This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic\_Proposals\_Help\_2019.

**Part 1:** **TITLE, AUTHORS, etc**

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| --- | --- | --- |
| **Code assigned:** | ***2019.030M*** |  |
| **Short title:** Create twelve new species in the genus *Cytorhabdovirus*, family *Rhabdoviridae* |
|  |
| **Author(s) and email address(es):**  |
| List authors in a single line *Archives of Virology* citation format (e.g. Smith AB, Huang C-L, Santos, F) | Provide email address for each author in a single line separated by semi-colons |
| Freitas-Astúa J, Dietzgen RG, Walker PJ, Blasdell KR, Breyta R, Fooks AR, Kondo H, Kurath G, Kuzmin IV, Stone DM, Tesh RB, Tordo N, Vasilakis N, Whitfield AE, Ramos-González PL | Juliana.astua@embrapa.br; r.dietzgen@uq.edu.au; peter.walker@uq.edu.au;kim.blasell@csiro.au; rbjmax@uw.edu;Tony.Fooks@apha.gov.uk; hkondo@okayama-u.ac.jp; gkurath@usgs.gov; ivkuzmin@yandex.ru; David.stone@cefas.co.uk; rtesh@utmb.edu; ntordo@pasteur.fr; nivasila@utmb.edu;awhitfi@ncsu.edu; plrg1970@gmail.com |

|  |  |  |
| --- | --- | --- |
| **Author(s) institutional address(es) (optional):**

|  |
| --- |
| Provide institutional addresses, each on a single line followed by author(s) initials (e.g. University of Woolloomooloo [SAB, HCL]) |
| Embrapa Cassava and Fruits, Brazil [JFA]University of Queensland, Australia [RGD, PJW]University of Washington, WA, USA [RB]CSIRO Australian Animal Health Laboratory, Geelong, Australia [KRB]Animal and Plant Health Agency (APHA), Weybridge, Surrey, UK [ARF]Okayama University, Kurashiki, Japan [HK]Western Fisheries Research Center, Seattle, WA, USA [GK]US Department of Agriculture, National Veterinary Services Laboratories [IVK]Centre for Environment, Fisheries and Aquaculture Science, Weymouth, UK [DMS]University of Texas Medical Branch, Galveston, TX, USA [RBT, NV]Institut Pasteur de Guinée, Conakry, French Guiana [NT]North Carolina State University, Raleigh, NC, USA [AEW]Instituto Biológico, São Paulo, Brazil [PLRG] |

 |
| **Corresponding author** |
| Ralf G Dietzgen; r.dietzgen@uq.edu.au  |
| **List the ICTV study group(s) that have seen this proposal:** |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | ICTV *Rhabdoviridae* Study Group |
| **ICTV Study Group comments (if any) and response of the proposer:** |
| Reviewed and supported by all responding ICTV *Rhabdoviridae* Study Group members |
|  |
| Date first submitted to ICTV: | 19 June 2019 |
| Date of this revision (if different to above): |       |

|  |
| --- |
| **ICTV-EC comments and response of the proposer:** |
|       |

**Part 3:** **PROPOSED TAXONOMY**

|  |
| --- |
| **Name of accompanying Excel module:** 2019.030M.A.v1.Cytorhabovirus\_12newsp.xlxs |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2019\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

|  |
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| In the past few years, several complete and coding-complete rhabdovirus genomes were determined mostly by next generation, high throughput sequencing approaches. Twelve of these genome sequences are most closely related phylogenetically (Fig. 1) and have highest sequence identity with viruses that are currently classified in species in the genus *Cytorhabdovirus* (Tables 1-5). We therefore propose to classify these viruses, listed in the associated spreadsheet in new species in the genus *Cytorhabdovirus*. Current species demarcation criteria for the genus *Cytorhabdovirus* listed in the ICTV 10th Report are: “Viruses assigned to different species within the genus Cytorhabdovirus have several of the following characteristics: A) minimum nucleotide sequence divergence >50 % in cognate genes; B) occupy different ecological niches as evidenced by differences in hosts and/or arthropod vectors; and C) can be clearly distinguished in serological tests or by nucleic acid hybridisation. Cytorhabdovirus species assignments are primarily determined by plant host range and vector specificity.” Based on the recent availability of an increased number of cytorhabdovirus genome sequences that provide a significantly broader spectrum of species and sequence diversity, we propose to revise these criteria as follows:Viruses assigned to different species within the genus *Cytorhabdovirus* have several of the following characteristics: 1. nucleotide sequence identity less than 75% for the complete genome sequence;
2. amino acid sequence identity in all cognate open reading frames less than 80%
3. occupy different ecological niches as evidenced by differences in hosts and/or arthropod vectors; and
4. can be clearly distinguished in serological tests or by nucleic acid hybridization.

