

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

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| **Code assigned:** | ***2022.022M*** |  |
| **Short title:** Create two new 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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| ICTV *Rhabdoviridae* Study Group |

**ICTV Study Group comments and response of proposer**

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| Minor typographical errors only |

**ICTV Study Group votes on proposal**

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| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| ICTV *Rhabdoviridae* Study Group | 12 | 0 | 2 |

**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 |

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

|  |  |
| --- | --- |
| Date first submitted to SC Chair | 27 May 2022 |
| 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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| 2022.022M.N.v1.Vesiculovirus\_2nsp.xlsx |

**Abstract**

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| Two new species in the genus *Vesiculovirus* are proposed to accommodate two newly discovered viruses detected in bats and bat flies infesting bats. The viruses cluster phylogenetically with the vesiculoviruses and have similar genome organisations to those of other vesiculoviruses. The proposed new species meet the established demarcation criteria. |

**Text of proposal**

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| --- | --- |
| |  | | --- | | **Proposed new members of the genus**  Wufeng Myotis altarium vesiculovirus 1 (WMalVV-1; sample WFB-Yunshu) was detected by metagenomic sequencing of Szechwan myotis bats (*Myotis altarium*) collected in China, in 2016. Mejal virus (MEJV; sample JAL10) was detected by metagenomic sequencing of streblid bat flies (*Trichobius* sp.) collected from Parnell's mustached bats (*Pteronotus parnellii*) sampled in Mexico, in 2018 [1].  We propose WMalVV-1 be assigned to the new species *Vesiculovirus wufeng* and MEJV be assigned to the new species *Vesiculovirus* *mejal.*  **Genome organizations**  The coding-complete genome sequence of WMalVV-1 (10,680 nt) is available, lacking only extreme 3' and 5' termini. The coding-complete genome sequence of MEJV (11,112 nt) is also available, lacking only extreme 3' and 5' termini and a possible corruption in the region between the G ORF and L ORF. Like most other vesiculoviruses, each contains only the five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*) (**Figure 1**).  **Phylogenetic analysis**  Based on ML trees generated from complete L protein sequences, WMalVV-1 and MEJV cluster with the vesiculoviruses in a distinct and well-supported monophyletic clade (**Figure 2**). By this analysis, WMalVV-1 falls within a sub-clade that also includes several viruses that have been detected in bats, including Mediterranean bat vesiculovirus (MBVV; species *Vesiculovirus mediterranean*) and American bat vesiculovirus (ABVV; species *Vesiculovirus eptesicus*). MEJV falls within a second sub-clade and is most closely related to Jurona virus (JURV; species *Vesiculovirus jurona*) which was isolated from mosquitoes.  **Amino acid sequence identities**  Pairwise sequence identities (p-distances) calculated in MEGA7 from ClustalW amino acid sequence alignments indicated that WMalVV-1 is most closely related to MBVV, ABVV and other viruses in the bat-associated subclade with which it shares maximum sequence identity of 60.0% in L, 38.9% in G and 60.9% in N (**Tables 1-3**). MEJV is most closely related to JURV with which it shares sequence identity of 73.9% in L, 52.8% in G and 72.0% in N.  **Ecology**  Phylogenetically, WMalVV-1 lies within a sub-clade of vesiculoviruses that have been detected in bats in North America, Europe and Asia. MEJV lies within a sub-clade of vesiculoviruses that have been isolated from mammals and/or arthropod vectors (Diptera).  **Species demarcation criteria**  According to current 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.  WMalVV-1 and MEJV meet criteria A, B and C. No neutralization test data are yet available as there are currently no isolates of these viruses. The genome organisations of WMalVV-1 and MEJV are similar to those of several other vesiculoviruses. As the viruses have been detected only by metagenomic sequencing, their natural ecology is uncertain but, uniquely amongst vesiculoviruses, WMalVV-1 was detected in Szechwan myotis bats and MJEV was detected in streblid bat flies.  **Other related viruses**  Longquan Rhinolophus sinicus vesiculovirus 1 (LRsiVV-1; sample LQB-Rsin) was detected by metagenomic sequencing of Chinese rufous horseshoe bats (*Rhinolophus sinicus*) collected in China, in 2016. The coding-complete genome sequence (11,063 nt) is available, lacking only extreme 3' and 5' termini. LRsiVV-01 shares very high levels of sequence identity with Yinshui bat virus (YsBV; species *Vesiculovirus yinshui*) and does not meet criteria for demarcation of separate species (**Tables 1-3**). LRsiVV-01 should be considered as an additional sample of YsBV.  Qiongzhong bat virus (QzBV; sample 1127) was detected by metagenomic sequencing of brain tissue from intermediate horseshoe bats (*Rhinolophus affinis*) collected in China, in 2007. Longquan Rhinolophus affinis vesiculovirus 1 (LRafVV-1) was detected by metagenomic sequencing of brain tissue from intermediate horseshoe bats (*Rhinolophus affinis*) collected in China, in 2016. The coding-complete genome sequences of QzBV (10,868 nt) and LRafVV-1 (10,915 nt) are available, lacking only extreme 3' and 5' termini. Each of these viruses share high levels of amino acid sequence identity with Jinghong bat virus (JhBV; species *Vesiculovirus jinghong*) and do not meet criteria for demarcation of separate species (**Tables 1-3**). They should be considered as additional samples of JhBV. | |

