

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

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| **Code assigned:** | **2020.010P** |  |
| **Short title:**  Create one new species in the genus *Blunervirus* (*Martellivirales*: *Kitaviridae*) | | |
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**Author(s) and email address(es)**

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**List the ICTV Study Group(s) that have seen this proposal**

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| Family *Kitaviridae* |

**ICTV study group comments and response of proposer**

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**Authority to use the name of a living person**

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | July 30, 2020 |
| Date of this revision (if different to above) |  |

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

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2020.010P.R.Kitaviridae\_1nsp.xlsx |

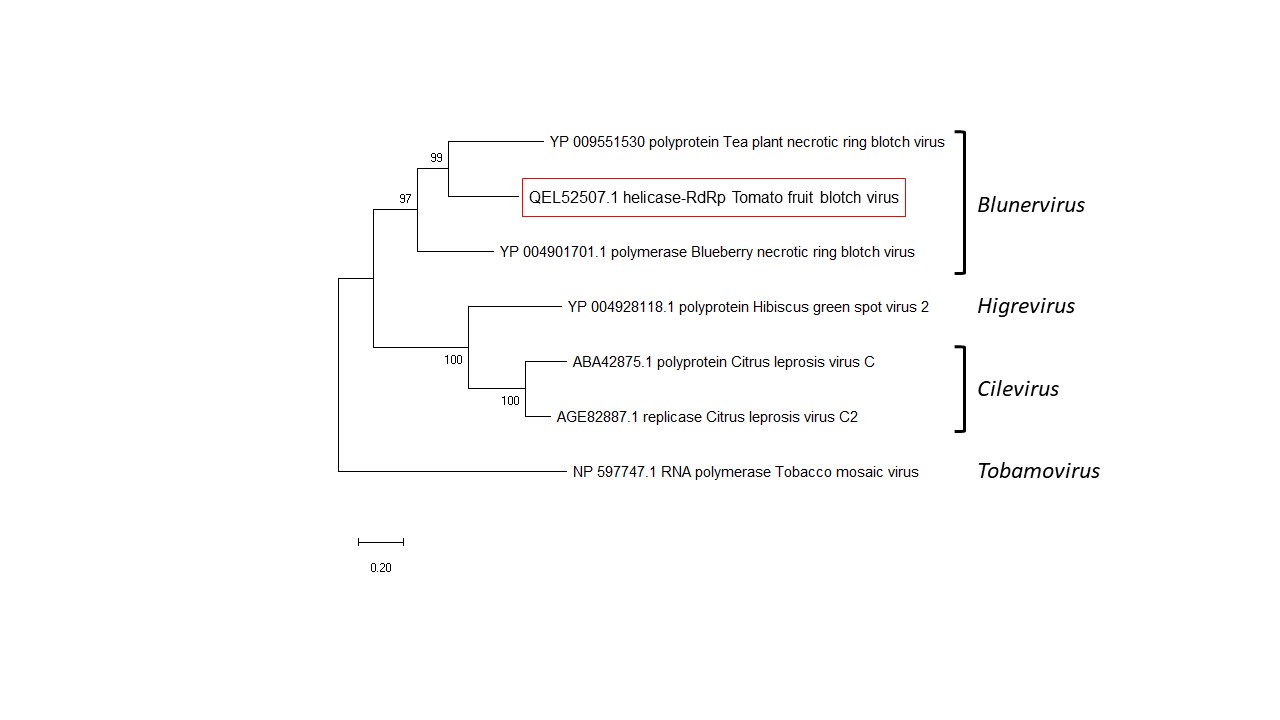
**Abstract**

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| This taxonomic proposal presents tomato fruit blotch virus as a new species in the genus *Blunervirus* (family *Kitaviridae*), which currently consists of two members: the type species *Blueberry necrotic ring blotch virus* and *Tea plant necrotic ring blotch virus*. Phylogenetic estimates clearly place tomato fruit blotch virus within the blunervirus clade. However, it possesses sufficient sequence and biological distinctions from recognized blunerviruses to be considered a new species within the genus. |