The following information is available for the newly classified viruses:**cabbage cytorhabdovirus 1 (CCyV-1)**The coding-complete genome sequence of CCyV-1 of 12,949 nucleotides was assembled from Illumina sequencing of rRNA-depleted total RNA from cabbage (*Brassica oleracea*) and validated by RT-PCR (Pecman et al., 2017). Host range and arthropod vector are unknown.**maize-associated cytorhabdovirus (MaCV)**The MaCV coding-complete genome of 11,877 nt was assembled from Illumina NGS data from maize plants. The genome sequence is 51% and 50% identical, respectively to those of cytorhabdoviruses barley yellow striate mosaic virus (BYSMV) and northern cereal mosaic virus (NCMV) (Willie and Stewart, 2017). Host range and arthropod vector are unknown. **maize yellow striate virus (MYSV)**The complete genome sequences of two isolates of MYSV was determined by Illumina sequencing and random amplification of cDNA ends (RACE) and determined to be 12,654 nt with 10 open reading frames (Maurino et al., 2018). The sequences have 71% nt sequence identity with the genome of BYSMV. Isolates from maize and wheat differed by only 0.4% at the nucleotide level. The wheat isolate was transmitted by a delphacid planthopper (*Delphacodes kuscheli*). **papaya virus E (PpVE)**The 13,469 nt complete genome of papaya virus E (PpVE) was assembled from NGS data and RACE from total RNA extracted from papaya (*Carica papaya*) in Ecuador (Medina-Salguero et al., 2019). An apparent isolate of the same virus was identified in common bean (*Phaseolus vulgaris*) in Brazil (Alves-Freitas et al., 2019). The genome of bean-associated cytorhabdovirus (BaCV; MK202584) was also determined by NGS; it is 13,467 nt long and the genome sequence is 97% identical to that of PpVE. Based on priority of submission date in GenBank, we propose BaCV as a strain of PpVE (Bejerman and Dietzgen, 2019). Host range and arthropod vector are unknown.**persimmon virus A (PeVA)**The genome of PeVA was assembled from NGS data and RACE of Japanese persimmon trees with fruit apex disorder. The complete genome consists of 13,467 nt (Ito et al., 2013). The L protein amino acid sequence of PeVA is 53% identical to that of strawberry crinkle virus (SCV), 42% to lettuce necrotic yellows virus (LNYV) and 43% to lettuce yellow mottle virus (LYMoV). Host range and arthropod vector are unknown.**raspberry vein chlorosis virus (RVCV)**Raspberry vines showing vein chlorosis symptoms were used to extract total RNA, depleted of rRNAs and analysed through Illumina sequencing and RACE (Jones et al., 2019). The complete genomes of two divergent isolates of RVCV were assembled to lengths of 14,512 nt (Hutt1) and 14,667 nt (Hutt2) with nt sequence identity of 68%. RVCV genomes were most closely related to those of SCV and alfalfa dwarf virus (ADV). We only propose to classify Hutton 1 strain here since more data will be required to determine if these isolates should be considered as strains of the same virus or represent different viruses. In earlier work, a small raspberry aphid (*Aphis idaei*) was suspected as the arthropod vector.**rice stripe mosaic virus (RSMV)**RSMV infects rice causing rice stripe mosaic disease in China. The virus has been shown experimentally to be transmitted by and replicate in a leafhopper (*Recilia dorsalis*). Virions are bacilliform and measure 300-375 nm x 45-55 nm. RSMV complete genome is 12,782 nt and was assembled from small RNA Illumina sequencing data and RACE (Yang et al., 2017).**tomato yellow mottle-associated virus (TYMaV)**The TYMaV coding-complete genome sequence of 13,389 nt was assembled from small RNA sequencing libraries in a tomato virome study in China (Xu et al., 2017). Phylogenetically, TYMaV clusters with ADV. Host range and arthropod vector are unknown.**yerba mate chlorosis-associated virus (YmCaV)**Yerba mate (*Ilex paraguariensis*) is a tropical South American shrub. Plants showing chlorotic line patterns and rings, and vein yellowing were used for total RNA extraction and small RNA Illumina sequencing and a cytorhabdovirus-like genome sequence identified. The YmCaV complete genome sequence of 12,876 nt has been determined following RACE (Bejerman et al., 2017). The virus is graft-transmissible. Host range and arthropod vector are unknown.**Wuhan insect viruses 4, 5, 6** Wuhan insect viruses 4, 5 and 6 RNA-directed RNA polymerase sequences (2105, 2098, 2079 nucleotides, respectively) were initially discovered in a pool of insects that included *Hyalopterus pruni* or *Aphelinus* sp. (Li et al., 2015). Coding-complete genome sequences were assembled for WuIV 4 (13,490 nt), WuIV 5 (12,734 nt) and WuIV 6 (14,191 nt) obtained from *H. pruni*. There is no information on any potential plant hosts. |

