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.

For guidance, see the notes written in blue, below, and the help notes in file Taxonomic\_Proposals\_Help\_2018.

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

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| **Code assigned:** | ***2018.025P*** | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)Seven new species in the genus *Orthotospovirus* |
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| **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) | ***Tospoviridae*** |
| **ICTV Study Group comments (if any) and response of the proposer:** |
|       |
|  |
| Date first submitted to ICTV: | June 5th, 2018 |
| Date of this revision (if different to above): |       |

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

**Part 2:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

| **Text of proposal:** |
| --- |
|  |

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

|  |
| --- |
| **Name of accompanying Excel module:** 2018.025P.N.v1.Orthotospovirus\_7sp.xlsx |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2017\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

| additional material in support of this proposal |
| --- |
| Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:* **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing.
* **Higher taxa**:
	+ There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.
	+ Please indicate the **origin of names** assigned to new taxa at genus level and above.
	+ For each new genus a **type species** must be designated to represent it. Please explain your choice.
* **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.
 |

The genus *Orthotospovirus* in the family *Tospoviridae* is comprised of insect- and plant-infecting viruses with tripartite single stranded RNA genomes. Individual RNAs are designated S (small), M (medium) or L (large) and contain five open reading frames (ORFs). The S and M RNAs are ambisense, whereas the L RNA is negative sense. Eight terminal nucleotides of each RNA are conserved among family members, and also complementary facilitating base-pairing of the termini of each RNA to form a panhandle structure. The S RNA encodes the nucleocapsid (N) and nonstructural (NSs, silencing suppressor) proteins. The M RNA encodes a glycoprotein precursor (proteolytically processed to yield two viral glycoproteins, GN and GC) and a second nonstructural protein (NSm, cell-to-cell movement). The L RNA encodes the viral RNA-dependent RNA polymerase (L). Phylogenetic analyses show segregation of orthotospovirus species into Old World and New World clades. Particles are pleomorphic or quasi-spherical, 80-120 nm in diameter, and enveloped with a host-derived membrane in which GN and GC are embedded to appear as ‘spike-like’ structures on the virion surface. Members of the family are transmitted by one or more species of thrips (Thysanoptera: Thripidae) in a persistent, propagative manner.

Species demarcation criteria for the genus *Orthotospovirus*:

• Genome sequence relatedness: different species have N protein amino acid pairwise identity less than 90%.

• Thrips species vector specificity.

• Plant host range.

• Antigenic properties: serological relatedness of N protein.

The seven viruses described below are proposed to represent new species in the genus *Orthotospovirus*. For each virus, there is at least one complete genome sequence in the public domain and this shows the expected ORFs and conserved nucleotide and/or amino acid motifs. The molecular criteria of pairwise identity to create new species have been fulfilled. Phylogenetic analysis of the complete S, M and L RNA genome segment sequences (Figures 1-3) supports the placement of these viruses in new species within genus *Orthotospovirus*.

**Seven proposed new species in genus *Orthotospovirus***

1. **Bean necrotic mosaic virus**

Bean necrotic mosaic virus (BeNMV) is endemic in Brazil where it was found naturally infecting common beans (De Oliveira et al., 2012). Experimental mechanical inoculation studies have shown that BeNMV has a narrow plant host range. The vector remains unknown. The complete genome sequence ([JN587268](https://www.ncbi.nlm.nih.gov/nuccore/JN587268.1), [JN587269](https://www.ncbi.nlm.nih.gov/nuccore/JN587269.1) and [JF417980](https://www.ncbi.nlm.nih.gov/nuccore/JF417980.1)) comprises three ssRNAs of 2584, 4886 and 9040 nt, respectively, with a genome organization typical of orthotospoviruses (De Oliveira et al., 2011, 2012). Phylogenetic analysis showed that BeNMV and soybean vein necrosis virus (SVNV; a member of another proposed orthotospovirus species – see #7 below), represent a novel evolutionary lineage of orthotospoviruses circulating in the New World (Americas). Functional and structural studies utilizing the BeNMV cell-to-cell movement (NSm) protein have been published (Leastro et al., 2015) further supporting BeNMV as a new species.

The *Tospoviridae* study group proposes that bean necrotic mosaic virus represents a new species, named *Bean necrotic mosaic orthotospovirus*, within the genus *Orthotospovirus* with BeNMV isolate TF-SP as the exemplar isolate.

