

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

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| **Code assigned:** | ***2023.018D*** |  |
| **Short title:** Establishing one new family, associated genera and species in the order *Mulpavirales* | | |
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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**

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

**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**

|  |  |
| --- | --- |
| 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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| --- |
| 2023.018D.N.v2. Mulpavirales\_1nf\_9ng\_9nsp.xlsx |

**Abstract**

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| We aim to establish a new family, *Anicreviridae,* in the order *Mulpavirales* to classify various new virus genomes (n=16) that have been identified from various sources. The new family will include 9 genera and 9 species. |

**Text of proposal**

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| |  | | --- | | There are currently three viral families (*Amesuviridae*, *Metaxyviridae* and *Nanoviridae*) in the order *Mulpavirales.* The Reps of *Alphasatellitidae* phylogenetically cluster with those of the members of *Mulpavirales* (Figure 1).Here we analyze the 16 virus genomes (Table 1) whose Reps are most closely related to those of the members of *Amesuviridae*, *Metaxyviridae*, *Nanoviridae* and *Alphasatellitidae* (Figure 1). This group of viruses has been informally referred to in the literature as CRESSV4 [1-4]. Whereas the monophyly of the *Amesuviridae* clade is well supported in the phylogenetic analyses, its position relative to other members of the *Mulpavirales* and *Gredzevirales* is less stable. We opted to include *Amesuviridae* into the order *Mulpavirales*, but its membership in this order might need revision once more members become available.  We propose the name *Anicreviridae*, for **ani**mal associated **CRE**SS viruses.  **Genus and species demarcation**  To analyze the relationships between viruses in the proposed family *Anicreviridae*, 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 other cressdnaviruses [5-7].  **Genera**  Etymology of genus names   1. *Manawavirus: oasis in Maori - kōmanawa* 2. *Rakkovirus: ocean in Muscogee - Uehvtkvrakko* 3. *Otevirus: beach in Muscogee - ote* 4. *Baranavirus: ocean in Garifuna - barana* 5. *Pekavirus: Flying fox in Tongan - peka* 6. *Kopavirus: fly in Maori - kopa* 7. *Ketkevirus: spider in Sencoteen (Saanich Dialect) - ḴETḴEĆOLE* 8. *Patavirus: drop of water in Maori - Pata* 9. *Uewvirus: water in Muscogee - Uewv*   Etymology of species epithets   1. *kapowais: dragonfly in Maori - kapowai* 2. *canuewis: fly in Muscogee - cana; water in Muscogee - uewv* 3. *soksuewis: bug in Muscogee – soksv; water in Muscogee - uewv* 4. *uduis: whale in Garifuna - udu* 5. *fuais: –fruit in Tongan - fua* 6. *kakawais: Cyanoramphus auriceps in Maori - Ḵākāwaiariki* 7. *silauonis: tent in Sencoteen (Saanich Dialect) - SILÁU¸TW̱; KELEJTEN* 8. *kakahis: Freshwater mussel; Hyridella menziesi in Maori - Kākahi* 9. *yahnais: fish in Muscogee - Yah-nah-sah* | |

