

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:** | In the subfamily *Alpharhabdovirinae*, create 9 new species in 6 existing genera (*Alphapaprhavirus*, *Sigmavirus*, *Merhavirus*, *Tupavirus*, *Alphanemrhavirus*, *Alpharicinrhavirus*), rename the existing genus *Thriprhavirus* (as *Alphathriprhavirus*), and create the new genus *Betathriprhavirus* including two new species (*Mononegavirales*: *Rhabdoviridae*) | |
| **Code assigned:** | 2024.001M.N.v1.Alpharhabdovirinae\_1ng\_11nsp |

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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 | 15 | 0 | 0 |
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| **Submission date:** | 09/06/2024 |

**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| W - Withdrawn |  |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:** | DD/MM/YYYY |

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

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| **Name of accompanying Excel module:** |
| 2024.001M.N.v1.Alpharhabdovirinae\_1ng\_11nsp.xlsx |

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

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| **Is any taxon name used here derived from that of a living person:** | | **N** |
| **Taxon name** | **Person from whom the name is derived** | **X** |

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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Genus and species (*Mononegavirales*: *Rhabdoviridae*: *Alpharhabdovirinae*)  *Description of current taxonomy*:  The subfamily *Alpharhabdovirinae* currently comprises 33 genera and 235 species.  *Proposed* *taxonomic change(s):*  Create 9 new species in 6 existing genera (*Alphapaprhavirus*, *Sigmavirus*, *Merhavirus*, *Tupavirus*, *Alphanemrhavirus* and *Alpharicinrhavirus*) for viruses recently detected in bats, shrew or various invertebrates by metagenomic sequencing. Rename the existing genus *Thriprhavirus* (as *Alphathriprhavirus*) and create a new genus *Betathriprhavirus* including 2 new species for viruses detected in thrips by metagenomic sequencing.  *Justification*:  The viruses cluster phylogenetically with others in the existing or proposed genera in ML trees inferred using L protein sequences. All new species in existing genera meet established demarcation criteria. The proposed renamed and new genera for viruses detected in thrips are well-separated phylogenetically. |

