

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

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| **Code assigned:** | **2020.016D** |  |
| **Short title:** Create six new genera and 42 new species (*Cremevirales*: *Smacoviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| *Circoviridae* 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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| --- | --- | --- |
| **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 | August 5, 2020 |
| Date of this revision (if different to above) | August 23, 2020 |

**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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| 2020.016D.R.Smacoviridae\_6ngen\_42nsp.xls |

**Abstract**

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| The family *Smacoviridae* currently includes 6 genera and 42 species. We revise the taxonomy of the family based on a large number of new genomic sequences deposited in GenBank. We propose to establish 6 new genera, 42 new species and propose a revision to species names to “Genus + freeform epithet” binomial system. |

**Text of proposal**

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| |  | | --- | | Smacoviruses have small circular ssDNA genomes (2.3-2.9 kb) encoding rolling-circle replication initiation proteins (Rep) and unique capsid proteins in an ambience orientation. The family *Smacoviridae* currently comprises 6 genera and 42 species, which were established based on 83 full genomes available in 2017:  *Bovismacovirus* (3 species, 3 genomes)  *Cosmacovirus* (1 species, 1 genomes)  *Dragsmacovirus* (1 species, 1 genomes)  *Drosmacovirus* (3 species, 3 genomes)  *Huchismacovirus* (7 species, 27 genomes)  *Porprismacovirus* (27 species, 47 genomes)  We propose to change the virus species names for this family to a manageable and easy to navigate option using a “Genus + freeform epithet” binomial system. The name changes are summarized in Table 1.  Since the last taxonomy proposal in 2017 [5], 138 new genomes of smacoviruses have been made available in GenBank. Using the previously established demarcation criteria [5], we use a Rep amino acid sequence-based phylogeny to first determine the genus-level classification of these viral sequences (Figure 1) and then use a genome-wide pairwise sequence identity to classify these into species-level taxa (77% pairwise identity threshold).  Based on the Rep phylogeny, we establish 6 new genera. Two of these genera accommodate two previously classified viruses in the genus *Huchismacovirus* (*Bovine associated huchismacovirus 1; Bovine associated huchismacovirus 2*). All the changes are summarized in Table 2.   * ***Babo****smacovirus* (name derived from **babo**on – the host /source of the virus) * ***Bonze****smacovirus* (name derived from **bo**vine **N**ew **Ze**aland – the host /source of the virus) * ***Bosta****smacovirus* (name derived from **Bos** **ta**urus– the host /source of the virus) * ***Felis****macovirus* (name derived from **feli**ne – the host /source of the virus) * ***Inpea****smacovirus* (name derived from **In**dian **pea**flowl– the host /source of the virus) * ***Simi****smacovirus* (name derived from **Simi**nan – the simian host /source of the virus). | |

