

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

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| **Code assigned:** | **2020.009M** |  |
| **Short title:**  Create one new species and rename one species in the genus *Vesiculovirus* (*Mononegavirales*: *Rhabdoviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| *Rhabdoviridae* Study Group |

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

Please provide comments/approval of each study group that has seen the proposal. Please indicate how you have responded to the comments.

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| Approved by all responding SG members (9 of 14) with minor revisions. |

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

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
|  |  |  |

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | 26 July 2020 |
| Date of this revision (if different to above) |  |

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

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2020.009M.R.Vesiculovirus\_1nsp\_renam1sp.xlxs |

**Abstract**

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| The new species *Rhinolophus vesiculovirus* is proposed for Jinghong bat virus. The virus clusters phylogenetically with members of the genus *Vesiculovirus* and meets demarcation criteria for assignment to a new species in the genus for which we propose the name *Rhinolophus vesiculovirus.* We also propose to rename the species *American bat vesiculovirus* as *Eptesicus vesiculovirus.* |

**Text of proposal**

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| --- | --- |
| |  | | --- | | Jinghong bat virus (JhBV; strain IH17) was detected in an intermediate horseshoe bat (*Rhinolophus affinis*) collected in 2011 in Jinghong city, Yunnan Province, China [1]. The near-complete genome sequence (10,866 nt) has been determined, including complete coding sequences but incomplete 3' and 5' termini [1]. We propose to assign Jinghong bat virus to a new species *Rhinolophus vesiculovirus* in the genus *Vesiculovirus*.  **Genome organization**  The JhBV genome is similar in organisation to those of other vesiculoviruses, containing the five canonical rhabdovirus structural protein genes (N, P, M, G and L) (**Figure 1**). There is no obvious alternative ORF in the P gene as occurs in vesicular stomatitis Indiana virus and some other vesiculoviruses.  Based on ML trees generated from complete L protein sequences JhBV falls within the vesiculovirus clade and is most closely related to American bat vesiculovirus (ABVV; species *American bat vesiculovirus*) (**Figure 2**). Amino acid sequence divergence between JhBV and ABVV in pair-wise alignments (p-distances) are 44.6% in the N proteins, 65.4% in the G proteins and 42.2% in the L proteins (**Tables 1-3**).  For consistency, we also propose to rename the species *American bat vesiculovirus* as *Eptesicus vesiculovirus.* ABVV was detected in big brown bats *(Eptesicus fuscus)* collected in Maryland, USA, in 2008 [2].  **Species demarcation criteria**  Viruses assigned to different species within the genus *Vesiculovirus* have several of the following characteristics: A) minimum amino acid sequence divergence of 20% in L; B) minimum amino acid sequence divergence of 10% in N; C) minimum amino acid sequence divergence of 15% in G; D) can be distinguished in serological tests; and E) occupy different ecological niches as evidenced by differences in hosts and or arthropod vectors.  JhBV meets demarcation criteria A, B, C and E. Serological tests (criterion D) have not been conducted as no virus isolate is currently available.  **Derivation of the species names**  *Rhinolophus* is derived from the bat of the species *Rhinolophus affinis* in which the virus detected.  *Eptesicus* is derived from the bat of the species *Eptesicus fuscus* in which the virus detected. | |

**Supporting evidence**

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**Figure 1.** Vesiculovirus genome organisations. Alternative ORFs in the P genes of some vesiculoviruses are shown as blue arrows.

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**Figure 2.** The evolutionary history was inferred from a Clustal W alignment of 169 complete L protein sequences of 168 animal rhabdoviruses currently assigned or recently proposed for assignment to species in other genera and Jinghong bat virus which we propose to be assigned to a new species in the genus *Vesiculovirus*. Phylogenetically informative sites were selected from the alignment using Gblocks resulting in 915 positions in the final dataset. The tree was inferred in MEGA7 by using the Maximum Likelihood method based on the Whelan and Goldman + Freq. model. The tree with the highest log likelihood (-127314.573) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Joining and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Bootstrap values (100 iterations) are shown for each node.

