MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	*2015.014a-cS*	(to be completed by ICTV officers)

Short title: In the family *Arteriviridae* create 10 species (1 unassigned, 9 in the genus *Arterivirus*) and rename one species.

Modules attached (modules 1 and 10 are required)	1 ☒ 2 ☒ 3 ☐ 4 ☐ 5 ☐ 6 ☐ 7 ☐ 8 ☒ 9 ☐ 10 ☒

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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 (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	Arterivirus Study Group Nidovirus Study Group

ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV: June 19, 2015
Date of this revision (if different to above):   November 10, 2015

ICTV-EC comments and response of the proposer:

The EC was glad to see taxonomic proposals which were aimed at advancing the taxonomy of the *Arteriviridae*, but were saddened to have to review two competing proposals. We have not yet made a decision on the suitability of either of the proposals, but would like to be able to

approve a new arterivirus taxonomy in the near future. The current arterivirus taxonomy consisting of four virus species in a single genus has been in existence with little change for a number of years and is not particularly useful.

The two proposals were eloquently presented to the EC by Sasha Gorbalenya and Jens Kuhn. The authors listed show that both proposals appear to be well supported by arterivirologists (in fact Magda Dunowska appears on both!).

Both proposals are in broad agreement regarding the assignment of virus species (although that of Bailey et al. suggest an additional species formed by Kinda baboon virus 1), but they differ in their naming conventions. The EC did not support the use of species names consisting of the current genus name, *Arterivirus*, and a number, especially as this was also applied to a virus not included in in that genus.

We (the EC) would like to see a joint proposal (between the Study Group and Bailey et al.) submitted by the end of October 2015 for us to consider. At the very least this should include new species names which would not require renaming if new genera were later proposed (along the lines of Bailey et al.). If possible any new genera should also be proposed at the same time.

Response of the proposers

We have addressed the major criticisms and have also provided GenBank IDs for all sequences (text and revised Fig. 1). Currently, the species and virus names of the classified arteriviruses are the same. In the revised proposal we have returned to this convention for the previously classified viruses and have also utilized it for the species names of new arteriviruses. In the Bailey et al. proposal, the species names are based on their proposed genera names. However, because the genera have not yet been firmly delineated in our analysis, we feel it would be premature to name virus species based on the genera names proposed by Bailey et al. All of the species names based on virus names would be revisited once the genera have been defined and named.

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	*2015.014aS*	(assigned by ICTV officers)

To create eight new species within:

Fill in all that apply.
- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Genus:	*Arterivirus*
Subfamily:	
Family:	*Arteriviridae*
Order:	*Nidovirales*

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Porcine reproductive and respiratory syndrome virus 2	Porcine reproductive and respiratory syndrome virus (American), PRRSV2	U87392
Kibale red-tailed guenon virus 1	Kibale red-tailed guenon virus 1, KRGTV	JX473849
Kibale red colobus virus 1	Kibale red colobus virus 1, KRCV-1	KC787630
Kibale red colobus virus 2	Kibale red colobus virus 2, KRCV-2	KC787658
Mikumi yellow baboon virus 1	Mikumi yellow baboon virus 1, MYBV-1	KM110938
Simian hemorrhagic encephalitis virus	Simian hemorrhagic encephalitis virus, SHEV	KM677927
DeBrazza's monkey arterivirus	"DeBrazza's monkey arterivirus", "DeMAV" *	KP126831
Forest pouched giant rat arterivirus	"Forest pouched giant rat arterivirus", "APRAV" *	KP026921
Pebjah virus	Pebjah virus, PBJV	KR139839
	*Not yet named	

