This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

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.

Part 1: **TITLE, AUTHORS, etc**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.005M*** | | | | (to be completed by ICTV officers) |
| **Short title:** One (1) new genus including two (2) new species in the family *Bornaviridae* (order *Mononegavirales*) | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Jens H. Kuhn, [kuhnjens@mail.nih.gov](mailto:kuhnjens@mail.nih.gov)  Mark Stenglein, [mark.stenglein@colostate.edu](mailto:mark.stenglein@colostate.edu)  Jim Wellehan, [wellehanj@ufl.edu](mailto:wellehanj@ufl.edu)  Dennis Rubbenstroth, [dennis.rubbenstroth@uniklinik-freiburg.de](mailto:dennis.rubbenstroth@uniklinik-freiburg.de)  Thomas Briese, [tb2047@cumc.columbia.edu](mailto:tb2047@cumc.columbia.edu)  Ralf Dürrwald, [ralf.duerrwald@t-online.de](mailto:ralf.duerrwald@t-online.de)  Masayuki Horie, [horie.masayuki.3m@kyoto-u.ac.jp](mailto:horie.masayuki.3m@kyoto-u.ac.jp)  Norbert Nowotny, [norbert.nowotny@vetmeduni.ac.at](mailto:norbert.nowotny@vetmeduni.ac.at)  Susan Payne, [SPayne@cvm.tamu.edu](mailto:SPayne@cvm.tamu.edu)  Martin Schwemmle, [martin.schwemmle@uniklinik-freiburg.de](mailto:martin.schwemmle@uniklinik-freiburg.de)  Keizo Tomonaga, [tomonaga@virus.kyoto-u.ac.jp](mailto:tomonaga@virus.kyoto-u.ac.jp)  Tim Hyndman, [T.Hyndman@murdoch.edu.au](mailto:T.Hyndman@murdoch.edu.au) | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Jens H. Kuhn, [kuhnjens@mail.nih.gov](mailto:kuhnjens@mail.nih.gov) | | | | | |
| **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 (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | | **ICTV *Bornaviridae* Study Group** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | June 8, 2017 | |
| Date of this revision (if different to above): | | | |  | |

|  |
| --- |
| **ICTV-EC comments and response of the proposer:** |
|  |

**Part 2**: **PROPOSED TAXONOMY**

|  |
| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet: 2017.005M.N.v1.Carbovirus** |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

**Part 4:** **APPENDIX**: supporting material

As of 2017, the family *Bornaviridae* includes one genus (*Bornavirus*) including eight species: *Elapid 1 bornavirus*, *Mammalian 1 bornavirus*, *Mammalian 2 bornavirus*, *Passeriform 1 bornavirus, Passeriform 2 bornavirus, Psittaciform 1 bornavirus, Psittaciform 2 bornavirus,* and *Waterbird 1 bornavirus* (see Excel spreadsheet)*.* The majority of known bornaviruses are classified in these species, but four additional bornaviruses remain unclassified due to insufficient sequence information.

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 relationships (Zimmermann *et al.*, 2014) and natural host ranges (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).

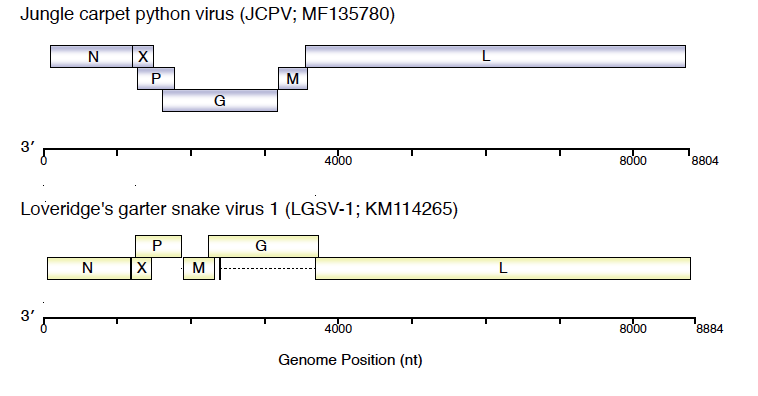
Two new bornaviruses were recently identified in carpet pythons (*Morelia spilota*) in Australia with neurological disease. These viruses were identified using metagenomic next generation sequencing and their coding-complete genome sequences were determined. The viruses were named southwest carpet python virus (SWCPV) and jungle carpet python virus (JCPV). The organization of their genomes and phylogenetic positioning support their designation as members of the family *Bornaviridae*, but they possess several distinguishing features, including a rearrangement of their M and G genes relative to classified members of the genus *Bornavirus* (Figure 1). SWCPV and JCPV have not been isolated in tissue culture and no antigenicity data have been generated.

