

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

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| **Code assigned:** | **2021.085B** |  |
| **Short title:** Create four genera including 16 new species in the family *Inoviridae*, and one new genus including one new species in the family *Plectrovridae* (*Tubulavirales*) | | |
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**Author(s) and email address(es)**

|  |  |
| --- | --- |
| Knezevic P, Adriaenssens EM, Kropinski AM, Lavigne R | [pknezevic20@gmail.com](mailto:pknezevic20@gmail.com)  [Evelien.Adriaenssens@gmail.com](mailto:Evelien.Adriaenssens@gmail.com)  [Phage.Canada@gmail.com](mailto:Phage.Canada@gmail.com);  rob.lavigne@kuleuven.be |

**Author(s) institutional address(es) (optional)**

|  |
| --- |
| University of Novi Sad, Serbia [PK]  Quadram Institute Bioscience, UK [EMA]  University of Guelph, Canada [AMK]  KU Leuven, Belgium [RL] |

**Corresponding author**

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| pknezevic20@gmail.com Petar Knezevic |

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

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| Tubulavirales SG |

**ICTV study group comments and response of proposer**

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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 |

|  |  |  |
| --- | --- | --- |
| **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 2021 |
| 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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| 2021.085B.R.Tubulavirales |

**Abstract**

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| --- |
| We propose twelve (12) new species within existing genera of the family *Inoviridae* and four new genera (*Vasivirus, Lophivirus, Porrectionivirus*, and *Siphunculivirus*) with four new species. Within the family *Plectroviridae* one (1) new genus (*Virgulavirus*) and one (1) new species are proposed. |

