This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

For guidance, see the notes written in blue and the separate document “Help with completing a taxonomic proposal”

Please try to keep related proposals within a single document.

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.011D*** | | | | (to be completed by ICTV officers) |
| **Short title:** New family called *Smacoviridae* with six genera and 43 species | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Arvind Varsani and Mart Krupovic | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| [arvind.varsani@asu.edu](mailto:arvind.varsani@asu.edu); [mart.krupovic@pasteur.fr](mailto:mart.krupovic@pasteur.fr) | | | | | |
| **List the ICTV study group(s) that have seen this proposal:** | | | | | |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | | **Chair of the Animal DNA Viruses and Retroviruses Subcommittee** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | 11 June 2017 | |
| Date of this revision (if different to above): | | | | 21 June 2017 | |

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

**Part 2**: **PROPOSED TAXONOMY**

|  |
| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet:** 2017.011D.N.v1.Smacoviridae |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

**Part 4:** **APPENDIX**: supporting material

The circular replication-initiation protein encoding single-stranded (CRESS) DNA viruses associated with eukaryotic hosts are currently classified by the International Committee on Taxonomy of Viruses (ICTV) into four families, namely *Circoviridae, Genomoviridae, Geminiviridae* and *Nanoviridae*. The replication-initiation protein (Rep) is reasonably well conserved across these four families, whereas the corresponding capsid proteins (CP) are not recognizably similar between viruses from different families.

With the advent of metagenomics approaches, a large diversity of unknown CRESS DNA viruses has been uncovered in various environmental, plant, and animal samples. Sampling of animal faecal matter has proved to be particularly efficient for the discovery of a wide variety of novel viral types, in particular CRESS DNA viruses and small dsDNA viruses. One of such virus groups, unofficially referred to as smacoviruses or chipoviruses, has been recently identified in faecal matter of various animals (Table 1):

*Alouatta caraya* (n=1),

*Bos taurus* (n=7),

*Camelus dromedarius* (n=6),

*Gallus gallus* (n=4),

*Gorilla gorilla* (n=2),

*Homo sapiens* (n=26),

*Lemur catta* (n=1),

*Lepus europaeus* (n=1),

*Libellula quadrimaculata* (n=1),

*Meleagris gallopavo* (n=1),

*Ovis aries* (n=3),

*Pan troglodytes* (n=7),

*Rattus norvegicus* (n=3),

*Sus scrofa domesticus* (n=18),

*Trichosurus vulpecula* (n=1).

In addition, two smacoviruses have been identified in the abdomen ofdragonflies:

*Erythrodiplax fusca* (n=1),

*Libellula quadrimaculata* (n=1).

None of these viruses have been cultured or found in animal tissue sample. Nonetheless, the viruses have been discovered using viral metagenomics approaches and for majority of the smacoviruses, the genomes have been verified by either PCR amplification using abutting primers and Sanger sequencing of these products or amplification, cloning and Sanger sequencing of the recombinant plasmids.

Smacoviruses have two main open reading frames, encoding the Rep and CP (Figure 1), and their genomes range in size from 2343 to 2861nucleotides. In most smacoviruses the two ORFs are bidirectionally organised. The Reps of smacoviruses are homologous but phylogenetically distinct from those of CRESS DNA viruses from other families (Figure 2). By contrast, although shared among smacoviruses, the CPs do not display recognizable sequence similarity to the CPs of other known viruses.

To recognize the distinctiveness of smacoviruses, we propose to classify them into a new family *Smacoviridae* (*smaco-* stands for *sma*ll *c*ircular DNA viruses). Analysis of the genome-wide pairwise identities of the 83 smacoviruses (Figure 3) shows 45% diversity amongst these genomes. The plot of the distribution of pairwise identities shows a trough between 76 and 88%. Hence, for this group of viruses, 77% genome-wide pairwise identity is proposed as a species demarcation threshold. Using this approach, the 83 smacoviruses can be assigned to 43 species.

