

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

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| **Code assigned:** | **2021.004M** |  |
| **Short title:** Create eight new species in the genus *Sunrhavirus*, create two new species in the genus *Hapavirus*, create two new species in the genus *Vesiculovirus* andcreate one species in the genus *Ledantevirus* (*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**

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| Approved by all responding SG members (12 of 15) with minor revisions. |

**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 |  |
| 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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| 2021.004M.R.Alpharhabdovirinae\_13nsp |

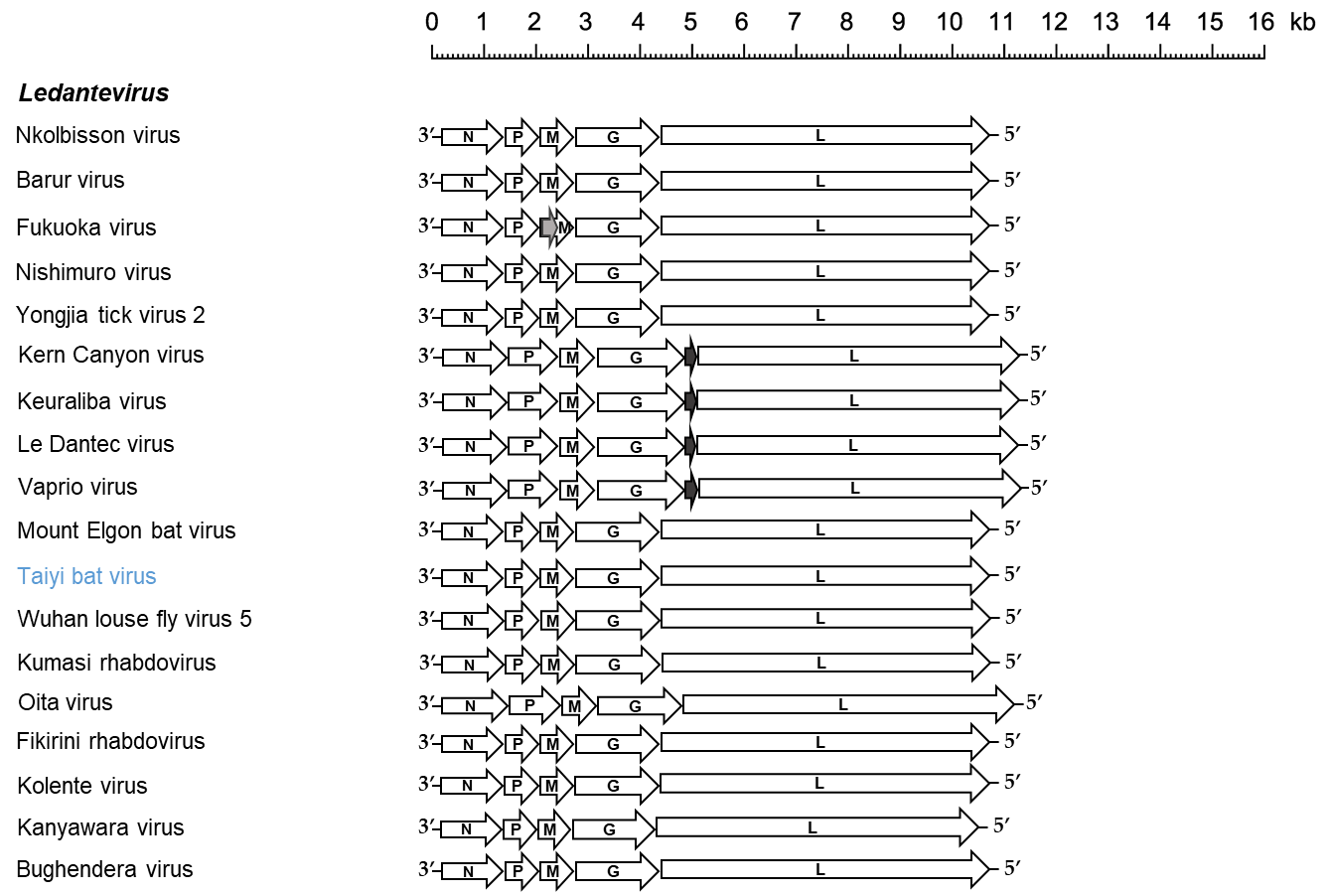
**Abstract**

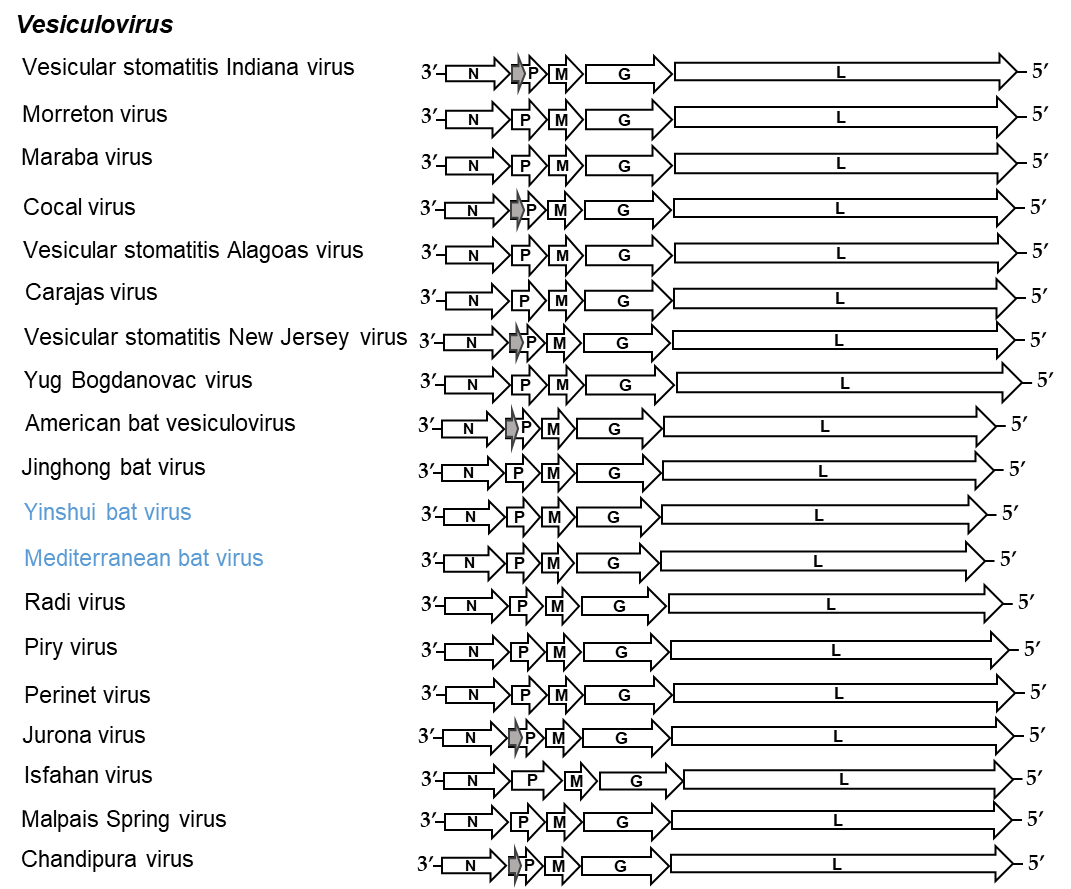
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| We propose the assignment of eight new species in the genus *Sunrhavirus*, two new species in the genus *Hapavirus*, one new species in the genus *Ledantevirus*, and two new species in the genus *Vesiculovirus.* |

