fei, Z., & Ling, K.-S. (2012). Deep sequencing of small RNAs in tomato for virus and viroid identification and strain differentiation. *PLoS ONE*, *7*(5), e37127. https://doi.org/10.1371/journal.pone.0037127

Ma, Y., Marais, A., Lefebvre, M., Faure, C., & Candresse, T. (2020). Metagenomic analysis of virome cross-talk between cultivated Solanum lycopersicum and wild Solanum nigrum. *Virology*, *540*(August 2019), 38–44. https://doi.org/10.1016/j.virol.2019.11.009

Ma, Y., Marais, A., Lefebvre, M., Theil, S., Svanella-Dumas, L., Faure, C., & Candresse, T. (2019). Phytovirome Analysis of Wild Plant Populations: Comparison of Double-Stranded RNA and Virion-Associated Nucleic Acid Metagenomic Approaches. *Journal of Virology*, *94*(1). https://doi.org/10.1128/JVI.01462-19

Maclot, F., Candresse, T., Filloux, D., Malmstrom, C. M., Roumagnac, P., van der Vlugt, R., & Massart, S. (2020). Illuminating an ecological blackbox: Using high throughput sequencing to characterize the plant virome across scales. *Frontiers in Microbiology*, *11*. https://doi.org/10.3389/fmicb.2020.578064

Mahlanza, T., Pierneef, R. E., Makwarela, L., Roberts, R., & Merwe, M. (2022). Metagenomic analysis for detection and discovery of plant viruses in wild Solanum spp. In South Africa. *Plant Pathology*. https://doi.org/10.1111/ppa.13585

Malpica, J. M., Sacristán, S., Fraile, A., & García-Arenal, F. (2006). Association and Host Selectivity in Multi-Host Pathogens. *PLoS ONE*, *1*(1), e41. https://doi.org/10.1371/journal.pone.0000041

Massart, S., Candresse, T., Gil, J., Lacomme, C., Predajna, L., Ravnikar, M., Reynard, J. S., Rumbou, A., Saldarelli, P., Škoric, D., Vainio, E. J., Valkonen, J. P. T., Vanderschuren, H., Varveri, C., & Wetzel, T. (2017). A framework for the evaluation of biosecurity, commercial, regulatory, and scientific impacts of plant viruses and viroids identified by NGS technologies. *Frontiers in Microbiology*, *8*(JAN). https://doi.org/10.3389/fmicb.2017.00045

Massart, S., Chiumenti, M., De Jonghe, K., Glover, R., Haegeman, A., Koloniuk, I., Komínek, P., Kreuze, J., Kutnjak, D., Lotos, L., Maclot, F., Maliogka, V., Maree, H. J., Olivier, T., Olmos, A., Pooggin, M. M., Reynard, J. S., Ruiz-García, A. B., Safarova, D., … Candresse, T. (2019). Virus detection by high-throughput sequencing of small RNAs: Large-scale performance testing of sequence analysis strategies. *Phytopathology*, *109*(3), 488–497. https://doi.org/10.1094/PHYTO-02-18-0067-R

McLeish, M. J., Fraile, A., & García-Arenal, F. (2019). Evolution of plant–virus interactions: Host range and virus emergence. *Current Opinion in Virology*, *34*, 50–55. https://doi.org/10.1016/j.coviro.2018.12.003

McLeish, M. J., Fraile, A., & García-Arenal, F. (2020). Trends and gaps in forecasting plant virus disease risk. *Annals of Applied Biology*, *176*(2), 102–108. https://doi.org/10.1111/aab.12553

McLeish, M. J., Fraile, A., & García-Arenal, F. (2021). Population Genomics of Plant Viruses: The Ecology and Evolution of Virus Emergence. *Phytopathology®*, *111*(1), 32–39. https://doi.org/10.1094/PHYTO-08-20-0355-FI

Mendes De Souza, J., Nascimento Da, K., Fragoso, S., Franco Orílio, A., Melo, F. L., Nagata, T., Fernandes, D., Valério, J. R., Zimermann, F., Torres, V., Barbosa Amaral, B., Benites, T., Pereira, C., Silva De Oliveira, A., & Oliveira Resende, R. (2021). Two viruses from Stylosanthes guianensis may represent a new genus within Potyviridae. *Virus Research*, *293*, 198257. https://doi.org/10.1016/j.virusres.2020.198257

Mifsud, J. C. O., Gallagher, R. V., Holmes, E. C., & Geoghegan, J. L. (2022). Transcriptome Mining Expands Knowledge of RNA Viruses across the Plant Kingdom. *Journal of Virology*. https://doi.org/10.1128/jvi.00260-22

