

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

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| **Code assigned:** | **2023.070B** |  |
| **Short title:** Create one (1) genus and eight (8) new species in the family *Inoviridae* (*Tubulavirales*) | | |
|  | | |

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**List the ICTV Study Group(s) that have seen this proposal**

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| Bacterial Viruses Subcommittee, *Tubulavirales* Study Group |

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

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**ICTV Study Group votes on proposal**

|  |  |  |  |
| --- | --- | --- | --- |
| **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)** |  |

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
|  |  |  |
|  |  |  |
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**Submission dates**

|  |  |
| --- | --- |
| 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**

|  |
| --- |
| 2023.070B.N.v1.Inoviridae\_8ns\_1ng.xlsx |

**Abstract**

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| We propose eight (8) new species within existing genera of the family *Inoviridae* and one (1) new genus *Anademivirus* with one (1) new species. |

**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | | The aim of the proposal is:   1. **To create new genus *Anademivirus* and species *Anademivirus* AFP**   The bacteriophage Alteromonas phage phiAFP1 belongs to family *Inoviridae*, and shows a distinct genome sequence in comparison to other known phages (<1.5% similarity) (Table 1). It shows negligible similarity of genome sequence of Enterobacteria phage If1, indicating a new species. The amino-acid sequence of Zot and CoaB are distinct from other bacteriophages (< 37.7% similarity; Figure 1A and 1B), indicating a new genus. We create a new genus *Anademivirus* (from lat. anadema, anadematis – band for the hair, head-band). The only species in the genus is *Anademivirus AFP1*. Its host is *Alteromonas macleodii* and the phage was isolated from South China Sea.   1. **To create two new species *Villovirus V5 and Villovirus FR***   Two strains infecting *Vibrio parachaemolyticus:*  [Vibrio phage V5](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_WAB24948) detected in shrimp pond water (India) and [Vibrio phage vB\_VpI\_FR1](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_WAB24948) isolated from the Bohai bay in TangShan, China show significant similarity with other members of the genus *Villovirus.* The new species *Villovirus V5* and *Villovirus FR* differ from other members of the genus, as genome sequences share 36.6-73.5% similarity. Their Zot and CoaB protein amino-acid sequences are similar to other members of genus *Villovirus* (80.5-100%) and significant number of proteins are homologous (supporting evidence Table 2; Fig. 2).   1. **To create 6 new species *Versovirus VipaK, Versovirus Vipa4291, Versovirus Vipa26, Versovirus Vipa36, Versovirus Vipa10 and Versovirus Vipa71***   They share characteristics with the members of the genus *Versovirus*, and genome sequence is similar 70.3-82.0%, indicating new species (Table 3). There is a significant similarity of Zot and CoaB protein amino-acid sequences (97.5-99.8%) and significant number of proteins are homologous (supporting evidence Table 3, Fig. 2).  Descriptions of the families *Inoviridae* and *Plectroviridae*, as well as demarcation criteria are described in the ICTV Report chapters and profiles [1, 2] (ictv.global/report/plectroviridae; ictv.global/report/inoviridae).  **Species demarcation:** „Phages of the same species share >95% DNA sequence similarity (identity × query coverage) and significant amino-acid sequence similarity of the adhesion protein (CoaA).“  **Genus demarcation:** “For genus demarcation, beside considerable similarity of DNA sequences confirmed by BLASTn, the phage should have significant similarity of both Zot and Coat B (major capsid) proteins. Each of the proposed genera comprise phages with similar DNA sequences; phages in different genera differ from each other by >50% in the amino-acid sequence of the major coat (CoaB; p8) and morphogenesis (Zot; p1) proteins as assessed using the BLASTp algorithm.” | |

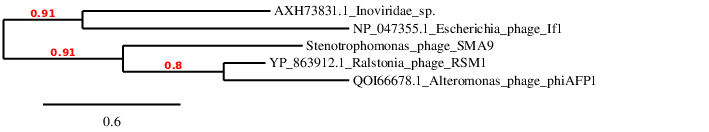
**Supporting evidence**

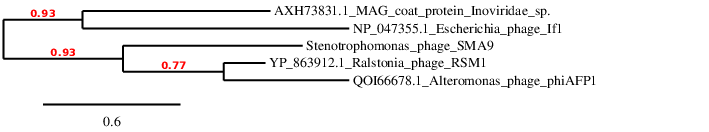
**Table 1.** New species (strain is in bold) and the new genus *Anademivirus* (members of the genus are highlighted in orange)

