

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

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| **Code assigned:** | ***2023.022D*** |  |
| **Short title:** Establishing one new order (*Ringavirales*), one new family and associated genera and species in the class *Arfiviricetes* (phylum *Cressdnaviricota*) | | |
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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**

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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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| 2023.022D.N.v2.Ringavirales\_1no\_1nf\_8ng\_15nsp.xlsx |

**Abstract**

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| We propose a new order, *Ringavirales*, in the class *Arfiviricetes* (phylum *Cressdnaviricota*), including a new family *Pecoviridae* with 8 genera and 15 species. |

**Text of proposal**

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| |  | | --- | | CRESSV1 is an informal group of viruses in the phylum *Cressdnaviricota* [1-4]. Within this group various viruses have been identified from animal samples, including primates.  In the global phylogeny of Rep proteins, CRESSV1 forms a clade outside of existing orders (Figure 1) and we propose considering it as a separate new order within the class *Arfiviricetes*. The order name, *Ringavirales*, is derived from Latin **ringa** for “ring”, referring to circularity of the virus genomes. Phan et al. [5] named the human derived viruses in this group as pecoviruses - **Pe**ruvian stool-associated cir**co**-like viruses. Thus, we propose to name the family *Pecoviridae.*  **Genus and species demarcation**  We undertook comparative genomics and phylogenetic analyses of the Rep proteins of members of this group to determine their relationships. 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 cressdnaviruses [6-8].  **Genera**  Etymology of genus names   1. *Intivirus: inti - sun (Quechua - Cuzco dialect)* 2. *Cinchivirus: Cinchi Roca - The second Inca, son of Manco Capac* 3. *Quillavirus: Quilla - Moon (Quechua)* 4. *Tambotovirus: Tambotoco - The cave from which the first mythical Incas emerged* 5. *Amaruvirus: Tupac Amaru - Youngest son of Manco Inca* 6. *Yaviravirus: Yavira - Shrine on the slope of Picchu mountain* 7. *Macochavirus: Mamacocha - Mother Lake* 8. *Capamivirus: Capac Raymi - Ritual month including the December solstice (Quechua)*   Etymology of species epithets   1. *Runais: runa - adult person (Quechua - Cuzco dialect)* 2. *quris: quri - gold (Quechua - Cuzco dialect)* 3. *surtixais: surtixa - ring (Quechua - Cuzco dialect)* 4. *asulis: asul - blue (Quechua - Cuzco dialect)* 5. *quwis: quwi - guinea pig (Quechua - Cuzco dialect)* 6. *pakuis: paku - alpaca (Quechua - Ayacucho dialect)* 7. *akarais: k'akara - crest of a bird (Quechua - Cuzco dialect)* 8. *tarukais: taruka - deer (Quechua - Cuzco dialect)* 9. *akais: aka - feces (Quechua - Cuzco dialect)* 10. *masis: masi - fellow man (Quechua - Cuzco dialect)* 11. *kapatais: kapatas - foreman (Quechua - Cuzco dialect)* 12. *kucis: k''ući - pig (Quechua - Cuzco dialect)* 13. *uywais: uywa - domestic animal (Quechua - Cuzco dialect)* 14. *cipis: ćipi - monkey (Quechua - Ayacucho dialect)* 15. *muyuis: muyu - round, spherical (Quechua - Cuzco dialect)* | |