Based on the nucleotide and deduced amino acid sequence information compiled in Tables 1 to 5, we propose to classify CCyV-1, MaCV, MYSV, PpVE, PeVA, RVCV, RSMV, TYMaV, YmCaV, WuIV-4, WuIV05 and WuIV-6 in the new species *Cabbage cytorhabdovirus*, *Maize-associated cytorhabdovirus*, *Maize yellow striate cytorhabdovirus*, *Papaya cytorhabdovirus*, *Persimmon cytorhabdovirus*, *Raspberry vein chlorosis cytorhabdovirus*, *Rice stripe mosaic cytorhabdovirus*, *Tomato yellow mottle-associated cytorhabdovirus*, *Yerba mate chlorosis-associated cytorhabdovirus*, *Wuhan 4 insect cytorhabdovirus*, *Wuhan 5 insect cytorhabdovirus*, and *Wuhan 6 insect cytorhabdovirus* in the genus *Cytorhabdovirus*, family *Rhabdoviridae*.

Viruses assigned to different species within the genus *Cytorhabdovirus* have several of the following characteristics:

1. nucleotide sequence identity less than 75% for the complete genome sequence;
2. amino acid sequence identity in all cognate open reading frames less than 80%
3. occupy different ecological niches as evidenced by differences in hosts and/or arthropod vectors; and
4. can be clearly distinguished in serological tests or by nucleic acid hybridization.

The viruses in both the currently accepted species and the proposed new species show < 75% nucleotide sequence identity across the genome (A; Table 1), show < 80% amino acid sequence identity in cognate ORFs (B; Tables 2-5), and infect different plant hosts and arthropod vectors (C), where this information is known.



**Figure 1.** A Maximum Likelihood phylogenetic tree of plant-adapted rhabdovirus L polymerase protein sequences. Amino acid sequences were aligned using MAFFT version 7 (Katoh et al., 2017) and then the alignment was filtered using Gblocks 0.91b (Talavera and Castresana 2007). The resulting alignment (783 amino acid positions remaining) was subjected to generate a phylogenetic tree using PhyML 3.0 (Guindon et al., 2010) with the best-fit model LG + G + I +F. For each genus, viruses belonging to either the proposed species or currently unassigned, related viruses are indicated by red color. The tree is rooted to two animal rhabdoviruses as outgroup. Numbers at the nodes indicate bootstrap support (100 replicates).