**Supporting evidence**

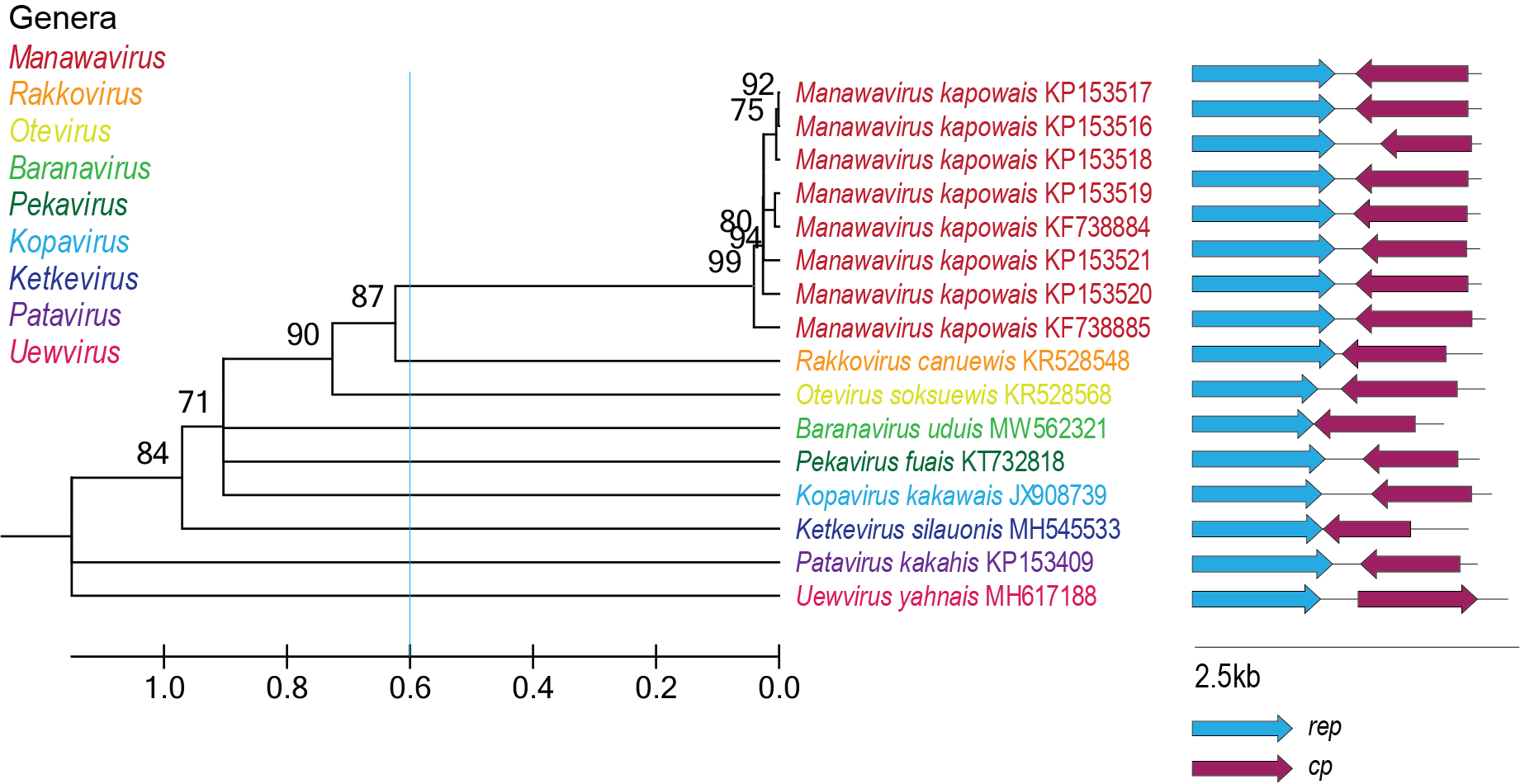
**Table 1:** Summary of the viruses classified in the new family *Anicreviridae*.

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| **Genus** | **Species** | **Accession #** | **Virus** | **Year** | **Country** | **Host /source** | **Isolate** |
| *Manawavirus* | *Manawavirus kapowais* | KP153517 | Dragonfly larvae associated circular virus-10 | 2013 | New Zealand | water | DflaCV-10-LSWA-2013 |
| *Manawavirus* | *Manawavirus kapowais* | KP153516 | Dragonfly larvae associated circular virus-10 | 2013 | New Zealand | *Musculium novaezelandiae* | DflaCV-10-LSCO-2013 |
| *Manawavirus* | *Manawavirus kapowais* | KP153518 | Dragonfly larvae associated circular virus-10 | 2013 | New Zealand | sediment | DflaCV-10-LSSO-2013 |
| *Manawavirus* | *Manawavirus kapowais* | KP153519 | Dragonfly larvae associated circular virus-10 | 2013 | New Zealand | *Echyridella menziesii* | DflaCV-10-LSMU-2013 |
| *Manawavirus* | *Manawavirus kapowais* | KF738884 | Dragonfly larvae associated circular virus-10 | 2012 | New Zealand | *Xanthocnemis zealandica* | DflaCV-10\_NZ-XZ2-LS |
| *Manawavirus* | *Manawavirus kapowais* | KP153521 | Dragonfly larvae associated circular virus-10 | 2013 | New Zealand | *Potamopyrgus antipodarum* | DflaCV-10-LSGA-2013 |
| *Manawavirus* | *Manawavirus kapowais* | KP153520 | Dragonfly larvae associated circular virus-10 | 2013 | New Zealand | *Procordulia grayi* | DflaCV-10-LSLA-2013 |
| *Manawavirus* | *Manawavirus kapowais* | KF738885 | Dragonfly larvae associated circular virus-10 | 2012 | New Zealand | *Xanthocnemis zealandica* | DflaCV-10\_NZ-XZ1-LH |
| *Rakkovirus* | *Rakkovirus canuewis* | KR528548 | Littorina sp. associated circular virus I0041 | - | USA | *Littorina sp.* | I0041 |
| *Otevirus* | *Otevirus soksuewis* | KR528568 | Palaemonetes sp. common grass shrimp associated circular virus I0006H | - | USA | *Palaemonetes sp.* | I0006H |
| *Baranavirus* | *Baranavirus uduis* | MW562321 | Delphin virus 1 | 2016 | Saint Vincent and the Grenadines | *Orcinus orca* | 3\_2016\_1939 |
| *Pekavirus* | *Pekavirus fuais* | KT732818 | Pacific flying fox faeces associated circular DNA virus-3 | 2014 | Tonga | *Pteropus tonganus* | Tbat\_38855 |
| *Kopavirus* | *Kopavirus kakawais* | JX908739 | Cyanoramphus nest associated circular X DNA virus | 2012 | New Zealand | *Cyanoramphus auriceps* | CynNCXV |
| *Ketkevirus* | *Ketkevirus silauonis* | MH545533 | Tentweb spider associated circular virus 1 | 2017 | Canada: Victoria, British Columbia | *Cyrtophora sp.* | BC\_I1608\_E1 |
| *Patavirus* | *Patavirus kakahis* | KP153409 | Lake Sarah-associated circular virus-11 | 2013 | New Zealand | *Echyridella menziesii* | LSaCV-11-LSMU-2013 |
| *Uewvirus* | *Uewvirus yahnais* | MH617188 | CRESS virus sp. ctcc62 | 2017 | USA | *rainbow trout tissue* | ctcc62 |

