

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

**Part 1a: Details of taxonomy proposals**

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| **Title:** | Create 2 new genera and 14 new species in the subfamily *Alpharhabdovirinae*, and move 5 species from the genus *Vesiculovirus* to the new genus *Chiroprhavirus* (*Mononegavirales: Rhabdoviridae*) |
| **Code assigned:** | 2025.001M.N.v3.Alpharhabdovirinae\_2ng\_14nsp | |

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**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:** | | | |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses |  |
| Animal minus-strand and dsRNA viruses | **X** | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses |  | Plant viruses |  |
| Archaeal viruses |  | General - |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:** |
| *Rhabdoviridae* SG |

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| **Optional – complete only if formally voted on by an ICTV Study Group:** | | | |
| **Study Group** | **Number of members** | | |
| **Votes in support** | **Votes against** | **No vote** |
| *Rhabdoviridae* SG | 14 |  | 1 |

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| **Submission date:** | 30/05/2025 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required |  |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J - Reject |  |
| W - Withdrawn |  |

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| **Comments from the Executive Committee:** |
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**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
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| **Revision date:** |  |

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

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| **Taxonomic changes proposed:** | | | |
| Establish new taxon | **X** | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename | **X** |

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| **Etymology (origin) of proposed taxonomic names:** | |
| **Taxon name** | **Etymology of the term** |
| *Chiroprhavirus* | The genus name is derived from the order Chiroptera (meaning hand-wing) which includes all species of bats, the animals in which all proposed members of the genus were detected. |
| *Artemrhavirus* | The genus name is derived from the genus name (*Artemia*) of the source shrimp sample from which the sequence of the virus was obtained, and rhabdovirus. |
| *Artemrhavirus blanca* | The species epithet is derived from the port city of Bahia Blanca in Argentina, the site of collection of the brine shrimp sample from which the sequence of the virus was obtained. |
| *Ledantevirus hipposideros* | The species epithet is adopted from *Hippersideros*, the genus of bat from which the sequence of the virus was obtained. |
| *Ohlsrhavirus bafoussam* | The species epithet is derived from Bafoussam, the city in Cameroon that was the site of collection of the mosquito sample from which the sequence of the virus was obtained. |
| *Ohlsrhavirus halifaxii* | The species epithet is adopted from *Lutzia halifaxii*, the species of mosquito from which the sequence of the virus was obtained. |
| *Merhavirus corixo* | The species epithet is derived from the Corixo Grande, a river in Brazil that was the site of collection of the mosquito sample from which the sequence of the virus was obtained. |
| *Ephemerovirus hardee* | The species epithet is derived from the Hardee County in Florida, the site of collection of the white-tailed deer tissue sample from which the sequence of the virus was obtained. |
| *Ephemerovirus hefer* | The species epithet is derived from the Hefer Valley in Israel, the site of collection of the bovine blood sample from which the sequence of the virus was obtained. |
| *Alpharicinrhavirus marginatum* | The species epithet is adopted from *Hyalomma marginatum*, the species of tick from which the sequence of the virus was obtained. |
| *Alpharicinrhavirus isaaci* | The species epithet is adopted from *Hyalomma isaaci*, the species of tick from which the sequence of the virus was first obtained. |
| *Betathriprhavirus pamplona* | The species epithet is derived from the city of Pamplona in Spain, in the region of origin of the thrips laboratory colony from which the sequence of the virus was obtained. |
| *Betathriprhavirus oviedo* | The species epithet is derived from the city of Oviedo in Spain, in the region of origin of the thrips laboratory colony from which the sequence of the virus was obtained. |
| *Sigmavirus cucurbitae* | The species epithet is adopted from *Zeugodacus cucurbitae*, the species of fly from which the sequence of the virus was obtained. |
| *Sigmavirus bangalore* | The species epithet is derived from Bangalore, the city in India that was the site of origin of the melon fly laboratory colony from which the sequence of the virus was obtained. |
| *Lyssavirus phala* | The species epithet is derived from the Phalaborwa, a town in Limpopo Province, South Africa, the site of collection of the bat brain sample from which the sequence of the virus was obtained. |

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| **Permission for use of names derived from a living person** | | |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached** |
| NA |  |  |

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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Create new genera, create new species, and move existing species in the subfamily *Alpharhabdovirinae*, family *Rhabdoviridae*.  *Description of current taxonomy*:  The subfamily *Alpharhabdovirinae* currently comprises 34 genera including 246 species for viruses infecting only vertebrates, only invertebrates, or vertebrate hosts and arthropod vectors.  *Proposed* *taxonomic change(s):*   1. Create the new genus *Chiroprhavirus* and move 5 existing species from the genus *Vesiculovirus* to the new genus. 2. Create the new genus *Artemrhavirus* to include 1 new species. 3. Create 1 new species in the genus *Ledantevirus*. 4. Create 1 new species in the genus *Merhavirus*. 5. Create 2 new species in the genus *Sigmavirus*. 6. Create 2 new species in the genus *Ohlsrhavirus*. 7. Create 2 new species in the genus *Ephemerovirus*. 8. Create 2 new species in the genus *Betathriprhavirus*. 9. Create 2 new species in the genus *Alpharicinrhavirus*. 10. Create 1 new species in the genus *Lyssavirus*.   *Justification*:   1. Five viruses assigned to five existing species in the genus *Vesiculovirus* are phylogenetically and ecologically distinct from all other members of the genus, justifying their re-assignment to a new genus. 2. A new virus detected in brine shrimp is phylogenetically and ecologically distinct from the members of other genera in the subfamily *Alpharhabdovirinae*, justifying the creation of a new genus including a single species. 3. Thirteen other viruses for which complete coding sequences are now available fall phylogenetically within clades representing 8 existing genera and meet demarcation criteria for the creation of new species. |