**Table 1.** Cytorhabdovirus - genome nucleotide sequence. Percent Identity Matrix - created by Clustal2.1.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Virus | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 |
| 1 | Northern\_cereal\_mosaic\_virus\_NC\_002251.1  | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 2 | Maize\_associated\_rhabdovirus\_strain\_Peru\_KY965147.1  | 57 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 3 | Barley\_yellow\_striate\_mosaic\_virus\_strain\_Hebei\_KM213865.1  | 55.94 | 54.91 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 4 | Maize\_yellow\_striate\_virus\_KY884303.1  | 56.13 | 54.84 | 66.51 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 5 | Colocasia\_bobone\_disease-associated\_virus\_strain\_SI\_KT381973.1  | 49.25 | 50.24 | 49.48 | 50.04 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 6 | Raspberry\_vein\_chlorosis\_virus\_isolate\_Hutton\_1\_MK240091.1  | 39.59 | 39.83 | 39.86 | 40.24 | 42.74 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |
| 7 | Alfalfa\_dwarf\_virus\_isolate\_Manfredi\_KP205452.2  | 40.04 | 39.76 | 39.76 | 39.94 | 40.2 | 52.09 | 100 |  |  |  |  |  |  |  |  |  |  |  |
| 8 | Tomato\_yellow\_mottle-associated\_virus\_KY075646.1  | 39.05 | 39.44 | 38.94 | 39.64 | 39.02 | 45.73 | 46.59 | 100 |  |  |  |  |  |  |  |  |  |  |
| 9 | Rice\_stripe\_mosaic\_virus\_isolate\_GD-LD\_KX525586.2  | 43.82 | 44.48 | 44.05 | 44.29 | 43.42 | 39.14 | 38.87 | 39.99 | 100 |  |  |  |  |  |  |  |  |  |
| 10 | Lettuce\_yellow\_mottle\_virus\_EF687738.1  | 38.17 | 38.38 | 38.06 | 39.09 | 39.03 | 42.95 | 43.46 | 42.9 | 38.33 | 100 |  |  |  |  |  |  |  |  |
| 11 | Lettuce\_necrotic\_yellows\_virus\_AJ867584.2  | 38.65 | 38.49 | 38.28 | 38.41 | 38.6 | 43.3 | 43.56 | 42.76 | 38.5 | 61.61 | 100 |  |  |  |  |  |  |  |
| 12 | Cabbagecytorhabdovirus\_1\_strain\_FERA\_050726\_KY810772.2 | 38.07 | 38.63 | 37.64 | 38.41 | 39.35 | 43.13 | 43.27 | 42.86 | 38.32 | 54.15 | 54.45 | 100 |  |  |  |  |  |  |
| 13 | Persimmon\_virus\_A\_clone\_\_Kaki13-14\_AB735628.2  | 38.41 | 39.82 | 38.97 | 39.22 | 39.52 | 44.5 | 44.77 | 44.17 | 38.38 | 45.88 | 46.13 | 45.42 | 100 |  |  |  |  |  |
| 14 | Wuhan\_Insect\_virus\_6\_strain\_SXCC01-1\_KM817652.1  | 38.8 | 38.88 | 38.41 | 38.76 | 39.02 | 47.57 | 47.54 | 47.31 | 39.62 | 44.64 | 44.95 | 44.72 | 49.18 | 100 |  |  |  |  |
| 15 | Wuhan\_Insect\_virus\_5\_strain\_YCYC02\_KM817651.  | 38.92 | 39.41 | 39.04 | 39.75 | 39.92 | 44.09 | 44.9 | 44.07 | 38.13 | 45.33 | 44.95 | 45.09 | 49.25 | 47.17 | 100 |  |  |  |
| 16 | Yerba\_mate\_chlorosis-associated\_virus\_isolate\_Montecarlo\_KY366322.2  | 39.93 | 40.32 | 39.61 | 40.48 | 39.69 | 39.06 | 37.8 | 38.56 | 39.17 | 37.58 | 38.65 | 37.9 | 38.56 | 38.96 | 38.03 | 100 |  |  |
| 17 | Wuhan\_Insect\_virus\_4\_strain\_YCYC03\_KM817650.1  | 38.94 | 39.58 | 38.79 | 39.66 | 39.14 | 42.9 | 42.96 | 42.38 | 39.03 | 45.32 | 45.44 | 44.67 | 44.12 | 44.63 | 44.44 | 40.81 | 100 |  |
| 18 | Papaya\_cytorhabdovirus\_isolate\_Los\_Rios\_Ec\_MH282832.1  | 41.99 | 42.16 | 42.03 | 42.29 | 42.47 | 39 | 38.73 | 37.97 | 41.45 | 39.28 | 38.7 | 39.23 | 39.38 | 39.61 | 38.69 | 40.18 | 39.24 | 100 |

