

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

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| **Code assigned:** | **2021.007F** |  |
| **Short title:** Create two new genera and three new species (*Tymovirales*: *Gammaflexiviridae*) | | |
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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, Fungal and Protist Viruses SC Chair |

**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) | September 14, 2021 |

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

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| **EC comments:** Please address minor changes in the text as proposed by one of the reviewers.  **Response:** Done |

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

**Name of accompanying Excel module**

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| 2021.007F.R.Gammaflexiviridae\_2ngen\_3nsp.xlsx |

**Abstract**

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| We propose creation of two new genera (*Gammaflexivirus*, *Xylavirus*) to classify three novel species in the family *Gammaflexiviridae*. |

**Text of proposal**

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| |  | | --- | | The relatively recently established family *Gammaflexiviridae* currently includes the single genus *Mycoflexivirus*, which contains a single species, *Botrytis virus F*. As a consequence, species demarcation criteria in the genus would include typical parameters such as host range and genome organization but sequence-based criteria have yet to be defined. It is however possible, as a first step to consider the demarcation criteria established in the related *Alpha*- and *Betaflexiviridae* families which currently stand at <72% nucleotide identity or <80% amino acid identity in the replication-associated protein (REP) of member viruses.  Here, we propose to create two new *Gammaflexiviridae* genera:   * Genus *Gammaflexivirus* to accommodate the recently described Entoleuca gammaflexivirus 1 (species *Gammaflexivirus EntGFV-1*) and Pistacia-associated flexivirus 1 (species *Gammaflexivirus PaGFV-1*) which share the same genome organization and have phylogenetically related REP proteins. * Genus *Xylavirus* to accommodate the recently described Entoleuca gammaflexivirus 2 by creating a new species *Xylavirus EntGFV-2*.   **Etymology**   1. After extensive debate about possible options to move to the new binomial nomenclature, the SG voted and decided by a majority vote (7-4) on a general format for species in the *Betaflexiviridae* family in which the "freeform epithet" accompanying the genus name will be the acronym derived from the virus common name. 2. Genus name *Gammaflexivirus* is derived from the name of the *Gammaflexiviridae* family. 3. Genus name *Xylavirus* is derived from *Xylariaceae* family of fungi that includes *Entoleuca* sp., host of the first member of this genus.   **Supporting evidence**  **Genome organization**    **Figure 1**. Figure from Park et al. (2020) showing the genome organization of Botrytis virus F (Genus *Mycoflexivirus*, family *Gammaflexiviridae*) and of proposed *Gammaflexivirus* members Entoleuca gammaflexivirus 1 (EnGFV1) and pistacia-associated flexivirus 1 (PAFV1) and of proposed *Xylavirus* member Entoleuca gammaflexivirus 2 (EnGFV2).  The 3 proteins of EnGFV1 and PAFV1 share ~38% (REP), ~40% (putative movement protein, MP) and ~37% (hypothetical protein, HP) sequence identity. The REPs of these viruses show only ~20% identity with that of BVF.  The REPs of of EnGFV2 and BVF exhibit only ~24% identity and the ribosomal readthrough strategy to express the RdRP domain of the REP protein is not adopted by EnGFV2 unlike BVF. The products of two additional ORFs of EnGFV2 have no detectable sequence similarity to the proteins encoded by BVF, EnGFV1 or PAFV1.    Figure 2. REP-based phylogenetic tree. The maximum-likelihood phylogenetic tree was inferred using Mega 7 on a multiple alignment prepared with Muscle. Distances were estimated using the LG+G+I substitution model determined as a best-fit for a given dataset. Robustness of branches was estimated by bootstrap analysis and only values >60% are shown. The GenBank accession numbers for all REP proteins used in analyses are shown, together with the virus name on branch tips. The REP of a single representative virus was used for each genus in the *Betaflexiviridae* family, while all 3 recognized members were used for the *Deltaflexiviridae* family. The position of REPs of the 3 newly proposed *Gammaflexiviridae* species are marked by red diamonds.  **References**   1. Velasco, L., Arjona-Girona, I., Cretazzo, E. & Lopez-Herrera, C., 2019. Viromes in Xylariaceae fungi infecting avocado in Spain. Virology 532, 11-21. PMID: **30986551** DOI: [10.1016/j.virol.2019.03.021](https://doi.org/10.1016/j.virol.2019.03.021) 2. Park, D., Goh, C.J., Lee, J.S., Sebastiani, F. & Hahn, Y., 2020. Identification of Pistacia-associated flexivirus 1, a putative mycovirus of the family Gammaflexiviridae, in the mastic tree (*Pistacia lentiscus*) transcriptome. Acta virologica 64,28-35. PMID: 32180416 DOI: [10.4149/av\_2020\_104](https://doi.org/10.4149/av_2020_104) 3. Pearson, M.N., Bailey, A.M., 2013. Viruses of *Botrytis*. Adv Virus Res., 86, 249-272. PMID: **23498909** DOI: [10.1016/B978-0-12-394315-6.00009-X](https://doi.org/10.1016/b978-0-12-394315-6.00009-x) | |