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| **Text of Taxonomy proposal:** |
| 1. **Create the new genus *Chiroprhavirus* and move 5 existing species from the genus *Vesiculovirus* to the new genus.**   Vesiculoviruses have been the subject of extensive investigations over many years, dating to the first isolation in 1927 of a virus causing the vesicular stomatitis [3], a disease that had been known in horses, pigs and cattle in the USA since 1801 [20]. Since that time, a total of 16 distinct vesiculoviruses have been isolated and/or detected in various mammals and vector-borne transmission involving sandflies, mosquitoes or biting flies has been established. Some of these viruses are zoonotic and can cause acute illness in humans [20]. In recent years, a further 5 related viruses have been detected, all in bats of various species from Asia and North America. Prior to this, there had been no evidence of the detection of vesiculoviruses in bats.  The genus *Vesiculovirus* currently comprises 21 species to accommodate these 21 member viruses. In ML trees using the complete L protein sequences the vesiculoviruses form a discrete clade within the family *Alpharhabdovirinae* (Figure 1). However, this clade resolves further into two well-supported sub-clades (**Figure 1A**). The first includes the 16 viruses that have ecological characteristics of the ‘classical’ vesiculoviruses, having been isolated from dipteran insects and/or various mammals with evidence of insect-borne transmission [19, 20]. The second sub-clade, which is ancestral to the first, includes the 5 viruses that were detected relatively recently in chiropid bats. They are as follows:   1. American bat vesiculovirus (ABVV; species *Vesiculovirus eptesicus*) was detected in big brown bats (*Eptesicus fuscus*) collected in the USA, in 2008 [16]. 2. Wufeng Myotis altarium vesiculovirus 1 (WMalVV1; species *Vesiculovirus wufeng*) was detected in Szechwan myotis bats (*Myotis altarium*) collected in China, in 2016. 3. Mediterranean bat virus (MBV; species *Vesiculovirus mediterranean*) was detected in *Miniopterus schreibersii*, *Rhinolophus ferrumequinum* and *Rhinolophus euryale* bats collected in 2008, 2009 and 2012 in Spain, Algeria, and Morocco. 4. Jinghong bat virus (JhBV; species *Vesiculovirus jinghong*) was detected in an intermediate horseshoe bat (*Rhinolophus affinis*) collected in 2011 in Jinghong city, Yunnan Province, China [27]. It had previously been detected in *Rhinolophus affinis* bats collected in 2007 in Qiongzhong city, Hainan Province, China and named Qiongzhong bat virus [12]. It was subsequently detected in bats of the same species in Guangxi and Fujian Provinces, China, in 2016. 5. Yinshui bat virus (YSBV; species *Vesiculovirus yinshui*) was found in the Chinese bats (*Rhinolophus sinicus*) collected in 2007 and 2017 in Hubei Province, China [12]. It was also detected in bats of the same species (two samples) in Yunnan Province, China, in 2008 and in *Rhinolophus* sp. bats collected in Guizhou Province, China, in 2022.   We propose re-assignment of these 5 species to a new genus for which we propose the name *Chiroprhavirus*. Evidence supporting this proposal is as follows:   1. The 5 member viruses cluster in well-supported sub-clade in ML trees based on aligned L protein sequences that is distinct and ancestral to the sub-clade representing other vesiculoviruses (**Figure 1A**) 2. The 5 member viruses share amino acid sequence identities in L (57.2–76.0%), N (53.8–89.6%) and G (26.5–73.4%) that are similar in range to the range of other vesiculoviruses, i.e., L (57.2–80.4%), N (51.0–90.5%) and G (36.3-–85.3%). This compares with lower ranges amino acid sequence identity between the 5 viruses and the other vesiculoviruses, i.e., L (52.2-57.7%), N (43.5-51.6%) and G (24.4-30.2%) (**Tables 1**–**3**). 3. The member viruses all have a common ecological association with bats that is distinct from the insect vector-borne association of other vesiculoviruses with other vertebrates.   We propose to move the five existing species (*Vesiculovirus eptesicus*, *Vesiculovirus wufeng*, *Vesiculovirus mediterranean*, *Vesiculovirus rhinolopus*, and *Vesiculovirus yinshui*) to the new genus and rename them (*Chiroprhavirus eptesicus*, *Chiroprhavirus wufeng*, *Chiroprhavirus mediterranean*, *Chiroprhavirus rhinolopus*, and *Chiroprhavirus yinshui*, respectively).   1. **Create the new genus *Artemrhavirus* to include one new species.**   Brine shrimp rhabdovirus 1 (BSRV1; isolate BB/16) was detected in brine shrimp (*Artemia* sp.) collected in the port of Bahia Blanca, Argentina, in 2016 [4]. The complete coding sequence of the virus (11426 nt; Genbank OL472789) has been reported. The genome lacks only extreme 3' and 5' termini.  Phylogenetic analysis  Based on ML trees using the complete L protein sequences, BSRV1 lies on a branch that clusters distantly with other viruses detected in aquatic animals (**Figure 1A**). These include the two existing members of the genus *Scophrhavirus*, each detected in marine finfish, and the sole member of the genus *Uniorhavirus*, detected in freshwater mussels.  Genome organisation  The genome organization of BSRV1 is similar to those of members of the genus *Scophrhavirus* (Scophthalmus maximus rhabdovirus, species *Scophrhavirus maximus*; and Whuan redfin culter dimarhabdovirus, species *Scophrhavirus chanodychthys*) each of which includes only the five rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*) (**Figure 2**). However, the genome organization differs from that of the sole member of the genus *Uniorhavirus* (killamcar virus 1, species *Uniorhavirus killamcar*) which contains two genes (*G1* and *G2*) encoding class I transmembrane glycoproteins.  Based on the distant phylogenetic relationship with members of other genera, difference in genome organization with the sole member of the most closely related genus (*Uniorhavirus*), and differences in the ecology of the source organism (brine shrimp), we propose the creation of the new genus *Artemrhavirus* and assignment of BSRV1 to the new species *Artemrhavirus bahia*.  Species demarcation criteria for the new genus  Similar to the criteria used for several other genera within the *Alpharhabdovirinae*, we propose that viruses assigned in future to different species within the genus *Artemrhavirus* should have several of the following characteristics: A) minimum amino acid sequence divergence of 10% in N proteins; B) minimum sequence divergence of 10% in the L proteins; C) minimum amino acid sequence divergence of 15% in G proteins; D) can be distinguished in virus neutralization tests; E) exhibit significant differences in genome organization as evidenced by numbers and locations of ORFs; and F) occupy different ecological niches as evidenced by differences in hosts and or vectors.   1. **Create one new species in the genus *Ledantevirus***   Bat ledantevirus 2 (BaLV2; strain Hi. Ruber\_rhab) was detected by metagenomic sequencing of a Noack's roundleaf bat (*Hipposideros aff. ruber*) collected in Sierra Leone, in 2022 (PRJNA1177529). We propose BaLV2 be assigned to the new species *Ledantevirus hipposideros.*  Ecology  Ledanteviruses have been reported in a range of mammals and arthropod vectors. Those, like BaLV2, that are assigned to phylogroup C (**Figure 2**) have been detected in bats of various species from Africa or East Asia. Two of these have been detected in roundleaf bats: Kolente virus (KOLEV: species *Ledantevirus kolente*) was detected in a Jones's roundleaf bat (*Hipposideros jonesi*) from Guinea, Fikirini virus (FIKV; species *Ledantevirus fikirini*) was detected in a Commerson's roundleaf bat (*Hipposideros commersoni*) from Kenya.  Genome organization  The complete genome coding sequence of BaLV2 (11119 nt; Genbank PQ541151) has been reported. The genome lacks only extreme 3' and 5' termini. The genome organization is similar to those of other ledanteviruses of phylogroup C, containing only the five canonical rhabdovirus structural protein genes (*N*, *P*, *M,* *G* and *L*) (**Figure 2**).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, BaLV2 falls with the ledanteviruses in a distinct and well-supported monophyletic clade (**Figure 1A**). BaLV2 lies on a sub-clade with FIKV and KOLEV.  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGA7 from ClustalW amino acid sequence alignments indicate that BaLV2 is most closely related to KOLEV in the L protein (79.6% identity), N protein (85.0% identity) and the G protein (55.0% identity) (**Tables 7–9**).  Species demarcation criteria  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 organisation as evidenced by numbers and locations of ORFs; D) can be distinguished in neutralisation tests; and E) occupy different ecological niches as evidenced by differences in hosts and/or arthropod vectors.  BaLV2 meets criteria A and B. The genome organisation is similar to those of ledanteviruses from the same phylogroup (criterion C). Neutralization tests have not been conducted as there is currently no isolate of this virus (criterion D). The virus has been detected in a bat of a species that has not previously been associated with ledanteviruses (criterion E).   1. **Create one new species in the genus *Merhavirus***   Corixo rhabdovirus (CRXRV; strain JARP9) was detected by metagenomic sequencing of mosquitoes (*Anopheles darlingi*) collected in the High Pantanal, Mato Grosso State, Brazil, in 2019 (BioProject PRJNA963176). Two samples of the same virus (named Corixo rhabdovirus 1 and Corixo rhabdovirus 2) have been reported from mosquitoes of the same species collected at the same location and year. We propose CRXRV be assigned to the new species *Merhavirus corixo*.  Ecology  The genus *Merhavirus* currently comprises 7 species for viruses detected in culicine mosquitos (Culicidae). Merida virus (MERDV; species *Merhavirus merida*) was detected in *Culex* spp. and *Ochlerotatus* spp. mosquitoes collected in Mexico, USA, and Turkey [2]. Culex tritaeniorhynchus rhabdovirus (CTRV; species *Merhavirus tritaeniorhynchus*) was detected in a laboratory colony of *Culex* sp. mosquitoes collected in Japan [9]. Formosus virus (FORMV; species *Merhavirus formosus*) was detected in mosquitoes (*Aedes aegypti*) from a laboratory colony originating from Bundibugyo, Uganda [18]. Hattula rhabdovirus (HTTRV; species *Merhavirus hattula*) and Inari virus (INARV; species *Merhavirus inari*) were each detected in mosquitoes of several species (*Ochlerotatus* spp.) collected in Finland [22]. Armigeres subalbatus rhabdovirus (AsubRV; species *Merhavirus subalbatus*) was detected by metagenomic sequencing in 2019 in a cell line (Ar-3) established from a laboratory colony of *Armigeres subalbatus* mosquitoes in Japan [7, 13]. Cambodia anopheles rhabdovirus (CamAnRV; species *Merhavirus cambodia*) was detected by metagenomic sequencing in *Anopheles vagus* mosquitoes collected in Cambodia in 2021 [15]. The detection of CRXRV in *Anopheles darlingi* mosquitoes in Brazil broadens both the number of mosquito species and geographic range in which merhaviruses have been detected.  Genome organization  The complete genome coding sequence of CRXRV (11334 nt; Genbank OQ968277) has been reported. The genome lacks only extreme 3' and 5' termini. The genome organization is similar to those of other merhaviruses, containing only the five canonical rhabdovirus structural protein genes (*N*, *P*, *M,* *G* and *L*) (**Figure 2**).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, CRXRV falls with the merhaviruses in a distinct and well-supported monophyletic clade (**Figure 1A**). CRXRV lies on a sub-clade with CamAnRV, MERDV and CTRV.  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGA7 from ClustalW amino acid sequence alignments indicate that CRXRV is most closely related to CamAnRV in the L protein (40.6% identity), and to MERDV in the N protein (20.8% identity) and the G protein (20.8% identity). (**Tables 7–9**).  Species demarcation criteria  According to current criteria, viruses assigned to different species within the genus *Merhavirus* have several of the following characteristics: A) minimum amino acid sequence divergence of 10% in N proteins; B) minimum sequence divergence of 10% in the L proteins; C) minimum amino acid sequence divergence of 15% in G proteins; D) significant differences in genome organisation as evidenced by numbers and locations of ORFs; E) can be distinguished in virus neutralisation tests; and F) occupy different ecological niches as evidenced by differences in vertebrate hosts and or arthropod vectors.  The proposed member of the new genus meets demarcation criteria A, B, and C. The genome organization does not vary significantly from other merhaviruses. Neutralization tests have not been conducted as there is currently no isolate of this virus (criterion E). CRXRV was detected in mosquitoes of a novel species, but the natural ecology is currently uncertain (criterion F).   1. **Create two new species in the genus *Sigmavirus***   Zeugodacus cucurbitae sigmavirus 1 (ZCucSV1) and Zeugodacus cucurbitae sigmavirus 2 (ZCucSV2) were each detected by metagenomic sequencing of melon flies (*Zeugodacus cucurbitae*) collected in Bangalore, India, in 2022 [8]. We propose ZCucSV1 be assigned to the new species *Sigmavirus cucurbitae* and ZCucSV2 be assigned to the new species *Sigmavirus bangalore.*  Ecology  The genus *Sigmavirus* currently comprises 22 species. Sigmaviruses have generally been detected in flies from various families in the order Diptera. The only exception is Apis rhabdovirus 3 (species *Sigmavirus sichuan*) which was detected in bees. The few sigmaviruses that have been studied in any detail have been shown to be transmitted vertically through both eggs and sperm [11]. The detection of ZCucSV1 and ZCucSV2 in dipteran flies is consistent with the ecology of most other sigmaviruses.  Genome organizations  The complete genome coding sequences of ZCucSV1 (12510 nt; Genbank OR714907) and ZCucSV2 (12714 nt; Genbank OR714908) have been reported. The genomes lack only extreme 3' and 5' termini. The genome organizations of ZCucSV1 and ZCucSV2 are similar to those of most other sigmaviruses, containing the five canonical rhabdovirus structural protein genes (*N*, *P*, *M,* *G* and *L*) and an additional gene (*X*) between the *P* and *M* genes (**Figure 3**).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, ZCucSV1 and ZCucSV2 fall with the sigmaviruses in a distinct and well-supported monophyletic clade (**Figure 1A**). ZCucSV1 lies on a sub-clade with Wuhan louse fly virus 9 (WhLFV9; species *Sigmavirus hippoboscid*) and Whuan louse fly virus 10 (WhLFV10; species *Sigmavirus lousefly*), and ZCucSV2 lies on a sub-clade with Drosophila sturtevanti sigmavirus (DStuSV; species *Sigmavirus sturtevanti*) and Drosophila affinis sigmavirus (DAffSV; species *Sigmavirus affinis*).  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGA7 from ClustalW amino acid sequence alignments indicate that ZCucSV1 is most closely related to WhLFV9 in the L protein (54.2% identity), Ceratitis capitata sigmavirus (CCapSV; species *Sigmavirus capitata*) in the N protein (26.4% identity) and Drosophila melanogaster sigmavirus (DMelSV; species *Sigmavirus melanogaster*) in the G protein (33.3% identity). ZCucSV2 is most closely related to Hubei diptera virus 10 (HbDV10; species *Sigmavirus myga*) in the L, N and G proteins (44.7%, 29.3% and 24.5% identity, respectively) (**Tables 10-12**).  Species demarcation criteria  Viruses assigned to different species within the genus *Sigmavirus*have one or both of the following characteristics: A) minimum amino acid sequence divergence of 10% in L; and B) occupy different ecological niches as evidenced by differences in hosts.  The proposed members of the genus meet demarcation criterion A. As the viruses have been detected only by metagenomic sequencing, their natural ecology is uncertain, but each has been detected in melon flies of the same species (criterion B).   1. **Create two new species in the genus *Ohlsrhavirus***   Bafoussam mosquito rhabdovirus (BFMRV; strain Pool12) was detected by metagenomic sequencing of mosquitoes (*Aedes africanus*) collected at Bafoussam, Cameroon, in 2020 [14]. Culex rhabdo-like virus 2 (CRLV2) was detected by metagenomic sequencing of mosquitoes (*Lutzia halifaxii*) collected from Yunnan Province, China, in 2018 [10]. We propose BFMRV be assigned to the new species *Ohlsrhavirus bafoussam* andCRLV2 be assigned to the new species *Ohlsrhavirus halifaxii*.  Ecology  The genus *Ohlsrhavirus* currently comprises 9 species. Ohlsrhaviruses have been detected exclusively in culicine mosquitoes (*Culex* spp., *Ochlerotatus* spp. or *Psorophora* sp., as well as an undetermined species) from Europe, Asia, Australia, Africa, and the Americas. The detection of BFMRV and CRLV2 in *Aedes africanus* and *Lutzia halifaxii*, respectively, broadens the range of culicine mosquitoes in which ohlsrhaviruses have been detected.  Genome organizations  The complete genome coding sequences of BFMRV (11965 nt; Genbank PP764659) and CRLV2 (11680 nt; Genbank OQ067690) have been reported. The genomes lack only extreme 3' and 5' termini. The genome organizations are similar to those of other ohlsrhaviruses, containing only the five canonical rhabdovirus structural protein genes (*N*, *P*, *M,* *G* and *L*) (**Figure 3**).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, BFMRV and CRLV2 fall with the ohlsrhaviruses in a distinct and well-supported monophyletic clade (**Figure 1A**). CRLV2 forms a sub-clade with Culex rhabdo-like virus Los Angeles (CRLVLA; species *Ohlsrhavirus angeles*) and BFMRV is ancestral to all other classified ohlsrhaviruses.  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGA7 from ClustalW amino acid sequence alignments indicate that BFMRV is most closely related to Ohlsdorf virus (OHLDV; species *Ohlsrhavirus ohlsdorf*) in the L, N and G proteins (58.4%, 39.9% and 30.1% identity, respectively). CRLVA is most closely related to CRLVLA in the L, N, and G proteins (72.3%, 61.1% and 50.7% identity, respectively). (**Tables 13–15**).  Species demarcation criteria  Viruses assigned to different species within the genus *Ohlsrhavirus* have several of the following characteristics: A) minimum amino acid sequence divergence of 10% in N; B) minimum amino acid sequence divergence of 10% in L; C) minimum amino acid sequence divergence of 15% in G; D) significant differences in genome organization as evidenced by numbers and locations of ORFs; E) can be distinguished in virus neutralisation tests; and F) occupy different ecological niches as evidenced by differences in hosts and or arthropod vectors.  BFMRV and CRLV2 each meet demarcation criteria A, B and C. They have similar genome organizations to other ohlsrhaviruses (criterion D). Neutralisation tests (criterion E) have not been conducted as no virus isolates are currently available. The species of mosquitos in which BFMRV and CRLV2 were detected are different and have not been reported previously as the source organisms of other ohlsrhaviruses (criterion F).   1. **Create two new species in the genus *Ephemerovirus***   Hefer Valley virus (HVV; strain ISR-1655/1/22) was detected by metagenomic sequencing in a blood sample taken in 2022 from a dairy cow in Israel with a severe and ultimately fatal respiratory illness [5]. Hardee County ephemerovirus 1 (HCEV1; strain CHeRI) was detected by metagenomic sequencing of C6/36 mosquito cells inoculated with spleen tissue collected from a white-tailed deer (*Odocoileus virginianus*) in Hardee County, Florida, in 2023 (Genbank PQ480188). We propose that HVV be assigned to the new species *Ephemerovirus hefer* and that HCEV1 be assigned to the new species *Ephemerovirus hardee*.  Ecology  The genus *Ephemerovirus* currently comprises 14 species. Ephemeroviruses have been isolated or detected primarily in bovines, including cattle, water buffalo and yaks from Australia, Asia, Africa, and North America, as well as in pigs in China and a wide range of wild ungulates in Africa [25, 26]. Some have been isolated from mosquitoes or biting midges which are considered biological vectors. Two ephemeroviruses, New Kent County virus (NKCV; species *Ephemerovirus kent*) and Huanggang rhabd tick virus 2 (HgRTV2; species *Ephemerovirus huanggang*) have been detected in ticks from the USA and China [17, 21], but it is not yet known if these active infections or carried passively by the ticks.  Genome organizations  The complete genome coding sequences of HVV (15033 nt; Genbank OQ679991) and HCEV1 (14682 nt; Genbank PQ480188) have been reported. The HVV genome sequence is complete; the HCEV1 genome lacks only extreme 3' and 5' termini. Like all other ephemeroviruses, each has a relatively complex genome containing the five canonical rhabdovirus structural protein genes (*N*, *P*, *M,* *G* and *L*) as well as several other genes between the *G* and *L* genes, including a gene (*GNS*) encoding non-structural glycoprotein followed by two genes (*a* and *b*) encoding a class I viroporin (a1) and two small proteins of unknown function (a2 and b). The HVV genome is similar to those of bovine ephemeral fever virus (BEFV; species *Ephemerovirus febris*) and other related ephemeroviruses such as Hayes Yard virus (HYV; species *Ephemerovirus hayes*) and Puchong virus (PUCV; species *Ephemerovirus puchong*) in that the *b* gene is followed by one other gene (*g*), also encoding a small protein of unknown function. The HCEV1 genome is similar to those of NKCV, kotonkan virus (KOTV; species *Ephemerovirus kotonkan*), and Koolpinyah virus (KOOLV; species *Ephemerovirus koolpinyah*) in that the *g* gene is followed by yet another additional gene (*d*) encoding a small protein of unknown function (**Figure 4**).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, HVV and HCEV1 fall with the ephemeroviruses in a distinct and well-supported monophyletic clade (**Figure 1B**). HVV lies on a sub-clade with HYV and PUCV. HCEV1 lies on a sub-clade with KOOLV, KOTV, NKCV and Yata virus (YATV; species *Ephemerovirus yata*).  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGA7 from ClustalW amino acid sequence alignments indicate that HVV is most closely related to HYV in the L protein (78.5% identity), to HYV and PUCV in the N protein (87.7% identity), and to PUCV in the G protein (64.9% identity). HCEV1 is most closely related to YATV in the L and G proteins (59.0% and 40.7% identity, respectively) and to KOTV in the N protein (58.5% identity) (**Tables 16–18**).  Species demarcation criteria  According to current criteria, viruses assigned to different species within the genus *Ephemerovirus* have several of the following characteristics: A) minimum amino acid sequence divergence of 12% in the G protein; B) minimum amino acid sequence divergence of 8% in the L protein; C) minimum amino acid sequence divergence of 4% in the N protein; D) can be distinguished in virus neutralization tests; and E) exhibit significant differences in genome organization as evidenced by numbers and locations of ORFs.  HVV and HCEV1 each meet criteria A, B and C. No neutralization test data have yet been reported (criterion D). The genome organisations of HVV and HCEV1 are similar to those of other ephemeroviruses (criterion E).  Two other potential new species rejected  Kokolu virus (KOKV; strain G04B) was detected by metagenomic sequencing of serum collected from a bovine in the Gulu District, Uganda, in 2017 [1]. The complete coding sequence of KOKV (14630 nt; Genbank OU592964) has been reported, the genome lacking only extreme 3' and 5' termini. The genome organization is similar to that of PUCV, as described above (**Figure 4**). In ML trees generated from complete L protein sequences, KOKV falls within the ephemerovirus clade and lies on a subclade with PUCV (**Figure 1B**). Pairwise sequence identities (p-distances) indicate that KOKV is most closely related to PUCV in the L, N and G proteins (90.4%, 96.2% and 83.8% identity, respectively) (**Tables 16–18**). Based on these levels of identity, KOKV does **not** meet the species demarcation criteria for the genus *Ephemerovirus* and is considered another exemplar member of the species *Ephemerovirus puchong*.  Ephemerovirus sp. 'akisim' isolate (AKSMV; strain UG11722) metagenomic sequencing of mosquitoes (*Mansonia uniformis* collected in Uganda, in 2014. The complete coding sequence of KOKV (15635 nt; Genbank PQ742170) has been reported, the genome lacking only extreme 3' and 5' termini. In ML trees generated from complete L protein sequences, AKSMV falls within the ephemerovirus clade and lies on a subclade with HgRTV2 (**Figure 1B**). Pairwise sequence identities (p-distances) indicate that AKSMV is most closely related to HgRTV2 in the L, N and G proteins (89.5%, 97.2% and 85.9% identity, respectively) (**Tables 13–15**). Based on these levels of identity, AKSMV does **not** meet the species demarcation criteria for the genus *Ephemerovirus* and is considered another exemplar member of the species *Ephemerovirus huanggang*.   1. **Create two new species in the genus *Betathriprhavirus***   Orius laevigatus rhabdovirus 2 (OlaeRV2) and Orius laevigatus rhabdovirus 3 (OlaeRV3) were detected by metagenomic sequencing of a mixed laboratory population the minute pirate bug *Orius laevigatus* that had been collected in the Pamplona and Oviedo regions of northern Spain in 2021 [6]. We propose that OlaeRV2 be assigned to the new species *Betathriprhavirus pamplona*,and that OlaeRV3 be assigned to the new species *Betathriprhavirus oviedo*.  Ecology  The genus *Betathriprhavirus* currently comprises two species for viruses that were detected by metagenomic sequencing of thrips. The minute pirate bug *Orius laevigatus* is a hemipteran predator that feeds on larval and adult thrips. It is not yet clear whether the minute pirate bug or thrips (or both) serve as the natural host of betathriprhaviruses.  Genome organizations  The complete genome coding sequences of OlaeRV2 (10996 nt; Genbank PP908636) and OlaeRV3 (10806 nt; Genbank PP908637) have been reported. The genome sequences lack only extreme 3' and 5' termini. The genomes are similar to those of other betathriprhaviruses containing the five canonical rhabdovirus structural protein genes (*N*, *P*, *M,* *G* and *L*) and a small additional gene between the *G* and *L* genes (**Figure 4**).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, OlaeRV2 and OlaeRV3 fall  with the betathriprhaviruses in a distinct and well-supported monophyletic clade (**Figure 1B**). OlaeRV2 forms a sub-clade with soybean thrips rhabdo-like virus 1 (STRLV1; species *Betathriprhavirus variabilis*) and OlaeRV3 forms a sub-clade with soybean thrips rhabdo-like virus 2 (STRLV2; species *Betathriprhavirus* *midwest*).  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGA7 from ClustalW amino acid sequence alignments indicate that OlaeRV2 is most closely related to STRLV1 in the L, N and G proteins (69.6%, 72.3% and 62.2% identity, respectively) and OlaeRV3 is most closely related to STRLV2 in the L, N and G proteins (51.2%, 51.5% and 36.1% identity, respectively) (**Tables 19–21**).  Species demarcation criteria  Viruses assigned to different species within the genus *Betathriprhavirus* have several of the following characteristics: A) minimum amino acid sequence divergence of 12% in the G protein; B) minimum amino acid sequence divergence of 8% in the L protein; C) minimum amino acid sequence divergence of 4% in the N protein; D) can be distinguished in virus neutralization tests; E) exhibit significant differences in genome organization as evidenced by numbers and locations of ORFs; and F) occupy different ecological niches as evidenced by differences in hosts and or arthropod vectors.  OlaeRV1 and OlaeRV2 meet criteria A, B and C. Neutralisation tests have not been conducted as there are currently no isolates of these viruses (criterion D). The genome organisations are very similar to those of other betathriprhaviruses (criterion E). As the viruses have been detected only by metagenomic sequencing, their natural ecology is uncertain, but they have been detected in samples of a predator of thrips of the same hemipteran species collected from the same geographic location (criterion F).   1. **Create two new species in the genus *Alpharicinrhavirus***   Hyalomma marginatum rhabdovirus (HmarRV; strain PG) was detected by metagenomic sequencing of ticks (*Hyalomma marginatum*) collected in Tulcea, Romania, in 2021. Zhangye rhabd tick virus 1 (ZyRTV1; strain tick\_108) was detected by metagenomic sequencing of ticks (*Hyalomma isaaci*) collected from cattle in Tibet, China in 2018 (PRJNA841744). It was subsequently detected in ticks (*Hyalomma marginatum*) collected in Yunnan Province, China, in 2023 (PRJNA1189840). We propose that HmarRV be assigned to the new species *Alpharicinrhavirus marginatum* and ZyRTV1 be assigned to the new species *Alpharicinrhavirus isaaci*.  Ecology  The genus *Alpharicinrhavirus* currently comprises 17 species. Alpharicinrhaviruses have been detected exclusively in hard ticks (Ixodidae) of various species. Viruses of only two species have been detected to date in ticks of the genus *Hyalomma*: Taishun tick virus (TsTV; species *Alpharicinrhavirus taishun*) was detected *Hyalomma asiaticum*, *Hyalomma detritum* and *Hyalomma scupense* in Zhejiang Province China and in Astrakhan, Russia. Bole tick virus 2 (BlTV2; species *Alpharicinrhavirus bole*) was detected in *Hyalomma asiaticum* ticks collected in Xinjiang Province, China.  Genome organization  The complete coding sequence of HmarRV (11217 nt; Genbank PQ036169) and ZyRTV1 (10990 nt; Genbank PQ754346) have been reported. The genomes lack only extreme 3' and 5' termini. The genome organizations are similar to those of several other alpharicinrhaviruses, containing only four of the five canonical rhabdovirus structural protein genes (*N*, *P*, *M,* and *L*) (**Figure 5**). Like closely related TsTV and Zhangjiakou rhabd tick virus 1 (ZjRTV1; species *Alpharicinrhavirus zhangjiakou*), HmarRV and ZyRTV1 have no *G* gene. There is an alternative ORF in the HmarRV *N* gene (Nx) encoding a putative protein of 93 amino acids that shares 40% identity with the putative Nx protein of closely related TsTV (**Figure 6)** but it does not occur in the *N* gene of ZyRTV1. It is not known if these putative Nx proteins are expressed. The alternative ORF (Px) in the *P* gene of TsTV is not present in the *P* gene of HmarRV or ZyRTV1.  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, HmarRV and ZyRTV1 fall with the alpharicinrhaviruses in a distinct and well-supported monophyletic clade (**Figure 1B**). HmarRV and ZyRTV1 form a sub-clade with TsTV and ZjRTV1 that is ancestral to all other classified alpharicinrhaviruses.  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGA7 from ClustalW amino acid sequence alignments indicate that HmarRV and ZyRTV1 are most closely related to each other in the L and N proteins (87.1% and 88.7% identity, respectively). The next closely related virus is TsTV with which HmarRV shares 72.5% in L and 68.6% identity in N, and ZyRTV1 shares 72.6% identity in L and 69.2% identity in N (**Tables 22–23**).  Species demarcation criteria  Viruses assigned to different species within the genus *Alpharicinrhavirus* have several of the following characteristics: A) minimum amino acid sequence divergence of 10% in N proteins; B) minimum sequence divergence of 10% in the L proteins; C) minimum amino acid sequence divergence of 15% in G proteins; D) significant differences in genome organization as evidenced by numbers and locations of ORFs; E) can be distinguished in virus neutralisation tests; and F) occupy different ecological niches as evidenced by differences in vertebrate hosts and or arthropod vectors.  The proposed new members of the genus meet demarcation criteria A and B. There are no G genes (criterion C). The genome organizations are similar to those of closely related alpharicinrhaviruses but differ in the number of alternative small ORFs in the *N* and *P* genes (criterion D). Neutralisation tests have not been conducted as there are currently no isolates of these viruses (criterion E). The proposed new members have been detected in ticks of a species that not previously been associated with alpharicinrhaviruses but each has been detected in ticks of the same species (criterion F).   1. **Create one new species in the genus *Lyssavirus***   Phala bat lyssavirus (PBLV; strain UP14561) was detected by metagenomic sequencing in the brain of a Schlieffen’s bat (*Nycticeinops schlieffeni*) with neurological signs collected in Phalaborwa, South Africa, in 2021 [23]. We propose that PBLV be assigned to the new species *Lyssavirus phala*.  Ecology  The genus *Lyssavirus* currently comprises 18 species. With a few exceptions, lyssaviruses have been detected primarily in bats of various species which serve as the natural reservoir hosts. Most lyssaviruses are geographically restricted, having co-evolved with their natural hosts. The detection of PBLV in bats of the species *Nycticeinops schlieffeni* which have a distribution limited to parts of Africa and the Arabian Peninsula suggests that it occupies a unique ecological niche [24].  Genome organisation  The complete genome coding sequence of PBLV (11978 nt; Genbank OQ970171) has been reported. The genome lacks only extreme 3' and 5' termini. The genome organization is similar to those of most other lyssaviruses, containing the five canonical rhabdovirus structural protein genes (*N*, *P*, *M,* *G* and *L*) with a very long (482 nt) non-coding region in the *G* gene that extends (in positive sense) from the end of the G ORF to the 3' polyadenylation signal (**Figure 4**).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, PBLV falls  with the lyssaviruses in a distinct and well-supported monophyletic clade (**Figure 1B**). It forms a sub-clade with European bat lyssavirus 1 (EBLV1; species *Lyssavirus hamburg*), Irkut virus (IRKV; species *Lyssavirus irkut*), Taiwan bat lyssavirus (TWBLV; species *Lyssavirus formosa*) and Duvenhage virus (DUVV; species *Lyssavirus duvenhage*). PBLV also lies within the subclade comprising lyssaviruses assigned to phylogroup I (**Figure 4**).  Nucleotide sequence identities  Pairwise sequence identities calculated in MEGA7 from ClustalW nucleotide sequence alignments indicate that PBLV is most closely related to EBLV1 in the complete *N* gene sequence (71.4% identity) and in the concatenated coding regions (ORFs) of N+P+M+G+L (70.1% identity) (**Tables 24–25**).  Species demarcation criteria  Viruses assigned to different species within the genus *Lyssavirus* have several of the following characteristics: A) Genetic distances, with the threshold of 78-80% nt identity for the complete *N* gene, provides better quantitative resolution compared to other genes, or 80% nt identity for concatenated coding regions of N+P+M+G+L; B) in phylogenetic trees based on the entire N, or G, or L gene sequences, or concatenated N+P+M+G+L coding sequences, the new virus does not represent a sister branch to a virus from an established species. Instead, it is placed ancestrally to a group (cluster) of phylogenetically related viruses that belong to several established species; C) can be distinguished serologically in virus-neutralization tests; D) occupies a distinct ecologic niche as evidenced by host species, pathobiological properties, or geographical range.  PBLV meets demarcation criteria A and B. Neutralisation tests have not been conducted as there is currently no isolate of the virus (criterion C). As the virus has been detected only by metagenomic sequencing, the natural ecology is uncertain, but PBLV has been detected in a bat of a species not previously identified as the reservoir host of other lyssaviruses (criterion D). |