Maximum likelihood phylogenetic analysis of the Rep sequences of all 83 smacoviruses reveals four main clusters with >90% branch support and two singletons (Figure 4). Rep sequences within each of the four clades in general share >40% pairwise identity, whereas sequences from different phylogenetic clades show less than 40% identity to each other. We note that phylogenetic trees produced using complete genome (Figure 5) and CP (Figure 6) sequences are not congruent with the Rep phylogeny, presumably due to intra-familial recombination between different smacovirus genomes resulting in chimeric entities encoding Rep and CP with different evolutionary histories. Given that smacovirus Reps are considerably more conserved than CPs and due to the fact that Reps are the only proteins shared across all CRESS DNA viruses, we propose establishing genera based on the phylogenetic analysis of the Rep sequences coupled with their pairwise sequence identity. Accordingly, 40% Rep amino acid sequence identity coupled with strong phylogenetic support is proposed as a genus level demarcation threshold.

We propose the following names for the six genera

Bovismacovirus: **Bovi**ne **smacovirus**

3 species (Table 1);

Drosmacovirus: **Dro**medary **smacovirus**

3 species (Table 1);

Huchismacovirus: **Hu**man and **chi**cken **smacovirus**

7 species (Table 1);

Porprismacovirus: **Por**cine and **pri**mate **smacovirus**

28 species (Table 1);

Cosmacovirus: **Co**w **smacovirus**

1 species (Table 1);

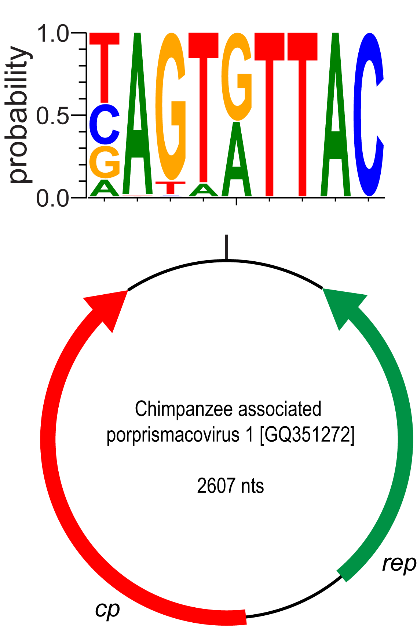
Dragsmacovirus: **Drag**onfly **smacovirus.**

1 species (Table 1).