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| **Text of Taxonomy proposal:**   1. **Create two new species in the genus *Alphapaprhavirus***   The genus *Alphapaprhavirus* currently comprises two species for viruses detected in moths or butterflies (Lepidoptera). Gata virus (GATV; strain M4) and Orgi virus (ORGIV; strain SP1) were each detected by metagenomic sequencing in Douglas-fir tussock moths (*Orgyia pseudotsugata*) collected in the USA in 2016 (BioProjects PRJNA485481 and PRJNA338014, respectively). We propose GATV be assigned to the new species *Alphapaprhavirus gata* and ORGIV be assigned to the new species *Alphapaprhavirus orgi.*  Ecology  Alphapaprhaviruses have been detected exclusively in lepidopteran insects. Pararge aegeria rhabdovirus (PAeRV; species *Alphapaprhavirus pararge*) was isolated from a laboratory population of speckled wood butterflies in Belgium [1]. Hubei lepidoptera virus 2 (HbLV2: species *Alphapaprhavirus hubei*) was detected in a mixed pool to lepidopteran insects collected in Hubei Province, China [2]. The detection of GATV and ORGIV in moths is consistent with the ecology of existing members of the genus.  Genome organizations  The complete genome coding sequences GATV (11238 nt; GenBank KX852388) and ORGIV (11306 nt; Genbank KX852386) have been reported. The genomes lack only extreme 3' and 5' termini. The genome organizations are similar to those of other alphapaprhaviruses. Each contains four canonical rhabdovirus structural protein genes (*N*, *P*, *M,* and *L*). However, unlike the viruses assigned to the two existing species which have duplicate transmembrane glycoprotein genes (*G1* and *G2*), each contains only a single gene (*G*) encoding a transmembrane glycoprotein (**Figure 1**). All glycoproteins share with vesicular stomatitis Indiana virus (VSIV; species *Vesiculovirus indiana*) the 12 conserved cysteine residues that form 6 disulphide bridges to stabilize the folded secondary structure but only ORGIV shares with the G1 protein of other alphapaprhaviruses the additional two cysteine residues that likely form an additional disulphide bridge (**Figure 3**). Thus, ORGIV appears to be intermediate in the evolutionary relationships between these viruses.  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, GATV and ORGIV cluster with the alphapaphaviruses in a distinct and well-supported monophyletic clade (**Figure 4**).  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGAX from ClustalW amino acid sequence alignments indicated that PAeRV and HbLV2 are most closely related (51.5% identity in N; 59.5% identity in L; 29.6% identity in G1; and 29.9% identity in G2). GATV and ORGIV are most closely related to each other sharing 29.4% identity in N, 46.9% identity in L and 20.2% identity in G (**Tables 1-3**).  Species demarcation criteria  According to current criteria, viruses assigned to different species within the genus *Alphapaprhavirus* have several of the following characteristics: A) minimum amino acid sequence divergence of 5% in N proteins; B) minimum sequence divergence of 10% in the L proteins; C) minimum amino acid sequence divergence of 15% in G1 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 (criterion D) vary significantly from existing members of the genus, containing only a single transmembrane glycoprotein gene (G) but they do not differ significantly from each other. Neutralization tests have not been conducted as there are currently no isolates of these viruses (criterion E). GATV and ORGIV have each been detected in moths of the same species collected in the USA (criterion F).  Derivation of the names of new taxa  The species epithets for *Alphapaprhavirus gata* and *Alphapaprhavirus orgi* have been derived from the assigned virus names, Gata virus and Orgi virus, respectively. The origin of these virus names is not known.   1. **Create two new species in the genus *Sigmavirus***   The genus *Sigmavirus* currently comprises 20 species for viruses detected primarily in flies (Diptera). Hangzhou rhabdovirus 4 (HzRV4; strain YSP1FY156) was detected by metagenomic sequencing in rice leaf miners (*Hydrellia griseola*) collected in Jiezhang Province, China in 2016 (BioProject PRJNA629998). Bactrocera dorsalis sigmavirus (BDorSV) was detected by metagenomic sequencing in oriental fruit flies (*Bactrocera dorsalis*) collected in China in 2018 [3]. We propose HzRV4 be assigned to the new species *Sigmavirus hangzhou* and BDorSV be assigned to the new species *Sigmavirus dorsalis.*  Ecology  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 [4]. The detection of JHzRV4 and BDorSV in dipteran flies is consistent with the ecology of most other sigmaviruses.  Genome organizations  The complete genome coding sequences of HzRV4 (12335 nt; GenBank MZ209737) and BDorSV (11302 nt; Genbank MN745080) have been reported. The genomes lack only extreme 3' and 5' termini. The genome organizations are similar to those of other sigmaviruses. Each contains the five canonical rhabdovirus structural protein genes (*N*, *P*, *M,* *G* and *L*). Like most sigmaviruses, HzRV4 contains an additional gene (*X*) between the *P* and *M* genes but, like all other sigmaviruses, BDorSV lacks the *X* gene (**Figure 1**).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, HzRV4 and BDorSV cluster with the sigmaviruses in a distinct and well-supported monophyletic clade (**Figure 4**).  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGA7 from ClustalW amino acid sequence alignments indicated that HzRV4 is most closely related to Jopcycgri virus 1(JPCGV1; species *Sigmavirus jopcycgri*) in the N protein (22.9% identity), Shayang fly virus 2 (SyFV2; species *Sigmavirus shayang*) in the L protein (45.6% identity) and both SyFV2 and Yushu rhabdovirus (YsRV; species *Sigmavirus yushu*) in the G protein (31.6% identity). BDorSV is most closely related to Bactrocera tryoni rhabdovirus (BtyrRV; species *Sigmavirus tyroni*) in the N, L and G proteins (69.3%, 78.8% and 53.0% identity, respectively) (**Tables 4-6**).  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 rice leaf miners (*Hydrellia griseola*) (HzRV4) and fruit flies of the species *Bactrocera dorsalis* (BDorSV) appear to represent novel hosts (criterion B).  Derivation of the names of new taxa  The species epithet for *Sigmavirus hangzhou* is derived from the city in China (Hangzhou) from which the source fly sample for the virus metagenomic sequencing was collected.  The species epithet for *Sigmavirus dorsalis* is derived from the species epithet of the source fly sample (*Bactrocera dorsalis*)in which the virus metagenomic sequencing was detected.   1. **Create one new species in the genus *Tupavirus***   The genus *Tupavirus* currently comprises eight species for viruses detected primarily in bats, but also in rodents, tupaia, and birds. Wufeng bat tupavirus 2 (WfBTV2; strain WF\_Rh.pearsonii\_rhabdo\_5) was detected by metagenomic sequencing in a Pearson's horseshoe bat (*Rhinolophus pearsonii*) collected in Hubei Province, China [5]. We propose WfBTV2 be assigned to the new species *Tupavirus wufeng*.  Ecology  Tupaviruses have been isolated from various mammals and birds. All bat tupaviruses reported to date have been detectedin China. Bat tupavirus BS1 (BtTVBS1; species *Tupavirus stheno*) and bat tupavirus BS1 (BtTVBS2; species Tupavirus *stoliczkanus*) were detected in bats of the two species (*Rhinolophus stheno* and *Aselliscus stoliczkanus*, respectively) in Yunnan Province; Wenzhou Rhinilophus laniger tupavirus 1 (WzMlaTV1; species *Tupavirus laniger*) and Wufeng *Rhinolophus pearsonii* tupavirus 1(WfRpeTV1; species *Tupavirus pearsonii*) and were detected in bats of two other species (*Myotis laniger* and *Rhinolophus pearsonii*, respectively) in Hubei Province. WfBTV2 was also detected in *Rhinolophus pearsonii* bats collected in Hubei Province.  Genome organization  The complete genome coding sequence of WfBTV2 (11468 nt; GenBank OQ715690) has been reported. The genome lacks only extreme 3' and 5' termini. Like all other tupaviruses, it contains the five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*), an alternative ORF in the *P* gene, and a gene encoding a small protein between the *M* and *G* genes. Like tupavirus SB8301 (TUPVSB; species *Tupavirus incomtus*), WfBTV2 contains an overlapping ORF in the small ORF between the *M* and *G* genes. Like most other bat tupaviruses, WfBTV2 also has a gene encoding a small protein between the *G* and *L* genes but, uniquely in WfBTV2, there is an alternative ORFs in this small gene (**Figure 1**).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, WfBTV2 clusters with the tupaviruses in a distinct and well-supported monophyletic clade (**Figure 4**).  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGAX from ClustalW amino acid sequence alignments indicated that WfBTV2 is most closely related to both TUPV (species *Tupavirus tupaia*) and WzMlaTV1 in the N protein (58.8% identity), KLAV (species *Tupavirus klamath*) in the L protein (62.4% identity) and TUPVSB in the G protein (34.8% identity).  Species demarcation criteria  Viruses assigned to different species within the genus *Tupavirus* have several of the following characteristics: A) minimum amino acid sequence divergence of 5% 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 serological tests; and F) occupy different ecological niches as evidenced by differences in hosts and or arthropod vectors.  The proposed new member of the genus meets demarcation criteria A, B, C and D. Neutralisation tests have not been conducted as there are currently no isolates of these viruses (criterion E). The member does not appear to meet criterion F as WfRpeTV1, which is assigned to another tupavirus species, was isolated from the same bat species from the same province of China.  Derivation of the names of the new taxon  The species epithet for *Tupavirus wufeng* is derived from Wufeng County, the district in China from which the source bat sample for virus metagenomic sequencing was collected.   1. **Create one new species in the genus *Alpharicinrhavirus***   The genus Alpharicinrhavirus currently comprises 16 species for viruses detected in hard ticks (Ixodidae). Tahe rhabdovirus 2 (ThRV2; strain NE-TH4) was detected by metagenomic sequencing in hard ticks (*Ixodes persulcatus*) collected in Heilongjiang Province, China in 2021 [6]. We propose ThRV2 be assigned to the new species *Alpharicinrhavirus heilongjiang*.  Ecology  Alpharicinrhaviruses have been detected exclusively in hard ticks (Ixodidae) of various species. Only two have been detected in ticks of the genus *Ixodes*: Norway mononegavirus 1 (NWMV1; species *Alpharicinrhavirus skanevik*) was detected *Ixodes ricinus* ticks collected in Norway [7]. Yanbian rhabd tick virus 1 (YbRTV1; species *Alpharicinrhavirus jilin*) was detected in *Ixodes persulcatus* ticks collected in Jilin Province, China. ThRV2 was also detected in Ixodes *persulcatus* ticks over 1000 km to the north in Heilongjiang Province, China.  