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:	***2014.010a,bV***	(to be completed by ICTV officers)

Short title: 4 new species in the genus *Bornavirus*; renaming of 1 species in the genus *Bornavirus*~~; and renaming of the family *Bornaviridae*~~
(e.g. 6 new species in the genus *Zetavirus*)

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

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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)	ICTV *Bornaviridae* Study Group (Kathryn Carbone, Wolfgang Garten, Norbert Nowotny, Martin Schwemmle, Keizo Tomonaga) ICTV *Mononegavirales* Study Group (Ralf Dietzgen, Jens H. Kuhn, Norbert Nowotny, and Linfa Wang)

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

Date first submitted to ICTV: July 2, 2014
Date of this revision (if different to above): September 9~~4~~, 2014

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	***2014.010aV***	(assigned by ICTV officers)

To create 4 new species within:

Genus:	***Bornavirus***
Subfamily:	
Family:	~~***Bordiviridae*** **(new, ex**~~ ***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)**
Psittaciform 1 bornavirus	parrot bornavirus 1 (PaBV-1) [ex ABV1] parrot bornavirus 2 (PaBV-2) [ex ABV2] parrot bornavirus 3 (PaBV-3) [ex ABV3] parrot bornavirus 4 (PaBV-4) [ex ABV4] parrot bornavirus 7 (PaBV-7) [ex ABV7]	GU249595, JX065207 EU781967, FJ620690 FJ169440 JX065209, JN014948, JN014949, JN035148 JX065210
Passeriform 1 bornavirus	canary bornavirus 1 (CnBV-1) [ex ABV C1] canary bornavirus 2 (CnBV-2) [ex ABV C2] canary bornavirus 3 (CnBV-3) [ex ABV C3] munia bornavirus 1 (MuBV-1) [ex ABV LS]	KC464471 KC464478 KC595273 HX776010, DC282008, DC290659
Passeriform 2 bornavirus	estrildid finch bornavirus 1 (EsBV-1) [ex ABV EF]	KF680099
Waterbird 1 bornavirus	aquatic bird bornavirus 1 (ABBV-1) [ex ABV 062$_{\mathrm{CG}}$]	KF578398

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

Variants of the mammalian Borna disease virus have extremely conserved genome sequences (>95% similarity) [4, 5, 10, 16, 17]. In 2008, novel viruses were discovered in psittacine birds that resemble Borna disease virus in genomic organization but differ considerable from this virus in sequence [7, 9]. These viruses were assigned to five different groups and provisionally named "avian bornaviruses 1-5 (ABV1-5)" [9]. ABV variant genomes are 91–100% similar within a group, 68-85% similar between groups, and 60–69% similar to the genome of Borna disease virus [9, 12]. By now, a total of 13 ABV groups are known. Six are associated with anseriform and passeriform birds [3, 8, 13-15, 19, 20]; an additional group may be of reptilian origin [6].

We used the PAirwise Sequence Comparison (PASC) methodology, a tool available from the National Center for Biotechnology Information (NCBI) website, to resolve the taxonomy of bornaviruses (for a description of this method see (1,2)). The results of this analysis (see Table 1 for used bornaviruses sequences) can be accessed on the PASC webpage at http://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?cmdresult=main&id=454. The results indicate the following reorganization of the family *Bornaviridae*:

- the family should stay monogeneric (the peak in PASC for the most distantly related viruses is located at 61-66%, a value in line with generic cut-offs for other viruses families);
- species differentiation may be achieved by setting three different sequence cut-offs: i) 66-69%; ii) 71-75%; and iii) 76-78%. Choice ii) seems most appropriate when additional factors, such as host range, geographical distribution, and genomic characteristics are taken into account. This choice leads to the need for creation of four species (nucleotide sequence cut-off of 75%):
    - Species 1 for mammalian Borna disease viruses
    - Species 2 for avian/psittacine bornaviruses 1, 2, and 4
    - Species 3 for avian/canary bornaviruses C1, C2, and C3
    - Species 4 for avian/anserine bornavirus 062_{CG}.

Traditional BLAST analyses using each bornavirus protein gene (nt BLAST and protein BLAST; data provided to the ICTV EC for review) confirm the PASC results and Choice 2. In addition, these analysis indicate that:

- avian/psittacine bornavirus 3 and avian bornavirus 7 should belong to Species 2;
- avian bornavirus LS should belong to Species 3;
- avian bornavirus EF should belong to a new Species 5;
- avian bornaviruses 5 and 6 and “reptile bornavirus/Gaboon viper virus” cannot yet be classified (only sequence fragments are available and there are no isolates).

Multiple sequence alignments, performed using BioEdit Sequence Alignment Editor Version 7.0.9.0 and verified by Clustal X (version 1.8), and the derived phylogenetic analyses performed with MEGA5 further confirm this classification (see Figures 1 and 2).