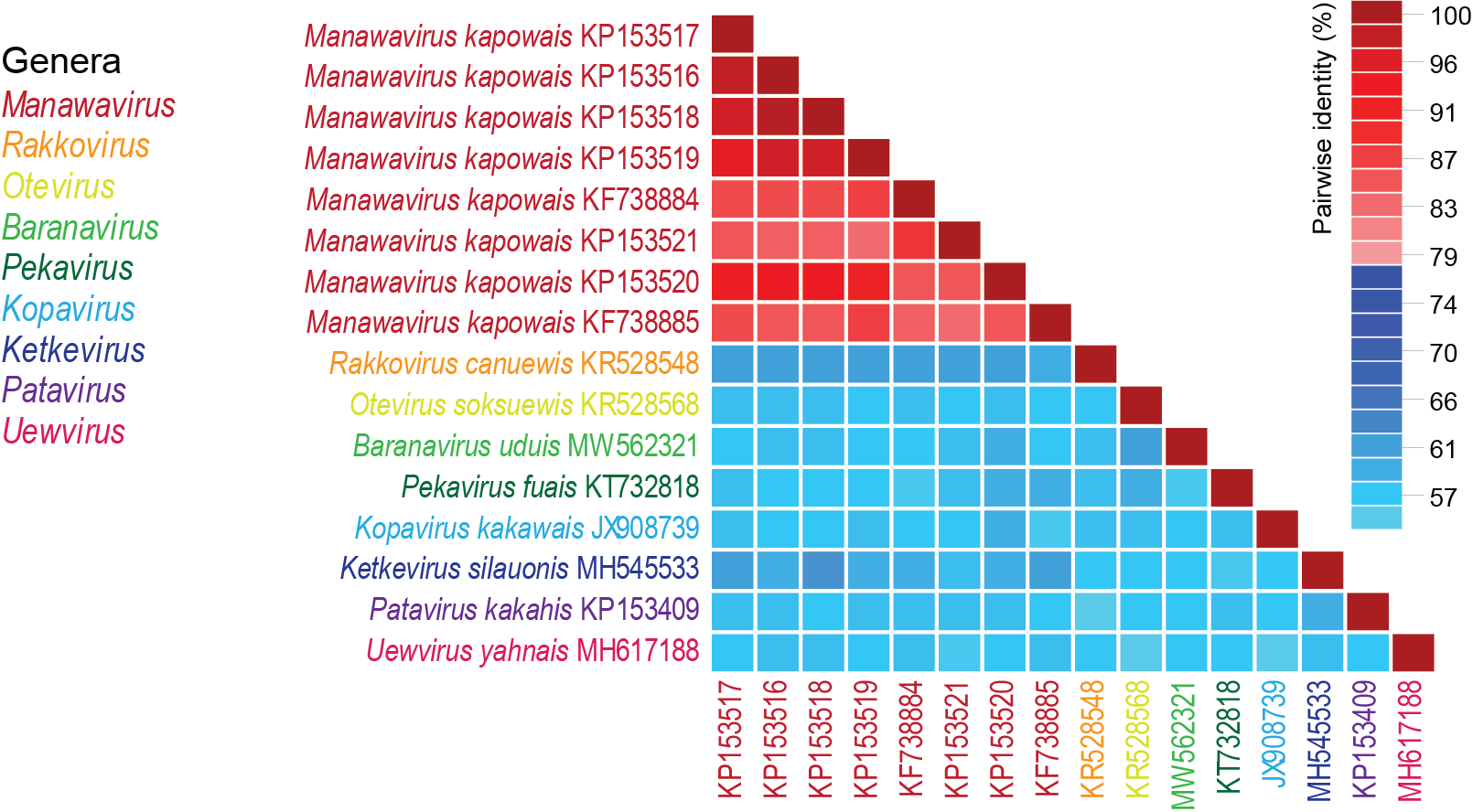
**A diagram of different colored lines

Description automatically generated with medium confidence**

**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 [8] with gap threshold of 0.2. The maximum likelihood phylogenetic tree was constructed using IQtree [9] 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*Anicreviridae* family inferred with PhyML 3.0 [10] with rtREV+I+G+F model determined as the best substitution model using ProtTest 3 [11] and rooted with representative sequences of members of the family *Smacoviridae*. 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 *Anicreviridae* with 78% species threshold, using full genome comparison, inferred using SDT v1.2 [12].

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