**Table 1.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of vesiculovirus N proteins.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | MSPV | CHNV | ISFV | JURV | PIRYV | PERV | RADV | YBV | ABVV | JhBV | VSNJV | CARV | VSAV | COCV | MARV | MORV | VSIV |
| MSPV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| CHNV | 59.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ISFV | 66.6 | 59.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| JURV | 70.9 | 63.0 | 67.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PIRYV | 63.4 | 56.9 | 62.7 | 63.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PERV | 66.6 | 55.4 | 61.7 | 65.1 | 66.3 |  |  |  |  |  |  |  |  |  |  |  |  |
| RADV | 56.7 | 52.8 | 55.7 | 57.4 | 55.9 | 56.9 |  |  |  |  |  |  |  |  |  |  |  |
| YBV | 53.8 | 50.6 | 54.7 | 55.0 | 53.3 | 53.0 | 76.0 |  |  |  |  |  |  |  |  |  |  |
| ABVV | 48.4 | 48.4 | 49.2 | 50.4 | 49.9 | 49.6 | 49.6 | 50.4 |  |  |  |  |  |  |  |  |  |
| JhBV | 47.7 | 43.8 | 45.3 | 47.5 | 45.8 | 46.2 | 45.3 | 48.9 | 55.4 |  |  |  |  |  |  |  |  |
| NSNJV | 56.7 | 51.1 | 52.8 | 55.7 | 52.5 | 56.2 | 56.4 | 54.2 | 47.5 | 47.5 |  |  |  |  |  |  |  |
| CARV | 56.4 | 51.8 | 51.8 | 53.0 | 50.6 | 55.7 | 55.7 | 54.7 | 48.4 | 47.2 | 72.9 |  |  |  |  |  |  |
| VSAV | 55.4 | 49.6 | 52.8 | 55.4 | 53.0 | 56.2 | 56.2 | 55.2 | 46.2 | 47.2 | 69.7 | 75.1 |  |  |  |  |  |
| COCV | 56.2 | 49.4 | 51.8 | 53.0 | 52.3 | 55.2 | 54.7 | 53.5 | 47.0 | 47.5 | 70.2 | 74.3 | 86.2 |  |  |  |  |
| MARV | 56.9 | 51.3 | 51.8 | 54.0 | 53.3 | 56.2 | 56.2 | 53.8 | 47.5 | 46.7 | 70.0 | 73.8 | 82.6 | 87.4 |  |  |  |
| MORV | 55.2 | 52.1 | 52.8 | 54.7 | 54.0 | 56.4 | 55.9 | 54.0 | 47.9 | 47.5 | 69.2 | 75.1 | 83.5 | 84.3 | 89.3 |  |  |
| VSIV | 56.4 | 52.1 | 52.5 | 54.7 | 54.2 | 56.4 | 57.1 | 54.7 | 47.5 | 48.7 | 69.7 | 76.0 | 84.7 | 84.3 | 90.6 | 90.8 |  |

**Table 2.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of vesiculovirus G proteins.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | MSPV | CHNV | ISFV | JURV | PIRYV | PERV | RADV | YBV | ABVV | JhBV | VSNJV | CARV | VSAV | COCV | MARV | MORV | VSIV |
| MSPV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| CHNV | 50.3 | ## |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ISFV | 50.3 | 55.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| JURV | 50.3 | 54.9 | 55.9 | ##### |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PIRYV | 50.1 | 54.9 | 51.3 | 51.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PERV | 50.7 | 53.8 | 52.2 | 53.8 | 59.4 | ### |  |  |  |  |  |  |  |  |  |  |  |
| RADV | 42.7 | 47.0 | 43.9 | 44.9 | 48.4 | 46.4 |  |  |  |  |  |  |  |  |  |  |  |
| YBV | 44.9 | 47.6 | 44.5 | 47.0 | 49.5 | 48.2 | 70.0 |  |  |  |  |  |  |  |  |  |  |
| ABVV | 27.7 | 25.9 | 26.9 | 27.5 | 29.0 | 27.1 | 27.3 | 27.3 | #### |  |  |  |  |  |  |  |  |
| JhBV | 27.1 | 29.2 | 29.8 | 28.8 | 28.2 | 28.6 | 28.4 | 28.6 | 34.6 |  |  |  |  |  |  |  |  |
| NSNJV | 39.5 | 40.0 | 39.1 | 38.3 | 40.4 | 40.4 | 36.9 | 35.2 | 25.5 | 28.2 |  |  |  |  |  |  |  |
| CARV | 40.2 | 43.9 | 40.8 | 41.0 | 43.1 | 41.4 | 38.9 | 39.3 | 28.2 | 31.3 | 52.4 | ### |  |  |  |  |  |
| VSAV | 38.7 | 41.8 | 39.3 | 39.1 | 39.8 | 41.6 | 38.3 | 37.9 | 24.4 | 29.8 | 48.7 | 56.7 |  |  |  |  |  |
| COCV | 38.5 | 42.0 | 43.5 | 41.6 | 39.8 | 40.4 | 38.5 | 37.1 | 25.3 | 30.4 | 48.7 | 57.6 | 68.3 | #### |  |  |  |
| MARV | 37.7 | 42.2 | 40.6 | 39.5 | 41.0 | 40.2 | 40.0 | 38.5 | 25.1 | 30.0 | 50.9 | 58.2 | 65.4 | 75.8 |  |  |  |
| MORV | 38.7 | 42.7 | 42.9 | 39.5 | 40.0 | 41.2 | 40.6 | 40.0 | 25.9 | 30.0 | 49.9 | 58.0 | 65.0 | 73.9 | 79.9 | #V! |  |
| VSIV | 37.3 | 40.8 | 42.2 | 39.1 | 40.6 | 41.0 | 39.3 | 39.1 | 25.7 | 30.8 | 50.9 | 57.1 | 64.2 | 73.3 | 79.1 | 87.6 |  |