**Text of proposal**

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| --- | --- |
| |  | | --- | | The aim of the proposal is:  A) To create new species belonging to the existing genera in family *Inoviridae*:   1. New species *Fibrovirus VP24* in the existing genus *Fibrovirus,* based on sequence of Vibrio phage VP24-2\_Ke   The strain infects *Vibrio cholerae* and was detected in Usenge Beach in Bondo, Siaya county (Kenya). It shares characteristics with the members of the genus *Fibrovirus*: Zot, CoaB and CoaA protein amino-acid sequences are similar >83% and significant number of proteins are homologous (support evidence Table A-1; Fig. 1). The new species *Fibrovirus VP24* differs from other members of the genus, as genome sequences share <91% similarity.   1. New species *Villovirus VALG8* in the existing genus *Villovirus,* based on sequence of Vibrio phage VALG\_phi8   The host is *Vibrio alginolyticus*. The phages share characteristics with the members of the genus *Villovirus*: Zot, CoaB and CoaA protein amino-acid sequences are similar >93% and significant number of proteins are homologous (support evidence Table A-2; Fig. 1). There are additional strains, Vibrio phage K05K4\_VK05K4\_1, K05K4\_VK05K4\_2 and K04M1\_VK0M1 that share >89% similarity to Vibrio phage VALG\_phi8, so they belong to the same species. The new species *Villovirus VALG8* differs from other members of the genus, as genome sequences share <85% similarity.   1. New species *Versovirus VALG6* in the existing genus *Versovirus*   It shares characteristics with the members of the genus *Verosvirus*: Zot, CoaB and CoaA protein amino-acid sequences are similar >91% and significant number of proteins are homologous (support evidence Table A-3, Fig. 1). The new species *Versovirus VALG6* differs from other members of the genus, as genome sequences share <78% (support evidence A-3; Fig. 1).   1. New species *Xylivirus XacF13* in the existing genus *Xylivirus,* based on sequence of Xanthomonas phage XacF13   It shares characteristics with the members of the genus *Xylivirus*: Zot, CoaB and CoaA protein amino-acid sequences are similar >78% and significant number of proteins are homologous (support evidence Table A-4, Fig. 1). The new species *Xylivirus XacF13* differs from other members of the genus, as genome sequences share <53% similarity.   1. New species *Restiviris RSBg* in the existing genus *Restivirus,* based on sequence of Ralstonia phage RSBg   The phage shares characteristics with the members of the genus *Restivirus*: Zot, CoaB and CoaA protein amino-acid sequences are similar >98% and significant number of proteins are homologous (support evidence Table A-5, Fig. 1). The new species differs from other members of the genus, as genome sequences share approx. 81% similarity.   1. New species *Lineavirus PEar* in the existing genus *Lineavirus,* based on sequence of Erwinia phage PEar6.   There are additional strains, Vibrio phage PEar1, PEar2, and Paer4, that share >98% genome similarity to Erwinia phage PEar1, so they belong to the same species. They share characteristics with the members of the genus *Lineavirus*: Zot, CoaB and CoaA protein amino-acid sequences are similar >71% and significant number of proteins are homologous (support evidence Table A-6, Fig. 1). The new species *Lineavirus PEar* differs from other members of the genus, as genome sequences share approx. 56-90% similarity.   1. New species *Primolicivirus Pf8* in the existing genus *Primolicivirus*, based on sequence of Pseudomonas phage pf8\_ST274-AUS411.   The phage infects *Pseudomonas aeruginosa.* It shares characteristics with the members of the genus *Primolicivirus*: Zot, CoaB and CoaA protein amino-acid sequences are similar >68% and significant number of proteins are homologous (support evidence Table A-7, Fig. 1). The new species *Lineavirus PEar* differs from other members of the genus, as genome sequences share approx. 69% similarity.   1. New species *Affertcholeramvirus preCTX1* ([KP972568.1](https://www.ncbi.nlm.nih.gov/nucleotide/KP972568.1?report=genbank&log$=nucltop&blast_rank=43&RID=93X4B3GA013)) and *Affertcholeramvirus preCTX2* ([KT728930.1](https://www.ncbi.nlm.nih.gov/nucleotide/KT728930.1?report=genbank&log$=nucltop&blast_rank=14&RID=93X4B3GA013)) in the existing genus *Affertcholeramvirus.*   They infect *V. cholerae* andshare characteristics with the members of the genus *Affertcholeramvirus*: Zot, CoaB and CoaA protein amino-acid sequences are similar >95% and significant number of proteins are homologous (support evidence Table A-8, Fig. 1). The two new species are similar less than 61% anddiffers from other members of the genus (approx. 50%) when sequence of their genomes are compared.  B) to create new species and new genera in family *Inoviridae*:   1. New genus *Vasivirus* (lat. vas, vasis – vase)   The genus comprises one new species *Vasivirus VAI*, with strains Vibrio phage VAI1 and Vibrio phage VAI2. The new species differs from other related phages, as genome sequences share <25% similarity. The CoaB and CoaA protein amino-acid sequences differ from other genera by >50% and there is a significant difference in number of homologous proteins (Table B-1, Fig. 1). The phage infects *V. anguillarum* and can integrate into several sites into host chromosome [6].   1. New genus *Lophivirus* (lat. lophos, lophi –crest)   Each strain, Xanthomonas phage phiXv2, Xanthomonas phage phiLfUK, Xanthomonas phage phiLf2 and Xanthomonas phage Cf2 represent a new species *Lophivirus Xv2, Lophivirus LfUK, Lophivirus Lf2* and *Lophivirus Cf2*, respectively, since differ in their nucleotide sequence for approx. 40-60% (Table B-2, Fig. 1). Their Zot, CoaB and CoaA protein amino-acid sequences show negligible similarity to members of other genera and there is a significant difference in number of homologous proteins.   1. New genus *Porrectionivirus* (lat. porrectio, porrectionis - straight line)   New species *Porrectionivirus p12J* show some similarities to Vibrio phage PE226 in the amino-acid sequence of Zot protein, but there is a difference in CoaB and Coa A, as well as in DNA sequence (Table B-3, Fig. 1). Thus, species belongs to a new genus. The new species *Porrectionivirus p12J* represent a new species, as its genome differs from other related phage genomes >66%.   1. New genus *Siphunculivirus* (lat. siphunculus, siphunculi - small tube)   The only member, a new species *Siphunculivirus SPH2* infects *Stenotrophomonas maltophilia,* and its genome sequence show less than 43% similarity when compared to other phages. The Zot, CoaB and CoaA show less than 38% similarity and there is a significant difference in number of homologous proteins (Table B-4, Fig. 1).  C) to create new species and new genera in family *Plectroviridae*   1. New genus *Virgulavirus* (virgula, virgulae - small rod)   The genus comprises one new species *Virgulavirus SVGII3,* whose genome is <35% similar to genome of other *Plectroviridae* members (Table C-1, Fig. 2). The core genes and phylogenetic tree based on genome sequences clearly indicate a new genus within family *Plectroviridae*.  Descriptions of the families *Inoviridae* and *Plectroviridae*, as well as demarcation criteria are described in the ICTV Report chapters and profiles [9,10] (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**

**A)** New species of existing genera in family *Inoviridae;* analysis was performed using BLASTN and BLASTP algorithms; for homologous proteins determination CoreGenes5.0 was used [8].

