

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

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| **Code assigned:** | **2021.003M** |  |
| **Short title:** Create one new species in the genus *Perhabdovirus*, and three new genera including six new species, for viruses of fish and marine mammals (*Mononegavirales*: *Rhabdoviridae*) | | |
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**Author(s) and email address(es)**

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**List the ICTV Study Group(s) that have seen this proposal**

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| ICTV *Rhabdoviridae* Study Group |

**ICTV study group comments and response of proposer**

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| The proposal was supported by all 15 members of the *Rhabdoviridae* SG - with minor revisions.  One issue was debated in some detail. The virus names for some rhabdoviruses in this proposal, include the name of the host fish species (e.g., Scophthalmus maximus rhabdovirus) and in these cases we decided to “adopt” the host species epithet for the virus species name (e.g., *Scophrhavirus maximus*). This raises the issue of whether there is a need for gender adjustment to comply with the neuter noun (e.g., *Scophrhavirus maximum*). On one hand, this is argued to be a correct expression of Latinisation. On the other hand, it is argued this is not intended to be Latinisation but a freeform adoption of a component of the host species name, and so consistent with the default option of freeform for animal rhabdoviruses. The importance of this is to ensure the species name maintains a direct connection with the host species name. It is also considered to be highly likely that most authors/reviewers/editors will not recognize or adhere to the gender adjustment when using the species name, causing unnecessary confusion in the literature.  A poll taken on this issue by the SG resulted in a split vote (8/5), but clearly in favor of no gender adjustment. Significantly, the votes reflected ethnic/cultural background of SG members - British/American/Asia-Pacific vs Latin/Euro. Those authors of the proposal who are not Rhabdo SG members also indicated that they wish to maintain the adopted epithet without gender adjustment.  The Rhabdo SG has now adopted this as an expression of the freeform option with no gender adjustment for all animal rhabdoviruses. |

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

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

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

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| Date first submitted to SC Chair | May 22, 2021 |
| Date of this revision (if different to above) | May 28, 2021 |

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

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

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2021.003M.R.Alpharhabdovirinae\_3ngen\_7nsp |

**Abstract**

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| We propose the assignment of one new species in the genus *Perhabdovirus* and the creation of three new genera (*Cetarhavirus*, *Siniperhavirus* and *Scophrhavirus*) each with two new species, to accommodate previously unclassified rhabdoviruses isolated from fish and aquatic mammals. |