**Supporting evidence**

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**Figure 1.** Schematic representation of vesiculovirus genomes. N, P, M, G and L represent ORFs encoding the structural proteins. Alternative ORFs in the P gene are shown in blue and an alternative ORF in the G gene of Mediterranean bat virus is shown in purple. Viruses representing proposed new species are listed in red text.

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**Figure 2.** The evolutionary history was inferred from a MUSCLE alignment of complete L protein sequences of 190 rhabdoviruses that are currently assigned to species in the subfamily *Alpharhabdovirinae* as well as 5 viruses considered for assignment to new species in the genus *Vesiculovirus*. Two viruses to be assigned to two new species are shown in red. Phylogenetically informative sites were selected from the alignment using Gblocks resulting in 967 positions in the final dataset. The tree was inferred in MEGA11 by using the Maximum Likelihood method based on the best-fit Le and Gascuel model with gamma distribution of evolutionary rates and invariable sites. The tree with the highest log likelihood (-146757.159) 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 identities (p-distance) of a CLUSTAL W alignment of vesiculovirus L protein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Virus | CHNV | ISFV | MSPV | PIRYV | PERV | JURV | **MEJV** | RADV | YBV | VSNJV | CARV | VSAV | COCV | MARV | MORV | VSIV | ABVV | **WfMaVV-1** | MBVV | YsBV | **LqRsVV-1** | **QzBV** | JhBV | **LqRaVV-1** |
| CHNV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ISFV | 68.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| MSPV | 67.7 | 68.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PIRYV | 67.0 | 66.5 | 67.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PERV | 66.4 | 66.7 | 66.9 | 67.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| JURV | 65.8 | 66.4 | 67.6 | 66.7 | 64.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **MEJV** | 64.7 | 66.1 | 65.9 | 65.2 | 64.0 | 73.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| RADV | 62.0 | 61.4 | 61.5 | 60.6 | 60.1 | 60.7 | 60.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YBV | 60.1 | 59.3 | 59.7 | 59.8 | 58.6 | 58.6 | 59.0 | 72.