**A-1.** New species (abbreviation in bold and italics) in the genus *Fibrovirus*

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | GenBank Access. No. | Genome lenght (nt) | Mol%G+C | No. CDS | DNA (% seq. Identiti) | Proteome (No. of homologous proteins) | Zot | CoaB | CoaA |
| ***VP24-2\_Ke*** | MN536023.1 | 7180 | 42.5 | 13 | 100 | 13 | 100 | 100 | 100 |
| fs1 | D89074.1 | 6340 | 43.4 | 15 | 90.1 | 8 | 96.4 | 90.9 | 86.5 |
| VGJ | AY242528.1 | 7543 | 43.4 | 13 | 78.4 | 11 | 83.3 | 88.6 | 97.8 |
| KSF1 | AY714348.1 | 7107 | 41.4 | 12 | 25.2 | 2 | 19.5 | 0 | 6.9 |

**A-2.** New species (abbreviation in bold and italics) in the genus *Fibrovirus,* with corresponding strains (abbreviation in bold)

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | GenBank Access. No. | Genome lenght (nt) | Mol%G+C | No. CDS | DNA (% seq. Identiti) | Proteome (No. of homologousp roteins) | Zot | CoaB | CoaA |
| ***VALG\_phi8*** | MN690600.1 | 7311 | 46.3 | 10 | 100 | 10 | 100 | 100 | 100 |
| **K05K4\_VK05K4\_1** | CP017905.1 | 21012 | 46.4 | 34 | 98.8 | 17 | 100 | 100 | 93.7 |
| **K05K4\_VK05K4\_2** | CP017906.1 | 13327 | 46.3 | 23 | 99.0 | 13 | 100 | 100 | 89.8 |
| **K04M1\_VK04M1** | CP017895.1 | 7079 | 46.1 | 11 | 99.0 | 8 | 100 | 100 | 100 |
| Vf33 | [NC\_005948](https://www.ncbi.nlm.nih.gov/nuccore/49248521) | 7965 | 45.7 | 7 | 84.9 | 7 | 99.2 | 97.4 | 100 |
| VALG phi6 | MN719123.1 | 8529 | 44.3 | 13 | 21.8 | 4 | 10.2 | 0 | 43.9 |
| VfO3K6 | [NC\_002362](https://www.ncbi.nlm.nih.gov/nuccore/9635467) | 8784 | 45.2 | 10 | 21.4 | 3 | 11.7 | 0 | 37.1 |

**A-3.** New species (abbreviation in bold and italics) in the genus *Villovirus*

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | GenBank Access. No. | Genome lenght (nt) | Mol%G+C | No. CDS | DNA (% seq. Identiti) | Proteome (No. of homologous proteins) | Zot | CoaB | CoaA |
| ***VALG phi6*** | MN719123.1 | 8529 | 44.3 | 13 | 100 | 13 | 100 | 100 | 100 |
| VfO3K6 | [NC\_002362](https://www.ncbi.nlm.nih.gov/nuccore/9635467) | 8784 | 45.2 | 10 | 77.6 | 9 | 99.4 | 96.3 | 91.3 |
| VALG\_phi8 | MN690600.1 | 7311 | 46.3 | 10 | 21.8 | 4 | 10.2 | 0 | 42.9 |
| Vf33 | [NC\_005948](https://www.ncbi.nlm.nih.gov/nuccore/49248521) | 7965 | 45.7 | 7 | 23.6 | 3 | 9.9 | 0 | 44.3 |

