

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

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| **Code assigned:** | **2021.021M** |  |
| **Short title:** Create one new species in genus *Orthobornavirus* (*Mononegavirales*: *Bornaviridae*) | | |
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**Author(s) and email address(es)**

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**List the ICTV Study Group(s) that have seen this proposal**

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| ICTV *Bornaviridae* Study Group |

**ICTV study group comments and response of proposer**

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**Authority to use the name of a living person**

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| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | May 28, 2021 |
| Date of this revision (if different to above) |  |

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

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2021.021M.R.Orthobornavirus\_1nsp |

**Abstract**

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| **Two novel reptilian orthobornaviruses, named “Caribbean watersnake bornavirus (CWBV)” and “Mexican black-tailed rattlesnake bornavirus (MRBV)” were identified in a Caribbean watersnake (*Tretanorhinus variabilis*) and a Mexican black-tailed rattlesnake (*Crotalus molossus nigrescens*), respectively [1]. The viral genome sequences were *de novo* assembled from archived raw transcriptomic read data of the host snake species.**  Based on the conserved genome organization, phylogenetic analysis, and pairwise nucleotide identity, we propose both viruses be assigned to a single new species within the bornaviral genus *Orthobornavirus.* We propose the name *Orthobornavirus caenophidiae* (genitive singular of Caenophidia, the alethinophidian clade harboring viperid and colubrid snakes). |

**Text of proposal**

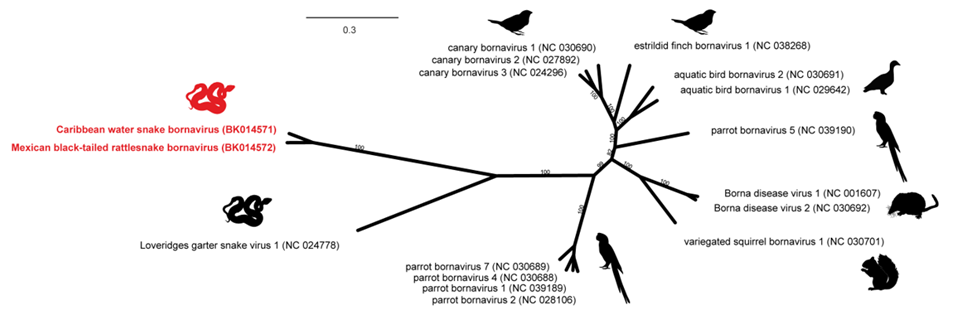
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| --- | --- |
| |  | | --- | | As of 2021, the family *Bornaviridae* includes three genera (*Carbovirus*, *Cultervirus*, and *Orthobornavirus*). The genus *Orthobornavirus* currently includes eight species for viruses that have been discovered in avian, reptilian, and mammalian hosts. Criteria for bornavirid genus affiliation and species demarcation are based on genomic characteristics, including genome organization, PAirwise Sequence Comparison (PASC) [2, 3], in combination with biological characteristics, such as antigenic relationships and natural host range [4]. In agreement with these criteria, the PASC species demarcation criterion was defined as 72–75% for coding-complete genome sequences[5, 6].  Two novel reptilian orthobornaviruses, named “Caribbean watersnake bornavirus (CWBV)” and “Mexican black-tailed rattlesnake bornavirus (MRBV)” were identified in archived raw transcriptomic read data of a Caribbean watersnake (*Tretanorhinus variabilis* **A.M.C. Duméril, Bibron & A.H.A. Duméril, 1854**; caenophidian family Colubridae) and a Mexican black-tailed rattlesnake (*Crotalus molossus nigrescens* **Gloyd, 1936**; caenophidian family Viperidae), respectively. Complete genome sequences from CWBV and MRBV were *de novo* assembled from the short read archive (SRA) datasets SRR5440420 and SRR9693197, and were deposited under the GenBank third party annotation accession numbers BK014571 and BK014572, respectively [1].  SRA dataset SRR5440420 contains raw reads from the Harderian gland transcriptome of a wild-caught adult Caribbean watersnake from Santa Fe, La Habana, Cuba [7]. SRA dataset SRR9693197 contains raw reads from the venom gland transcriptome of a wild-caught juvenile Mexican black-tailed rattlesnake from Nuevo León, Mexico.  The genomes of CWBV and MRBV are approximately 8,900 nucleotides long, and the overall genomic makeup and predicted gene content is typical for members of the genus *Orthobornavirus*. Alternative splicing was identified for transcripts derived from the L and M genes (Figure 1) based on the detection of multiple sequence reads that covered the splice junctions over the intronic sequences.  Phylogenetic analysis of concatenated alignments of N-P-M-G-L amino acid sequences from both viruses along with representative bornavirus sequences showed that both viruses are distinct from currently classified members of the genus *Orthobornavirus* (Figure 2). PASC of complete genome sequences showed that CWBV and MRBV are 76.6% identical and that both viral genomes are 56.6–57.3% identical to the next most closely related orthobornavirus (Figure 3).  Based on the conserved genome organization, phylogenetic analysis, and pairwise nucleotide identity, we propose both viruses to be assigned to a single new species within the bornaviral genus *Orthobornavirus.* We propose the name *Orthobornavirus caenophidiae* (genitive singular of Caenophidia, the alethinophidian clade harboring viperid and colubrid snakes [8]). | |