**Text of proposal**

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| |  | | --- | | **Genus *Perhabdovirus***  One new species is proposed for the existing genus *Perhabdovirus*. Leman rhabdovirus (LeRV; strain18/193) was isolated from perch fry collected at Lake Leman in France, in 1999 [8]. The complete genome sequence (11,1619 nt) has been determined [8].  **Genus *Cetarhavirus***  The new genus *Cetarhavirus* is proposed for rhabdoviruses infecting aquatic mammals (Cetacea) and will include two new species.  Dolphin rhabdovirus (DRV; isolate pxV1) was isolated from a white-beaked dolphin (*Lagenorhynchus albirostris* (Gray, 1846)) stranded on the Dutch island of Schiermonnikoog in 1992 [7]. The virus replicates in Vero cell cultures and displays bullet-shaped morphology (125-145 nm x 75-85 nm) by negative-contrast electron microscopy of infected cell lysates [7]. DRV failed to cross-react with rabies virus, bovine ephemeral fever virus or several vesiculoviruses in indirect immunofluorescence or virus neutralisation tests [7]. Neutralising antibody was detected in various cetaceans (dolphins, porpoises, whales) and pinnipeds (seals) sampled from the costa of northwest Europe or the Mediterranean Sea [7, 10]. The complete genome sequence (11,141 nt) has been determined [10]. Dolphin rhabdovirus will be assigned to the proposed new species *Cetarhavirus lagenorhynchus*.  Harbour porpoise rhabdovirus (HPRV; isolate WVL17017A) was isolated from a harbour porpoise (*Phocoena phocoena* (Linnaeus, 1758)) stranded off the coast of Alaska in 2013 [2]. The virus was shown to replicate in primary beluga whale (*Delphinapterus leucas* (Pallas, 1776)) kidney (BWK) cells [2]. Enveloped, bullet-shaped virions (approximately 111 nm x 73 nm) were observed in ultrathin sections to bud from the surface of the BWK cells [2]. The complete coding genome sequence (10,988 nt) has been determined [2]. Harbour porpoise rhabdovirus will be assigned to the proposed new species *Cetarhavirus phocoena*.  **Genus *Siniperhavirus***  The new genus *Siniperhavirus* is proposed for rhabdoviruses infecting ray-finned fish (Actinopterygii) to include two new species. Based on maximum-likelihood trees inferred using complete L protein sequences, viruses assigned to the new genus are phylogenetically distinct from other rhabdoviruses infecting ray-finned fish which are assigned to other genera (*Perhabdovirus*, *Sprivivirus*, *Novirhabdovirus* and proposed new genera *Scophrhavirus*).  Eelpout rhabdovirus (EpRV; isolate FSK0523) was detected by high-throughput sequencing in samples of eelpout (*Zoarces viviparous* (Linnaeus, 1758)) collected during mass fish mortalities near Stockholm, Sweden, in 2014 [1]. Bullet-shaped virions (approximately 80 nm x 140 nm) were observed in lysates of bluegill fry (BF-2) cells infected with extracts of diseased fish [1]. The complete coding genome sequence (11,139 nt) has been determined [1]. Eelpout rhabdovirus will be assigned to the proposed new species *Siniperhavirus zoarces*.  Siniperca chuatsi rhabdovirus (SCRV) was isolated from mandarin fish (*Siniperca chuatsi* (Basilewsky, 1855)) collected in Guangdong Province, China, in 1997 [13, 15]. Bullet-shaped particles (80-100 nm x 110-130 nm) were observed by negative-contrast electron microscopy of virions purified from infected grass carp fin (GCF) cell cultures [11]. The complete genome sequence (11,545 nt) has been determined [11]. Siniperca chuatsi rhabdovirus will be assigned to the proposed new species *Siniperhavirus chuatsi*.  