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| VSNJV | 57.4 | 57.7 | 57.5 | 57.9 | 57.3 | 57.4 | 56.9 | 57.3 | 56.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| CARV | 59.2 | 59.4 | 59.6 | 59.1 | 59.2 | 58.8 | 58.7 | 58.1 | 58.2 | 69.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| VSAV | 58.9 | 58.9 | 59.3 | 58.3 | 57.9 | 58.4 | 57.9 | 58.0 | 57.8 | 66.8 | 69.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| COCV | 58.6 | 59.0 | 59.4 | 57.6 | 58.3 | 58.3 | 57.8 | 58.4 | 58.2 | 65.3 | 68.9 | 78.2 |  |  |  |  |  |  |  |  |  |  |  |  |
| MARV | 58.6 | 59.1 | 58.9 | 57.4 | 57.6 | 58.0 | 57.7 | 57.3 | 57.6 | 65.4 | 68.5 | 77.2 | 79.0 |  |  |  |  |  |  |  |  |  |  |  |
| MORV | 58.4 | 58.8 | 58.9 | 58.0 | 58.7 | 57.7 | 58.2 | 57.2 | 57.9 | 65.4 | 69.0 | 75.4 | 77.3 | 78.8 |  |  |  |  |  |  |  |  |  |  |
| VSIV | 59.1 | 58.7 | 59.3 | 57.9 | 57.6 | 58.6 | 57.4 | 57.2 | 57.2 | 65.5 | 69.7 | 75.6 | 76.5 | 78.0 | 80.4 |  |  |  |  |  |  |  |  |  |
| ABVV | 56.0 | 56.3 | 57.2 | 57.5 | 55.5 | 57.6 | 56.4 | 56.3 | 55.2 | 54.0 | 54.4 | 54.5 | 53.7 | 53.1 | 53.6 | 53.7 |  |  |  |  |  |  |  |  |
| **WfMaVV-1** | 53.7 | 54.7 | 55.2 | 54.7 | 54.1 | 54.8 | 54.7 | 54.8 | 54.9 | 52.9 | 54.0 | 53.8 | 54.2 | 54.4 | 54.2 | 53.5 | 57.9 |  |  |  |  |  |  |  |
| MBVV | 54.3 | 53.6 | 54.4 | 53.6 | 52.8 | 53.8 | 53.7 | 55.2 | 54.5 | 52.6 | 53.7 | 54.0 | 53.1 | 53.2 | 53.0 | 53.0 | 57.3 | 59.7 |  |  |  |  |  |  |
| YsBV | 55.4 | 55.2 | 54.8 | 53.4 | 54.2 | 54.3 | 53.6 | 54.8 | 53.5 | 52.4 | 53.4 | 53.6 | 53.8 | 52.8 | 53.2 | 52.3 | 57.9 | 59.8 | 67.2 |  |  |  |  |  |
| **LqRsVV-1** | 55.2 | 54.7 | 54.7 | 53.0 | 54.1 | 54.0 | 53.4 | 54.4 | 53.5 | 52.5 | 53.4 | 53.6 | 53.7 | 52.8 | 53.2 | 52.2 | 57.5 | 59.7 | 67.1 | 96.9 |  |  |  |  |
| **QzBV** | 55.7 | 54.4 | 55.6 | 54.1 | 54.2 | 53.9 | 53.5 | 53.8 | 53.0 | 52.4 | 53.2 | 52.9 | 52.9 | 52.4 | 53.8 | 52.7 | 57.9 | 60.0 | 66.4 | 75.5 | 75.8 |  |  |  |
| JhBV | 55.3 | 54.3 | 55.0 | 53.7 | 54.1 | 53.7 | 53.0 | 53.5 | 53.3 | 52.2 | 53.0 | 52.6 | 52.9 | 52.3 | 53.2 | 52.4 | 57.3 | 59.2 | 66.0 | 76.0 | 76.5 | 91.4 |  |  |
| **LqRaVV-1** | 55.6 | 54.5 | 55.2 | 53.9 | 53.6 | 54.1 | 53.4 | 53.2 | 53.3 | 52.8 | 53.4 | 52.8 | 53.2 | 52.4 | 53.2 | 52.7 | 57.9 | 59.7 | 66.6 | 75.6 | 76.0 | 90.7 | 91.3 |  |

