

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

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| **Code assigned:** | ***2023.015M*** |  |
| **Short title:** Create17 new species in the subfamily *Alpharhabdovirinae* (*Mononegavirales*: *Rhabdoviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| ICTV *Rhabdoviridae* Study Group |

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

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| One proposed new species was deleted due to sequence similarity members of another proposed new species. Corrected in the final proposal. |

**ICTV Study Group votes on proposal**

|  |  |  |  |
| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| ICTV *Rhabdoviridae* Study Group | 13 | o | 1 |

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

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

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

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | June 23, 2023 |
| Date of this revision (if different to above) |  |

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

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

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| N/A |

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

**Name of accompanying Excel module**

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| 2023.015M.N.v1.Alpharhabdovirinae\_17nsp.xlsx |

**Abstract**

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| In the subfamily *Alpharhabdovirinae,* we propose the creation of 17 new species: three in the genus *Merhavirus*, one in the genus *Ohlsrhavirus,* one in the genus *Amplylivirus*, and twelve in the genus *Alpharicinrhavirus*. Members of each of the proposed new species have been detected by metagenomic sequencing of vertebrates or invertebrates to obtain complete coding sequences. Each meets the demarcation criteria established for each genus. |

**Text of proposal**

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| --- | --- |
| |  | | --- | | 1. **Create three new species in the genus *Merhavirus***   Formosus virus (FORMV; sample U30) was detected by metagenomic sequencing of mosquitoes (*Aedes aegypti*) from a laboratory colony originating from Bundibugyo, Uganda [1]. We propose FORMV be assigned to the new species *Merhavirus formosus.*  Hattula rhabdovirus (HTTRV; sample FIN/PK-2018/62) was detected by metagenomic sequencing of mosquitoes (*Ochlerotatus communis*) collected in Ilomantsi, Finland, in 2015. The virus was also detected in mosquitoes of two other species (*O. pullatus* and *O. hexodontus*) from the same region of eastern Finland in 2015 [5]. We propose HTTRV be assigned to the new species *Merhavirus hattula.*  Inari rhabdovirus (INARV; sample FIN/L-2018/84) was detected by metagenomic sequencing of mosquitoes (*Ochlerotatus communis*) collected in Lappi, Finland, in 2015 [5]. We propose INARV be assigned to the new species *Merhavirus inari.*  Genome organizations  The near-complete genome sequences of FORMV (12,151 nt), HTTRV (11,971 nt) and INARV (12,040 nt) are available, lacking only extreme 3' and 5' termini. The genome organizations are similar to those of other merhaviruses, containing only the putative five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*) (**Figure 1**).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, FORMV, HTTRV and INARV cluster with the merhaviruses in a distinct and well-supported monophyletic clade (**Figure 3**).  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGAX from ClustalW amino acid sequence alignments indicated that FORMV and INARV are most closely related in N (47.5% identity), and that HTTRV and INARV are the most closely related in L (67.0% identity) and G (53.2% identity) (**Tables 1-3**).  Ecology  Merhaviruses have been detected exclusively in culicine mosquitoes (Cluicidae). Merida virus (MERDV; species *Merhavirus merida*) in *Culex* spp. and *Ochlerotatus* spp. mosquitoes collected in Mexico, USA, and Turkey. Culex *tritaeniorhynchus* rhabdovirus (CTRV: species *Merhavirus tritaeniorhynchus*) was isolated from *Culex* sp. mosquitoes collected in Japan. The viruses to be assigned to the three new species have also been detected in culicine mosquitoes, extending the geographic range to Uganda and Finland.  