This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). 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; you can copy the modules to create more than one genus within a new family, for example.

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

Code assigned:	***2015.003a-eS***	(to be completed by ICTV officers)

Short title: Create 12 new species in the family *Coronaviridae*
(e.g. 6 new species in the genus *Zetavirus*)

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)	This proposal is filed by the *Coronaviridae* Study Group (CSG) in consultation with the *Nidovirales* Study Group (NSG)

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

The CSG members agree with this proposal.

Date first submitted to ICTV:	19/06/2015
Date of this revision (if different to above):	16/09/2015

ICTV-EC comments and response of the proposer:

MODULE 2a: **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	***2015.003aS***	(assigned by ICTV officers)

To create three new species within:

Genus:	***Alphacoronavirus***
Subfamily:	***Coronavirinae***
Family:	***Coronaviridae***
Order:	***Nidovirales***

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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Bat coronavirus HKU10	Rousettus bat coronavirus HKU10, BtCoV_HKU10	JQ989271 (publication)
Bat coronavirus CDPHE15	Bat coronavirus CDPHE15/USA/2006, BtCoV_CDPHE15	KF430219 (only GenBank)
Mink coronavirus 1	Mink coronavirus strain WD1127, MCoV	HM245925

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

The subfamily *Coronavirinae*, family *Coronaviridae*, order *Nidovirales* includes 20 established species in four genera (de Groot et al., 2012). This classification was designed using quantitative criteria on genetic divergence obtained through application of DEmARC software (Lauber & Gorbalenya 2012a) as described for picornaviruses (Lauber & Gorbalenya 2012b). After the last revision of the *Coronavirinae* taxonomy in 2012, a number of new coronaviruses have been identified in different hosts through genome sequencing, which, in most cases, was extended to an initial functional and structural characterization (Corman et al., 2014; Lau et al., 2012; Van Boheemen et al., 2012; Vlasova et al., 2011; Woo et al., 2012). The authors of the respective papers proposed to recognize these viruses as new species.

In the preparation of this proposal, these assignments were verified and confirmed. Based on phylogenetic analysis of a multiple sequence alignment of the most conserved nonstructural proteins (nsps) of coronaviruses, the newly recognized viruses group within monophyletic clusters that define the genera *Alphacoronavirus*, *Betacoronavirus* and *Deltacoronavirus* (see **Annex**). Using DEmARC for partitioning density distribution of pair-wise evolutionary distances of these viruses, 10 new species were recognized. They conform to the previously established family-wide demarcation threshold of having less than 90% identity with viruses of the previously characterized species, while belonging to the three genera *Alphacoronavirus* (3 new species), *Betacoronavirus* (2 new species) and *Deltacoronavirus* (5 new species).

The naming convention of coronavirus species is in the transition from a system that largely copied virus names to a generic system that includes a reference to species and genus. Currently the CSG is reviewing the rank structure of the *Coronaviridae* which may lead to a considerable revision. Due to this uncertainty, CSG decided to take a conservative approach to the naming of the new species and followed largely the names of the prototype viruses. In the case of the high-profile MERS-CoV (de Groot et al., 2013), the name for this species was designed by incorporating “-related” in the name, following the example set for SARS-CoV a few years ago. This name is inclusive for closely related viruses isolated from humans, camels or other animals.

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	***2015.003bS***	(assigned by ICTV officers)

To create two new species within:

Genus:	***Betacoronavirus***
Subfamily:	***Coronavirinae***
Family:	***Coronaviridae***
Order:	***Nidovirales***

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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Middle East respiratory syndrome-related coronavirus	MERS coronavirus EMC/2012, MERS-CoV	JX869059.2
Hedgehog coronavirus 1	Betacoronavirus Erinaceus/VMC/DEU/2012, EriCoV	KC545383

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

See comments to Module 2a

MODULE 2c: **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	***2015.003cS***	(assigned by ICTV officers)

To create five new species within:

Genus:	***Deltacoronavirus***
Subfamily:	***Coronavirinae***
Family:	***Coronaviridae***
Order:	***Nidovirales***