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| **Tables, Figures:**  **Figure 1 (A and B).** The evolutionary history was inferred from a multiple sequence alignment of complete L protein sequences of 246 rhabdoviruses that are currently assigned to species in the subfamily *Alpharhabdovirinae* as well as 16 viruses proposed to be assigned to 14 new species in the subfamily. The alignment was constructed in MAFFT using the E-INS-I iterative refinement method. Phylogenetically informative sites were selected from the alignment using TrimAl, resulting in 1604 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 (-443532.49) is shown. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log-likelihood values. 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.    **Figure 2.** Schematic illustration of the genome organisations of brine shrimp rhabdovirus 1 (proposed new genus *Artemrhavirus*), ledanteviruses and merhaviruses. Arrows represent long open reading frames (ORFs) with the N, P, M, G and L ORFs shown, the additional ORF of the Fukuoka virus shown in blue, and the additional ORF in the phylogroup B ledanteviruses shown in burgundy. The RNA splice site in Culex tritaeniorhynchus rhabdovirus is also shown. |
| **Figure 3.** Schematic illustration of the genome organisations of sigmaviruses and ohlsrhaviruses. Arrows represent long open reading frames (ORFs) with the N, P, M, G and L ORFs shown and the additional ORF (X) of sigmaviruses shown in light blue/aqua. |
| **Figure 4.** Schematic illustration of the genome organisations of ephemeroviruses and betathriprhaviruses. Arrows represent long open reading frames (ORFs) with the N, P, M, G and L ORFs shown and additional ORFs encoding homologous proteins shown in the same colour. |
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| **Figure 5.** Schematic illustration of the genome organisations of alpharicinrhaviruses and lyssaviruses. Arrows represent long open reading frames (ORFs) with the N, P, M, G and L ORFs shown. Alternative ORFs in the N genes of TSTV and HmarRV encoding homologous proteins are shown in green. In other alpharicinrhaviruses, other alternative ORFs are shown in grey. In WCBV, an alternative ORFs in the M ORF and following the G ORF is shown in orange and blue, respectively. It is not known if any of these alternative ORFs are expressed.  TsTV\_Nx MFSRWKLGSCLPSRSCLQLQTNPRRGLHRGRHKNRRKRQNGQPTPLVNSDSSARRVRPAK  HmarRV\_Nx MFARWKYRGSLSTRAGLQLQTSARRGPLIRRDTDREKGRNCHTGKFPRYRKVASSVSSAK  \*\*:\*\*\* \*.\*.:\*: \*\*\*\*\*..\*\*\* \*..:\*.\* \* :. . . .. \* \* .\*\*  TsTV\_Nx NRNCRPRPLFPRGRSVLDLFLPSNGQCGGLGNN  HmarRV\_Nx TRHSRPQTVSSRGSCLSHLLLPSNGECRDSSNH  .\*:.\*\*:.: .\*\*\*.: .\*.\*\*\*\*\*:\* . .\*:  **Figure 6.** Clustal W amino acid sequence alignment of the HmarRV and TsTV Nx proteins. |

