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:	***2016.013aM***	(to be completed by ICTV officers)

Short title: One (1) new species in the genus *Bornavirus*
(e.g. 6 new species in the genus *Zetavirus*)

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

Author(s) with e-mail address(es) of the proposer:

The ICTV *Bornaviridae* Study Group:

Rubbenstroth, Dennis	Chair	Germany	Dennis.Rubbenstroth@uniklinik-freiburg.de
Briese, Thomas	Member	USA	thomas.briese@columbia.edu
Duerrwald, Ralf	Member	Germany	Ralf.Duerrwald@idt-biologika.de
Horie, Masayuki	Member	Japan	mhorie@vet.kagoshima-u.ac.jp
Kuhn, Jens H.	Member	USA	kuhnjens@mail.nih.gov
Nowotny, Norbert	Member	Austria	NorbertNowotny@gmx.at
Payne, Susan	Member	USA	SPayne@cvm.tamu.edu
Schwemmle, Martin	Member	Germany	martin.schwemmle@uniklinik-freiburg.de
Tomonaga, Keizo	Member	Japan	tomonaga@virus.kyoto-u.ac.jp

and:
Yiming Bao, bao@ncbi.nlm.nih.gov
Martin Beer, Martin.Beer@fli.bund.de

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)	

ICTV-EC or Study Group comments and response of the proposer:

Date first submitted to ICTV:	July 12, 2016
Date of this revision (if different to above):	

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	***2016.013aM***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Bornavirus***
Subfamily:	
Family:	***Bornaviridae***
Order:	***Mononegavirales***

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:**	**GenBank sequence accession number(s)**
Mammalian 2 bornavirus	variegated squirrel bornavirus 1 (VSBV-1) isolate "squirrel brain"	LN713681

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

As of 2016, the family *Bornaviridae* includes one genus (*Bornavirus*). Until early 2015, this genus included a single species (*Borna disease virus*) for viruses originating from mammalian hosts. However, since 2008 several distinct bornaviruses have been discovered in avian, reptilian, and mammalian hosts. In the past two years, bornavirus taxonomy was adapted to accommodate this increased variability (see newest taxonomy release by the ICTV). The family remains mono-generic, but the genus now includes seven species: *Elapid 1 bornavirus*, *Mammalian 1 bornavirus* (formerly *Borna disease virus*), *Passeriform 1 bornavirus*, *Passeriform 2 bornavirus*, *Psittaciform 1 bornavirus*, *Psittaciform 2 bornavirus*, and *Waterbird 1 bornavirus* (Kuhn et al., 2015; Rubbenstroth et al., 2015). The majority of known bornaviruses are classified in these species, but four additional bornaviruses remain unclassified due to insufficient sequence information (Table 2).

Criteria for bornavirus species demarcation are based on genomic characteristics, including PAirwise Sequence Comparison (PASC) (Bao et al., 2012, 2014), in combination with biological characteristics, such as antigenic relationship (Zimmermann et al., 2014) and natural host range (Kuhn et al., 2015). In agreement with these additional criteria, the range of the species differentiation cut-off for PASC of coding-complete genome sequences was defined as 72–75% (Kuhn et al., 2015; Rubbenstroth et al., 2015).

Within the past year, a new mammalian bornavirus, named "variegated squirrel bornavirus 1 (VSBV-1)", was identified. The virus was discovered in Germany in healthy captive squirrels of the family *Sciuridae*, such as variegated squirrels (*Sciurus variegatoides*) (Hoffmann et al., 2015). VSBV-1 is a zoonotic virus as accidental transmission to humans exposed to infected squirrels resulted in fatal neurologic disease in at least three cases (Hoffmann et al., 2015). VSVB-1 coding-complete genomes were deposited to GenBank (LN713680, LN713681). The highest nucleotide identity of the VSBV-1 genome (67.5%) is shared with the genome of Borna disease virus 1 (species *Mammalian 1 bornavirus*). This value is below the previously defined bornavirus species differentiation cut-off of 71%, but within the range of sequence identities found between bornaviruses of distinct species (58.1–71.0%). Based on the known host range and genome sequence identity values, we propose to assign VSBV-1 to a new species "*Mammalian 2 bornavirus*" within the genus *Bornavirus*.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Bao, Y., Chetvernin, V., Tatusova, T., 2012. PAirwise Sequence Comparison (PASC) and its application in the classification of filoviruses. Viruses 4, 1318-1327.

Bao, Y., Chetvernin, V., Tatusova, T., 2014. Improvements to pairwise sequence comparison (PASC): a genome-based web tool for virus classification. Arch Virol 159, 3293-3304.