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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Coronavirus HKU15	Porcine coronavirus HKU15, PoCoV HKU15	JQ065043
White-eye coronavirus HKU16	White-eye coronavirus HKU16, WECoV HKU16	JQ065044
Night heron coronavirus HKU19	Night heron coronavirus HKU19, NHCoV HKU19	JQ065047
Wigeon coronavirus HKU20	Wigeon coronavirus HKU20, WiCoV HKU20	JQ065048
Common moorhen coronavirus HKU21	Common moorhen coronavirus HKU21, CMCoV HKU21	JQ065049

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

See comments to Module 2a

MODULE 2d: **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	***2015.003dS***	(assigned by ICTV officers)

To create one new species within:

Genus:	***Bafinivirus***
Subfamily:	***Torovirinae***
Family:	***Coronaviridae***
Order:	***Nidovirales***

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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Fathead minnow nidovirus 1	Fathead minnow nidovirus, FHMNV	GU002364.2

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

The subfamily *Torovirinae*, family *Coronaviridae*, order *Nidovirales* currently includes 3 established species in two genera (de Groot et al., 2012). This classification was designed using quantitative criteria on genetic divergence obtained through application of the DEmARC software (Lauber & Gorbalenya 2012a) as described for picornaviruses (Lauber & Gorbalenya 2012b). More recently, researchers have reported the identification of Fathead minnow nidovirus, which is distantly related to White bream virus (WBV) in the *Bafinivirus* genus (Batts et al., 2012). Two other groups reported the identification of closely related nidoviruses isolated from different python species (Bodewes et al., 2014; Stenglein et al., 2014). These viruses were found to be distantly related to all other members of this subfamily and lack the ORF1a-encoded ADRP domain that is otherwise strictly conserved in viruses of the entire family.

In the preparation of this proposal, these tentative assignments were verified and confirmed using phylogenetic analysis of a multiple sequence alignment of the RdRp of nidoviruses (see **Annex**). Using DEmARC for partitioning density distribution of pair-wise evolutionary distances of the *Coronaviridae*, two new species were recognized. They conform to the previously established family-wide demarcation threshold of less than 90% identity in the most conserved nonstructural proteins encoded by viruses of previously established species in the *Torovirinae*. One of these species is proposed to be assigned to the *Bafinivirus* genus, while the other, infecting python, remains unassigned in the *Torovirinae* subfamily. The names of the respective species were generated following the reasoning outlined in Module 2a.

MODULE 2e: **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	***2015.003eS***	(assigned by ICTV officers)

To create one new species within:

Genus:	***unassigned***
Subfamily:	***Torovirinae***
Family:	***Coronaviridae***
Order:	***Nidovirales***

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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Ball python nidovirus 1	Ball python nidovirus strain 07-53, BPNV	KJ541759

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

See comments to Module 2d

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Batts,W.N., Goodwin,A.E. and Winton,J.R. (2012) Genetic analysis of a novel nidovirus from fathead minnows. J. Gen. Virol. 93 (PT 6), 1247-1252.

Bodewes,R., Lempp,C., Schurch,A.C., Habierski,A., Hahn,K., Lamers,M., von Dornberg,K., Wohlsein,P., Drexler,J.F., Haagmans,B.L., Smits,S.L., Baumgartner,W. and Osterhaus,A.D. (2014) Novel divergent nidovirus in a python with pneumonia. J. Gen. Virol. 95 (PT 11), 2480-2485.

Corman,V.M., Kallies,R., Philipps,H., Gopner,G., Muller,M.A., Eckerle,I., Brunink,S., Drosten,C. and Drexler,J.F. (2014) Characterization of a novel betacoronavirus related to middle East respiratory syndrome coronavirus in European hedgehogs. J. Virol. 88 (1), 717-724.

de Groot, R.J, Baker, S.C., Baric, R.S., Brown, C.S., Drosten, C., Enjuanes, L., Fouchier, R.A.M., Galiano, M., Gorbalenya, A.E., Memish, Z., Perlman, S., Poon, L.L.M., Snijder, E.J., Stephens, G.M., Woo, P.C.Y., Zaki, A.M., Zambon, M., and J. Ziebuhr (2013) Middle East Respiratory Syndrome Coronavirus (MERS-CoV): Announcement of the Coronavirus Study Group. *J. Virol.*, 87 (14): 7790-7792.