**Table 3.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of vesiculovirus L proteins.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | MSPV | CHNV | ISFV | JURV | PIRYV | PERV | RADV | YBV | ABVV | JhBV | VSNJV | CARV | VSAV | COCV | MARV | MORV | VSIV |
| MSPV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| CHNV | 68.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ISFV | 69.2 | 69.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| JURV | 68.3 | 66.2 | 66.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PIRYV | 68.3 | 67.6 | 66.9 | 67.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PERV | 67.5 | 66.9 | 67.2 | 65.1 | 67.6 |  |  |  |  |  |  |  |  |  |  |  |  |
| RADV | 61.9 | 62.5 | 62.0 | 61.2 | 61.2 | 60.7 |  |  |  |  |  |  |  |  |  |  |  |
| YBV | 60.2 | 60.6 | 59.7 | 59.0 | 60.3 | 59.2 | 73.2 |  |  |  |  |  |  |  |  |  |  |
| ABVV | 57.7 | 56.4 | 56.6 | 57.8 | 57.8 | 55.9 | 56.9 | 55.8 |  |  |  |  |  |  |  |  |  |
| JhBV | 55.3 | 55.6 | 54.8 | 54.0 | 54.2 | 54.5 | 54.0 | 53.7 | 57.8 |  |  |  |  |  |  |  |  |
| NSNJV | 58.0 | 57.9 | 58.1 | 58.0 | 58.3 | 57.7 | 57.8 | 57.1 | 54.4 | 52.7 |  |  |  |  |  |  |  |
| CARV | 60.2 | 59.6 | 59.8 | 59.5 | 59.6 | 59.7 | 58.7 | 58.9 | 54.9 | 53.5 | 70.4 |  |  |  |  |  |  |
| VSAV | 59.8 | 59.2 | 59.2 | 58.9 | 58.7 | 58.4 | 58.5 | 58.4 | 55.0 | 53.0 | 67.5 | 70.4 |  |  |  |  |  |
| COCV | 60.1 | 58.9 | 59.4 | 58.9 | 58.1 | 58.9 | 59.0 | 58.7 | 54.2 | 53.2 | 66.1 | 69.6 | 78.9 |  |  |  |  |
| MARV | 59.3 | 58.9 | 59.4 | 58.5 | 57.7 | 58.1 | 57.8 | 58.2 | 53.7 | 52.7 | 66.2 | 69.0 | 77.7 | 79.6 |  |  |  |
| MORV | 59.5 | 58.7 | 59.2 | 58.3 | 58.3 | 59.2 | 57.8 | 58.4 | 54.1 | 53.6 | 66.3 | 69.9 | 76.1 | 78.0 | 79.2 |  |  |
| VSIV | 59.9 | 59.5 | 59.1 | 59.2 | 58.3 | 58.1 | 57.7 | 57.8 | 54.2 | 52.8 | 66.2 | 70.4 | 76.2 | 77.4 | 78.7 | 81.2 |  |

**References**

1. Xu L, Wu J, Jiang T, Qin S, Xia L, Li X, He B, Tu C (2018) Molecular detection and sequence characterization of diverse rhabdoviruses in bats, China. *Virus Res* 244: 208-212. PMID: **29196194** DOI: 10.1016/j.virusres.2017.11.028
2. Ng TF, Driscoll C, Carlos MP, Prioleau A, Schmieder R, Dwivedi B, Wong J, Cha Y, Head S, Breitbart M, Delwart E (2013) Distinct lineage of vesiculovirus from big brown bats, United States. *Emerg Inf Dis* 19: 1978-1980. PMID: 24274823 DOI: 10.3201/eid1912.121506