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 members of the new genus meet demarcation criteria A, B, and C. The genome organisations do not vary significantly. Neutralization tests have not been conducted as there are currently no isolates of these viruses (criterion E). FORMV has been detected in a novel geographic location and mosquitoes of a novel species. HTTRV and INARV have each been detected in mosquitoes of the same species and geographic location, each of which is novel (criterion F).   1. **Create one new species in the genus *Ohlsrhavirus***   Adumi virus (ADUMV; sample Ug2012-CVR1) was detected by metagenomic sequencing of mosquitoes (species not recorded) collected in Uganda in 2012. We propose to assign ADUMV to the new species *Ohlsrhavirus adumi*.  Genome organization  The near-complete genome sequence of ADUMV (11,727 nt) has been determined, including complete coding sequences but incomplete 3' and 5' termini. The ADUMV genome is similar in organisation to that of other ohlsrhaviruses, containing only the putative five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*) (**Figure 1**).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, ADUMV clusters with the other known ohlsrhaviruses in a distinct and well-supported monophyletic clade and is most closely related to Culex rhabdo-like virus Los Angeles (CRLVLA; species *Ohlsrhavirus angeles*) (**Figure 3**).  Amino acid sequence identities  ADUMV is most closely related to CRLVLA in amino acid sequence with identity in pair-wise alignments (p-distances) is 58.2% in N, 67.9% in L and 40.0% in G **(Tables 4-6).**  Ecology  All eight currently assigned ohlsrhaviruses were isolated from or detected in culicine mosquitoes (*Culex* spp., *Ochlerotatus* spp. or *Psorophora* sp.) from Europe, Asia, Australia and the Americas. ADUMV has also been detected in mosquitoes of undetermined species, extending the geographic range to Africa.    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.  ADUMV meets demarcation criteria A, B and C. ADUMV has a similar genome organization to other ohlsrhaviruses (criterion D). Neutralisation tests (criterion E) have not been conducted as no virus isolate is currently available. The species of mosquito in which ADUMV was detected has not been identified but uniquely amongst known ohlsrhaviruses, the mosquitoes were collected in Africa (criterion F).   1. **Create one new species in the genus *Amplylivirus***   Boana pugnax lyssa-like virus 1 (BpugLLV1; strain Antioquia) was detected in Chirique-Flusse tree frogs (*Boana pugnax*) collected in Colombia, in 2016. We propose BpugLLV1 be assigned to the new species *Amplylivirus pugnax.*  Genome organization  The near-complete genome sequence of BpugLLV1 (12,482 nt) is available, lacking only extreme 3' and 5' termini. The genome organization is similar to that of the only existing member of the genus, frog lyssa-like virus 1 (FLLV1; species *Amplylivirus cinereus*), containing only the putative five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*) (**Figure 1**).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, BpugLLV1 clusters with FLLV1 in a distinct and well-supported monophyletic clade (**Figure 3**).  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGAX from ClustalW amino acid sequence alignments indicated that BpugLLV1 and FLLV1 share 45.6% identity in N, 51.5% identity in L, and 30.7% identity in G.  Ecology  FLLV1 was identified in the brain of the American green tree frog (*Hyla cinerea* or *Dryophytes cinereus* in different classifications) collected in the USA in 2016. BpugLLV1 was detected in frogs of a different genus and different geographic location.  Species demarcation criteria  According to current criteria, viruses assigned to different species within the genus *Amplylivirus* 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 neutralisation tests; and E) 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 organisations do not vary significantly. Neutralization tests have not been conducted as there are currently no isolates of these viruses (criterion D). BpugLLV1 has been detected in a novel geographic location and frogs of a novel genus (criterion E).   1. **Create 12 new species in the genus *Alpharicinrhavirus***   Zhangjaikou rhabd tick virus 1 (ZjRTV1; sample TIGMIC7) was detected by metagenomic sequencing of hard ticks (*Dermacentor silvarum*) collected in Inner Mongolia, China, in 2018 (BioProject PRJNA841744). We propose ZjRTV1 be assigned to the new species *Alpharicinrhavirus zhangjiakou.