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Lau,S.K., Li,K.S., Tsang,A.K., Shek,C.T., Wang,M., Choi,G.K., Guo,R., Wong,B.H., Poon,R.W., Lam,C.S., Wang,S.Y., Fan,R.Y., Chan,K.H., Zheng,B.J., Woo,P.C. and Yuen,K.Y. (2012) Recent Transmission of a Novel Alphacoronavirus, Bat Coronavirus HKU10, from Leschenault's Rousettes to Pomona Leaf-Nosed Bats: First Evidence of Interspecies Transmission of Coronavirus between Bats of Different Suborders. J. Virol. 86 (21), 11906-11918

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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.

Stenglein,M.D., Jacobson,E.R., Wozniak,E.J., Wellehan,J.F.X., Kincaid,A., Gordon,M., Porter,B.F., Baumgartner,W., Stahl,S., Kelley,K., Wellehan,J.F.X., Towner,J.S. and DeRisi,J.L. (2014). Ball python nidovirus: a candidate etiologic agent for severe respiratory disease in Python regius. MBio 5 (4), e01484-14.

Van Boheemen, S., de Graaf, M., Lauber, C., Bestebroer, T.M., Stalin Raj, V., Moh Zaki, A., Osterhaus, A.D.M.E., Haagmans, B.L., Gorbalenya, A.E., Snijder, E.J., & R. A.M. Fouchier (2012) Genomic Characterization of a Newly Discovered Coronavirus Associated with Acute Respiratory Distress Syndrome in Humans, mBio 3 (6): e00473-12.

Vlasova,A.N., Halpin,R., Wang,S., Ghedin,E., Spiro,D.J. and Saif,L.J. (2011) Molecular characterization of a new species in the genus Alphacoronavirus associated with mink epizootic catarrhal gastroenteritis. J. Gen. Virol. 92 (PT 6), 1369-1379.

Woo,P.C., Lau,S.K., Lam,C.S., Lau,C.C., Tsang,A.K., Lau,J.H., Bai,R., Teng,J.L.,

additional material in support of this proposal

References:

Tsang,C.C., Wang,M., Zheng,B.J., Chan,K.H. and Yuen,K.Y. (2012) Discovery of seven novel mammalian and avian coronaviruses in Deltacoronavirus supports bat coronaviruses as the gene source of Alphacoronavirus and Betacoronavirus and avian coronaviruses as the gene source of Gammacoronavirus and Deltacoronavirus, J. Virol. 86 (7), 3995-4008.

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.

Table 1. Virus sequences used for phylogenetic trees in Figures 1 and 2.

GenBank ID	Virus (species) acronym
AB257344	SARS-CoV
AY903459	BetaCoV-1
AY884001	HCoV-HKU1
AB551247	MCoV (MHV)
JX869059	MERS-CoV
EF065505	BatCoV-HKU4
EF065509	BatCov-HKU5
KC545383	BetaCoV-Erinaceus (Hedgehog)
EF065513	BatCoV-HKU9
GU937797	PEDV
DQ445911	HCoV-NL63
JQ410000	HCoV-229E
JQ989266	BatCoV-HKU10
EF203064	BatCoV-HKU2
DQ648858	BatCoV-512
EU420138	BatCoV-1A
EU420139	BatCoV-HKU8
KF430219	BatCoV-CDPHE15
AY994055	AlphaCoV-1
HM245925	Mink-CoV
AJ311317	ACoV(IBV)
EU111742	Beluga/Dolphin-CoV
JQ065042	CoV-HKU15/17
FJ376619	CoV-HKU11
FJ376622	CoV-HKU13/18
FJ376621	CoV-HKU12
JQ065044	CoV-HKU16
JQ065049	CoV-HKU21
JQ065047	CoV-HKU19
JQ065048	CoV-HKU20
DQ898157	WBV
GU002364.2	FHMNV
JQ860350	PToV SH1
AY427798	BRV-1
KJ541759	BPNV