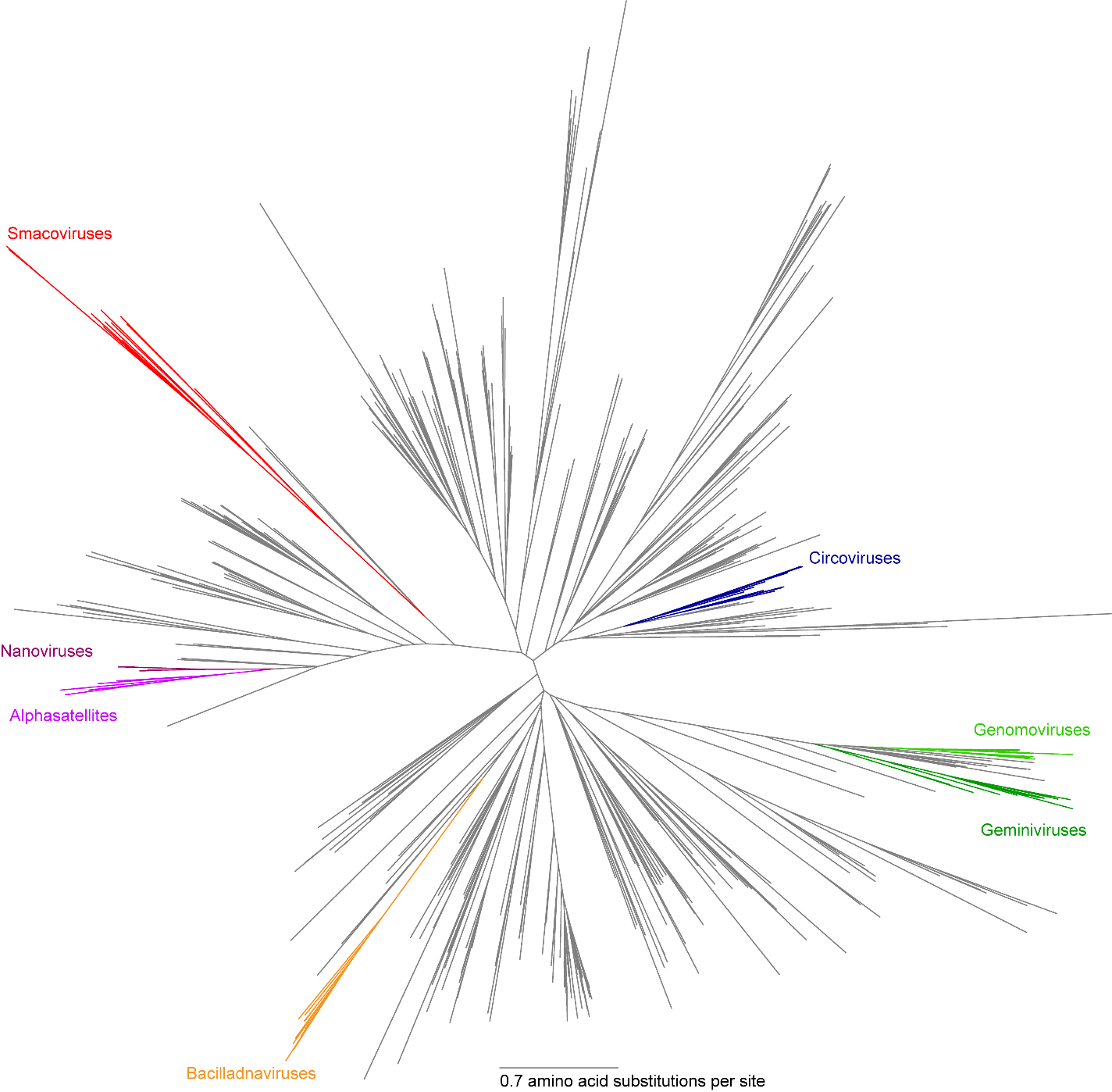
We would like to note that the species Sheep associated porprismacovirus 3, Bovine associated huchismacovirus 1 and Bovine associated huchismacovirus 2 have been tentatively assigned to Proprosmavirus and Huchismacovirus. It is highly likely that as the more sequences become available the divergent taxa (Figures 4 and 5) of these species may represent new genera.

