

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Create 2 new species in the genus *Betaplatrhavirus*,1 new species in the genus *Alphacrustrhavirus* and 1 new species in the genus *Novirhabdovirus* (*Mononegavirales: Rhabdoviridae*) |
| **Code assigned:** | 2025.009M.Ac.v4.Rhabdoviridae\_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 |

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| **Optional – complete only if formally voted on by an ICTV Study Group:** | | | |
| **Study Group** | **Number of members** | | |
| **Votes in support** | **Votes against** | **No vote** |
| *Rhabdoviridae* SG | 14 |  | 1 |
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| **Submission date:** | 30/05/2025 |

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

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required | **x** |
| 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| W - Withdrawn |  |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:** |
| Ac for minor typographical edits and consistent Abstract format across all Subcommittees. |

**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer** |
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| **Revision date:** | 19/08/2025 |

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

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

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| **Etymology (origin) of proposed taxonomic names:** | |
| **Taxon name** | **Etymology of the term** |
| *Betaplatrhavirus pipistrellus* | The species epithet is adopted from the genus name of the Japanese house bat (*Pipistrellus abramus*), the source of the pharyngeal and anal swab in which the member virus was detected. |
| *Betaplatrhavirus robustula* | The species epithet is adopted from the species epithet of the greater bamboo bat (*Tylonycteris robustula*), the source of the pharyngeal and anal swab in which the member virus was detected. |
| *Alphacrustrhavirus vison* | The species epithet is adopted from the species epithet of American mink (*Neogale vison*), the source of the fecal sample in which the member virus was detected. |
| *Novirhabdovirus carpione* | The species epithet is adopted from the virus name (carpione rhabdovirus) which itself has been named from Lake Garda carpione (S*almo carpio*) the common name for the fish from which the member virus was first isolated. |

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| **Permission for use of names derived from a living person** | | |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached** X |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Species in the family *Rhabdoviridae*.  *Description of current taxonomy*:   * The genus *Betaplatrhavirus* is not assigned to a subfamily. It currently includes 12 species for viruses detected in platyhelminth parasites, or in gill, gut or anal swab samples taken from vertebrates. * The subfamily *Deltarhabdovirinae* currently comprises 11 genera including 38 species for viruses detected in invertebrates. These include 2 species in the genus *Alphacrustrhavirus* for viruses detected in crustaceans. * The subfamily *Gammarhabdovirinae* currently comprises 2 genera including 4 species in the genus *Novirhabdovirus* for viruses infecting or detected in ray-finned fish and 1 species in the genus *Margarhavirus* for a virus detected in freshwater molluscs.   *Proposed* *taxonomic change(s):*   1. Create 2 new species in the genus *Betaplatrhavirus*. 2. Create 1 new species in the genus *Alphacrustrhavirus.* 3. Create 1 new species in the genus *Novirhabdovirus*.   *Justification*:  Four viruses for which complete coding sequences are now available fall phylogenetically within clades representing these three genera and meet demarcation criteria for the creation of new species. |