Hoffmann, B., Tappe, D., Hoper, D., Herden, C., Boldt, A., Mawrin, C., Niederstrasser, O., Muller, T., Jenckel, M., van der Grinten, E., Lutter, C., Abendroth, B., Teifke, J.P., Cadar, D., Schmidt-Chanasit, J., Ulrich, R.G., Beer, M., 2015. A Variegated Squirrel Bornavirus Associated with Fatal Human Encephalitis. N Engl J Med 373, 154-162.

Kuhn, J.H., Durrwald, R., Bao, Y., Briese, T., Carbone, K., Clawson, A.N., deRisi, J.L., Garten, W., Jahrling, P.B., Kolodziejek, J., Rubbenstroth, D., Schwemmle, M., Stenglein, M., Tomonaga, K., Weissenbock, H., Nowotny, N., 2015. Taxonomic reorganization of the family *Bornaviridae*. Arch. Virol. 160, 621-632.

Rubbenstroth, D., Briese, T., Durrwald, R., Horie, M., Kuhn, J.H., Nowotny, N., Payne, S., Schwemmle, M., Tomonaga, K., Banyai, K., Bao, Y., Farkas, S., Marton, S. 2015. Two new species in the family *Bornaviridae*.

Zimmermann, V., Rinder, M., Kaspers, B., Staeheli, P., Rubbenstroth, D., 2014. Impact of antigenic diversity on laboratory diagnosis of Avian bornavirus infections in birds. J. Vet. Diagn. Invest. 26, 769-777.

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. Sequences used for PASC analysis

GenBank acc. no.	Virus	Variant characteristics	Sequence information
AB032031	BoDV-1	Japanese laboratory variant of "strain" V	complete genome
AB246670	BoDV-1	Japanese laboratory variant Bo/04w of "strain" V	complete genome
AB258389	BoDV-1	Japanese laboratory variant huP2br of "strain" V	complete genome
AJ311521	BoDV-1	Freiburg laboratory variant of "strain" V	complete genome
AJ311522	BoDV-1	Freiburg laboratory variant of "strain" He/80	complete genome
AJ311523	BoDV-1	"strain" H1766 of sequence cluster 4 originally isolated from a horse	complete genome
AY114161	BoDV-1	US laboratory variant of "strain" V	complete genome
AY114162	BoDV-1	US laboratory variant of "strain" V	complete genome
AY114163	BoDV-1	US laboratory variant of "strain" V	complete genome
L27077	BoDV-1	"strain" He/80 of BDV1 sequence cluster 1A originally isolated from a horse	complete genome
NC_001607	BoDV-1	"strain" V of sequence cluster 4 originally isolated from a horse	complete genome
AJ311524	BoDV-2	"strain" No/98 originally isolated from a horse in Austria	complete genome
LN713680	VSBV-1	"strain" squirrel brain isolated from a variegated squirrel in Germany	coding-complete genome
LN713681	VSBV-1	"strain" patient 3 isolated from a human in Germany	coding-complete genome
GU249595	PaBV-1	"strain" M25 isolated from a red-shouldered macaw in the USA	coding-complete genome
JX065207	PaBV-1	"strain" 16234 isolated from a kea in Germany	coding-complete genome
EU781967	PaBV-2	"strain" bil isolated from a sun parakeet in the USA	complete genome
FJ620690	PaBV-2	"strain" 6609 isolated from a Hispaniolan amazon in Austria	complete genome
GU249596	PaBV-4	"strain" AG5 isolated from an African grey parrot in the USA	complete genome
JN014948	PaBV-4	"strain" NM_06 isolated from Goffin's cockatoo in the USA	coding-complete genome
JN014949	PaBV-4	"strain" NM_20 isolated from a blue-and-yellow macaw in the USA	coding-complete genome
JN035148	PaBV-4	"strain" NM_01 isolated from Jandaya parakeet in the USA	coding-complete genome
JX065209	PaBV-4	"strain" 6758 isolated from a blue-and-yellow macaw in Germany	complete genome
JX065210	PaBV-7	"strain" 16667a isolated from a salmon-crested cockatoo in Germany	coding-complete genome
KR612223	PaBV-5	"strain" 2014-A isolated from a blue-and-yellow macaw in Hungary	coding-complete genome
KT378600	PaBV-5	"strain" Cockg5 isolated from a cockatoo in the USA	coding-complete genome
KF578398	ABBV-1	"strain" 062-CG isolated from a Canada goose in the USA	complete genome
KP972428	ABBV-1	"strain" CG-N1489 isolated from a Canada goose in the USA	coding-complete genome
KJ756399	ABBV-2	"strain" duck-89 isolated from a wild duck in the USA	coding-complete genome
KC464471	CnBV-1	"strain" 7293 isolated from a domestic canary bird in Germany	coding-complete genome
KC464478	CnBV-2	"strain" 15864 isolated froma domestic canary bird in Germany	coding-complete genome
KC595273	CnBV-3	"strain" VS-4424 isolated froma domestic canary bird in Germany	coding-complete genome
KM114265	LGSV-1	"strain" 251327 detected in a wild caught Loveridge's garter snake in Tanzania	coding-complete genome