**Table 1:** Summary of taxa that are part of the family *Smacoviridae*

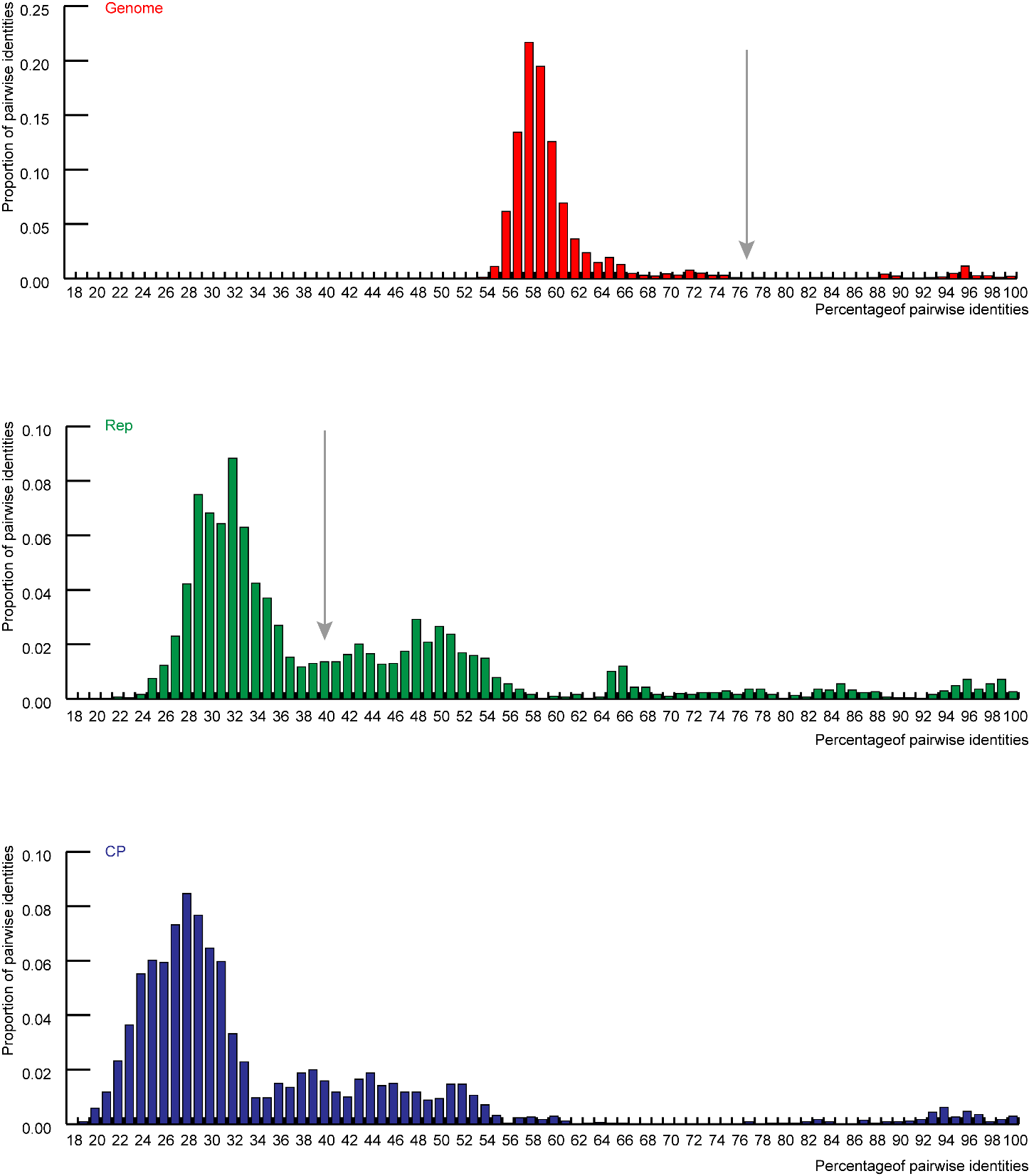
|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | **Isolation source** | | |  |
| **Genus** | **Species** | **Accession #** | **Isolate** | **Common**  **name** | **Host** | **Country** | **Reference** |
| *Bovismacovirus* | *Bovine associated bovismacovirus 1* | JN634851 | CP11-49-3 | Cow | *Bos taurus* | South Korea | (Kim et al., 2012) |
|  | *Bovine associated bovismacovirus 2* | KT862222 | 48\_Fec5\_cow | Cow | *Bos taurus* | New Zealand | (Steel et al., 2016) |
|  | *Dragonfly associated bovismacovirus 1* | KM598409 | OdasCV-21-US-1679SC3-12 | Dragonfly | *Erythrodiplax fusca* | USA | (Dayaram et al., 2015) |
| *Drosmacovirus* | *Camel associated drosmacovirus 1* | KM573769 | DcSCV\_c1359 | Camel | *Camelus dromedarius* | United Arab Emirates | (Woo et al., 2014) |
|  | *Camel associated drosmacovirus2* | KM573774 | DcSCV\_c1330 | Camel | *Camelus dromedarius* | United Arab Emirates | (Woo et al., 2014) |
|  | *Bovine associated drosmacovirus 1* | KT862224 | 48\_Fec9\_cow | Cow | *Bos taurus* | New Zealand | (Steel et al., 2016) |
| *Huchismacovirus* | *Bovine associated huchismacovirus 1* | KT862223 | 48\_Fec59973\_cow | Cow | *Bos taurus* | New Zealand | (Steel et al., 2016) |
|  | *Bovine associated huchismacovirus 2* | KT862229 | GP3\_46075\_cow | Cow | *Bos taurus* | New Zealand | (Steel et al., 2016) |
|  | *Chicken associated huchismacovirus 1* | KY086301 | RS/BR/2015/2 | Chicken | *Gallus gallus* | Brazil | (Lima et al., 2017) |
|  | *Chicken associated huchismacovirus 2* | KY086300 | RS/BR/2015/3 | Chicken | *Gallus gallus* | Brazil | (Lima et al., 2017) |
|  | *Human associated huchismacovirus 1* | KP233180 | Oregon/6/2011/GottageGrove/5A1 | Human | *Homo sapiens* | USA | (Ng et al., 2015) |
|  |  | KP233181 | Oregon/6/2011/GottageGrove/B3 | Human | *Homo sapiens* | USA | (Ng et al., 2015) |
|  |  | KP233182 | Oregon/6/2011/GottageGrove/B45 | Human | *Homo sapiens* | USA | (Ng et al., 2015) |
|  |  | KP233183 | Oregon/8/2011/Portland/D56 | Human | *Homo sapiens* | USA | (Ng et al., 2015) |
|  |  | KP233185 | Virginia/2/2012/Albemarle/5I17 | Human | *Homo sapiens* | USA | (Ng et al., 2015) |
|  |  | KP233186 | Virginia/2/2012/Chesapeake/J23 | Human | *Homo sapiens* | USA | (Ng et al., 2015) |
|  |  | KP233188 | Virginia/12/2011/Albemarle/G16 | Human | *Homo sapiens* | USA | (Ng et al., 2015) |
