

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

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| **Code assigned:** | ***2023.020D*** |  |
| **Short title:** Establishing one new family, associated genera and species in the order *Geplafuvirales* |
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**List the ICTV Study Group(s) that have seen this proposal**

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**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)** | 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 | 14 July 2023 |
| Date of this revision (if different to above) | 5 Oct 2023 |

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

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| The proposal was deemed acceptable in the form presented at the EC meeting. |

**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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| 2023.020D.N.v2. Geplafuvirales\_1nf\_18ng\_30nsp.xlsx |

**Abstract**

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| We aim to establish a new family, *Geplanaviridae*, in the order *Geplafuvirales* to classify new virus genomes that have been identified from various sources. The new family will include 18 genera and 30 species.  |

**Text of proposal**

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| *Geplafuvirales* currently is comprised of two virus families, *Geminiviridae* and *Genomoviridae*. An informal group called CRESSV6 of cressdnaviruses has been previously described [1-4]. Here we analyze the 37 virus genomes that are part of this group (based on the Rep protein sequences) that have been identified from various sources (Table 1) (Figure 1). The Reps of these 37 viruses all have the geminivirus Rep sequence (GRS) motif [5] characteristic and specific of Reps encoded by viruses in the families *Geminiviridae* and *Genomoviridae.* We have named the family *Geplanaviridae* which is derived from **ge**mini-like Rep **pl**ant and **an**imal **a**ssociated viruses.**Genus and species demarcation**To analyze the relationships between viruses within the proposed family, we performed comparative genomics and phylogenetic analyses of the Rep proteins. Genera were delineated based on phylogenetic analyses coupled with pairwise identities and also the genome organization relative to the *rep* open reading frame (Figures 2 - 3). For species demarcation we used a 78% pairwise nucleotide genome-wide sequence identity which is similar to that used for other cressdnaviricots [6-8].GeneraEtymology of genus names - the genera names are all based on spells from Harry Potter literature. 1. *Acciovirus*
2. *Aguamentivirus*
3. *Alohovirus*
4. *Aparevirus*
5. *Avadavirus*
6. *Densaugvirus*
7. *Diffindovirus*
8. *Engorgivirus*
9. *Episkevirus*
10. *Expellivirus*
11. *Impedivirus*
12. *Lumovirus*
13. *Oblivivirus*
14. *Patrovirus*
15. *Protegovirus*
16. *Riddikuvirus*
17. *Stupevirus*
18. *Wingardivirus*

Etymology of species epithets1. *tongis: Pteropus tonganus*
2. *mintis: minnow tissue*
3. *ailuris: Ailurus fulgens*
4. *austrosis: Austrosimulium australense*
5. *phoenis: Phoenicopteridae*
6. *bromis: Bromus hordeaceus*
7. *ailgensis: Ailurus fulgens*
8. *bromhordis: Bromus hordeaceus*
9. *trifolis: Trifolium resupinatum*
10. *kummerois: Kummerowia striata*
11. *airobis: airborne particulate matter*
12. *arcechis: Arctopus echinatus*
13. *copteris: Phoenicopteridae*
14. *libequis: Libellula quadrimaculata*
15. *racskinis: raccoon* skin
16. *avheatis: Avon-Heathcote Estuary*
17. *arilais: Arizlama virus AZLM\_683*
18. *capibaris: Capybara virus 11\_cap1\_98*
19. *mincris: minnow cressvirus - tissue*
20. *musculis: Musculium novaezelandiae*
21. *maspris: Manatee spring*
22. *trichosis: Trichosanthes kirilowii*
23. *kirilis: Trichosanthes kirilowii*
24. *yangtsis: water samples from river ports along the Yangtze River in China*
25. *manatis: Manatee Spring*
26. *forpesis: Forsythia suspensa*
27. *dianchis: Dianchi freshwater lake*
28. *arizlamas: Arizlama virus*
29. *quadrimis: Libellula quadrimaculata*
30. *minnis: minnow tissue*
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**Supporting evidence**