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| **Text of Taxonomy proposal:** |
| 1. **Create 2 new species in the genus *Betaplatrhavirus***   Bat-associated rhabdovirus 1 (BaRV1; strain GD2018) was detected by high-throughput sequencing of a pharyngeal and anal swab from a Japanese house bat (*Pipistrellus abramus*) collected in China in 2018 (PRJNA994658). Bat-associated rhabdovirus 3 (BaRV3; strain GX2016) was detected by high-throughput sequencing of a pharyngeal and anal swab from a greater bamboo bat (*Tylonycteris robustula*) collected in China in 2016 (PRJNA994658). We propose BaRV1 be assigned to the new species *Betaplatrhavirus pipistrellus* and BaRV3 be assigned to the new species *Betaplatrhavirus robustula*.  Ecology  The genus *Betaplatrhavirus* currently comprises 12 species for viruses detected by metagenomic sequencing in platyhelminth parasites, or in gill, gut or anal swab samples taken from vertebrates. The detection of BaRV1 and BaRV3 in pharyngeal and anal swabs from bats is consistent with this ecology and suggests that platyhelminth parasite infestations are the true source. Bat-associated rhabdovirus 2 (BaRV2; species *Betaplatrhavirus abramus*) was also detected in a pharyngeal and anal swab from a Japanese house bat (*Pipistrellus abramus*) collected in China.  Genome organisations  The complete genome coding sequences of BaRV1 (11884 nt; GenBank OR951391) and BaRV3 (11798 nt; GenBank OR951389) have been reported. The genomes lack only extreme 3' and 5' termini. The genome organizations are similar to those of some other betaplatrhaviruses, containing only the five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*). Some other betaplatrhaviruses lack a *G* gene and Eptesticus fuscus rhabdovirus (EfusRV; species *Betaplatrhavirus fuscus*) contains an additional small gene between the *G* and *L* genes (**Figure 1**).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, BaRV1 and BaRV3 fall with the betaplatrhaviruses in a distinct and well-supported monophyletic clade (**Figure 2**). BaRv1 lies on a sub-clade with Behai dimarhabdovirus 1 (BhDRV1; species *Betaplatrhavirus behai*) and triaenorhabdovirus 2 (TriRV2; species *Betaplatrhavirus nodulosis*). BaRV3 lies on a sub-clade with BaRV2 and rhabdovirus HAGXC131516/2 (HAGXCRV; species *Betaplatrhavirus armiger*).  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGA7 from ClustalW amino acid sequence alignments indicate that BaRV1 is most closely related to both TriRV2 and BaRV3 in the L protein (31.7% identity), to Wenling dimarhabdovirus 1 (WlDRV1; species *Betaplatrhavirus wenling*) in the N protein (15.6% identity) and psilorhabdovirus 2 (PsiRV2; species *Betaplatrhavirus simillimum*) the G protein (14.9% identity); BaRV3 is most closely related to HAGXCRV in the L, N and G proteins (73.7%, 79.6% and 63.5% identity, respectively) (**Tables 1–3**).  Species demarcation criteria  The species demarcation criteria for the genus *Betaplatrhavirus* 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 two proposed members of the genus meet criteria A and B. The divergence between BaRV1 and one other member virus (PsiRV2) is marginally below the demarcation point (criterion C). There are significant differences in genome organization between these viruses and some other members of the genus, but other members are similar (criterion D). No neutralization test data are yet available as there are currently no isolates of the viruses (criterion E). One other betaplatrhavirus has been detected in a pharyngeal and anal swab from a bat from China (criterion F).   1. **Create 1 new species in the genus *Alphacrustrhavirus***   Mink stool-associated rhabdovirus (MSaRV; strain PJSD13) was detected in the feces of farmed American mink (*Neogale vison*) from China in 2023 (GenBank submission). We propose MSaRV be assigned to the new species *Alphacrustrhavirus vison*.  Ecology  There are currently two species in the genus *Alphacrustrhavirus*. Wenling crustacean virus 10 (WlCV10; species *Alphacrustrhavirus wenling*) and Wenling crustacean virus 11 (WlCV11; species *Alphacrustrhavirus zhezhang*) were each discovered by high throughput sequencing in a pool of marine crustaceans (multiple families) collected in Zhezhang Province, China, in 2014. The detection of MSaRV in the feces of farmed mink appears to be consistent with their common diet which consists primarily of waste from fish and poultry processing plants (https://fur.ca/fur-farming/mink-farming/). In the wild, crustaceans can be a component of their natural diet [8, 9].  Genome organization  The complete genome coding sequence of MSaRV (12362 nt; GenBank PQ182562) has been reported. The genome lacks only extreme 3' and 5' termini. The genome organization is similar to those of other alphacrustrhaviruses which contain only five genes (*N*, *P*, *M*, *G* and *L*) encoding canonical rhabdovirus structural proteins, although one other alphacrustrhavirus (WlCV11) has an alternative long ORF in the *P* gene. Uniquely amongst known animal rhabdoviruses, the MSaRV genome features a complete additional gene following the *L* gene. It contains a single ORF encoding a putative 21.5 kDa polypeptide (**Figure 1**).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, MSaRV falls with the alphacrustrhaviruses in a distinct and well-supported monophyletic clade in the subfamily *Deltarhabdovirinae* **(Figure 2**). MSaRV lies on a sub-clade with WlCV11.  