**Text of proposal**

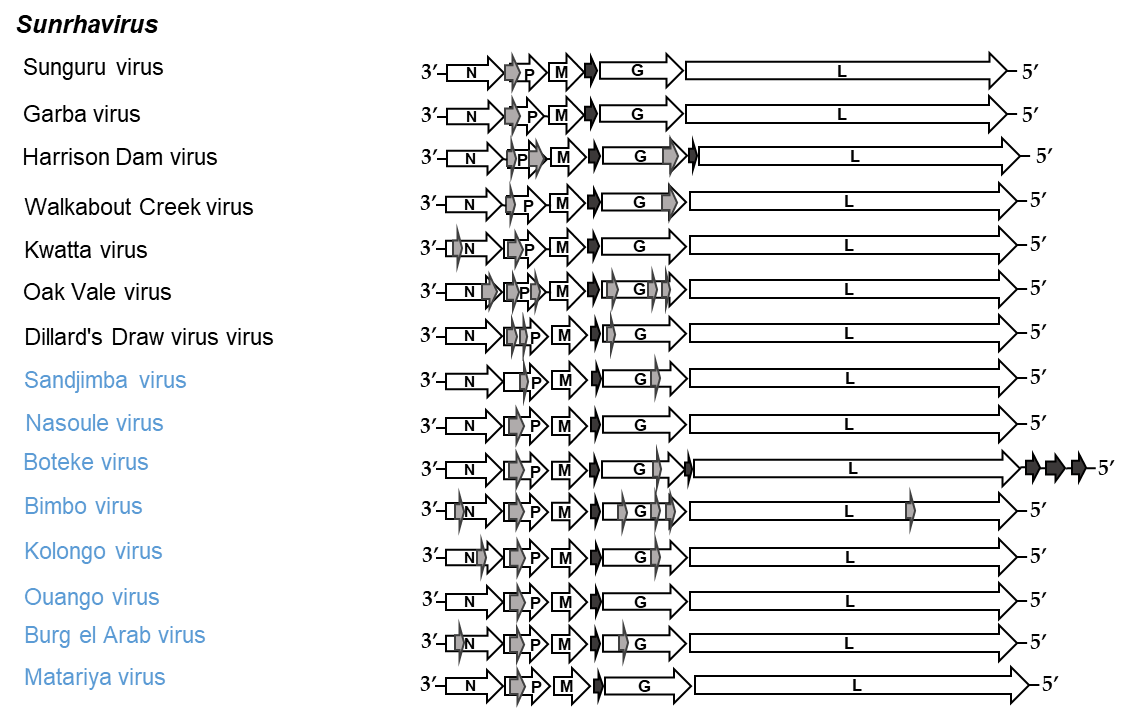
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| --- | --- |
| |  | | --- | | **Genus *Vesiculovirus***  Yinshui bat virus (YSBV; four strains: 1017, D170001, D170022, D170190; GenBank number: MN607594 - MN607597) was found in the Chinese bats (*Rhinolophus sinicus*) collected in 2007 and 2017 in two caves of Xianning city, Hubei Province, China [1]. The near-coding-complete genome sequences (average in 10935 nt) have been obtained by NGS and Sanger sequencing without the 3’ and 5’ terminal sequences [1]. We propose to assign Yinshui bat virus to the new species *Vesiculovirus yinshui.*  Mediterranean bat virus (MBV; 16 strains: 2012096, A08011, A08065, A09061, A09097, A09145, A09151, A09153, A09181, A09193, A09197, M08013, M08017, M08051, M09005, M09009, GenBank numbers: MW557328 - MW557343) was found in the *Miniopterus schreibersii*, *Rhinolophus ferrumequinum* and *Rhinolophus euryale* collected in 2008, 2009 and 2012 in the six caves of the three Mediterranean countries Spain, Algeria and Morocco (unpublished). The coding-complete genome sequences (average in 11000 nt) have been obtained by NGS and Sanger sequencing without the 3’ and 5’ terminal sequences (unpublished). We propose to assign Mediterranean bat virus to the new species *Vesiculovirus mediterranean*.  Qiongzhong bat virus (QZBV; strain: 1127; GenBank: MN607593) was found in the *Rhinolophus affinis* collected in 2007 in Qiongzhong city, Hainan Province, China [1]. The near-coding-complete genome sequence (10868 nt) has been obtained by NGS and Sanger sequencing without the 3’ and 5’ terminal sequences [1]. We consider Qiongzhong bat virus to be a second isolate of Jinghong bat virus (JhBV; strain IH17) [2] and so would be assigned as a second exemplar same existing species (*Vesiculovirus* *jinghong*).  **Genus *Ledantevirus***  Taiyi bat virus (TYBV; strain: 958; GenBank: MN607592) was found in the *Rhinolophus sinicus* collected in 2007 in Taiyi cave of Xianning city, Hainan Province, China [1]. The near-coding-complete genome sequence (10933 nt) has been obtained by NGS and Sanger sequencing without the 3’ and 5’ terminal sequences [1]. We propose to assign Taiyi bat virus to the new species *Ledantevirus* *taiyi*.  **Genus *Sunrhavirus***  Sandjimba virus (SJAV; strain: DakAnB 373d; GenBank: MW491754) was found in birds (*Acrocephalus schoenbaeus*) collected in 1970 in Landjia in Central African Republic (3,4). The coding-complete genome sequence (10951 nt) has been obtained by NGS without the 3’ and 5’ terminal sequences (unpublished). We propose to assign Sandjimba virus to the new species *Sunrhavirus sandjimba*.  Nasoule virus (NASV; strain: DakAnB 4289; GenBank: MW491755) was found in birds (*Andropadus virens*) collected in 1973 in Nasoule in Central African Republic (3,4). The coding-complete genome sequence (10977 nt) has been obtained by NGS without the 3’ and 5’ terminal sequences (unpublished). We propose to assign Nasoule virus to the new species *Sunrhavirus nasoule*.  Boteke virus (BOTV; strain: DakAnB 1077; GenBank: MW491753) was found in mosquitoes (*Coquillettidia maculipennis*) collected in 1968 in Boteke of Central African Republic (3,4). The coding-complete genome sequence (12466 nt) has been obtained by NGS without the 3’ and 5’ terminal sequences (unpublished). We propose to assign Boteke virus to the new species *Sunrhavirus boteke*.  Bimbo virus (BBOV; strain: DakAnB 1054; GenBank: MW491756) was found in birds (*Euplectes afra*) collected in 1970 in Kolongo in Central African Republic (3,4). The coding-complete genome sequence (10969 nt) has been obtained by NGS without the 3’ and 5’ terminal sequences (unpublished). We propose to assign Bimbo virus to the new species *Sunrhavirus bimbo*.  Kolongo virus (KOLV; strain: DakAnB 1094; GenBank: MW491757) was found in the birds (*Euplectes afra*) collected in 1970 in Bangui in Central African Republic (3,4). The coding-complete genome sequence (10971 nt) has been obtained by NGS without the 3’ and 5’ terminal sequences (unpublished). We propose to assign Kolongo virus to the new species *Sunrhavirus kolongo*.  Ouango virus (OUAV; strain: DakAnB 1582; GenBank: MW491758) was found in birds (*Ploceus melanocephalus*) collected in 1970 in Landjia in Central African Republic (3,4). The coding-complete genome sequence (10805 nt) has been obtained by NGS without the 3’ and 5’ terminal sequences (unpublished). We propose to assign Ouango virus to the new species *Sunrhavirus ouango*.  Burg el Arab virus (BEAV; strain: An 3782-62; GenBank: MW491759) was found in birds (*Sylvia curraca*) collected in 1962 in Bahig of Egypt (3). The coding-complete genome sequence (10846 nt) has been obtained by NGS without the 3’ and 5’ terminal sequences (unpublished). We propose to assign Burg el Arab virus to the new species *Sunrhavirus alexandria*.  Matariya virus (MTYV; strain: An 1477-61; GenBank: MW491760) was found in birds (*Sylvia curraca*) collected in 1961 in Port Saïd in Egypt (3). The coding-complete genome sequence (11021 nt) has been obtained by NGS without the 3’ and 5’ terminal sequences (unpublished). We propose to assign Matariya virus to the new species *Sunrhavirus matariya*.  **Genus *Hapavirus***  Porton virus (PORV; strain: S 1643; GenBank: MW491751) was found in mosquitoes (*Mansonia uniformis*) collected in 1960s in Sarawak region of Malaysia (3). The coding-complete genome sequence (12077 nt) has been obtained by NGS without the 3’ and 5’ terminal sequences (unpublished). We propose to assign Porton’s virus to the new species *Hapavirus* *porton*.  Bangoran virus (BGNV; strain: DakArB 2053; GenBank: MW491752) was found in mosquitoes (*Culex perfuscus*) collected in 1969 in Bangoran in Central African Republic (3,4). The coding-complete genome sequence (14053 nt) has been obtained by NGS without the 3’ and 5’ terminal sequences (unpublished). We propose to assign Bangoran virus to the new species *Hapavirus* *bangoran*.  **Genome architecture**  The genomes of viruses assigned to each genus contain the five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*). For the proposed sunrhaviruses and hapaviruses, there are diverse alternative ORFs within the genomes (**Figure 1**).  **Phylogeny**  Based on ML trees inferred from a Clustal W alignment of the complete L protein sequences of the available rhabdoviruses in the subfamily *Alpharhabdovirinae*, family *Rhabdoviridae*. The proposed rhabdoviruses are indicated in blue of the ML phylogenetic tree (**Figure 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.  Viruses assigned to different species within the genus *Ledantevirus* have several of the following characteristics: A) minimum amino acid sequence divergence of 7% in L; B) minimum amino acid sequence divergence of 15% in G; C) significant differences in genome organization as evidenced by numbers and locations of ORFs; D) can be distinguished in serological tests; and E) occupy different ecological niches as evidenced by differences in hosts and/or arthropod vectors.  Viruses assigned to different species within the genus Sunrhavirus have several of the following characteristics: A) a minimum amino acid sequence divergence of 10% in their N proteins; B) a minimum sequence divergence of 10% in their L proteins; C) a minimum amino acid sequence divergence of 15% in their G proteins; D) significant differences in genome organization as evidenced by numbers and locations of ORFs; E) they can be distinguished in virus neutralization tests; and F) they occupy different ecological niches as evidenced by differences in vertebrate hosts and or arthropod vectors.  Viruses assigned to different species within the genus Hapavirus display several of the following characteristics: A) minimum amino acid sequence divergence of 5% in N; B) minimum sequence divergence of 10% in L; C) minimum amino acid sequence divergence of 15% G; D) significant differences in genome organization as evidenced by numbers and locations of ORFs; E) can be distinguished in virus neutralization tests; and F) occupy different ecological niches as evidenced by differences in hosts and/or arthropod vectors.  All rhabdoviruses peoposed to assigned to genera *Vesiculovirus* and *Ledantevirus* meet the demarcation criteria A, B, C and E. Serological tests (criterion D) have not been conducted as no virus isolate is currently available. The rhabdoviruses proposed to be assigned to genera *Sunrhavirus* and *Hapavirus* meet the demarcation criteria A, B, C, D and F. Serological tests (criterion E) have not been conducted (**Tables 1-12**).  **Derivation of the species names**  *Vesiculovirus yinshui:* the species name is taken from the name of the virus (Yinshui bat virus) after Yinshui cave of Xianning city, China, where the virus was discovered.  *Vesiculovirus mediterranean:* the virus was found in several bat species, in three Mediterranean countries - Spain, Algeria and Morocco.  *Ledantevirus taiyi:* the species name is taken from the name of the virus (Taiyi bat virus) after Taiyi cave of Xianning city, China, where the virus was discovered.  *Sunrhavirus sandjimba:* the species name is taken from the name of the virus (Sandjimba virus) from Sandjimba village localized near Landjia, Central African Republic, where the virus was first isolated.  *Sunrhavirus nasoule:* the species name is taken from the name of the virus (Nasoule virus) from Nasoule village, Central African Republic, where the virus was first isolated.  *Sunrhavirus boteke:* the species name is taken from the name of the virus (Boteke virus) from Boteke village, Central African Republic, where the virus was first isolated.  *Sunrhavirus bimbo*:the species name is taken from the name of the virus (Bimbo virus) from Bimbo city, Central African Republic, where the virus was first isolated.  *Sunrhavirus kolongo*:the species name is taken from the name of the virus (Kolongo virus) from Kolongo district in the city of Bangui, Central African Republic, where the virus was first isolated.  *Sunrhavirus ouango*: the species name is taken from the name of the virus (Ouango virus) from Ouango district in the city of Bangui, Central African Republic, where the virus was first isolated.  *Sunrhavirus alexandria*: the species name is taken from Alexandria city, Egypt, where the virus was first isolated.  *Sunrhavirus matariya*: the species name is taken from the name of the virus (Matariya virus) from Matariya district in Cairo, Egypt, where the virus was first isolated.  *Hapavirus porton*: the species name is taken from the name of the virus (Porton virus). The origin of this virus name has not been determined but it is suggested that it may have been derived from the Porton Down laboratory.  *Hapavirus bangoran*: the species name is taken from the name of the virus (Bangoran virus) from Bangoran city, Central African Republic, where the virus was first isolated. | |