**A-4.** New species (abbreviation in bold and italics) in the genus *Xylivirus*

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | GenBank Access. No. | Genome lenght (nt) | Mol%G+C | No. CDS | DNA (% seq. Identiti) | Proteome (No. of homologous proteins) | Zot | CoaB | CoaA |
| ***XacF13*** | [MN335248.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN335248.1?report=genbank&log$=nucltop&blast_rank=33&RID=2BHFD971016) | 7045 | 60.3 | 14 | 100 | 14 | 100 | 100 | 100 |
| Xf409 | [KY853667.1](https://www.ncbi.nlm.nih.gov/nucleotide/KY853667.1?report=genbank&log$=nucltop&blast_rank=10&RID=2BSVY70G013) | 8280 | 59.7 | 14 | 52.6 | 5 | 85.5 | 98.7\* | 78.5 |
| Cf1c | NC\_001396.1 | 7308 | 58.15 | 9 | 10.1 | 2 | 7.5 | 0 | 8.7 |
| SMA6 | [NC\_043029.1](https://www.ncbi.nlm.nih.gov/nucleotide/NC_043029.1?report=genbank&log$=nucltop&blast_rank=3&RID=2BHFD971016) | 7648 | 62.6 | 10 | 31.3 | 5 | 68.1 | 0 | 50.0 |
| phiXv2 | [MH206183.1](https://www.ncbi.nlm.nih.gov/nucleotide/MH206183.1?report=genbank&log$=nucltop&blast_rank=1&RID=2BJ8K33E016) | 6564 | 59.6 | 12 | 1.6 | 0 | 0 | 0 | 30.9 |
| PSH1 | NC\_010429.1 | 6867 | 61.1 | 7 | 7.7 | 3 | 28.7 | 0 | 67.1 |

\* reannotated

**A-5.** New species (abbreviation in bold and italics) in the genus *Restivirus*

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | GenBank Access. No. | Genome lenght (nt) | Mol%G+C | No. CDS | DNA (% seq. Identiti) | Proteome (No. of homologous proteins) | Zot | CoaB | CoaA |
| ***RSBg*** | MT495635.1 | 7540 | 61.7 | 11 | 100 | 11 | 100 | 100 | 100 |
| RSS1 | [AB259124.1](https://www.ncbi.nlm.nih.gov/nucleotide/AB259124.1?report=genbank&log$=nucltop&blast_rank=10&RID=1S5X2WNM016) | 6633 | 62.6 | 11 | 80.3 | 9 | 98.3 | 100 | 98 |
| PE226 | HM064452.1 | 5475 | 61.7 | 9 | 20.5 | 3 | 28.0 | 0 | 0 |
| RS603 | [AB937974.1](https://www.ncbi.nlm.nih.gov/nucleotide/AB937974.1?report=genbank&log$=nucltop&blast_rank=3&RID=1S5X2WNM016) | 7679 | 59.4 | 13 | 10.1 | 2 | 13.0 | 0 | 25.0 |

\* Contain internal stop codons

**A-6.** New species (abbreviation in bold and italics) whit corresponding strains (abbreviations in bold) in the genus *Lineavirus*

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | GenBank Access. No. | Genome lenght (nt) | Mol%G+C | No. CDS | DNA (% seq. Identiti) | Proteome (No. of homologous proteins) | Zot | CoaB | CoaA |
| ***PEar6*** | MT901800.1 | 6608 | 41.7 | 11 | 100 | 11 | 100 | 100 | 100 |
| **PEar2** | MT901798.1 | 6651 | 41.7 | 10 | 99.8 | 10 | 100 | 100 | 100 |
| **PEar1** | MT901797.1 | 6646 | 41.7 | 10 | 99.4 | 10 | 100 | 100 | 100 |
| **PEar4** | MT901799.1 | 6801 | 41.7 | 10 | 98.0 | 10 | 100 | 100 | 100 |
| Ike | [NC\_002014](https://www.ncbi.nlm.nih.gov/nuccore/9626232) | 6883 | 40.5 | 10 | 89.6 | 10 | 97.3 | 89.0 | 80.5 |
| I22 | [NC\_001332](https://www.ncbi.nlm.nih.gov/nuccore/9625381) | 6744 | 42.7 | 9 | 55.7 | 6 | 86.6 | 71.4 | 80 |
| M13 | [NC\_003287](https://www.ncbi.nlm.nih.gov/nuccore/56718463) | 6407 | 40.75 | 10 | 19.6 | 8 | 51.4 | 41.6 | 24.4 |
| If1 | [NC\_001954](https://www.ncbi.nlm.nih.gov/nuccore/9630747) | 8454 | 43.7 | 10 | 6.2 | 5 | 56.5 | 36.5 | 8.8 |