|  |  | KP233193 | Orgeon/8/2011/Portland/D53 | Human | *Homo sapiens* | USA | (Ng et al., 2015) |
|  |  | KP264964 | France/2/2008/2548 | Human | *Homo sapiens* | France | (Ng et al., 2015) |
|  |  | KP264966 | France/12/2008/3454 | Human | *Homo sapiens* | France | (Ng et al., 2015) |
|  |  | KP264969 | France/6/2008/2871 | Human | *Homo sapiens* | France | (Ng et al., 2015) |
|  |  | KY086299 | RS/BR/2015/4 | Chicken | *Gallus gallus* | Brazil | (Lima et al., 2017) |
|  | *Human associated huchismacovirus 2* | KP233174 | France/8/2008/2444 | Human | *Homo sapiens* | France | (Ng et al., 2015) |
|  |  | KP233175 | France/1/2008/2610 | Human | *Homo sapiens* | France | (Ng et al., 2015) |
|  |  | KP233176 | France/8/2008/2449 | Human | *Homo sapiens* | France | (Ng et al., 2015) |
|  |  | KP233177 | France/4/2009/4265 | Human | *Homo sapiens* | France | (Ng et al., 2015) |
|  |  | KP233184 | Virginia/1/2012/Mecklenburg/H19 | Human | *Homo sapiens* | USA | (Ng et al., 2015) |
|  |  | KP233187 | Virginia/2/2012/Middlesex/I22 | Human | *Homo sapiens* | USA | (Ng et al., 2015) |
|  |  | KP264965 | France/3/2008/2623 | Human | *Homo sapiens* | France | (Ng et al., 2015) |
|  |  | KP264967 | France/12/2008/3454 | Human | *Homo sapiens* | France | (Ng et al., 2015) |
|  | *Human associated huchismacovirus 3* | KP233178 | France/1/2009/3664 | Human | *Homo sapiens* | France | (Ng et al., 2015) |
|  |  | KP233179 | France/1/2009/3663 | Human | *Homo sapiens* | France | (Ng et al., 2015) |
|  |  | KP264968 | France/3/2009/4191 | Human | *Homo sapiens* | France | (Ng et al., 2015) |
| *Porprismacovirus* | *Bovine associated porprismacovirus 1* | KT862218 | 23\_Fec30587\_cow | Cow | *Bos taurus* | New Zealand | (Steel et al., 2016) |
|  | *Camel associated porprismacovirus 1* | KM573772 | DcSCV\_c1378 | Camel | *Camelus dromedarius* | United Arab Emirates | (Woo et al., 2014) |
|  | *Camel associated porprismacovirus 2* | KM573770 | DcSCV\_c1072 | Camel | *Camelus dromedarius* | United Arab Emirates | (Woo et al., 2014) |
|  | *Camel associated porprismacovirus 3* | KM573771 | DcSCV\_c1345 | Camel | *Camelus dromedarius* | United Arab Emirates | (Woo et al., 2014) |
|  | *Camel associated porprismacovirus 4* | KM573775 | DcSCV\_c1358 | Camel | *Camelus dromedarius* | United Arab Emirates | (Woo et al., 2014) |
|  | *Chimpanzee associated porprismacovirus 1* | GQ351272 | DP152 | Chimpanzee | *Pan troglodytes* | Cameroon | (Blinkova et al., 2010) |