Because the results of all three types of analyses are compatible with each other, and in line with the known biological properties of the viruses, we propose the bornavirus taxonomy outlined in Table 2. Species 2-5 are named *Psittaciform 1 bornavirus*, *Passeriform 1 bornavirus*, *Waterbird 1 bornavirus*, and *Passeriform 2 bornavirus*, respectively.

MODULE 8: **NON-STANDARD**

Template for any proposal not covered by modules 2-7. This includes proposals to change the name of existing taxa (but note that stability of nomenclature is encouraged wherever possible).

non-standard proposal

Code	***2014.010bV***	(assigned by ICTV officers)

Title of proposal: ~~(i) Change the name of the family *Bornaviridae* to *Bordiviridae*. (ii)~~ In the genus *Bornavirus*, change the name of species *Borna disease virus* to *Mammalian 1 bornavirus*

Text of proposal:

~~The increasing diversity of borna-like viruses, unpublished data available to the authors, and preliminary analyses of the thus far unclassified “reptile bornavirus/Gaboon viper virus 1” indicate that it is not unlikely that a second genus will have to be created within the family fairly soon. The creation of a second genus in the family *Bornaviridae* would create an ambiguity in regard to the words “bornaviral”, “bornavirus”, and “bornaviruses” – as all three words could refer to members of the entire family *Bornaviridae* (members of the genus *Bornavirus* and those of the second genus) or only to those of the genus *Bornavirus*. We therefore propose to change the family name *Bornaviridae* to remove the ambiguity. By keeping the genus name *Bornavirus*, impact of the renaming on the bornavirus research community is minimal (the term “bornavirus” would still refer to all currently described and classified members of the family). We propose the name *Bordiviridae* for the family (sigil of “Borna disease” and the family suffix “-viridae”):~~

~~*Bornaviridae* → *Bordiviridae* (Table 2).~~

At the moment, the one accepted bornavirus species name is identical in spelling to the name of its member and only differs by presence or absence of italics (i.e., the species *Borna disease virus* is the taxonomic home for Borna disease virus). Consequently, species and virus names are constantly confused. To remove this ambiguity and achieve better alignment with ICVCN’s Rules (in particular, Rules 2.1(ii), 3.14, and 3.24), we propose to replace the current species name with a non-Latinized binomial name distinct from the virus names (21), which is also in line with the four new species proposed to be included into the genus *Bornavirus* above:

Borna disease virus → *Mammalian 1 bornavirus* (Table 2).

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Bao Y, Kapustin Y, Tatusova T (2008). Virus Classification by Pairwise Sequence Comparison (PASC). In Encyclopedia of Virology (Third Edition), BWJ Mahy, MH Regenmortel, eds. (Oxford: Academic Press), pp. 342–348
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4. Dürrwald R, Kolodziejek J, Muluneh A, Herzog S, Nowotny N (2006) Epidemiological pattern of classical Borna disease and regional genetic clustering of Borna disease viruses point towards the existence of to-date unknown endemic reservoir host populations. Microbes and infection 8:917-929
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6. Fujino K, Horie M, Honda T, Nakamura S, Matsumoto Y, Francischetti IM, Tomonaga K (2012) Evolutionarily conserved interaction between the phosphoproteins and X proteins of bornaviruses from different vertebrate species. PloS One 7:e51161
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11. **Kuhn JH, Dürrwald R, Bào~~Bao~~ Y, Briese T, Carbone K, Clawson AN, deRisi JL, Garten W, Jahrling PJ, Kolodziejek J, Rubbenstroth D, Schwemmle M, Stenglein M, Tomonaga K, Weissenböck H, Nowotny N (2014). ~~Current~~ ~~t~~Taxonomic ~~status and proposal for~~ reorganization ~~and expansion~~ of the family *Bornaviridae*. Revised version submitted~~In preparation~~ (draft provided to ICTV**

References:

EC for review; the text in this proposal is largely derived from this draft).