**A-7.** New species (abbreviation in bold and italics) in the genus *Primolicivirus*

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | GenBank Access. No. | Genome lenght (nt) | Mol%G+C | No. CDS | DNA (% seq. Identiti) | Proteome (No. of homologous proteins) | Zot | CoaB | CoaA |
| **Pf8** | MN710383.1 | 10061 | 58.1 | 16 | 100 | 16 | 100 | 100 | 100 |
| Pf1 | AY324828.1 | 10675 | 59.4 | 14 | 68.6 | 11 | 99.5 | 100 | 68 |

**A-8.** Two new species (abbreviation in bold and italics) in the genus *Affertcholeramvirus*

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | GenBank Access. No. | Genome lenght (nt) | Mol%G+C | No. CDS | DNA (% seq. Identiti) | Proteome (No. of homologous proteins) | Zot | CoaB | CoaA |
| ***Vibrio phage pre-CTX (1)*** | [KP972568.1](https://www.ncbi.nlm.nih.gov/nucleotide/KP972568.1?report=genbank&log$=nucltop&blast_rank=43&RID=93X4B3GA013) | 6,722 | 46.7 | 7 | 100 | 7 | 100 | 100 | 100 |
| ***Vibrio phage pre-CTX (2)*** | [KT728930.1](https://www.ncbi.nlm.nih.gov/nucleotide/KT728930.1?report=genbank&log$=nucltop&blast_rank=14&RID=93X4B3GA013) | 5,215 | 46.7 | 7 | 60.6 | 4 | 98.3 | 97.6 | 96.5 |
| CTXphi | [NC\_015209.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_015209.1) | 10,638 | 44.7 | 13 | 50.0 | 4 | 95.7 | 97.6 | 97.0 |

**B)** New species and new genera in family *Inoviridae;* analysis was performed using BLASTN and BLASTP algorithms; for homologous proteins determination CoreGenes5.0 was used [8].

**B-1.** New species (abbreviation in bold and italics) in the new genus *Vasivirus,* with additional strain (abbreviation in bold)

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | GenBank Access. No. | Genome lenght (nt) | Mol%G+C | No. CDS | DNA (% seq. Identiti) | Proteome (No. of homologous proteins) | Zot | CoaB | CoaA |
| ***VAI1*** | [MN200778.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN200778.1?report=genbank&log$=nucltop&blast_rank=1&RID=1N297ATW013) | 6117 | 42.5 | 11 | 100 | 11 | 100 | 100 | 100 |
| **VAI2** | [MN200777.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN200777.1?report=genbank&log$=nucltop&blast_rank=2&RID=1N297ATW013) | 6117 | 42.5 | 11 | 100 | 11 | 100 | 100 | 100 |
| VCY | NC\_016162.1 | 7103 | 41.1 | 11 | 24.2 | 6 | 64.5 | 45.2 | 26.5 |
| KSF | NC\_006294.1 | 7107 | 44.4 | 12 | 15.4 | 4 | 64.5 | 21.2 | 24.5 |
| CTX | MF155889.1 | 6698 | 44.5 | 9 | 12.7 | 3 | 16.6 | 0 | 0 |

**B-2.** Four new species (abbreviation in bold and italics) in the new genus *Lophivirus*

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | GenBank Access. No. | Genome lenght (nt) | Mol%G+C | No. CDS | DNA (% seq. Identiti) | Proteome (No. of homologous proteins) | Zot | CoaB | CoaA |
| ***phiLfUK*** | [MH206184.1](https://www.ncbi.nlm.nih.gov/nucleotide/MH206184.1?report=genbank&log$=nucltop&blast_rank=2&RID=2BJ8K33E016) | 6062 | 59.9 | 10 | 100 | 10 | 100 | 100 | 100 |
| ***phiLf2*** | M[H218848.1](https://www.ncbi.nlm.nih.gov/nucleotide/MH218848.1?report=genbank&log$=nucltop&blast_rank=4&RID=2BJ8K33E016) | 6372 | 60.2 | 11 | 67.9 | 7 | 93.6 | 100 | 75.8 |
| ***phiXv2*** | [MH206183.1](https://www.ncbi.nlm.nih.gov/nucleotide/MH206183.1?report=genbank&log$=nucltop&blast_rank=1&RID=2BJ8K33E016) | 6564 | 59.6 | 12 | 63.2 | 9 | 93.4 | 100 | 22.8 |
| ***Cf2*** | [MK512531.1](https://www.ncbi.nlm.nih.gov/nucleotide/MK512531.1?report=genbank&log$=nucltop&blast_rank=17&RID=2BSVY70G013) | 6454 | 58.2 | 12 | 43.9 | 7 | 79.7 | 76.2 | 17.1 |
| Xf409 | [KY853667.1](https://www.ncbi.nlm.nih.gov/nucleotide/KY853667.1?report=genbank&log$=nucltop&blast_rank=10&RID=2BSVY70G013) | 8280 | 59.7 | 14 | 29.0 | 3 | 5.0 | 0 | 0.9 |
| XacF1 | [AB910602.1](https://www.ncbi.nlm.nih.gov/nucleotide/AB910602.1?report=genbank&log$=nucltop&blast_rank=15&RID=2BSVY70G013) | 7325 | 58.13 | 13 | 24.7 | 4 | 0 | 0 | 0 |