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

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Virus | CHNV | ISFV | MSPV | PIRYV | PERV | JURV | **MEJV** | RADV | YBV | VSNJV | CARV | VSAV | COCV | MARV | MORV | VSIV | ABVV | **WfMaVV-1** | MBVV | YsBV | **LqRsVV-1** | **QzBV** | JhBV | **LqRaVV-1** |
| CHNV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ISFV | 54.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| MSPV | 48.8 | 49.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PIRYV | 51.9 | 50.2 | 49.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PERV | 51.4 | 50.1 | 49.1 | 57.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| JURV | 53.1 | 54.5 | 49.2 | 49.9 | 50.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **MEJV** | 47.9 | 45.6 | 43.5 | 47.0 | 45.6 | 52.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| RADV | 44.7 | 42.5 | 41.2 | 46.2 | 43.9 | 43.2 | 39.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YBV | 45.6 | 44.0 | 43.5 | 48.4 | 46.1 | 45.4 | 41.7 | 67.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| VSNJV | 38.9 | 38.3 | 38.7 | 39.3 | 39.0 | 37.4 | 35.7 | 35.8 | 35.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| CARV | 42.0 | 39.6 | 38.9 | 42.0 | 39.5 | 39.4 | 36.6 | 37.8 | 38.5 | 51.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| VSAV | 41.1 | 37.9 | 38.8 | 39.1 | 40.2 | 38.1 | 35.2 | 37.2 | 37.3 | 47.5 | 55.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| COCV | 41.4 | 42.0 | 37.6 | 38.9 | 38.2 | 40.1 | 34.4 | 37.6 | 36.3 | 46.9 | 55.3 | 67.1 |  |  |  |  |  |  |  |  |  |  |  |  |
| MARV | 41.6 | 39.4 | 37.2 | 40.2 | 38.8 | 38.5 | 36.0 | 38.7 | 37.4 | 49.4 | 55.9 | 64.3 | 74.2 |  |  |  |  |  |  |  |  |  |  |  |
| MORV | 41.5 | 41.5 | 38.6 | 39.2 | 39.4 | 38.7 | 37.0 | 39.1 | 39.0 | 48.8 | 56.7 | 64.2 | 71.7 | 77.9 |  |  |  |  |  |  |  |  |  |  |
| VSIV | 39.9 | 40.9 | 36.7 | 39.7 | 38.9 | 38.0 | 36.9 | 38.0 | 38.1 | 49.8 | 55.6 | 62.5 | 71.2 | 77.5 | 85.3 |  |  |  |  |  |  |  |  |  |
| ABVV | 25.6 | 26.1 | 27.5 | 27.3 | 26.2 | 25.9 | 27.4 | 26.6 | 27.1 | 24.9 | 27.7 | 24.9 | 25.3 | 24.7 | 25.7 | 25.1 |  |  |  |  |  |  |  |  |
| **WfMaVV-1** | 28.0 | 26.9 | 30.1 | 28.3 | 28.0 | 26.6 | 26.2 | 25.8 | 26.3 | 27.2 | 26.8 | 26.1 | 27.7 | 27.2 | 27.3 | 27.8 | 28.7 |  |  |  |  |  |  |  |
| MBVV | 29.5 | 27.8 | 27.8 | 29.0 | 29.5 | 28.6 | 28.6 | 26.9 | 26.0 | 27.0 | 27.8 | 28.0 | 28.2 | 29.5 | 29.7 | 29.4 | 32.3 | 37.2 |  |  |  |  |  |  |
| YsBV | 28.3 | 29.4 | 28.8 | 28.9 | 30.0 | 29.4 | 28.3 | 27.6 | 27.9 | 28.8 | 29.6 | 28.8 | 29.2 | 29.9 | 29.5 | 31.0 | 30.8 | 38.9 | 62.9 |  |  |  |  |  |
| **LqRsVV-1** | 28.3 | 30.0 | 28.2 | 28.7 | 29.0 | 29.1 | 28.1 | 27.6 | 28.1 | 28.6 | 29.4 | 28.6 | 29.2 | 29.7 | 29.3 | 30.6 | 30.6 | 38.9 | 63.7 | 96.9 |  |  |  |  |
| **QzBV** | 27.4 | 27.8 | 26.7 | 27.3 | 28.0 | 27.9 | 29.5 | 27.6 | 27.5 | 27.2 | 29.2 | 29.1 | 29.1 | 28.9 | 28.3 | 29.5 | 32.1 | 36.3 | 60.5 | 73.8 | 73.6 |  |  |  |
| JhBV | 27.6 | 27.8 | 27.1 | 27.5 | 28.0 | 27.7 | 30.1 | 27.0 | 28.1 | 28.0 | 29.7 | 29.1 | 29.1 | 29.3 | 28.9 | 29.7 | 32.5 | 36.8 | 60.5 | 73.2 | 73.6 | 84.8 |  |  |
| **LqRaVV-1** | 27.6 | 27.1 | 27.1 | 27.7 | 28.6 | 26.9 | 29.3 | 27.2 | 27.1 | 27.6 | 29.4 | 30.3 | 29.7 | 29.5 | 28.3 | 29.5 | 32.9 | 36.5 | 60.7 | 73.8 | 74.0 | 83.7 | 83.3 |  |