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | GenBank Access. No. | Genome lenght (nt) | Mol% G+C | No. CDS | DNA (% seq. Identity) | Proteome (No. of homologous proteins) | Zot | CoaB |
| Alteromonas phage phiAFP1 | [MT975991.1](https://www.ncbi.nlm.nih.gov/nuccore/MT975991.1) | 5859 | 40.6 | 8 | 100 | 8 | 100 | 100 |
| Inoviridae sp. Isolate ctbf525 | [MH616815.1](https://www.ncbi.nlm.nih.gov/nucleotide/MH616815.1?report=genbank&log$=nucltop&blast_rank=3&RID=77ZJD046013) | 5715 | 50.8 | 9 | 1.5 | 1 | 0 | 0 |
| Enterobacteria phage If1 | [NC\_001954](https://www.ncbi.nlm.nih.gov/nuccore/9630747) | 8454 | 43.7 | 10 | 1.0 | 1 | 0 | 0 |
| Ralstonia phage RSM1 | [NC\_008574](https://www.ncbi.nlm.nih.gov/nuccore/565323596) | 9004 | 60.0 | 15 | 0 | 4 | 33.7 | 33.7 |
| Stenotrophomonas phage SMA9 | [NC\_007189](https://www.ncbi.nlm.nih.gov/nuccore/70727678) | 6907 | 62.4 | 7 | 0 | 3 | 27.4 | 0 |

**Figure 1.** “One click” phylogeny tree [3] of *Inoviridae*, based on amino-acid sequences of morphogenesis protein (A) and coat protein (B); the new species and genus is indicated by orange color

**A)**





**B)**

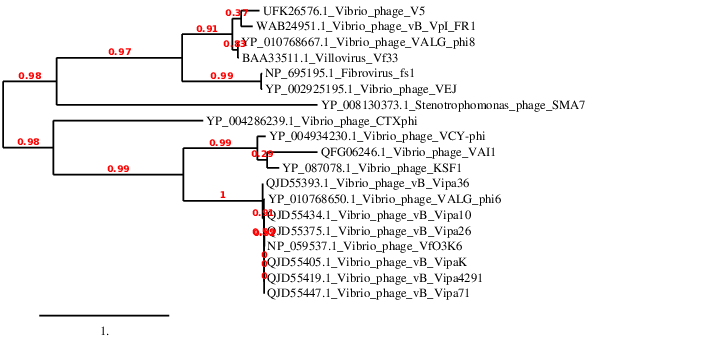
**Table 2.** New species (in bold) in the genus *Villovirus* (members of the genus are highlighted in green)

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | GenBank Access. No. | Genome lenght (nt) | Mol%G+C | No. CDS | DNA (% seq. Identiti) | Proteome (No. of homologous proteins) | Zot | CoaB |
| **Vibrio phage V5** | [OL512807.1](https://www.ncbi.nlm.nih.gov/nuccore/OL512807.1) | 6658 | 43.7 | 10 | 100 | 10 | 100 | 100 |
| [**Vibrio phage vB\_VpI\_FR1**](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_WAB24948) | [OP628074.1](https://www.ncbi.nlm.nih.gov/nuccore/OP628074.1) | 6080 | 42.9 | 9 | 73.5 | 7 | 80.5 | 82.9 |
| Vibrio phage Vf33 | [NC\_005948.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_005948.1) | 7965 | 45.7 | 7 | 36.6 | 6 | 77.1 | 74.0 |
| Vibrio phage VALG phi8 | [NC\_073760.1](https://www.ncbi.nlm.nih.gov/nucleotide/NC_073760.1?report=genbank&log$=nucltop&blast_rank=6&RID=777C414D013) | 7311 | 46.3 | 10 | 36.6 | 6 | 77.1 | 71.4 |
| *Fibrovirus fs1* | [NC\_004306](https://www.ncbi.nlm.nih.gov/nuccore/23455823) | 6340 | 43.4 | 15 | 0 | 6 | 45.9 | 63.2 |
| Vibrio phage VEJ | [NC\_012757](https://www.ncbi.nlm.nih.gov/nuccore/238821372) | 6842 | 43.0 | 11 | 0 | 6 | 45.6 | 63.2 |
| *Vasivirus VAI* | [NC\_073758.1](https://www.ncbi.nlm.nih.gov/nucleotide/NC_073758.1?report=genbank&log$=nucltop&blast_rank=11&RID=7PFX4U8G016) | 6117 | 42.5 | 10 | 20.1 | 2 | 11.5 | 9.5 |
| *Affertcholeramvirus CTXphi* | [NC\_015209.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_015209.1) | 10638 | 44.6 | 13 | 16.6 | 4 | 19.4 | 0 |
| *Subteminivirus SMA7* | [NC\_021569](https://www.ncbi.nlm.nih.gov/nuccore/514361131) | 7069 | 62.3 | 10 | 0 | 3 | 20.0 | 0 |