**Table 1.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of vesiculovirus and chiroprhavirus L protein sequences.

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|  | MSPV | ISFV | PIRYV | PERV | CHNV | JURV | MEJV | RADV | YBV | VSNJV | CARV | VSAV | COCV | MARV | MORV | VSIV | **ABVV** | **WfMaVV1** | **MBV** | **JhBV** | **YsBV** |
| MSPV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ISFV | 68.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PIRYV | 67.8 | 66.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PERV | 66.9 | 66.7 | 67.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| CHNV | 67.7 | 68.9 | 67.0 | 66.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| JURV | 67.6 | 66.4 | 66.7 | 64.7 | 65.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| MEJV | 65.9 | 66.1 | 65.2 | 64.0 | 64.7 | 73.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| RADV | 61.5 | 61.4 | 60.6 | 60.1 | 62.0 | 60.7 | 60.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YBV | 59.7 | 59.3 | 59.8 | 58.6 | 60.1 | 58.6 | 59.0 | 72.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| VSNJV | 57.5 | 57.7 | 57.9 | 57.3 | 57.4 | 57.4 | 56.9 | 57.3 | 56.6 |  |  |  |  |  |  |  |  |  |  |  |  |
| CARV | 59.6 | 59.4 | 59.1 | 59.2 | 59.2 | 58.8 | 58.7 | 58.1 | 58.2 | 69.5 |  |  |  |  |  |  |  |  |  |  |  |
| VSAV | 59.3 | 58.9 | 58.3 | 57.9 | 58.9 | 58.4 | 57.9 | 58.0 | 57.8 | 66.8 | 69.7 |  |  |  |  |  |  |  |  |  |  |
| COCV | 59.4 | 59.0 | 57.6 | 58.3 | 58.6 | 58.3 | 57.8 | 58.4 | 58.2 | 65.3 | 68.9 | 78.2 |  |  |  |  |  |  |  |  |  |
| MARV | 58.9 | 59.1 | 57.4 | 57.6 | 58.6 | 58.0 | 57.7 | 57.3 | 57.6 | 65.4 | 68.5 | 77.2 | 79.0 |  |  |  |  |  |  |  |  |
| MORV | 58.9 | 58.8 | 58.0 | 58.7 | 58.4 | 57.7 | 58.2 | 57.2 | 57.9 | 65.4 | 69.0 | 75.4 | 77.3 | 78.8 |  |  |  |  |  |  |  |
| VSIV | 59.3 | 58.7 | 57.9 | 57.6 | 59.1 | 58.6 | 57.4 | 57.2 | 57.2 | 65.5 | 69.7 | 75.6 | 76.5 | 78.0 | 80.4 |  |  |  |  |  |  |
| **ABVV** | 57.2 | 56.3 | 57.6 | 55.5 | 56.1 | 57.7 | 56.5 | 56.3 | 55.2 | 54.1 | 54.5 | 54.6 | 53.8 | 53.2 | 53.6 | 53.8 |  |  |  |  |  |
| **WfMaVV1** | 55.2 | 54.8 | 54.7 | 54.2 | 53.9 | 54.7 | 54.6 | 54.9 | 54.9 | 53.0 | 54.1 | 53.8 | 54.3 | 54.4 | 54.3 | 53.5 | 58.0 |  |  |  |  |
| **MBV** | 54.4 | 53.7 | 53.6 | 52.9 | 54.4 | 53.7 | 53.7 | 55.2 | 54.5 | 52.7 | 53.8 | 54.0 | 53.2 | 53.2 | 53.0 | 53.0 | 57.2 | 59.7 |  |  |  |
| **JhBV** | 55.0 | 54.3 | 53.7 | 54.1 | 55.3 | 53.7 | 53.0 | 53.5 | 53.3 | 52.2 | 53.1 | 52.6 | 52.9 | 52.4 | 53.3 | 52.4 | 57.3 | 59.2 | 66.0 |  |  |
| **YsBV** | 54.8 | 55.3 | 53.4 | 54.2 | 55.4 | 54.2 | 53.6 | 54.8 | 53.5 | 52.4 | 53.5 | 53.6 | 53.8 | 52.8 | 53.2 | 52.3 | 57.9 | 59.7 | 67.2 | 76.0 |  |

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

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | MSPV | ISFV | PIRYV | PERV | CHNV | JURV | MEJV | RADV | YBV | VSNJV | CARV | VSAV | COCV | MARV | MORV | VSIV | **ABVV** | **WfMaVV1** | **MBV** | **JhBV** | **YsBV** |
| MSPV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ISFV | 65.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PIRYV | 62.8 | 61.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PERV | 65.6 | 60.5 | 65.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| CHNV | 58.5 | 58.5 | 55.9 | 54.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| JURV | 70.4 | 66.6 | 63.0 | 64.2 | 61.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| MEJV | 68.7 | 62.3 | 58.1 | 63.3 | 58.1 | 72.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| RADV | 54.6 | 54.7 | 54.1 | 55.1 | 51.7 | 56.2 | 54.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YBV | 52.8 | 53.8 | 51.8 | 52.0 | 49.6 | 54.6 | 52.0 | 75.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| VSNJV | 55.8 | 51.9 | 52.0 | 55.2 | 50.4 | 54.7 | 52.7 | 55.6 | 53.3 |  |  |  |  |  |  |  |  |  |  |  |  |
| CARV | 55.8 | 51.0 | 49.9 | 55.0 | 51.1 | 52.7 | 53.9 | 54.6 | 54.8 | 72.0 |  |  |  |  |  |  |  |  |  |  |  |
| VSAV | 54.9 | 51.9 | 52.3 | 55.2 | 48.9 | 55.1 | 53.9 | 55.3 | 54.8 | 69.0 | 74.9 |  |  |  |  |  |  |  |  |  |  |
| COCV | 55.6 | 51.0 | 51.8 | 54.5 | 48.7 | 52.7 | 54.9 | 53.7 | 53.1 | 69.4 | 73.9 | 85.3 |  |  |  |  |  |  |  |  |  |
| MARV | 56.3 | 51.0 | 52.5 | 55.2 | 50.6 | 53.7 | 54.4 | 55.1 | 53.6 | 69.2 | 73.5 | 82.5 | 86.7 |  |  |  |  |  |  |  |  |
| MORV | 54.7 | 51.9 | 53.0 | 55.5 | 51.3 | 54.4 | 53.7 | 55.1 | 53.6 | 68.2 | 74.9 | 83.4 | 83.4 | 88.9 |  |  |  |  |  |  |  |
| VSIV | 55.8 | 51.7 | 53.2 | 55.5 | 51.3 | 54.4 | 53.7 | 56.5 | 54.3 | 68.7 | 75.8 | 84.8 | 83.6 | 90.0 | 90.5 |  |  |  |  |  |  |
| **ABVV** | 47.9 | 48.7 | 49.3 | 49.2 | 47.6 | 49.5 | 48.3 | 48.3 | 49.4 | 46.4 | 47.4 | 45.3 | 46.0 | 46.4 | 46.9 | 46.4 |  |  |  |  |  |
| **WfMaVV1** | 48.9 | 47.1 | 47.5 | 50.2 | 48.7 | 51.6 | 49.6 | 51.3 | 51.4 | 46.8 | 48.0 | 48.9 | 47.5 | 48.2 | 48.2 | 49.2 | 55.6 |  |  |  |  |
| **MBV** | 47.1 | 44.4 | 44.5 | 46.8 | 44.0 | 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 |  |  |  |
| **JhBV** | 47.6 | 44.9 | 45.0 | 45.6 | 43.5 | 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 |  |  |
| **YsBV** | 48.6 | 47.0 | 47.1 | 47.3 | 44.0 | 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 | 89.6 |  |

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

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | MSPV | ISFV | PIRYV | PERV | CHNV | JURV | MEJV | RADV | YBV | VSNJV | CARV | VSAV | COCV | MARV | MORV | VSIV | **ABVV** | **WfMaVV1** | **MBV** | **JhBV** | **YsBV** |
| MSPV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ISFV | 49.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PIRYV | 49.3 | 50.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PERV | 49.1 | 50.1 | 57.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| CHNV | 48.8 | 54.9 | 51.9 | 51.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| JURV | 49.2 | 54.5 | 49.9 | 50.4 | 53.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| MEJV | 43.5 | 45.6 | 47.0 | 45.6 | 47.9 | 52.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| RADV | 41.2 | 42.5 | 46.2 | 43.9 | 44.7 | 43.2 | 39.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YBV | 43.5 | 44.0 | 48.4 | 46.1 | 45.6 | 45.4 | 41.7 | 67.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| VSNJV | 38.7 | 38.3 | 39.3 | 39.0 | 38.9 | 37.4 | 35.7 | 35.8 | 35.3 |  |  |  |  |  |  |  |  |  |  |  |  |
| CARV | 38.9 | 39.6 | 42.0 | 39.5 | 42.0 | 39.4 | 36.6 | 37.8 | 38.5 | 51.4 |  |  |  |  |  |  |  |  |  |  |  |
| VSAV | 38.8 | 37.9 | 39.1 | 40.2 | 41.1 | 38.1 | 35.2 | 37.2 | 37.3 | 47.5 | 55.0 |  |  |  |  |  |  |  |  |  |  |
| COCV | 37.6 | 42.0 | 38.9 | 38.2 | 41.4 | 40.1 | 34.4 | 37.6 | 36.3 | 46.9 | 55.3 | 67.1 |  |  |  |  |  |  |  |  |  |
| MARV | 37.2 | 39.4 | 40.2 | 38.8 | 41.6 | 38.5 | 36.0 | 38.7 | 37.4 | 49.4 | 55.9 | 64.3 | 74.2 |  |  |  |  |  |  |  |  |
| MORV | 38.6 | 41.5 | 39.2 | 39.4 | 41.5 | 38.7 | 37.0 | 39.1 | 39.0 | 48.8 | 56.7 | 64.2 | 71.7 | 77.9 |  |  |  |  |  |  |  |
| VSIV | 36.7 | 40.9 | 39.7 | 38.9 | 39.9 | 38.0 | 36.9 | 38.0 | 38.1 | 49.8 | 55.6 | 62.5 | 71.2 | 77.5 | 85.3 |  |  |  |  |  |  |
| **ABVV** | 27.5 | 25.4 | 27.4 | 26.2 | 24.7 | 26.3 | 27.5 | 26.6 | 26.8 | 24.8 | 28.1 | 24.6 | 25.2 | 25.2 | 25.3 | 24.4 |  |  |  |  |  |
| **WfMaVV1** | 29.5 | 26.6 | 27.9 | 28.4 | 27.1 | 27.0 | 27.2 | 26.0 | 26.5 | 26.4 | 27.9 | 25.5 | 25.9 | 26.3 | 27.4 | 27.7 | 26.5 |  |  |  |  |
| **MBV** | 27.6 | 27.2 | 27.2 | 27.8 | 28.8 | 26.8 | 28.4 | 26.7 | 26.4 | 27.4 | 26.0 | 27.4 | 27.1 | 29.5 | 29.1 | 28.5 | 30.3 | 37.2 |  |  |  |
| **JhBV** | 26.7 | 26.8 | 27.0 | 27.3 | 27.1 | 26.8 | 29.2 | 26.0 | 27.5 | 27.5 | 28.3 | 28.4 | 28.3 | 28.7 | 28.1 | 29.1 | 31.2 | 36.6 | 60.9 |  |  |
| **YsBV** | 28.5 | 28.7 | 27.9 | 28.3 | 28.3 | 28.1 | 28.1 | 26.8 | 26.7 | 27.8 | 28.8 | 28.7 | 28.6 | 29.9 | 29.3 | 30.2 | 28.9 | 38.3 | 63.1 | 73.4 |  |

**Table 4.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of ledantevirus L protein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | BARV | FUKV | NISV | NKOV | LqNcoLV1 | TrRTV2 | YjTV2 | KEUV | LDV | VAPV | KCV | MEBV | TYBV | KYAV | BUGV | WLFV5 | OITAV | WzRpuLV1 | KRV | FKRV | **BaLV2** | KOLEV |
| BARV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| FUKV | 92.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| NISV | 87.6 | 89.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| NKOV | 61.4 | 61.8 | 61.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| LqNcoLV1 | 55.4 | 55.1 | 55.6 | 56.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| TrRTV2 | 55.8 | 55.7 | 56.0 | 55.5 | 85.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YjTV2 | 54.1 | 54.0 | 54.2 | 54.3 | 53.8 | 53.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| KEUV | 50.6 | 51.3 | 51.1 | 51.1 | 49.2 | 49.2 | 50.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| LDV | 50.1 | 50.2 | 50.0 | 50.5 | 49.1 | 49.0 | 50.2 | 80.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| VAPV | 50.8 | 50.6 | 50.8 | 50.9 | 49.7 | 50.0 | 49.1 | 69.9 | 69.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| KCV | 50.1 | 50.6 | 50.8 | 51.1 | 49.8 | 49.8 | 50.5 | 62.8 | 62.8 | 63.1 |  |  |  |  |  |  |  |  |  |  |  |  |
| MEBV | 48.9 | 49.0 | 49.1 | 49.1 | 48.6 | 48.3 | 47.5 | 49.2 | 48.8 | 49.8 | 49.0 |  |  |  |  |  |  |  |  |  |  |  |
| TYBV | 49.2 | 49.3 | 49.1 | 49.6 | 48.3 | 48.2 | 48.3 | 48.9 | 48.6 | 50.0 | 48.3 | 75.5 |  |  |  |  |  |  |  |  |  |  |
| KYAV | 49.0 | 48.8 | 48.7 | 48.3 | 48.2 | 48.0 | 48.4 | 48.4 | 47.8 | 48.8 | 48.4 | 63.8 | 63.1 |  |  |  |  |  |  |  |  |  |
| BUGV | 46.7 | 47.0 | 46.8 | 47.5 | 47.8 | 47.9 | 47.3 | 47.8 | 47.4 | 47.8 | 47.6 | 62.8 | 62.0 | 71.6 |  |  |  |  |  |  |  |  |
| WLFV5 | 47.8 | 47.9 | 48.1 | 47.9 | 47.7 | 47.7 | 46.8 | 49.1 | 49.0 | 50.2 | 48.5 | 61.6 | 61.1 | 59.1 | 57.0 | 1 |  |  |  |  |  |  |
| OITAV | 47.9 | 48.1 | 47.8 | 48.1 | 46.9 | 46.7 | 46.9 | 47.7 | 47.8 | 50.0 | 48.7 | 54.8 | 54.9 | 53.5 | 52.7 | 55.8 |  |  |  |  |  |  |
| WzRpuLV1 | 47.2 | 47.8 | 47.7 | 47.1 | 46.7 | 46.7 | 47.2 | 48.7 | 48.2 | 49.7 | 48.0 | 54.9 | 55.1 | 54.1 | 52.9 | 56.3 | 74.1 |  |  |  |  |  |
| KRV | 47.8 | 47.7 | 47.0 | 47.2 | 46.5 | 46.5 | 48.2 | 49.1 | 49.1 | 50.1 | 48.7 | 55.7 | 55.4 | 54.8 | 53.6 | 55.3 | 63.3 | 63.2 |  |  |  |  |
| FKRV | 47.8 | 47.6 | 47.8 | 47.0 | 46.6 | 46.5 | 46.7 | 47.8 | 47.1 | 48.7 | 48.4 | 54.9 | 53.6 | 53.1 | 52.3 | 53.8 | 62.2 | 62.8 | 61.7 |  |  |  |
| **BaLV2** | 47.5 | 47.5 | 47.3 | 48.3 | 46.9 | 46.2 | 47.5 | 48.3 | 47.7 | 49.8 | 48.6 | 55.0 | 54.7 | 54.0 | 52.8 | 53.7 | 62.7 | 62.3 | 62.4 | 74.9 |  |  |
| KOLEV | 47.4 | 48.0 | 47.6 | 48.3 | 47.2 | 46.8 | 47.9 | 49.3 | 48.5 | 49.6 | 49.2 | 55.1 | 54.6 | 54.6 | 53.4 | 54.3 | 62.2 | 62.9 | 62.5 | 75.3 | 79.6 |  |