**Supporting evidence**

**Table 1:** Summary of the viruses classified in the new order *Ringavirales* and family *Pecoviridae.*

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| **Genus** | **Species** | **Accession #** | **Virus** | **Year** | **Country** | **Host /source** | **Isolate** |
| *Intivirus* | *Intivirus runa* | KT600066 | human feces pecovirus PeCV-NI | 2005 | Nicaragua | *Homo sapiens* | PeCV-NI |
| *Intivirus* | *Intivirus runa* | KT600067 | human feces pecovirus PeCV-CH | 2006 | Chile | *Homo sapiens* | PeCV-CH |
| *Intivirus* | *Intivirus runa* | KT600065 | human feces pecovirus PeCV-PE | 2013 | Peru | *Homo sapiens* | PeCV-PE |
| *Intivirus* | *Intivirus runa* | LC708000 | pecovirus sp. CRESSV1-84-AMS-02 DNA | 1984 | Netherlands | *Homo sapiens* | CRESSV1-84-AMS-02 |
| *Intivirus* | *Intivirus quri* | KU043425 | unidentified circular ssDNA virus cg8094 | 2014 | USA | *Macaca mulatta* | cg8094 |
| *Intivirus* | *Intivirus surtixa* | MG571897 | unidentified circular ssDNA virus V11B | 2015 | Venezuela | *Homo sapiens* | V11B |
| *Intivirus* | *Intivirus surtixa* | MG571895 | unidentified circular ssDNA virus clone V9C2 | 2015 | Venezuela | *Homo sapiens* | V9C2 |
| *Cinchivirus* | *Cinchivirus asul* | OQ599927 | nanfec virus 3 V16\_S08a | - | USA: Arizona | *Canis latrans* | V16\_S08a |
| *Cinchivirus* | *Cinchivirus quwi* | KY370035 | rodent circovirus RtBi-CV-1/FJ2015 | 2015 | China | *Bandicota indica* | RtBi-CV-1/FJ2015 |
| *Quillavirus* | *Quillavirus paku* | KM573766 | dromedary stool-associated circular ssDNA virus DcSCV\_c1054 | 2013 | United Arab Emirates | *Camelus dromedarius* | DcSCV\_c1054 |
| *Tambotovirus* | *Tambotovirus akara* | MN379592 | chicken virus mg8\_273 | 2017 | USA | *Gallus gallus* | mg8\_273 |
| *Tambotovirus* | *Tambotovirus akara* | MN379585 | chicken virus mg4\_657 | 2017 | USA | *Gallus gallus* | mg4\_657 |
| *Tambotovirus* | *Tambotovirus akara* | MK012530 | circoviridae sp. ctbf43 | 2017 | USA | *turkey tissue* | ctbf43 |
| *Tambotovirus* | *Tambotovirus akara* | MT138080 | CRESS virus sp. w3chi091cir4 | 2016 | China | Avian | w3chi091cir4 |
| *Tambotovirus* | *Tambotovirus akara* | MN928925 | CRESS virus sp. gps222cir1 | 2018 | China | Chrysolophuspictus | gps222cir1 |
| *Amaruvirus* | *Amaruvirus taruka* | MN621476 | CRESS virus sp. UJSL017 | 2016 | China | *Moschus erezovskii* | UJSL017 |
| *Amaruvirus* | *Amaruvirus aka* | KJ206566 | human circovirus VS6600022 | - | Netherlands | *Homo sapiens* | VS6600022 |
| *Amaruvirus* | *Amaruvirus masi* | LC708001 | pecovirus sp. CRESSV1-84-AMS-03 DNA | 1984 | Netherlands | *Homo sapiens* | CRESSV1-84-AMS-03 |
| *Amaruvirus* | *Amaruvirus masi* | KU043411 | unidentified circular ssDNA virus cg1855 | 2014 | USA | *Macaca mulatta* | cg1855 |
| *Yaviravirus* | *Yaviravirus kapata* | KU043424 | unidentified circular ssDNA virus cg5269 | 2014 | USA | *Macaca mulatta* | cg5269 |
| *Yaviravirus* | *Yaviravirus kapata* | LC708002 | pecovirus sp. CRESSV1-84-AMS-04 DNA | 1984 | Netherlands | *Homo sapiens* | CRESSV1-84-AMS-04 |
| *Yaviravirus* | *Yaviravirus kapata* | KJ417134 | porcine stool-associated circular virus 4 CP2 | 2011 | USA | *Sus scrofa domesticus* | CP2 |
| *Macochavirus* | *Macochavirus kuci* | MW601954 | porcine associated circular DNA virus-3 P20\_37\_BR | 2014 | Brazil | *Sus scrofa domesticus* | P20\_37\_BR |
| *Macochavirus* | *Macochavirus uywa* | MW601953 | porcine associated circular DNA virus-2 P20\_36\_BR | 2014 | Brazil | *Sus scrofa domesticus* | P20\_36\_BR |
| *unclassified* | *unclassified* | KT862256 | bovine faeces associated circular DNA molecule 1 5\_Fec60361\_cow | 2011 | New Zealand | *Sus scrofa domesticus* | 5\_Fec60361\_cow |
| *Macochavirus* | *Macochavirus uywa* | MK462122 | fur seal faeces associated circular DNA virus CHN | 2017 | China | *Sus scrofa domesticus* | CHN |
| *Macochavirus* | *Macochavirus uywa* | LC133373 | fur seal faeces associated circular DNA virus DNA, isolate: JPN1 | 2014 | Japan | *Sus scrofa domesticus* | JPN1 |
| *Macochavirus* | *Macochavirus uywa* | KF246569 | fur seal faeces associated circular DNA virus as50 | 2012 | New Zealand | *Arctocephalus forsteri* | as50 |
| *Macochavirus* | *Macochavirus uywa* | MW847284 | fur seal faeces associated circular DNA virus 451\_2 | 2012 | Hungary | *Sus scrofa* | 451\_2 |
| *Macochavirus* | *Macochavirus uywa* | MW847283 | fur seal faeces associated circular DNA virus 306\_2 | 2012 | Hungary | *Sus scrofa* | 306\_2 |
| *Capamivirus* | *Capamivirus cipi* | MH616647 | Circoviridae sp. ctia25 | 2017 | USA | *Macaca mulatta* | ctia25 |
| *Capamivirus* | *Capamivirus muyu* | LC708004 | pecovirus sp. CRESSV1-94-AMS-01 | 1994 | Netherlands | *Homo sapiens* | CRESSV1-94-AMS-01 |
| *Capamivirus* | *Capamivirus muyu* | LC708003 | pecovirus sp. CRESSV1-84-AMS-05 DNA | 1984 | Netherlands | *Homo sapiens* | CRESSV1-84-AMS-05 |
| *Capamivirus* | *Capamivirus muyu* | LC707999 | pecovirus sp. CRESSV1-84-AMS-01 DNA | 1984 | Netherlands | *Homo sapiens* | CRESSV1-84-AMS-01 |

**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 [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.

**A screen shot of a computer

Description automatically generated**

**Figure 2:** Maximum likelihood phylogenetic tree of the Rep sequences of the members of the*Pecoviridae* 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 *Bacilladnaviridae*. 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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Description automatically generated**

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

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