*  Taishun tick virus (TsTV; sample BL198)was detected by metagenomic sequencing in East Asian mountain haemaphysalid ticks (*Haemaphysalis hystricis*) collected in Zhejiang Province, China, in 2013 [4]. It was also detected in hard ticks (*Hyalomma asiaticum*, *Dermacentor marginatus* and *Hyalomma detritum*) collected in China, in 2017, and in hard ticks (*Hyalomma scupense*) collected in the Kharabali district, Astrakhan, Russia, in 2018. We propose TsTV be assigned to the new species *Alpharicinrhavirus taishun.*  Norway mononegavirus 1 (NWMV1; sample NOR/H3/Skanevik/2014) was detected by metagenomic sequencing in hard ticks (*Ixodes ricinus*) collected in Skanevik, Norway, in 2014 [2]. It was also detected in ticks of the same species in Bronnoya, Norway, in the same year and has been reported to be endogenous in the IRE/CTVM19 tick (*Ixodes ricinus*) cell line (unpublished). We propose NWMV1 be assigned to the new species *Alpharicinrhavirus skanevik.*  Yanbian rhabd tick virus 1 (YbRTV1; sample TIGMIC4) was detected by metagenomic sequencing in taiga ticks (*Ixodes persulcatu*) collected in Jilin Province, China, in 2014 (BioProject PRJNA841744). We propose YbRTV1 be assigned to the new species *Alpharicinrhavirus jilin.*  Haemaphysalis bancrofti rhabdovirus (HbanRV; sample K23) was detected by metagenomic sequencing in wallaby ticks (*Haemaphysalis bancrofti*) collected in Australia, in 2020. We propose HbanRV be assigned to the new species *Alpharicinrhavirus bancrofti.*  Huangpi tick virus 3(HpTV3; sample H124-2) was detected by metagenomic sequencing in Doenitz' Oriental-Australian bird baemaphysalid ticks (*Haemaphysalis doenitzi*) collected in the Huangpi District of Wuhan, Hubei Province, China, in 2012 [4]. We propose HpTV3 be assigned to the new species *Alpharicinrhavirus huangpi.*  Tahe rhabdovirus 1 (ThRV1; sample NE-TH2) was detected by metagenomic sequencing in relict ticks (*Haemaphysalis concinna*) collected in Tahe, Heilongjiang Province, China, in 2021. The virus was also detected in hard ticks (*Dermacentor silvarum* and *Haemaphysalis japonica*) collected in Jilin Province, China, in 2020 and 2021. Yanbian rhabd tick virus 4 (YbRTV4; sample TIGMIC5) was detected by metagenomic sequencing in hard ticks (*Haemaphysalis japonica*) collected in Jilin Province, China, in 2019 (BioProject PRJNA841744). It is almost identical to ThRV1 in sequence and is considered to be an isolate of the same virus. Yanbian rhabd tick virus 5 (YbRTV5; sample TIGMIC, reported as detected in hard ticks (*Haemaphysalis concinna*) in Jilin Province, China, in 2019 (BioProject PRJNA841744), is also very closely related to ThRV1 and is considered to be an isolate of the same virus (see below). We propose ThRV1 be assigned to the new species *Alpharicinrhavirus tahe.*  Nanning rhabd tick virus 1 (NnRTV1; sample TIGMIC1) was detected by metagenomic sequencing in Asian monitor lizard ticks (*Amblyomma varanense*) collected in Guangxi Province, China, in 2019 (BioProject PRJNA841744). We propose NnRTV1 be assigned to the new species *Alpharicinrhavirus nanning.*  Huanggang rhabd tick virus 1 (HgRTV1; sample TIGMIC22) was detected by metagenomic sequencing in hard ticks (*Rhipicephalus microplus*) collected from cattle in Hubei Province, China, in 2019 (BioProject PRJNA841744). We propose HgRTV1 be assigned to the new species *Alpharicinrhavirus huanggang.*  Dermacentor reticulatus rhabdovirus 1 (DretRV1; sample CT3) was detected by metagenomic sequencing in ornate cow ticks (*Dermacentor reticulatus*) collected in Croatia, in 2012. We propose DretRV1 be assigned to the new species *Alpharicinrhavirus reticulatis* [3].  Yushu rhabd tick virus 2 (YsRTV2; sample TIGMIC1) was detected by metagenomic sequencing in hard ticks (*Dermacentor everestianus*) collected from cattle in Qinghai Province, China, in 2018 (BioProject PRJNA841744). We propose YsRTV2 be assigned to the new species *Alpharicinrhavirus qinghai.*  Guyuan rhabd tick virus 1 (GyRTV1; sample TIGMIC3) was detected by metagenomic sequencing in hard ticks (*Haemaphysalis japonica*) collected from sheep in Ningxia Hui Autonomous Region, China, in 1905 (BioProject PRJNA841744). We propose GyRTV1 be assigned to the new species *Alpharicinrhavirus ningxia.