1. **Calla lily chlorotic spot virus**

Calla lily chlorotic spot virus (CCSV) was first isolated from calla lily (*Zantedeschia* spp.) in Taiwan in 2001 (Chen et al., 2005). Calla lily is the usual host, with symptoms of chlorotic spots on leaves and stems but CCSV has more recently been identified infecting other ornamental and agronomic plants (Lin et al., 2005; Wu et al., 2018). Thrips palmi is reported as a vector of CCSV. Comparison of data on serological relationships and N gene sequences revealed that CCSV is most closely but distantly related to the watermelon silver mottle virus (WSMoV) serogroup of orthotospoviruses. The first complete genome sequence (AY867502, FJ822961 and FJ822962) is from calla lily characterized in Taiwan and comprises three ssRNAs of 3172, 4704 and 8911 nt, respectively, with a genome organization typical of orthotospoviruses (Chen et al., 2012; Lin et al., 2005).

The *Tospoviridae* study group proposes that Calla lily chlorotic spot virus represents a new species within the genus *Orthotospovirus,* named *Calla lily chlorotic spot orthotospovirus,* with CCSV isolate calla lily as the exemplar isolate.

1. **Capsicum chlorosis virus**

Capsicum chlorosis virus (CaCV) was first characterized from Capsicum (pepper) in Australia in the late 1990s (Persley et al., 2006). The virus was subsequently identified in multiple vegetable (tomato, chilli, capsicum), legume (peanut) and ornamental (orchid) plant hosts in several Asian countries. More recently, CaCV was identified in an ornamental (Hoya) in Hawaii. Symptoms vary greatly by plant host and include general chlorosis and mottling of leaves, ringspots and chlorotic leaf spots and apical necrosis of shoots. Infected vegetable plants often produce distorted fruits that may exhibit concentric rings on the surface. Three thrips species, Ceratothripoides claratris, Frankliniella schultzei and Thrips palmi are reported as vectors of CaCV (Persley et al., 2006; Premachandra et al. 2005). The first complete genome sequence (DQ256123, DQ256125 and DQ256124) is from an isolate infecting tomato in Thailand and comprises three ssRNAs of 3477, 4823 and 8912 nt, respectively, with a genome organization typical of orthotospoviruses (Knierim et al. 2006). Subsequent complete genome sequences from multiple plant hosts in multiple Asian countries are generally quite similar (Gamage et al., 2015; Kunkalikar et al., 2010). Comparison of the N gene sequences and data on serological relationships revealed that CaCV is most closely related to the watermelon silver mottle virus (WSMoV) serogroup of orthotospoviruses. The overall identities of L-, M-, and S-RNA sequences with members of the WSMoV serogroup and other orthotospoviruses were less than 80%, well below the threshold for establishing a distinct orthotospovirus species. Recent phylogenetic analysis of the S RNA revealed segregation of CaCV isolates into two distinct clades, with isolates from Australia, Taiwan, Thailand and India forming one clade and a few isolates from China and Thailand forming another clade. It has been suggested that the Chinese and Thai isolates in this separate clade may be sufficiently distinct to merit consideration as prototypes of different species (Gamage et al., 2015). However, this suggestion was based solely on S RNA sequence data; the lack of sequence data for M and L RNA segments makes this conclusion premature.

Thus, the *Tospoviridae* study group proposes that Capsicum chlorosis virus represents a new species within the genus *Orthotospovirus*, named *Capsicum chlorosis orthotospovirus*, with CaCV isolate AIT as the exemplar isolate.

1. **Chrysanthemum stem necrosis virus**

Chrysanthemum stem necrosis virus (CSNV) was first characterized in the 1990s and to date has been identified in several countries in South America, Europe and Asia (Bezerra et al., 1999; Verhoeven et al., 1996). Chrysanthemum and other ornamental crops are usual hosts, with symptoms of chlorotic and necrotic spots on leaves and stems, and leaf distortion. Two thrips species, *Frankliniella schultzei* and *F. occidentalis*, have been experimentally demonstrated to transmit CSNV (Nagata and De Avila, 2000). The complete genome sequence ([KM114548](https://www.ncbi.nlm.nih.gov/nuccore/KM114548.1), [KM11454](https://www.ncbi.nlm.nih.gov/nuccore/KM114548.1)7 and [KM11454](https://www.ncbi.nlm.nih.gov/nuccore/KM114548.1)6) comprises three ssRNAs of 2947, 4830 and 8955 nt, respectively, with a genome organization typical of orthotospoviruses (Dullemans et al., 2015). Melon severe mosaic virus (MSMV; a virus belonging to another proposed orthotospovirus species – see #5 below) has the most closely related sequence present in public databases. CSNV and MSMV share 61% identity of aligned N proteins, well below the threshold for a establishing a distinct orthotospovirus species.