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGA7 from ClustalW amino acid sequence alignments indicate that MSaRV is most closely related to WlCV11 in the L, N and G proteins (61.2%, 43.5% and 48.7% identity, respectively) (**Tables 4–6**).  Species demarcation criteria  Viruses assigned to different species within the genus *Alphacrustrhavirus* 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, C and D. As no virus isolates are currently available neutralisation tests have not been conducted (criterion E). As the virus was detected in a fecal sample, the source host is not entirely certain (criterion F).   1. **Create 1 new species in the genus *Novirhabdovirus***   Carpione rhabdovirus (CAPRV; strain LG1988) was first isolated from whole fry of Lake Garda carpione (S*almo carpio*) collected in Italy in 1988 [2]. It was subsequently isolated from the spleen and trunk kidney of cultured golden pompano (*Trachinotus ovatus*) suffering mass mortalities in Zhanjiang, Guangdong Province, China, in 2023 [11]. We propose CAPRV be assigned to the new species *Novirhabdovirus carpione*.  Ecology  Novirhabdoviruses infect ray-finned fish. There are currently four species in the genus. Infectious hematopoietic necrosis virus (IHNV; species *Novirhabdovirus salmonid*) has a host range restricted largely to salmonid fish. It is enzootic in North America but has also been reported in other parts of the world [3, 12]. Viral hemorrhagic septicemia virus (VHSV; species *Novirhabdovirus piscine*) has a very broad host range in finfish from diverse families. It occurs naturally in wild fish species in the northern Atlantic and Pacific Oceans [3, 12]. Snakehead rhabdovirus (SHRV; species *Novirhabdovirus snakehead*) was first isolated from the tissues of diseased snakehead fish (*Ophicephalus striatus*) during an epizootic ulcerative syndrome (EUS) outbreak in Thailand [5] and appears to be restricted in distribution to South-East Asia. Hirame rhabdovirus (HIRRV; species *Novirhabdovirus hirame*) was first detected in Japanese flounder (*Paralichthys olivaceus*) in Japan [7] and subsequently in Korea [6] but appears to have a wide host range amongst ray-finned fish. It has also been shown in Japan to infect ayu (*Plecoglossus olivaceus*), black seabream (*Milio macrocephalus*), mebaru (*Sebastes inermis*) and rainbow trout, (*Oncorhynchus mykiss*) [7, 10, 14], as well as stone flounder (*Paralichthys bicoloratu*) in China [13], and greyling (*Thymallus thymallus*) in Poland [1].  Genome organisation  The complete genome coding sequence of CAPRV (11285 nt; GenBank LC630942) has been reported [4]. The genome lacks only extreme 3' and 5' termini. The genome organization is similar to those of other novirhabdoviruses, containing the five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*) and an additional gene (*NV*) between the *G* and *L* genes encoding a small non-structural protein (**Figure 1**).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, the two samples of CAPRV fall with the novirhabdoviruses in a distinct and well-supported monophyletic clade (**Figure 2**). The CAPRV samples lie on a sub-clade with SHRV. ML trees were inferred using two different models for multiple sequence alignment of L and N proteins of two samples of CAPRV, a single available sample of SHRV, three available samples of HIRRV, and large data sets of available VHSV and IHNV sequences from diverse sources (**Figure 3**). In each case, the CAPRV isolates form a distinct monophyletic clade, albeit with a level of sequence divergence that exceeds that observed for viruses assigned to other novirhabdovirus species.  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGA7 from ClustalW nucleotide and amino acid sequence alignments indicate that CAPRV (strain LG1988) is most closely related to SHRV in the *G* gene (55.0–55.2% identity) and in the G protein (54.3–55.1% identity) (**Tables 7–8**). The two CAPRV isolates (1988 and 2023) share 80.5% identity in the *G* gene and 86.3% identity in the G protein.  Serology  CAPRV has been reported to not be neutralized by rabbit antisera to IHNV or VHSV [2]. CAPRV does cross-react by immunofluorescence with VHSV antiserum and with monoclonal antibodies (MAbs) directed at the VHSV N protein and G protein, but not with rabbit antiserum to IHNV [2]. Rabbit antiserum to CAPRV did not cross-react by immunofluorescence with VHSV or IHNV. By immunoblotting VHSV rabbit antiserum was shown to cross-react with the CAPRV G protein and a VHSV N protein MAb cross-reacted with the CAPRV N protein. No cross-reactions with CAPRV proteins were detected using IHNV rabbit antiserum [2].  Species demarcation criteria  Viruses assigned to different species within the genus *Novirhabdovirus* have some of the following characteristics: A) minimum of 31% nucleotide divergence and 26% amino acid divergence in the G gene and G protein, respectively; B) phylogenetic structure as distinct monophyletic clades in phylogenetic analyses with various genome regions, obtained with various evolutionary models; C) distinguished by serological tests; and D) occupy different ecological niches as indicated by non-overlapping or partially overlapping host ranges, and non-overlapping or partially overlapping geographic ranges.  The proposed new member of the genus meets criteria A, B and C. The species of fish and geographic locations in which the virus has been detected are novel amongst novirhabdoviruses but the possible host range and geographic range have not yet been determined (criterion D). The nucleotide and amino acid sequence divergence of the two isolates of the virus fall below that required for assignment to different species. |