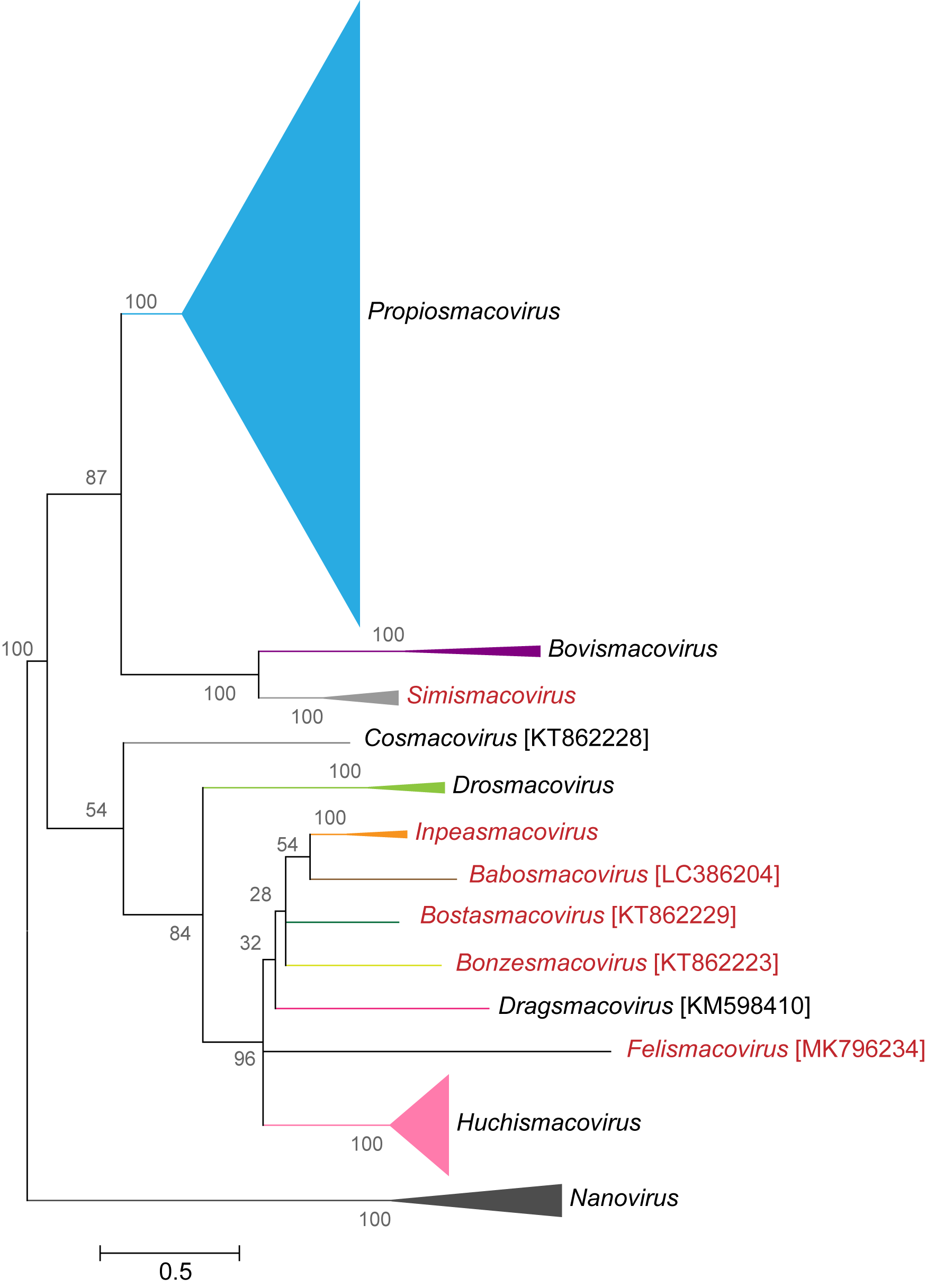
**Supporting evidence**

**Table 1:** Summary of name changes from current species names to binomial system (Genus + freeform epithet). New names are in red font.