**Table 1:** Summary of the viruses classified into various genera and species in the family *Geplanaviridae* in the order *Geplafuvirales*

|  |  |  |  |  |  |  |  |
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| **Genus** | **Species** | **Accession #** | **Virus** | **Year** | **Country** | **Host /source** | **Isolate** |
| *Protegovirus* | *Protegovirus tongis* | KT732831 | Pacific flying fox faeces associated circular DNA virus-2 | 2015 | Tonga | *Pteropus tonganus* | Tbat\_H\_103763 |
| *Protegovirus* | *Protegovirus tongis* | KT732829 | Pacific flying fox faeces associated circular DNA virus-2 | 2015 | Tonga | *Pteropus tonganus* | Tbat\_A\_103763 |
| *Protegovirus* | *Protegovirus mintis* | MH617562 | CRESS virus sp. ctbg173 | 2017 | USA | Minnow tissue | ctbg173 |
| *Protegovirus* | *Protegovirus ailuris* | MZ556147 | Red panda feces-associated circular DNA virus 11 | 2015 | China: Sichuan Province | *Ailurus fulgens* | AliP02cress04-2015 |
| *Diffindovirus* | *Diffindovirus austrosis* | MK433230 | Blackfly DNA Virus 16 | 2015 | New Zealand: Canterbury | *Austrosimulium australense* | SF02\_377 |
| *Avadavirus* | *Avadavirus phoenis* | MN928944 | CRESS virus sp. fmg067cre2 | 2018 | China | *Phoenicopteridae* | fmg067cre2 |
| *Alohovirus* | *Alohovirus bromis* | KM510190 | Bromus-associated circular DNA virus 1 | 2012 | New Zealand | *Bromus hordeaceus* | BasCV-1\_NZ-NZG03\_Wel-2012 |
| *Alohovirus* | *Alohovirus bromis* | KM510189 | Bromus-associated circular DNA virus 1 | 2012 | New Zealand | *Bromus sp.* | BasCV-1\_NZ-NZG01\_Sef-2012 |
| *Alohovirus* | *Alohovirus ailgensis* | MZ556204 | Red panda feces-associated circular DNA virus 12 | 2020 | China: Sichuan Province | *Ailurus fulgens* | Rpf011unssDNA01-5 |
| *Alohovirus* | *Alohovirus bromhordis* | KP005454 | Bromus-associated circular DNA virus 4 | 2013 | France | *Bromus hordeaceus* | BasCV-4\_FR38-38-Cam |
| *Alohovirus* | *Alohovirus trifolis* | KP005453 | Trifolium-associated circular DNA virus 1 | 2013 | France | *Trifolium resupinatum* | TasCV-1\_FR34-34-Cam |
| *Stupevirus* | *Stupevirus kummerois* | MN891814 | Kummerowia striata CRESS virus pt119-nep-9 | - | China | *Kummerowia striata* | pt119-nep-9 |
| *Aparevirus* | *Aparevirus airobis* | MW678915 | Virus sp. D1\_753 | 2009 | USA: Pinal County, Arizona | airborne particulate matter | D1\_753 |
| *Lumovirus* | *Lumovirus arcechis* | MH425569 | Arctopus echinatus-associated virus 2-76-E | 2012 | South Africa | *Arctopus echinatus* | 2-76-E |
| *Impedivirus* | *Impedivirus copteris* | MN928943 | CRESS virus sp. fmg067cir3 | 2018 | China | *Phoenicopteridae* | fmg067cir3 |
| *Impedivirus* | *Impedivirus libequis* | KM598398 | Odonata-associated circular virus-15 | 2012 | USA | *Libellula quadrimaculata* | OdasCV-15-US-1640LM1-12 |
| *Aguamentivirus* | *Aguamentivirus racskinis* | MK012475 | Circoviridae sp. ctcc28 | 2017 | USA | *Procyon lotor* | ctcc28 |