*  Genome organizations  The near-complete genome sequences of ZjRTV1 (10,716 nt), TsTV (11,280 nt), NWMV1 (12,040 nt), YbRTV1 (10,366 nt), HbanRV (13,109 nt), HpTV3 (13,169 nt), ThRV1 (11,349 nt), NnRTV1 (11,408 nt), HgRTV1 (11,556 nt), DretRV1 (10,313 nt), YsRTV2 (10,456 nt) and GyRTV1 (11,578 nt) are available, lacking only extreme 3' and 5' termini (**Figure 2**). The genome compositions are similar to those of the four currently classified alpharicinrhaviruses: Wuhan tick virus 1 (WhTV1; species *Alpharicinrhavirus wuhan*), Blanchseco virus (BCOV; species *Alpharicinrhavirus blanchseco*); Hubei tick rhabdovirus 1 (HbTRV1; species *Alpharicinrhavirus hubei*), and Bole tick virus 2 (BlTV2; species *Alpharicinrhavirus bole*). They contain either four or five of the putative canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*). Most contain all five of these genes but as previously observed for WhTV1, five of the newly proposed viruses (ZjRTV1, TsTV, TbRTV1, DretRV1 and YsRTV2) lack the *G* gene. Viruses lacking the *G* gene are not uncommon in ticks. Additional overlapping ORFs occur commonly in most of these viruses, either commencing close to the start of the structural protein ORFs or of significant length, suggesting that they may have the potential to be expressed.  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, all viruses proposed for classification cluster with the alpharicinrhaviruses in a distinct and well-supported monophyletic clade (**Figure 3**).  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGAX from ClustalW amino acid sequence alignments indicated that HbanRV and HpTV3 are the most closely related in sequence of the viruses to be assigned to new species, sharing 78.9% identity in N, 82.5% identity in L and 90.8% identity in G (**Tables 7-9**). The close relationships between the ThRV1, YbRTV4 and YbRTV5 are also shown. ThRV1 and YbRTV4 share 99.6-100% amino acid sequence identity in the N, L and G; YbRTV5 also displays low levels of sequence divergence with ThRV1 and YbRTV4, below that required for assignment to a separate species (see below) (**Tables 7-9**).  Ecology  Alpharicinrhaviruses have been detected exclusively in hard ticks (Ixodidae). Viruses assigned already to species were detected in hard ticks of two species (*Hyalomma asiaticum* or *Rhipicephalus microplus*) from China or in hard ticks (*Amblyomma ovale)* from Trinidad*.* All but one of the newly proposed viruses have been detected in hard ticks of various species in China; NWMV1 was detected in hard ticks (*Ixodes ricinus*) in Norway and in a cell line from the same tick species in Russia.  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.  All proposed members of the new genus, except for HbanRV and HpTV3, meet demarcation criteria A, B and C. The level of sequence identity between the G proteins of HbanRV and HpTV3 is surprisingly high (90.8%) which exceeds the level of identity defined in the demarcation criterion C. These two viruses have similar genome organisations but HbanRV has alternative ORFs in the *P* and *G* genes whereas HpTV3 has alternative ORFs in the *M* and *G* genes (criterion D). As there are no isolates of these viruses, cross-neutralization data are not available (criterion E). They were detected in ticks of the same genus but different species in China, in two relatively distant provinces: Hubei and Jilin (criterion F). On balance, HbanRV and HpTV3 have a sufficient level of demarcation to be classified to separate species.  Sequence divergence between YbRTV5 and ThRV1/YbRTV4 is insufficient for assignment to separate species. Although N protein divergence (15.2%) is above the required threshold, divergence in G (9.2%) and L (6.6%) fall well below the threshold for species demarcation.  Other viruses are adequately divergent in the *N*, *L* and *G* genes to justify classification to separate species.  Other likely alpharicinrhaviruses  Several other viruses detected by metagenomic sequencing of hard ticks from China also cluster phylogenetically with the alpharicinrhaviruses but are not proposed for taxonomic classification due either to incomplete or corrupted genome coding sequences, or very high levels of sequence identity to viruses that have already been classified. These include Guandong tick Manly virus (Genbank OM264164), Qingyang rhabd tick virus 1 (Genbank ON746522). Zhangjiakou rhabd tick virus 2 (Genbank ON746533), Tongren rhabd tick virus 3 (Genbank ON746535) and Zhanhye rhabd tick virus 1 (Genbank ON746538).  Comment  As proposed, the genus *Alpharicinrhavirus*, although clearly monophyletic based on L protein sequences and comprised entirely of viruses detected in hard ticks, incorporates quite significant sequence diversity. It is possible that further discoveries may present the need to split the genus, should viruses with inconsistent ecology or genome organization intervene in the phylogeny. However, at this point, inclusion in a single genus appears to be well justified. | |