Other related viruses in the genus  Hybrid snakehead rhabdovirus (HSHRV; isolate C1207) was isolated from a moribund hybrid snakehead fish (*Channa maculata* (Lacépède, 1801) x *Channa argus (Cantor, 1842)* cross) collected in Guangdong Province, China, in 2012 [12]. The virus was subsequently isolated from hybrid snakehead fish from the same province of China in 2014 and shown to infect mandarin fish [4]. A third isolate was obtained from snakehead fish (*Channa argus*)in China in 2019*.*  Complete genome sequences have been reported for all three isolates [4, 12]. Hybrid snakehead rhabdovirus is considered to be a variant of Siniperca chuatsi rhabdovirus and will be assigned to the same species (*Siniperhavirus chuatsi*).  Chinese rice-field eel rhabdovirus (CrERV) was isolated from diseased Asian swamp eels (*Monopterus albus* (Zuiew, 1793)) collected from Hubei Province, China, in 2017 [3]. The virus replicates in a gibel carp brain (GiCB) cell line [3]. Bullet-shaped virions (approximately 60 nm x 120 nm) were observed in thin sections of infected GiBC cells and in the tissues of infected eels [3]. The complete genome sequence (11,545 nt) has been determined [3]. Chinese rice-field eel rhabdovirus is considered to be a variant of Siniperca chuatsi rhabdovirus and will be assigned to the same species (*Siniperhavirus chuatsi*).  Micropterus salmoides rhabdovirus (MSRV; isolate YH01) was isolated from moribund largemouth bass (*Micropterus salmoides* (Lacépède, 1802)) collected in Zhejiang Province, China, in 2017 [5]. The virus had previously been discovered in juvenile mandarin fish collected in Guangdong Province, China, in 2011 [6]. Bullet-shaped virions (reported to be 120-200 nm x 300-500 nm) were observed in ultrathin sections of infected grass carp ovary (GCO) cells [5]. The complete coding genome sequence (11,526 nt) has been determined [5]. Micropterus salmoides rhabdovirus is considered to be a variant of Siniperca chuatsi rhabdovirus and will be assigned to the same species (*Siniperhavirus chuatsi*).  **Genus *Scophrhavirus***  The new genus *Scophrhavirus* is proposed for rhabdoviruses infecting ray-finned fish (Actinopterygii) to include two new species. Based on maximum-likelihood trees inferred using complete L protein sequences, viruses assigned to the new genus are phylogenetically distinct from other rhabdoviruses infecting ray-finned fish which are assigned to other genera (*Perhabdovirus*, *Sprivivirus*, *Novirhabdovirus* and proposed new genera *Siniperhavirus*).  Scophthalmus maximus rhabdovirus (SMRV) was isolated from turbot fish (*Scophthalmus maximus* (Linnaeus, 1758)) with signs of haemorrhagic disease collected from Shandong Province, China [14]. Bullet-shaped particles were observed in ultrathin sections of infected carp leucocyte (CLC) cell cultures and for virions purified from cell culture supernatants. The complete genome sequence (11,492 nt) has been determined [11, 16]. Scophthalmus maximus rhabdovirus will be assigned to the proposed new species *Scophrhavirus maximus*.  Wuhan redfin culter dimarhabdovirus (WhRCDRV; sample DSYS6218) was detected by high-throughput sequencing in redfin culter (*Chanodichthys erythropterus* (Basilewsky, 1855)) collected in Hubei Province, China [9]. The complete coding genome sequence (10,882 nt) has been determined [9]. Wuhan redfin culter dimarhabdovirus will be assigned to the proposed new species *Scophrhavirus* *chanodichthys*.  **Genome architecture**  The genomes of viruses assigned to each genus contain the five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*). In the proposed genera *Perhabdovirus*, *Siniperhavirus* and *Scophrhavirus*, some viruses have alternative ORFs within the *P* genes; it is not known if these are expressed (**Figure 1**).  **Amino acid sequence relationships**  Pair-wise sequence identities (p-distances) were estimated from Clustal W alignments of the amino acid sequences of the L, N and G proteins of all available isolates of viruses to be assigned to the genera *Perhabdovirus*, *Cetarhavirus*, *Siniperhavirus* and *Scophrhavirus*. For viruses within existing or proposed new species amino acid sequence identities were in the range 94.8–100% for L, 93.9–100% for N, and 88.4–99.8% for G. For viruses assigned to different species, amino acid sequence identities were ≤86.9 for L, ≤84.1 for N, and ≤83.3 for G (**Tables 1-3**).  **Phylogeny**  Based on ML trees inferred from a Clustal W alignment of the complete L protein sequences of all available isolates, viruses assigned to each species or genus form a well-supported monophyletic clade. Clades representing each new genus are distinct from all currently assigned genera (**Figure 2**).  **Species demarcation criteria**  Viruses assigned to different species within each of the genera *Perhabdovirus, Siniperhavirus, Scophrhavirus* and *Cetarhavirus* have several of the following characteristics: A) minimum amino acid sequence divergence of 10% in N proteins; B) minimum sequence divergence of 10% in the L proteins; C) minimum amino acid sequence divergence of 15% in G proteins; D) can be distinguished in virus neutralisation tests; and E) occupy different ecological niches as evidenced by differences in vertebrate hosts.  Viruses assigned to each of the proposed new species meet demarcation criteria A, B and C. Virus neutralization tests to distinguish individual viruses have not yet been conducted (criterion D). There is insufficient evidence at this stage to establish the specificity of the natural host range for the viruses (criterion E).  **Derivation of the genus names**  *Cetarhavirus -* Sigla for cetacean rhabdovirus after the dolphin and porpoise hosts of viruses in the two member species.  *Siniperhavirus -* Sigla for the genus of the source host (mandarin fish; *Siniperca chuatsi*) of the first rhabdovirus reported from this genus (Siniperca chuatsi rhabdovirus).  *Scophrhavirus -* Sigla for the genus of the source host (turbot fish; *Scophthalmus maximus*) of the first rhabdovirus reported from this genus, (Scophthalmus maximus rhabdovirus).  **Derivation of species epithet names**  *Perhabdovirus leman* – from Lake Leman*,* the site of isolation of the virus assigned to this species (18/193)  *Cetarhavirus lagenorhynchus* – from the genus name of the source host (white-beaked dolphin; *Lagenorhynchus albirostris*) of the virus assigned to the species (dolphin rhabdovirus).  *Cetarhavirus phocoena –* from the genus name of the source host (harbour porpoise; *Phocoena phocoena*) of the virus assigned to the species (harbour porpoise rhabdovirus).  *Siniperhavirus chuatsi* – from the species epithet of the source host (mandarin fish; *Siniperca chuatsi*) of the virus assigned to the species (Siniperca chuatsi rhabdovirus).  *Siniperhavirus zoarces* – from the genus name of the source host (eelpout; *Zoarces viviparous*) of the virus assigned to the species (eelpout rhabdovirus).  *Scophrhavirus maximus* – from the species epithet of the source host (turbot fish; *Scophthalmus maximus*) of the virus assigned to the species (Scophthalmus maximus rhabdovirus).  *Scophrhavirus chanodichthys –* from the genus name of the source host (redfin culter; *Chanodichthys erythropterus*) of the virus assigned to the species (Wuhan redfin culter dimarhabdovirus). | |