12. Payne S, Shivaprasad HL, Mirhosseini N, Gray P, Hoppes S, Weissenböck H, Tizard I (2011) Unusual and severe lesions of proventricular dilatation disease in cockatiels (Nymphicus hollandicus) acting as healthy carriers of avian bornavirus (ABV) and subsequently infected with a virulent strain of ABV. Avian pathology : journal of the WVPA 40:15-22
13. Rubbenstroth D, Rinder M, Kaspers B, Staeheli P (2012) Efficient isolation of avian bornaviruses (ABV) from naturally infected psittacine birds and identification of a new ABV genotype from a salmon-crested cockatoo (Cacatua moluccensis). Veterinary microbiology 161:36-42
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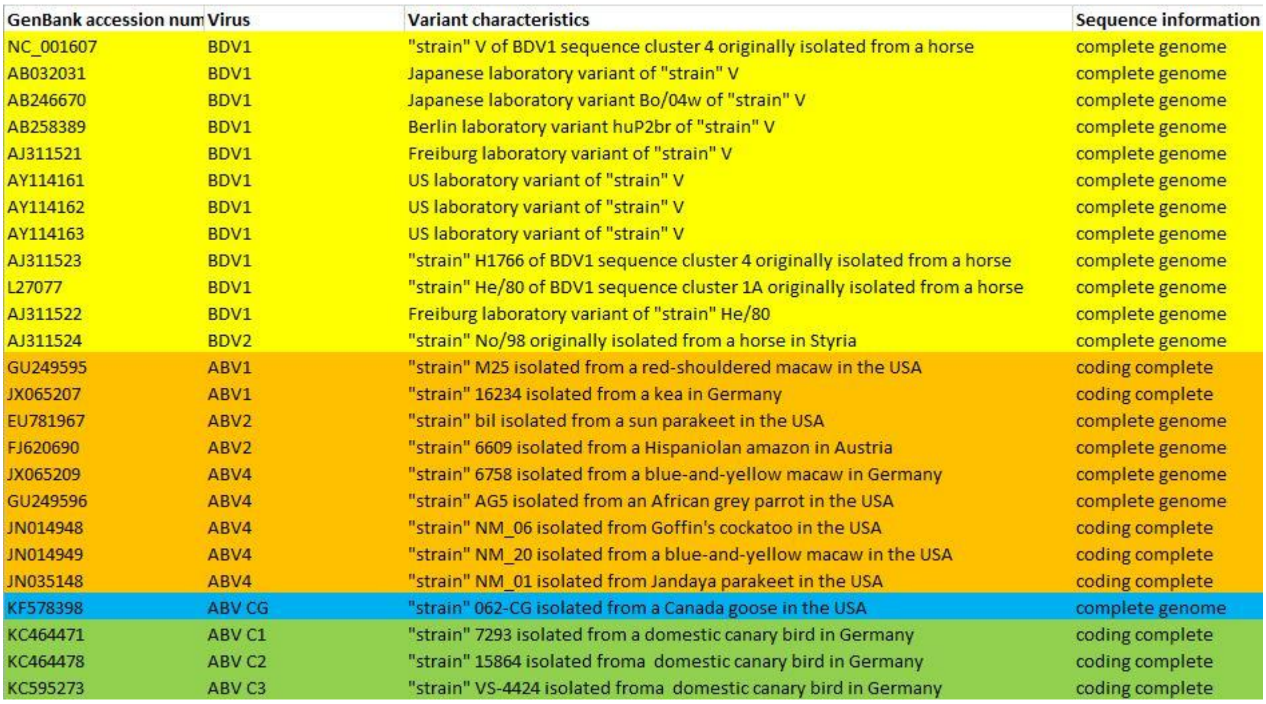
Annex:

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 accession num	Virus	Variant characteristics	Sequence information
NC_001607	BDV1	"strain" V of BDV1 sequence cluster 4 originally isolated from a horse	complete genome
AB032031	BDV1	Japanese laboratory variant of "strain" V	complete genome
AB246670	BDV1	Japanese laboratory variant Bo/04w of "strain" V	complete genome
AB258389	BDV1	Berlin laboratory variant huP2br of "strain" V	complete genome
AJ311521	BDV1	Freiburg laboratory variant of "strain" V	complete genome
AY114161	BDV1	US laboratory variant of "strain" V	complete genome
AY114162	BDV1	US laboratory variant of "strain" V	complete genome
AY114163	BDV1	US laboratory variant of "strain" V	complete genome
AJ311523	BDV1	"strain" H1766 of BDV1 sequence cluster 4 originally isolated from a horse	complete genome
L27077	BDV1	"strain" He/80 of BDV1 sequence cluster 1A originally isolated from a horse	complete genome
AJ311522	BDV1	Freiburg laboratory variant of "strain" He/80	complete genome
AJ311524	BDV2	"strain" No/98 originally isolated from a horse in Styria	complete genome
GU249595	ABV1	"strain" M25 isolated from a red-shouldered macaw in the USA	coding complete
JX065207	ABV1	"strain" 16234 isolated from a kea in Germany	coding complete
EU781967	ABV2	"strain" bil isolated from a sun parakeet in the USA	complete genome
FJ620690	ABV2	"strain" 6609 isolated from a Hispaniolan amazon in Austria	complete genome
JX065209	ABV4	"strain" 6758 isolated from a blue-and-yellow macaw in Germany	complete genome
GU249596	ABV4	"strain" AG5 isolated from an African grey parrot in the USA	complete genome
JN014948	ABV4	"strain" NM_06 isolated from Goffin's cockatoo in the USA	coding complete
JN014949	ABV4	"strain" NM_20 isolated from a blue-and-yellow macaw in the USA	coding complete
JN035148	ABV4	"strain" NM_01 isolated from Jandaya parakeet in the USA	coding complete
KF578398	ABV CG	"strain" 062-CG isolated from a Canada goose in the USA	complete genome
KC464471	ABV C1	"strain" 7293 isolated from a domestic canary bird in Germany	coding complete
KC464478	ABV C2	"strain" 15864 isolated froma domestic canary bird in Germany	coding complete
KC595273	ABV C3	"strain" VS-4424 isolated froma domestic canary bird in Germany	coding complete