**Supporting evidence**

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**Figure 1.** Schematic representation of merhavirus, ohlsrhavirus and amplylivirus (-) ssRNA genomes shown in reverse polarity. N, P, M, G and L represent ORFs encoding the structural proteins. The viruses representing proposed new species are listed in red text.

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**Figure 2.** Schematic representation of alpharicinrhavirus (-) ssRNA genomes shown in reverse polarity. N, P, M, G and L represent open reading frames (ORFs) encoding the structural proteins. Additional overlapping ORFs shown in grey commence close to the start of the structural protein ORFs or are of significant length, suggesting that they may have the potential to be expressed. Viruses representing proposed new species are listed in red text.

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**Figure 3.** The evolutionary history was inferred from a MAFFT alignment of complete L protein sequences of 207 rhabdoviruses that are currently assigned to species in the subfamily *Alpharhabdovirinae*, 17 viruses (shown in bold red) to be assigned to new species in the genera *Merhavirus*, *Ohlsrhavirus*, *Amplylivirus* and *Alpharicinrhavirus*. Also included are YbTRV5 (shown in green) which is not proposed for species assignment (see above) and two unclassified insect viruses (shown in blue) that lie phylogenetically between the two genera *Merhavirus* and *Ohlsrhavirus*, each of which included members that have been detected only in mosquitoes. Viruses already assigned to species are shown in black. Phylogenetically informative sites were selected from the alignment using TrimAl resulting in 1650 positions in the final dataset. The tree was inferred in MEGAX 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 (-413344.33) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Several genera have been condensed together into single branches. Bootstrap values (100 iterations) are shown for each node.

**Table 1.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of merhavirus N protein sequences.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | MERDV | CTRV | **FORMV** | **INARV** | **HTTRV** |
| MERDV | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| CTRV | 25.1 | 100.0 | 100.0 | 100.0 | 100.0 |
| **FORMV** | 22.5 | 22.1 | 100.0 | 100.0 | 100.0 |
| **INARV** | 20.3 | 22.5 | 47.5 | 100.0 | 100.0 |
| **HTTRV** | 19.3 | 22.0 | 26.7 | 25.6 | 100.0 |

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | MERDV | CTRV | **FORMV** | **INARV** | **HTTRV** |
| MERDV |  |  |  |  |  |
| CTRV | 43.7 |  |  |  |  |
| **FORMV** | 38.5 | 38.0 |  |  |  |
| **INARV** | 37.8 | 37.9 | 49.9 |  |  |
| **HTTRV** | 39.1 | 38.1 | 50.6 | 67.0 |  |

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | MERDV | CTRV | **FORMV** | **INARV** | **HTTRV** |
| MERDV |  |  |  |  |  |
| CTRV | 38.5 |  |  |  |  |
| **FORMV** | 23.4 | 21.7 |  |  |  |
| **INARV** | 22.4 | 22.5 | 40.9 |  |  |
| **HTTRV** | 23.6 | 22.3 | 39.7 | 53.2 |  |