**Table 2.** Cytorhabdovirus - N gene\_nts. Percent Identity Matrix - created by Clustal2.1.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Virus | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 |
| 1 | Northern\_cereal\_mosaic\_virus\_NC\_002251.1 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 2 | Barley\_yellow\_striate\_mosaic\_virus\_strain\_Hebei\_KM213865.1 | 53.45 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 3 | Maize\_yellow\_striate\_virus\_KY884303.1 | 54.89 | 66.98 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 4 | Rice\_stripe\_mosaic\_virus\_isolate\_GD-LD\_KX525586.2 | 43.43 | 47.76 | 49.24 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 5 | Maize\_associated\_rhabdovirus\_strain\_Peru\_KY965147.1 | 52.01 | 50.71 | 51.14 | 44.95 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 6 | Papaya\_cytorhabdovirus\_isolate\_Los\_Rios\_Ec\_MH282832.1 | 41.06 | 39.51 | 42.03 | 43.95 | 40.54 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |
| 7 | Wuhan\_Insect\_virus\_5\_strain\_YCYC02\_KM817651. | 39.59 | 39.33 | 40.22 | 40.74 | 40.2 | 39.74 | 100 |  |  |  |  |  |  |  |  |  |  |  |
| 8 | Yerba\_mate\_chlorosis-associated\_virus\_isolate\_Montecarlo\_KY366322.2 | 44.3 | 43.26 | 45.8 | 44.15 | 44.64 | 38.81 | 39.97 | 100 |  |  |  |  |  |  |  |  |  |  |
| 9 | Lettuce\_yellow\_mottle\_virus\_EF687738.1 | 39.92 | 39.42 | 39.33 | 37.58 | 38.64 | 40.35 | 44.41 | 39.24 | 100 |  |  |  |  |  |  |  |  |  |
| 10 | Lettuce\_necrotic\_yellows\_virus\_AJ867584.2 | 39.75 | 39.24 | 38.96 | 37.53 | 37.99 | 38.47 | 42.88 | 37.78 | 60.03 | 100 |  |  |  |  |  |  |  |  |
| 11 | Cabbagecytorhabdovirus\_1\_strain\_FERA\_050726\_KY810772.1 | 40.62 | 38.18 | 40.6 | 39.19 | 39.41 | 41.43 | 44.33 | 40.48 | 55.01 | 53.99 | 100 |  |  |  |  |  |  |  |
| 12 | Persimmon\_virus\_A\_clone\_\_Kaki13-14\_AB735628.2 | 39.56 | 40.15 | 39.39 | 40.1 | 38.9 | 38.23 | 48.74 | 39.81 | 47.38 | 46.93 | 46.79 | 100 |  |  |  |  |  |  |
| 13 | Alfalfa\_dwarf\_virus\_isolate\_Manfredi\_KP205452.2 | 38.09 | 38.29 | 38 | 38.14 | 39.51 | 38.49 | 45.89 | 37.67 | 43.89 | 42.89 | 46.07 | 47.75 | 100 |  |  |  |  |  |
| 14 | Raspberry\_vein\_chlorosis\_virus\_isolate\_Hutton\_1\_MK240091.1 | 37.23 | 36.49 | 36.22 | 36.86 | 38.55 | 39.57 | 44.47 | 38.57 | 43.1 | 43.16 | 41.31 | 46.15 | 52.24 | 100 |  |  |  |  |
| 15 | Tomato\_yellow\_mottle-associated\_virus\_KY075646.1 | 37.38 | 38.15 | 38.52 | 38.38 | 40.14 | 38.89 | 42.95 | 37.83 | 44.01 | 43.51 | 44.88 | 44.57 | 46.33 | 47.5 | 100 |  |  |  |
| 16 | Wuhan\_Insect\_virus\_4\_strain\_YCYC03\_KM817650.1 | 40.37 | 38.64 | 40.02 | 36.86 | 38.42 | 38.63 | 43.07 | 38.77 | 45.78 | 46.26 | 47.45 | 45.21 | 45.53 | 43.82 | 46.07 | 100 |  |  |
| 17 | Wuhan\_Insect\_virus\_6\_strain\_SXCC01-1\_KM817652.1 | 39.9 | 39.71 | 38.54 | 39.78 | 39.18 | 40.57 | 44.33 | 40.17 | 44.28 | 45.02 | 45.49 | 46.73 | 47.01 | 48.17 | 45.51 | 49.17 | 100 |  |
| 18 | Colocasia\_bobone\_disease-associated\_virus\_strain\_SI\_KT381973.1 | 47.01 | 44.51 | 45.42 | 44.77 | 47.91 | 40.65 | 38.81 | 42.5 | 41.4 | 39.29 | 40.16 | 39.91 | 41.31 | 39.72 | 39.77 | 40.99 | 38.78 | 100 |