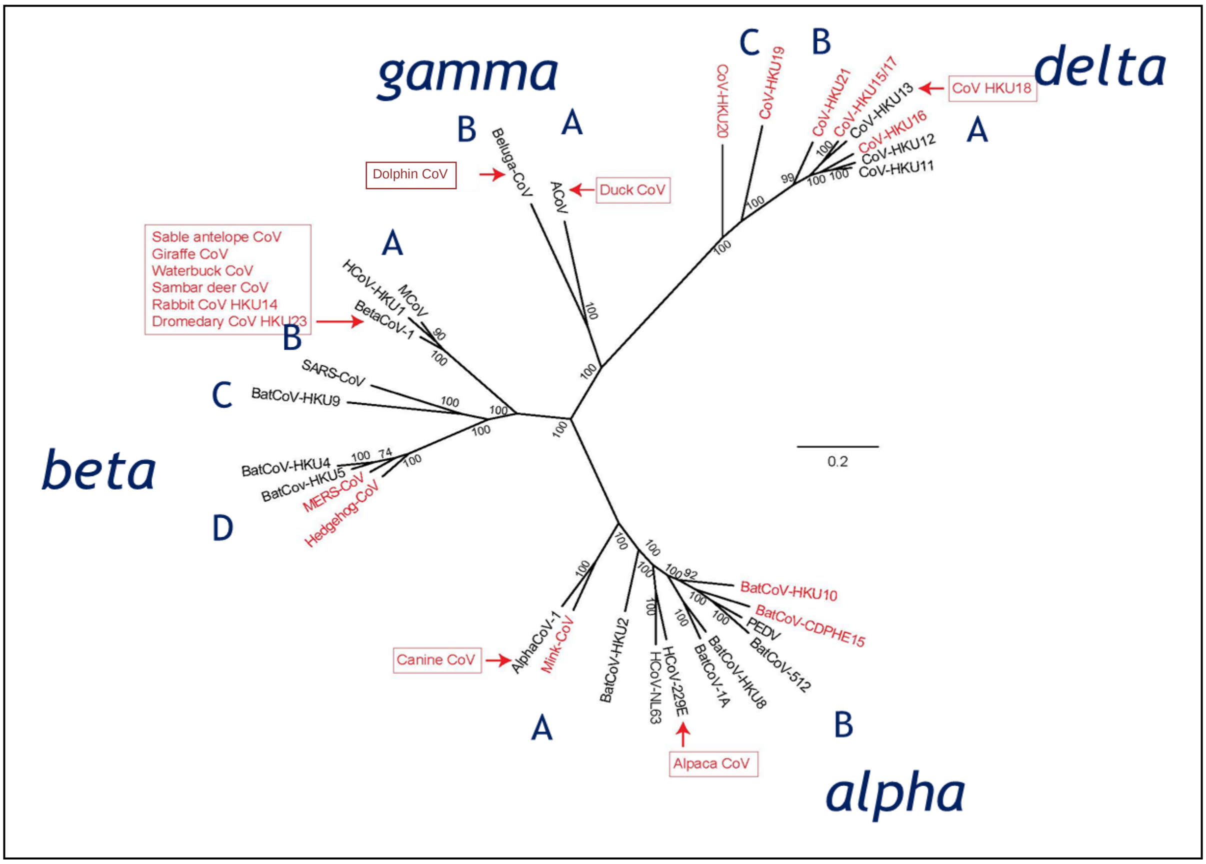

Fig. 1. Phylogenetic analysis of the *Coronavirinae* subfamily. This unrooted tree was generated using PhyML using WAG aa substitution matrix, 4 substitution rate categories, and 100 non-parametric bootstraps, which applied to a concatenated multiple sequence alignment of several domains of nsp3 and the nsp4-nsp16 region of coronavirus replicase polyproteins. Acronyms of names of the ten newly proposed species next to terminal nodes are shown in red. Names of new coronaviruses that expand the host range of already established species are shown in red boxes. Arrows indicate the respective species that these viruses belong to. Also indicated are the names of the four genera (*alpha, beta, gamma,* and *delta*) and of phylogenetically compact subgenera (A, B, C, and D), which may form a separate rank according to DEmARC analysis of more than 800 coronaviruses. The