Morens, D. M., Daszak, P., Markel, H., & Taubenberger, J. K. (2020). Pandemic COVID-19 Joins History's Pandemic Legion. *MBio*, *11*(3). https://doi.org/10.1128/mBio.00812-20

Neri, U., Wolf, Y. I., Roux, S., Camargo, A. P., Lee, B., Kazlauskas, D., Chen, I. M., Ivanova, N., Allen, L. Z., Paez-Espino, D., Bryant, D. A., Bhaya, D., Consortium, R. V. D., Krupovic, M., Dolja, V. V., Kyrpides, N. C., Koonin, E. V., & Gophna, U. (2022). A five-fold expansion of the global RNA virome reveals multiple new clades of RNA bacteriophages. *BioRxiv*, 2022.02.15.480533. https://doi.org/10.1101/2022.02.15.480533

NIH-NHGRI. (2021). *DNA sequencing costs: Data.* https://www.genome.gov/about-genomics/fact-sheets/DNA-Sequencing-Costs-Data

Oerke, E. C. (2006). Crop losses to pests. *Journal of Agricultural Science*, *144*(1), 31–43. https://doi.org/10.1017/S0021859605005708

Oladokun, J. O., Halabi, M. H., Barua, P., & Nath, P. D. (2019). Tomato brown rugose fruit disease: Current distribution, knowledge and future prospects. *Plant Pathology*, *68*(9), 1579–1586. https://doi.org/10.1111/ppa.13096

Ong, S. N., Taheri, S., Othman, R. Y., & Teo, C. H. (2020). Viral disease of tomato crops (Solanum lycopesicum L.): An overview. *Journal of Plant Diseases and Protection*. https://doi.org/10.1007/s41348-020-00330-0

Paez-Espino, D., Eloe-Fadrosh, E. A., Pavlopoulos, G. A., Thomas, A. D., Huntemann, M., Mikhailova, N., Rubin, E., Ivanova, N. N., & Kyrpides, N. C. (2016). Uncovering Earth's virome. *Nature*, *536*(7617), 425–430. https://doi.org/10.1038/nature19094

Pappas, N., Roux, S., Hölzer, M., Lamkiewicz, K., Mock, F., Marz, M., & Dutilh, B. E. (2021). Virus Bioinformatics. In *Encyclopedia of Virology* (pp. 124–132). Elsevier. https://doi.org/10.1016/B978-0-12-814515-9.00034-5

Pecman, A., Kutnjak, D., Gutiérrez-Aguirre, I., Adams, I., Fox, A., Boonham, N., & Ravnikar, M. (2017). Next Generation Sequencing for Detection and Discovery of Plant Viruses and Viroids: Comparison of Two Approaches. *Frontiers in Microbiology*, *8*(OCT), 1–10. https://doi.org/10.3389/fmicb.2017.01998

Ramos-González, P. L., Chabi-Jesus, C., Tassi, A. D., Calegario, R. F., Harakava, R., Nome, C. F., Kitajima, E. W., & Freitas-Astua, J. (2022). A Novel Lineage of Cile-Like Viruses Discloses the Phylogenetic Continuum Across the Family Kitaviridae. *Frontiers in Microbiology*, *13*. https://doi.org/10.3389/fmicb.2022.836076

Rego-Machado, C. M., Nakasu, E. Y. T., Blawid, R., Nagata, T., & Inoue-Nagata, A. K. (2019). Complete genome sequence of a new bipartite begomovirus infecting tomato in Brazil. *Archives of Virology*, *164*(11), 2873–2875. https://doi.org/10.1007/s00705-019-04380-0

Ristaino, J. B., Anderson, P. K., Bebber, D. P., Brauman, K. A., Cunniffe, N. J., Fedoroff, N. V., Finegold, C., Garrett, K. A., Gilligan, C. A., Jones, C. M., Martin, M. D., MacDonald, G. K., Neenan, P., Records, A., Schmale, D. G., Tateosian, L., & Wei, Q. (2021). The persistent threat of emerging plant disease pandemics to global food security. *Proceedings of the National Academy of Sciences*, *118*(23), e2022239118. https://doi.org/10.1073/pnas.2022239118

Rivarez, M. P. S., Kogej, Z., Jakoš, N., Pecman, A., Seljak, G., Vučurović, A., Ravnikar, M., Mehle, N., & Kutnjak, D. (2022). First Report of Ranunculus White Mottle Ophiovirus in Slovenia in Pepper with Yellow Leaf Curling Symptom and in Tomato. *Plant Disease*, *106*(7), 2003. https://doi.org/10.1094/PDIS-08-21-1624-PDN

Rivarez, M. P. S., Vučurović, A., Mehle, N., Ravnikar, M., & Kutnjak, D. (2021). Global Advances in Tomato Virome Research: Current Status and the Impact of High-Throughput Sequencing. *Frontiers in Microbiology*, *12*. https://doi.org/10.3389/fmicb.2021.671925