**Table 3.** Cytorhabdovirus - N gene\_aa. Percent Identity Matrix - created by Clustal2.1.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Virus | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 |
| 1 | Northern\_cereal\_mosaic\_virus\_NP\_057954.1 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 2 | Barley\_yellow\_striate\_mosaic\_virus\_strain\_Hebei\_AJP67515.1 | 46.91 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 3 | Maize\_yellow\_striate\_virus\_ATN96434.1 | 48.48 | 70.59 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 4 | Maize\_associated\_rhabdovirus\_strain\_Peru\_ARS22490.1 | 45.56 | 42.94 | 40.94 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 5 | Colocasia\_bobone\_disease-associated\_virus\_strain\_SI\_ALU34429.1 | 35.84 | 36.13 | 37.11 | 35.28 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 6 | Rice\_stripe\_mosaic\_virus\_isolate\_GD-LD\_APR74648.1 | 30.71 | 33.33 | 35.58 | 32.54 | 32.1 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |
| 7 | Yerba\_mate\_chlorosis-associated\_virus\_isolate\_Montecarlo\_AYR67253.1 | 27.45 | 28.2 | 29.48 | 25.31 | 26.01 | 25.74 | 100 |  |  |  |  |  |  |  |  |  |  |  |
| 8 | Papaya\_cytorhabdovirus\_isolate\_Los\_Rios\_Ec\_AYD37618.1 | 23.87 | 23.65 | 25.36 | 24.28 | 21.74 | 26.89 | 23.73 | 100 |  |  |  |  |  |  |  |  |  |  |
| 9 | Lettuce\_yellow\_mottle\_virus\_ABV56124.1 | 21.34 | 24.25 | 22.77 | 22.83 | 21.79 | 18.36 | 19.9 | 20.35 | 100 |  |  |  |  |  |  |  |  |  |
| 10 | Lettuce\_necrotic\_yellows\_virus\_CAI30421.1 | 21.98 | 24.93 | 24.26 | 23.51 | 20.61 | 21.2 | 20.25 | 19.32 | 58.44 | 100 |  |  |  |  |  |  |  |  |
| 11 | Cabbagecytorhabdovirus\_1\_strain\_FERA\_050726\_ATS17308.1 | 21.55 | 23.03 | 24.44 | 23.75 | 22.02 | 21.31 | 20.36 | 20.9 | 47.32 | 45.45 | 100 |  |  |  |  |  |  |  |
| 12 | Wuhan\_Insect\_virus\_4\_strain\_YCYC03\_AJG39174.1 | 20.15 | 21.32 | 22.33 | 20.45 | 20.62 | 21.2 | 18.99 | 18.18 | 32.21 | 33.63 | 30.13 | 100 |  |  |  |  |  |  |
| 13 | Alfalfa\_dwarf\_virus\_isolate\_Manfredi\_AKD44211.2 | 20.15 | 19.8 | 20.18 | 20.14 | 21.85 | 18.81 | 17.88 | 18.77 | 30.56 | 28.16 | 33.71 | 29.62 | 100 |  |  |  |  |  |
| 14 | Raspberry\_vein\_chlorosis\_virus\_isolate\_Hutton\_1\_QBS46629.1 | 18 | 16.97 | 16.17 | 19.76 | 19.9 | 17.92 | 18.48 | 18.36 | 30.11 | 28.89 | 29.62 | 29.87 | 45.86 | 100 |  |  |  |  |
| 15 | Wuhan\_Insect\_virus\_6\_strain\_SXCC01-1\_AJG39186.1 | 19.1 | 23.48 | 21.75 | 19.65 | 18.44 | 20.88 | 21.39 | 20 | 30.14 | 29.8 | 30.02 | 32.23 | 36.88 | 36.47 | 100 |  |  |  |
| 16 | Tomato\_yellow\_mottle-associated\_virus\_AQY17511.1 | 21.07 | 23.1 | 22.84 | 22.9 | 20.53 | 19.75 | 19.64 | 19.27 | 32.33 | 32.75 | 31.82 | 32.75 | 34.74 | 34.67 | 35.59 | 100 |  |  |
| 17 | Persimmon\_virus\_A\_clone\_\_Kaki13-14\_BAM36030.2 | 22.11 | 23.78 | 23 | 22.17 | 20.52 | 23 | 20.36 | 19.4 | 34.26 | 33.33 | 31.42 | 29.21 | 32.64 | 32.81 | 33.78 | 32.57 | 100 |  |
| 18 | Wuhan\_Insect\_virus\_5\_strain\_YCYC02\_AJG39180.1 | 20.4 | 24.7 | 23.76 | 21.78 | 20.82 | 22.46 | 20.45 | 19.21 | 30.79 | 29.89 | 31.49 | 30.68 | 30.66 | 30.27 | 31.64 | 29.19 | 39.86 | 100 |