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

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | LOBV | OHLDV | CRLVLA | **ADUMV** | RISV | CRLV | NORCV | TCHV1 | CpRLV |
| LOBV |  |  |  |  |  |  |  |  |  |
| OHLDV | 46.2 |  |  |  |  |  |  |  |  |
| CRLVLA | 47.1 | 53.2 |  |  |  |  |  |  |  |
| **ADUMV** | 44.8 | 51.6 | 58.2 |  |  |  |  |  |  |
| RISV | 44.4 | 49.7 | 52.0 | 53.1 |  |  |  |  |  |
| CRLV | 48.7 | 51.6 | 58.3 | 57.7 | 52.4 |  |  |  |  |
| NORCV | 48.4 | 50.1 | 56.6 | 56.4 | 51.6 | 88.1 |  |  |  |
| TCHV1 | 47.3 | 54.0 | 59.7 | 57.0 | 56.1 | 78.9 | 76.9 |  |  |
| CpRLV | 49.2 | 52.0 | 58.5 | 57.9 | 50.1 | 80.2 | 78.1 | 77.8 |  |

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

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | LOBV | OHLDV | CRLVLA | **ADUMV** | RISV | CRLV | NORCV | TCHV1 | CpRLV |
| LOBV |  |  |  |  |  |  |  |  |  |
| OHLDV | 59.3 |  |  |  |  |  |  |  |  |
| CRLVLA | 57.7 | 62.5 |  |  |  |  |  |  |  |
| **ADUMV** | 55.8 | 62.0 | 67.9 |  |  |  |  |  |  |
| RISV | 58.5 | 68.0 | 66.9 | 66.4 | 1 |  |  |  |  |
| CRLV | 57.0 | 63.4 | 66.4 | 65.9 | 66.3 |  |  |  |  |
| NORCV | 56.6 | 62.5 | 65.6 | 64.7 | 65.9 | 90.8 |  |  |  |
| TCHV1 | 57.0 | 64.2 | 66.2 | 66.1 | 67.2 | 90.0 | 87.8 |  |  |
| CpRLV | 57.4 | 63.7 | 66.8 | 66.0 | 67.5 | 87.3 | 85.6 | 88.3 |  |

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

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | LOBV | OHLDV | CRLVLA | **ADUMV** | RISV | CRLV | NORCV | TCHV1 | CpRLV |
| LOBV |  |  |  |  |  |  |  |  |  |
| OHLDV | 26.1 |  |  |  |  |  |  |  |  |
| CRLVLA | 28.0 | 26.8 |  |  |  |  |  |  |  |
| **ADUMV** | 28.3 | 26.5 | 40.0 |  |  |  |  |  |  |
| RISV | 27.2 | 27.9 | 43.6 | 39.1 |  |  |  |  |  |
| CRLV | 26.8 | 29.3 | 39.3 | 37.9 | 39.6 |  |  |  |  |
| NORCV | 26.2 | 26.0 | 37.9 | 37.5 | 36.5 | 68.0 |  |  |  |
| TCHV1 | 27.4 | 26.7 | 37.3 | 38.6 | 36.3 | 57.1 | 57.7 |  |  |
| CpRLV | 28.7 | 28.1 | 38.3 | 37.9 | 37.1 | 55.7 | 54.0 | 54.0 |  |

