

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

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| **Code assigned:** | ***2023.053B*** |  |
| **Short title:** Create five (5) new species in the genus *Przondovirus* (*Caudoviricetes*) | | |
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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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| *Caudoviricetes* Study Group |

**ICTV Study Group comments and response of proposer**

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| No comments |

**ICTV Study Group votes on proposal**

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| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
|  |  |  |  |
|  |  |  |  |

**Authority to use the name of a living person**

|  |  |
| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

|  |  |  |
| --- | --- | --- |
| **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 2023 |
| Date of this revision (if different to above) |  |

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

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2023.053B.N.v1.Przondovirus\_5ns.xlsx |

**Abstract**

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| There are currently 29 species within the *Przondovirus* genus. With this proposal we add another ten przondoviruses, assigned to five new species. The average genome sizes for members of this taxon are: 41.103 kb (52.64 mol%G+C) encoding for 55 proteins. |

**Text of proposal**

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| --- | --- |
| |  | | --- | | **Demarcation criteria**  **Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.  These values were calculated using intergenomic distance calculator VIRIDIC (1).  **Genus demarcation criteria:** In search for criteria that create cohesive and distinct genera that are reproducible and monophyletic, the Bacterial Viruses Subcommittee has established 70% nucleotide identity of the genome length as the cut-off for genera. Genus-level groupings should always be monophyletic in the signature genes, as tested with a phylogenetic tree (2).  **Five new species in the genus *Przondovirus***  Comparison of the genomes of 10 new phages (Table 1) with reference phages from GenBank (3) showed high levels of sequence similarity with phages from the genus *Przondovirus* in the subfamily *Studiervirinae*, family *Autographiviridae*. The assignment to the genus *Przondovirus* was confirmed using nucleotide similarity with existing members of the genus at over 70% nucleotide similarity (Fig. 1) and phylogenetic analysis of the hallmark RNA polymerase gene showing robust clustering (Fig. 2).  Using the demarcation criteria for at the species level, six phages (Oda, Toyotomi, Mera, Speegle, Cornelius, and Tokugawa) were assigned to the new species *Przondovirus oda*, while phages Emom, Amrap, Saitama and Whistle each were the sole representatives of four new species (Table 1). | |

**Supporting evidence**

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**A close-up of a barcode

Description automatically generated with low confidence**

**Fig. 1. Nucleotide-based intergenomic similarities of przondoviruses in the collection and a selection of related phages within the *Studiervirinae* subfamily, using VIRIDIC.** A heatmap of hierarchical clustering of the intergenomic similarity values was generated and given as percentage values (right half, blue-green heatmap). Each genome pair is represented by three values (left half), where the top and bottom (blue scale) represent the aligned genome fraction for the genome in the row and column, respectively, where darker colour indicates a lower fraction of the genome was aligned. The middle value (grey scale) represents the genome length ratio for each genome pair, where darker colour indicates increasing distance between phages. The new przondovirus isolates are highlighted in blue-grey.

**A screenshot of a computer

Description automatically generated with medium confidence**

**Fig. 2. Maximum-likelihood phylogeny of the RNA polymerase for przondoviruses in this study and a selection of related *Studiervirinae* phages.** All phages for this proposal (purple highlight) clustered with related przondoviruses (purple). Outgroups, *Berlinvirus* (orange), *Apidecimavirus* (yellow), *Teseptimavirus* (green), and *Teetrevirus* (blue). Tree is midpoint rooted. Bootstrap support values at ≥0.7 are given in blue (500 replicates). Scale bar represents number of amino acid substitutions per site.

**Table 1.** New przondoviruses

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage Name | Genome size (bp) | GC content (%) | No. CDS | Accession | Species |
| Klebsiella phage Oda | 41,642 | 52.64 | 58 | OQ579023 | *Przondovirus oda* |
| Klebsiella phage Toyotomi | 41,268 | 52.64 | 55 | OQ579024 | *Przondovirus oda* |
| Klebsiella phage Mera | 41,400 | 52.58 | 56 | OQ579025 | *Przondovirus oda* |
| Klebsiella phage Speegle | 41,395 | 52.64 | 58 | OQ579026 | *Przondovirus oda* |
| Klebsiella phage Cornelius | 40,437 | 52.72 | 55 | OQ579027 | *Przondovirus oda* |
| Klebsiella phage Tokugawa | 41,414 | 52.64 | 56 | OQ579028 | *Przondovirus oda* |
| Klebsiella phage Saitama | 40,741 | 53.06 | 51 | OQ579029 | *Przondovirus saitama* |
| Klebsiella phage Emom | 40,788 | 52.56 | 53 | OQ579030 | *Przondovirus emom* |
| Klebsiella phage Amrap | 41,209 | 52.47 | 57 | OQ579031 | *Przondovirus amrap* |
| Klebsiella phage Whistle | 40,735 | 52.40 | 54 | OQ579032 | *Przondovirus whistle* |

**References**

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