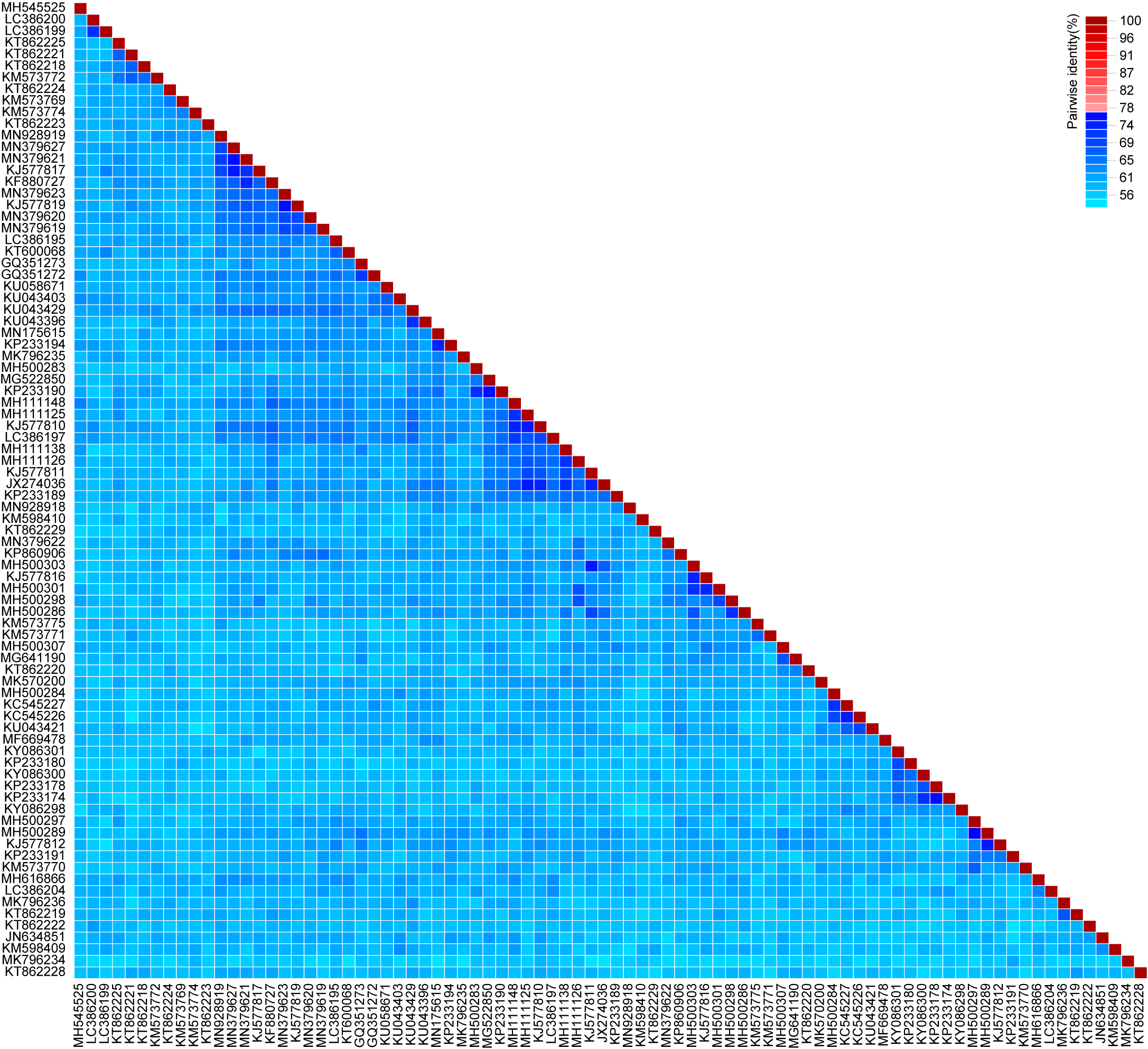
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| --- | --- | --- | --- | --- |
| **Genus** | **New species name** | **Current species name** | **Virus name** | **Accession #** |
| *Bovismacovirus* | *Bovismacovirus bovas1* | *Bovine associated bovismacovirus 1* | Circoviridae bovine stool/BK/KOR/2011 | JN634851 |
|  | *Bovismacovirus bovas2* | *Bovine associated bovismacovirus 2* | bovine faeces associated smacovirus 3 | KT862222 |
|  | *Bovismacovirus draga1* | *Dragonfly associated bovismacovirus 1* | Odonata-associated circular virus-21 | KM598409 |
| *Cosmacovirus* | *Cosmacovirus bovas1* | *Bovine associated cosmacovirus 1* | bovine faeces associated smacovirus 4 | KT862228 |
| *Dragsmacovirus* | *Dragsmacovirus draga1* | *Dragonfly associated dragsmacovirus 1* | Odonata-associated circular virus-5 | KM598410 |
| *Drosmacovirus* | *Drosmacovirus bovas1* | *Bovine associated drosmacovirus 1* | bovine faeces associated smacovirus 5 | KT862224 |
|  | *Drosmacovirus camas1* | *Camel associated drosmacovirus 1* | dromedary stool-associated circular ssDNA virus | KM573769 |
|  | *Drosmacovirus camas2* | *Camel associated drosmacovirus2* | dromedary stool-associated circular ssDNA virus | KM573774 |
| *Huchismacovirus* | *Huchismacovirus chicas1* | *Chicken associated huchismacovirus 1* | chicken associated smacovirus | KY086301 |
|  | *Huchismacovirus chicas2* | *Chicken associated huchismacovirus 2* | chicken associated smacovirus | KY086300 |
|  | *Huchismacovirus humas1* | *Human associated huchismacovirus 1* | human smacovirus 1 | KP233180 |
|  | *Huchismacovirus humas2* | *Human associated huchismacovirus 2* | human smacovirus 1 | KP233174 |
|  | *Huchismacovirus humas3* | *Human associated huchismacovirus 3* | human smacovirus 1 | KP233178 |
| *Porprismacovirus* | *Porprismacovirus bovas1* | *Bovine associated porprismacovirus 1* | bovine faeces associated smacovirus 2 | KT862218 |
|  | *Porprismacovirus camas1* | *Camel associated porprismacovirus 1* | dromedary stool-associated circular ssDNA virus | KM573772 |
|  | *Porprismacovirus camas2* | *Camel associated porprismacovirus 2* | dromedary stool-associated circular ssDNA virus | KM573770 |
|  | *Porprismacovirus camas3* | *Camel associated porprismacovirus 3* | dromedary stool-associated circular ssDNA virus | KM573771 |
|  | *Porprismacovirus camas4* | *Camel associated porprismacovirus 4* | dromedary stool-associated circular ssDNA virus | KM573775 |
|  | *Porprismacovirus chimas1* | *Chimpanzee associated porprismacovirus 1* | chimpanzee stool associated circular ssDNA virus | GQ351272 |