**Table 7.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of alpharicinrhavirus N protein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **ZjRTV1** | **YbRTV1** | **HpTV3** | **HbanRV** | **ThRV1** | YbRTV4\* | YbRTV5\* | **NnRTV1** | **HgRTV1** | WhTV1 | **YsRTV2** | **DretRV1** | BCOV | BlTV2 | HbTRV1 | **GyRTV1** | **NWMV1** | **TsTV** |
| **ZjRTV1** | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| **YbRTV1** | 18.6 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| **HpTV3** | 19.8 | 22.3 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| **HbanRV** | 19.3 | 23.3 | 78.9 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| **ThRV1** | 19.3 | 21.9 | 22.6 | 22.7 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| YbRTV4 | 19.3 | 21.9 | 22.6 | 22.7 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| YbRTV5 | 19.1 | 22.6 | 21.7 | 22.1 | 84.8 | 84.8 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| **NnRTV1** | 17.4 | 23.7 | 24.1 | 23.1 | 55.8 | 55.8 | 55.1 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| **HgRTV1** | 19.0 | 21.5 | 24.1 | 23.6 | 46.8 | 46.8 | 46.8 | 48.8 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| WhTV1 | 17.9 | 20.4 | 20.9 | 20.8 | 31.1 | 31.1 | 31.8 | 32.0 | 34.1 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| **YsRTV2** | 17.9 | 22.9 | 21.3 | 20.4 | 32.0 | 32.0 | 32.7 | 32.2 | 34.1 | 50.1 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| **DretRV1** | 17.3 | 23.4 | 23.0 | 23.1 | 32.6 | 32.6 | 32.6 | 34.8 | 33.3 | 51.5 | 67.9 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| BCOV | 16.7 | 22.7 | 20.9 | 21.7 | 24.4 | 24.4 | 24.7 | 25.5 | 24.9 | 25.4 | 27.3 | 28.1 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| BlTV2 | 16.4 | 21.7 | 23.5 | 23.2 | 23.9 | 23.9 | 24.3 | 25.6 | 27.6 | 24.9 | 26.4 | 28.8 | 36.6 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| HbTRV1 | 14.9 | 23.8 | 20.4 | 20.4 | 25.1 | 25.1 | 24.9 | 27.1 | 24.9 | 26.9 | 26.5 | 28.4 | 37.3 | 41.1 | 100.0 | 100.0 | 100.0 | 100.0 |
| **GyRTV1** | 18.6 | 21.6 | 22.6 | 21.3 | 24.3 | 24.3 | 24.1 | 26.5 | 25.7 | 25.2 | 26.6 | 28.5 | 35.9 | 41.4 | 45.1 | 100.0 | 100.0 | 100.0 |
| **NWMV1** | 20.2 | 28.4 | 24.3 | 22.9 | 25.5 | 25.5 | 24.8 | 25.9 | 26.2 | 22.8 | 24.2 | 23.5 | 23.4 | 21.4 | 22.2 | 23.0 | 100.0 | 100.0 |
| **TsTV** | 24.7 | 19.2 | 20.0 | 19.7 | 19.5 | 19.5 | 20.0 | 19.2 | 18.8 | 17.1 | 17.8 | 18.1 | 18.0 | 17.6 | 16.0 | 19.5 | 18.8 | 100.0 |

\* Considered to be variants of ThRV1.