**Table 4.** Cytorhabdovirus - L\_gene nts. Percent Identity Matrix - created by Clustal2.1.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Virus | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 |
| 1 | Northern\_cereal\_mosaic\_virus\_NC\_002251.1 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 2 | Barley\_yellow\_striate\_mosaic\_virus\_strain\_Hebei\_KM213865.1 | 61.48 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 3 | Maize\_yellow\_striate\_virus\_KY884303.1 | 62.45 | 70.47 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 4 | Maize\_associated\_rhabdovirus\_strain\_Peru\_KY965147.1 | 60.37 | 59.53 | 60.26 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 5 | Colocasia\_bobone\_disease-associated\_virus\_strain\_SI\_KT381973.1 | 55.64 | 56.35 | 56.41 | 55.88 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 6 | Rice\_stripe\_mosaic\_virus\_isolate\_GD-LD\_KX525586.2 | 47.9 | 48.2 | 48.7 | 49.69 | 47.59 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |
| 7 | Papaya\_cytorhabdovirus\_isolate\_Los\_Rios\_Ec\_MH282832.1 | 47.77 | 47.55 | 48.38 | 47.54 | 47.92 | 46.62 | 100 |  |  |  |  |  |  |  |  |  |  |  |
| 8 | Yerba\_mate\_chlorosis-associated\_virus\_isolate\_Montecarlo\_KY366322.2 | 45.32 | 44.38 | 44.86 | 43.94 | 44.22 | 43.19 | 44.34 | 100 |  |  |  |  |  |  |  |  |  |  |
| 9 | Lettuce\_yellow\_mottle\_virus\_EF687738.1 | 41.35 | 41.22 | 42.12 | 41.85 | 41.89 | 40.51 | 41.21 | 40.96 | 100 |  |  |  |  |  |  |  |  |  |
| 10 | Lettuce\_necrotic\_yellows\_virus\_AJ867584.2 | 41.23 | 41.1 | 42.06 | 41.36 | 41.13 | 40.74 | 40.12 | 41.29 | 64.32 | 100 |  |  |  |  |  |  |  |  |
| 11 | Cabbagecytorhabdovirus\_1\_strain\_FERA\_050726\_KY810772.1 | 41.19 | 41.14 | 41.58 | 42.35 | 41.8 | 41.48 | 42.5 | 40.41 | 56.67 | 57.56 | 100 |  |  |  |  |  |  |  |
| 12 | Wuhan\_Insect\_virus\_4\_strain\_YCYC03\_KM817650.1 | 41.05 | 41.16 | 41.34 | 41.82 | 41.05 | 40.9 | 41.13 | 40.55 | 49.28 | 50.09 | 48.61 | 100 |  |  |  |  |  |  |
| 13 | Alfalfa\_dwarf\_virus\_isolate\_Manfredi\_KP205452.2 | 41.44 | 41.44 | 41.68 | 41.4 | 41.13 | 40.71 | 41.41 | 40.39 | 48.76 | 48.03 | 48.35 | 46.92 | 100 |  |  |  |  |  |
| 14 | Raspberry\_vein\_chlorosis\_virus\_isolate\_Hutton\_1\_MK240091.1 | 41.71 | 41.77 | 42.08 | 41.88 | 40.51 | 40.55 | 41.54 | 40.92 | 48.27 | 48.62 | 48.39 | 46.9 | 60.52 | 100 |  |  |  |  |
| 15 | Persimmon\_virus\_A\_clone\_\_Kaki13-14\_AB735628.2 | 41.81 | 42.29 | 42.71 | 43.09 | 42.08 | 40.26 | 41.67 | 40.73 | 51.23 | 51.28 | 49.98 | 50.28 | 51.03 | 51.02 | 100 |  |  |  |
| 16 | Wuhan\_Insect\_virus\_6\_strain\_SXCC01-1\_KM817652.1 | 41.36 | 41.29 | 41.93 | 41.43 | 41.09 | 41.84 | 41.29 | 40.38 | 49.35 | 49.63 | 48.91 | 48.4 | 54.24 | 54.89 | 52.83 | 100 |  |  |
| 17 | Tomato\_yellow\_mottle-associated\_virus\_KY075646.1 | 40.41 | 40.69 | 40.94 | 40.44 | 40.4 | 41.58 | 40.2 | 40.56 | 47.39 | 47.4 | 47.18 | 46.93 | 51.11 | 51.74 | 49.75 | 53 | 100 |  |
| 18 | Wuhan\_Insect\_virus\_5\_strain\_YCYC02\_KM817651. | 41.44 | 42.22 | 42.8 | 42.62 | 41.83 | 40.59 | 40.86 | 40.77 | 50.29 | 49.68 | 49.15 | 49.24 | 50.41 | 49.3 | 52.97 | 50.87 | 48.21 | 100 |

