

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

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| **Code assigned:** | ***2023.013F*** |  |
| **Short title:** Rename existing species and create 1 new species (*Tymovirales*: *Deltaflexiviridae*) |
|  |

**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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| Candresse T |

**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* | 10 | 0 | 1 |
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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)** | N |

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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 | 20/6/2023 |
| 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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| 2023.013F.v2.Deltaflexiviridae\_1nsp\_spren.xlsx |

**Abstract**

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| We propose the creation of one novel species in the genus *Deltaflexivirus*, family *Deltaflexiviridae* to classify a recently characterized virus from *Pleurotus ostreatus.* In addition, we adopt Latinized binomial nomenclature for all species in the family.  |

**Text of proposal**

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| The family *Deltaflexiviridae* currently includes a single genus, *Deltaflexivirus,* which contains three species. Species demarcation criteria in the genus 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 expand the family *Deltaflexiviridae* by creation of new species to classify a recently discovered novel virus [1]. 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.In addition, after extensive debate about possible options for the new binomial nomenclature, the SG voted and decided to change previous decision and adopt “Genus + latinized binomial” format for species names in the family *Deltaflexiviridae.* Accordingly, with this proposal we also rename the three previously recognized species, so that overall nomenclature in the family complies with recently adopted ICTV standards.  |

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**References**

1. Xiao J, Wang X, Zheng Z, Wu Y, Wang Z, Li H, Li P (2023) Molecular characterization of a novel deltaflexivirus infecting the edible fungus *Pleurotus ostreatus*. Arch Virol 168(6):162. <https://doi.org/10.1007/s00705-023-05789-4>

**Supporting evidence**

**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. A *Betaflexiviridae* representative member and all *Gammaflexiviridae* members were included for reference. The proposed novel species is indicated by a black diamond.