**Supporting evidence**

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**Figure 1.** Genome organisations of viruses to be assigned as exemplars of each species in the genera *Perhabdovirus*, *Cetarhavirus*, *Siniperhavirus* and *Scophrhavirus*. Each genome contains five long open reading frames (ORFs) in the N, P, M, G and L genes (open arrows). In several viruses, alternative ORFs (>180 nt) occur in the P genes (grey arrows) but they share no recognizable sequence identity.

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**Figure 2.** The evolutionary history was inferred from a Clustal W alignment of 191 complete L protein sequences of animal rhabdoviruses currently assigned or recently proposed for assignment to species in the subfamily *Alpharhabdovirinae*, family *Rhabdoviridae*. Phylogenetically informative sites were selected from the alignment using Gblocks resulting in 1029 positions in the final dataset. The tree was inferred in MEGA7 by using the Maximum Likelihood method based on the Whelan and Goldman + Freq. model. The tree with the highest log likelihood (-151963.70) 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-Joining and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Bootstrap values (100 iterations) are shown for each node.

**Table 1.** Percentage amino acid sequence identities (p-distances) estimated from a CLUSTAL W alignment of perhabdovirus, cetarhavirus, siniperhavirus and scophrhavirus L proteins.

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| **Species** |  | Virus | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 |
| ***Perhabdovirus perca\**** | 1 | PRV\_Dorson\_JX679246 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 2 | PRV\_16/121\_MN964000 | 96.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 3 | PRV\_P8350\_MN963998 | 95.5 | 96.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *Perhabdovirus leman* | 4 | LEMV\_18/193\_MN963996 | 85.2 | 86.6 | 86.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ***Perhabdovirus trutta\**** | 5 | STRV\_R6146\_MN963999 | 80.2 | 81.2 | 81.5 | 81.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 6 | STRV\_18/203\_MN963997 | 80.0 | 80.9 | 81.3 | 81.6 | 94.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 7 | STRV\_CH17\_MN510774 | 80.0 | 81.0 | 81.4 | 81.7 | 95.0 | 99.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ***Perhabdovirus anguilla\**** | 8 | EVA\_J6B4\_KC608038 | 70.6 | 71.4 | 71.8 | 72.4 | 71.9 | 72.3 | 72.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 9 | EVEX\_CV1153311\_FN557213 | 70.8 | 71.6 | 72.0 | 72.7 | 72.5 | 72.9 | 72.9 | 97.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 10 | EVEX\_C30\_JN639009 | 70.9 | 71.7 | 72.1 | 72.7 | 72.4 | 72.8 | 72.8 | 98.3 | 99.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 11 | EVEX\_DF25/04\_KC608037 | 70.8 | 71.6 | 72.0 | 72.6 | 72.3 | 72.8 | 72.8 | 97.9 | 99.1 | 99.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 12 | EVEX\_DK3545\_KC608034 | 70.8 | 71.7 | 72.0 | 72.7 | 72.3 | 72.8 | 72.8 | 98.2 | 99.1 | 99.7 | 99.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 13 | EVEX\_DK3631\_KC608035 | 70.7 | 71.5 | 71.9 | 72.5 | 72.2 | 72.7 | 72.7 | 97.8 | 98.9 | 99.4 | 99.0 | 99.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 14 | EVEX\_DK5743\_KC608036 | 70.9 | 71.7 | 72.1 | 72.7 | 72.4 | 72.8 | 72.8 | 98.2 | 99.3 | 99.9 | 99.5 | 99.7 | 99.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 15 | EVEX\_GG129\_JN639010 | 70.7 | 71.6 | 71.9 | 72.6 | 72.4 | 72.9 | 72.9 | 97.8 | 98.9 | 99.4 | 99.1 | 99.2 | 98.9 | 99.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 16 | EVEX\_GG184\_KC608033 | 70.7 | 71.6 | 71.9 | 72.6 | 72.4 | 72.9 | 72.9 | 97.8 | 98.8 | 99.4 | 99.1 | 99.2 | 98.9 | 99.2 | 100.0 |  |  |  |  |  |  |  |  |  |  |  |  |