Figure 1. Histogram of *Bornaviridae* PASC analysis. Distribution of pairwise identities among complete sequences of 22 viruses in the family *Bornaviridae*. The histogram is colored as if the taxonomy proposed here was accepted by the ICTV and then adopted by NCBI. Peaks above 72% identity (green) represent genome pairs belonging to the same species. Peaks below 71% identity (yellow) represent genome pairs belonging to different species but the same genus. X-axis, percentage of identity; y-axis, number of genome pairs.

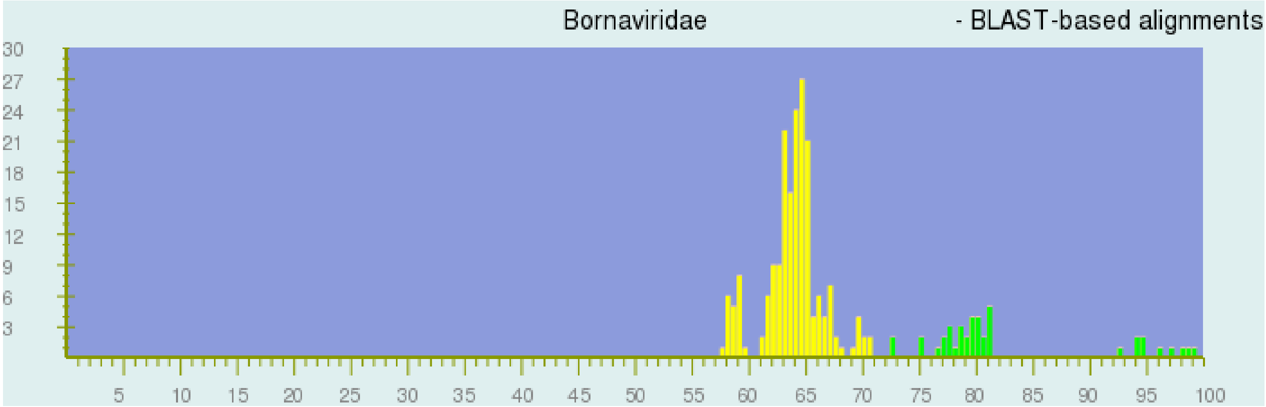

Table 2. Proposed classification and nomenclature of bornaviruses

Family (name of taxon members)	**Genus (name of taxon members)**	**Species**	**Virus (virus abbreviation)**
Bornaviridae (bornavirids, bornaviruses)			
	Bornavirus (bornaviruses)		
		Mammalian 1 bornavirus	
			Borna disease virus 1 (BoDV-1)
			Borna disease virus 2 (BoDV-2)
		Mammalian 2 bornavirus	
			variegated squirrel bornavirus 1 (VSBV-1)
		Psittaciform 1 bornavirus	
			parrot bornavirus 1 (PaBV-1)
			parrot bornavirus 2 (PaBV-2)
			parrot bornavirus 3 (PaBV-3)
			parrot bornavirus 4 (PaBV-4)
			parrot bornavirus 7 (PaBV-7)
		Passeriform 1 bornavirus	
			canary bornavirus 1 (CnBV-1)
			canary bornavirus 2 (CnBV-2)
			canary bornavirus 3 (CnBV-3)
		Waterbird 1 bornavirus	
			aquatic bird bornavirus 1 (ABBV-1)
			aquatic bird bornavirus 2 (ABBV-2)
		Passeriform 2 bornavirus	
			estrildid finch bornavirus 1 (EsBV-1)
		Psittaciform 2 bornavirus	
			parrot bornavirus 5 (PaBV-5)
		Elapid 1 bornavirus	
			Loveridge´s garter snake virus 1 (LGSV-1)
		tentative, unclassified bornaviruses	
			Gaboon viper virus 1 (GaVV-1)
			munia bornavirus 1 (MuBV-1)
			parrot bornavirus 6 (PaBV-6)
			parrot bornavirus 8 (PaBV-8)

[1] Type species is underlined.

red new virus, previously unclassified

Figure 2. Phylogenetic tree of a 5,571 nt stretch coding for complete N, X, P, M, and G proteins and partial L proteins of 16 bornaviruses (corresponding to pos. 54 to 5,553 of BoDV-1 [U04608]). Phylogenetic neighbor joining analysis was conducted with Geneious R8. The evolutionary distances were computed using the Jukes-Cantor model. Bootstrap resampling analysis with 1,000 replicates was employed; percentages ≥70% are shown next to the branches.