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| **References:** |
| 1. Borzym E, Matras M, Maj-Paluch J, Baud M, De Boisseson C, Talbi C, Olesen NJ, Bigarre L (2014) First isolation of hirame rhabdovirus from freshwater fish in Europe. Journal of Fish Diseases 37:423-430. PMID: 23962315  2. Bovo G, Olesen NJ, Jorgensen PEV, Ahne W, Winton JR (1995) Characterization of a rhabdovirus isolated from carpione Salmo trutta carpio in Italy. Diseases of Aquatic Organisms 21:115-122. DOI:10.3354/dao021115  3. Epizooties OId (2021) Manual of Diagnostic Tests for Aquatic Animals. World Organisation of Animal Health, Paris, pp https://www.woah.org/en/what-we-do/standards/codes-and-manuals/aquatic-manual-online-access/  4. Ito T, Mekata T, Olesen NJ, Lorenzen N (2023) Epitope mapping of the monoclonal antibody IP5B11 used for detection of viral haemorrhagic septicaemia virus facilitated by genome sequencing of carpione novirhabdovirus. Vetinary Research 54:e35. PMID: 37069579  5. Kasornchandra J, Engelking HM, Lannan CN, Rohovec JS, Fryer JL (1992) Characteristics of three rhabdoviruses from snakehead fish *Ophicephalus striatus*. Diseases of Aquatic Organisms 13:89-94. DOI:10.3354/dao013089  6. Kim DH, Oh HK, Eou JI, Seo HJ, Kim SK, Oh MJ, Nam SW, Choi TJ (2005) Complete nucleotide sequence of the hirame rhabdovirus, a pathogen of marine fish. Virus Res 107:1-9. PMID: 15567027  7. Kimura T, Yoshimizu M, Gorie S (1986) A new rhabdovirus isolated in Japan from cultured hirame (Japanese flounder) *Paralichthys olivaceus* and ayu *Plecoglossus altivelis*. Diseases of Aquatic Organisms 1:209-217. DOI: 10.3354/dao001209  8. Malmkvist J, Palme R, Svendsen PM, Hansen SW (2013) Additional foraging elements reduce abnormal behaviour – fur-chewing and stereotypic behaviour – in farmed mink (*Neovison vison*). Applied Animal Behaviour Science 149:77-86. DOI:10.1016/j.applanim.2013.10.001  9. Rørbæk RW, Andersen TA, Pertoldi C, Jørgensen A, Pagh S (2023) Diet of free ranging American Mink (*Neovison vison*) in Denmark. Animals (Basel) 13:e461. PMID: 36766350  10. Sano T, Fukuda H (1987) Principal microbial disease of mariculture in Japan. Aquaculture 67:59-70. DOI: 10.1016/0044-8486(87)90008-1  11. Sun H, Huang J, Wang H, Zhang Y, Fei Q, Zhou J, Yang L, Li Y, Jian J, Lu Y, Cai S, Huang Y (2025) Mass mortality associated with carpione rhabdovirus in golden pompano (*Trachinotus ovatus*) in China: First report. Aquaculture 595:e741638. DOI:10.1016/j.aquaculture.2024.741638  12. Walker PJ, Winton JR (2010) Emerging viral diseases of fish and shrimp. Vet Res 41:e51. PMID: 20409453  13. Yingjie S, Min Z, Hong L, Zhiqin Y, Xiaocong Z, Zhe W (2011) Analysis and characterization of the complete genomic sequence of the Chinese strain of hirame rhabdovirus. Journal of Fish Diseases 34:167-171. PMID: 21241324  14. Yoshimizu M, Nishizawa T, O’seko N, Kimura T (1987) Rhabdovirus disease of hirame (Japanese flounder). Fish Pathology 22:54-55. |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |

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| **Tables, Figures:** |



**Figure 1.** Schematic illustration of the genome organisations of betaplatrhaviruses, alphacrustrhaviruses and novirhabdoviruses. Arrows represent long open reading frames (ORFs) with the N, P, M, G and L ORFs shown and additional ORFs shaded. Apparently unique ORFs are shaded in grey and ORFs encoding homologous novirhabdovirus NV proteins shown in crimson.



**Figure 2.** The evolutionary history was inferred from a multiple sequence alignment of complete L protein sequences of 79 rhabdoviruses that are currently assigned to species in the subfamily *Gammarhabdovirinae*, subfamily *Deltarhabdovirinae* and the genera *Alphaplatrhavirus*, *Betaplatrhavirus* and *Gammaplatrhavirus*, as well as 4 viruses proposed to be assigned to 4 new species in the family. 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 902 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 (-108365.67) is shown. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log-likelihood values. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Bootstrap values (100 iterations) are shown for each node.



**Figure 3.** **A.** The evolutionary history was inferred from a MUSCLE multiple sequence alignment of complete L protein sequences of 155 rhabdoviruses that are currently assigned to species in the subfamily *Gammarhabdovirinae*, as well as two isolates of carpione rhabdovirus proposed to be assigned to a new species in the genus *Novirhabdovirus.* **B.** The evolutionary history was inferred from a CLUSTAL W multiple sequence alignment of complete L protein sequences of 139 rhabdoviruses that are currently assigned to species in the subfamily *Gammarhabdovirinae*, as well as two isolates of carpione rhabdovirus proposed to be assigned to a new species in the genus *Novirnabdovirus.* Each 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 (-28611.17 in tree A and 0.8191.63 in tree B) is shown. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log-likelihood values. The trees are 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 betaplatrhavirus L sequences.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | HAGXCRV | BaRV2 | **BaRV3** | PsiRV2 | SphRV2 | PsiRV1 | SphRV3 | EfusRV | FjDRV | HIMRV1 | WlDRV1 | **BaRV1** | BhDRV1 | TriRV2 |
| HAGXCRV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| BaRV2 | 77.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **BaRV3** | 73.7 | 73.3 |  |  |  |  |  |  |  |  |  |  |  |  |
| PsiRV2 | 56.9 | 58.0 | 56.6 |  |  |  |  |  |  |  |  |  |  |  |
| SphRV2 | 57.5 | 58.1 | 57.5 | 64.8 |  |  |  |  |  |  |  |  |  |  |
| PsiRV1 | 49.0 | 48.4 | 49.2 | 51.0 | 49.6 |  |  |  |  |  |  |  |  |  |
| SphRV3 | 50.0 | 49.6 | 49.9 | 51.5 | 50.7 | 55.7 |  |  |  |  |  |  |  |  |
| EfusRV | 45.6 | 45.2 | 45.4 | 45.7 | 46.9 | 45.2 | 44.4 |  |  |  |  |  |  |  |
| FjDRV | 44.5 | 43.6 | 44.3 | 45.0 | 45.5 | 45.0 | 44.9 | 41.7 |  |  |  |  |  |  |
| HIMRV1 | 41.8 | 41.7 | 41.7 | 43.8 | 43.5 | 42.6 | 42.9 | 42.6 | 41.8 |  |  |  |  |  |
| WlDRV1 | 35.2 | 35.5 | 35.3 | 35.6 | 35.9 | 34.6 | 34.3 | 34.6 | 34.5 | 34.4 |  |  |  |  |
| **BaRV1** | 30.6 | 31.5 | 31.7 | 31.0 | 30.9 | 31.2 | 30.2 | 31.0 | 30.0 | 30.3 | 27.6 |  |  |  |
| BhDRV1 | 28.1 | 28.5 | 27.7 | 27.6 | 27.8 | 27.1 | 27.5 | 27.9 | 27.2 | 26.8 | 26.6 | 28.9 |  |  |
| TriRV2 | 30.2 | 30.3 | 31.1 | 30.9 | 30.5 | 30.3 | 29.8 | 29.6 | 31.5 | 31.2 | 28.7 | 31.7 | 34.4 |  |