**B-3.** New species (abbreviation in bold and italics) in the new genus *Porrectionivirus*

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | GenBank Access. No. | Genome lenght (nt) | Mol%G+C | No. CDS | DNA (% seq. Identiti) | Proteome (No. of homologous proteins) | Zot | CoaB | CoaA |
| ***p12J*** | AY374414.2 | 7118 | 57.0 | 9 | 100 | 9 | 100 | 100 | 100 |
| PE226 | HM064452.1 | 5475 | 61.7 | 9 | 34.4 | 5 | 71.21 | 28.0 | 38.2 |
| RS603 | [AB937974.1](https://www.ncbi.nlm.nih.gov/nucleotide/AB937974.1?report=genbank&log$=nucltop&blast_rank=3&RID=1S5X2WNM016) | 7679 | 59.4 | 13 | 7.3 | 4 | 4.3 | 0 | 6.7 |

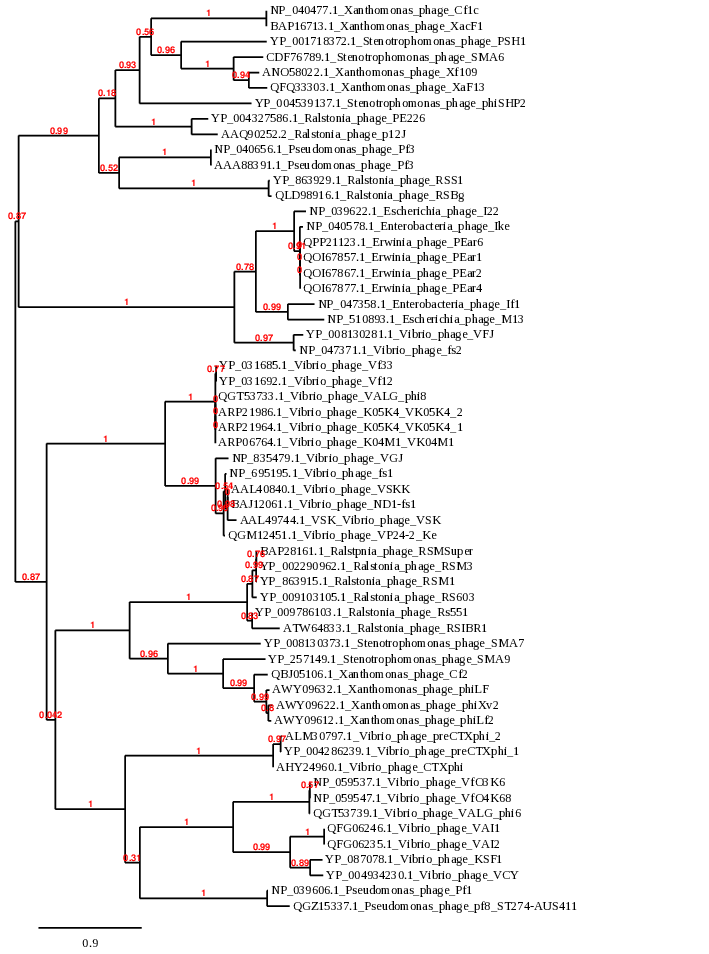
**B-4.** New species (abbreviation in bold and italics) in the new genus *Siphunculivirus*