|  |  | GQ351275 | GM510 | Chimpanzee | *Pan troglodytes* | Tanzania | (Blinkova et al., 2010) |
|  | *Chimpanzee associated porprismacovirus 2* | GQ351273 | GM495 | Chimpanzee | *Pan troglodytes* | Tanzania | (Blinkova et al., 2010) |
|  |  | GQ351274 | GM476 | Chimpanzee | *Pan troglodytes* | Tanzania | (Blinkova et al., 2010) |
|  |  | GQ351276 | GM488 | Chimpanzee | *Pan troglodytes* | Tanzania | (Blinkova et al., 2010) |
|  |  | GQ351277 | GM415 | Chimpanzee | *Pan troglodytes* | Tanzania | (Blinkova et al., 2010) |
|  | *Chicken associated porprismacovirus 1* | KY086298 | RS/BR/2015/1 | Chicken | *Gallus gallus* | Brazil | (Lima et al., 2017) |
|  | *Gorilla associated porprismacovirus 1* | KP233191 | SF3 | Gorilla | *Gorilla gorilla* | USA | (Ng et al., 2015) |
|  |  | KP233192 | SF4 | Gorilla | *Gorilla gorilla* | USA | (Ng et al., 2015) |
|  | *Howler monkey associated porprismacovirus 1* | KP233189 | SF1 | Howler monkey | *Alouatta caraya* | USA | (Ng et al., 2015) |
|  | *Human associated porprismacovirus 1* | KT600068 | SmaCV2\_ID31 | Human | *Homo sapiens* | Peru | (Phan et al., 2016) |
|  | *Human associated porprismacovirus 2* | KP233190 | SF2 | Chimpanzee | *Pan troglodytes* | USA | (Ng et al., 2015) |
|  |  | KT600069 | SmaCV3\_ID16 | Human | *Homo sapiens* | Peru | (Phan et al., 2016) |
|  |  | KX838317 | BWA1115 | Human | *Homo sapiens* | Botswana | - |
|  |  | KX838318 | BWA7684 | Human | *Homo sapiens* | Botswana | - |
|  | *Lemur associated porprismacovirus 1* | KP233194 | SF5 | Lemur | *Lemur catta* | USA | (Ng et al., 2015) |
|  | *Porcine associated porprismacovirus 1* | JX274036 | Cass | Pig | *Sus scrofa domesticus* | New Zealand | (Sikorski et al., 2013) |
|  |  | KF193403 | J481 | Pig | *Sus scrofa domesticus* | South Korea | (Kim et al., 2014) |
|  |  | KT862226 | 56\_Coc3310\_hare | Hare | *Lepus europaeus* | New Zealand | (Steel et al., 2016) |
|  |  | KT862227 | 59\_Coc3310\_possum | Possum | *Trichosurus vulpecula* | New Zealand | (Steel et al., 2016) |
|  | *Porcine associated porprismacovirus 2* | KC545226 | f | Pig | *Sus scrofa domesticus* | USA | (Cheung et al., 2013) |
|  |  | KJ577818 | TP3 | Pig | *Sus scrofa domesticus* | USA | (Cheung et al., 2015) |
|  | *Porcine associated porprismacovirus 3* | KC545227 | 3L7 | Pig | *Sus scrofa domesticus* | USA | (Cheung et al., 2013) |
|  |  | KC545228 | 4L13 | Pig | *Sus scrofa domesticus* | USA | (Cheung et al., 2013) |
|  |  | KC545229 | 4L5 | Pig | *Sus scrofa domesticus* | USA | (Cheung et al., 2013) |