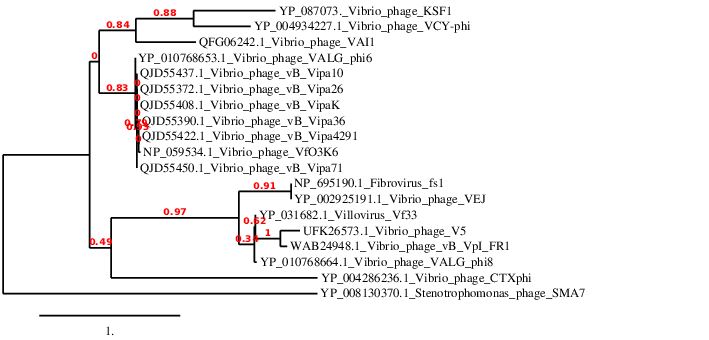
**Table 3.** New species (strains in bold) in the genus *Versovirus* (members of the genus are highlighted in violet)

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | GenBank Access. No. | Genome lenght (nt) | Mol%G+C | No. CDS | DNA (% seq. Identiti) | Proteome (No. of homologous proteins) | Zot | CoaB |
| [**Vibrio phage vB\_VipaK**](https://www.ncbi.nlm.nih.gov/genome/107228) | [MT188664.1](https://www.ncbi.nlm.nih.gov/nuccore/MT188664.1) | 10809 | 44.0 | 15 | 100 | 15 | 100 | 100 |
| [**Vibrio phage vB\_Vipa4291**](https://www.ncbi.nlm.nih.gov/genome/107227) | [MT188665.1](https://www.ncbi.nlm.nih.gov/nuccore/MT188665.1) | 9663 | 45.0 | 15 | 81.0 | 12 | 100 | 99.8 |
| [**Vibrio phage vB\_Vipa36**](https://www.ncbi.nlm.nih.gov/genome/107226) | [MT188663.1](https://www.ncbi.nlm.nih.gov/nuccore/MT188663.1) | 9721 | 44.7 | 15 | 78.0 | 11 | 98.8 | 99.8 |
| [**Vibrio phage vB\_Vipa26**](https://www.ncbi.nlm.nih.gov/genome/107226) | [MT188662.1](https://www.ncbi.nlm.nih.gov/nuccore/MT188662.1) | 10893 | 44.7 | 18 | 70.3 | 11 | 99.8 | 100 |
| [**Vibrio phage vB\_Vipa10**](https://www.ncbi.nlm.nih.gov/genome/107224) | [MT188666.1](https://www.ncbi.nlm.nih.gov/nuccore/MT188666.1) | 9318 | 45.0 | 14 | 82.0 | 11 | 99.8 | 100 |
| [**Vibrio phage vB\_Vipa71**](https://www.ncbi.nlm.nih.gov/genome/103313) | [MT193890.1](https://www.ncbi.nlm.nih.gov/nuccore/MT193890.1) | 10295 | 44.5 | 13 | 72.2 | 11 | 100 | 100 |
| Vibrio phage VfO3K6 | [NC\_002362.1](https://www.ncbi.nlm.nih.gov/nucleotide/NC_002362.1?report=genbank&log$=nucltop&blast_rank=5&RID=77EBVDET013) | 8784 | 45.2 | 10 | 73.1 | 8 | 99.8 | 97.5 |
| Vibrio phage VALG phi6 | [NC\_073759.1](https://www.ncbi.nlm.nih.gov/nucleotide/NC_073759.1?report=genbank&log$=nucltop&blast_rank=9&RID=77EBVDET013) | 8529 | 44.3 | 13 | 74.5 | 10 | 99.6 | 98.8 |
| *Villovirus Vf33* | [AB012573.1](https://www.ncbi.nlm.nih.gov/nucleotide/AB012573.1?report=genbank&log$=nucltop&blast_rank=17&RID=77EBVDET013) | 7965 | 45.7 | 7 | 36.8 | 3 | 9.8 | 0 |
| *Vicialiavirus VCY* | [NC\_016162](https://www.ncbi.nlm.nih.gov/nuccore/358356470) | 7103 | 41.4 | 11 | 0.8 | 6 | 68.6 | 28.7 |
| *Capistrivirus KSF1* | [NC\_006294](https://www.ncbi.nlm.nih.gov/nuccore/52221121) | 7107 | 44.4 | 12 | 0 | 5 | 40.6 | 19.9 |

**Figure 2.** “One click” phylogeny tree [3] of *Inoviridae*, based on amino-acid sequences of morphogenesis protein (A) and coat protein (B); the new species in genera *Villovirus* and *Versovirus* are indicated by green and violet color, respectively.



**A)**



**B)**

**References**

1. Knezevic P, Adriaenssens EM, ICTV Report Consortium (2021) ICTV Virus Taxonomy Profile: *Plectroviridae*, J Gen Virol https://doi.org/10.1099/jgv.0.001597
2. Knezevic P, Adriaenssens EM, ICTV Report Consortium (2021) ICTV Virus Taxonomy Profile: *Inoviridae*, J Gen Virol *in press*
3. Dereeper A.. Guignon V., Blanc G., Audic S., Buffet S., Chevenet F., Dufayard J.F., Guindon S., Lefort V., Lescot M., Claverie J.M., Gascuel O. (2008). Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res. W465-9. <https://doi.org/10.1186/1756-0500-6-140>
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