|  | *Porprismacovirus chimas2* | *Chimpanzee associated porprismacovirus 2* | chimpanzee stool associated circular ssDNA virus | GQ351273 |
|  | *Porprismacovirus goras1* | *Gorilla associated porprismacovirus 1* | gorilla smacovirus | KP233191 |
|  | *Porprismacovirus howas1* | *Howler monkey associated porprismacovirus 1* | black howler monkey smacovirus | KP233189 |
|  | *Porprismacovirus humas1* | *Human associated porprismacovirus 1* | human feces smacovirus 2 | KT600068 |
|  | *Porprismacovirus humas2* | *Human associated porprismacovirus 2* | chimpanzee smacovirus | KP233190 |
|  | *Porprismacovirus lemas1* | *Lemur associated porprismacovirus 1* | lemur smacovirus | KP233194 |
|  | *Porprismacovirus porci1* | *Porcine associated porprismacovirus 1* | porcine associated stool circular virus | JX274036 |
|  | *Porprismacovirus porci2* | *Porcine associated porprismacovirus 2* | porcine stool-associated circular virus 2 | KC545226 |
|  | *Porprismacovirus porci3* | *Porcine associated porprismacovirus 3* | porcine stool-associated circular virus 3 | KC545227 |
|  | *Porprismacovirus porci4* | *Porcine associated porprismacovirus 4* | porcine stool-associated circular virus 1 | KJ577810 |
|  | *Porprismacovirus porci5* | *Porcine associated porprismacovirus 5* | porcine stool-associated circular virus 1 | KJ577811 |
|  | *Porprismacovirus porci6* | *Porcine associated porprismacovirus 6* | porcine stool-associated circular virus 6 | KJ577819 |
|  | *Porprismacovirus porci7* | *Porcine associated porprismacovirus 7* | porcine stool-associated circular virus 7 | KJ577812 |
|  | *Porprismacovirus porci8* | *Porcine associated porprismacovirus 8* | porcine stool-associated circular virus 8 | KJ577817 |
|  | *Porprismacovirus porci9* | *Porcine associated porprismacovirus 9* | porcine stool-associated circular virus 9 | KJ577816 |
|  | *Porprismacovirus porci10* | *Porcine associated porprismacovirus 10* | porcine faeces associated smacovirus 1 | KT862225 |
|  | *Porprismacovirus ratas1* | *Rat associated porprismacovirus 1* | rat stool-associated circular ssDNA virus | KP860906 |
|  | *Porprismacovirus sheas1* | *Sheep associated porprismacovirus 1* | sheep faeces associated smacovirus 1 | KT862220 |
|  | *Porprismacovirus sheas2* | *Sheep associated porprismacovirus 2* | sheep faeces associated smacovirus 2 | KT862221 |
|  | *Porprismacovirus sheas3* | *Sheep associated porprismacovirus 3* | sheep faeces associated smacovirus 3 | KT862219 |
|  | *Porprismacovirus turas1* | *Turkey associated porprismacovirus 1* | turkey stool associated circular ssDNA virus | KF880727 |