PASC analysis was performed using the coding-complete genome sequences of JCPV and SWCPV (GenBank #MF135780 and #MF135781, respectively). These genomes share 69% pairwise nucleotide identity, indicating that they should be classified in different species according to the existing bornavirus species demarcation threshold. The predicted JCPV and SWCPV L proteins share 35.1–37% pairwise amino acid identity with the L proteins of classified bornaviruses. The JCPV and SWCPV genome sequences share ≤37.1% identity with any other classified bornavirus genome, which lies well below the pairwise identities of previously described bornaviruses, which all share >≈57% pairwise identity (Figure 2).

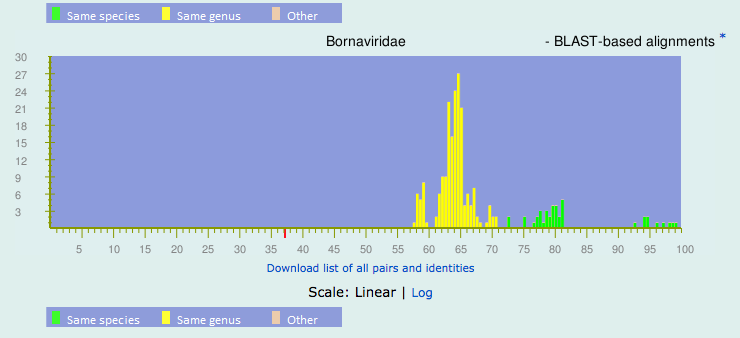
Phylogenies inferred from alignments of the predicted L and N protein sequences of JCPV and SWCPV and related sequences show that JCPV and SWCPV represent a lineage distinct from that of known bornaviruses (Figures 3–4). In fact, JCPV and SWCPV are more closely related to endogenous bornavirus elements in various mammalian genomes than they are to the sequences of extant exogenous bornaviruses.

PASC, phylogenetic analyses, and the rearranged M-G gene order support the assertion that JCPV and SWCPV ought to be classified into a new bornavirus genus. A genus-demarcation cut-off could initially be set at ≈45%.