**Table 5.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of ledantevirus N protein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | BARV | FUKV | NISV | NKOV | LqNcoLV1 | TrRTV2 | YjTV2 | KEUV | LDV | VAPV | KCV | MEBV | TYBV | KYAV | BUGV | WLFV5 | OITAV | WzRpuLV1 | KRV | FKRV | **BaLV2** | KOLEV |
| BARV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| FUKV | 96.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| NISV | 94.1 | 95.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| NKOV | 76.2 | 77.2 | 75.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| LqNcoLV1 | 52.5 | 53.0 | 52.3 | 52.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| TrRTV2 | 52.5 | 52.7 | 52.0 | 52.5 | 92.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YjTV2 | 52.7 | 53.0 | 52.7 | 53.4 | 47.6 | 47.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| KEUV | 40.1 | 40.1 | 39.6 | 40.3 | 39.9 | 39.2 | 38.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| LDV | 39.6 | 39.6 | 38.9 | 39.4 | 41.3 | 39.9 | 38.6 | 80.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| VAPV | 43.0 | 42.2 | 42.0 | 43.7 | 39.7 | 38.7 | 38.6 | 62.5 | 63.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| KCV | 39.7 | 39.9 | 38.5 | 40.1 | 37.4 | 36.9 | 39.8 | 46.9 | 47.9 | 47.9 |  |  |  |  |  |  |  |  |  |  |  |  |
| MEBV | 41.7 | 41.2 | 41.0 | 40.2 | 42.8 | 42.5 | 39.7 | 42.0 | 41.1 | 37.1 | 38.1 |  |  |  |  |  |  |  |  |  |  |  |
| TYBV | 40.7 | 40.2 | 39.8 | 39.3 | 42.0 | 41.3 | 38.7 | 42.5 | 40.1 | 38.5 | 37.4 | 87.1 |  |  |  |  |  |  |  |  |  |  |
| KYAV | 40.0 | 40.2 | 39.5 | 39.8 | 40.6 | 39.7 | 39.0 | 41.8 | 39.2 | 38.0 | 35.9 | 75.2 | 77.3 |  |  |  |  |  |  |  |  |  |
| BUGV | 39.3 | 39.8 | 38.8 | 40.7 | 38.7 | 38.0 | 37.3 | 39.0 | 37.3 | 37.8 | 37.1 | 74.7 | 75.9 | 85.2 |  |  |  |  |  |  |  |  |
| WLFV5 | 37.6 | 37.4 | 37.6 | 38.3 | 39.9 | 39.2 | 36.1 | 39.4 | 38.5 | 38.0 | 37.1 | 72.6 | 72.6 | 67.4 | 69.3 |  |  |  |  |  |  |  |
| OITAV | 37.9 | 37.6 | 37.1 | 37.9 | 41.6 | 40.4 | 36.6 | 38.5 | 38.7 | 35.6 | 38.8 | 54.8 | 55.3 | 51.1 | 52.5 | 52.2 |  |  |  |  |  |  |
| WzRpuLV1 | 38.1 | 37.6 | 36.7 | 38.1 | 42.0 | 40.9 | 37.5 | 39.0 | 39.2 | 36.8 | 36.9 | 54.1 | 54.6 | 51.8 | 50.6 | 51.3 | 71.2 |  |  |  |  |  |
| KRV | 42.9 | 41.9 | 41.0 | 42.6 | 40.6 | 39.9 | 39.2 | 39.7 | 39.0 | 35.9 | 38.1 | 60.2 | 61.4 | 57.6 | 56.0 | 58.3 | 58.5 | 54.1 |  |  |  |  |
| FKRV | 40.2 | 40.0 | 40.2 | 40.5 | 39.2 | 38.5 | 40.6 | 36.6 | 37.1 | 34.9 | 36.9 | 60.4 | 60.0 | 58.1 | 57.8 | 56.7 | 56.9 | 55.5 | 60.0 |  |  |  |
| **BaLV2** | 40.8 | 40.3 | 39.4 | 40.8 | 40.5 | 39.5 | 39.3 | 38.3 | 39.0 | 38.8 | 39.3 | 62.0 | 63.4 | 59.2 | 59.9 | 62.2 | 59.9 | 54.9 | 66.7 | 72.8 |  |  |
| KOLEV | 40.1 | 40.1 | 40.3 | 40.3 | 43.1 | 41.7 | 40.2 | 38.3 | 39.8 | 37.6 | 38.6 | 62.4 | 61.3 | 60.1 | 58.2 | 62.4 | 58.0 | 55.2 | 63.4 | 73.7 | 85.0 |  |

**Table 6.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of ledantevirus G protein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | BARV | FUKV | NISV | NKOV | LqNcoLV1 | TrRTV2 | YjTV2 | KEUV | LDV | VAPV | KCV | MEBV | TYBV | KYAV | BUGV | WLFV5 | OITAV | WzRpuLV1 | KRV | FKRV | **BaLV2** | KOLEV |
| BARV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| FUKV | 84.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| NISV | 77.9 | 78.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| NKOV | 47.1 | 46.8 | 49.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| LqNcoLV1 | 40.8 | 41.4 | 41.6 | 43.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| TrRTV2 | 40.8 | 40.4 | 42.4 | 42.6 | 80.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YjTV2 | 38.3 | 40.7 | 39.0 | 40.2 | 42.0 | 40.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| KEUV | 30.6 | 31.5 | 31.8 | 32.6 | 34.1 | 33.6 | 34.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| LDV | 30.9 | 31.6 | 31.1 | 31.5 | 33.1 | 32.5 | 33.6 | 69.8 | 0 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| VAPV | 33.6 | 33.6 | 33.0 | 34.7 | 31.6 | 32.2 | 36.2 | 57.0 | 58.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| KCV | 33.8 | 34.8 | 33.5 | 33.0 | 32.3 | 33.5 | 36.2 | 48.5 | 49.1 | 51.4 |  |  |  |  |  |  |  |  |  |  |  |  |
| MEBV | 28.2 | 28.7 | 29.2 | 29.0 | 28.1 | 28.9 | 30.9 | 29.7 | 30.6 | 31.6 | 32.2 |  |  |  |  |  |  |  |  |  |  |  |
| TYBV | 29.8 | 31.9 | 30.0 | 30.8 | 28.1 | 28.5 | 29.8 | 30.8 | 30.2 | 32.8 | 29.9 | 64.4 |  |  |  |  |  |  |  |  |  |  |
| KYAV | 30.5 | 30.1 | 30.2 | 30.2 | 27.0 | 27.4 | 29.6 | 30.7 | 29.9 | 31.2 | 31.0 | 47.0 | 47.0 |  |  |  |  |  |  |  |  |  |
| BUGV | 29.9 | 31.4 | 30.5 | 31.0 | 28.7 | 29.5 | 30.0 | 30.8 | 30.1 | 32.9 | 32.1 | 45.8 | 47.4 | 70.0 |  |  |  |  |  |  |  |  |
| WLFV5 | 29.8 | 29.8 | 29.9 | 32.8 | 29.8 | 29.6 | 29.7 | 29.5 | 29.4 | 30.7 | 29.9 | 43.6 | 44.5 | 43.2 | 41.7 |  |  |  |  |  |  |  |
| OITAV | 26.3 | 25.9 | 26.4 | 27.7 | 27.8 | 26.7 | 28.2 | 26.3 | 23.8 | 26.7 | 25.7 | 29.4 | 31.3 | 30.1 | 29.3 | 29.0 |  |  |  |  |  |  |
| WzRpuLV1 | 28.4 | 28.2 | 28.7 | 27.0 | 26.7 | 26.1 | 27.2 | 26.2 | 25.8 | 25.3 | 25.9 | 29.4 | 31.1 | 31.0 | 29.7 | 27.9 | 58.0 |  |  |  |  |  |
| KRV | 25.2 | 25.8 | 24.3 | 23.6 | 23.1 | 21.7 | 25.0 | 24.3 | 24.7 | 25.1 | 27.5 | 27.2 | 26.8 | 28.9 | 28.0 | 24.7 | 32.1 | 34.3 |  |  |  |  |
| FKRV | 25.0 | 24.2 | 25.0 | 26.6 | 27.4 | 26.5 | 27.7 | 26.2 | 26.8 | 26.9 | 25.2 | 31.4 | 32.4 | 30.2 | 29.8 | 27.9 | 43.3 | 41.2 | 32.1 |  |  |  |
| **BaLV2** | 25.7 | 25.9 | 25.9 | 25.6 | 25.1 | 25.5 | 27.4 | 25.7 | 26.1 | 26.0 | 25.9 | 29.3 | 31.5 | 30.1 | 29.2 | 29.5 | 38.3 | 36.7 | 31.6 | 48.4 |  |  |
| KOLEV | 27.1 | 27.6 | 26.9 | 28.7 | 27.2 | 27.2 | 27.7 | 27.6 | 27.7 | 26.2 | 26.9 | 29.9 | 31.4 | 32.6 | 31.3 | 31.2 | 39.1 | 41.0 | 33.3 | 50.9 | 55.0 |  |

**Table 7.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of merhavirus L sequences.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | MERDV | CTRV | CamAnRV | **CRXRV** | HTTRV | INARV | AsRV | FORMV |
| MERDV |  |  |  |  |  |  |  |  |
| CTRV | 43.7 |  |  |  |  |  |  |  |
| CamAnRV | 41.0 | 41.0 |  |  |  |  |  |  |
| **CRXRV** | 39.8 | 40.1 | 40.6 |  |  |  |  |  |
| HTTRV | 39.2 | 38.1 | 37.5 | 37.4 |  |  |  |  |
| INARV | 37.8 | 37.9 | 37.8 | 37.7 | 67.0 |  |  |  |
| AsRV | 38.5 | 38.2 | 37.9 | 38.0 | 51.0 | 51.0 |  |  |
| FORMV | 38.5 | 38.0 | 37.1 | 37.5 | 50.6 | 50.0 | 72.2 |  |

**Table 8.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of merhavirus N sequences.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | MERDV | CTRV | CamAnRV | **CRXRV** | HTTRV | INARV | AsRV | FORMV |
| MERDV |  |  |  |  |  |  |  |  |
| CTRV | 24.9 |  |  |  |  |  |  |  |
| CamAnRV | 16.0 | 18.8 |  |  |  |  |  |  |
| **CRXRV** | 20.8 | 18.7 | 17.5 |  |  |  |  |  |
| HTTRV | 22.3 | 22.3 | 15.2 | 19.7 |  |  |  |  |
| INARV | 20.3 | 22.7 | 18.2 | 19.6 | 47.5 |  |  |  |
| AsRV | 17.5 | 23.7 | 17.9 | 18.8 | 24.9 | 26.8 |  |  |
| FORMV | 19.3 | 22.7 | 18.4 | 19.0 | 26.6 | 24.8 | 56.0 |  |

**Table 9.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of merhavirus G sequences.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | MERDV | CTRV | CamAnRV | **CRXRV** | HTTRV | INARV | AsRV | FORMV |
| MERDV |  |  |  |  |  |  |  |  |
| CTRV | 38.5 |  |  |  |  |  |  |  |
| CamAnRV | 18.1 | 19.3 |  |  |  |  |  |  |
| **CRXRV** | 20.8 | 19.4 | 14.8 |  |  |  |  |  |
| HTTRV | 23.4 | 20.9 | 16.6 | 17.4 |  |  |  |  |
| INARV | 22.0 | 22.3 | 16.5 | 15.6 | 53.2 |  |  |  |
| AsRV | 22.4 | 23.7 | 15.5 | 16.5 | 38.2 | 40.5 |  |  |
| FORMV | 22.8 | 21.5 | 15.9 | 16.5 | 38.8 | 40.6 | 62.9 |  |