**Table 2:** Summary of new species in established genera. Species names are prosed with Genus + freeform epithet. New names are in red font.

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| --- | --- | --- | --- | --- |
| **Genus** | **New species name** | **Current species name** | **Virus name** | **Accession #** |
| *Babosmacovirus* | *Babosmacovirus babas1* |  | Papio cynocephalus associated smacovirus | LC386204 |
| *Bonzesmacovirus* | *Bonzesmacovirus bovas1* | *Bovine associated huchismacovirus 1* | bovine faeces associated smacovirus 1 | KT862223 |
| *Bostasmacovirus* | *Bostasmacovirus bovas1* | *Bovine associated huchismacovirus 2* | bovine faeces associated smacovirus 6 | KT862229 |
| *Felismacovirus* | *Felismacovirus lynas1* |  | Lynx rufus smacovirus 1 | MK796234 |
| *Inpeasmacovirus* | *Inpeasmacovirus peafo1* |  | Smacoviridae sp. | MN928918 |
|  | *Inpeasmacovirus humas1* |  | human associated porprismacovirus | MH500283 |
| *Simismacovirus* | *Simismacovirus malbas1* |  | Chlorocebus cynosuros associated smacovirus | LC386199 |
|  | *Simismacovirus malbas2* |  | Chlorocebus cynosuros associated smacovirus | LC386200 |
| *Porprismacovirus* | *Porprismacovirus alecas1* |  | Alces alces faeces associated smacovirus MP78 | MG641190 |
|  | *Porprismacovirus avias1* |  | avian associated porprismacovirus | MN175615 |
|  | *Porprismacovirus capas1* |  | capybara associated smacovirus 1\_cap1\_104 | MK570200 |
|  | *Porprismacovirus bovas2* |  | cattle blood-associated circovirus-like virus | MF669478 |
|  | *Porprismacovirus chicas1* |  | chicken associated smacovirus | KY086298 |
|  | *Porprismacovirus chicas2* |  | chicken smacovirus mg4\_881 | MN379619 |
|  | *Porprismacovirus chicas4* |  | chicken smacovirus mg4\_885 | MN379620 |
|  | *Porprismacovirus chicas6* |  | chicken smacovirus mg4\_964 | MN379621 |
|  | *Porprismacovirus chicas7* |  | chicken smacovirus mg5\_1081 | MN379622 |
|  | *Porprismacovirus chicas3* |  | chicken smacovirus mg5\_1212 | MN379623 |
|  | *Porprismacovirus chicas5* |  | chicken smacovirus mg7\_67 | MN379627 |
|  | *Porprismacovirus malbas1* |  | Chlorocebus cynosuros associated smacovirus | LC386195 |
|  | *Porprismacovirus flas1* |  | fly associated circular virus 4 | MH545525 |
|  | *Porprismacovirus goas1* |  | goat associated porprismacovirus | MH500307 |
|  | *Porprismacovirus humas4* |  | human associated porprismacovirus 3 | MH111125 |
|  | *Porprismacovirus humas3* |  | human feces smacovirus 3 | MG522850 |
|  | *Porprismacovirus lynas2* |  | Lynx rufus smacovirus 2 | MK796235 |
|  | *Porprismacovirus macas6* |  | Macaca mulatta feces associated virus 10 | KU043396 |
|  | *Porprismacovirus macas4* |  | Macaca mulatta feces associated virus 2 | KU043403 |
|  | *Porprismacovirus macas3* |  | Macaca mulatta feces associated virus 3 | KU058671 |
|  | *Porprismacovirus macas2* |  | Macaca mulatta feces associated virus 4 | KU043429 |
|  | *Porprismacovirus macas1* |  | Macaca mulatta feces associated virus 7 | KU043421 |
|  | *Porprismacovirus macas5* |  | macaque stool associated virus 11 | MH616866 |
|  | *Porprismacovirus leo1* |  | Panthera leo smacovirus 1 | MK796236 |
|  | *Porprismacovirus babas1* |  | Papio cynocephalus associated smacovirus | LC386197 |
|  | *Porprismacovirus porci11* |  | porcine associated porprismacovirus | MH111138 |
|  | *Porprismacovirus porci12* |  | porcine associated porprismacovirus | MH500297 |
|  | *Porprismacovirus porci13* |  | porcine associated porprismacovirus | MH500303 |
|  | *Porprismacovirus porci14* |  | porcine associated porprismacovirus | MH500301 |
|  | *Porprismacovirus porci15* |  | porcine associated porprismacovirus | MH500286 |
|  | *Porprismacovirus porci16* |  | porcine associated porprismacovirus | MH500298 |
|  | *Porprismacovirus porci17* |  | porcine associated porprismacovirus | MH500284 |
|  | *Porprismacovirus porci18* |  | porcine associated porprismacovirus | MH111148 |
|  | *Porprismacovirus porci19* |  | porcine associated porprismacovirus | MH111126 |
|  | *Porprismacovirus porci20* |  | porcine associated porprismacovirus | MH500289 |
|  | *Porprismacovirus peafo1* |  | Smacoviridae sp. | MN928919 |