Table 2. Proposed classification and nomenclature of bornaviruses

Family (name of taxon members)	**Genus (name of taxon members)**	**Species**	**Virus (virus abbreviation)**
Borna~~di~~viridae (borna~~di~~virids, borna~~di~~viruses)			
	Bornavirus (bornaviruses)		
		Mammalian 1 bornavirus	
			Borna disease virus 1 (BoDV-1)
			Borna disease virus 2 (BoDV-2)
		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)
			munia bornavirus 1 (MuBV-1)
		Waterbird 1 bornavirus	
			aquatic bird bornavirus 1 (ABBV-1)
		Passeriform 2 bornavirus	
			estrildid finch bornavirus 1 (EsBV-1)
		tentative, unclassified bordiviruses	
			Gaboon viper virus 1 (GaVV-1)
			parrot bornavirus 5 (PaBV-5)
			parrot bornavirus 6 (PaBV-6)

[1] Type species is underlined.

Figure 1. Phylogentic tree of a 1824 nt stretch of 17~~6~~ nucleic acid sequences coding for N, X, and P proteins and the N/X intergenic region of “bornaviruses”. Phylogenetic neighbor joining analysis was conducted with the MEGA5 program (18). The evolutionary distances were computed using the Kimura 2-parameter model. Bootstrap resampling analysis with 1,000 replicates was employed; percentages ≥60% are shown next to the branches.

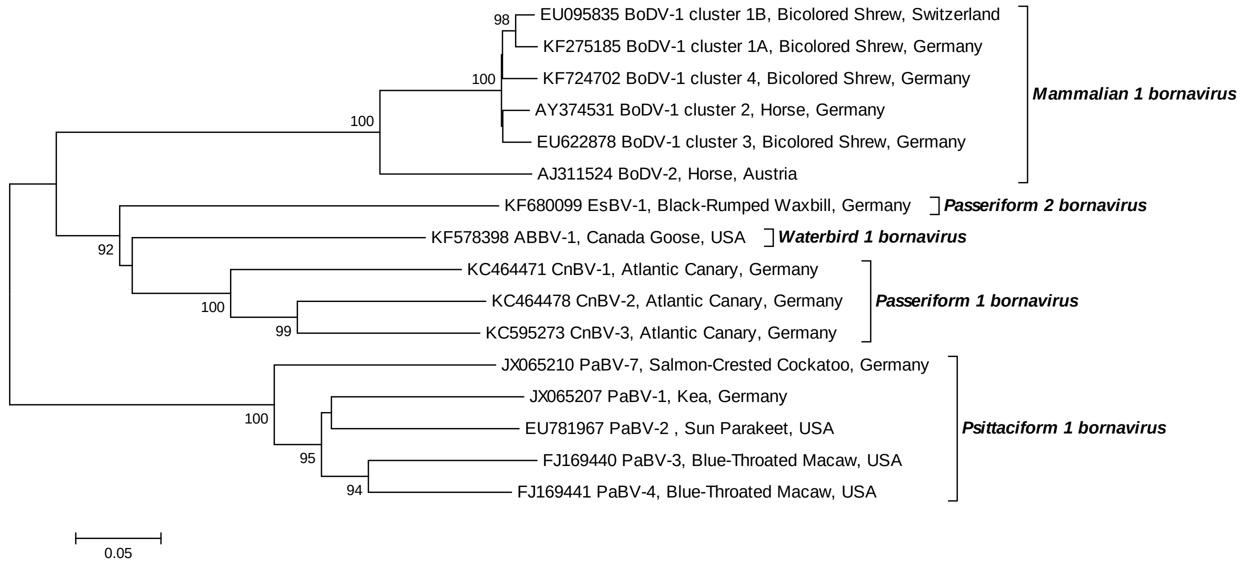


Figure 2. Phylogenetic tree of 15~~4~~ selected amino acid sequences representing the X protein of “bornaviruses”. Phylogenetic neighbor joining analysis was conducted with the MEGA5 program (18). The evolutionary distances were computed using the p-distance method. Bootstrap resampling analysis with 1,000 replicates was employed; percentages ≥60% are shown next to the branches.