**Table 3.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of vesiculovirus N protein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Virus | CHNV | ISFV | MSPV | PIRYV | PERV | JURV | **MEJV** | RADV | YBV | VSNJV | CARV | VSAV | COCV | MARV | MORV | VSIV | ABVV | **WfMaVV-1** | MBVV | YsBV | **LqRsVV-1** | **QzBV** | JhBV | **LqRaVV-1** |
| CHNV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ISFV | 58.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| MSPV | 58.5 | 65.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PIRYV | 55.9 | 61.6 | 62.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PERV | 54.7 | 60.5 | 65.6 | 65.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| JURV | 61.6 | 66.6 | 70.4 | 63.0 | 64.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **MEJV** | 58.1 | 62.3 | 68.7 | 58.1 | 63.3 | 72.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| RADV | 51.7 | 54.7 | 54.6 | 54.1 | 55.1 | 56.2 | 54.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YBV | 49.6 | 53.8 | 52.8 | 51.8 | 52.0 | 54.6 | 52.0 | 75.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| VSNJV | 50.4 | 51.9 | 55.8 | 52.0 | 55.2 | 54.7 | 52.7 | 55.6 | 53.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| CARV | 51.1 | 51.0 | 55.8 | 49.9 | 55.0 | 52.7 | 53.9 | 54.6 | 54.8 | 72.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| VSAV | 48.9 | 51.9 | 54.9 | 52.3 | 55.2 | 55.1 | 53.9 | 55.3 | 54.8 | 69.0 | 74.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| COCV | 48.7 | 51.0 | 55.6 | 51.8 | 54.5 | 52.7 | 54.9 | 53.7 | 53.1 | 69.4 | 73.9 | 85.3 |  |  |  |  |  |  |  |  |  |  |  |  |
| MARV | 50.6 | 51.0 | 56.3 | 52.5 | 55.2 | 53.7 | 54.4 | 55.1 | 53.6 | 69.2 | 73.5 | 82.5 | 86.7 |  |  |  |  |  |  |  |  |  |  |  |
| MORV | 51.3 | 51.9 | 54.7 | 53.0 | 55.5 | 54.4 | 53.7 | 55.1 | 53.6 | 68.2 | 74.9 | 83.4 | 83.4 | 88.9 |  |  |  |  |  |  |  |  |  |  |
| VSIV | 51.3 | 51.7 | 55.8 | 53.2 | 55.5 | 54.4 | 53.7 | 56.5 | 54.3 | 68.7 | 75.8 | 84.8 | 83.6 | 90.0 | 90.5 |  |  |  |  |  |  |  |  |  |
| ABVV | 47.6 | 48.7 | 47.9 | 49.3 | 49.2 | 49.5 | 48.3 | 48.3 | 49.4 | 46.4 | 47.4 | 45.3 | 46.0 | 46.4 | 46.9 | 46.4 |  |  |  |  |  |  |  |  |
| **WfMaVV-1** | 48.7 | 47.1 | 48.9 | 47.5 | 50.2 | 51.6 | 49.6 | 51.3 | 51.4 | 46.8 | 48.0 | 48.9 | 47.5 | 48.2 | 48.2 | 49.2 | 55.6 |  |  |  |  |  |  |  |
| MBVV | 44.0 | 44.4 | 47.1 | 44.5 | 46.8 | 45.7 | 46.9 | 47.4 | 49.2 | 46.4 | 48.1 | 47.1 | 47.4 | 46.2 | 46.9 | 47.9 | 53.8 | 60.9 |  |  |  |  |  |  |
| YsBV | 44.0 | 47.0 | 48.6 | 47.1 | 47.3 | 47.4 | 46.4 | 46.7 | 47.7 | 47.9 | 46.4 | 46.7 | 46.7 | 46.2 | 48.3 | 48.1 | 54.5 | 57.6 | 75.6 |  |  |  |  |  |
| **LqRsVV-1** | 44.0 | 47.0 | 48.8 | 47.1 | 47.3 | 47.4 | 46.7 | 46.7 | 47.7 | 47.9 | 46.4 | 46.7 | 46.7 | 46.2 | 48.3 | 48.1 | 54.5 | 57.6 | 75.8 | 99.8 |  |  |  |  |
| **QzBV** | 43.5 | 44.9 | 47.6 | 45.0 | 45.6 | 46.9 | 45.7 | 44.3 | 48.2 | 46.7 | 46.4 | 46.7 | 46.9 | 46.2 | 46.7 | 48.1 | 55.0 | 58.3 | 74.6 | 89.8 | 89.6 |  |  |  |
| JhBV | 43.5 | 44.9 | 47.6 | 45.0 | 45.6 | 46.9 | 45.7 | 44.5 | 48.2 | 46.7 | 46.4 | 46.4 | 46.7 | 46.0 | 46.7 | 47.9 | 54.7 | 58.3 | 74.6 | 89.6 | 89.3 | 99.8 |  |  |
| **LqRaVV-1** | 43.5 | 44.9 | 47.6 | 45.0 | 45.3 | 46.9 | 45.7 | 44.5 | 48.2 | 46.7 | 46.4 | 46.2 | 46.7 | 45.7 | 46.4 | 47.6 | 54.7 | 58.3 | 74.9 | 90.0 | 89.8 | 99.3 | 99.5 |  |

**References**

1. Ramirez-Martinez MM, Bennett AJ, Dunn CD, Yuill TM, Goldberg TL (2021) Bat flies of the family Streblidae (Diptera: Hippoboscoidea) host relatives of medically and agriculturally Important “bat-associated" viruses. Viruses 13:e860. DOI: 10.3390/v13050860