Roberts, J. M. K., Anderson, D. L., & Durr, P. A. (2018). Metagenomic analysis of Varroa-free Australian honey bees (Apis mellifera) shows a diverse Picornavirales virome. *Journal of General Virology*, *99*(6), 818–826. https://doi.org/10.1099/jgv.0.001073

Roberts, J. M. K., Ireland, K. B., Tay, W. T., & Paini, D. (2018). Honey bee-assisted surveillance for early plant virus detection. *Annals of Applied Biology*, *173*(3), 285–293. https://doi.org/10.1111/aab.12461

Roossinck, M. J. (2015). Plants, viruses and the environment: Ecology and mutualism. *Virology*, *479–480*, 271–277. https://doi.org/10.1016/j.virol.2015.03.041

Roossinck, M. J. (2019). Viruses in the phytobiome. *Current Opinion in Virology*, *37*, 72–76. https://doi.org/10.1016/j.coviro.2019.06.008

Roossinck, M. J., & García-Arenal, F. (2015). Ecosystem simplification, biodiversity loss and plant virus emergence. In *Current Opinion in Virology* (Vol. 10, pp. 56–62). Elsevier B.V. https://doi.org/10.1016/j.coviro.2015.01.005

Roossinck, M. J., Martin, D. P., & Roumagnac, P. (2015). Plant virus metagenomics: Advances in virus discovery. *Phytopathology*, *105*(6), 716–727. https://doi.org/10.1094/PHYTO-12-14-0356-RVW

Roux, S., Brum, J. R., Dutilh, B. E., Sunagawa, S., Duhaime, M. B., Loy, A., Poulos, B. T., Solonenko, N., Lara, E., Poulain, J., Pesant, S., Kandels-Lewis, S., Dimier, C., Picheral, M., Searson, S., Cruaud, C., Alberti, A., Duarte, C. M., Gasol, J. M., … Sullivan, M. B. (2016). Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. *Nature*, *537*(7622), 689–693. https://doi.org/10.1038/nature19366

Rwahnih, M. A., Daubert, S., Úrbez-Torres, J. R., Cordero, F., & Rowhani, A. (2011). Deep sequencing evidence from single grapevine plants reveals a virome dominated by mycoviruses. *Archives of Virology*, *156*(3), 397–403. https://doi.org/10.1007/s00705-010-0869-8

Saqib, M., Wylie, S. J., & Jones, M. G. K. (2015). Serendipitous identification of a new Iflavirus -like virus infecting tomato and its subsequent characterization. *Plant Pathology*, *64*(3), 519–527. https://doi.org/10.1111/ppa.12293

Sastry, K. S. (2013). *Plant Virus and Viroid Diseases in the Tropics*. Springer Netherlands. https://doi.org/10.1007/978-94-007-6524-5

Schoelz, J. E., & Stewart, L. R. (2018). The Role of Viruses in the Phytobiome. *Annual Review of Virology*, *5*(1), 93–111. https://doi.org/10.1146/annurev-virology-092917-043421

Sharma, D., Priyadarshini, P., & Vrati, S. (2015). Unraveling the Web of Viroinformatics: Computational Tools and Databases in Virus Research. *Journal of Virology*, *89*(3), 1489–1501. https://doi.org/10.1128/JVI.02027-14

Shates, T. M., Sun, P., Malmstrom, C. M., Dominguez, C., & Mauck, K. E. (2019). Addressing research needs in the field of plant virus ecology by defining knowledge gaps and developing wild dicot study systems. *Frontiers in Microbiology*, *9*(JAN), 1–20. https://doi.org/10.3389/fmicb.2018.03305

Shi, M., Lin, X.-D., Tian, J.-H., Chen, L.-J., Chen, X., Li, C.-X., Qin, X.-C., Li, J., Cao, J.-P., Eden, J.-S., Buchmann, J., Wang, W., Xu, J., Holmes, E. C., & Zhang, Y.-Z. (2016). Redefining the invertebrate RNA virosphere. *Nature*, *540*(7634), 539–543. https://doi.org/10.1038/nature20167

Smith, E., & Dombrovsky, A. (2020). Aspects in Tobamovirus Management in Intensive Agriculture. In *Plant Diseases—Current Threats and Management Trends*. IntechOpen. https://doi.org/10.5772/intechopen.87101

Smith, S. E., Huang, W., Tiamani, K., Unterer, M., Khan Mirzaei, M., & Deng, L. (2022). Emerging technologies in the study of the virome. *Current Opinion in Virology*, *54*, 101231. https://doi.org/10.1016/J.COVIRO.2022.101231