Currently, the taxonomy of the family *Arteriviridae* includes a single genus *Arterivirus* with only four species, all recognized many years ago (Faaberg et al., 2012). The names of the prototype viruses are used for naming the respective species. Viruses of these species differ in many aspects of genome organization and molecular biology, and are considerably separated in the phylogenetic tree of the family. Consequently, the demarcation criteria for these species are very broad. During the preparation of the last report on the taxonomy of the family (Faaberg et al., 2012), the ASG noted that two types of viruses, American and European, that belong to the most economically important arterivirus species *Porcine reproductive and respiratory syndrome virus* form two very distinct phylogenetic clusters and therefore may be qualified for classification as separate species. Over the last few years, many new arteriviruses were identified in the field, predominantly in different monkey species, although few have yet been characterized beyond genome sequencing (Dunowska et al., 2012; Bailey et al., 2014ab; Lauck et al., 2011, 2013, 2015). The authors of these important discoveries made suggestions about how to classify the newly identified arteriviruses. While considering these developments, the ASG recognized that accommodation of the new arteriviruses would require a considerable revision of the existing taxonomy that would be done with little input about the properties of the new arteriviruses obtained from experiments. To accomplish this revision, the ASG discussed different options and decided to follow a path similar to that taken by the Coronavirus SG, which used input from a DEmARC-mediated analysis of genomic variation to set family-wide demarcation criteria for ranks to reorganize the taxonomy of the *Coronaviridae* (de Groot et al., 2012).

Some 500 full genomic sequences of arteriviruses were selected for this analysis. They were used to produce an expert-curated multiple sequence alignment of most conserved non-structural proteins (nsps), including two domains of nsp2, the entire nsp3-nsp5, nsp7a, nsp8-9 regions, and the conserved part of nsp10, and nsp11. In agreement with published results, a phylogenetic analysis of arteriviruses by PhyML revealed a highly uneven distribution of viruses over many clusters (**Fig. 1 in Annex**). To inform taxonomy, we employed the DEmARC framework (Lauber & Gorbalenya, 2012ab), which provided thresholds to partition pairwise evolutionary distance (PED) distribution (**Fig. 2**). These thresholds could be used as candidates to set demarcation criteria for ranks. They were satisfied to two requirements: clusters formed under these thresholds were monophyletic in the tree of arteriviruses (**Fig. 1**), and all intra- and inter-cluster PEDs were, respectively, smaller and larger than the respective threshold (clustering cost of zero according to DEmARC) (**Fig. 2**). In total, 10 PED thresholds satisfying these conditions were identified; if all were used, the taxonomy of the family would include 10 ranks, many more than the currently available 3 ranks. This observation, which is likely due to the relatively small virus sampling, indicated that the taxonomy of arteriviruses could be devised in many ways that all would be perfectly compatible with current knowledge. However, if the goal is to devise a sustainable taxonomy structure, additional yet-to-be designed filters must be employed. Due to this large uncertainty about the choice of thresholds (and criteria), the ASG decided to first focus on setting a threshold for species to classify arteriviruses at this rank, while recognizing that the decisions on other ranks would be made later. With this in mind, three most supported PED thresholds (demarcation criteria) were selected; they are at 0.172, 0.844, and 1.433 PEDs, which correspond to 14, 5 and 2 clusters, respectively (**Fig. 3**). The 0.172 PED threshold was used to define arterivirus species, which

include 3 existing species, two derived by splitting one of the existing species, and 8 new species. Two other thresholds could potentially be used to demarcate higher ranks and are used here mainly for illustration of what is being considered by ASG for revising the *Arteriviridae* taxonomy in the future. One immediate application of the DEmARC thresholds was devising one species, *Wobbly possum disease virus,* which is the most distantly related to the others, as unassigned outside the genus *Arterivirus*.

There is a nearly perfect match between the species structures of two proposals on arterivirus taxonomy, this one and that of Bailey et al. The only exception concerns the species *Mikumi yellow baboon virus 1,* which is split into two species that are prototyped by the closely related MYBV-1 and SWBV-1, respectively (see **Fig. 1**), in the other proposal. According to DEmARC, this split is not supported by the clustering persistence measure (Fig. 2), and it would need to be accompanied by splitting two other species into two (Fig. 3) to maintain consistency in demarcation criteria for arterivirus species. Consequently we choose to retain the species structure described in our original proposal. The large overlap between the two proposals in respect to species served as the basis for revision of our proposal. However, this agreement does not extend to the species naming which follow two different conventions in the respective original proposals. Although we are willing to consider a binominal naming convention for species involving genus names proposed by Bailey et al., this was not feasible due to the current uncertainty regarding the genus structure in our proposal. Accordingly, and in line with the established practice for this family, species are named after the respective prototype viruses in our revised proposal.