**Supporting evidence**

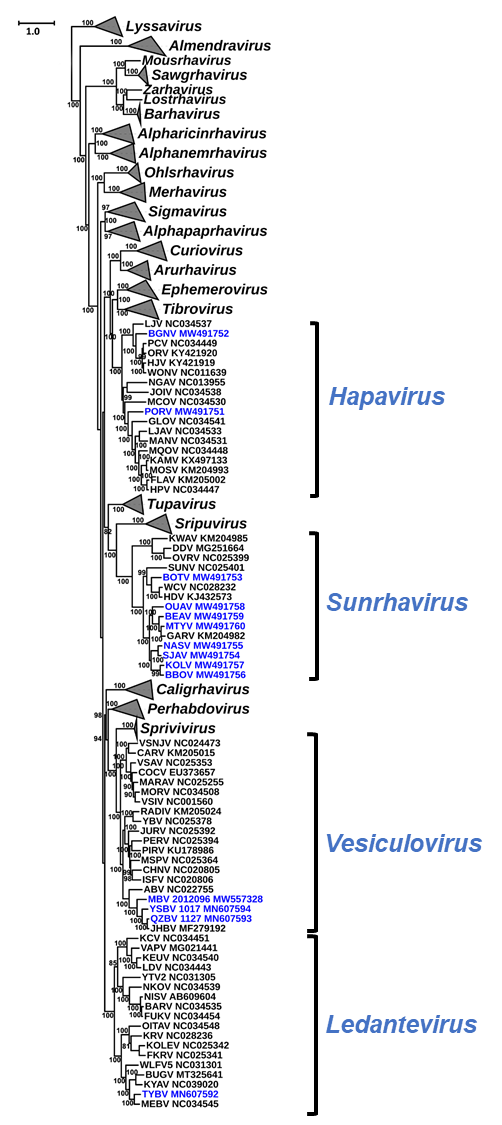








**Figure 1.** Genome organizations of viruses to be assigned as exemplars of each species in the genera *Vesiculovirus*, *Ledantevirus*, *Sunrhavirus,* and *Hapavirus*. Each genome contains five long open reading frames (ORFs) in the N, P, M, G, and L genes (open arrows). In some viruses, alternative ORFs (>180 nt) were indicated in the figure.



**Figure 2.** The phylogenetic tree was inferred from a Clustal W alignment of the complete L protein sequences of animal rhabdoviruses currently assigned or recently proposed for assignment to species in the subfamily *Alpharhabdovirinae*, family *Rhabdoviridae*. The tree was done by IQ-tree based on the Maximum Likelihood method in the LG + G + I + F model. Bootstrap values > 80% (10000 iterations) are shown for each node.