Sommers, P., Chatterjee, A., Varsani, A., & Trubl, G. (2021). Integrating Viral Metagenomics into an Ecological Framework. *Annual Review of Virology*, *8*(1), 133–158. https://doi.org/10.1146/annurev-virology-010421-053015

Souiri, A., Khataby, K., Kasmi, Y., Zemzami, M., Amzazi, S., & Ennaji, M. M. (2019). Emerging and reemerging viral diseases of solanaceous crops and management strategies for detection and eradication. In *Emerging and Reemerging Viral*

*Pathogens: Volume 1: Fundamental and Basic Virology Aspects of Human, Animal and Plant Pathogens* (pp. 847–877). Elsevier. https://doi.org/10.1016/B978-0-12-819400-3.00038-7

Temple, C., Blouin, A. G., De Jonghe, K., Foucart, Y., Botermans, M., Westenberg, M., Schoen, R., Gentit, P., Visage, M., Verdin, E., Wipf-Scheibel, C., Ziebell, H., Gaafar, Y. Z. A., Kutnjak, D., Vučurović, A., Rivarez, M. P. S., Richert-Pöggeler, K. R., Ulrich, R., Zia, A., … Massart, S. (2022). Biological and genetic characterization of Physostegia chlorotic mottle virus in Europe based on host range, location, and time. *Plant Disease*. https://doi.org/10.1094/PDIS-12-21-2800-RE

Tisza, M. J., Pastrana, D. V., Welch, N. L., Stewart, B., Peretti, A., Starrett, G. J., Pang, Y.-Y. S., Krishnamurthy, S. R., Pesavento, P. A., McDermott, D. H., Murphy, P. M., Whited, J. L., Miller, B., Brenchley, J., Rosshart, S. P., Rehermann, B., Doorbar, J., Ta'ala, B. A., Pletnikova, O., … Buck, C. B. (2020). Discovery of several thousand highly diverse circular DNA viruses. *ELife*, *9*, e51971. https://doi.org/10.7554/eLife.51971

Trebicki, P. (2020). Climate change and plant virus epidemiology. *Virus Research*, *286*, 198059. https://doi.org/10.1016/j.virusres.2020.198059

Vaira, A. M., Vecchiati, M., Lisa, V., & Milne, R. G. (2000). First Report of Anemone Plants Infected by Ranunculus white mottle virus. *Plant Disease*, *84*(9), 1046–1046. https://doi.org/10.1094/PDIS.2000.84.9.1046B

Villamor, D. E. V., Ho, T., Al Rwahnih, M., Martin, R. R., & Tzanetakis, I. E. (2019). High Throughput Sequencing For Plant Virus Detection and Discovery. *Phytopathology®*, *109*(5), 716–725. https://doi.org/10.1094/PHYTO-07-18-0257-RVW

Vučurović, A., Kutnjak, D., Mehle, N., Stanković, I., Pecman, A., Bulajić, A., Krstić, B., & Ravnikar, M. (2021). Detection of Four New Tomato Viruses in Serbia Using Post Hoc High-Throughput Sequencing Analysis of Samples From a Large-Scale Field Survey. *Plant Disease*, *105*(9), 2325–2332. https://doi.org/10.1094/PDIS-09-20-1915-RE

Wren, J. D., Roossinck, M. J., Nelson, R. S., Scheets, K., Palmer, M. W., & Melcher, U. (2006). Plant virus biodiversity and ecology. In *PLoS Biology* (Vol. 4, Issue 3, pp. 0314–0315). https://doi.org/10.1371/journal.pbio.0040080

Wu, H., Fu, P., Fu, Q., Zhang, Z., Zheng, H., Mao, L., Li, X., Yu, F., & Peng, Y. (2022). Plant Virus Database: A resource for exploring the diversity of plant viruses and their interactions with hosts. *BioRxiv*, 2022.03.20.485054. https://doi.org/10.1101/2022.03.20.485054

Xing, Y., Hernandez Nopsa, J. F., Andersen, K. F., Andrade-Piedra, J. L., Beed, F. D., Blomme, G., Carvajal-Yepes, M., Coyne, D. L., Cuellar, W. J., Forbes, G. A., Kreuze, J. F., Kroschel, J., Kumar, P. L., Legg, J. P., Parker, M., Schulte-Geldermann, E., Sharma, K., & Garrett, K. A. (2020). Global Cropland Connectivity: A Risk Factor for Invasion and Saturation by Emerging Pathogens and Pests. *BioScience*, *70*(9), 744–758. https://doi.org/10.1093/biosci/biaa067

Xu, C., Sun, X., Taylor, A., Jiao, C., Xu, Y., Cai, X., Wang, X., Ge, C., Pan, G., Wang, Q., Fei, Z., & Wang, Q. (2017). Diversity, Distribution, and Evolution of Tomato Viruses in China Uncovered by Small RNA Sequencing. *Journal of Virology*, *91*(11). https://doi.org/10.1128/JVI.00173-17