Genome organization  The near-complete genome sequence of ThRV2 (11485 nt; GenBank ON408171) has been reported. The genome lacks only extreme 3' and 5' termini (**Figure 2**). The genome organisation is similar to those of most other alpharicinrhaviruses, containing the five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*). Unlike some alpharicinrhaviruses, ThRV2 contains no long alternative ORFs in the structural protein genes. Several other alpharicinrhaviruses lack a *G* gene.  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, ThRV2 clusters with the alpharicinrhaviruses in a distinct and well-supported monophyletic clade (**Figure 4**).  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGAX from ClustalW amino acid sequence alignments indicated that ThRV2 is most closely related to NWMNV1 with 59.8% identity  in the N protein, 79.3% identity in the L protein and 69.4% identity in the G protein.  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 member of the genus meets demarcation criteria A, B and C. The genome organization is similar to that of several other alpharicinrhaviruses (criterion D). Neutralisation tests have not been conducted as there are currently no isolates of these viruses (criterion E). The member does not appear to meet criterion F as YbRTV1, which is assigned to another alpharicinrhavirus species, was isolated from the same bat species in China.  Derivation of the names of the new taxon  The species epithet for *Alpharicinrhavirus heilongjiang* is derived from Heilongjiang Province, the district in China from which the source tick sample for virus metagenomic sequencing was collected.   1. **Create two new species in the genus *Merhavirus***   The genus Merhavirus currently contains five species for viruses isolated from or detected in culicine mosquitoes (Culicidae). Armigeres subalbatus rhabdovirus (AsubRV; strain Ar-3) was detected by metagenomic sequencing in 2019 in a cell line (Ar-3) established from a laboratory colony of *Armigeres subalbatus* mosquitoes in Japan [8, 9]. Cambodia anopheles rhabdovirus (CamAnRV; strain A4) was detected by metagenomic sequencing in *Anopheles vagus* mosquitoes collected in Cambodia in 2021 [10]. We propose AsubRV be assigned to the new species *Merhavirus subalbatus* and CamAnRV be assigned to the new species *Merhavirus cambodia*.  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 [11]. Culex tritaeniorhynchus rhabdovirus (CTRV: species *Merhavirus tritaeniorhynchus*) was detected in a laboratory colony of *Culex* sp. mosquitoes collected in Japan [12]. Formosus virus (FORMV; species *Merhavirus formosus*) was detected in mosquitoes (*Aedes aegypti*) from a laboratory colony originating from Bundibugyo, Uganda [13]. 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 [14]. The detection of AsubRV and CamAnRV in *Armigeres* sp. and *Anophales* sp. mosquitoes broadens the range of culicine mosquitoes known to harbour merhaviruses.  Genome organizations  The near-complete genome sequences of AsubRV (12152 nt; GenBank LC775065) and CamAnRV (12039 nt; Genbank OR479699) have been reported. The genome lacks only extreme 3' and 5' termini (**Figure 2**). The genome organisations are similar to those of other merhaviruses, containing only the five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*). There is no evidence in either virus of a splice site in the L gene, as has been reported for CTRV.  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, AsubRV and CamAnRV cluster with the merhaviruses in a distinct and well-supported monophyletic clade (**Figure 4**).  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGAX from ClustalW amino acid sequence alignments indicated that AsubRV is most closely related to FORMV with 56.0% identity  in the N protein, 72.2% identity in the L protein and 62.9% identity in the G protein. CamAnRV is most closely related to CTRV in the N protein and G protein (18.8% in each) and to MERDV in the L protein (41.5% identity).  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). AsRV and CamAnRV have each been detected in cells of mosquitoes of a novel species but their natural ecologies are currently uncertain (criterion F).  Derivation of the names of the new taxon  The species epithet for *Merhavirus subalbatus* is derived from the species epithet of the mosquito species (*Armigeres subalbatus*) that was the source of the cell line in which the virus was first detected.  The species epithet for *Merhavirus cambodia* is derived from the country (Cambodia)  from which the source mosquito sample for virus metagenomic sequencing was collected.   1. **Create one new species in the genus *Alphanemrhavirus***   The genus *Alphanemrhavirus* comprises four species for viruses detected in round worms (Nematoda). Wufeng shrew rhabdovirus 1 (WfSRV1: strain WF\_An.squamipes\_rhabdo\_1) was detected by metagenomic sequencing of the internal organs of a shrew (*Anourosorex squamipes*) collected in Hubei Province, China [5]. We propose WfSRV1 be assigned to the new species *Alphanemrhavirus wufeng*.  Ecology  Alphanemrhaviruses have been detected by metagenomic sequencing in nematode worms or in mammals suspected of being infested with worms. Xingshan nematode virus 4 (XsNV-4; species *Alphanemrhavirus xingshan*) was detected in a spirurian parasitic nematode in Hubei Province, China, in 2014 [2]. Xinzhou nematode virus 4(XzNV-4; species *Alphanemrhavirus xinzhou*) was detected in snake-associated nematodes collected in Shanxi Province, China, in 2014 [2]. Sodak rhabdovirus 1 (SDRV-1; species *Alphanemrhavirus sodak*) was detected in visceral homogenates from big brown bats (*Eptesicus fuscus*) collected in 2020 in South Dakota, USA [15]. It was recognized by those reporting the virus that it may well have originated from internal nematodes parasitizing the bats [15]. Rattus tanezumi rhabdovirus 1 (RtaRV-1; species *Alphanemrhavirus bangkok*) was detected in the lung tissue of Asian house rats (*Rattus tanezumi*) collected in 2018 from Bangkok, Thailand [16]. It appears likely that WfSRV1 has also been derived from nematode worms infecting the shrew in which it was detected by metagenomic sequencing.  Genome organizations  The near-complete genome sequences of WfSRV1 (11489 nt; GenBank OQ715689) has been reported. The genome lacks only extreme 3' and 5' termini (**Figure 3**). The genome organization is similar to most other alphanemrhaviruses, containing only the five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, WfSRV1 clusters with the alphanemrhaviruses in a distinct and well-supported monophyletic clade within the *Alpharhabdovirinae* (**Figure 4**).  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGAX from ClustalW amino acid sequence alignments indicated that WfSRV1 is most closely related to RtaRV1 with 52.4% identity  in the N protein, 56.4% identity in the L protein and 26.1% identity in the G protein.  Species demarcation criteria  Viruses assigned to different species within the genus *Alphanemrhavirus* 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 species meets demarcation criteria A, B and C. The genome organisation of WfSRV1 is similar to those of other alphanemrhaviruses (criterion D). Neutralisation tests have not been conducted as there are currently no isolates of these viruses (criterion E). As the viruses has been detected only by metagenomic sequencing, the natural ecology is uncertain (criterion F).   1. **Rename the genus *Thriprhavirus* (as *Alphathriprhavirus*), create the new genus *Betathriprhavirus* including two new species**   The genus *Thriprhavirus* comprises two species for viruses detected in thrips (Thripidae). Thrips tabaci associated dimarhabdovirus 1 (TtaDRV1; strain Tamono1) was detected by metagenomic sequencing of onion thrips (*Thrips tabaci*) collected in Italy in 2018 [17]. It has been assigned to the species *Thriprhavirus tabaci*. Hangzhou Frankliniella intonsa rhabdovirus 1 (HFinRV1; strain JM1FY86115) was detected by metagenomic sequencing of European flower thrips (*Frankliniella intonsa*) collected in China in 2016. It has been assigned to the species *Thriprhavirus intonsa*.  Two novel viruses have recently been detected by metagenomic sequencing of thrips. Soybean trips rhabdo-like virus 1 (STRLV1; strain STN1) and soybean trips rhabdo-like virus 2 (STRLV2; strain STN1) were each detected in a pool of soybean thrips (*Neohydatothrips variabilis*) samples collected at various locations, primarily in the midwestern states (Illinois, Iowa, Kansas, Michigan, Minnesota, Missouri and Wisconsin) of the USA, in 2018 [18]. These viruses are phylogenetically distant from those currently assigned to the genus *Thriprhavirus*. We propose the creation of the new genus *Betathriprhavirus* to accommodate the new viruses, the assignment of STRLV1 to the new species *Betathriprhavirus variabilis*, and the assignment of STRLV2 to the new species *Betathriprhavirus midwest*. We also propose to rename the genus *Thriprhavirus* as the genus *Alpharthriprhavirus*.  Genome organizations  The near-complete genome sequences of STRLV1 (10848 nt; GenBank MT224147) and STRLV2 (10807 nt; Genbank MT224148) have been reported. The genomes lack only extreme 3' and 5' termini (**Figure 3**). Each genome contains the five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*) as well as an additional gene (*U1*) located between the *G* gene and *L* gene, encoding a small protein of unknown function. The genome organization of these viruses differs from that of the viruses currently assigned to the genus *Thriprhavirus* **(Figure 3)**.  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, STRLV1 and STRVL2 form a distinct and well-supported monophyletic clade within the *Alpharhabdovirinae* that is phylogenetically quite separate from the existing thriprhavirus clade (**Figure 4**).  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGA7 from ClustalW amino acid sequence alignments indicated that STRLV1 and STRLV2 share 36.8% identity in the N protein, 46.2% identity in the L protein and 32.5% identity in the G protein.  Species demarcation criteria for the new genus  Similar to the criteria used for several other genera within the *Alpharhabdovirinae*, we propose that viruses assigned to different species within the genus *Betathriprhavirus* should 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.  STRLV1 and STRLV2 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; the U1 genes encode proteins that, although clearly homologous, are somewhat different in length (criterion E). As the viruses have been detected only by metagenomic sequencing, their natural ecology is uncertain but they have been detected in pooled samples of thrips of the same species from different geographic locations (criterion F).  Derivation of the names of the new taxa  The renamed genus *Alphathriprhavirus* and the new genus *Betathriprhavirus* are named for the alpha and beta clusters of thrips rhabdoviruses.  The species epithet for *Betathriprhavirus variabilis* is derived from the species epithet of the thrips species (*Neohydatothrips variabilis*) in which the virus was first detected.  The species epithet for *Betathriprhavirus midwest* is derived from the region of the USA (midwestern states) where the source thrips sample was collected for virus metagenomic sequencing. |