Future development of arterivirus taxonomy will be conducted taking into account other aspects of the proposal of Bailey et al., and in close cooperation with other nidovirus SGs to benefit from this a larger knowledge base and to ensure coherence of demarcation criteria and taxonomy structure across the order. As part of this process, the names of the new arterivirus species could be reviewed, the benefits of binominal naming conventions will be considered, and, if necessary, the species names revised.

MODULE 2b: **NEW SPECIES**

creating and naming one or more new species.
If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	*2015.014bS*		(assigned by ICTV officers)

To create one new species within:

		Fill in all that apply.
Genus:	*Unassigned*	• If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
Subfamily:		
Family:	*Arteriviridae*	• If no genus is specified, enter "**unassigned**" in the genus box.
Order:	*Nidovirales*	

Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
Wobbly possum disease virus	Wobbly possum disease virus (WPDV)	JN116253

Reasons to justify the creation and assignment of the new species:
- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 9

Please see our comments in Module 2a

MODULE 8: **RENAME**

Use this module to change the name of one or more existing taxa (but note that stability of nomenclature is encouraged wherever possible). Insert extra lines in the table if needed.
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Renaming one or more taxa

Code	*2015.014cS*	(assigned by ICTV officers)

To rename the following species:

Current name	Proposed name
Porcine reproductive and respiratory syndrome virus	*Porcine reproductive and respiratory syndrome virus 1*

Reasons to justify the renaming: Explain why the taxon (or taxa) should be renamed
We propose to split the species *Porcine respiratory and reproductive syndrome virus* into two new species defined as *Porcine respiratory and reproductive syndrome virus 1* and *Porcine respiratory and reproductive syndrome virus 2* (see Module 2a). The reason for this splitting is to conform to a new species demarcation criterion designed for the *Arteriviridae* (see our comments in Module 2a).

additional material in support of this proposal

References:

Bailey AL, Lauck M, Sibley SD, Pecotte J, Rice K, Weny G, Tumukunde A, Hyeroba D, Greene J, Correll M, Gleicher M, Friedrich TC, Jahrling PB, Kuhn JH, Goldberg TL, Rogers J, O'Connor DH (2014a) Two novel simian arteriviruses in captive and wild baboons (Papio spp.). *Journal of virology* 88:13231-13239

Bailey AL, Lauck M, Weiler A, Sibley SD, Dinis JM, Bergman Z, Nelson CW, Correll M, Gleicher M, Hyeroba D, Tumukunde A, Weny G, Chapman C, Kuhn JH, Hughes AL, Friedrich TC, Goldberg TL, O'Connor DH (2014b) High genetic diversity and adaptive potential of two simian hemorrhagic fever viruses in a wild primate population. *PloS one 9*:e90714

de Groot, R.J., Baker, S.C., Baric, R.S., Brian, D.A., Enjuanes, L., Gorbalenya, A.E., Holmes, K. V., Perlman, S., Poon, L.L., Rottier, P.J.M., Talbot, P.J., Woo, P.C.Y., & J. Ziebuhr (2012) Family *Coronaviridae*. In: Virus Taxonomy, the 9th Report of the International Committee on Taxonomy of Viruses, King, A.M.Q., Adams, M.J., Carstens, E.B. & E.J Lefkowitz, Eds. Academic Press, pp. 806-828.

Dunowska M, Biggs PJ, Zheng T, Perrott MR (2012) Identification of a novel nidovirus associated with a neurological disease of the Australian brushtail possum (Trichosurus vulpecula). *Veterinary microbiology*, 156:418-424

Faaberg KS, Balasuriya UB, Brinton MA, Gorbalenya AE, Leung FC-C, Nauwynck H, Snijder EJ, Stadejek T, Yang H, Yoo D (2012) Family Arteriviridae. In: Virus Taxonomy, the 9th Report of the International Committee on Taxonomy of Viruses, King, A., Adams, M., Carstens, E. & E.J Lefkowitz, Eds. Academic Press, pp 796-805.

Gorbalenya, A. E., Enjuanes, L., Ziebuhr, J. and E. J. Snijder (2006) Nidovirales: Evolving the largest RNA virus genome, Virus Research, 117: 17-37.

Lauber, C. & A.E. Gorbalenya (2012a). Partitioning the genetic diversity of a virus family: approach and evaluation through a case study of picornaviruses, *J. Virol.* 86 (7): 3890-3904.