**Table 10.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of sigmavirus L protein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | SyFV2 | WhFV2 | YsRV | HbDV10 | **ZCucSV2** | WhHFV1 | HbDV9 | ApRV3 | HzRV4 | BtyrRV1 | BDorSV | JPCGV1 | DAnaSV | DObsSV | DImmSV | DStuSV | DAffSV | CCapSV | HbDRV1 | DMelSV | ADMSV | WhLFV9 | **ZCucSV1** | WhLFV10 |
| SyFV2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WhFV2 | 82.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YsRV | 74.0 | 73.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbDV10 | 53.1 | 52.6 | 52.4 | 100.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **ZCucSV2** | 43.9 | 44.4 | 44.0 | 44.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WhHFV1 | 50.9 | 51.2 | 50.0 | 52.1 | 44.4 | 1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbDV9 | 50.4 | 50.3 | 51.3 | 52.5 | 43.8 | 51.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ApRV3 | 48.6 | 49.1 | 47.9 | 48.8 | 41.5 | 46.4 | 45.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HzRV4 | 45.5 | 45.0 | 45.6 | 44.8 | 43.0 | 44.4 | 45.2 | 44.4 | 1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| BtyrRV1 | 47.7 | 47.4 | 47.1 | 46.8 | 43.9 | 45.5 | 47.5 | 43.6 | 44.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| BDorSV | 47.6 | 47.2 | 47.3 | 46.6 | 44.2 | 46.0 | 46.7 | 43.1 | 45.2 | 78.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| JPCGV1 | 46.9 | 46.0 | 46.8 | 46.6 | 44.1 | 45.2 | 47.2 | 43.1 | 45.0 | 68.3 | 68.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DAnaSV | 44.2 | 43.6 | 43.1 | 45.9 | 41.4 | 42.7 | 43.7 | 42.0 | 43.2 | 43.3 | 44.4 | 44.1 | 1 |  |  |  |  |  |  |  |  |  |  |  |
| DObsSV | 43.0 | 43.5 | 43.1 | 42.6 | 40.6 | 41.5 | 43.9 | 41.6 | 41.4 | 43.8 | 43.6 | 43.5 | 41.9 |  |  |  |  |  |  |  |  |  |  |  |
| DImmSV | 42.6 | 42.1 | 42.2 | 42.2 | 39.5 | 42.7 | 43.4 | 41.5 | 41.9 | 44.0 | 43.7 | 43.4 | 42.4 | 55.1 |  |  |  |  |  |  |  |  |  |  |
| DStuSV | 41.8 | 42.1 | 42.4 | 43.6 | 40.8 | 41.9 | 42.5 | 39.9 | 40.9 | 42.0 | 41.9 | 42.3 | 41.5 | 41.2 | 39.8 |  |  |  |  |  |  |  |  |  |
| DAffSV | 41.1 | 41.8 | 41.6 | 44.0 | 40.6 | 41.6 | 41.6 | 40.5 | 40.9 | 41.9 | 41.6 | 41.9 | 40.8 | 41.1 | 39.4 | 60.3 |  |  |  |  |  |  |  |  |
| CCapSV | 43.8 | 43.7 | 43.2 | 45.0 | 41.3 | 43.8 | 43.1 | 41.5 | 41.3 | 43.5 | 44.3 | 44.0 | 42.1 | 41.1 | 41.4 | 40.7 | 40.5 |  |  |  |  |  |  |  |
| HbDRV1 | 42.9 | 42.5 | 42.0 | 43.2 | 40.4 | 42.0 | 42.0 | 41.5 | 41.6 | 43.0 | 43.6 | 43.1 | 41.5 | 41.2 | 41.7 | 40.9 | 39.5 | 47.6 |  |  |  |  |  |  |
| DMelSV | 42.3 | 41.8 | 42.0 | 43.1 | 41.0 | 41.1 | 42.6 | 40.5 | 41.7 | 41.6 | 43.3 | 43.6 | 40.8 | 41.0 | 41.1 | 40.5 | 39.0 | 48.0 | 48.8 | 1 |  |  |  |  |
| ADMSV | 43.1 | 42.4 | 43.5 | 42.8 | 41.8 | 42.8 | 42.6 | 40.2 | 41.8 | 43.1 | 43.9 | 43.5 | 39.8 | 41.5 | 41.5 | 39.9 | 38.3 | 50.5 | 50.2 | 50.0 |  |  |  |  |
| WhLFV9 | 42.4 | 41.6 | 42.0 | 42.7 | 40.2 | 42.0 | 41.8 | 40.0 | 41.8 | 43.7 | 44.1 | 43.6 | 41.1 | 40.9 | 40.7 | 40.4 | 40.2 | 49.6 | 50.9 | 51.2 | 52.0 |  |  |  |
| **ZCucSV1** | 43.3 | 43.6 | 42.6 | 42.5 | 41.2 | 42.3 | 42.5 | 40.7 | 43.7 | 43.6 | 43.9 | 42.8 | 42.5 | 42.1 | 41.7 | 41.5 | 41.2 | 50.9 | 50.7 | 50.2 | 52.1 | 54.2 |  |  |
| WhLFV10 | 42.5 | 42.2 | 42.0 | 42.6 | 41.0 | 42.2 | 42.1 | 39.8 | 41.3 | 43.4 | 43.7 | 43.3 | 41.8 | 41.3 | 40.6 | 40.2 | 39.6 | 49.8 | 50.3 | 50.9 | 51.9 | 67.6 | 54.0 |  |

**Table 11.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of sigmavirus N protein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | SyFV2 | WhFV2 | YsRV | HbDV10 | **ZCucSV2** | WhHFV1 | HbDV9 | ApRV3 | HzRV4 | BtyrRV1 | BDorSV | JPCGV1 | DAnaSV | DObsSV | DImmSV | DStuSV | DAffSV | CCapSV | HbDRV1 | DMelSV | ADMSV | WhLFV9 | **ZCucSV1** | WhLFV10 |
| SyFV2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WhFV2 | 83.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YsRV | 65.5 | 65.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbDV10 | 34.6 | 34.4 | 33.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **ZCucSV2** | 25.9 | 25.2 | 25.7 | 29.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WhHFV1 | 28.3 | 27.8 | 29.4 | 27.2 | 26.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbDV9 | 30.8 | 30.1 | 30.6 | 28.3 | 24.3 | 28.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ApRV3 | 24.8 | 25.1 | 25.5 | 23.7 | 25.3 | 23.7 | 26.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HzRV4 | 21.0 | 20.8 | 21.2 | 17.8 | 22.0 | 19.8 | 22.1 | 18.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| BtyrRV1 | 28.5 | 27.1 | 30.2 | 26.1 | 27.1 | 23.6 | 27.5 | 23.7 | 21.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| BDorSV | 30.0 | 28.4 | 31.0 | 26.3 | 25.9 | 24.6 | 27.8 | 24.1 | 23.1 | 69.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| JPCGV1 | 29.4 | 30.3 | 29.2 | 28.7 | 26.9 | 25.7 | 26.4 | 24.3 | 23.7 | 59.1 | 59.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DAnaSV | 26.6 | 26.9 | 25.5 | 24.4 | 24.7 | 23.0 | 20.6 | 19.7 | 20.2 | 24.8 | 25.6 | 26.4 |  |  |  |  |  |  |  |  |  |  |  |  |
| DObsSV | 20.1 | 20.8 | 21.7 | 19.8 | 20.3 | 19.8 | 20.9 | 18.3 | 20.7 | 23.7 | 23.5 | 21.2 | 21.8 |  |  |  |  |  |  |  |  |  |  |  |
| DImmSV | 21.3 | 21.3 | 21.8 | 20.7 | 22.2 | 19.9 | 23.4 | 20.3 | 20.4 | 23.9 | 23.8 | 24.6 | 21.6 | 43.5 |  |  |  |  |  |  |  |  |  |  |
| DStuSV | 26.3 | 27.5 | 26.2 | 26.2 | 20.2 | 23.1 | 24.1 | 22.9 | 18.6 | 24.4 | 24.5 | 26.0 | 22.7 | 21.1 | 19.5 |  |  |  |  |  |  |  |  |  |
| DAffSV | 27.7 | 27.4 | 28.4 | 25.9 | 22.4 | 24.1 | 24.3 | 27.0 | 19.5 | 25.3 | 26.7 | 26.5 | 23.4 | 22.7 | 19.4 | 43.3 |  |  |  |  |  |  |  |  |
| CCapSV | 22.6 | 22.1 | 21.2 | 21.3 | 20.9 | 19.0 | 23.5 | 20.1 | 21.9 | 23.2 | 21.7 | 22.7 | 19.7 | 22.4 | 21.7 | 20.2 | 20.9 |  |  |  |  |  |  |  |
| HbDRV1 | 19.5 | 18.1 | 20.0 | 18.8 | 21.1 | 20.4 | 19.2 | 19.0 | 19.1 | 19.0 | 19.8 | 18.6 | 18.6 | 18.3 | 16.7 | 18.9 | 20.0 | 23.8 |  |  |  |  |  |  |
| DMelSV | 23.0 | 21.8 | 24.8 | 23.0 | 21.1 | 22.8 | 22.9 | 22.3 | 22.4 | 21.2 | 23.0 | 22.5 | 18.9 | 22.9 | 19.6 | 20.3 | 20.3 | 29.9 | 24.6 |  |  |  |  |  |
| ADMSV | 23.1 | 23.6 | 23.9 | 22.1 | 19.2 | 24.4 | 20.2 | 21.6 | 21.2 | 21.2 | 22.8 | 22.9 | 18.2 | 20.3 | 19.8 | 22.1 | 20.6 | 28.5 | 26.1 | 27.7 |  |  |  |  |
| WhLFV9 | 23.4 | 24.1 | 22.7 | 21.5 | 24.1 | 21.9 | 20.7 | 20.7 | 20.8 | 26.3 | 23.2 | 24.7 | 21.9 | 20.6 | 19.1 | 22.2 | 21.9 | 27.9 | 22.0 | 33.9 | 27.8 |  |  |  |
| **ZCucSV1** | 17.9 | 17.0 | 18.4 | 17.9 | 18.6 | 21.0 | 18.1 | 16.7 | 22.6 | 16.4 | 17.0 | 19.1 | 17.9 | 18.9 | 17.3 | 19.2 | 20.5 | 26.4 | 24.4 | 27.4 | 24.7 | 24.9 |  |  |
| WhLFV10 | 22.5 | 22.7 | 21.3 | 19.0 | 20.8 | 22.1 | 23.8 | 21.2 | 21.5 | 25.8 | 26.6 | 25.2 | 18.9 | 19.7 | 19.5 | 20.3 | 21.6 | 27.9 | 24.6 | 34.5 | 29.2 | 50.0 | 26.3 | 1 |

**Table 12.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of sigmavirus Gprotein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | SyFV2 | WhFV2 | YsRV | HbDV10 | **ZCucSV2** | WhHFV1 | HbDV9 | ApRV3 | HzRV4 | BtyrRV1 | BDorSV | JPCGV1 | DAnaSV | DObsSV | DImmSV | DStuSV | DAffSV | CCapSV | HbDRV1 | DMelSV | ADMSV | WhLFV9 | **ZCucSV1** | WhLFV10 |
| SyFV2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WhFV2 | 67.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YsRV | 58.4 | 59.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbDV10 | 36.1 | 35.8 | 37.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **ZCucSV2** | 22.8 | 23.4 | 22.9 | 24.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WhHFV1 | 26.5 | 24.3 | 26.9 | 25.7 | 22.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbDV9 | 28.4 | 25.9 | 27.3 | 29.6 | 21.1 | 22.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ApRV3 | 31.2 | 30.1 | 30.9 | 30.6 | 20.0 | 25.7 | 26.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HzRV4 | 20.2 | 19.4 | 20.6 | 22.2 | 18.3 | 20.7 | 19.2 | 19.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| BtyrRV1 | 22.3 | 21.5 | 22.8 | 23.4 | 23.2 | 21.2 | 21.7 | 18.8 | 21.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| BDorSV | 23.6 | 23.5 | 22.9 | 23.5 | 22.0 | 22.7 | 23.3 | 21.7 | 20.2 | 53.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| JPCGV1 | 24.7 | 22.4 | 26.3 | 25.1 | 22.5 | 22.2 | 24.3 | 23.6 | 20.2 | 42.8 | 39.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DAnaSV | 22.7 | 22.3 | 20.8 | 22.4 | 23.4 | 22.9 | 20.6 | 20.9 | 19.1 | 22.9 | 24.2 | 24.0 |  |  |  |  |  |  |  |  |  |  |  |  |
| DObsSV | 18.8 | 20.6 | 20.5 | 19.6 | 20.7 | 22.8 | 17.9 | 18.8 | 19.1 | 20.7 | 22.0 | 21.6 | 20.4 |  |  |  |  |  |  |  |  |  |  |  |
| DImmSV | 20.4 | 21.4 | 20.5 | 21.9 | 23.3 | 23.7 | 19.9 | 19.4 | 15.8 | 21.1 | 20.3 | 21.6 | 20.2 | 36.2 |  |  |  |  |  |  |  |  |  |  |
| DStuSV | 23.2 | 22.6 | 23.4 | 23.3 | 23.4 | 23.3 | 21.5 | 21.2 | 17.9 | 18.6 | 20.1 | 22.1 | 19.0 | 22.2 | 21.0 |  |  |  |  |  |  |  |  |  |
| DAffSV | 22.1 | 23.6 | 22.8 | 24.0 | 23.0 | 22.7 | 20.2 | 22.5 | 19.3 | 18.8 | 18.7 | 19.4 | 20.3 | 21.4 | 19.9 | 46.2 |  |  |  |  |  |  |  |  |
| CCapSV | 22.6 | 24.2 | 21.4 | 24.1 | 24.5 | 22.6 | 20.6 | 21.1 | 18.8 | 21.5 | 22.2 | 22.6 | 21.7 | 21.0 | 19.9 | 20.4 | 19.8 |  |  |  |  |  |  |  |
| HbDRV1 | 19.7 | 21.1 | 21.6 | 23.3 | 21.4 | 23.7 | 22.7 | 21.2 | 21.6 | 24.7 | 23.6 | 25.9 | 23.0 | 21.4 | 19.6 | 20.1 | 20.9 | 25.5 |  |  |  |  |  |  |
| DMelSV | 20.4 | 21.2 | 21.9 | 23.3 | 20.0 | 22.3 | 21.3 | 21.6 | 20.5 | 23.8 | 23.4 | 25.3 | 23.4 | 21.4 | 18.7 | 22.1 | 21.8 | 27.8 | 26.1 |  |  |  |  |  |
| ADMSV | 21.6 | 19.3 | 19.1 | 21.9 | 19.8 | 19.7 | 19.1 | 20.6 | 17.0 | 22.8 | 21.6 | 24.3 | 20.4 | 17.8 | 19.4 | 18.2 | 20.5 | 23.3 | 23.5 | 20.6 |  |  |  |  |
| WhLFV9 | 19.8 | 20.2 | 20.3 | 19.7 | 21.3 | 22.8 | 21.1 | 21.0 | 19.5 | 22.8 | 25.1 | 20.6 | 22.5 | 20.3 | 19.9 | 18.7 | 18.2 | 24.2 | 24.4 | 22.5 | 20.2 |  |  |  |
| **ZCucSV1** | 21.2 | 21.7 | 21.8 | 22.6 | 23.6 | 23.5 | 21.7 | 21.3 | 20.8 | 21.3 | 22.5 | 23.2 | 23.4 | 19.5 | 19.8 | 22.6 | 21.8 | 26.3 | 29.2 | 33.3 | 20.7 | 26.0 |  |  |
| WhLFV10 | 20.8 | 19.7 | 21.4 | 21.3 | 19.7 | 20.6 | 22.6 | 20.7 | 18.2 | 20.3 | 21.7 | 21.6 | 19.9 | 19.9 | 20.5 | 19.6 | 19.1 | 23.3 | 22.3 | 23.5 | 21.4 | 35.1 | 23.8 |  |