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

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **MEBV** | **TYBV** | **KYAV** | **BUGV** | **WLFV5** | **FKRV** | **KOLEV** | **KRV** | **OITAV** | **FUKV** | **BARV** | **NISV** | **NKOV** | **YTV2** | **LDV** | **KEUV** | **VAPV** | **KCV** |
| **MEBV** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **TYBV** | 87.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **KYAV** | 75.1 | 77.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **BUGV** | 73.0 | 74.2 | 83.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **WLFV5** | 72.5 | 72.5 | 67.4 | 67.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **FKRV** | 60.4 | 59.9 | 58.0 | 57.1 | 56.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **KOLEV** | 62.2 | 61.1 | 59.9 | 57.1 | 62.2 | 73.5 |  |  |  |  |  |  |  |  |  |  |  |  |
| **KRV** | 60.1 | 61.3 | 57.6 | 54.5 | 58.3 | 59.9 | 63.2 |  |  |  |  |  |  |  |  |  |  |  |
| **OITAV** | 54.6 | 54.6 | 51.1 | 51.6 | 51.8 | 56.0 | 57.2 | 57.9 |  |  |  |  |  |  |  |  |  |  |
| **FUKV** | 39.3 | 38.9 | 38.2 | 37.9 | 36.8 | 38.4 | 38.4 | 39.8 | 35.9 |  |  |  |  |  |  |  |  |  |
| **BARV** | 39.8 | 39.3 | 37.9 | 37.5 | 37.0 | 38.6 | 38.4 | 40.5 | 36.1 | 96.4 |  |  |  |  |  |  |  |  |
| **NISV** | 39.1 | 38.4 | 37.5 | 37.0 | 37.0 | 38.6 | 38.6 | 38.9 | 35.4 | 95.2 | 94.0 |  |  |  |  |  |  |  |
| **NKOV** | 39.1 | 38.4 | 38.2 | 38.9 | 37.7 | 38.4 | 38.9 | 41.2 | 36.8 | 77.1 | 76.2 | 75.5 |  |  |  |  |  |  |
| **YTV2** | 38.3 | 37.2 | 36.9 | 35.5 | 34.6 | 39.0 | 38.3 | 37.9 | 34.9 | 52.7 | 52.4 | 52.4 | 53.1 |  |  |  |  |  |
| **LDV** | 39.4 | 38.7 | 37.5 | 35.4 | 37.3 | 35.9 | 38.5 | 38.2 | 38.3 | 38.9 | 38.9 | 38.2 | 39.4 | 38.4 |  |  |  |  |
| **KEUV** | 40.1 | 40.3 | 39.6 | 36.8 | 38.2 | 35.4 | 37.3 | 38.2 | 38.1 | 39.4 | 39.4 | 38.9 | 40.1 | 38.1 | 80.6 |  |  |  |
| **VAPV** | 35.9 | 36.6 | 35.7 | 36.1 | 36.8 | 33.8 | 36.1 | 34.3 | 34.6 | 41.7 | 42.4 | 41.5 | 43.6 | 37.9 | 63.9 | 62.5 |  |  |
| **KCV** | 36.4 | 36.1 | 34.5 | 35.2 | 35.9 | 35.4 | 37.1 | 36.8 | 37.4 | 39.9 | 39.4 | 38.4 | 39.9 | 39.1 | 47.6 | 46.7 | 47.6 |  |

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

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **FUKV** | **BARV** | **NISV** | **NKOV** | **YTV2** | **LDV** | **KEUV** | **VAPV** | **KCV** | **KYAV** | **BUGV** | **MEBV** | **TYBV** | **WLFV5** | **FKRV** | **KOLEV** | **OITAV** | **KRV** |
| **FUKV** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **BARV** | 84.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **NISV** | 78.0 | 77.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **NKOV** | 46.5 | 46.9 | 49.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **YTV2** | 40.1 | 37.9 | 38.3 | 39.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **LDV** | 30.0 | 29.5 | 29.3 | 29.3 | 30.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **KEUV** | 29.7 | 29.2 | 30.2 | 30.2 | 31.4 | 69.0 |  |  |  |  |  |  |  |  |  |  |  |  |
| **VAPV** | 31.5 | 31.6 | 31.1 | 32.2 | 33.4 | 57.3 | 55.9 |  |  |  |  |  |  |  |  |  |  |  |
| **KCV** | 32.2 | 31.3 | 31.0 | 30.1 | 34.2 | 47.9 | 48.0 | 50.7 |  |  |  |  |  |  |  |  |  |  |
| **KYAV** | 26.8 | 27.7 | 27.8 | 27.5 | 27.1 | 26.5 | 27.6 | 27.4 | 27.4 |  |  |  |  |  |  |  |  |  |
| **BUGV** | 28.5 | 27.3 | 27.5 | 28.4 | 27.1 | 27.2 | 27.6 | 29.3 | 28.9 | 69.7 |  |  |  |  |  |  |  |  |
| **MEBV** | 26.8 | 25.9 | 26.4 | 27.7 | 29.3 | 27.9 | 26.3 | 28.5 | 28.0 | 45.4 | 43.8 |  |  |  |  |  |  |  |
| **TYBV** | 30.0 | 27.6 | 28.4 | 28.6 | 27.0 | 27.0 | 27.3 | 29.1 | 26.7 | 44.8 | 45.2 | 63.9 |  |  |  |  |  |  |
| **WLFV5** | 27.1 | 27.1 | 27.3 | 29.1 | 27.1 | 27.2 | 27.5 | 28.4 | 27.5 | 41.8 | 40.5 | 41.4 | 41.5 |  |  |  |  |  |
| **FKRV** | 22.9 | 23.5 | 22.6 | 24.2 | 25.1 | 24.4 | 24.3 | 25.2 | 22.9 | 28.0 | 27.1 | 29.4 | 29.7 | 27.5 |  |  |  |  |
| **KOLEV** | 24.7 | 24.7 | 24.5 | 25.8 | 25.6 | 25.6 | 24.7 | 25.0 | 24.8 | 30.5 | 28.4 | 27.8 | 28.6 | 28.5 | 50.5 |  |  |  |
| **OITAV** | 23.6 | 23.9 | 24.1 | 25.6 | 25.9 | 22.3 | 24.0 | 24.9 | 23.2 | 28.4 | 27.5 | 27.4 | 28.8 | 28.2 | 42.8 | 38.6 |  |  |
| **KRV** | 23.9 | 23.0 | 23.0 | 22.2 | 23.9 | 23.3 | 22.6 | 23.0 | 24.6 | 26.6 | 25.7 | 24.5 | 24.0 | 23.7 | 31.8 | 32.6 | 32.0 |  |