| *Aguamentivirus* | *Aguamentivirus avheatis* | MW588038 | Avon-Heathcote Estuary associated circular virus 25 | 2016 | United Kingdom | *Cygnus olor*  | Abbotsbury/A/2016 |
| *Aguamentivirus* | *Aguamentivirus avheatis* | KM874355 | Avon-Heathcote Estuary associated circular virus 25 | 2012 | New Zealand | *Austrovenus stutchburyi* | AHEaCV-25-NZ-2942CO-2012 |
| *Aguamentivirus* | *Aguamentivirus avheatis* | KM874356 | Avon-Heathcote Estuary associated circular virus 25 | 2012 | New Zealand | *Paphies subtriangulata* | AHEaCV-25-NZ-2250TU-2012 |
| *Aguamentivirus* | *Aguamentivirus avheatis* | KM874358 | Avon-Heathcote Estuary associated circular virus 25 | 2012 | New Zealand | *Amphibola crenata* | AHEaCV-25-NZ-3789GA-2012 |
| *Aguamentivirus* | *Aguamentivirus avheatis* | KM874357 | Avon-Heathcote Estuary associated circular virus 25 | 2012 | New Zealand | Benthic sediment | AHEaCV-25-NZ-1935SG-2012 |
| *Wingardivirus* | *Wingardivirus arilais* | MW697535 | Arizlama virus AZLM\_683 | 12-Jul | USA | Lake water sample | AZLM\_683 |
| *Wingardivirus* | *Wingardivirus capibaris* | MK570173 | Capybara virus 11\_cap1\_98 | 2016 | Brazil | *Hydrochoerus hydrochaeris* | cap1\_98 |
| *Engorgivirus* | *Engorgivirus mincris* | MH616705 | CRESS virus sp. ctce103 | 2017 | USA | Minnow tissue | ctce103 |
| *Engorgivirus* | *Engorgivirus musculis* | KP153501 | Lake Sarah-associated circular virus-45 | 2013 | New Zealand | *Musculium novaezelandiae* | LSaCV-45-LSCO-2013 |
| *Densaugvirus* | *Densaugvirus maspris* | MW202708 | CRESS virus sp. ctrLR020 | 2019 | USA | Manatee Spring | ctrLR020 |
| *Episkevirus* | *Episkevirus trichosis* | MW202452 | CRESS virus sp. ctrD6136 | 2019 | USA | Manatee Spring | ctrD6136 |
| *Episkevirus* | *Episkevirus kirilis* | MN891804 | Trichosanthes kirilowii CRESS virus t111-nep-5 | - | China | *Trichosanthes kirilowii* | pt111-nep-5 |
| *Oblivivirus* | *Oblivivirus yangtsis* | MW346688 | CRESS virus sp. 1aq-CRESS-1 | 2017 | China: Yangtze River | Water samples from river ports along the Yangtze River in China | 1aq-CRESS-1 |
| *Riddikuvirus* | *Riddikuvirus manatis* | MW202840 | CRESS virus sp. ctKR5164 | 2019 | USA | Manatee Spring | ctKR5164 |
| *Riddikuvirus* | *Riddikuvirus forpesis* | MN891803 | Trichosanthes kirilowii CRESS virus pt111-nep-4 | - | China | *Trichosanthes kirilowii* | pt111-nep-4 |
| *Riddikuvirus* | *Riddikuvirus forpesis* | MN891795 | Forsythia suspensa CRESS virus pt110-nep-1 | - | China | *Forsythia suspensa* | pt110-nep-1 |
| *Patrovirus* | *Patrovirus dianchis* | KT149395 | Circovirus-like genome DCCV-2 | 2010 | China | Freshwater lake (Dianchi) sample (< 0.5m) | DCCV-2 |
| *Acciovirus* | *Acciovirus arizlamas* | MW697536 | Arizlama virus AZLM\_678 | 2012 | USA | Lake water sample | AZLM\_678 |
| *Acciovirus* | *Acciovirus quadrimis* | KM598390 | Odonata-associated circular virus-7 | 2012 | USA | *Libellula quadrimaculata* | OdasCV-7-US-1706LM1-12 |
| *Expellivirus* | *Expellivirus minnis* | MH616944 | CRESS virus sp. ctdg299 | 2017 | USA | Minnow tissue | ctdg299 |