|  |  | KC545230 | L2T | Pig | *Sus scrofa domesticus* | USA | (Cheung et al., 2013) |
|  | *Porcine associated porprismacovirus 4* | KJ577810 | DP2 | Pig | *Sus scrofa domesticus* | USA | (Cheung et al., 2015) |
|  | *Porcine associated porprismacovirus 5* | KJ577811 | DP3 | Pig | *Sus scrofa domesticus* | USA | (Cheung et al., 2015) |
|  | *Porcine associated porprismacovirus 6* | KJ577819 | XP1 | Pig | *Sus scrofa domesticus* | USA | (Cheung et al., 2015) |
|  | *Porcine associated porprismacovirus 7* | KJ577812 | EP2-A | Pig | *Sus scrofa domesticus* | USA | (Cheung et al., 2015) |
|  |  | KJ577813 | EP2-B | Pig | *Sus scrofa domesticus* | USA | (Cheung et al., 2015) |
|  |  | KJ577814 | EP3-C | Pig | *Sus scrofa domesticus* | USA | (Cheung et al., 2015) |
|  |  | KJ577815 | EP3-D | Pig | *Sus scrofa domesticus* | USA | (Cheung et al., 2015) |
|  | *Porcine associated porprismacovirus 8* | KJ577817 | GP2 | Pig | *Sus scrofa domesticus* | USA | (Cheung et al., 2015) |
|  | *Porcine associated porprismacovirus 9* | KJ577816 | FP1 | Pig | *Sus scrofa domesticus* | USA | (Cheung et al., 2015) |
|  | *Porcine associated porprismacovirus 10* | KT862225 | 49\_Fec25\_pig | Pig | *Sus scrofa domesticus* | New Zealand | (Steel et al., 2016) |
|  | *Rat associated porprismacovirus 1* | KP860906 | KS/11/0577 | Rat | *Rattus norvegicus* | Germany | (Sachsenroder et al., 2014) |
|  |  | KP860907 | Mu/10/1799 | Rat | *Rattus norvegicus* | Germany | (Sachsenroder et al., 2014) |
|  |  | KP860908 | KS/11/0582 | Rat | *Rattus norvegicus* | Germany | (Sachsenroder et al., 2014) |
|  | *Sheep associated porprismacovirus 1* | KT862220 | 47\_Fec58729\_sheep | Sheep | *Ovis aries* | New Zealand | (Steel et al., 2016) |
|  | *Sheep associated porprismacovirus 2* | KT862221 | 47\_Fec60415\_sheep | Sheep | *Ovis aries* | New Zealand | (Steel et al., 2016) |
|  | *Sheep associated porprismacovirus 3* | KT862219 | 47\_Fec58091\_sheep | Sheep | *Ovis aries* | New Zealand | (Steel et al., 2016) |
|  | *Turkey associated porprismacovirus 1* | KF880727 | TuSCV | Turkey | *Meleagris gallopavo* | Hungary | (Reuter et al., 2014) |
| *Cosmacovirus* | *Bovine associated cosmacovirus 1* | KT862228 | GP3\_45917\_cow | Cow | *Bos taurus* | New Zealand | (Steel et al., 2016) |
| *Dragsmacovirus* | *Dragonfly associated dragsmacovirus 1* | KM598410 | OdasCV-5-US-1683LM1-12 | Dragonfly | *Libellula quadrimaculata* | USA | (Dayaram et al., 2015) |