Zayed, A. A., Wainaina, J. M., Dominguez-Huerta, G., Pelletier, E., Guo, J., Mohssen, M., Tian, F., Pratama, A. A., Bolduc, B., Zablocki, O., Cronin, D., Solden, L., Delage, E., Alberti, A., Aury, J.-M., Carradec, Q., da Silva, C., Labadie, K., Poulain, J., … Wincker, P. (2022). Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome. *Science*, *376*(6589), 156–162. https://doi.org/10.1126/SCIENCE.ABM5847

Zhang, S., Griffiths, J. S., Marchand, G., Bernards, M. A., & Wang, A. (2022). Tomato brown rugose fruit virus: An emerging and rapidly spreading plant RNA virus that threatens tomato production worldwide. *Molecular Plant Pathology*. https://doi.org/10.1111/mpp.13229

Zhang, Y.-Z., Shi, M., & Holmes, E. C. (2018). Using Metagenomics to Characterize an Expanding Virosphere. *Cell*, *172*(6), 1168–1172. https://doi.org/10.1016/j.cell.2018.02.043

# Bibliography

## Publications Related to the Thesis

### Journal Articles

**Rivarez, Mark Paul Selda,** Ana Vučurović, Nataša Mehle, Maja Ravnikar, and Denis Kutnjak. 2021. "Global Advances in Tomato Virome Research: Current Status and the Impact of High-Throughput Sequencing." *Frontiers in Microbiology* 12. doi: 10.3389/fmicb.2021.671925.

**Rivarez, Mark Paul Selda**, Pecman, A., Bačnik, K., Ferreira, O. M. C., Vučurović, A., Seljak, G., Mehle, N., Gutiérrez-Aguirre, I., Ravnikar, M., & Kutnjak, D. 2022. **"**In-depth study of tomato and weed viromes reveals undiscovered plant virus diversity in an agroecosystem.**"** *BioRxiv.* doi.org/10.1101/2022.06.30.498278**.**

**Rivarez, Mark Paul Selda,** Zala Kogej, Nejc Jakos, Anja Pecman, Gabrijel Seljak, Ana Vučurović, Natasa Mehle, Maja Ravnikar, and Denis Kutnjak. 2021. "First Report of Ranunculus White Mottle Ophiovirus in Slovenia in Pepper with Yellow Leaf Curling Symptom and in Tomato." *Plant Disease.* doi: 10.1094/PDIS-08-21-1624-PDN.

### Conference Paper

Kogej, Zala, **Rivarez, Mark Paul Selda,** Pecman, Anja, Vučurović, Ana, Jakoš, Nejc, Seljak, Gabrijel, Mehle, Nataša, Ravnikar, Maja, Kutnjak, Denis. First discovery of Ranunculus white mottle virus in tomato and assembly of its first full genome. In: Programme and abstracts : International Advances in Plant Virology 2021 : virtually via Zoom : 20th April - 22nd April 2021. [S. l.: Association of Applied Biologists], 2021. str. [9]. https://custom.cvent.com/05F40F40EA964BBB968323D70A3E1C38/files/event/ef4ceb27d30d4676a7f14cb5d4dd7663/bd3a825c81194b88a904a9bd5738cd44.pdf. [COBISS.SI-ID 62527235]

**Rivarez, Mark Paul Selda,** Parac, Elizabeth, Dimasingkil, Shajara Fatima M., Magdalita, Pablito M. In Altruism, Size Doesn't Matter : The Heroic Case for Kosakonia vs Erwinia in Papaya. In: JOVIČEVIĆ KLUG, Patricia (ed.), et al. Knjiga povzetkov = Book of abstracts. 12. študentska konferenca Mednarodne podiplomske šole Jožefa Stefana in 14. dan mladih raziskovalcev (Konferenca KMBO) = 12th Jožef Stefan International Postgraduate School Students' Conference and 14th Young Researchers' Day, 15th May 2020. Ljubljana: Mednarodna podiplomska šola Jožefa Stefana: = Jožef Stefan International Postgraduate School: Inštitut Jožef Stefan: = Jožef Stefan Institute, 2020. str. 51. http://ipssc.mps.si/2020/BookOfAbstracts.pdf. [COBISS.SI-ID 60184835]

Kutnjak, Denis, **Rivarez, Mark Paul Selda,** Maksimović, Olivera, Bačnik, Katarina, Kogej, Zala, Pecman, Anja, Lengar, Živa, Mehle, Nataša, Vučurović, Ana, Gutiérrez-Aguirre, Ion, Ravnikar, Maja. In-depth virome study linking tomato, associated weed plants and irrigation water sources in Slovenia reveals many new and known plant viruses. In: Plant health 2021 : seismic shifts in disease risk : August 2-6, 2021 :

virtual meeting. [S. l.: s. n., 2021]. 1 spletni vir. https://events.rdmobile.com/Lists/Details/1179651. [COBISS.SI-ID 90988291]

