

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 *Deltarhabdovirinae*, create 1 new species in the genus *Stangrhavirus*, 1 new species in the genus *Primrhavirus*, and 2 new species in the genus *Alphahymrhavirus* | |
| **Code assigned:** | 2024.N.v1.Deltarhabdovirinae\_4nsp |

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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 |

|  |  |  |  |
| --- | --- | --- | --- |
| **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| W - Withdrawn |  |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 |

Enter date of the revised version.

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

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| --- |
| **Name of accompanying Excel module:** |
| 2024.N.v1.Deltarhabdovirinae\_4nsp.xlsx |

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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 |  |

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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** | **Attached X** |
|  |  |  |

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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Species (*Mononegavirales*: *Rhabdoviridae: Deltarhabdovirinae*)  *Description of current taxonomy*:  The subfamily *Deltarhabdovirinae* currently comprises 11 genera including  34 species for viruses detected in various invertebrates (arthropods, nematodes and crustaceans).  *Proposed* *taxonomic change(s):*  Create 4 new species in the subfamily *Deltarhabdovirinae*, 1 in the genus *Stangrhavirus* for a virus detected in mosquitoes, 1 in the genus *Primrhavirus* for a virus detected in mosquitoes, and 2 in the genus *Alphahymrhavirus* for aviruses detected in ants and wasps.  *Justification*:  The viruses cluster phylogenetically with others in the existing genera in ML trees inferred using L protein sequences. All new species meet established demarcation criteria for the genera. |