**Table 8.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of alpharicinrhavirus L protein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **ZjRTV1** | **YbRTV1** | **HpTV3** | **HbanRV** | **ThRV1** | YbRTV4\* | YbRTV5\* | **NnRTV1** | **HgRTV1** | WhTV1 | **YsRTV2** | **DretRV1** | BCOV | BlTV2 | HbTRV1 | **GyRTV1** | **NWMV1** | **TsTV** |
| **ZjRTV1** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **YbRTV1** | 38.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **HpTV3** | 37.2 | 44.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **HbanRV** | 37.8 | 43.8 | 82.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **ThRV1** | 39.2 | 44.5 | 43.8 | 43.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YbRTV4\* | 39.2 | 44.5 | 43.8 | 43.8 | 99.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YbRTV5\* | 39.4 | 44.4 | 43.8 | 43.8 | 93.5 | 93.4 |  |  |  |  |  |  |  |  |  |  |  |  |
| **NnRTV1** | 39.5 | 45.1 | 43.8 | 43.8 | 69.6 | 69.6 | 70.2 |  |  |  |  |  |  |  |  |  |  |  |
| **HgRTV1** | 39.4 | 44.7 | 42.8 | 42.3 | 66.0 | 66.0 | 66.0 | 66.0 |  |  |  |  |  |  |  |  |  |  |
| WhTV1 | 36.2 | 41.9 | 41.8 | 41.5 | 49.3 | 49.2 | 49.2 | 49.7 | 50.5 |  |  |  |  |  |  |  |  |  |
| **YsRTV2** | 37.6 | 42.9 | 43.1 | 43.2 | 52.0 | 52.0 | 52.3 | 51.3 | 51.3 | 64.0 |  |  |  |  |  |  |  |  |
| **DretRV1** | 36.9 | 42.8 | 42.8 | 42.5 | 51.2 | 51.2 | 51.5 | 50.2 | 49.7 | 63.4 | 72.2 |  |  |  |  |  |  |  |
| BCOV | 37.1 | 42.4 | 42.3 | 41.9 | 48.0 | 48.0 | 47.9 | 48.4 | 48.2 | 46.7 | 47.9 | 48.6 |  |  |  |  |  |  |
| BlTV2 | 37.5 | 41.6 | 41.4 | 41.3 | 49.3 | 49.2 | 49.2 | 50.2 | 48.6 | 47.1 | 48.7 | 48.3 | 56.5 |  |  |  |  |  |
| HbTRV1 | 37.7 | 43.1 | 42.1 | 41.6 | 49.6 | 49.7 | 49.5 | 50.1 | 48.8 | 48.6 | 49.1 | 48.8 | 55.3 | 63.0 |  |  |  |  |
| **GyRTV1** | 37.9 | 42.9 | 41.3 | 41.9 | 50.4 | 50.3 | 50.2 | 50.1 | 49.8 | 47.4 | 49.3 | 48.9 | 55.8 | 64.7 | 66.2 |  |  |  |
| **NWMV1** | 41.1 | 48.8 | 47.5 | 47.2 | 50.8 | 50.8 | 51.2 | 50.0 | 49.6 | 45.6 | 47.0 | 46.2 | 45.5 | 46.4 | 45.8 | 46.3 |  |  |
| **TsTV** | 45.2 | 38.6 | 37.3 | 37.6 | 37.3 | 37.4 | 37.1 | 37.7 | 37.3 | 36.9 | 36.4 | 36.7 | 35.7 | 35.8 | 37.1 | 36.3 | 40.7 |  |

\* Considered to be variants of ThRV1.

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

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **HpTV3** | **HbanRV** | **ThRV1** | YbRTV4\* | YbRTV5\* | **NnRTV1** | **HgRTV1** | BCOV | BlTV2 | HbTRV1 | **GyRTV1** | **NWMV1** |
| **HpTV3** |  |  |  |  |  |  |  |  |  |  |  |  |
| **HbanRV** | 35.1 |  |  |  |  |  |  |  |  |  |  |  |
| **ThRV1** | 12.4 | 12.9 |  |  |  |  |  |  |  |  |  |  |
| YbRTV4\* | 12.4 | 12.9 | 99.6 |  |  |  |  |  |  |  |  |  |
| YbRTV5\* | 12.4 | 13.5 | 90.8 | 90.4 |  |  |  |  |  |  |  |  |
| **NnRTV1** | 13.1 | 15.0 | 47.6 | 47.6 | 46.5 |  |  |  |  |  |  |  |
| **HgRTV1** | 12.4 | 12.7 | 38.7 | 39.1 | 37.9 | 40.9 |  |  |  |  |  |  |
| BCOV | 14.1 | 13.1 | 31.0 | 30.8 | 31.4 | 30.1 | 31.2 |  |  |  |  |  |
| BlTV2 | 11.4 | 12.1 | 31.3 | 31.3 | 31.5 | 31.5 | 33.3 | 36.0 |  |  |  |  |
| HbTRV1 | 12.4 | 12.7 | 29.5 | 29.5 | 29.9 | 30.5 | 30.0 | 36.6 | 42.7 |  |  |  |
| **GyRTV1** | 14.4 | 14.8 | 31.1 | 31.3 | 31.3 | 28.5 | 29.4 | 36.1 | 44.9 | 42.5 |  |  |
| **NWMV1** | 14.1 | 14.8 | 30.2 | 30.4 | 30.6 | 30.0 | 30.5 | 29.3 | 30.7 | 29.3 | 31.1 |  |

\* Considered to be variants of ThRV1.

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