The *Tospoviridae* study group proposes that Chrysanthemum stem necrosis virus represents a new species within the genus *Orthotospovirus*, named *Chrysanthemum stem necrosis orthotospovirus*, with CSNV isolate PD4412741 as the exemplar isolate.

1. **Melon severe mosaic virus**

Melon severe mosaic virus (MSMV) was first characterized from melon samples collected in the Guerrero state of Mexico in 2007 (Ciuffo et al., 2009). The natural host range is limited to melon and watermelon. To date, MSMV has only been detected in Mexico and the vector remains unknown. Serological characterization shows that MSMV is distinct from a number of other tospoviruses. The complete genome sequence (KX698422, KX698423 and KX698424) comprises three ssRNAs of 3283, 4873 and 8911 nt, respectively, with a genome organization typical of orthotospoviruses (Ciuffo et al., 2017). Phylogenetic analysis shows that MSMV belongs to the New World orthotospovirus clade. Chrysanthemum stem necrosis virus (CSNV; member of another proposed orthotospovirus species – see #4 above) has the most closely related sequence present in public databases. MSMV and CSNV share 61% identity of aligned N proteins, well below the threshold for establishing a distinct orthotospovirus species.

The *Tospoviridae* study group proposes that melon severe mosaic virus represents a new species within the genus *Orthotospovirus,* named *Melon severe mosaic orthotospovirus,* with MSMV isolate VE440-A as the exemplar isolate.

1. **Melon yellow spot virus**

Melon yellow spot virus (MYSV) was first characterized from netted melon samples in Japan in 2000 (Kato and Hanada, 2000). The virus was subsequently detected in other Asian countries (China, Thailand, India) and, more recently, was also detected and characterized from melon samples in Ecuador, the first report of MYSV outside of Asia (Quito-Avila et al., 2014). MYSV is transmitted by *Thrips palmi*. The complete genome sequence (AB038343, AB061773 and AB061774) comprises three ssRNAs of 3232, 4815 and 8918 nt, respectively, with a genome organization typical of orthotospoviruses (Kato and Hanada, 2000; Okuda et al., 2004, 2006). Phylogenetic analysis shows that MYSV belongs to the Old World (Asian) orthotospovirus clade. Groundnut bud necrosis virus (GBNV) has the most closely related sequence present in public databases. MYSV and GBNV share 61% identity of aligned N proteins, well below the threshold for establishing a distinct orthotospovirus species. Based on the deduced protein sequence, Physalis severe mottle virus, a putative orthotospovirus first characterized from *Physalis minima* in Thailand in 2001 (Cortez et al., 2001), should be considered an isolate of MYSV.

The *Tospoviridae* study group proposes that melon yellow spot virus represents a new species within the genus *Orthotospovirus,* named *Melon yellow spot orthotospovirus,* with MYSV isolate Tospo-melo as the exemplar isolate.

1. **Soybean vein necrosis virus**

Soybean vein necrosis virus (SVNV) was first characterized from soybean in southern and mid-southern regions of the United States (Zhou et al., 2011). Early virus symptoms in soybean include yellowing along the veins; as infection progresses these areas become necrotic. SVNV is transmitted by several thrips species including *Neohydatothrips variabilis* (soybean thrips), *Frankliniella tritici* (eastern flower thrips) and *Frankliniella fusca* (tobacco thrips) (Keough et al., 2016). The complete genome sequence (HQ728387, HQ728386 and HQ728385) comprises three ssRNAs of 2603, 4955 and 9010 nt, respectively, with a genome organization typical of orthotospoviruses (Zhou et al., 2011). The genome sequence was generated by Sanger sequencing of plasmid clones from dsRNA isolated from symptomatic plants. Both SVNV and bean necrotic mosaic virus (BeNMV; virus representing another proposed orthotospovirus species – see #1 above) appear to have a unique lysine rich C-terminal extension of the L protein not found in other orthotospoviruses described to date. Phylogenetic analysis showed that SVNV and BeNMV represent a novel evolutionary lineage of orthotospoviruses circulating in the New World (Americas).