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| **Text of Taxonomy proposal:**   1. **Create 1 new species in the genus *Stangrhavirus***   The genus *Stangrhavirus* comprises four species for members detected by metagenomic sequencing in mosquitoes (Culicidae) of various species. Stang virus (STNGV; species *Stangrhavirus stang*) was detected in *Culex erythrothorax* mosquitoes collected in the Placer Valley, California, in 2017 [1]. Elisy virus (ELSYV; species *Stangrhavirus elisy*) was detected in *Culex tarsalis* mosquitoes collected in Alameda County, California, USA, in 2017 [1]. Wuhan mosquito virus 9 (WhMV9; species *Stangrhavirus wuhan*) was detected in *Culex tritaeniorhynchus* mosquitoes collected in Yunnan, China, in 2018 [2]. Guadeloupe Culex rhabdovirus (GCRV; species *Stangrhavirus guadeloupe*) has been detected in mosquitoes of several species (*Culex quinquefasciatus*, *Deinocerites* sp., *Aedes aegypti*) collected in Guadeloupe, Grenada and Brazil, in 2015 and 2017 [3-5].  Xiangyun mono-chu-like virus 11 (XyMCLV11; strain XY234924) was detected by metagenomic sequencing of *Culex pipiens* mosquitoes collected in Yunnan Province, China, in 2018. We propose XyMCLV11 be assigned to the new species *Stangrhavirus yunnan*.  Genome organization  The complete genome coding sequence of XyMCLV11 (Genbank OL700136; 14,251 nt) has been reported, lacking only extreme 3’ and 5’ termini (**Figure 1**). Like other stangrhaviruses, the genome contains the five canonical rhabdovirus structural protein genes (*N*, *P*, *M,* *G* and *L*) and an additional gene (*U1*) encoding a small protein between the G and L genes. The U1 proteins of stangrhaviruses are homologous. Uniquely, in XyMCLV11 the *U1* gene is followed immediately by a second gene (*U2*) encoding a small protein that has no identifiable sequence homology with the stangrhavirus U1 proteins. The U1 and U2 ORFs are in independent transcriptional units and so very likely to be expressed.  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, XyMCLV11 clusters with the 4 viruses already assigned to the genus, forming a distinct and well-supported monophyletic clade (**Figure 2**).  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGAX from ClustalW amino acid sequence alignments for all viruses in the genus indicated that XyMCLV11 is most closely related to ELSYV in N (39.3% identity) and L (61.8% identity), and most closely related to WhMV9 in G (41.6% identity). (**Tables 1-3**).  Species demarcation criteria  The species demarcation criteria for the genus *Stangrhavirus* are that viruses assigned to different species within the genus 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 neutralization tests; and F) occupy different ecological niches as evidenced by differences in hosts and/or vectors.  The proposed new member of the genus meets criteria A, B and C. XyMCLV11 is similar in genome organization to other members of the genus but, uniquely, has an additional gene designated *U2.* It therefore also meets criterion D. No neutralization test data are yet available as there are currently no isolates of the viruses (criterion E). XyMCLV11 was detected in mosquitoes of a different species to those of other stangrhaviruses and in a different geographic location. It therefore also meets criterion F.  Derivation of the name of the new taxon  The species epithet for the new species was derived as follows:   |  |  | | --- | --- | | *Stangrhavirus yunnan* | derived from the Chinese province (Yunnan) from which the source mosquito sample was collected for virus metagenomic sequencing |  1. **Create 1 new species in the genus *Primrhavirus***   The genus *Primrhavirus* comprises three species for viruses detected by metagenomic sequencing in mosquitoes (Culicidae) of various species. Primus virus (PRIMV; species *Primrhavirus primus*) was discovered in *Aedes vexans* mosquitoes collected in Senegal, in 2014. Atrato rhabdo-like virus 3 (AtRLV3; species *Primrhavirus atrato*) was discovered in *Culex sp.* mosquitoes collected in Colombia, in 2016. San Gabriel mononegavirus (SGMNV; species *Primrhavirus gabriel*) was first discovered in an RNA-Seq library generated from an *Aedes albopictus* mosquito colony and then detected in wild-caught mosquitoes and various cell lines from *Aedes* spp. mosquitoes from various parts of the world.  XiangYun mono-chu-like virus 4 (XyMCLV4; strain XY19495) was detected by metagenomic sequencing of mosquitoes (*Culex theileri*) collected in Yunnan Province, China, in 2018. We propose XyMCLV4 be assigned to the new species *Primrhavirus yunnan*.  Genome organization  The complete genome coding sequence of XyMCLV4 (Genbank OL700129; 12,160 nt) has been reported, lacking only extreme 3’ and 5’ termini (**Figure 1**). Like other primrhaviruses, the genome contains only the five canonical rhabdovirus structural protein genes (*N*, *P*, *M,* *G* and *L*). There are no alternative long ORFs as have been detected in other primrhaviruses but which may or may not be expressed.  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, XyMCLV4 clusters with the 3 viruses already assigned to the genus, forming a distinct and well-supported monophyletic clade (**Figure 2**).  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGAX from ClustalW amino acid sequence alignments for all viruses in the genus indicated that XyMCLV4 is most closely related to PRIMV (71.1% identity in N; 84.2% identity in L; 83.6% identity in G) (**Tables 4-6**).  Species demarcation criteria  The species demarcation criteria for the genus *Primrhavirus* are that viruses assigned to different species within the genus 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 neutralization tests; and F) occupy different ecological niches as evidenced by differences in hosts and/or vectors.  The proposed new member of the genus meets criteria A, B and C. XyMCLV4 is similar in genome organization to other members of the genus (criterion D). No neutralization test data are yet available as there are currently no isolates of the viruses (criterion E). XyMCLV4 was detected in mosquitoes of a different species to those of other primrhaviruses. It therefore also meets criterion F.  **NOTE:**  Armigeres rhabdo-like virus 2 (ArmRLV2; strain G) was detected by metagenomic sequencing of mosquitoes (*Armigeres subalbatus*) collected in Jinghong, Yunnan Province, China, in 2018 [6]. Although it is a likely member of the genus *Primrhavirus* (**Figure 2**), it was not considered for classification as the genome sequence is incomplete, lacking the *N* gene and part of the *P* gene.  