**Rivarez, Mark Paul Selda,** Kutnjak, Denis, Vučurović, Ana, Maksimović, Olivera, Bačnik, Katarina, Kogej, Zala, Pecman, Anja, Lengar, Živa, Seljak, Gabrijel, Gutiérrez-Aguirre, Ion, Mehle, Nataša, Ravnikar, Maja. Phytoviromics and datamining added insights on the recent intercontinental detection of an iflavirus and kitavirus in tomato. In: Plant health 2021 : seismic shifts in disease risk : August 2-6, 2021 : virtual meeting. [S. l.: s. n., 2021]. 1 spletni vir. https://events.rdmobile.com/Lists/Details/1179532. [COBISS.SI-ID 90992643]

**Rivarez, Mark Paul Selda,** Kutnjak, Denis, Vučurović, Ana, Maksimović, Olivera, Bačnik, Katarina, Kogej, Zala, Pecman, Anja, Lengar, Živa, Seljak, Gabrijel, Stanković, Ivana, Gutiérrez-Aguirre, Ion, Mehle, Nataša, Ravnikar, Maja. Scanning tomato and associated weeds virosphere composition using high-throughput sequencing. In: Programme and abstracts : International Advances in Plant Virology 2021 : virtually via Zoom : 20th April - 22nd April 2021. [S. l.: Association of Applied Biologists], 2021. str. 113. https://custom.cvent.com/05F40F40EA964BBB968323D70A3E1C38/files/event/ef4ceb27d30d4676a7f14cb5d4dd7663/bd3a825c81194b88a904a9bd5738cd44.pdf. [COBISS.SI-ID 62648835]

**Rivarez, Mark Paul Selda,** Kutnjak, Denis, Vučurović, Ana, Maksimović, Olivera, Bačnik, Katarina, Stanković, Ivana, Seljak, Gabrijel, Mehle, Nataša, Gutiérrez-Aguirre, Ion, Ravnikar, Maja. Virome screening of tomatoes and wild plants in Slovenia and Serbia using high-throughput sequencing. In: Plant health 2020 : APS Annual Meeting : August 10-14. [S. l.: s. n., 2020]. 1 spletni vir. https://apsnet.confex.com/apsnet/2020/meetingapp.cgi/Paper/17646. [COBISS.SI-ID 43114243]

## Other Publications

Magdalita, Pablito M., **Mark Paul Selda Rivarez**, Fe M. dela Cueva, Alangelico O. San Pascual, and Lorele C. Trinidad. 2022. Ultrastructural characterization and field performance of papaya regrowth selections recovered from bacterial crown rot infection for disease tolerance breeding. Philippine Journal of Crop Science (*in press*).

Temple, Coline, Arnaud G. Blouin, Kris De Jonghe, Yoika Foucart, Marleen Botermans, Marcel Westenberg, Ruben Schoen, Pascal Gentit, Michele Visage, Eric Verdin, Catherine Wipf-Scheibel, Heiko Ziebell, Yahya Z. A. Gaafar, Denis Kutnjak, Ana Vučurović, **Mark Paul Selda Rivarez**, Katja R. Richert-Pöggeler, Roswitha Ulrich, Amjad Zia, Xiao-Hua Yan, and Sebastian Massart. 2022. “Biological and Genetic Characterization of Physostegia Chlorotic Mottle Virus in Europe Based on Host Range, Location, and Time.” Plant Disease. doi: 10.1094/PDIS-12-21-2800-RE.

**Rivarez, Mark Paul Selda**, Elizabeth P. Parac, Niño R. Laurel, Benjamin V. Cunanan, Angelie B. Magarro, and Shajara Fatima M. Dimasingkil. 2021. “Antagonistic Activity of Bacteria from Wild Honey against Colletotrichum Musae, and Testing of Wild Honey as Biopesticide Spray to Control Banana Anthracnose.” Bioscience Journal 37:e37089. doi: 10.14393/BJ-v37n0a2021-49921.

**Rivarez, Mark Paul Selda**, Elizabeth P. Parac, Shajara Fatima M. Dimasingkil, and Pablito M. Magdalita. 2021. “Influence of Native Endophytic Bacteria on the Growth and Bacterial Crown Rot Tolerance of Papaya (Carica Papaya).” European Journal of Plant Pathology 161(3):593–606. doi: 10.1007/s10658-021-02345-1.