**Supporting evidence**

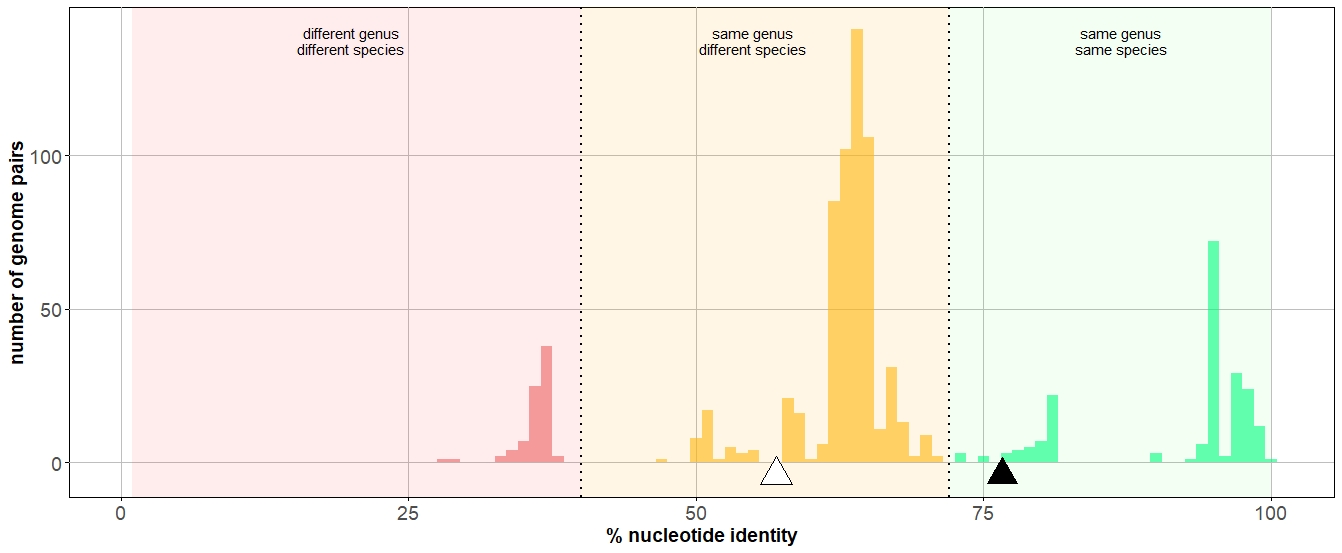
**Figure 1. Genome organization of Caribbean watersnake bornavirus (CWBV) and Mexican black-tailed rattlesnake bornavirus (MRBV).** Canonical bornaviral gene order N-X/P-M-G-L (pink arrows) flanked by untranslated regions (UTR – blue arrows). Introns have been detected in M and L genes (grey arrows). Three transcription initiation sites (S1-3) and four transcription termination sites (T1-4) have been predicted.



**Figure 2. Maximum likelihood phylogenetic analysis of orthobornaviruses.** The unrooted phylogenetic tree is based on the concatenated amino acid alignments of N-P-M-G-L of the novel snake bornaviruses (highlighted red) together with all available complete orthobornavirus genome sequences. The tree was calculated using IQ-TREE (version 2.1.2; 1 million ultrafast bootstraps; optimal substitution model for each alignment / alignment partition).

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**Figure 3. Histogram of *Bornaviridae* PASC analysis.** Distribution of pairwise nucleotide identities among coding-complete sequences of viruses classified in the genera *Carbovirus* and *Orthobornavirus*. The histogram is colored as if the taxonomy proposed here was accepted by the ICTV and then adopted by NCBI. Peaks above 72% nucleotide identity (green) represent genome pairs belonging to the same species. Peaks below 72% nucleotide identity (yellow) represent genome pairs belonging to different species but the same genus. Peaks below 40% nucleotide identity (red) represent genome pairs belonging to different species and different genus. White triangle indicates nucleotide identity between Mexican black-tailed rattlesnake bornavirus and the top matched bornavirus genome. Black triangle indicates nucleotide identity between Mexican black-tailed rattlesnake bornavirus and Caribbean water snake bornavirus.



**References**

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