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| **Tables, Figures:**  Below    **Firgure 1 (above).** Clustal Omega multiple sequence alignment of alphapaprhavirus glycoproteins and the vesicular stomatitis Indiana virus (VSIV) G protein, for which disulphide bridges have been determined in a structural model informed by X-ray crystallography.    **Figure 2 (above).** Schematic illustration of the genome organisations of alphapaprhaviruses, sigmaviruses and tupaviruses. Arrows represent long open reading frames (ORFs) with those encoding proteins demonstrating sequence homology shown in the same colour.  **Figure 3 (below).** Schematic illustration of the genome organisations of alpharicinrhaviruses, merhaviruses, alphanemrhaviruses, alphathriprhaviruses and betathriprhaviruses. Arrows represent long open reading frames (ORFs) with those encoding proteins demonstrating sequence homology shown in the same colour.      **Figure 4 (above).** The evolutionary history was inferred from a multiple sequence alignment of complete L protein sequences of 235 rhabdoviruses that are currently assigned to species in the subfamily *Alpharhabdovirinae* as well as 11 viruses proposed to be assigned to 11 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 1621 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 (-1418703.04) 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 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. |

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | PAeRV | HbLV2 | **GATV** | **ORGIV** |
| PAeRV |  |  |  |  |
| HbLV2 | 51.5 |  |  |  |
| **GATV** | 24.5 | 28.3 |  |  |
| **ORGIV** | 33.5 | 31.8 | 29.4 |  |

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | PAeRV | HbLV2 | **GATV** | **ORGIV** |
| PAeRV |  |  |  |  |
| HbLV2 | 59.5 |  |  |  |
| **GATV** | 44.4 | 44.8 |  |  |
| **ORGIV** | 42.4 | 43.5 | 46.9 |  |

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

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | PAeRV | HbLV2 | **GATV** | **ORGIV** | PAeRV G2 | HbLV2 G2 |
| PAeRV G1 |  |  |  |  |  |  |
| HbLV2 G1 | 29.6 |  |  |  |  |  |
| **GATV G** | 18.0 | 19.2 |  |  |  |  |
| **ORGIV G** | 19.8 | 20.5 | 20.2 |  |  |  |
| PAeRV G2 | 17.7 | 18.7 | 12.5 | 12.0 |  |  |
| HbLV2 G2 | 18.7 | 21.9 | 17.0 | 13.9 | 29.9 |  |