Lauber, C. & A.E. Gorbalenya (2012b). Toward Genetics-Based Taxonomy: Comparative Analysis of a Genetics-Based Classification and the Taxonomy of Picornaviruses, *J. Virol.* 86 (7): 3905-3915.

Lauber, C., Ziebuhr, J., Junglen, S., Drosten, S., Zirkel, F., Nga, P. T., Morita, K., Snijder, E.J., & A.E. Gorbalenya (2012). Mesoniviridae: a new family in the order Nidovirales formed by a single species of mosquito-borne viruses, *Arch. of Virology*, 157 (8): 1623-1628.

Lauck M, Hyeroba D, Tumukunde A, Weny G, Lank SM, Chapman CA, O'Connor DH, Friedrich TC, Goldberg TL (2011) Novel, divergent simian hemorrhagic fever viruses in a wild Ugandan red colobus monkey discovered using direct pyrosequencing. *PloS one* 6:e19056

Lauck M, Sibley SD, Hyeroba D, Tumukunde A, Weny G, Chapman CA, Ting N, Switzer WM, Kuhn JH, Friedrich TC, O'Connor DH, Goldberg TL (2013) Exceptional simian hemorrhagic fever virus diversity in a wild African primate community. *Journal of virology* 87:688-691

References:

Lauck M, Alkhovsky SV, Bao Y, Bailey AL, Shevtsova ZV, Shchetinin AM, Vishnevskaya TV, Lackemeyer MG, Postnikova E, Mazur S, Wada J, Radoshitzky SR, Friedrich TC, Lapin BA, Deriabin PG, Jahrling PB, Goldberg TL, O'Connor DH, Kuhn JH (2015) Historical Outbreaks of Simian Hemorrhagic Fever in Captive Macaques Were Caused by Distinct Arteriviruses. *J Virol*: JVI01046-15