The *Tospoviridae* study group proposes that soybean vein necrosis virus represents a new species within the genus *Orthotospovirus*, named *Soybean vein necrosis orthotospovirus*, with SVNV isolate TN as the exemplar isolate.

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**Figure 1 -** Estimated phylogeny of the complete S RNA genome segment sequences of viruses belonging to recognized and proposed species within the genus *Orthotospovirus* in the family *Tospoviridae*. The seven viruses proposed to represent new species are indicated with red text. The midpoint-rooted tree was deduced in MEGA v. 7.0.26 after alignment in Muscle, using the maximum likelihood method based on the GTR+I+G substitution model with 500 bootstrap replications. The scale bar indicates the number of substitutions per site. Bootstrap support for branches is shown at the junctions of branches where it was >50%. Accession numbers correspond to the nucleotide sequence of each virus genome sequence used in the tree: BeNMV, bean necrotic mosaic virus; CCSV, calla lily chlorotic spot virus; CaCV, Capsicum chlorosis virus; CNSV, chrysanthemum stem necrosis virus; GBNV, groundnut bud necrosis virus; GRSV, groundnut ringspot virus; GYSV, groundnut yellow spot virus; INSV, impatiens necrotic spot virus; IYSV, iris yellow spot virus; MSMV, melon severe mosaic virus; MYSV, melon yellow spot virus; PolRSV, polygonum ringspot virus; SVNV, soybean vein necrosis virus; TCSV, tomato chlorotic spot virus; TSWV, tomato spotted wilt virus; WBNV, watermelon bud necrosis virus; WSMoV, watermelon silver mottle virus; ZLCV, zucchini lethal chlorosis virus.

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**Figure 2 -** Estimated phylogeny of the complete M RNA genome segment sequences of viruses belonging to recognized and proposed species within the genus *Orthotospovirus* in the family *Tospoviridae*. The seven viruses proposed to represent new species are indicated with red text. The midpoint-rooted tree was deduced in MEGA v. 7.0.26 after alignment in Muscle, using the maximum likelihood method based on the GTR+I+G substitution model with 500 bootstrap replications. The scale bar indicates the number of substitutions per site. Bootstrap support for branches is shown at the junctions of branches where it was >50%. Accession numbers correspond to the nucleotide sequence of each virus genome sequence used in the tree: BeNMV, bean necrotic mosaic virus; CCSV, calla lily chlorotic spot virus; CaCV, Capsicum chlorosis virus; CNSV, chrysanthemum stem necrosis virus; GBNV, groundnut bud necrosis virus; GRSV, groundnut ringspot virus; INSV, impatiens necrotic spot virus; IYSV, iris yellow spot virus; MSMV, melon severe mosaic virus; MYSV, melon yellow spot virus; PolRSV, polygonum ringspot virus; SVNV, soybean vein necrosis virus; TCSV, tomato chlorotic spot virus; TSWV, tomato spotted wilt virus; WBNV, watermelon bud necrosis virus; WSMoV, watermelon silver mottle virus; ZLCV, zucchini lethal chlorosis virus.

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**Figure 3 -** Estimated phylogeny of the complete L RNA genome segment sequences of viruses belonging to recognized and proposed species within the genus *Orthotospovirus* in the family *Tospoviridae*. The seven viruses proposed to represent new species are indicated with red text. The midpoint-rooted tree was deduced in MEGA v. 7.0.26 after alignment in Muscle, using the maximum likelihood method based on the GTR+I+G substitution model with 500 bootstrap replications. The scale bar indicates the number of substitutions per site. Bootstrap support for branches is shown at the junctions of branches where it was >50%. Accession numbers correspond to the nucleotide sequence of each virus genome sequence used in the tree: BeNMV, bean necrotic mosaic virus; CCSV, calla lily chlorotic spot virus; CaCV, Capsicum chlorosis virus; CNSV, chrysanthemum stem necrosis virus; GBNV, groundnut bud necrosis virus; GRSV, groundnut ringspot virus; INSV, impatiens necrotic spot virus; IYSV, iris yellow spot virus; MSMV, melon severe mosaic virus; MYSV, melon yellow spot virus; PolRSV, polygonum ringspot virus; SVNV, soybean vein necrosis virus; TCSV, tomato chlorotic spot virus; TSWV, tomato spotted wilt virus; WBNV, watermelon bud necrosis virus; WSMoV, watermelon silver mottle virus; ZLCV, zucchini lethal chlorosis virus.