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

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | WhLFV9 | WhLFV10 | DMelSV | HbDRV1 | CCapSV | DStuSV | DAffSV | DAanSV | DObsSV | DImmSV | SyFV2 | WhFV2 | HbDV10 | HbDV9 | WhHFV1 | ApRV3 | **HzRV4** | YsRV | ADMSV | BtyrRV1 | **BDorSV** | JPCGV1 |
| WhLFV9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WhLFV10 | 50.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DMelSV | 33.9 | 34.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbDRV1 | 21.4 | 24.2 | 24.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| CCapSV | 27.2 | 27.2 | 29.2 | 25.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DStuSV | 22.2 | 20.8 | 20.5 | 19.7 | 22.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DAffSV | 22.1 | 21.9 | 20.3 | 20.2 | 21.7 | 43.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DAanSV | 21.5 | 19.0 | 19.9 | 18.8 | 19.8 | 22.7 | 23.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DObsSV | 21.0 | 20.0 | 22.6 | 19.2 | 22.9 | 21.1 | 22.7 | 21.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DImmSV | 19.4 | 18.7 | 20.0 | 17.9 | 21.8 | 19.5 | 19.4 | 21.6 | 43.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SyFV2 | 22.6 | 21.4 | 22.8 | 19.9 | 20.9 | 26.3 | 27.7 | 26.6 | 20.1 | 21.3 |  |  |  |  |  |  |  |  |  |  |  |  |
| WhFV2 | 23.5 | 21.9 | 21.9 | 18.7 | 20.9 | 27.5 | 27.4 | 26.9 | 20.8 | 21.3 | 83.1 |  |  |  |  |  |  |  |  |  |  |  |
| HbDV10 | 21.8 | 19.0 | 22.0 | 19.1 | 21.2 | 26.2 | 25.9 | 24.4 | 19.8 | 20.7 | 34.6 | 34.4 |  |  |  |  |  |  |  |  |  |  |
| HbDV9 | 20.3 | 23.3 | 22.9 | 18.5 | 23.1 | 23.9 | 24.5 | 21.3 | 20.9 | 23.0 | 30.3 | 29.6 | 28.6 |  |  |  |  |  |  |  |  |  |
| WhHFV1 | 21.2 | 21.9 | 22.6 | 19.7 | 18.6 | 23.1 | 23.6 | 23.0 | 20.3 | 21.3 | 27.8 | 27.1 | 27.5 | 29.5 |  |  |  |  |  |  |  |  |
| ApRV3 | 21.0 | 21.9 | 23.0 | 19.7 | 20.1 | 22.7 | 26.5 | 19.1 | 18.1 | 19.9 | 24.1 | 24.1 | 23.3 | 26.5 | 23.7 |  |  |  |  |  |  |  |
| **HzRV4** | 21.4 | 21.6 | 21.6 | 19.1 | 20.9 | 18.6 | 19.3 | 21.1 | 20.5 | 21.4 | 21.3 | 20.9 | 18.7 | 22.1 | 19.8 | 18.7 |  |  |  |  |  |  |
| YsRV | 22.6 | 21.9 | 24.5 | 20.1 | 20.7 | 26.2 | 28.4 | 25.5 | 21.7 | 21.8 | 65.5 | 65.1 | 33.8 | 30.6 | 29.4 | 25.1 | 21.1 |  |  |  |  |  |
| ADMSV | 28.2 | 28.9 | 29.2 | 25.9 | 29.1 | 21.0 | 20.0 | 19.1 | 20.3 | 20.0 | 23.2 | 24.2 | 21.7 | 19.7 | 24.3 | 21.2 | 21.0 | 24.9 |  |  |  |  |
| BtyrRV1 | 25.5 | 25.5 | 21.0 | 18.6 | 22.8 | 24.4 | 25.3 | 24.8 | 23.7 | 23.9 | 28.5 | 27.1 | 26.1 | 27.3 | 24.1 | 23.5 | 20.6 | 30.2 | 20.3 |  |  |  |
| **BDorSV** | 22.7 | 26.1 | 22.2 | 19.3 | 21.8 | 24.5 | 26.7 | 25.6 | 23.5 | 23.8 | 30.0 | 28.4 | 26.3 | 27.6 | 24.6 | 24.4 | 21.6 | 31.0 | 22.7 | 69.3 |  |  |
| JPCGV1 | 24.7 | 24.9 | 21.8 | 18.6 | 22.3 | 26.0 | 26.5 | 26.4 | 21.2 | 24.6 | 29.4 | 30.3 | 28.7 | 27.1 | 25.7 | 24.3 | 22.9 | 29.2 | 23.2 | 59.1 | 59.0 |  |

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

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | WhLFV9 | WhLFV10 | DMelSV | HbDRV1 | CCapSV | DStuSV | DAffSV | DAanSV | DObsSV | DImmSV | SyFV2 | WhFV2 | HbDV10 | HbDV9 | WhHFV1 | ApRV3 | **HzRV4** | YsRV | ADMSV | BtyrRV1 | **BDorSV** | JPCGV1 |
| WhLFV9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WhLFV10 | 67.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DMelSV | 51.2 | 50.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbDRV1 | 50.8 | 50.4 | 48.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| CCapSV | 49.8 | 49.5 | 48.1 | 47.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DStuSV | 40.7 | 40.8 | 40.6 | 40.8 | 40.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DAffSV | 40.3 | 39.9 | 39.5 | 39.6 | 40.6 | 60.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DAanSV | 40.9 | 41.8 | 41.1 | 41.9 | 42.3 | 41.5 | 40.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DObsSV | 41.0 | 41.4 | 41.2 | 41.2 | 40.9 | 41.1 | 40.9 | 41.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DImmSV | 40.6 | 40.6 | 41.3 | 41.6 | 41.6 | 39.5 | 39.0 | 42.4 | 55.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SyFV2 | 42.2 | 42.6 | 42.3 | 43.1 | 43.8 | 42.2 | 41.2 | 44.0 | 43.1 | 42.7 |  |  |  |  |  |  |  |  |  |  |  |  |
| WhFV2 | 41.4 | 42.6 | 42.0 | 42.8 | 43.6 | 42.3 | 41.8 | 43.6 | 43.5 | 42.1 | 82.2 |  |  |  |  |  |  |  |  |  |  |  |
| HbDV10 | 42.6 | 42.8 | 43.2 | 43.1 | 44.6 | 43.7 | 43.8 | 45.5 | 42.7 | 42.1 | 53.1 | 52.6 |  |  |  |  |  |  |  |  |  |  |
| HbDV9 | 41.7 | 42.3 | 42.9 | 42.4 | 43.2 | 42.4 | 41.7 | 43.7 | 43.9 | 43.2 | 50.4 | 50.3 | 52.5 |  |  |  |  |  |  |  |  |  |
| WhHFV1 | 41.9 | 42.4 | 41.3 | 42.1 | 43.8 | 42.1 | 41.6 | 42.6 | 41.4 | 42.6 | 50.9 | 51.2 | 52.1 | 51.0 |  |  |  |  |  |  |  |  |
| ApRV3 | 39.8 | 39.9 | 40.7 | 41.3 | 40.9 | 39.8 | 40.4 | 41.7 | 41.6 | 41.2 | 48.6 | 49.2 | 48.8 | 46.0 | 46.4 |  |  |  |  |  |  |  |
| **HzRV4** | 41.8 | 41.3 | 41.5 | 41.8 | 41.3 | 40.9 | 41.1 | 42.8 | 41.0 | 41.3 | 45.6 | 45.0 | 44.9 | 45.2 | 44.4 | 44.4 |  |  |  |  |  |  |
| YsRV | 42.1 | 42.1 | 42.5 | 42.2 | 43.3 | 42.2 | 41.6 | 42.9 | 43.4 | 42.1 | 74.0 | 73.6 | 52.4 | 51.3 | 50.0 | 47.8 | 45.5 |  |  |  |  |  |
| ADMSV | 52.0 | 51.7 | 50.1 | 50.0 | 50.6 | 40.2 | 38.6 | 39.6 | 41.7 | 41.5 | 43.4 | 42.5 | 42.8 | 42.8 | 43.0 | 40.6 | 42.1 | 43.7 |  |  |  |  |
| BtyrRV1 | 43.6 | 43.6 | 41.8 | 42.9 | 43.4 | 42.1 | 42.1 | 43.3 | 43.6 | 43.5 | 47.7 | 47.4 | 46.9 | 47.5 | 45.5 | 43.5 | 44.8 | 47.1 | 43.2 |  |  |  |
| **BDorSV** | 44.2 | 43.9 | 43.5 | 43.6 | 44.4 | 42.2 | 41.9 | 44.4 | 43.4 | 43.3 | 47.6 | 47.2 | 46.7 | 46.9 | 46.1 | 43.2 | 45.1 | 47.3 | 44.3 | 78.8 |  |  |
| JPCGV1 | 43.7 | 43.7 | 43.9 | 43.5 | 44.1 | 42.5 | 41.8 | 43.7 | 43.3 | 42.8 | 46.9 | 46.0 | 46.6 | 47.2 | 45.2 | 43.1 | 45.1 | 46.8 | 43.8 | 68.3 | 68.9 |  |

