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:	***2016.019aS***	(to be completed by ICTV officers)

Short title: Create 2 new species unassigned in the subfamily *Torovirinae*, family *Coronaviridae*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 11 are required)	**2** ☒ **3** ☐ **4** ☐ **5** ☐ **6** ☐ **7** ☐ **8** ☐ **9** ☐ **10** ☐

Author(s):

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de Groot, R.J., Member
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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:

Date first submitted to ICTV: 05/08/2016
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

MODULE 2: **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	***2016.019aS***	(assigned by ICTV officers)

To create two 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)**
Bovine nidovirus 1	Bovine nidovirus TCH5	KM589359
Chinook salmon nidovirus 1	Chinook salmon bafinivirus NIDO	KJ681496

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 11

The subfamily *Torovirinae*, family *Coronaviridae*, order *Nidovirales* currently includes 4 established species in two genera and one assigned species (de Groot et al., 2012; Ziebuhr et al., 2015; Adams et al., 2016). 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).

Over the past year, genome sequences were reported for many viruses of the family, which we used to update the taxonomy. In total 1381 genome sequences were analysed and a Maximum Likelihood phylogenetic tree was generated using multiple sequence alignments of the 10 most conserved replicative domains, including the Cys-rich domain of nsp3, C-terminal domain of nsp4, catalytic domain of the nsp5 3CL protease, nsp8, NiRAN and RdRp domains of nsp12, ZBD and Helicase core domains of nsp13, ExoN of nsp14, and OMT domain of nsp16 (see **Annex**). Using DEmARC for partitioning density distribution of pair-wise patristic distances (PPD) of the *Coronaviridae*, two new species were recognized, each including a single virus. 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 family. While these viruses clustered with viruses of the *Torovirinae* subfamily, in line with the results reported by the discoverers of one of these viruses (Tokarz et a., 2015), they were separated from each other and any other virus of all known species by the PPD of more than one replacement per position on average, exceeding considerably the observed intra-genus PPDs. As a result, both species are left unassigned in the *Torovirinae* subfamily. The names of the respective species were devised after names of the prototype viruses.

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

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.

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.

Tokarz, R., Sameroff, S., Hesse, R. A., Hause, B. M., Desai, A., Jain, K., & Lipkin, W. I. (2015). Discovery of a novel nidovirus in cattle with respiratory disease. *J. Gen. Virol.* 96: 2188-2193.

Ziebuhr J, Baric RS, Baker S, de Groot RJ, Drosten C, Gulyaeva A, Haagmans BL, Lauber C, Neuman BW, Perlman S, Poon LLM, Sola I, & Gorbalenya AE (2015). ICTV taxonomic proposal 2015.003a-eS.A.v2.Coronaviridae_12sp. Create 12 species in the family *Coronaviridae*. http://www.ictvonline.org/proposals-15/2015.003a-eS.A.v2.Coronaviridae_12sp.pdf

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.

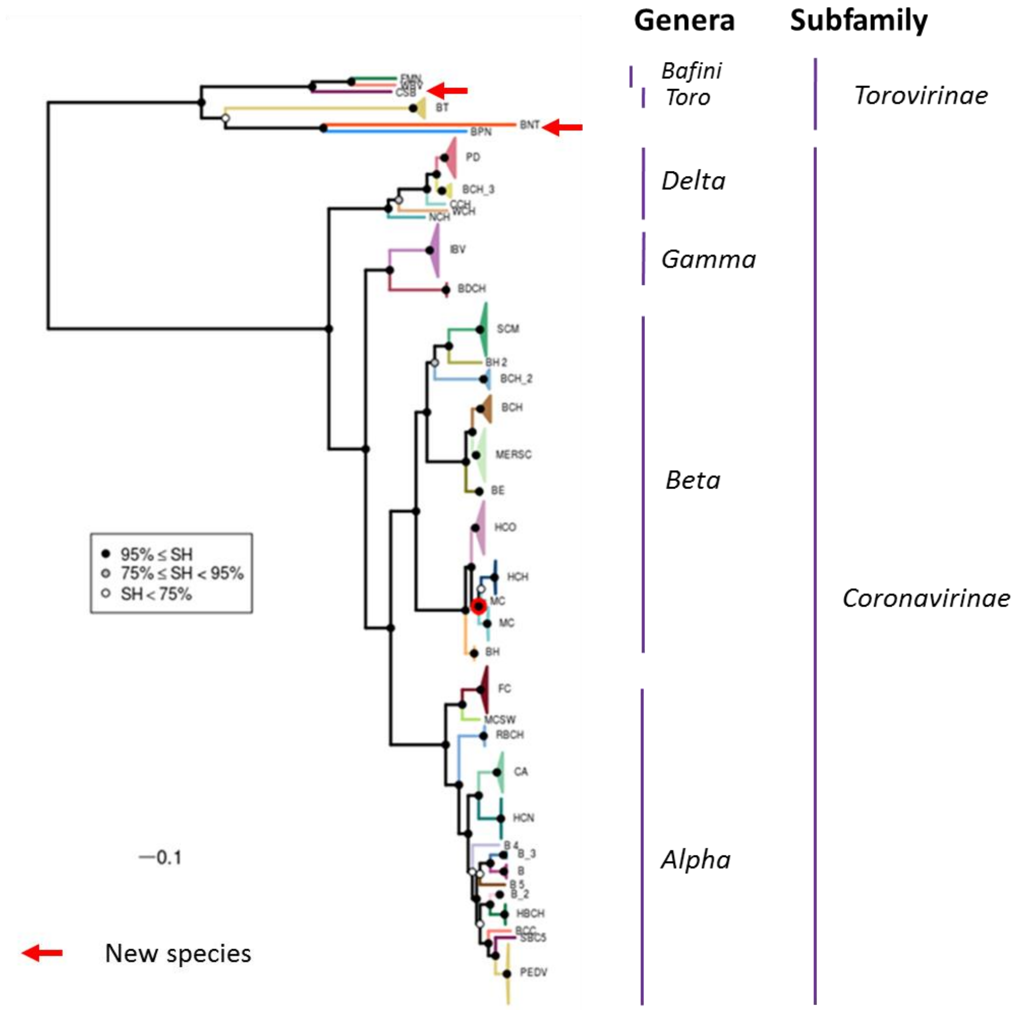

Fig. 1. Phylogenetic analysis of the *Coronaviridae* family. This midpoint rooted tree was generated by applying FastTree, WAG aa substitution matrix, 4 substitution rate categories, and 1000 non-parametric bootstraps, to a multiple sequence alignment described in Module 2. The scale is in aa replacements per position on average, and support for internal nodes by SH test is indicated. Each separately colored branch is a species, in total 37 each with acronym automatically derived from annotation of one of the GenBank entries of that species. Height and width of triangles at the tip of branches reflect the number and diversity, respectively, of respective species using a log scale. Red arrows, new species, BNT, bovine nidovirus 1; CSN, chinook salmon nidovirus 1. (Gulyaeva et al & Gorbalenya, unpublished).