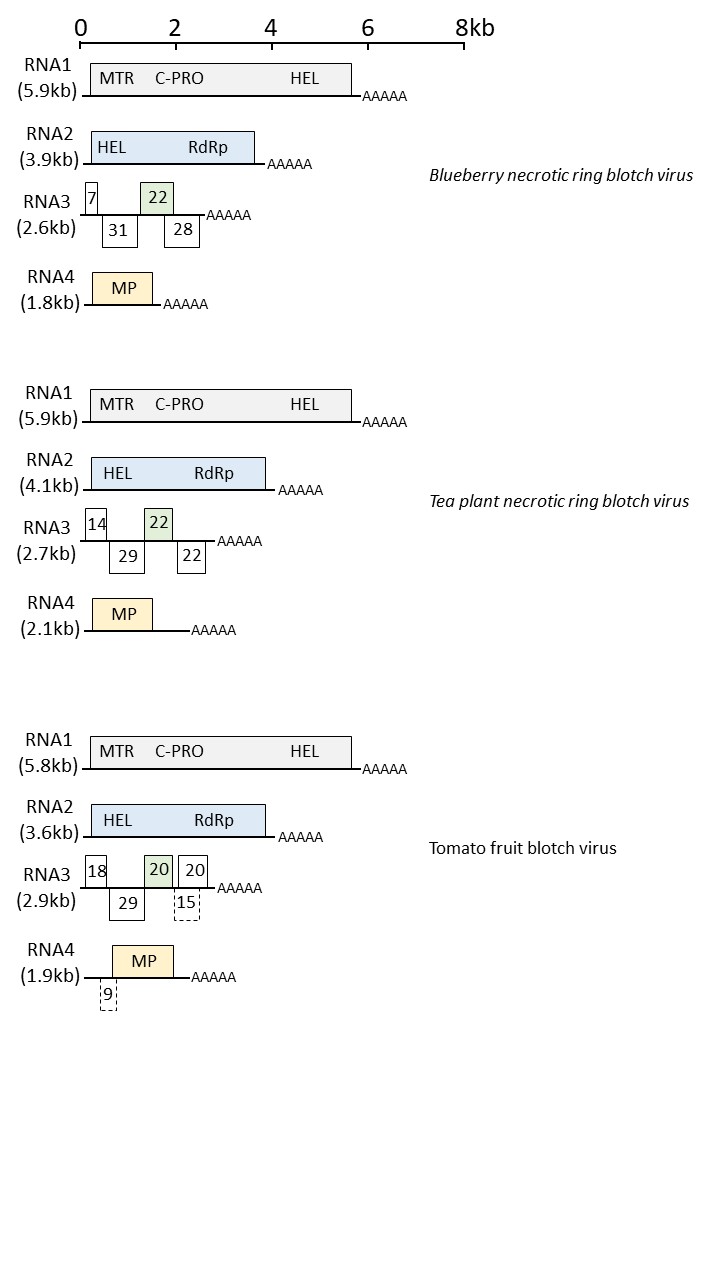
**Text of proposal**

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| |  | | --- | | The genus *Blunervirus* was established in 2016 and is composed of two species, *Blueberry necrotic ring blotch virus* (type species), and *Tea plant necrotic ring blotch virus*. The genome of blunerviruses is quadripartite, with positive sense ssRNA molecules. RNA1 and RNA2 each encode a polyprotein that putatively cleaves into replication associated products: methyltransferase, RNA-dependent RNA polymerase (RdRp), two helicases, and a protease. These conserved products are informative for predicting phylogenetic relationships between species and establishing new species in the genus. Species demarcation criteria for this genus currently include i) the extent of the serological relationship as determined by immunodiffusion and/or ELISA; ii) less than 75% amino acid sequence identity for the polyprotein; iii) natural host range; and iv) experimental host range symptom reactions.  Tomato fruit blotch virus  The putatively complete genome of a virus with similarity to current blunerviruses was uploaded to GenBank in May 2020 (MK517477-80). This virus, originally designated tomato blunervirus 1 in the GenBank accession, was isolated from tomato (*Solanum lycopersicum* L.) in Italy and its genome sequenced by HTS (Illumina). The genome is quadripartite, with RNA1 (5790 nt excluding the polyA tail) encoding a single ORF containing methyltransferase and helicase domains. RNA2 (3621 nt excluding the polyA tail) encodes a single ORF with helicase and RdRp domains. RNA3 (2842 nt excluding the polyA tail) encodes four ORFs, including the putative virion protein (p24). A fifth ORF may also be present, largely overlapping the 3’-terminal ORF in a different reading frame. RNA4 (1924 nt excluding the polyA tail) encodes two ORFs, with the 3’-terminal ORF encoding the putative movement protein. This genome organization is consistent with that of other blunerviruses, and phylogenetic analysis using the RdRp amino acid sequence places this virus in the blunervirus clade, most closely to tea plant necrotic ring blotch virus (Figure 1).  Pairwise global alignment (without end gap penalty) of the concatenated polyprotein sequences of RNA1 and RNA2 revealed tomato fruit blotch virus had amino acid identities of 26.5% and 33.1% with blueberry necrotic ring blotch virus and tea plant necrotic ring blotch virus, respectively.  Tomato fruit blotch virus was also independently identified by HTS in tomato grown in Australia (GenBank MT434819-22) with genome segments >96% identical to the Italian isolate.  Considering the phylogenetic placement of tomato fruit blotch virus within the blunervirus clade, the consistency of its genome organization with members of the genus *Blunervirus*, its limited (<75%) amino acid identity with these members, and its distinct host range, we propose that tomato fruit blotch virus represents a new species in the genus *Blunervirus*. | |

**Supporting evidence**

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**Figure 1.** Phylogenetic placement of tomato fruit blotch virus with members of the *Blunervirus*, *Higrevirus*, and *Cilevirus* genera, which comprise the family *Kitaviridae*. The RNA-dependent RNA polymerase domain (RNA2) was used in a Neighbor-Joining algorithm to predict this placement. Node numbers indicate branch support following 1000 bootstrap replications. The scale bar represents the number of substitutions for the given branch length. The RdRp of *Tobacco mosaic virus* (genus *Tobamovirus*, family *Virgaviridae*) was used as an outgroup.

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**Figure 2.** Genome organization tomato fruit blotch virus compared to those of *Blueberry necrotic ring blotch virus* (genus *Blunervirus* type species) and *Tea plant necrotic ring blotch virus* (genus *Blunervirus*). Boxes represent open reading frames, and those with similar fill color are orthologs. Boxes with a dashed perimeter are author-predicted open reading frames in the Genbank accession of tomato fruit blotch virus. Boxes are labelled with either the predicted molecular weight (kDa) of the protein product, or its predicted function. MTR, methyltransferase; C-PRO, cysteine-like protease; HEL, helicase; RdRp, RNA-dependent RNA polymerase; MP, movement protein.

**References**

1. Ciuffo M, Forgia M, Chiapello M, Peracchio C, Turina M (2019) A new blunervirus species from tomato. Direct submission to GenBank (NCBI:txid2607480) on Feb 2019.
2. Ciuffo M, Kinoti W, Tiberini A, Forgia M, Tomassoli L, Constable F, Turina M (2020) A new blunervirus infects tomato crops in Italy and Australia. Arch Virol PMID: 32761427 DOI: 10.1007/s00705-020-04760-x