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

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | WhLFV9 | WhLFV10 | DMelSV | HbDRV1 | CCapSV | DStuSV | DAffSV | DAanSV | DObsSV | DImmSV | SyFV2 | WhFV2 | HbDV10 | HbDV9 | WhHFV1 | ApRV3 | **HzRV4** | YsRV | ADMSV | BtyrRV1 | **BDorSV** | JPCGV1 |
| WhLFV9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WhLFV10 | 35.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DMelSV | 21.0 | 22.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbDRV1 | 22.4 | 21.2 | 27.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| CCapSV | 23.2 | 21.1 | 26.0 | 26.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DStuSV | 20.8 | 21.3 | 22.3 | 20.7 | 19.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DAffSV | 20.0 | 20.9 | 22.6 | 20.6 | 19.5 | 46.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DAanSV | 20.6 | 18.7 | 23.6 | 23.7 | 21.9 | 19.3 | 20.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DObsSV | 19.6 | 17.9 | 21.9 | 22.1 | 20.4 | 21.6 | 20.4 | 21.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DImmSV | 19.8 | 20.3 | 20.3 | 20.6 | 20.4 | 20.9 | 18.9 | 19.6 | 36.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SyFV2 | 18.7 | 19.4 | 21.1 | 20.1 | 22.0 | 25.0 | 23.3 | 22.6 | 19.6 | 21.1 |  |  |  |  |  |  |  |  |  |  |  |  |
| WhFV2 | 19.6 | 20.2 | 21.0 | 21.0 | 22.9 | 25.5 | 26.0 | 21.4 | 21.7 | 21.6 | 67.9 |  |  |  |  |  |  |  |  |  |  |  |
| HbDV10 | 18.4 | 20.7 | 23.5 | 23.0 | 23.1 | 24.0 | 24.7 | 24.1 | 20.8 | 21.8 | 36.1 | 35.8 |  |  |  |  |  |  |  |  |  |  |
| HbDV9 | 19.7 | 20.8 | 21.2 | 23.4 | 20.5 | 22.4 | 20.9 | 21.5 | 20.2 | 20.5 | 28.0 | 27.1 | 28.6 |  |  |  |  |  |  |  |  |  |
| WhHFV1 | 22.7 | 21.3 | 23.0 | 23.7 | 22.7 | 23.2 | 22.6 | 22.7 | 22.1 | 24.0 | 27.6 | 24.6 | 27.0 | 22.2 |  |  |  |  |  |  |  |  |
| ApRV3 | 17.4 | 16.7 | 21.3 | 21.6 | 18.1 | 18.3 | 18.5 | 17.8 | 18.1 | 17.0 | 19.9 | 19.7 | 21.6 | 18.0 | 19.0 |  |  |  |  |  |  |  |
| **HzRV4** | 20.3 | 20.3 | 22.1 | 20.5 | 21.2 | 21.7 | 21.4 | 20.6 | 19.7 | 19.9 | 31.6 | 30.0 | 30.8 | 27.3 | 26.8 | 18.7 |  |  |  |  |  |  |
| YsRV | 19.2 | 21.3 | 22.4 | 21.5 | 20.3 | 25.8 | 25.2 | 20.9 | 22.0 | 21.4 | 58.4 | 59.4 | 37.1 | 28.7 | 28.0 | 20.6 | 31.6 |  |  |  |  |  |
| ADMSV | 18.9 | 20.9 | 20.0 | 21.5 | 21.4 | 18.3 | 18.8 | 20.4 | 18.4 | 19.0 | 21.9 | 20.7 | 22.1 | 20.0 | 19.2 | 18.0 | 21.1 | 19.6 |  |  |  |  |
| BtyrRV1 | 21.5 | 20.8 | 23.9 | 23.4 | 21.6 | 18.5 | 18.9 | 22.0 | 20.8 | 20.5 | 23.1 | 22.6 | 23.6 | 22.0 | 21.1 | 19.1 | 18.5 | 22.9 | 24.0 |  |  |  |
| **BDorSV** | 23.4 | 22.1 | 23.0 | 22.6 | 22.1 | 20.4 | 18.6 | 24.5 | 23.0 | 20.7 | 23.1 | 24.0 | 23.2 | 22.2 | 22.0 | 20.2 | 21.0 | 22.4 | 22.4 | 53.0 |  |  |
| JPCGV1 | 19.1 | 21.1 | 25.1 | 26.1 | 22.1 | 21.4 | 19.1 | 24.2 | 22.4 | 21.9 | 22.8 | 22.4 | 23.6 | 23.8 | 22.5 | 19.4 | 22.4 | 25.6 | 23.6 | 42.8 | 39.7 |  |

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

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | DURV | KLAV | TUPVSB | **WfBTV2** | TUPV | WzMlaTV1 | BtTVBS2 | WfRpeTV1 | BtTVBS1 |
| DURV |  |  |  |  |  |  |  |  |  |
| KLAV | 47.1 |  |  |  |  |  |  |  |  |
| TUPVSB | 48.3 | 71.4 |  |  |  |  |  |  |  |
| **WfBTV2** | 54.1 | 57.4 | 58.6 |  |  |  |  |  |  |
| TUPV | 57.1 | 55.1 | 55.3 | 58.8 |  |  |  |  |  |
| WzMlaTV1 | 53.6 | 52.1 | 53.0 | 58.8 | 70.2 |  |  |  |  |
| BtTVBS2 | 55.5 | 51.6 | 53.0 | 54.7 | 68.1 | 67.2 |  |  |  |
| WfRpeTV1 | 55.2 | 52.6 | 55.3 | 55.6 | 67.2 | 66.7 | 81.4 |  |  |
| BtTVBS1 | 53.8 | 52.1 | 56.0 | 56.0 | 67.7 | 66.5 | 80.9 | 85.6 |  |