Derivation of the name of the new taxon  The species epithet for the new species was derived as follows:   |  |  | | --- | --- | | *Primrhavirus yunnan* | derived from the Chinese province (Yunnan) from which the source mosquito sample was collected for virus metagenomic sequencing |  1. **Create 2 new species in the genus *Alphahymrhavirus***   The genus *Alphahymrhavirus* comprises six species for viruses detected by metagenomic sequencing, primarily in hymenopteran insects (Hymenoptera). Four of the viruses were detected in wasps of various species (*Pompilus cinereus*, *Chrysura radians, Chlorion hirtum,* *Lariophagus distinguendus),* one was detected in ants *(Lasius neglectus)* [7-9],and one was detected in a mixed sample of insects (Hymenoptera; Diptera; Lepidoptera).  Electric ant rhabdovirus (EARV) was detected by metagenomic sequencing of little fire ants (*Wasmannia auropunctata*) collected from various locations in Argentina, 2019-2021 [10]. We propose EARV be assigned to the new species *Alphahymrhavirus electrico*.  Ectemnius rhabdovirus (EctRV) was discovered in a digger wasp (*Ectemnius lituratus*) collected in Oxfordshire, England [11] by data mining of the NCBI Sequence Read Archive (SRA) repository. We propose EARV be assigned to the new species *Alphahymrhavirus ectemnius*.  Genome organization  The near-complete genome sequence of EARV (Genbank OP518027; 12,034 nt) has been reported, lacking only extreme 3’ and 5’ termini (**Figure 1**). Although the authors claim to have determined the exact terminal sequences by 5’ and 3’ RACE [10], the termini are not anti-complementary, suggesting they remain incomplete. Like other alphahymrhaviruses, the genome contains only the five canonical rhabdovirus structural protein genes (*N*, *P*, *M,* *G* and *L*). The coding complete genome sequence of EctRV (Gernbank BK063699; 12,682 nt) has been reported, lacking only extreme 3’ and 5’ termini. The genome contains the five canonical rhabdovirus structural protein genes (*N*, *P*, *M,* *G* and *L*). Uniquely amongst alphahymrhaviruses, in the *M* gene there is a long overlapping ORF of 453 nt that commences 323 nt upstream of the M ORF stop codon and terminates within the M transcriptional unit. If expressed, the overlapping ORF could encode a 17.4 kD basic protein or, by ribosomal frameshift, provide an alternative C-terminal domain for the M protein.  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, EARV and EctRV cluster with the viruses already assigned to the genus, forming a distinct and well-supported monophyletic clade (**Figure 2**).  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGAX from ClustalW amino acid sequence alignments for all viruses in the genus indicated that EARV is most closely related to Lasius neglectus virus 2 (LnegV2; species *Alphahymrhavirus neglectus*) in N (45.0% identity) and L (56.7% identity), and most closely related to EctRV in G (23.2% identity). EctRV is also most closely related to LnegV2 in N (28.2% identity) and L (48.2% identity), and most closely related to hymenopteran rhabdo-related virus 38 (HyRRV38; species *Alphahymrhavirus cinereus*) in G (23.7% identity) (**Tables 7-9**).  Species demarcation criteria  The species demarcation criteria for the genus *Alphahymrhavirus* are that viruses assigned to different species within the genus 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 neutralization tests; and F) occupy different ecological niches as evidenced by differences in hosts and/or vectors.  The proposed new members of the genus meet criteria A, B and C. EARV is similar in genome organization to other members of the genus, but EctRV varies in the structure of the M gene (criterion D). No neutralization test data are yet available as there are currently no isolates of the viruses (criterion E). Each new member was detected in ants or wasps of different species to those of other alphahymrhaviruses. They therefore also meet criterion F.  **NOTE:**  Wuhan ant virus (WhAV; strain WHMY02) was discovered in a pool of a Japanese carpenter ants (*Camponotus japonicus*) collected in Hubei Province, China, in 2013. Although a likely member of the genus, it was not considered for classification as the genome sequence is incomplete, comprising only partial *G* gene and the complete *L* gene [2].  Derivation of the name of the new taxon  The species epithet for the new species was derived as follows:   |  |  | | --- | --- | | *Alphahymrhavirus electrico* | derived from one common name of the ant species (electric ant) that was the source sample collected for virus metagenomic sequencing. This name was proposed by the authors of the associated manuscript. | | *Alphahymrhavirus ectemnius* | derived from the genus name of the wasp species (*Ectemnius lituratus*) that was the source sample for the SRA in which the virus sequence was detected. | |
| |  | | --- | | **References:** | | 1. **Batson J, Dudas G, Haas-Stapleton E, Kistler AL, Li LM et al.** (2021) Single mosquito metatranscriptomics identifies vectors, emerging pathogens and reservoirs in one assay. Elife 10:e68353. PMID: 33904402  2. **Li CX, Shi M, Tian JH, Lin XD, Kang YJ et al.** (2015) Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative-sense RNA viruses. Elife 4:e05378. PMID: 25633976  3. **Shi C, Beller L, Deboutte W, Yinda KC, Delang L et al.** (2019) Stable distinct core eukaryotic viromes in different mosquito species from Guadeloupe, using single mosquito viral metagenomics. Microbiome 7:e121. PMID: 31462331  4. **Xu CL, Cantalupo PG, Sáenz-Robles MT, Baldwin A, Fitzpatrick D et al.** (2018) Draft genome sequence of a novel rhabdovirus isolated from *Deinocerites* mosquitoes. Genome Announcements 6:e01438-01417. PMID: 29748415  5. **da Silva Ferreira R, de Toni Aquino da Cruz LC, de Souza VJ, da Silva Neves NA, de Souza VC et al.** (2020) Insect-specific viruses and arboviruses in adult male culicids from Midwestern Brazil. Infection Genetics and Evolution 85:e104561. PMID: 32961364  6. **Li C, Liu S, Zhou H, Zhu W, Cui M et al.** (2023) Metatranscriptomic sequencing reveals host species as an important factor shaping the mosquito virome. Microbiology Spectrum 11:e0465522. PMID: 36786616  7. **Kleanthous E, Olendraite I, Lukhovitskaya NI, Firth AE**. (2019) Discovery of three RNA viruses using ant transcriptomic datasets. Arch Virol 164:643-647. PMID: 30415391  8. **Kafer S, Paraskevopoulou S, Zirkel F, Wieseke N, Donath A et al.** (2019) Re-assessing the diversity of negative strand RNA viruses in insects. PLoS Pathogens15:e1008224. PMID: 31830128  9. **Wang F, Yuan B, Xiao S, Zhang J, Jia W et al.** (2021) Diverse RNA viruses discovered in three parasitoid wasps of the rice weevil *Sitophilus oryzae*. *mSphere* 6:e00331-21. PMID: 33952664  10. **Valles SM, Zhao C, Rivers AR, Iwata RL, Oi DH et al.** (2023) RNA virus discoveries in the electric ant, *Wasmannia auropunctata*. *Virus Genes* 59:276-289. PMID: 36729322  11. **Caldas-Garcia GB, Santos VC, Fonseca PLC, de Almeida JPP, Costa MA et al.** (2023) The viromes of six ecosystem service provider parasitoid wasps. *Viruses* 15:e2448. PMID: 38140687 | |