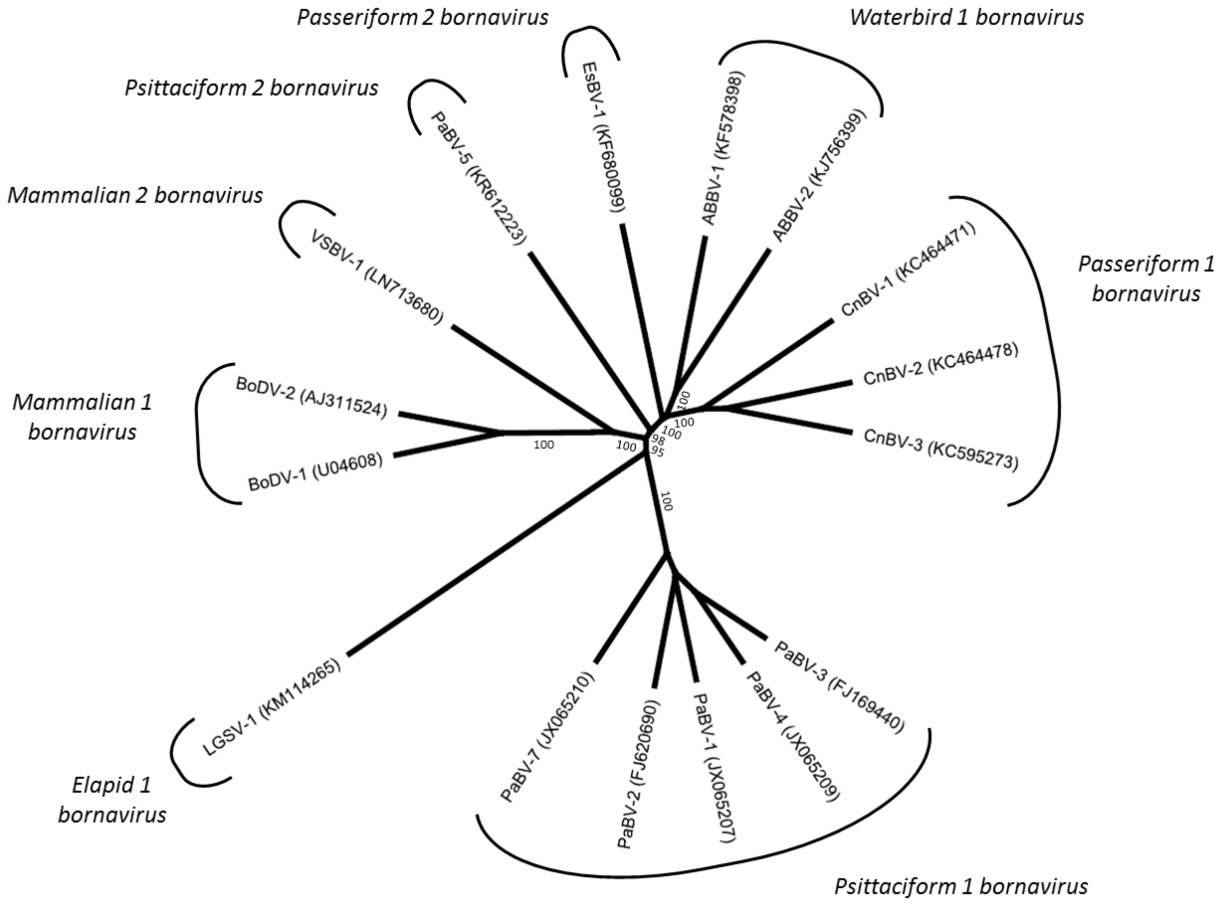

Figure 3. Phylogenetic tree of selected nucleotide sequences (A) or amino acid sequences (B) of the P protein gene of 18 bornaviruses. Phylogenetic neighbor joining analysis was conducted with Geneious R8. The evolutionary distances were computed using the Jukes-Cantor model. Bootstrap resampling analysis with 1,000 replicates was employed; percentages ≥70% are shown next to the branches. (*) Asterisks indicate bornaviruses not classified due to lack of sufficient sequence information.