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

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | DURV | KLAV | TUPVSB | **WfBTV2** | TUPV | WzMlaTV1 | BtTVBS2 | WfRpeTV1 | BtTVBS1 |
| DURV |  |  |  |  |  |  |  |  |  |
| KLAV | 52.5 |  |  |  |  |  |  |  |  |
| TUPVSB | 51.8 | 68.9 |  |  |  |  |  |  |  |
| **WfBTV2** | 53.4 | 62.4 | 60.3 |  |  |  |  |  |  |
| TUPV | 52.6 | 56.4 | 56.1 | 57.6 |  |  |  |  |  |
| WzMlaTV1 | 53.3 | 58.9 | 57.1 | 60.0 | 61.7 |  |  |  |  |
| BtTVBS2 | 54.4 | 57.9 | 56.9 | 59.4 | 62.4 | 63.6 |  |  |  |
| WfRpeTV1 | 53.7 | 57.7 | 57.3 | 60.0 | 62.8 | 63.6 | 72.5 |  |  |
| BtTVBS1 | 53.0 | 59.2 | 57.6 | 59.8 | 62.0 | 63.3 | 71.3 | 75.5 |  |

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

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | DURV | KLAV | TUPVSB | **WfBTV2** | TUPV | WzMlaTV1 | BtTVBS2 | WfRpeTV1 | BtTVBS1 |
| DURV |  |  |  |  |  |  |  |  |  |
| KLAV | 19.2 |  |  |  |  |  |  |  |  |
| TUPVSB | 23.0 | 51.0 |  |  |  |  |  |  |  |
| **WfBTV2** | 26.0 | 33.9 | 34.8 |  |  |  |  |  |  |
| TUPV | 25.5 | 27.9 | 26.6 | 28.7 |  |  |  |  |  |
| WzMlaTV1 | 24.9 | 26.0 | 27.8 | 32.2 | 40.3 |  |  |  |  |
| BtTVBS2 | 27.1 | 30.4 | 29.1 | 33.0 | 40.6 | 51.6 |  |  |  |
| WfRpeTV1 | 26.9 | 29.6 | 30.2 | 33.7 | 41.9 | 50.9 | 75.2 |  |  |
| BtTVBS1 | 25.7 | 29.4 | 28.9 | 32.6 | 40.9 | 51.6 | 67.5 | 75.2 |  |

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

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | ZjRTV1 | YbRTV1 | HpTV3 | HbanRV | ThRV1 | NnRTV1 | HgRTV1 | WhTV1 | YsRTV2 | DretRV1 | BCOV | BlTV2 | HbTRV1 | GyRTV1 | **ThRV2** | NWMV1 | TsTV |
| ZjRTV1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YbRTV1 | 19.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HpTV3 | 19.9 | 22.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbanRV | 19.4 | 23.5 | 78.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ThRV1 | 19.2 | 22.4 | 22.7 | 22.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| NnRTV1 | 17.4 | 24.1 | 23.9 | 23.1 | 55.8 |  |  |  |  |  |  |  |  |  |  |  |  |
| HgRTV1 | 19.3 | 21.5 | 23.9 | 23.6 | 46.8 | 48.6 |  |  |  |  |  |  |  |  |  |  |  |
| WhTV1 | 18.0 | 20.6 | 20.5 | 20.6 | 31.4 | 32.4 | 34.7 |  |  |  |  |  |  |  |  |  |  |
| YsRTV2 | 18.3 | 23.6 | 21.1 | 20.2 | 32.3 | 32.4 | 34.5 | 50.1 |  |  |  |  |  |  |  |  |  |
| DretRV1 | 17.7 | 23.9 | 22.8 | 23.0 | 32.9 | 34.8 | 34.0 | 51.5 | 67.9 |  |  |  |  |  |  |  |  |
| BCOV | 16.4 | 22.4 | 20.9 | 21.4 | 24.3 | 25.2 | 24.2 | 26.0 | 27.1 | 28.5 |  |  |  |  |  |  |  |
| BlTV2 | 16.2 | 21.3 | 23.9 | 23.1 | 23.9 | 25.8 | 28.0 | 24.8 | 26.2 | 29.0 | 36.6 |  |  |  |  |  |  |
| HbTRV1 | 14.4 | 23.6 | 20.4 | 20.3 | 25.1 | 27.3 | 25.9 | 27.5 | 26.7 | 28.4 | 37.3 | 41.1 |  |  |  |  |  |
| GyRTV1 | 17.7 | 21.8 | 22.6 | 21.3 | 24.0 | 26.7 | 25.7 | 24.8 | 26.6 | 28.8 | 35.9 | 41.4 | 45.1 |  |  |  |  |
| **ThRV2** | 19.5 | 27.5 | 23.7 | 21.6 | 25.2 | 25.2 | 26.7 | 23.9 | 23.8 | 24.0 | 22.7 | 20.4 | 19.3 | 19.4 |  |  |  |
| NWMV1 | 19.7 | 28.2 | 23.7 | 22.3 | 24.9 | 25.2 | 25.6 | 23.0 | 23.8 | 23.5 | 23.1 | 21.4 | 22.0 | 22.6 | 59.8 |  |  |
| TsTV | 24.9 | 19.9 | 20.2 | 19.9 | 19.7 | 19.3 | 18.9 | 17.3 | 18.0 | 18.3 | 18.2 | 17.5 | 16.0 | 19.1 | 19.9 | 18.8 |  |

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

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | ZjRTV1 | YbRTV1 | HpTV3 | HbanRV | ThRV1 | NnRTV1 | HgRTV1 | WhTV1 | YsRTV2 | DretRV1 | BCOV | BlTV2 | HbTRV1 | GyRTV1 | **ThRV2** | NWMV1 | TsTV |
| ZjRTV1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YbRTV1 | 38.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HpTV3 | 37.4 | 44.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbanRV | 37.9 | 43.9 | 82.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ThRV1 | 39.1 | 44.5 | 43.9 | 44.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| NnRTV1 | 39.2 | 45.0 | 44.1 | 44.2 | 69.6 |  |  |  |  |  |  |  |  |  |  |  |  |
| HgRTV1 | 39.3 | 44.9 | 42.8 | 42.7 | 66.0 | 66.0 |  |  |  |  |  |  |  |  |  |  |  |
| WhTV1 | 36.2 | 41.9 | 41.7 | 41.7 | 49.3 | 49.7 | 50.5 |  |  |  |  |  |  |  |  |  |  |
| YsRTV2 | 37.4 | 43.0 | 43.2 | 43.2 | 52.0 | 51.3 | 51.4 | 64.0 |  |  |  |  |  |  |  |  |  |
| DretRV1 | 36.8 | 42.9 | 42.7 | 42.5 | 51.2 | 50.2 | 49.8 | 63.4 | 72.2 |  |  |  |  |  |  |  |  |
| BCOV | 36.9 | 42.3 | 42.3 | 41.9 | 48.2 | 48.4 | 48.2 | 46.6 | 47.7 | 48.6 |  |  |  |  |  |  |  |
| BlTV2 | 37.5 | 41.4 | 41.5 | 41.5 | 49.5 | 50.4 | 48.7 | 47.1 | 48.7 | 48.3 | 56.5 |  |  |  |  |  |  |
| HbTRV1 | 37.6 | 43.2 | 41.8 | 41.4 | 49.8 | 50.2 | 48.9 | 48.6 | 49.1 | 48.8 | 55.3 | 63.0 |  |  |  |  |  |
| GyRTV1 | 37.8 | 42.8 | 41.1 | 41.8 | 50.6 | 50.3 | 50.0 | 47.3 | 49.3 | 48.8 | 55.8 | 64.7 | 66.2 |  |  |  |  |
| **ThRV2** | 41.2 | 48.3 | 47.2 | 47.4 | 50.3 | 49.4 | 49.5 | 45.4 | 46.7 | 45.8 | 45.7 | 45.9 | 45.0 | 45.6 |  |  |  |
| NWMV1 | 41.3 | 48.7 | 47.5 | 47.3 | 51.0 | 50.1 | 49.5 | 45.7 | 47.1 | 46.3 | 45.5 | 46.2 | 45.6 | 45.8 | 79.3 |  |  |
| TsTV | 45.2 | 38.6 | 37.5 | 37.6 | 37.4 | 37.9 | 37.6 | 37.2 | 36.4 | 36.7 | 35.8 | 36.0 | 37.3 | 36.4 | 40.0 | 40.7 |  |