**Table 5.** Cytorhabdovirus - L gene\_aa. Percent Identity Matrix - created by Clustal2.1.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Virus | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 |
| 1 | Northern\_cereal\_mosaic\_virus\_NP\_597914.1 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 2 | Barley\_yellow\_striate\_mosaic\_virus\_strain\_Hebei\_AJP67524.1 | 62.28 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 3 | Maize\_yellow\_striate\_virus\_ATN96443.1 | 63.16 | 79.91 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 4 | Maize\_associated\_rhabdovirus\_strain\_Peru\_ARS22495.1 | 59.51 | 60.51 | 60.46 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 5 | Colocasia\_bobone\_disease-associated\_virus\_strain\_SI\_ALU34427.1 | 52.64 | 54 | 53.56 | 51.29 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 6 | Rice\_stripe\_mosaic\_virus\_isolate\_GD-LD\_APR74654.1 | 39.24 | 39.84 | 39.89 | 39.58 | 39.28 | 100 |  |  |  |  |  |  |  |  |  |  |  |  |
| 7 | Papaya\_cytorhabdovirus\_isolate\_Los\_Rios\_Ec\_AYD37624.1 | 37.67 | 38.24 | 37.84 | 36.76 | 38.1 | 34.5 | 100 |  |  |  |  |  |  |  |  |  |  |  |
| 8 | Yerba\_mate\_chlorosis-associated\_virus\_isolate\_Montecarlo\_ARA91091.1 | 32.07 | 32.25 | 31.81 | 30.74 | 31.73 | 29.6 | 31.48 | 100 |  |  |  |  |  |  |  |  |  |  |
| 9 | Lettuce\_yellow\_mottle\_virus\_ABV56129.1 | 27.2 | 27.61 | 28.16 | 27.37 | 27.97 | 26.9 | 27.03 | 23.76 | 100 |  |  |  |  |  |  |  |  |  |
| 10 | Lettuce\_necrotic\_yellows\_virus\_CAI30426.1 | 27.01 | 27.68 | 28.08 | 26.88 | 27.94 | 27.11 | 25.55 | 24.96 | 66.15 | 100 |  |  |  |  |  |  |  |  |
| 11 | Cabbagecytorhabdovirus\_1\_strain\_FERA\_050726\_ATS17313.1 | 28.09 | 28.21 | 28.51 | 28.11 | 28.61 | 28.44 | 26.68 | 23.96 | 53.63 | 53.39 | 100 |  |  |  |  |  |  |  |
| 12 | Alfalfa\_dwarf\_virus\_isolate\_Manfredi\_AKD44217.1 | 28.21 | 27.83 | 28.48 | 27.23 | 27.24 | 27.65 | 26.52 | 24.11 | 40.36 | 38.79 | 39.47 | 100 |  |  |  |  |  |  |
| 13 | Raspberry\_vein\_chlorosis\_virus\_isolate\_Hutton\_1\_QBS46636.1 | 28.67 | 28.19 | 28.54 | 28.39 | 27.91 | 28.51 | 26.13 | 25.07 | 39.26 | 39.74 | 39.69 | 60.71 | 100 |  |  |  |  |  |
| 14 | Wuhan\_Insect\_virus\_6\_strain\_SXCC01-1\_AJG39191.1 | 28.65 | 28.78 | 28.98 | 28.13 | 28.44 | 28.94 | 26.32 | 24.25 | 39.9 | 39.78 | 39.6 | 47.92 | 48.04 | 100 |  |  |  |  |
| 15 | Tomato\_yellow\_mottle-associated\_virus\_AQY17505.1 | 27.02 | 27.3 | 27.95 | 27.25 | 27.51 | 28.54 | 25.83 | 25.42 | 39.01 | 38.17 | 38.37 | 45.34 | 45.58 | 47.31 | 100 |  |  |  |
| 16 | Persimmon\_virus\_A\_clone\_\_Kaki13-14\_BAM36035.2 | 28.5 | 29.18 | 29.23 | 28.9 | 28.62 | 27.29 | 27.09 | 25.09 | 43.21 | 42.57 | 41.95 | 42.7 | 42.43 | 44.43 | 41.36 | 100 |  |  |
| 17 | Wuhan\_Insect\_virus\_5\_strain\_YCYC02\_AJG39185.1 | 29.31 | 30.32 | 30.47 | 29.64 | 30.76 | 27.93 | 26.72 | 24.98 | 42.96 | 42.62 | 42.14 | 42.93 | 40.83 | 42.99 | 40.07 | 47.86 | 100 |  |
| 18 | Wuhan\_Insect\_virus\_4\_strain\_YCYC03\_AJG39179.1 | 26.97 | 27.37 | 28.02 | 27.42 | 27.56 | 26.83 | 26 | 23.7 | 40.39 | 40.15 | 39.43 | 37.56 | 37.3 | 38.16 | 36.56 | 40.06 | 40.86 | 100 |

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