scale represents aa replacements per position on average. Support for internal nodes by bootstrap (BS) is indicated (Lauber & Gorbalenya, unpublished). For GenBank accession numbers, see Table 1.

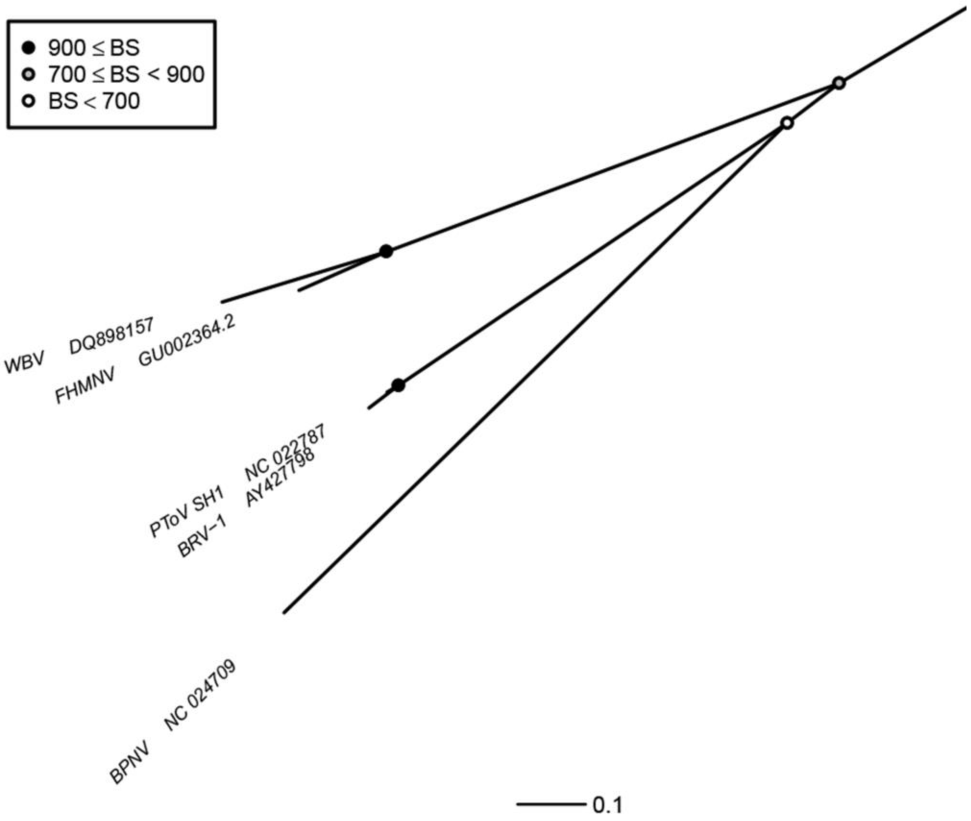

Fig. 2. Phylogenetic analysis of the *Torovirinae* subfamily. This rooted tree is a branch of a nidovirus tree that was generated by applying PhyML, WAG aa substitution matrix, 4 substitution rate categories, and 1000 non-parametric bootstraps, to a multiple sequence alignment of RdRp domains of 50 nidoviruses. Shown are five viruses that prototype the three previously established and the two proposed (FHMNV and BPNV) torovirus species. The scale is in aa replacements per position on average, and support for internal nodes by bootstrap (BS) is indicated (Gulyaeva & Gorbalenya, unpublished). For a complete list of GenBank accession numbers, see Table 1.