**Table 12.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of alpharicinrhavirus G protein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | HpTV3 | HbanRV | ThRV1 | NnRTV1 | HgRTV1 | BCOV | BlTV2 | HbTRV1 | GyRTV1 | **ThRV2** | NWMV1 |
| HpTV3 |  |  |  |  |  |  |  |  |  |  |  |
| HbanRV | 35.1 |  |  |  |  |  |  |  |  |  |  |
| ThRV1 | 14.2 | 14.1 |  |  |  |  |  |  |  |  |  |
| NnRTV1 | 14.1 | 14.6 | 47.5 |  |  |  |  |  |  |  |  |
| HgRTV1 | 15.0 | 13.5 | 38.7 | 40.9 |  |  |  |  |  |  |  |
| BCOV | 12.5 | 13.4 | 31.2 | 31.8 | 30.4 |  |  |  |  |  |  |
| BlTV2 | 12.4 | 12.7 | 30.2 | 30.7 | 33.1 | 36.0 |  |  |  |  |  |
| HbTRV1 | 13.1 | 13.1 | 29.7 | 29.7 | 29.5 | 36.6 | 42.7 |  |  |  |  |
| GyRTV1 | 14.8 | 15.9 | 30.0 | 27.9 | 28.7 | 36.1 | 44.9 | 42.5 |  |  |  |
| **ThRV2** | 13.8 | 13.7 | 32.1 | 30.2 | 29.9 | 28.5 | 29.7 | 27.9 | 30.3 |  |  |
| NWMV1 | 14.6 | 14.9 | 30.3 | 31.1 | 30.3 | 28.9 | 29.7 | 30.1 | 30.1 | 69.4 |  |

**Table 13.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of merhavirus N protein sequences.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | MERDV | CTRV | **CamAnRV** | FORMV | **AsubRV** | INARV | HTTRV |
| MERDV |  |  |  |  |  |  |  |
| CTRV | 24.9 | 0 |  |  |  |  |  |
| **CamAnRV** | 16.0 | 18.8 |  |  |  |  |  |
| FORMV | 19.3 | 22.7 | 18.4 |  |  |  |  |
| **AsubRV** | 17.5 | 23.7 | 17.9 | 56.0 | 1 |  |  |
| INARV | 20.3 | 22.7 | 18.2 | 24.8 | 26.8 |  |  |
| HTTRV | 22.3 | 22.3 | 15.2 | 26.6 | 24.9 | 47.5 |  |

**Table 14.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of merhavirus L protein sequences.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | MERDV | CTRV | **CamAnRV** | FORMV | **AsubRV** | INARV | HTTRV |
| MERDV |  |  |  |  |  |  |  |
| CTRV | 43.7 |  |  |  |  |  |  |
| **CamAnRV** | 41.5 | 41.1 | 1 |  |  |  |  |
| FORMV | 38.7 | 38.1 | 37.1 |  |  |  |  |
| **AsubRV** | 38.5 | 38.1 | 37.5 | 72.2 |  |  |  |
| INARV | 38.0 | 37.9 | 37.9 | 50.0 | 51.0 |  |  |
| HTTRV | 38.9 | 38.0 | 37.7 | 50.6 | 51.0 | 67.0 |  |

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

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | MERDV | CTRV | **CamAnRV** | FORMV | **AsubRV** | INARV | HTTRV |
| MERDV |  |  |  |  |  |  |  |
| CTRV | 38.5 |  |  |  |  |  |  |
| **CamAnRV** | 18.1 | 18.8 | 1 |  |  |  |  |
| FORMV | 22.6 | 21.7 | 15.3 |  |  |  |  |
| **AsubRV** | 22.2 | 23.9 | 15.1 | 62.9 |  |  |  |
| INARV | 21.8 | 22.5 | 16.3 | 40.6 | 40.5 |  |  |
| HTTRV | 23.4 | 20.9 | 16.5 | 38.8 | 38.2 | 53.2 |  |

**Table 16.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of alphanemrhavirus N protein sequences.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | XsNV4 | XzNV4 | SDRV1 | RtaRV | **WfSRV1** |
| XsNV4 |  |  |  |  |  |
| XzNV4 | 35.2 |  |  |  |  |
| SDRV1 | 47.2 | 34.8 |  |  |  |
| RtaRV | 45.5 | 37.9 | 42.1 |  |  |
| **WfSRV1** | 37.9 | 35.3 | 37.5 | 52.4 |  |

**Table 17.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of alphanemrhavirus L protein sequences.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | XsNV4 | XzNV4 | SDRV1 | RtaRV | **WfSRV1** |
| XsNV4 |  |  |  |  |  |
| XzNV4 | 45.9 |  |  |  |  |
| SDRV1 | 53.0 | 46.0 |  |  |  |
| RtaRV | 51.8 | 47.3 | 52.3 |  |  |
| **WfSRV1** | 50.0 | 45.3 | 51.8 | 56.4 |  |

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | XsNV4 | XzNV4 | SDRV1 | RtaRV | **WfSRV1** |
| XsNV4 |  |  |  |  |  |
| XzNV4 | 20.6 |  |  |  |  |
| SDRV1 | 17.6 | 20.4 |  |  |  |
| RtaRV | 23.0 | 21.4 | 19.0 |  |  |
| **WfSRV1** | 19.9 | 18.7 | 19.3 | 26.1 |  |