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | GenBank Access. No. | Genome lenght (nt) | Mol%G+C | No. CDS | DNA (% seq. Identiti) | Proteome (No. of homologous proteins) | Zot | CoaB | CoaA |
| **SHP2** | [HM150760.1](https://www.ncbi.nlm.nih.gov/nucleotide/HM150760.1?report=genbank&log$=nucltop&blast_rank=13&RID=BJKHWCDG016) | 5812 | 61.5 | 9 | 100 | 9 | 100 | 100 | 100 |
| SMA7 | NC\_021569.1 | 7069 | 62.3 | 10 | 42.5 | 4 | 37.5 | 0 | 0 |
| PSH1 | NC\_010429.1 | 6867 | 61.1 | 7 | 28.0 | 4 | 30.9 | 0 | 13.6 |
| phiLf2 | MH218848.1 | 6372 | 60.2 | 11 | 20.8 | 4 | 7.5 | 0 | 13.7 |

**C)** New species and new genus in family *Plectroviridae;* analysis was performed using BLASTN and BLASTP algorithms; for homologous proteins determination CoreGenes5.0 was used [8].

**C-1.** New species (abbreviation in bold and italics) in the new genus *Virgulavirus*

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | GenBank Access. No. | Genome lenght (nt) | Mol%G+C | No. CDS | DNA (% seq. Identiti) | Proteome (No. of homologous proteins) | Zot | CoaB | CoaA |
| **SVGII3** | [AJ969242.1](https://www.ncbi.nlm.nih.gov/nucleotide/AJ969242.1?report=genbank&log$=nucltop&blast_rank=1&RID=2G89CM0G013) | 7878 | 23.0 | 11 | 100 | 11 | 100 | 100 | 100 |
| SVTS2 | [AF133242.2](https://www.ncbi.nlm.nih.gov/nucleotide/AF133242.2?report=genbank&log$=nucltop&blast_rank=2&RID=2G89CM0G013) | 6825 | 22.7 | 13 | 34.2 | 8 | 36.2 | 44.1 | 37.7 |
| R8A2B | [X51344.1](https://www.ncbi.nlm.nih.gov/nucleotide/X51344.1?report=genbank&log$=nucltop&blast_rank=4&RID=2G89CM0G013) | 8273 | 22.9 | 12 | 0 | 2 | 6.8 | 0 | 30.3 |

Figure 1. “One click” phylogeny tree [7] of *Inoviridae*, based on amino-acid sequences of morphogenesis protein; the new species and/or genera are indicated 

***Vasivirus***

***Porrectionivirus***

***Restivirus***

***Primolicivirus***

***Siphunculivirus***

***Fibrovirus***

***Xylivirus***

***Lineavirus***

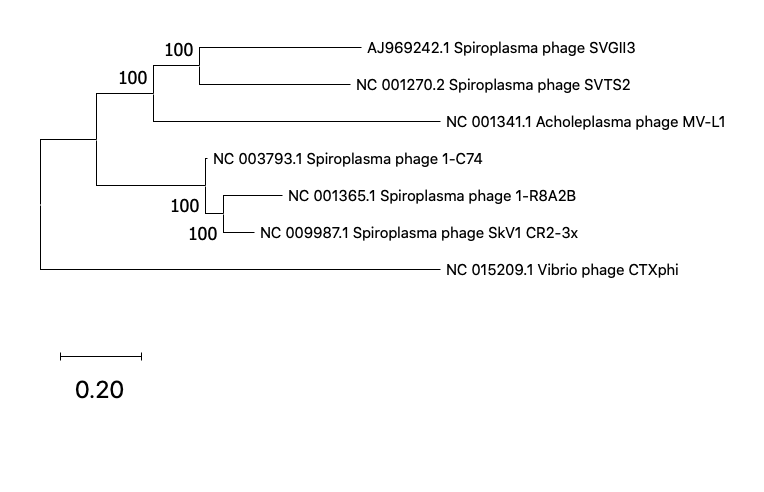
***Villovirus***

***Lophivirus***

***Affertcholeramvirus***

***Villovirus***

Figure 2. The evolutionary history was inferred based on whole genome sequences of *Plectroviridae*, using the Neighbor-Joining method [1]. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (100 replicates) are shown next to the branches [2]. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Kimura 2-parameter method [3] and are in the units of the number of base substitutions per site. This analysis involved 7 nucleotide sequences. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were a total of 12049 positions in the final dataset. Evolutionary analyses were conducted in MEGA [4,5]. The tree was rooted using Vibrio phage CTXphi as an outlier.



***Virgulavirus***

***Suturavirus***

***Vespertiliovirus***

***Plectrovirus***

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