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**Figure 1:** Maximum likelihood phylogenetic tree inferred from Rep proteins of members of the phylum *Cressdnaviricota*. Related sequence groups are collapsed into triangles, the side lengths of which are proportional to the distances between the closest and farthest leaf nodes. The alignment was trimmed with TrimAL [9] with gap threshold of 0.2. The maximum likelihood phylogenetic tree was constructed using IQtree [10] with automatic selection of the best-fit substitution model for a given alignment, which was Q.pfam+F+R10. Numbers at the nodes represent aLRT branch supports. The scale bar represents the number of substitutions per site.

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**Figure 2:** Maximum likelihood phylogenetic tree of the Rep sequences of the members of the*Geplanaviridae* family inferred with PhyML 3.0 [11] with LG+I+G model determined as the best substitution model using ProtTest 3 [12] and rooted with representative sequences of members of the family *Geminiviridae*. The species belonging to the same genus are indicated with the same color. Numbers at the nodes represent aLRT branch supports. The cyan line shows a proposed demarcation of genera. The genome organization relative to the *rep* ORF is shown to the right of the phylogeny.

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**Figure 3:** A ‘two color’ pairwise identity matrix of members of the family *Geplanaviridae* with 78% species threshold, using full genome comparison, inferred using SDT v1.2 [13].

**References**

1. Kazlauskas D, Varsani A, Krupovic M (2018) Pervasive Chimerism in the Replication-Associated Proteins of Uncultured Single-Stranded DNA Viruses. Viruses 10:187. doi:10.3390/v10040187. PMID:29642587
2. Kazlauskas D, Varsani A, Koonin EV, Krupovic M (2019) Multiple origins of prokaryotic and eukaryotic single-stranded DNA viruses from bacterial and archaeal plasmids. Nat Commun 10:3425. doi:10.1038/s41467-019-11433-0. PMID:31366885
3. Kinsella CM, Deijs M, Becker C, Broekhuizen P, van Gool T, Bart A, Schaefer AS, van der Hoek L. (2022). Host prediction for disease-associated gastrointestinal cressdnaviruses. Virus Evol. 8(2):veac087. doi: 10.1093/ve/veac087. PMID: 36325032; PMCID: PMC9615429.
4. Krupovic M, Varsani A, Kazlauskas D, Breitbart M, Delwart E, Rosario K, Yutin N, Wolf YI, Harrach B, Zerbini FM, Dolja VV, Kuhn JH, Koonin EV (2020) Cressdnaviricota: A virus phylum unifying seven families of Rep-encoding viruses with single-stranded, circular DNA genomes. J Virol 94:e00582-20. doi:10.1128/JVI.00582-20. PMID:32269128
5. Nash TE, Dallas MB, Reyes MI, Buhrman GK, Ascencio-Ibañez JT, Hanley-Bowdoin L. (2011). Functional analysis of a novel motif conserved across geminivirus Rep proteins. J Virol. 85(3):1182-92. doi: 10.1128/JVI.02143-10.. PMID: 21084480; PMCID: PMC3020519.
6. Krupovic M, Varsani A. (2022). *Naryaviridae*, *Nenyaviridae*, and *Vilyaviridae*: three new families of single-stranded DNA viruses in the phylum *Cressdnaviricota*. Arch. Virol. 167, 2907–2921.PMID: 36098801 DOI: 10.1007/s00705-022-05557-w
7. Varsani A, Krupovic M (2017) Sequence-based taxonomic framework for the classification of uncultured single-stranded DNA viruses of the family Genomoviridae. Virus Evol 3:vew037. doi:10.1093/ve/vew037. PMID:28458911
8. Varsani A, Krupovic M (2018) Smacoviridae: a new family of animal-associated single-stranded DNA viruses. Arch Virol 163:2005-2015. doi:10.1007/s00705-018-3820-z. PMID:29572596
9. Capella-Gutierrez S, Silla-Martinez JM, Gabaldon T (2009) trimAl: a tool for automated alignment trimming in large-scale phylogenetic analyses. Bioinformatics 25:1972-3. doi:10.1093/bioinformatics/btp348. PMID:19505945
10. Minh BQ, Schmidt HA, Chernomor O, Schrempf D, Woodhams MD, von Haeseler A, Lanfear R (2020) IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. Mol Biol Evol 37:1530-1534. doi:10.1093/molbev/msaa015. PMID:32011700
11. Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O (2010) New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. Syst Biol 59:307-321. PMID: 20525638; doi: 10.1093/sysbio/syq010
12. Darriba D, Taboada GL, Doallo R, Posada D. (2011). ProtTest 3: fast selection of best-fit models of protein evolution. Bioinformatics. 27(8):1164-5. doi: 10.1093/bioinformatics/btr088. Epub 2011 Feb 17. PMID: 21335321; PMCID: PMC5215816.
13. Muhire BM, Varsani A, Martin DP (2014) SDT: A Virus Classification Tool Based on Pairwise Sequence Alignment and Identity Calculation. Plos One 9:e108277. PMID: 25259891; PMCID: PMC4178126.