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

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **KRV** | **OITAV** | **FKRV** | **KOLEV** | **MEBV** | **TYBV** | **KYAV** | **BUGV** | **WLFV5** | **FUKV** | **BARV** | **NISV** | **NKOV** | **YTV2** | **LDV** | **KEUV** | **VAPV** | **KCV** |
| **KRV** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **OITAV** | 62.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **FKRV** | 61.4 | 61.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **KOLEV** | 62.3 | 61.7 | 75.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **MEBV** | 54.9 | 53.8 | 54.1 | 54.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **TYBV** | 54.7 | 53.8 | 52.7 | 53.9 | 75.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **KYAV** | 54.0 | 52.5 | 52.4 | 53.8 | 63.6 | 63.0 |  |  |  |  |  |  |  |  |  |  |  |  |
| **BUGV** | 52.9 | 51.5 | 51.6 | 52.6 | 62.5 | 61.9 | 71.3 |  |  |  |  |  |  |  |  |  |  |  |
| **WLFV5** | 54.6 | 54.5 | 53.0 | 53.4 | 61.2 | 60.7 | 58.7 | 56.5 |  |  |  |  |  |  |  |  |  |  |
| **FUKV** | 46.5 | 46.7 | 46.7 | 47.2 | 48.1 | 48.2 | 47.8 | 46.2 | 46.9 |  |  |  |  |  |  |  |  |  |
| **BARV** | 46.7 | 46.7 | 46.8 | 46.5 | 48.0 | 48.2 | 47.8 | 45.8 | 46.8 | 92.1 |  |  |  |  |  |  |  |  |
| **NISV** | 46.1 | 46.4 | 46.8 | 46.9 | 48.3 | 48.1 | 47.7 | 46.1 | 47.1 | 89.0 | 87.5 |  |  |  |  |  |  |  |
| **NKOV** | 46.3 | 46.8 | 46.2 | 47.1 | 48.0 | 48.5 | 47.3 | 46.5 | 46.9 | 61.7 | 61.3 | 60.9 |  |  |  |  |  |  |
| **YTV2** | 47.1 | 45.6 | 45.6 | 47.0 | 46.4 | 47.4 | 47.4 | 46.2 | 45.6 | 53.6 | 53.5 | 53.8 | 54.1 |  |  |  |  |  |
| **LDV** | 47.9 | 46.5 | 46.3 | 47.4 | 47.9 | 47.6 | 46.8 | 46.4 | 48.1 | 49.7 | 49.5 | 49.5 | 50.0 | 49.4 |  |  |  |  |
| **KEUV** | 48.0 | 46.8 | 47.1 | 48.5 | 48.2 | 47.8 | 47.5 | 47.0 | 48.2 | 50.7 | 50.0 | 50.7 | 50.6 | 49.6 | 80.9 |  |  |  |
| **VAPV** | 49.2 | 48.7 | 48.0 | 48.7 | 49.0 | 49.0 | 48.0 | 46.8 | 49.2 | 50.1 | 50.3 | 50.3 | 50.3 | 48.4 | 69.0 | 69.9 |  |  |
| **KCV** | 47.8 | 47.7 | 47.6 | 48.2 | 48.2 | 47.7 | 47.5 | 46.8 | 47.6 | 49.9 | 49.5 | 50.1 | 50.3 | 49.6 | 62.5 | 62.6 | 62.8 |  |

**Table 4.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of vesiculovirus N proteins.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **MBV\_2012096** | **YSBV\_1017** | **QZBV\_1127** | **JHBV** | **ABV** | **YBV** | **CARV** | **VSIV** | **VSAV** | **COCV** | **MORV** | **RADIV** | **MSPV** | **VSNJV** | **MARAV** | **JURV** | **PIRV** | **ISFV** | **CHNV** | **PERV** |
| **MBV\_2012096** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **YSBV\_1017** | 75.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **QZBV\_1127** | 74.6 | 89.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **JHBV** | 74.6 | 89.5 | 99.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **ABV** | 53.5 | 54.2 | 54.7 | 54.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **YBV** | 47.8 | 46.7 | 47.4 | 47.4 | 48.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **CARV** | 46.9 | 45.5 | 45.5 | 45.5 | 46.4 | 53.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **VSIV** | 46.4 | 46.9 | 46.9 | 46.7 | 45.5 | 52.9 | 75.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **VSAV** | 46.2 | 45.5 | 45.5 | 45.3 | 44.6 | 53.3 | 74.8 | 84.8 |  |  |  |  |  |  |  |  |  |  |  |  |
| **COCV** | 46.0 | 45.5 | 45.7 | 45.5 | 45.3 | 51.7 | 73.9 | 83.6 | 85.3 |  |  |  |  |  |  |  |  |  |  |  |
| **MORV** | 46.0 | 47.1 | 45.5 | 45.5 | 46.2 | 52.2 | 74.8 | 90.5 | 83.4 | 83.4 |  |  |  |  |  |  |  |  |  |  |
| **RADIV** | 46.0 | 45.5 | 43.2 | 43.4 | 47.4 | 74.5 | 53.1 | 54.7 | 53.8 | 51.7 | 53.6 |  |  |  |  |  |  |  |  |  |
| **MSPV** | 45.5 | 46.9 | 45.8 | 45.8 | 46.5 | 51.9 | 55.2 | 55.2 | 54.3 | 55.0 | 53.8 | 54.2 |  |  |  |  |  |  |  |  |
| **VSNJV** | 45.5 | 47.4 | 46.2 | 46.2 | 46.9 | 52.9 | 72.5 | 69.1 | 69.4 | 70.1 | 68.7 | 54.5 | 55.5 |  |  |  |  |  |  |  |
| **MARAV** | 45.3 | 45.0 | 45.0 | 44.8 | 45.7 | 52.2 | 73.4 | 90.0 | 82.4 | 86.7 | 88.8 | 53.3 | 55.7 | 69.6 |  |  |  |  |  |  |
| **JURV** | 44.1 | 46.2 | 45.7 | 45.7 | 48.5 | 54.0 | 52.4 | 54.1 | 54.8 | 52.4 | 54.3 | 55.3 | 70.3 | 54.1 | 53.4 |  |  |  |  |  |
| **PIRV** | 43.7 | 46.0 | 43.9 | 43.9 | 48.6 | 51.2 | 49.5 | 52.5 | 51.4 | 50.9 | 52.1 | 53.9 | 61.5 | 51.4 | 51.6 | 62.0 |  |  |  |  |
| **ISFV** | 43.3 | 45.9 | 43.7 | 43.7 | 47.7 | 53.6 | 51.1 | 51.8 | 52.1 | 51.1 | 51.8 | 54.3 | 65.2 | 51.8 | 51.1 | 66.2 | 60.9 |  |  |  |
| **CHNV** | 42.8 | 42.8 | 42.6 | 42.6 | 47.0 | 48.9 | 50.2 | 50.4 | 48.1 | 48.1 | 50.4 | 50.9 | 58.1 | 50.2 | 50.0 | 61.4 | 55.0 | 58.3 |  |  |
| **PERV** | 38.3 | 38.0 | 36.6 | 36.6 | 39.6 | 42.5 | 45.0 | 45.3 | 45.0 | 45.3 | 45.3 | 44.0 | 52.8 | 46.2 | 45.7 | 49.8 | 51.6 | 47.0 | 43.7 |  |