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| **Tables, Figures:**    **Figure 1 (above).** Schematic scale illustration of the genome organisations of stangrhaviruses, primrhaviruses and alphahymrhaviruses. Arrows represent long open reading frames (ORFs). ORFs encoding small homologous proteins are shown in cherry red. A long ORF in XyMCLV11 that lies within an independent transcriptional unit is shown in blue. Other alternative or overlapping ORFs of moderate length within the canonical structural protein genes are shown in grey; these may or may not be expressed.    **Figure 2 (above).** The evolutionary history was inferred from a multiple sequence alignment of complete L protein sequences of 34 rhabdoviruses that are currently assigned to species in the family *Rhabdoviridae* as well as 4 viruses proposed to be assigned to existing genera in the family and 2 viruses that are likely to be members but for which the genome sequences are incomplete. 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 1776 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 (-116487.89) 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 mid-rooted 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 stangrhavirus N protein sequences.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | GCRV | **XyMCLV11** | WhMV9 | ELSYV | STNGV |
| GCRV |  |  |  |  |  |
| **XyMCLV11** | 24.0 |  |  |  |  |
| WhMV9 | 28.4 | 38.5 |  |  |  |
| ELSYV | 25.2 | 39.3 | 47.7 |  |  |
| STNGV | 25.5 | 39.2 | 48.8 | 51.8 |  |