**Table 13.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of ohlsrhavirus L sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | LOBV | OHLDV | **BFMRV** | RISV | CRLVLA | **CRLV2** | ADUMV | CpRLV | TCHV1 | CRLV | NORCV |
| LOBV |  |  |  |  |  |  |  |  |  |  |  |
| OHLDV | 59.3 |  |  |  |  |  |  |  |  |  |  |
| **BFMRV** | 53.7 | 58.4 |  |  |  |  |  |  |  |  |  |
| RISV | 58.5 | 68.0 | 56.7 |  |  |  |  |  |  |  |  |
| CRLVLA | 57.7 | 62.5 | 56.7 | 66.9 |  |  |  |  |  |  |  |
| **CRLV2** | 57.2 | 61.7 | 56.3 | 65.7 | 73.2 |  |  |  |  |  |  |
| ADUMV | 55.8 | 62.0 | 55.4 | 66.4 | 67.9 | 67.8 |  |  |  |  |  |
| CpRLV | 57.4 | 63.7 | 56.6 | 67.5 | 66.8 | 66.2 | 66.0 |  |  |  |  |
| TCHV1 | 57.0 | 64.2 | 56.3 | 67.2 | 66.2 | 66.3 | 66.1 | 88.3 |  |  |  |
| CRLV | 57.0 | 63.4 | 55.9 | 66.3 | 66.4 | 67.3 | 65.9 | 87.3 | 90.0 |  |  |
| NORCV | 56.6 | 62.5 | 55.4 | 65.9 | 65.6 | 66.0 | 64.7 | 85.6 | 87.8 | 90.8 |  |

**Table 14.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of ohlsrhavirus N sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | LOBV | OHLDV | **BFMRV** | RISV | CRLVLA | **CRLV2** | ADUMV | CpRLV | TCHV1 | CRLV | NORCV |
| LOBV |  |  |  |  |  |  |  |  |  |  |  |
| OHLDV | 46.2 |  |  |  |  |  |  |  |  |  |  |
| **BFMRV** | 35.6 | 39.9 |  |  |  |  |  |  |  |  |  |
| RISV | 44.7 | 49.7 | 37.0 |  |  |  |  |  |  |  |  |
| CRLVLA | 47.3 | 53.5 | 39.6 | 52.0 |  |  |  |  |  |  |  |
| **CRLV2** | 42.8 | 50.7 | 38.4 | 49.4 | 61.1 |  |  |  |  |  |  |
| ADUMV | 45.1 | 51.4 | 35.0 | 53.1 | 57.8 | 57.1 |  |  |  |  |  |
| CpRLV | 49.7 | 52.4 | 37.6 | 49.9 | 58.5 | 57.1 | 58.4 |  |  |  |  |
| TCHV1 | 47.9 | 54.0 | 38.5 | 56.4 | 59.7 | 55.1 | 57.5 | 77.8 |  |  |  |
| CRLV | 49.2 | 51.6 | 37.7 | 52.7 | 58.3 | 56.7 | 58.2 | 80.2 | 78.9 |  |  |
| NORCV | 48.4 | 50.5 | 35.1 | 51.6 | 56.9 | 54.8 | 56.6 | 78.1 | 76.9 | 88.1 |  |

**Table 15.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of ohlsrhavirus G sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | LOBV | OHLDV | **BFMRV** | RISV | CRLVLA | CRLV2 | ADUMV | CpRLV | TCHV1 | CRLV | NORCV |
| LOBV |  |  |  |  |  |  |  |  |  |  |  |
| OHLDV | 26.2 |  |  |  |  |  |  |  |  |  |  |
| **BFMRV** | 26.6 | 30.1 |  |  |  |  |  |  |  |  |  |
| RISV | 27.1 | 28.4 | 29.9 |  |  |  |  |  |  |  |  |
| CRLVLA | 27.9 | 26.9 | 29.9 | 41.7 |  |  |  |  |  |  |  |
| CRLV2 | 27.9 | 28.5 | 29.2 | 38.9 | 50.7 |  |  |  |  |  |  |
| ADUMV | 27.6 | 27.4 | 27.0 | 38.9 | 39.0 | 39.9 |  |  |  |  |  |
| CpRLV | 26.9 | 27.6 | 28.5 | 36.5 | 39.1 | 38.7 | 38.1 |  |  |  |  |
| TCHV1 | 27.1 | 26.0 | 27.5 | 36.9 | 37.3 | 37.3 | 38.4 | 54.0 |  |  |  |
| CRLV | 26.5 | 28.7 | 26.4 | 40.3 | 39.3 | 37.7 | 38.4 | 55.7 | 57.1 |  |  |
| NORCV | 25.5 | 25.2 | 27.5 | 36.5 | 36.9 | 37.1 | 38.1 | 54.0 | 57.7 | 68.0 |  |

**Table 16.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of ephemerovirus L sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | BEFV | BRMV | KIMV | **AKSMV** | HgRTV2 | **KOKV** | PUCV | **HVV** | HYV | OBOV | ARV | PoEV1 | PoEV2 | **HCEV1** | YATV | NKCV | KOTV | KOOLV |
| BEFV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| BRMV | 84.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| KIMV | 64.6 | 64.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **AKSMV** | 64.9 | 65.1 | 85.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HgRTV2 | 65.1 | 65.4 | 86.4 | 89.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **KOKV** | 63.3 | 63.9 | 62.5 | 62.6 | 62.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PUCV | 63.3 | 63.6 | 63.2 | 62.9 | 62.7 | 90.4 |  |  |  |  |  |  |  |  |  |  |  |  |
| **HVV** | 63.6 | 64.1 | 63.9 | 63.4 | 64.0 | 77.4 | 77.5 |  |  |  |  |  |  |  |  |  |  |  |
| HYV | 63.5 | 64.2 | 63.5 | 63.6 | 63.1 | 86.8 | 86.8 | 78.5 |  |  |  |  |  |  |  |  |  |  |
| OBOV | 49.6 | 48.9 | 49.5 | 49.2 | 49.3 | 48.0 | 48.1 | 48.4 | 48.1 |  |  |  |  |  |  |  |  |  |
| ARV | 49.3 | 48.7 | 48.2 | 48.0 | 47.8 | 47.0 | 47.1 | 48.2 | 47.3 | 78.1 |  |  |  |  |  |  |  |  |
| PoEV1 | 49.5 | 49.5 | 49.9 | 50.2 | 49.8 | 49.1 | 49.2 | 49.5 | 49.3 | 47.2 | 47.0 |  |  |  |  |  |  |  |
| PoEV2 | 49.0 | 49.5 | 50.2 | 49.7 | 50.0 | 48.6 | 48.7 | 48.4 | 48.8 | 47.4 | 47.8 | 70.7 |  |  |  |  |  |  |
| **HCEV1** | 49.9 | 50.2 | 50.9 | 50.5 | 49.9 | 49.9 | 49.5 | 49.5 | 49.6 | 45.6 | 46.0 | 55.1 | 54.8 |  |  |  |  |  |
| YATV | 50.3 | 50.8 | 50.9 | 51.3 | 50.9 | 51.2 | 51.0 | 51.1 | 51.3 | 46.8 | 46.9 | 56.3 | 56.0 | 59.0 |  |  |  |  |
| NKCV | 51.1 | 51.4 | 51.1 | 50.9 | 50.9 | 50.0 | 49.9 | 50.3 | 50.5 | 47.1 | 46.4 | 56.4 | 56.6 | 58.6 | 59.8 |  |  |  |
| KOTV | 50.3 | 51.2 | 50.0 | 50.6 | 50.8 | 49.7 | 49.5 | 50.2 | 50.0 | 47.8 | 47.6 | 57.0 | 57.0 | 56.7 | 58.9 | 64.9 | 0 |  |
| KOOLV | 50.6 | 50.8 | 50.6 | 51.4 | 50.8 | 49.6 | 49.5 | 50.0 | 49.9 | 48.3 | 47.8 | 56.7 | 57.0 | 56.8 | 59.2 | 65.7 | 84.2 |  |

**Table 17.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of ephemerovirus N sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | BEFV | BRMV | KIMV | **AKSMV** | HgRTV2 | **KOKV** | PUCV | **HVV** | HYV | OBOV | ARV | PoEV1 | PoEV2 | **HCEV1** | YATV | NKCV | KOTV | KOOLV |
| BEFV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| BRMV | 91.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| KIMV | 77.3 | 77.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **AKSMV** | 76.3 | 76.8 | 94.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HgRTV2 | 75.6 | 76.6 | 93.5 | 97.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **KOKV** | 75.7 | 77.4 | 73.4 | 76.1 | 74.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PUCV | 75.6 | 77.5 | 73.6 | 75.5 | 75.0 | 96.2 |  |  |  |  |  |  |  |  |  |  |  |  |
| **HVV** | 72.3 | 74.5 | 71.9 | 73.6 | 73.1 | 89.4 | 87.7 |  |  |  |  |  |  |  |  |  |  |  |
| HYV | 75.4 | 77.0 | 74.1 | 76.2 | 75.5 | 94.8 | 95.1 | 87.7 |  |  |  |  |  |  |  |  |  |  |
| OBOV | 50.1 | 49.9 | 51.3 | 51.0 | 50.1 | 53.2 | 51.0 | 49.9 | 51.3 |  |  |  |  |  |  |  |  |  |
| ARV | 48.7 | 49.2 | 50.1 | 50.1 | 50.1 | 53.2 | 49.9 | 50.4 | 50.1 | 86.9 |  |  |  |  |  |  |  |  |
| PoEV1 | 46.6 | 47.5 | 49.4 | 50.1 | 49.9 | 49.9 | 50.8 | 48.9 | 49.4 | 43.3 | 44.0 |  |  |  |  |  |  |  |
| PoEV2 | 49.2 | 48.5 | 51.8 | 51.5 | 51.1 | 47.9 | 48.9 | 48.4 | 48.7 | 47.3 | 48.0 | 78.1 |  |  |  |  |  |  |
| **HCEV1** | 48.6 | 48.6 | 48.4 | 50.0 | 49.1 | 51.1 | 49.8 | 48.3 | 49.5 | 44.6 | 45.8 | 53.1 | 52.6 |  |  |  |  |  |
| YATV | 45.0 | 45.5 | 47.4 | 48.8 | 48.6 | 47.2 | 45.0 | 45.3 | 45.8 | 39.2 | 41.5 | 49.5 | 48.3 | 52.7 |  |  |  |  |
| NKCV | 50.6 | 51.1 | 53.0 | 52.7 | 52.7 | 53.5 | 53.7 | 51.9 | 53.2 | 46.1 | 47.3 | 61.2 | 60.3 | 57.6 | 51.0 |  |  |  |
| KOTV | 51.3 | 51.5 | 53.2 | 53.9 | 53.2 | 52.6 | 52.9 | 52.3 | 52.5 | 46.4 | 47.8 | 59.9 | 58.7 | 58.5 | 51.4 | 71.9 |  |  |
| KOOLV | 51.8 | 51.5 | 52.7 | 53.2 | 52.5 | 51.8 | 52.5 | 51.1 | 52.0 | 46.6 | 47.1 | 59.2 | 58.7 | 57.5 | 50.5 | 71.9 | 92.7 |  |

**Table 18.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of ephemerovirus G sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | BEFV | BRMV | KIMV | **AKSMV** | HgRTV2 | **KOKV** | PUCV | **HVV** | HYV | OBOV | ARV | PoEV1 | PoEV2 | **HCEV1** | YATV | NKCV | KOTV | KOOLV |
| BEFV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| BRMV | 75.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| KIMV | 48.1 | 47.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **AKSMV** | 46.2 | 47.5 | 73.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HgRTV2 | 47.3 | 48.6 | 75.1 | 85.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **KOKV** | 48.4 | 48.2 | 44.1 | 44.6 | 44.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| PUCV | 48.4 | 48.6 | 44.1 | 44.6 | 44.9 | 83.8 |  |  |  |  |  |  |  |  |  |  |  |  |
| **HVV** | 48.6 | 46.8 | 47.2 | 45.4 | 45.9 | 63.9 | 64.9 |  |  |  |  |  |  |  |  |  |  |  |
| HYV | 48.9 | 47.7 | 46.0 | 45.8 | 45.3 | 74.6 | 76.0 | 64.1 |  |  |  |  |  |  |  |  |  |  |
| OBOV | 28.0 | 28.3 | 27.4 | 27.5 | 27.1 | 26.6 | 26.9 | 27.2 | 27.5 |  |  |  |  |  |  |  |  |  |
| ARV | 28.9 | 28.2 | 25.4 | 25.8 | 25.4 | 26.3 | 27.0 | 27.7 | 27.6 | 68.6 |  |  |  |  |  |  |  |  |
| PoEV1 | 26.6 | 27.0 | 28.1 | 27.1 | 27.8 | 24.9 | 25.4 | 24.5 | 25.2 | 27.8 | 28.4 |  |  |  |  |  |  |  |
| PoEV2 | 25.9 | 26.9 | 25.2 | 28.1 | 26.9 | 25.4 | 26.5 | 25.4 | 24.2 | 27.5 | 29.4 | 59.9 |  |  |  |  |  |  |
| **HCEV1** | 31.8 | 31.8 | 29.9 | 30.9 | 29.6 | 30.1 | 30.3 | 27.7 | 29.6 | 29.8 | 29.1 | 36.3 | 37.0 |  |  |  |  |  |
| YATV | 29.5 | 29.9 | 29.8 | 30.0 | 29.7 | 29.1 | 29.3 | 29.1 | 29.3 | 29.1 | 27.6 | 33.1 | 34.0 | 40.6 |  |  |  |  |
| NKCV | 28.0 | 28.0 | 29.6 | 30.2 | 29.6 | 27.6 | 27.1 | 28.3 | 26.6 | 28.2 | 28.1 | 33.7 | 34.7 | 34.4 | 40.2 |  |  |  |
| KOTV | 29.0 | 28.6 | 30.0 | 30.3 | 30.3 | 28.1 | 27.5 | 26.9 | 26.5 | 27.4 | 27.4 | 34.7 | 37.0 | 34.9 | 39.1 | 59.0 |  |  |
| KOOLV | 29.1 | 28.3 | 29.8 | 29.9 | 29.8 | 26.8 | 26.6 | 26.5 | 25.9 | 27.2 | 26.5 | 33.4 | 37.0 | 35.9 | 38.5 | 61.4 | 80.0 |  |

**Table 19.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of betathriprhavirus L sequences.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | STRLV1 | **OlaRV2** | STRLV2 | **OlaRV3** |
| STRLV1 |  |  |  |  |
| **OlaRV2** | 69.6 |  |  |  |
| STRLV2 | 46.0 | 46.4 |  |  |
| **OlaRV3** | 46.6 | 47.0 | 51.2 |  |

**Table 20.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of betathriprhavirus N sequences.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | STRLV1 | **OlaRV2** | STRLV2 | **OlaRV3** |
| STRLV1 |  |  |  |  |
| **OlaRV2** | 72.3 |  |  |  |
| STRLV2 | 36.2 | 37.8 |  |  |
| **OlaRV3** | 40.7 | 40.6 | 51.5 |  |

**Table 21.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of betathriprhavirus G sequences.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | STRLV1 | **OlaRV2** | STRLV2 | **OlaRV3** |
| STRLV1 |  |  |  |  |
| **OlaRV2** | 62.2 |  |  |  |
| STRLV2 | 32.3 | 32.0 |  |  |
| **OlaRV3** | 33.1 | 34.2 | 36.1 |  |