Annex:
Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.
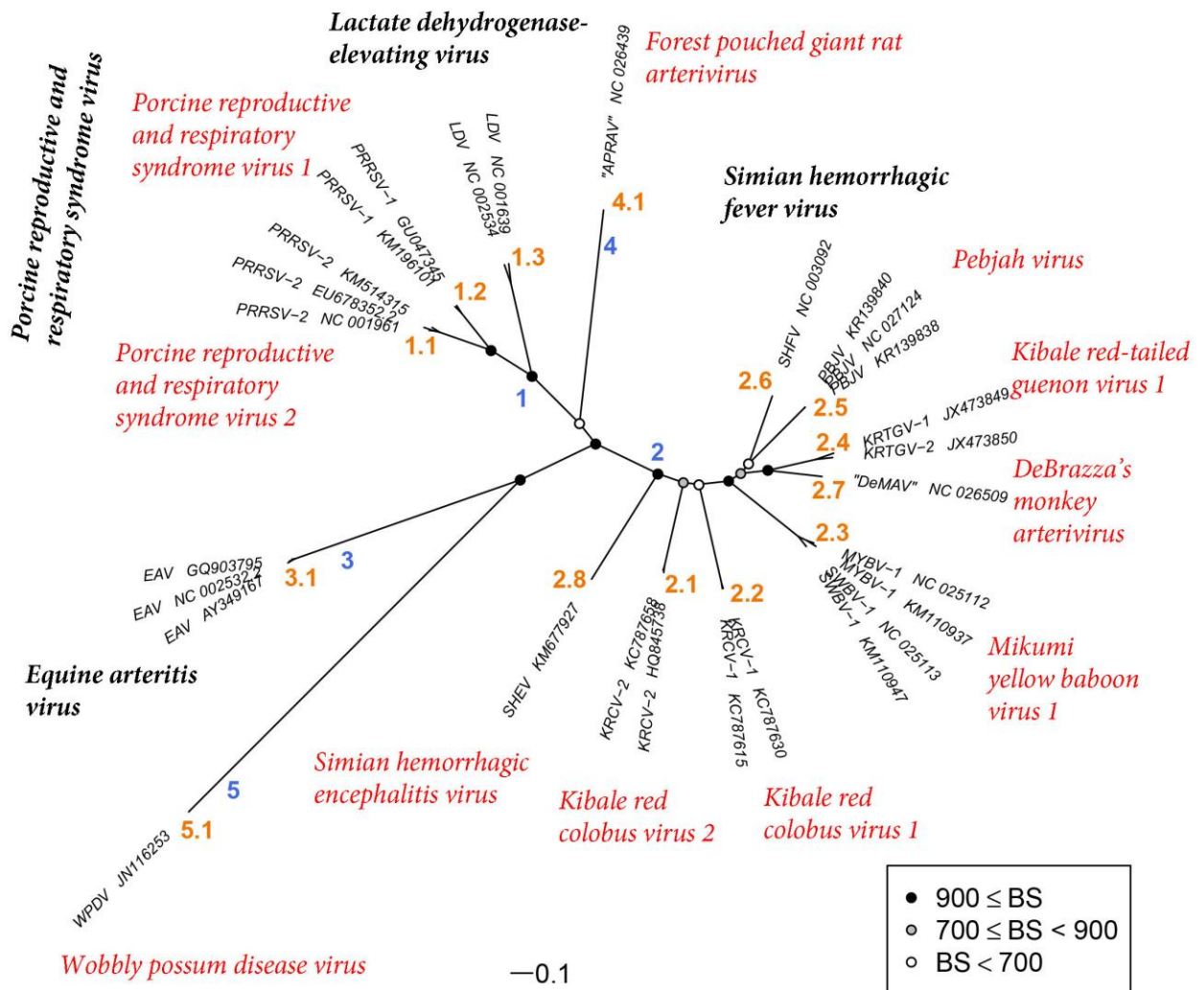
Fig. 1. Phylogenetic analysis of arteriviruses. This unrooted tree was generated using PhyML 3.0 with the following parameters: WAG aa substitution matrix, 4 substitution rate categories, and 1000 non-parametric bootstraps. Names of the currently recognized four species are in black bold. Virus acronyms, GenBank and RefSeq accession numbers for the most divergent available sequences in each species, and proposed species names are indicated in red. The listed RefSeq IDs correspond to the following GenBank IDs: NC_025112 to KM110938; NC_025113 to KM110946; NC_026509 to KP126831; NC_026439 to KP026921; NC_027124 to KR139839; NC_003092 to AF180391; NC_001639 to U15146; NC_002534 (removed from RefSeq) to L13298; NC_001961 to AF046869; NC_002532 to X53459. Clusters of different hierarchical levels according to DEmARC are indicated with orange and blue numbers, which correspond to species and (tentative) genera, respectively (see Figures 2 and 3 for other details on clustering). The scale is in aa replacements per position on average, and support for internal nodes by bootstrap (BS) is indicated. (Gulyaeva & Gorbalenya, unpublished).