**Figure 1:** Genome organization of a representative smacovirus (chimpanzee associated porprismacovirus 1 [GQ351272]) and a weblogo of the nonanucleotide motif found in smacoviruses.



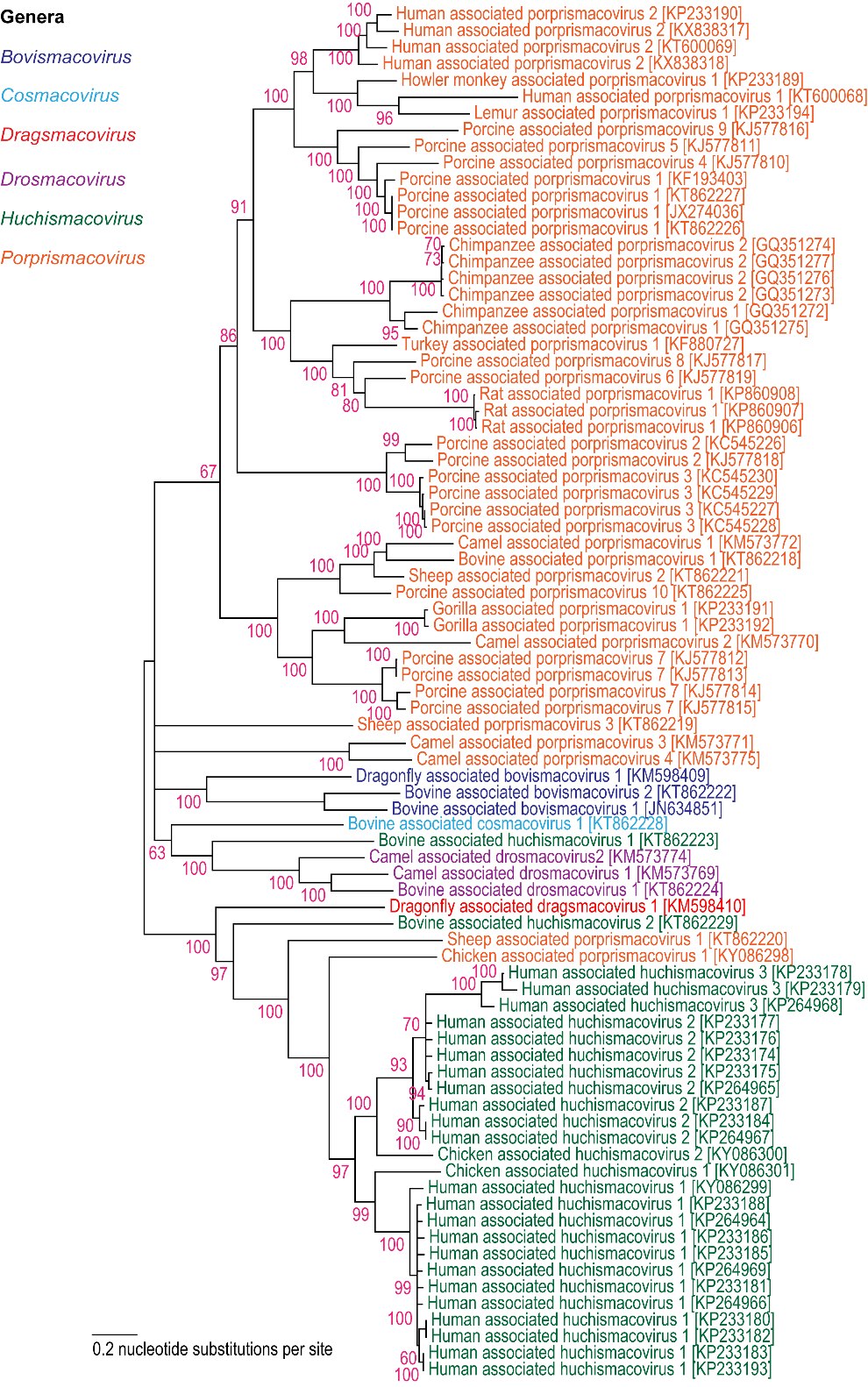
**Figure 2:** Unrooted approximate maximum likelihood phylogenetic tree of Reps of CRESS DNA viruses inferred using FastTree (Price et al., 2010). Major groups of classified viruses (circoviruses, geminiviruses, genomoviruses and nanoviruses) are colour coded. Proposals for the classifications of bacilladnaviruses and alphasatellites associated with geminiviruses and nanoviruses have been submitted to ICTV. Smacoviruses are highlighted in red.



**Figure 3:** Distribution of pairwise identities if the full genome (upper panel), the replication initiation protein (middle panel) and the capsid protein sequences determined using SDT v1.2 (Muhire et al., 2014).

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**Figure 4:** Maximum likelihood phylogenetic tree of the Rep protein sequences of the smacoviruses inferred using PhyML (Guindon et al., 2010) with the LG+G+I+F substitution model. The tree is rooted with the Rep sequences of nanoviruses.

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**Figure 5:** Maximum likelihood phylogenetic tree of the genome sequences inferred using IQ-TREE (Nguyen et al., 2015) with K3Pu+I+G4 substitution model. Branches with <60% bootstrap support have been collapsed and the tree is mid-point rooted.



**Figure 6:** Maximum likelihood phylogenetic tree of the CP sequences of the smacoviruses inferred using PhyML (Guindon et al., 2010) with the LG+G+I+F substitution model. The phylogenetic tree is mid-point rooted.

| additional material in support of this proposal |
| --- |
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| **References:** |
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| **Annex:**  Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance. |