

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

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| **Code assigned:** | **2021.007P** |  |
| **Short title:** Create two new genera and 23 new species (*Tymovirales*: *Betaflexiviridae*) | | |
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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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| ICTV *Beta*-, *Delta*- and *Gammaflexiviridae* Study Group |

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

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**Submission dates**

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| Date first submitted to SC Chair | May 21, 2021 |
| Date of this revision (if different to above) |  |

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

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

**Name of accompanying Excel module**

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| 2021.007P.A.v1.Betaflexiviridae\_2ng\_23nsp.xlsx |

**Abstract**

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| We propose the establishment of two new monospecific genera (*Banmivirus*, *Sustrivirus*) to classify two previously unassigned *Betaflexiviridae* species, and creation of 20 novel species in the family *Betaflexiviridae* (8 new species in genus *Carlavirus*, 2 in genus *Foveavirus*, 1 in genus *Capillovirus*, 1 in genus *Prunevirus*, 3 in genus *Tepovirus*, 3 in genus *Trichovirus* and 2 in genus *Vitivirus*). |

**Text of proposal**

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| |  | | --- | | The family *Betaflexiviridae* currently includes two subfamilies, *Trivirinae* and *Quinvirinae*. The *Trivirinae* contains 10 genera, the *Quinvirinae* contains 3 genera as well as 3 species, *Banana mild mosaic virus* (BanMMV), *Sugarcane striate mosaic-associated virus* (SCSMaV) and *Banana virus X* (BVX) currently unassigned to any of the three recognized genera. With the exception of *Citrivirus, Ravavirus* and *Wamavirus* which are currently monospecific, all other *Betaflexiviridae* genera already contain multiple species which are differentiated on the basis of multiple criteria, including sequence-based ones. The currently approved species demarcation criteria based on sequence identity for the family are <72% nucleotide identity, or <80% amino acid identity in the replication-associated (REP) or capsid (CP) proteins, of the member viruses.  Here, we propose (1) to create two new *Quinvirinae* genera to accomodate two well-characterized and previously unassigned species *Banana mild mosaic virus* (*Banmivirus*) [6] and *Sugarcane striate mosaic-associated virus* (*Sustrivirus*) [18] and (2) to expand the betaflexivirid taxonomy by creation of new species for recently discovered novel viruses [1-5, 7-17, 19-21]. In performing its analyses the SG considered only novel recently described viruses for which a publication provided solid evidence that at least the sequence corresponding to the full coding capacity of the genome was available.  Application of the current sequence-based criteria results in the expansion of the currently accepted species by a total of 20 species allocated to the following genera: *Carlavirus* (8), *Foveavirus* (2), *Capillovirus* (1), *Prunevirus* (1), *Tepovirus* (3), *Trichovirus* (3) and *Vitivirus* (2).  **Etymology**   1. After extensive debate about possible options for the new binomial nomenclature, the SG voted and decided to adopt “Genus + Acronym” format for species names in the family *Betaflexiviridae* (Note: the acronym being derived from the virus common name). 2. Genus name *Banmivirus* is derived from a contraction of the name of its only member virus, Banana mild mosaic virus. 3. Genus name *Sustrivirus* is derived from a contraction of the name of its only member virus, Sugarcane striate mosaic-associated virus.   **Supporting evidence**    Figure 1. The maximum-likelihood phylogenetic tree was inferred using Mega 7 and a multiple alignment of replication-associated proteins (REP) prepared using Muscle. Bootstrap values >70% are shown. Tree branches are proportional to genetic distances between sequences, and the scale bars at the bottom indicats substitutions per amino acid. Accession numbers are shown next to the respective virus taxon. The two species for which monospecific genera are created are indicated by a blue diamond while novel species are indicated by a red diamond.  **References**   1. Alabi OJ, Appel DN, McBride S, Al Rwahnih M, Pontasch FM (2020) Complete genome sequence analysis of a genetic variant of grapevine virus L from the grapevine cultivar Blanc du Bois. Arch Virol 165:1905-1909. PMID: 32472290. DOI: 10.1007/s00705-020-04682-8 2. Artemis Rumbou A, Candresse T, Marais A, Svanella-Dumas L, Landgraf M, von Bargen S, Büttner C (2020) Unravelling the virome in birch: RNA-Seq reveals a complex of known and novel viruses. PLoS ONE 15: e0221834 PMID: **32589631.** DOI: [10.1371/journal.pone.0221834](https://doi.org/10.1371/journal.pone.0221834) 3. Brewer E, Cao M, Gutierrez B, Bateman M, Li R (2020) Discovery and molecular characterization of a novel trichovirus infecting sweet cherry. Virus Genes 56:380-385. 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