De Jesus, Anna Pamela O., **Mark Paul Selda Rivarez**, Ranzivelle Marianne L. Roxas-Villanueva, and Marvin U. Herrera. 2021. “Assessment of Shellac and Lemongrass Oil Blend as Edible Coating to Prolong Shelf Life of Pili Nut (Canarium Ovatum).”

Key Engineering Materials 902:121–25. doi: 10.4028/www.scientific.net/KEM.902.121.

Butković, Anamarija, Rubén González, **Mark Paul Selda Rivarez**, and Santiago F. Elena. 2021. “A Genome-Wide Association Study Identifies Arabidopsis Thaliana Genes That Contribute to Differences in the Outcome of Infection with Two Turnip Mosaic Potyvirus Strains That Differ in Their Evolutionary History and Degree of Host Specialization.” Virus Evolution 7(2). doi: 10.1093/ve/veab063.

González, Rubén, Anamarija Butković, **Mark Paul Selda Rivarez**, and Santiago F. Elena. 2020. “Natural Variation in Arabidopsis Thaliana Rosette Area Unveils New Genes Involved in Plant Development.” Scientific Reports 10(1):17600. doi: 10.1038/s41598-020-74723-4.

**Rivarez, Mark Paul Selda**, and Elizabeth P. Parac. 2019. “Rapid Molecular Detection and Transmission of Bacterial Leaf Streak Pathogen, Xanthomonas Oryzae Pv. Oryzicola, in Rice Seeds.” Bioscience and Biotechnology Research Asia 16:509–20.

**Rivarez, Mark Paul Selda**, Elizabeth P. Parac, Shajara Fatima M. Dimasingkil, and Cheek S. Fadriquela. 2019. “Identification of Wood Rot Fungi in the Historic Baker Memorial Hall at the University of the Philippines, Los Baños Campus.” Bioscience Research 16:3421–31.

**Rivarez, Mark Paul Selda**, Roy Nino M. Lucila, and Pablito M. Magdalita. 2017. “Stomatal Penetration and Temporal Dynamics of Ingress of Two Fungal Isolates Associated with Leaf Spot Disease of Jasmine (Jasminum Sambac).” International Journal of Agriculture and Biological Science 1:1–12

# Biography

(as of July 31, 2022)

Mark Paul Selda Rivarez was born on May 4, 1994, in Marinduque, Philippines, where he obtained his primary and secondary education. He obtained his Bachelor and Master of Science (BSc and MSc) degrees at the University of the Philippines Los Baños (UPLB), in Laguna, Philippines. His major field is agricultural biotechnology (BSc) and plant pathology (MSc), with specializations in crop protection biotechnology and plant virology (BSc), and phytobacteriology and plant breeding (MSc).

At the virology group of the International Rice Research Institute (IRRI), led by Dr. Il-Ryong Choi, he did his BSc research thesis on the responses of rice (*Oryza sativa*) upon infection of the *Rice tungro bacilliform virus* (genus *Tungrovirus*) and *Rice tungro spherical virus* (genus *Waikavirus*). He investigated differential regulation of host developmental and resistance genes, in relation to plant biomass and symptomatology, and virus population dynamics, in single and mixed infection regimes of the two viruses. The virology group at IRRI later used his findings to narrow down candidate genes that could possibly contribute to host resistance against the two viruses, for future breeding activities. He earned a distinction of *magna cum laude* (with high honours) with his BSc studies and thesis in 2014.

Mr. Rivarez was hired as a college instructor at UPLB in 2014 and studied part-time to obtain his MSc degree. Within his time as a teaching personnel of UPLB, he did *pro bono* research work at the Institute of Weed Science, Entomology and Plant Pathology (IWEP), where he investigated the seed-to-plant transmission of, and developed a diagnostic protocol for, the bacterial leaf streak pathogen (*Xanthomonas oryzae* pv. *oryzicola*) of rice. The method he developed was later used in the field for early pathogen detection in seeds to prevent unwanted spread and disease outbreaks. Thereafter, he became an affiliate researcher at the Institute of Plant Breeding (IPB) under the supervision of Prof. Pablito Magdalita. In IPB, he studied the possible influence of beneficial microbes to host resistance of papaya (*Carica papaya*) against the bacterial crown rot pathogen (*Erwinia mallotivora*) for his master's thesis. He identified two bacterial endophytes under genus *Sphingomonas* and *Kosakonia*, and three rhizosphere-derived *Bacillus* species, which have antibacterial properties against *E. mallotivora.* These bacteria were shown to influence on growth and resistance of papaya to crown rot. Through this research, the group at IPB aimed to promote biological alternative to bactericides, and to augment resistance breeding programs. He obtained his MSc degree in 2018, with an excellent mark for his thesis research, which was later published at the *European Journal of Plant Pathology* and *Philippine Journal of Crop Science.* He was involved in various mycological research, published with Filipino colleagues, and helped them obtain funding for research in post-harvest plant pathology and soil-microbe-plant biotechnology (now currently funded), before undertaking training and research work in Europe.