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**Figure 1:** Maximum likelihood phylogenetic tree of the Rep amino acid sequences of 545 smacovirus sequences together with a subset of nanoviruses, which were used as an outgroup. The Rep sequence alignment was constructed with MAFFT [3] and trimmed with TrimAL [1] using the gappyout option. The final alignment contained 202 amino-acid sites and was used to infer a Maximum likelihood phylogenetic with PhyML [2] with LG+F+I+G4 substitution model. Numbers at the nodes represent bootstrap support values (%).

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**Figure 2:** Pairwise identity matrix of the genome sequences of a representative member from each species of smacoviruses (n=84) determined using SDT v1.2 [4]

**References**

1. Capella-Gutierrez S, Silla-Martinez JM, Gabaldon T (2009) trimAl: a tool for automated alignment trimming in large-scale phylogenetic analyses. Bioinformatics 25:1972-1973. PMID: 19505945; DOI: 10.1093/bioinformatics/btp348

2. 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

3. Katoh K, Rozewicki J, Yamada KD (2019) MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. Brief Bioinform 20:1160-1166. PMID: 28968734; DOI: 10.1093/bib/bbx108

4. 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: 2525989; DOI: 10.1371/journal.pone.0108277

5. Varsani A, Krupovic M (2018) Smacoviridae: a new family of animal-associated single-stranded DNA viruses. Arch Virol 163:2005-2015. PMID: 29572596; DOI: 10.1007/s00705-018-3820-z