**Table 5.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of vesiculovirus G proteins.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **MBV\_2012096** | **YSBV\_1017** | **QZBV\_1127** | **JHBV** | **ABV** | **YBV** | **CARV** | **VSIV** | **VSAV** | **COCV** | **MORV** | **RADIV** | **MSPV** | **VSNJV** | **MARAV** | **JURV** | **PIRV** | **ISFV** | **CHNV** | **PERV** |
| **MBV\_2012096** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **YSBV\_1017** | 62.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **QZBV\_1127** | 59.3 | 71.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **JHBV** | 59.5 | 71.7 | 84.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **ABV** | 31.2 | 29.6 | 30.9 | 30.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **YBV** | 24.2 | 24.3 | 24.1 | 24.3 | 23.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **CARV** | 25.9 | 27.5 | 28.3 | 28.7 | 26.5 | 35.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **VSIV** | 27.5 | 29.0 | 28.6 | 28.6 | 23.4 | 34.1 | 54.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **VSAV** | 27.5 | 27.5 | 28.4 | 28.2 | 22.2 | 33.5 | 53.7 | 62.3 |  |  |  |  |  |  |  |  |  |  |  |  |
| **COCV** | 26.9 | 28.0 | 28.7 | 28.5 | 22.6 | 32.6 | 54.1 | 71.2 | 66.9 |  |  |  |  |  |  |  |  |  |  |  |
| **MORV** | 27.6 | 27.8 | 27.6 | 28.0 | 24.1 | 35.1 | 55.6 | 84.4 | 63.9 | 71.5 |  |  |  |  |  |  |  |  |  |  |
| **RADIV** | 24.9 | 24.9 | 24.2 | 24.0 | 23.9 | 67.0 | 34.9 | 34.3 | 33.8 | 34.1 | 35.5 |  |  |  |  |  |  |  |  |  |
| **MSPV** | 26.7 | 27.4 | 25.3 | 25.5 | 26.1 | 40.2 | 36.9 | 35.6 | 37.1 | 36.3 | 37.0 | 38.1 |  |  |  |  |  |  |  |  |
| **VSNJV** | 26.4 | 27.5 | 27.5 | 27.3 | 23.8 | 31.4 | 50.5 | 49.2 | 47.9 | 47.2 | 48.8 | 32.0 | 36.9 |  |  |  |  |  |  |  |
| **MARAV** | 27.7 | 28.1 | 28.6 | 28.4 | 23.4 | 33.7 | 54.6 | 77.3 | 63.9 | 73.8 | 77.4 | 35.2 | 36.1 | 49.7 |  |  |  |  |  |  |
| **JURV** | 26.3 | 27.8 | 27.0 | 26.4 | 25.2 | 41.8 | 38.5 | 36.4 | 36.8 | 38.7 | 37.3 | 40.1 | 48.6 | 36.7 | 37.1 |  |  |  |  |  |
| **PIRV** | 27.0 | 27.5 | 26.0 | 25.6 | 26.1 | 44.2 | 40.5 | 37.6 | 36.8 | 36.8 | 37.4 | 42.9 | 47.7 | 37.0 | 38.2 | 48.8 |  |  |  |  |
| **ISFV** | 27.0 | 27.9 | 26.4 | 26.4 | 24.4 | 40.1 | 38.4 | 38.4 | 36.0 | 40.0 | 39.6 | 39.2 | 47.9 | 37.1 | 37.5 | 53.5 | 50.0 |  |  |  |
| **CHNV** | 27.4 | 26.7 | 26.1 | 26.1 | 23.7 | 41.9 | 41.1 | 38.3 | 39.2 | 39.6 | 39.8 | 41.5 | 48.3 | 37.0 | 39.8 | 52.4 | 51.5 | 54.1 |  |  |
| **PERV** | 27.7 | 28.0 | 26.5 | 26.7 | 24.8 | 43.3 | 38.7 | 37.7 | 38.9 | 37.3 | 38.2 | 41.6 | 49.0 | 38.2 | 37.9 | 51.0 | 56.5 | 49.1 | 50.9 |  |

**Table 6.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of vesiculovirus L proteins.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **MBV\_2012096** | **YSBV\_1017** | **QZBV\_1127** | **JHBV** | **ABV** | **YBV** | **CARV** | **VSIV** | **VSAV** | **COCV** | **MORV** | **RADIV** | **MSPV** | **VSNJV** | **MARAV** | **JURV** | **PIRV** | **ISFV** | **CHNV** | **PERV** |
| **MBV\_2012096** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **YSBV\_1017** | 67.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **QZBV\_1127** | 66.0 | 75.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **JHBV** | 65.9 | 76.0 | 91.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **ABV** | 56.8 | 57.5 | 57.6 | 57.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **YBV** | 53.9 | 53.2 | 52.7 | 53.0 | 54.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **CARV** | 53.1 | 53.0 | 52.8 | 52.5 | 54.0 | 57.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **VSIV** | 52.5 | 51.9 | 52.2 | 52.1 | 53.4 | 56.7 | 69.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **VSAV** | 53.5 | 53.2 | 52.4 | 52.1 | 54.0 | 57.4 | 69.7 | 75.5 |  |  |  |  |  |  |  |  |  |  |  |  |
| **COCV** | 52.6 | 53.3 | 52.5 | 52.5 | 53.2 | 57.7 | 68.9 | 76.4 | 78.2 |  |  |  |  |  |  |  |  |  |  |  |
| **MORV** | 52.5 | 52.8 | 53.3 | 52.8 | 53.1 | 57.3 | 69.0 | 80.3 | 75.3 | 77.2 |  |  |  |  |  |  |  |  |  |  |
| **RADIV** | 54.7 | 54.5 | 53.5 | 53.2 | 55.9 | 72.3 | 57.5 | 56.8 | 57.4 | 57.8 | 56.7 |  |  |  |  |  |  |  |  |  |
| **MSPV** | 53.9 | 54.2 | 55.1 | 54.5 | 56.7 | 59.3 | 59.2 | 58.9 | 59.0 | 59.1 | 58.4 | 61.0 |  |  |  |  |  |  |  |  |
| **VSNJV** | 52.5 | 52.4 | 52.4 | 52.2 | 53.8 | 56.6 | 69.7 | 65.8 | 67.3 | 65.6 | 65.9 | 57.4 | 57.9 |  |  |  |  |  |  |  |
| **MARAV** | 52.6 | 52.3 | 52.0 | 51.9 | 52.6 | 57.2 | 68.5 | 78.0 | 77.1 | 78.9 | 78.7 | 56.8 | 58.4 | 65.7 |  |  |  |  |  |  |
| **JURV** | 52.9 | 53.4 | 53.2 | 53.2 | 56.9 | 58.1 | 58.4 | 58.1 | 57.9 | 57.9 | 57.2 | 60.1 | 67.4 | 57.5 | 57.6 |  |  |  |  |  |
| **PIRV** | 53.0 | 52.8 | 53.7 | 53.2 | 56.9 | 59.2 | 58.7 | 57.3 | 57.6 | 57.0 | 57.3 | 60.1 | 67.6 | 57.9 | 56.9 | 66.5 |  |  |  |  |
| **ISFV** | 52.9 | 54.8 | 53.9 | 53.9 | 55.6 | 58.6 | 58.8 | 58.2 | 58.3 | 58.4 | 58.3 | 61.0 | 68.6 | 57.5 | 58.5 | 66.1 | 66.4 |  |  |  |
| **CHNV** | 53.3 | 54.3 | 54.5 | 54.0 | 55.3 | 59.8 | 58.6 | 58.8 | 58.2 | 57.8 | 58.0 | 61.6 | 67.4 | 57.6 | 58.5 | 66.5 | 66.7 | 68.5 |  |  |
| **PERV** | 52.4 | 53.7 | 53.5 | 53.5 | 54.8 | 58.3 | 58.7 | 57.1 | 57.3 | 57.8 | 58.1 | 59.6 | 66.7 | 57.1 | 57.3 | 64.5 | 66.9 | 66.5 | 66.3 |  |

**Table 7.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of sunrhavirus N proteins.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **SJAV** | **NASV** | **BBOV** | **KOLV** | **OUAV** | **BEAV** | **MTYV** | **BOTV** | **GARV** | **HDV** | **WCV** | **SUNV** | **KWAV** | **DDV** | **OVRV** |
| **SJAV** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **NASV** | 81.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **BBOV** | 48.9 | 49.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **KOLV** | 51.3 | 50.4 | 81.0 |  |  |  |  |  |  |  |  |  |  |  |  |
| **OUAV** | 46.5 | 45.3 | 48.4 | 46.7 |  |  |  |  |  |  |  |  |  |  |  |
| **BEAV** | 48.2 | 47.5 | 49.4 | 49.0 | 53.9 |  |  |  |  |  |  |  |  |  |  |
| **MTYV** | 49.1 | 47.0 | 47.5 | 46.4 | 56.0 | 79.9 |  |  |  |  |  |  |  |  |  |
| **BOTV** | 35.3 | 35.8 | 39.0 | 38.9 | 34.2 | 35.4 | 34.9 |  |  |  |  |  |  |  |  |
| **GARV** | 50.8 | 48.9 | 48.9 | 48.5 | 54.8 | 79.6 | 86.6 | 36.3 |  |  |  |  |  |  |  |
| **HDV** | 37.4 | 36.7 | 37.8 | 38.5 | 33.0 | 36.9 | 35.5 | 55.8 | 36.9 |  |  |  |  |  |  |
| **WCV** | 37.4 | 37.2 | 37.3 | 38.2 | 31.4 | 37.6 | 34.8 | 57.7 | 36.7 | 86.5 |  |  |  |  |  |
| **SUNV** | 35.9 | 37.3 | 37.0 | 37.5 | 33.9 | 35.8 | 33.7 | 47.9 | 37.2 | 46.6 | 48.4 |  |  |  |  |
| **KWAV** | 26.1 | 25.5 | 26.9 | 26.2 | 24.5 | 25.6 | 26.0 | 28.8 | 26.5 | 26.2 | 26.8 | 29.2 |  |  |  |
| **DDV** | 24.1 | 23.6 | 26.5 | 25.8 | 26.5 | 26.7 | 24.7 | 28.8 | 25.6 | 27.9 | 28.3 | 27.9 | 33.1 |  |  |
| **OVRV** | 23.8 | 23.6 | 26.7 | 25.3 | 25.1 | 25.8 | 26.0 | 28.5 | 26.0 | 26.9 | 27.6 | 28.7 | 34.6 | 68.5 |  |