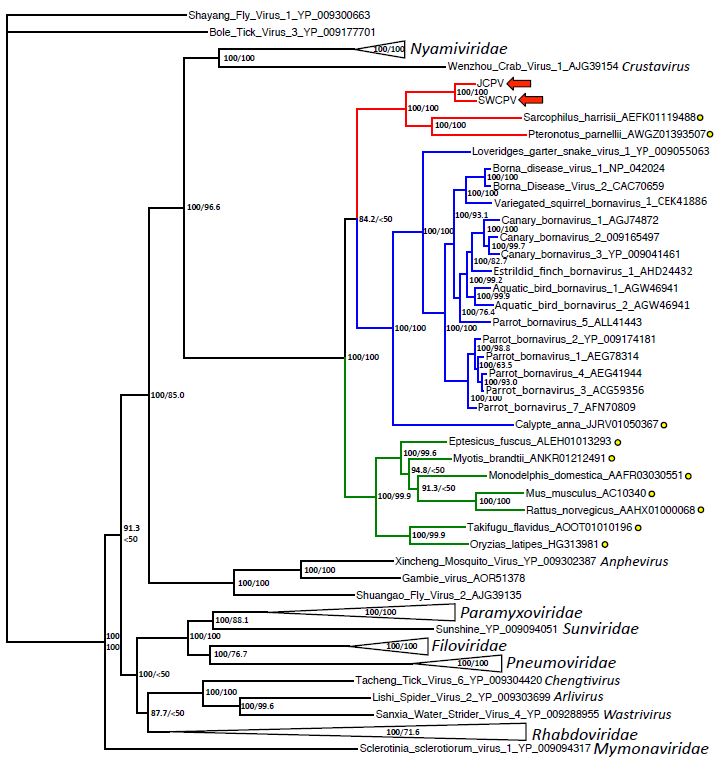
The name of the new genus is proposed to be *Carbovirus* (from “**CA**irns”, the place of the initial isolation, “**R**eptilian” and “**BO**rnavirus”). The genus will include the species *Queensland carbovirus* (encompassing JCPV) and *Southwest carbovirus* (encompassing SWCPV).



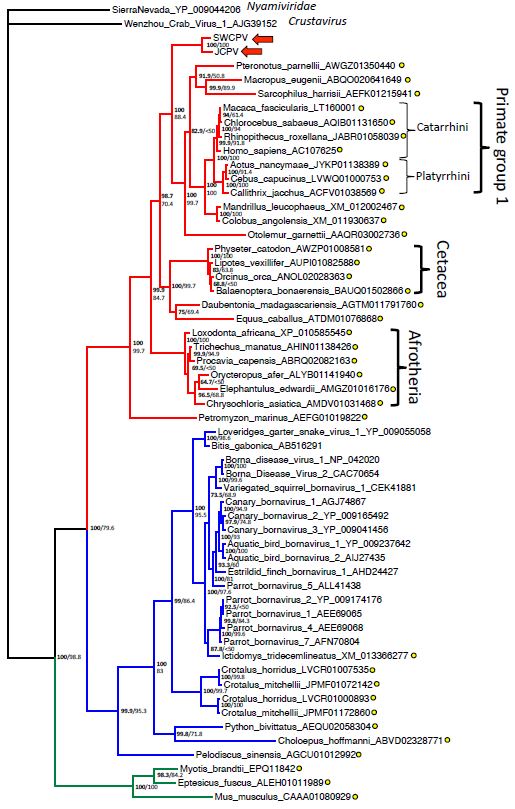
**Figure 1. Genome organization of JCPV and LGSV-1.** The genome organization of JCPV and Loveridge’s garter snake virus 1, a previously described and classified member of the genus *Bornavirus* (Stenglein *et al*., 2014). Note the rearrangement of the predicted M and G genes.

****

**Figure 2. Histogram of *Bornaviridae* PASC analysis.** Distribution of pairwise identities among complete sequences of viruses in the family *Bornaviridae*. 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. The JCPV and SWCPV genomes shared < 37.1% pairwise identity with any of the previously described extant bornavirus genomes (indicated by red tick mark).



**Figure 3 Phylogeny based on alignment of mononegavirus L sequences.** Classified and putative members of the family *Bornaviridae* are shown at the end of colored (non-black) branches. Endogenous bornavirus-like element sequences are indicated by yellow circles.



**Figure 4.** **Phylogeny based on alignment of mononegavirus N sequences.** Classified and putative members of the family *Bornaviridae* are shown at the end of colored (non-black) branches. Endogenous bornavirus-like element sequences are indicated by yellow circles.

|  |
| --- |
| **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.  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.  Stenglein MD, Leavitt EB, Abramovitch MA, McGuire JA, DeRisi JL. Genome Sequence of a Bornavirus Recovered from an African Garter Snake (*Elapsoidea loveridgei*). Genome Announc. 2014 Oct 9;2(5). pii: e00779-14.  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:**  Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance. |