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | GCRV | **XyMCLV11** | WhMV9 | ELSYV | STNGV |
| GCRV |  |  |  |  |  |
| **XyMCLV11** | 42.7 |  |  |  |  |
| WhMV9 | 42.4 | 60.5 |  |  |  |
| ELSYV | 42.8 | 61.8 | 63.9 |  |  |
| STNGV | 41.9 | 60.3 | 65.1 | 65.6 |  |

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | GCRV | **XyMCLV11** | WhMV9 | ELSYV | STNGV |
| GCRV |  |  |  |  |  |
| **XyMCLV11** | 28.2 |  |  |  |  |
| WhMV9 | 30.2 | 41.6 |  |  |  |
| ELSYV | 26.8 | 41.4 | 46.6 |  |  |
| STNGV | 27.2 | 40.3 | 45.4 | 47.7 |  |

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | AtRLV3 | SGMNV | PRIMV | **XyMCLV4** |
| AtRLV3 |  |  |  |  |
| SGMNV | 24.9 |  |  |  |
| PRIMV | 25.6 | 37.3 |  |  |
| **XyMCLV4** | 24.8 | 38.0 | 71.1 |  |

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | AtRLV3 | SGMNV | PRIMV | **XyMCLV4** |
| AtRLV3 |  |  |  |  |
| SGMNV | 45.4 |  |  |  |
| PRIMV | 45.7 | 60.4 |  |  |
| **XyMCLV4** | 44.9 | 60.5 | 84.2 |  |

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | AtRLV3 | SGMNV | PRIMV | **XyMCLV4** |
| AtRLV3 |  |  |  |  |
| SGMNV | 23.8 |  |  |  |
| PRIMV | 23.7 | 39.7 |  |  |
| **XyMCLV4** | 22.7 | 39.4 | 83.6 |  |

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

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | HyRRV46 | HyRRV109 | XsRLV3 | LdisNSV1 | **EctRV** | HyRRV38 | LnegV2 | **EARV** |
| HyRRV46 |  |  |  |  |  |  |  |  |
| HyRRV109 | 55.5 |  |  |  |  |  |  |  |
| XsRLV3 | 44.4 | 40.7 |  |  |  |  |  |  |
| LdisNSV1 | 37.6 | 38.3 | 37.1 |  |  |  |  |  |
| **EctRV** | 21.8 | 20.5 | 21.9 | 20.3 |  |  |  |  |
| HyRRV38 | 23.7 | 23.0 | 20.5 | 24.4 | 24.6 |  |  |  |
| LnegV2 | 28.4 | 24.4 | 22.0 | 26.8 | 28.2 | 35.6 |  |  |
| **EARV** | 24.2 | 23.1 | 23.2 | 24.5 | 27.1 | 31.2 | 45.0 |  |

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

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | HyRRV46 | HyRRV109 | XsRLV3 | LdisNSV1 | **EctRV** | HyRRV38 | LnegV2 | **EARV** |
| HyRRV46 |  |  |  |  |  |  |  |  |
| HyRRV109 | 64.6 |  |  |  |  |  |  |  |
| XsRLV3 | 50.3 | 51.0 |  |  |  |  |  |  |
| LdisNSV1 | 48.0 | 48.4 | 48.0 |  |  |  |  |  |
| **EctRV** | 40.1 | 39.7 | 40.6 | 38.2 |  |  |  |  |
| HyRRV38 | 40.0 | 39.8 | 40.4 | 39.3 | 46.9 |  |  |  |
| LnegV2 | 41.6 | 41.0 | 41.4 | 39.2 | 48.2 | 49.3 |  |  |
| **EARV** | 42.1 | 40.8 | 41.0 | 40.0 | 47.2 | 48.8 | 56.7 |  |

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

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | HyRRV46 | HyRRV109 | XsRLV3 | LdisNSV1 | **EctRV** | HyRRV38 | LnegV2 | **EARV** |
| HyRRV46 |  |  |  |  |  |  |  |  |
| HyRRV109 | 41.8 |  |  |  |  |  |  |  |
| XsRLV3 | 25.2 | 22.8 |  |  |  |  |  |  |
| LdisNSV1 | 27.1 | 24.9 | 23.8 |  |  |  |  |  |
| **EctRV** | 18.8 | 18.9 | 20.9 | 15.0 |  |  |  |  |
| HyRRV38 | 18.9 | 18.5 | 17.2 | 16.6 | 23.7 |  |  |  |
| LnegV2 | 18.5 | 17.8 | 17.2 | 16.9 | 21.6 | 23.2 |  |  |
| **EARV** | 20.3 | 18.9 | 19.5 | 19.1 | 23.2 | 21.9 | 22.3 |  |