In Spain, Mr. Rivarez did a research stint at the Institute of Integrative Systems Biology, CSIC-University of Valencia in 2019, under the supervision of Prof. Dr. Santiago Elena, working alongside with Dr. Anamarija Butković and Dr. Ruben González. He was involved in studies that uncovered candidate genes in *Arabidopsis thaliana*, using genome-wide association studies, which could have a role in the adaptation of turnip mosaic potyvirus to new host genotypes, and separately, novel genes involved in plant development. These studies were published in *Virus Evolution* and *Scientific Reports.* Shortly after, he joined Department of Biotechnology and Systems Biology of the National Institute of Biology (NIB) in Slovenia, for his doctoral studies under the supervision of Dr. Denis Kutnjak and Prof. Dr. Maja Ravnikar. He specifically worked as a full-time employee under the EU Horizon 2020 project called "Innovative network for the next generation training and sequencing of the virome (INEXTVIR)". Together with colleagues at NIB, he systematically reviewed the current status of tomato viruses and how high-throughput sequencing (HTS) has helped accelerate their discovery. This review was published in *Frontiers in Microbiology.* His doctoral research primarily focused on characterizing the viromes of tomato and weed plants from Slovenia. He used HTS and various bioinformatic analyses pipelines, to uncover the diversity and phylogenetic relationships of viruses in tomatoes, and in various weed species nearby selected tomato-growing areas. He has identified more than 100 known and novel species of viruses, viroids and satellite RNAs of viruses. A research paper regarding this work is currently under consideration for publication in *Microbiome.* He later reported the detection of Ranunculus white mottle virus in Slovenian tomatoes and peppers through HTS in the *Plant Disease* journal, and compared their diversity together with Italian isolates.

Mr. Rivarez expanded his research work through visits at the National Research Institute for Agriculture, Food and the Environment (INRAE), France, and Abiopep, S.L. Plant Health and Center for Edaphology and Applied Biology of Segura (CEBAS)-CSIC in Spain. Through these collaborative works, he aimed to uncover the global diversity of recently discovered tomato viruses, examine their phylogenetic relationships, and characterize some of their biological properties. Through collaboration with the team of Dr. Thierry Candresse at INRAE, he implemented research in characterizing the global diversity, transmission, host range and infectivity of Solanum nigrum ilarvirus 1 (SnIV1). He resumed this research in NIB where he aimed to expand experimental host range and histopathology of SnIV1. He is currently preparing a manuscript regarding their studies on SnIV1. It was selected to be considered for publication in an special issue of *Phytopathology*, in the recently concluded *International Symposium of Plant Virus Epidemiology* in Madrid, Spain. At Abiopep, S.L. and CEBAS, he collaborated with the team of Prof. Dr. Miguel A. Aranda to study the diversity, develop infectious clones, and identify possible vector of tomato fruit blotch virus (ToFBV). This research is a part of an international collaboration with researchers from other European countries (Italy, Slovenia, Netherlands, Belgium, France, and Spain), Brazil, and Australia to better understand the recent detection of ToFBV. He also contributed in the characterization of Physostegia chlorotic mottle virus (PhCMoV), a recently emerging virus in tomato and other crops, which were detected across Europe. This study is published in the *Plant Disease* journal. Lastly, he is also expanding his initial efforts in viroid discovery through the collaboration with researchers mainly from National Institutes of Health, USA. During his doctoral studies, Mr. Rivarez has participated in various workshops focusing on bioinformatics tools in virology, and presented in Slovenian and international scientific conferences, with the aim to disseminate his results and foster research collaborations, globally.

After finishing his doctoral research at NIB, Mr. Rivarez will take up a *Balik Scientist* (Returning Scientist) fellowship in the Philippines, funded by the Philippine Department of Science and Technology (DOST), at the Virology and Vaccinology Institute of the Philippines ($V^2IP$) and Caraga State University (CarSU), to help establish plant virology and agricultural biotechnology research and technology development with his Filipino colleagues. By early 2023, he will take up a National Science Foundation (NSF)-funded postdoctoral researcher position at the Department of Entomology and Plant Pathology and Bioinformatics Research Center of the North Carolina State University (NCSU) in the USA. He will be under the mentorship of Dr. David A. Rasmussen, an infectious disease evolutionary biologist and epidemiologist. They will focus on investigating the natural history, evolution and phylodynamics of super-generalist plant viruses, with tomato spotted wilt virus as a model. He will continue his on-going work and advocacy on virus and viroid discovery and characterization, and aim to publish the remaining collaborative studies that he contributed to, under the INEXTVIR research network.

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