

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

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| **Code assigned:** | **2022.001P** |  |
| **Short title:** Create 12 new species (*Tymovirales*: *Betaflexiviridae*) |
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**Author(s) and email address(es)**

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| --- | --- |
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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 | 0 | 0 |

**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 | May 16, 2022 |
| Date of this revision (if different to above) | May 26, 2022 |

**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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| 2022.001P.A.v2.Betaflexiviridae\_12ns.xlsx |

**Abstract**

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| We propose the creation of 12 novel species in extant genera in the family *Betaflexiviridae* (6 new species in genus *Carlavirus*, 2 in genus *Foveavirus*, 1 in genus *Capillovirus*, 2 in genus *Chordovirus*, 1 in genus *Banmivirus*). |

**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, Banmivirus, 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 [1-10]. 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 12 species allocated to the following genera: *Carlavirus* (6), *Foveavirus* (2), *Chordovirus* (2), *Capillovirus* (1), *Banmivirus* (1).**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).
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**Supporting evidence**

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**Figure 1**. The maximum-likelihood phylogenetic tree was inferred using Mega 11 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 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 red diamond.

**References**

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