**Table 8.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of sunrhavirus G proteins.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **SJAV** | **NASV** | **BBOV** | **KOLV** | **OUAV** | **BEAV** | **MTYV** | **BOTV** | **GARV** | **HDV** | **WCV** | **SUNV** | **KWAV** | **DDV** | **OVRV** |
| **SJAV** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **NASV** | 72.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **BBOV** | 39.0 | 39.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **KOLV** | 41.3 | 39.5 | 66.4 |  |  |  |  |  |  |  |  |  |  |  |  |
| **OUAV** | 44.2 | 45.3 | 39.0 | 36.1 |  |  |  |  |  |  |  |  |  |  |  |
| **BEAV** | 42.9 | 40.8 | 36.7 | 39.0 | 47.2 |  |  |  |  |  |  |  |  |  |  |
| **MTYV** | 43.9 | 41.1 | 38.5 | 38.7 | 48.4 | 68.4 |  |  |  |  |  |  |  |  |  |
| **BOTV** | 32.9 | 32.2 | 29.0 | 29.9 | 34.8 | 31.7 | 32.4 |  |  |  |  |  |  |  |  |
| **GARV** | 42.0 | 40.0 | 37.3 | 39.1 | 47.5 | 66.9 | 73.5 | 32.4 |  |  |  |  |  |  |  |
| **HDV** | 28.1 | 27.7 | 25.9 | 26.4 | 30.5 | 31.6 | 30.6 | 45.6 | 31.1 |  |  |  |  |  |  |
| **WCV** | 28.8 | 28.0 | 26.5 | 26.9 | 30.6 | 31.0 | 31.0 | 46.2 | 31.0 | 75.5 |  |  |  |  |  |
| **SUNV** | 30.7 | 29.4 | 26.4 | 27.3 | 31.5 | 30.3 | 30.8 | 42.7 | 31.4 | 39.7 | 40.0 |  |  |  |  |
| **KWAV** | 23.5 | 24.2 | 23.8 | 24.0 | 24.7 | 24.8 | 24.1 | 26.2 | 23.9 | 23.9 | 22.4 | 22.4 |  |  |  |
| **DDV** | 21.2 | 19.8 | 21.6 | 21.5 | 23.0 | 21.0 | 21.5 | 24.2 | 21.5 | 20.9 | 19.9 | 22.0 | 42.5 |  |  |
| **OVRV** | 22.0 | 20.9 | 21.9 | 22.3 | 22.8 | 23.4 | 23.2 | 23.5 | 22.1 | 21.9 | 20.7 | 21.7 | 40.2 | 72.5 |  |

**Table 9.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of sunrhavirus L proteins.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **SJAV** | **NASV** | **BBOV** | **KOLV** | **OUAV** | **BEAV** | **MTYV** | **BOTV** | **GARV** | **HDV** | **WCV** | **SUNV** | **KWAV** | **DDV** | **OVRV** |
| **SJAV** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **NASV** | 83.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **BBOV** | 63.8 | 61.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **KOLV** | 62.9 | 61.9 | 82.5 |  |  |  |  |  |  |  |  |  |  |  |  |
| **OUAV** | 61.6 | 60.9 | 59.4 | 58.9 |  |  |  |  |  |  |  |  |  |  |  |
| **BEAV** | 63.2 | 62.8 | 60.5 | 60.4 | 63.8 |  |  |  |  |  |  |  |  |  |  |
| **MTYV** | 64.6 | 62.6 | 61.1 | 60.8 | 63.3 | 79.6 |  |  |  |  |  |  |  |  |  |
| **BOTV** | 53.9 | 53.3 | 53.2 | 53.1 | 53.8 | 54.5 | 53.3 |  |  |  |  |  |  |  |  |
| **GARV** | 63.4 | 62.9 | 59.6 | 60.3 | 63.8 | 78.2 | 82.9 | 53.5 |  |  |  |  |  |  |  |
| **HDV** | 54.1 | 54.2 | 53.4 | 52.4 | 54.5 | 54.0 | 53.6 | 65.2 | 53.2 |  |  |  |  |  |  |
| **WCV** | 54.2 | 53.6 | 53.0 | 52.5 | 54.2 | 53.5 | 53.7 | 65.2 | 53.3 | 85.2 |  |  |  |  |  |
| **SUNV** | 51.1 | 50.8 | 50.0 | 49.8 | 49.5 | 50.1 | 48.7 | 54.3 | 49.5 | 53.8 | 52.9 |  |  |  |  |
| **KWAV** | 39.9 | 39.3 | 39.2 | 39.6 | 39.7 | 40.8 | 40.0 | 40.0 | 40.3 | 40.8 | 39.8 | 38.9 |  |  |  |
| **DDV** | 38.3 | 38.7 | 38.3 | 39.0 | 39.2 | 39.4 | 39.1 | 39.8 | 38.9 | 40.6 | 39.5 | 38.1 | 53.4 |  |  |
| **OVRV** | 39.1 | 39.5 | 38.5 | 39.7 | 38.7 | 39.1 | 38.6 | 39.2 | 39.2 | 39.4 | 39 | 37.9 | 54.3 | 71.6 |  |

**Table 10.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of hapavirus N proteins.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **PORV** | **BGNV** | **FLAV** | **HPV** | **KAMV** | **MOSV** | **MQOV** | **LJAV** | **MANV** | **GLOV** | **ORV** | **HJV** | **JOIV** | **PCV** | **WONV** | **LJV** | **NGAV** | **MCOV** |
| **PORV** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **BGNV** | 40.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **FLAV** | 45.1 | 41.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **HPV** | 44.6 | 41.0 | 94.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **KAMV** | 41.9 | 41.0 | 72.2 | 72.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **MOSV** | 41.9 | 41.0 | 72.2 | 72.2 | 99.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **MQOV** | 43.2 | 43.2 | 70.3 | 69.4 | 73.1 | 73.3 |  |  |  |  |  |  |  |  |  |  |  |  |
| **LJAV** | 46.8 | 42.9 | 53.2 | 52.3 | 52.7 | 52.7 | 54.5 |  |  |  |  |  |  |  |  |  |  |  |
| **MANV** | 42.3 | 39.9 | 52.5 | 52.7 | 53.4 | 53.2 | 52.1 | 70.2 |  |  |  |  |  |  |  |  |  |  |
| **GLOV** | 43.4 | 46.4 | 52.5 | 52.5 | 52.5 | 52.5 | 54.3 | 51.1 | 51.9 |  |  |  |  |  |  |  |  |  |
| **ORV** | 40.5 | 68.8 | 43.2 | 43.7 | 43.9 | 44.1 | 44.6 | 41.8 | 40.5 | 49.4 |  |  |  |  |  |  |  |  |
| **HJV** | 41.0 | 69.5 | 43.0 | 43.7 | 43.2 | 43.5 | 44.6 | 41.8 | 40.5 | 48.7 | 92.6 |  |  |  |  |  |  |  |
| **JOIV** | 42.2 | 43.5 | 43.0 | 42.3 | 42.5 | 42.5 | 44.8 | 44.1 | 41.0 | 47.5 | 43.7 | 43.7 |  |  |  |  |  |  |
| **PCV** | 41.2 | 69.8 | 42.8 | 43.2 | 43.0 | 43.2 | 44.1 | 42.2 | 41.9 | 49.6 | 90.9 | 89.6 | 44.4 |  |  |  |  |  |
| **WONV** | 40.1 | 68.4 | 42.1 | 42.3 | 42.8 | 43.0 | 44.3 | 40.4 | 39.7 | 48.4 | 92.7 | 94.5 | 42.6 | 89.0 |  |  |  |  |
| **LJV** | 39.5 | 59.2 | 42.1 | 41.0 | 43.2 | 43 | 43.9 | 42.7 | 39.6 | 45.9 | 63.8 | 63.1 | 42.8 | 62.6 | 62.5 |  |  |  |
| **NGAV** | 36.0 | 40.5 | 40.3 | 40.7 | 40.2 | 40.2 | 40.2 | 39.8 | 37.9 | 43.0 | 40.3 | 40.3 | 43.8 | 40.7 | 39.6 | 40.5 |  |  |
| **MCOV** | 28.4 | 31.1 | 31.4 | 31.6 | 31.6 | 31.6 | 32.5 | 31.6 | 30.1 | 34.0 | 31.5 | 31.1 | 34.4 | 30.2 | 31.1 | 30.9 | 28.9 |  |