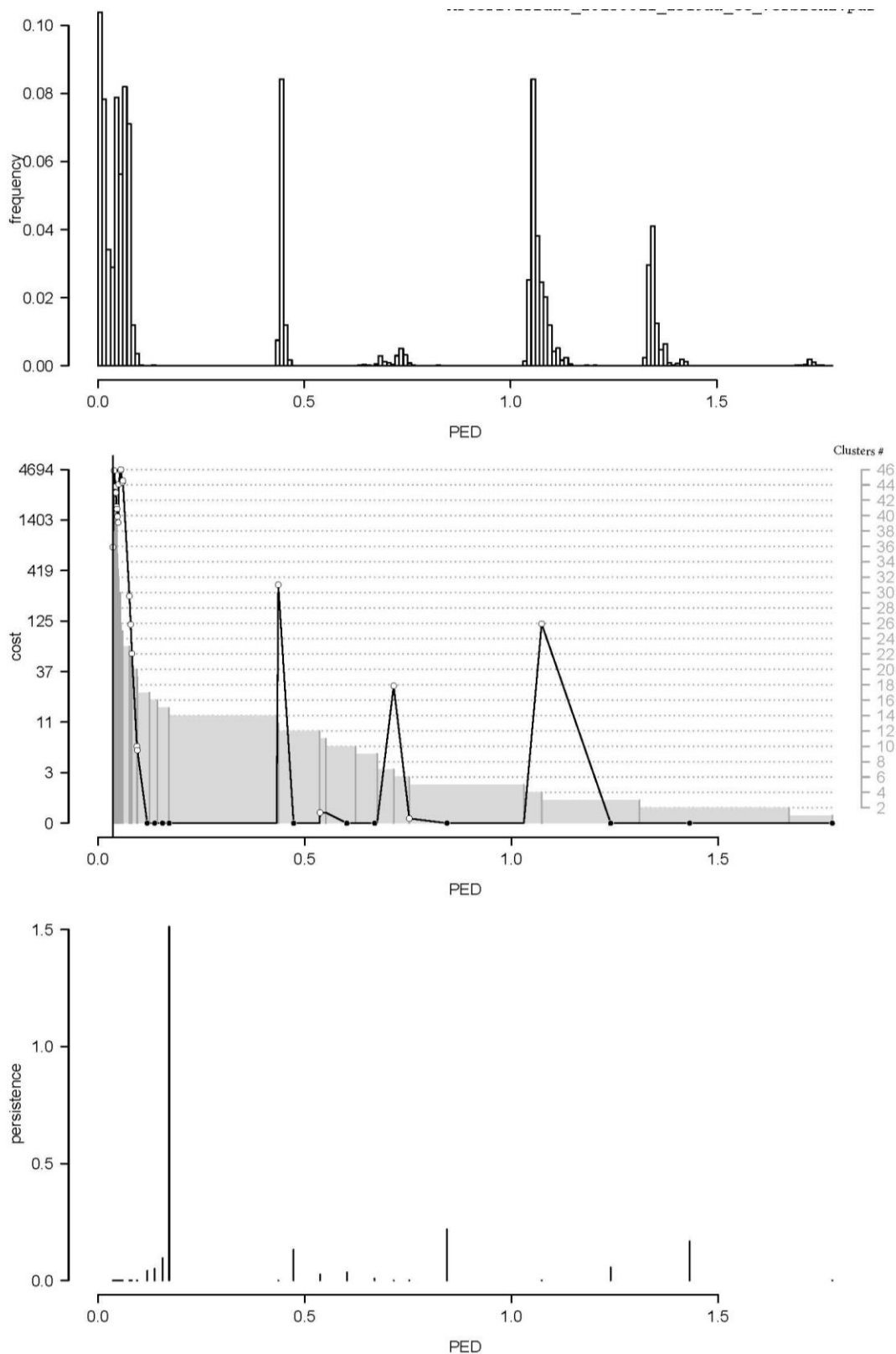
Fig. 2. Arterivirus-wide pairwise evolutionary distance distribution and distance thresholds for partitioning. The three panels starting from the top depict, respectively, frequency distribution of PEDs, change of clustering of viruses and clustering cost associated with partitioning at each PED, and threshold persistence of particular clustering over the PED range. The pairwise distance scale reflects the estimated number of amino acid substitutions per site on average. The three most supported thresholds are at 0.172, 0.844, and1.433 PED, and correspond to 14, 5 and 2 clusters, respectively. (Gulyaeva & Gorbalenya, unpublished).
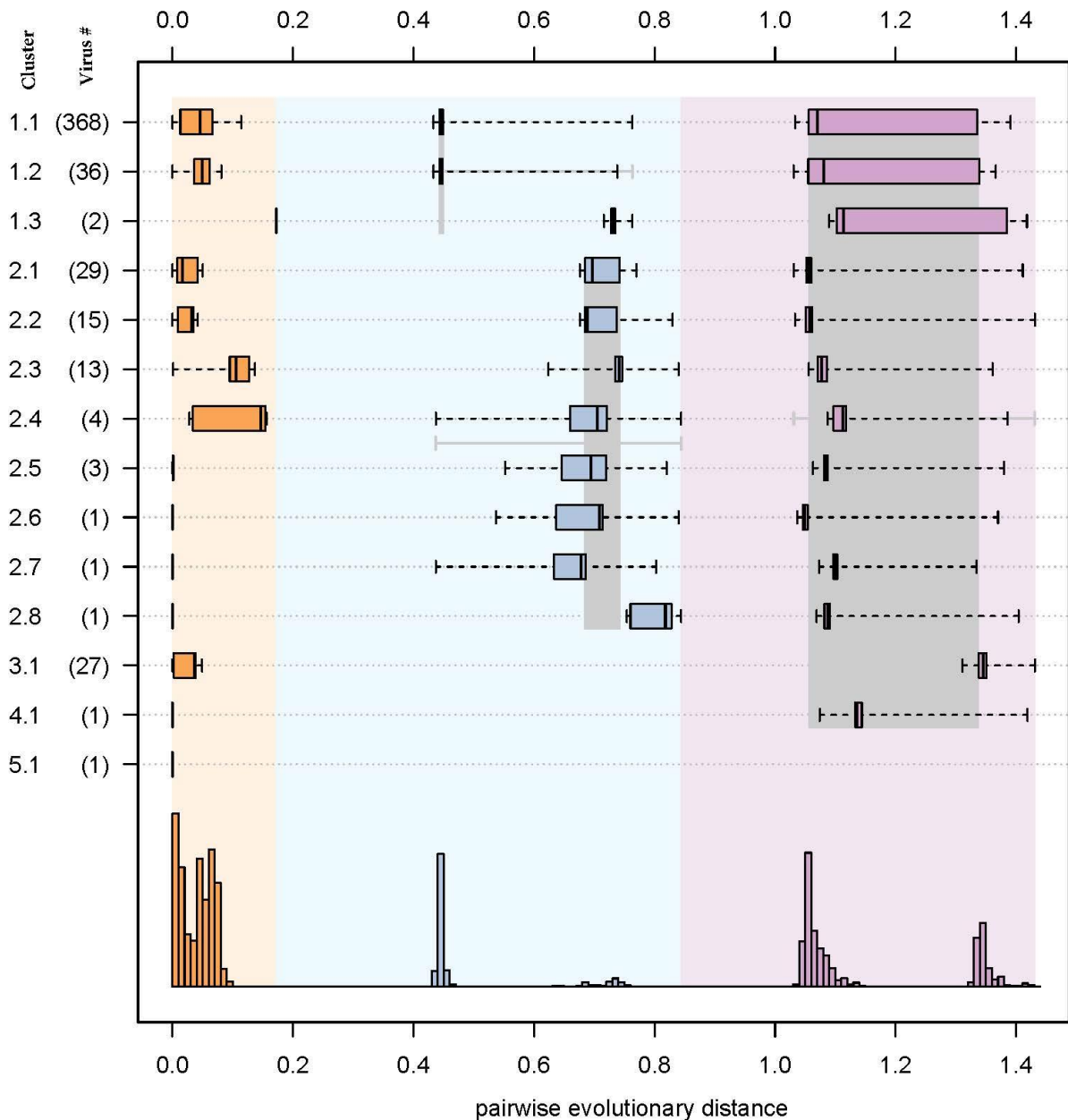
Fig. 3. Intra-group genetic divergence in three-level hierarchical clustering of arteriviruses by DEmARC. Levels are defined by the three strongest PED thresholds defined in the bottom panel of Fig. 2. For simplicity, species identities are indicated via a binary system where