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

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | HAGXCRV | BaRV2 | **BaRV3** | PsiRV2 | SphRV2 | PsiRV1 | SphRV3 | EfusRV | FjDRV | HIMRV1 | WlDRV1 | **BaRV1** | BhDRV1 | TriRV2 |
| HAGXCRV |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| BaRV2 | 82.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **BaRV3** | 79.6 | 77.6 |  |  |  |  |  |  |  |  |  |  |  |  |
| PsiRV2 | 52.6 | 52.6 | 53.3 |  |  |  |  |  |  |  |  |  |  |  |
| SphRV2 | 55.0 | 54.6 | 54.8 | 63.1 |  |  |  |  |  |  |  |  |  |  |
| PsiRV1 | 38.3 | 37.8 | 39.1 | 39.5 | 37.7 |  |  |  |  |  |  |  |  |  |
| SphRV3 | 35.4 | 34.3 | 36.5 | 37.4 | 37.7 | 43.6 |  |  |  |  |  |  |  |  |
| EfusRV | 32.9 | 33.1 | 32.4 | 36.9 | 33.3 | 30.6 | 31.0 |  |  |  |  |  |  |  |
| FjDRV | 36.5 | 36.8 | 36.1 | 37.9 | 34.7 | 34.2 | 32.4 | 35.4 |  |  |  |  |  |  |
| HIMRV1 | 26.0 | 24.9 | 24.7 | 26.5 | 27.3 | 28.3 | 28.0 | 26.0 | 30.0 |  |  |  |  |  |
| WlDRV1 | 18.3 | 18.3 | 18.0 | 19.4 | 19.2 | 19.6 | 18.0 | 18.8 | 18.9 | 17.8 |  |  |  |  |
| **BaRV1** | 12.9 | 12.9 | 13.1 | 12.8 | 10.4 | 12.7 | 10.7 | 12.2 | 14.2 | 11.6 | 15.6 |  |  |  |
| BhDRV1 | 10.0 | 8.3 | 8.0 | 9.7 | 8.6 | 9.4 | 8.2 | 7.5 | 9.8 | 9.5 | 7.8 | 8.8 |  |  |
| TriRV2 | 11.1 | 10.0 | 9.3 | 10.0 | 8.9 | 9.7 | 8.5 | 7.0 | 8.8 | 10.2 | 9.5 | 7.6 | 10.1 |  |

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

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | HAGXCRV | **BaRV3** | PsiRV2 | SphRV2 | EfusRV | WlDRV1 | **BaRV1** |
| HAGXCRV |  |  |  |  |  |  |  |
| **BaRV3** | 63.5 |  |  |  |  |  |  |
| PsiRV2 | 36.5 | 34.7 |  |  |  |  |  |
| SphRV2 | 45.6 | 42.9 | 44.3 |  |  |  |  |
| EfusRV | 23.5 | 25.8 | 22.7 | 24.5 |  |  |  |
| WlDRV1 | 21.3 | 19.5 | 17.3 | 21.5 | 18.5 |  |  |
| **BaRV1** | 14.6 | 13.6 | 14.9 | 12.3 | 14.2 | 12.0 |  |

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

|  |  |  |  |
| --- | --- | --- | --- |
|  | WlCV10 | WLCV11 | **MSaRV** |
| WlCV10 |  |  |  |
| WlCV11 | 41.8 |  |  |
| **MSaRV** | 40.9 | 61.2 |  |

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

|  |  |  |  |
| --- | --- | --- | --- |
|  | WlCV10 | WLCV11 | **MSaRV** |
| WlCV10 |  |  |  |
| WlCV11 | 29.8 |  |  |
| **MSaRV** | 26.0 | 43.5 |  |

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

|  |  |  |  |
| --- | --- | --- | --- |
|  | WlCV10 | WLCV11 | **MSaRV** |
| WlCV10 |  |  |  |
| WlCV11 | 19.8 |  |  |
| **MSaRV** | 19.2 | 48.7 |  |

**Table 7.** Percentage nucleotide identities (p-distance) of a CLUSTAL W alignment of novirhabdovirus G gene sequences.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | IHNV | HIRRV | VHSV | SHRV | **CAPRV 1988** | **CAPRV 2023** |
| IHNV |  |  |  |  |  |  |
| HIRRV | 69.7 |  |  |  |  |  |
| VHSV | 47.8 | 48.1 |  |  |  |  |
| SHRV | 49.7 | 47.8 | 56.0 |  |  |  |
| **CAPRV 1988** | 50.1 | 48.5 | 53.6 | 55.0 |  |  |
| **CAPRV 2023** | 50.6 | 49.5 | 51.8 | 55.2 | 80.5 |  |

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

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | IHNV | HIRRV | VHSV | SHRV | **CAPRV 1988** | **CAPRV 2023** |
| IHNV |  |  |  |  |  |  |
| HIRRV | 73.6 |  |  |  |  |  |
| VHSV | 38.4 | 38.0 |  |  |  |  |
| SHRV | 40.0 | 40.0 | 47.6 |  |  |  |
| **CAPRV 1988** | 39.5 | 40.5 | 46.8 | 54.3 |  |  |
| **CAPRV**  **2023** | 38.5 | 40.9 | 46.0 | 55.1 | 86.3 |  |