**Table 11.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of hapavirus G proteins.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **PORV** | **BGNV** | **FLAV** | **HPV** | **KAMV** | **MOSV** | **MQOV** | **LJAV** | **MANV** | **GLOV** | **ORV** | **HJV** | **JOIV** | **PCV** | **WONV** | **LJV** | **NGAV** | **MCOV** |
| **PORV** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **BGNV** | 23.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **FLAV** | 28.0 | 26.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **HPV** | 28.7 | 24.5 | 80.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **KAMV** | 25.5 | 25.9 | 52.8 | 52.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **MOSV** | 26.8 | 25.1 | 51.6 | 52.5 | 79.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **MQOV** | 27.1 | 25.3 | 46.9 | 47.9 | 47.3 | 46.6 |  |  |  |  |  |  |  |  |  |  |  |  |
| **LJAV** | 29.9 | 25.4 | 41.0 | 40.9 | 38.2 | 38.0 | 39.4 |  |  |  |  |  |  |  |  |  |  |  |
| **MANV** | 27.9 | 27.0 | 38.8 | 40.5 | 35.3 | 35.6 | 36.9 | 50.7 |  |  |  |  |  |  |  |  |  |  |
| **GLOV** | 30.1 | 26.3 | 33.6 | 33.7 | 33.6 | 34.5 | 35.3 | 33.9 | 35.3 |  |  |  |  |  |  |  |  |  |
| **ORV** | 23.9 | 46.8 | 25.9 | 24.6 | 24.5 | 24.6 | 24.1 | 26.3 | 27.3 | 28.9 |  |  |  |  |  |  |  |  |
| **HJV** | 23.4 | 47.6 | 26.5 | 25.8 | 24.8 | 24.8 | 24.7 | 25.5 | 26.1 | 28.2 | 67.4 |  |  |  |  |  |  |  |
| **JOIV** | 20.4 | 25.0 | 20.2 | 20.9 | 22.1 | 20.8 | 22.0 | 20.0 | 21.4 | 20.5 | 25.2 | 24.6 |  |  |  |  |  |  |
| **PCV** | 23.2 | 46.9 | 25.9 | 25.0 | 24.5 | 24.4 | 25.0 | 23.9 | 25.3 | 27.8 | 70.4 | 65.8 | 26.2 |  |  |  |  |  |
| **WONV** | 23.1 | 47.2 | 25.7 | 25.5 | 24.5 | 25.1 | 25.3 | 25.1 | 25.9 | 28.5 | 69.0 | 82.8 | 24.6 | 65.8 |  |  |  |  |
| **LJV** | 23.9 | 36.3 | 25.8 | 24.8 | 22.9 | 24.6 | 24.5 | 25.5 | 23.8 | 25.9 | 38.1 | 37.7 | 21.6 | 39.0 | 38.8 |  |  |  |
| **NGAV** | 20.4 | 22.8 | 21.0 | 20.7 | 20.7 | 20.5 | 21.6 | 19.9 | 22.3 | 19.6 | 21.2 | 20.1 | 27.9 | 22.3 | 20.7 | 22.0 |  |  |
| **MCOV** | 18.5 | 22.2 | 19.7 | 21.1 | 19.9 | 19.8 | 19.5 | 21.1 | 20.0 | 20.6 | 21.1 | 21.9 | 18.4 | 20.7 | 20.1 | 22.2 | 18.6 |  |

**Table 12.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of hapavirus L proteins.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **PORV** | **BGNV** | **FLAV** | **HPV** | **KAMV** | **MOSV** | **MQOV** | **LJAV** | **MANV** | **GLOV** | **ORV** | **HJV** | **JOIV** | **PCV** | **WONV** | **LJV** | **NGAV** | **MCOV** |
| **PORV** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **BGNV** | 50.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **FLAV** | 55.5 | 50.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **HPV** | 55.3 | 49.6 | 90.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **KAMV** | 55.7 | 50.0 | 72.9 | 73.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **MOSV** | 56.0 | 50.3 | 72.8 | 73.2 | 91.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **MQOV** | 55.7 | 50.1 | 69.3 | 68.9 | 69.3 | 69.5 |  |  |  |  |  |  |  |  |  |  |  |  |
| **LJAV** | 56.3 | 49.7 | 63.8 | 63.9 | 64.2 | 64.4 | 63.3 |  |  |  |  |  |  |  |  |  |  |  |
| **MANV** | 55.1 | 50.5 | 64.1 | 64.4 | 63.9 | 64.4 | 63.4 | 70.4 |  |  |  |  |  |  |  |  |  |  |
| **GLOV** | 55.5 | 49.5 | 58.6 | 59.0 | 59.5 | 59.6 | 58.9 | 58.5 | 58.4 |  |  |  |  |  |  |  |  |  |
| **ORV** | 50.5 | 64.8 | 50.5 | 50.3 | 50.2 | 50.5 | 51.2 | 49.4 | 50.9 | 50.0 |  |  |  |  |  |  |  |  |
| **HJV** | 50.7 | 65.1 | 50.4 | 50.5 | 51.1 | 50.7 | 51.4 | 49.6 | 50.5 | 49.3 | 83.4 |  |  |  |  |  |  |  |
| **JOIV** | 49.5 | 46.9 | 48.2 | 48.4 | 47.8 | 48.3 | 49.5 | 49.6 | 49.6 | 48.2 | 48.7 | 48.2 |  |  |  |  |  |  |
| **PCV** | 50.7 | 65.4 | 50.1 | 49.9 | 50.7 | 50.9 | 51.4 | 49.9 | 51.1 | 50.0 | 85.7 | 83.7 | 48.1 |  |  |  |  |  |
| **WONV** | 51.5 | 65.0 | 50.7 | 51.0 | 51.5 | 51.8 | 51.7 | 50.2 | 51.3 | 50.4 | 83.6 | 88.1 | 48.3 | 83.1 |  |  |  |  |
| **LJV** | 49.7 | 61.9 | 50.1 | 49.6 | 49.6 | 49.9 | 50.8 | 50.4 | 50.9 | 49.9 | 64.5 | 64.7 | 47.5 | 65.4 | 65.8 |  |  |  |
| **NGAV** | 50.5 | 47.9 | 49.5 | 49.3 | 49.4 | 50.1 | 49.6 | 49.2 | 50.4 | 48.2 | 48.2 | 48.2 | 48.0 | 47.5 | 47.6 | 47.7 |  |  |
| **MCOV** | 51.1 | 49.6 | 50.1 | 49.7 | 51.6 | 51.6 | 50.7 | 50.7 | 51.0 | 49.2 | 50.2 | 50.0 | 46.8 | 50.6 | 50.5 | 50.5 | 47.5 |  |

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