**Table 22.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of alpharicinrhavirus L sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | TsTV | **HmarRV** | **ZyRTV1** | ZjRTV1 | NWMNV1 | ThRV2 | YbRTV1 | HbanRV | HpTV3 | HbTRV1 | GyRTV1 | BlTV2 | BCOV | DretRV1 | YsRTV2 | WhTV1 | HgRTV1 | NnRTV1 | ThRV1 |
| TsTV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **HmarRV** | 72.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **ZyRTV1** | 72.6 | 87.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ZjRTV1 | 45.2 | 46.1 | 46.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| NWMNV1 | 40.7 | 40.9 | 40.6 | 41.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ThRV2 | 39.9 | 40.3 | 40.1 | 41.0 | 79.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YbRTV1 | 38.5 | 38.5 | 37.8 | 38.1 | 48.7 | 48.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbanRV | 37.2 | 37.4 | 37.7 | 37.2 | 47.3 | 47.4 | 43.9 |  |  |  |  |  |  |  |  |  |  |  |  |
| HpTV3 | 37.0 | 37.5 | 37.5 | 36.7 | 47.5 | 47.2 | 44.0 | 82.5 | 100. |  |  |  |  |  |  |  |  |  |  |
| HbTRV1 | 37.3 | 37.2 | 36.8 | 37.5 | 45.6 | 44.9 | 43.3 | 41.3 | 41.8 |  |  |  |  |  |  |  |  |  |  |
| GyRTV1 | 36.5 | 37.6 | 37.0 | 37.7 | 45.9 | 45.6 | 42.8 | 41.8 | 41.1 | 66.2 |  |  |  |  |  |  |  |  |  |
| BlTV2 | 35.9 | 36.7 | 36.2 | 37.3 | 46.4 | 46.0 | 41.5 | 41.4 | 41.5 | 63.0 | 64.7 |  |  |  |  |  |  |  |  |
| BCOV | 36.0 | 36.8 | 37.1 | 37.0 | 45.5 | 45.8 | 42.4 | 41.9 | 42.2 | 55.3 | 55.8 | 56.5 |  |  |  |  |  |  |  |
| DretRV1 | 37.0 | 37.2 | 36.8 | 36.8 | 46.4 | 45.9 | 42.9 | 42.4 | 42.7 | 48.9 | 48.8 | 48.3 | 48.7 |  |  |  |  |  |  |
| YsRTV2 | 36.6 | 37.2 | 36.3 | 37.1 | 47.3 | 46.9 | 43.1 | 43.3 | 43.2 | 49.2 | 49.4 | 48.8 | 47.8 | 72.2 |  |  |  |  |  |
| WhTV1 | 37.1 | 36.5 | 36.2 | 36.1 | 45.7 | 45.4 | 42.1 | 41.8 | 41.8 | 48.8 | 47.5 | 47.2 | 46.7 | 63.4 | 64.0 |  |  |  |  |
| HgRTV1 | 37.5 | 38.0 | 37.9 | 39.1 | 49.6 | 49.5 | 44.9 | 42.6 | 42.8 | 48.9 | 50.0 | 48.7 | 48.1 | 49.7 | 51.3 | 50.5 |  |  |  |
| NnRTV1 | 38.0 | 38.9 | 38.1 | 39.2 | 50.0 | 49.3 | 45.0 | 44.1 | 44.1 | 50.2 | 50.3 | 50.3 | 48.4 | 50.2 | 51.3 | 49.7 | 66.0 |  |  |
| ThRV1 | 37.4 | 38.3 | 37.3 | 38.9 | 50.9 | 50.3 | 44.4 | 44.1 | 44.0 | 49.7 | 50.3 | 49.4 | 48.1 | 51.2 | 52.0 | 49.3 | 66.0 | 69.6 |  |

**Table 23.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of alpharicinrhavirus N sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | TsTV | **HmarRV** | **ZyRTV1** | ZjRTV1 | NWMNV1 | ThRV2 | YbRTV1 | HbanRV | HpTV3 | HbTRV1 | GyRTV1 | BlTV2 | BCOV | DretRV1 | YsRTV2 | WhTV1 | HgRTV1 | NnRTV1 | ThRV1 |
| TsTV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **ZyRTV1** | 68.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **HmarRV** | 69.2 | 88.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ZjRTV1 | 24.6 | 24.2 | 24.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| NWMNV1 | 18.8 | 17.3 | 17.9 | 19.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ThRV2 | 19.6 | 18.7 | 19.1 | 19.3 | 59.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YbRTV1 | 19.5 | 18.6 | 19.3 | 18.6 | 28.8 | 28.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbanRV | 19.8 | 20.5 | 19.7 | 19.6 | 22.7 | 22.3 | 23.3 |  |  |  |  |  |  |  |  |  |  |  |  |
| HpTV3 | 19.4 | 20.2 | 20.0 | 20.1 | 23.5 | 24.0 | 22.0 | 78.9 |  |  |  |  |  |  |  |  |  |  |  |
| HbTRV1 | 15.8 | 15.6 | 16.0 | 14.4 | 22.5 | 20.0 | 24.1 | 20.0 | 20.6 |  |  |  |  |  |  |  |  |  |  |
| GyRTV1 | 19.1 | 17.8 | 17.3 | 17.8 | 22.4 | 19.6 | 22.0 | 20.7 | 22.0 | 45.1 |  |  |  |  |  |  |  |  |  |
| BlTV2 | 17.0 | 15.2 | 15.9 | 15.9 | 21.5 | 20.2 | 21.3 | 22.8 | 23.3 | 41.1 | 41.4 |  |  |  |  |  |  |  |  |
| BCOV | 17.7 | 16.2 | 17.3 | 16.7 | 23.4 | 23.6 | 22.9 | 21.9 | 21.1 | 37.3 | 35.9 | 36.6 |  |  |  |  |  |  |  |
| DretRV1 | 18.6 | 17.3 | 17.5 | 17.4 | 24.1 | 24.2 | 24.0 | 22.5 | 22.1 | 28.4 | 28.8 | 29.0 | 28.5 |  |  |  |  |  |  |
| YsRTV2 | 18.1 | 17.0 | 17.4 | 17.8 | 25.2 | 24.0 | 23.6 | 20.2 | 20.9 | 26.7 | 26.6 | 26.2 | 27.1 | 67.9 |  |  |  |  |  |
| WhTV1 | 16.6 | 14.3 | 15.5 | 17.6 | 23.5 | 24.3 | 20.9 | 20.1 | 20.2 | 27.5 | 24.8 | 24.8 | 26.0 | 51.5 | 50.1 |  |  |  |  |
| HgRTV1 | 19.0 | 19.2 | 19.6 | 18.6 | 27.4 | 27.4 | 22.0 | 23.2 | 23.3 | 25.9 | 25.7 | 28.0 | 24.2 | 34.0 | 34.5 | 34.7 |  |  |  |
| NnRTV1 | 19.2 | 18.1 | 17.7 | 17.3 | 26.4 | 26.1 | 24.3 | 22.5 | 23.3 | 27.3 | 26.7 | 25.8 | 25.2 | 34.8 | 32.4 | 32.4 | 48.6 |  |  |
| ThRV1 | 19.6 | 17.9 | 18.3 | 18.8 | 26.1 | 25.8 | 22.2 | 22.3 | 21.9 | 25.1 | 24.0 | 23.9 | 24.3 | 32.9 | 32.3 | 31.4 | 46.8 | 55.8 |  |

**Table 24.** Percentage nucleotide identities of a CLUSTAL W alignment of lyssavirus N gene sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | IKOV | LLEBV | WCBV | SHIBV | LBV | MOKV | EBLV1 | IRKV | TWBLV | DUVV | **PBLV** | RABV | ABLV | GBLV | BBLV | ARAV | EBLV2 | KHUV | KBLV |
| IKOV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| LLEBV | 68.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WCBV | 62.6 | 63.6 | 100.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SHIBV | 60.8 | 65.0 | 67.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| LBV | 60.3 | 62.3 | 68.1 | 70.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| MOKV | 58.5 | 61.0 | 64.3 | 69.9 | 69.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| EBLV1 | 58.8 | 60.0 | 63.5 | 64.3 | 67.8 | 62.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| IRKV | 58.2 | 60.5 | 62.6 | 66.6 | 62.9 | 62.6 | 73.0 | 1 |  |  |  |  |  |  |  |  |  |  |  |
| TWBLV | 58.3 | 57.3 | 63.2 | 64.4 | 63.4 | 61.8 | 73.0 | 74.0 |  |  |  |  |  |  |  |  |  |  |  |
| DUVV | 57.5 | 60.2 | 66.0 | 66.4 | 65.0 | 64.0 | 74.3 | 71.7 | 71.9 | 10 |  |  |  |  |  |  |  |  |  |
| **PBLV** | 59.6 | 60.9 | 64.5 | 65.4 | 65.5 | 61.6 | 71.4 | 68.3 | 70.3 | 69.8 |  |  |  |  |  |  |  |  |  |
| RABV | 56.8 | 59.1 | 63.8 | 64.9 | 64.6 | 62.9 | 67.0 | 66.0 | 67.0 | 65.9 | 66.2 |  |  |  |  |  |  |  |  |
| ABLV | 55.3 | 61.7 | 65.0 | 65.6 | 65.7 | 62.9 | 70.7 | 68.8 | 69.0 | 70.3 | 70.6 | 72.7 |  |  |  |  |  |  |  |
| GBLV | 55.5 | 57.9 | 62.8 | 63.4 | 62.6 | 61.0 | 70.6 | 67.1 | 67.5 | 69.9 | 69.4 | 71.9 | 75.7 |  |  |  |  |  |  |
| BBLV | 56.2 | 56.7 | 62.0 | 66.7 | 65.3 | 60.7 | 70.1 | 68.4 | 66.8 | 68.0 | 69.7 | 66.9 | 73.1 | 70.4 |  |  |  |  |  |
| ARAV | 57.9 | 59.0 | 64.8 | 66.9 | 67.4 | 65.8 | 72.4 | 69.9 | 69.3 | 72.2 | 70.5 | 67.3 | 70.0 | 72.1 | 73.4 |  |  |  |  |
| EBLV2 | 56.9 | 58.1 | 63.9 | 63.0 | 61.5 | 59.3 | 69.2 | 70.6 | 67.7 | 68.4 | 66.8 | 65.7 | 69.6 | 69.7 | 73.3 | 70.6 |  |  |  |
| KHUV | 57.9 | 58.6 | 60.7 | 64.1 | 64.4 | 58.3 | 71.5 | 69.0 | 66.0 | 68.6 | 67.4 | 67.4 | 71.4 | 71.7 | 75.4 | 74.3 | 75.5 |  |  |
| KBLV | 57.6 | 56.7 | 63.1 | 64.6 | 64.3 | 62.1 | 70.5 | 70.6 | 67.3 | 69.0 | 67.6 | 68.1 | 71.7 | 72.0 | 73.5 | 74.6 | 74.7 | 77.6 |  |

**Table 25.** Percentage nucleotide identities of a CLUSTAL W alignment of lyssavirus concatenated N+P+M+G+L coding sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | IKOV | LLEBV | WCBV | SHIBV | LBV | MOKV | EBLV1 | IRKV | TWBLV | DUVV | **PBLV** | RABV | ABLV | GBLV | BBLV | ARAV | EBLV2 | KHUV | KBLV |
| IKOV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| LLEBV | 62.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WCBV | 48.2 | 50.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SHIBV | 49.0 | 50.9 | 54.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| LBV | 47.4 | 47.8 | 53.3 | 67.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| MOKV | 47.6 | 47.9 | 52.8 | 65.1 | 68.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| EBLV1 | 47.2 | 47.8 | 52.7 | 58.4 | 58.6 | 57.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| IRKV | 45.8 | 48.7 | 52.7 | 58.9 | 57.6 | 58.2 | 71.7 |  |  |  |  |  |  |  |  |  |  |  |  |
| TWBLV | 47.0 | 47.7 | 51.6 | 57.9 | 57.4 | 56.3 | 69.8 | 67.9 |  |  |  |  |  |  |  |  |  |  |  |
| DUVV | 46.9 | 47.4 | 53.5 | 57.5 | 57.2 | 57.0 | 71.5 | 68.4 | 66.3 |  |  |  |  |  |  |  |  |  |  |
| **PBLV** | 46.9 | 48.5 | 52.2 | 58.6 | 58.3 | 57.3 | 70.1 | 67.6 | 67.5 | 67.1 |  |  |  |  |  |  |  |  |  |
| RABV | 45.7 | 46.9 | 51.4 | 56.5 | 55.7 | 55.7 | 64.6 | 63.9 | 62.0 | 63.4 | 62.6 |  |  |  |  |  |  |  |  |
| ABLV | 47.0 | 48.0 | 52.2 | 57.9 | 57.6 | 57.2 | 66.9 | 65.8 | 64.1 | 64.6 | 64.4 | 67.8 |  |  |  |  |  |  |  |
| GBLV | 46.7 | 48.7 | 52.4 | 57.8 | 57.9 | 57.2 | 67.1 | 65.4 | 63.8 | 64.7 | 64.6 | 71.2 | 72.4 |  |  |  |  |  |  |
| BBLV | 46.6 | 47.3 | 51.7 | 59.1 | 57.6 | 56.9 | 68.1 | 67.4 | 65.3 | 66.6 | 66.1 | 66.2 | 70.9 | 69.9 |  |  |  |  |  |
| ARAV | 47.1 | 46.6 | 53.2 | 58.2 | 58.2 | 57.4 | 70.2 | 68.1 | 66.5 | 67.2 | 66.7 | 66.0 | 69.5 | 69.6 | 71.6 |  |  |  |  |
| EBLV2 | 47.5 | 46.1 | 52.6 | 58.1 | 56.8 | 56.6 | 68.2 | 67.4 | 65.1 | 67.1 | 65.3 | 65.8 | 70.0 | 69.3 | 74.3 | 72.4 |  |  |  |
| KHUV | 46.6 | 48.2 | 52.3 | 57.7 | 57.7 | 55.9 | 69.0 | 68.4 | 65.5 | 67.2 | 65.7 | 66.8 | 70.9 | 70.3 | 74.7 | 73.3 | 75.4 |  |  |
| KBLV | 47.8 | 47.1 | 52.3 | 58.2 | 58.2 | 57.6 | 69.4 | 68.4 | 66.4 | 67.3 | 66.1 | 67.6 | 71.8 | 71.8 | 75.8 | 73.2 | 76.8 | 76.8 |  |