the first number and the second number represent the tentative genus and the proposed species, respectively (left axis); the number of viruses in the identified clusters are shown in brackets. All identified clusters correspond to monophyletic groups in the tree of Fig. 1. Box-and-whisker graphs were used to plot distributions of distances between viruses from the same species (orange), and between viruses from different species but the same genus (blue), and between viruses from different genera but the same "supergenus" (pink). The boxes span from the first to the third quartile and include the median (bold line), and the whiskers (dashed lines) extend to the extreme values. The corresponding part of the PED distribution (see panel C of Fig. 2) is depicted below. (Gulyaeva & Gorbalenya, unpublished).
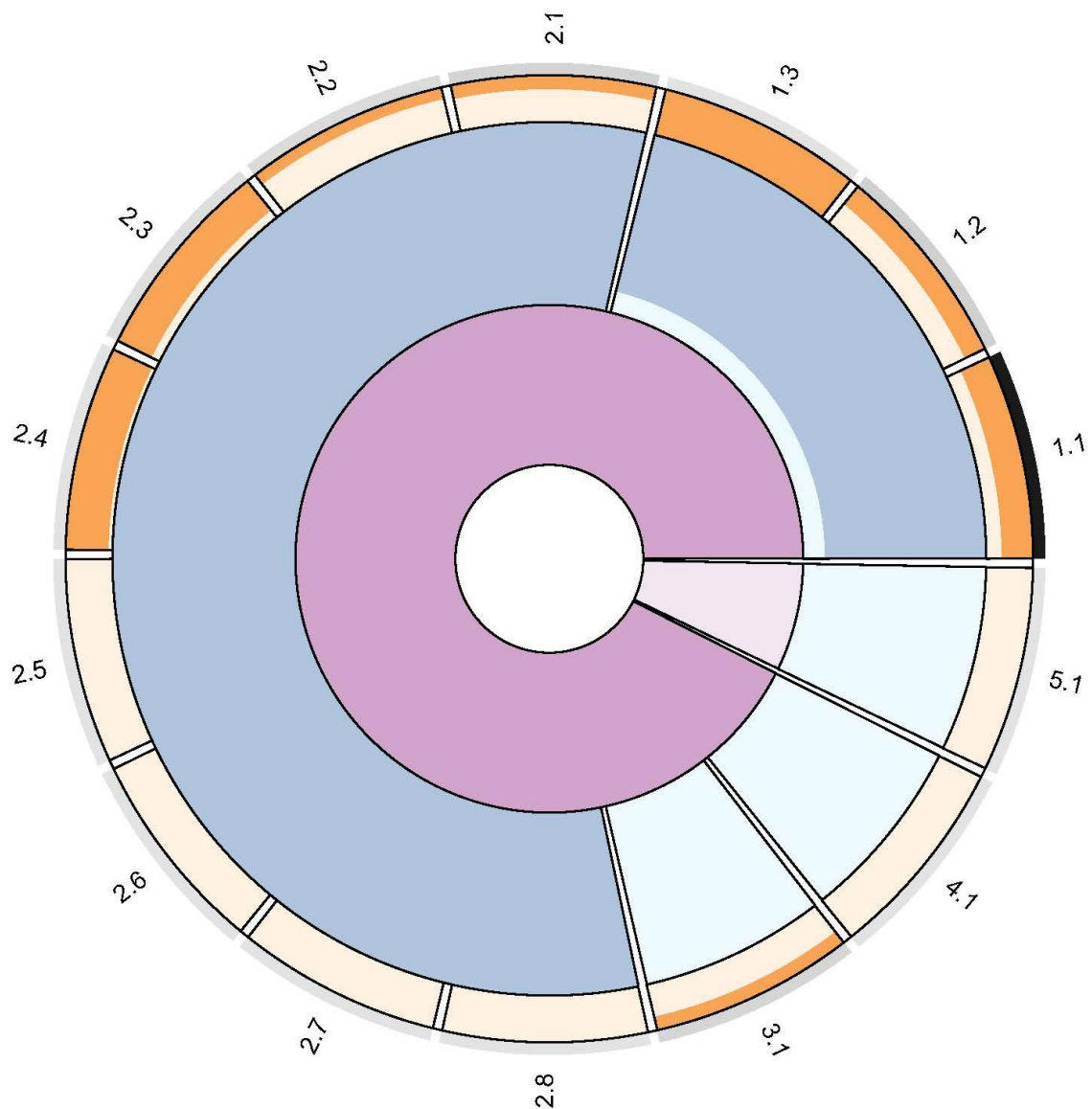
Fig. 4. Taxonomy diagram. A taxonomy diagram for arteriviruses under the DEmARC framework is shown. Intervirus genetic divergence (as PED) increases linearly from the perimeter (PED of zero) toward the center of the circle (maximum PED of 1.68). Delimited taxa are shown as curved rectangle-like shapes. Taxa are filled using the coloring scheme from Fig. 3; the three basic colors represent the species (orange), genus (blue), and supergenus (purple) levels. Each color exists in two shadings that highlight the limit on intragroup genetic divergence according to a distance threshold (soft shading) and the maximum observed intragroup genetic divergence (bright shading) of a taxon. Outside the circle, the relative density of virus sampling per species is shown as gray shadings from low (light) to high (dark) sampling, which is in the range of 1 (least sampled species) to 369 (most sampled species). Species identities are as in Fig. 3. In the DEmARC framework, taxa are treated equally at each level and they must conform to family-wide distance thresholds (equal, level-specific heights of taxon shapes). The space inside taxon shapes colored in soft shading highlights the genetic diversity that may be missed by the current arterivirus sampling, when assuming a universal, level-wide threshold that limits the actual diversity of each taxon. (Gulyaeva & Gorbalenya, unpublished).