

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

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| **Code assigned:** | **2023.028P** |  |
| **Short title:** Create 13 new species (*Tymovirales*: *Betaflexiviridae*) |
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**Author(s) and email address(es)**

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

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**Corresponding author**

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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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**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members 11** |
| **Votes support** | **Votes against** | **No vote** |
| *Beta-, Delta-, Gammaflexiviridae* | 11 |  |  |
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**Authority to use the name of a living person**

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| **Is any taxon name used here derived from that of a living person (Y/N)** | NO |

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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 | June 26, 2023 |
| 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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| 2023.028P.A.v1.Betaflexiviridae\_13nsp |

**Abstract**

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| We propose the creation of 13 novel species in extant genera in the family *Betaflexiviridae* (7 new species in genus *Carlavirus*, 1 in genus *Foveavirus*, 2 in genus *Capillovirus*, 1 in genus *Citrivirus*, 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, while the *Quinvirinae* contains 5 genera. With the exception of *Citrivirus*, *Ravavirus*, *Sustrivirus* 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 to expand the family *Betaflexiviridae* by creation of new species for recently discovered novel viruses [1-8]. In performing its analyses the SG considered only novel recently described viruses for which publications provided solid evidence that the sequence corresponding to the full coding capacity of the genome was at least available.Application of the current sequence-based criteria results in the expansion of the currently accepted species by a total of 13 species allocated to the following genera: *Carlavirus* (7), *Foveavirus* (1), *Capillovirus* (2), *Citrivirus* (1), and *Vitivirus* (2).**Etymology**1. After extensive debate about possible options for the new binomial nomenclature, the SG voted and decided to change it previous decision and adopt “Genus + latinized binomial” format for species names in the family *Betaflexiviridae*.
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**Supporting evidence**

**Figure 1**. The maximum-likelihood phylogenetic tree was inferred using FastTree 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 bar at the bottom indicates substitutions per amino acid. Accession numbers are shown next to the respective virus taxon. Novel species proposed in extant genera are indicated by a black diamond.

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**References**

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