| 17 | EVEX\_JP77\_JX827265 | 70.9 | 71.7 | 72.1 | 72.7 | 72.4 | 72.8 | 72.8 | 98.3 | 99.4 | 100.0 | 99.6 | 99.7 | 99.4 | 99.9 | 99.4 | 99.4 |  |  |  |  |  |  |  |  |  |  |  |
| *Cetarhavirus lagalorhynchus* | 18 | DRV\_KF958252 | 55.3 | 56.2 | 55.8 | 55.7 | 55.0 | 55.7 | 55.4 | 55.9 | 55.9 | 55.7 | 55.8 | 55.7 | 55.6 | 55.7 | 55.7 | 55.7 | 55.7 |  |  |  |  |  |  |  |  |  |  |
| *Cetarhavirus phocoena* | 19 | HPRV\_MN103537 | 55.2 | 55.7 | 55.6 | 55.5 | 55.4 | 55.4 | 55.2 | 55.8 | 55.7 | 55.8 | 55.6 | 55.7 | 55.7 | 55.8 | 55.8 | 55.8 | 55.8 | 68.7 |  |  |  |  |  |  |  |  |  |
| *Siniperhavirus zoarces* | 20 | EPRV\_KR612230 | 51.8 | 52.3 | 52.1 | 52.6 | 52.2 | 52.5 | 52.3 | 51.5 | 52.0 | 51.9 | 51.9 | 51.8 | 51.7 | 51.9 | 51.8 | 51.8 | 51.9 | 53.9 | 52.5 |  |  |  |  |  |  |  |  |
| *Siniperhavirus chuatsi* | 21 | HSHV\_C1207\_KC519324 | 51.8 | 52.2 | 52.3 | 52.1 | 52.2 | 52.4 | 52.4 | 51.3 | 51.6 | 51.6 | 51.6 | 51.6 | 51.6 | 51.6 | 51.6 | 51.6 | 51.6 | 54.2 | 54.0 | 71.2 |  |  |  |  |  |  |  |
| 22 | HSHV\_SHVV19\_MW291462 | 51.7 | 52.2 | 52.2 | 52.2 | 52.2 | 52.3 | 52.3 | 51.3 | 51.6 | 51.6 | 51.6 | 51.6 | 51.6 | 51.6 | 51.6 | 51.6 | 51.6 | 54.4 | 54.3 | 71.1 | 98.9 |  |  |  |  |  |  |
| 23 | CrERV\_MH319839 | 52.0 | 52.3 | 52.5 | 52.3 | 52.4 | 52.5 | 52.5 | 51.5 | 51.8 | 51.8 | 51.8 | 51.8 | 51.8 | 51.8 | 51.8 | 51.8 | 51.8 | 54.2 | 54.0 | 70.8 | 97.6 | 97.2 |  |  |  |  |  |
| 24 | MSRV\_MK397811 | 51.9 | 52.2 | 52.5 | 52.0 | 52.3 | 52.5 | 52.5 | 51.4 | 51.7 | 51.7 | 51.7 | 51.7 | 51.7 | 51.7 | 51.7 | 51.7 | 51.7 | 54.2 | 54.2 | 71.0 | 97.0 | 96.4 | 96.9 |  |  |  |  |
| 25 | SCRV\_DQ399789 | 51.6 | 52.0 | 52.2 | 51.7 | 51.9 | 52.1 | 52.1 | 51.1 | 51.4 | 51.4 | 51.4 | 51.4 | 51.4 | 51.4 | 51.4 | 51.4 | 51.4 | 53.9 | 53.9 | 70.7 | 97.6 | 97.1 | 97.4 | 97.9 |  |  |  |
| *Scophrhavirus maximus* | 26 | SMRV\_HQ003891 | 46.6 | 47.2 | 46.9 | 46.6 | 47.1 | 46.9 | 46.8 | 46.2 | 46.3 | 46.4 | 46.4 | 46.4 | 46.3 | 46.4 | 46.5 | 46.5 | 46.4 | 46.8 | 46.7 | 46.0 | 46.5 | 46.4 | 46.6 | 46.6 | 46.5 |  |  |
| *Scophrhavirus chanodychthys* | 27 | WhRCDRV\_MG600013 | 45.3 | 45.5 | 45.8 | 45.6 | 45.2 | 44.6 | 44.5 | 45.0 | 44.9 | 45.0 | 44.9 | 44.9 | 44.8 | 45.0 | 44.9 | 44.9 | 45.0 | 47.2 | 46.1 | 44.9 | 44.7 | 44.7 | 44.7 | 44.9 | 44.8 | 53.5 |  |

\*Existing species

**Table 2.** Percentage amino acid sequence identities (p-distances) estimated from a CLUSTAL W alignment of perhabdovirus, cetarhavirus, siniperhavirus and scophrhavirus N proteins.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
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| **Species** |  | Virus | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 |
| ***Perhabdovirus perca\**** | 1 | PRV\_Dorson\_JX679246 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 2 | PRV\_16/121\_MN964000 | 97.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 3 | PRV\_P8350\_MN963998 | 98.0 | 97.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *Perhabdovirus leman* | 4 | LEMV\_18/193\_MN963996 | 84.1 | 82.6 | 83.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ***Perhabdovirus trutta\**** | 5 | LTRV\_AF434991 | 75.1 | 74.1 | 74.8 | 72.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 6 | STRV\_R6146\_MN963999 | 75.1 | 74.1 | 74.8 | 72.6 | 99.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 7 | STRV\_18/203\_MN963997 | 74.1 | 73.1 | 73.8 | 72.1 | 94.1 | 94.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 8 | STRV\_CH17\_MN510774 | 73.8 | 73.1 | 73.6 | 71.9 | 93.9 | 93.9 | 98.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ***Perhabdovirus anguilla\**** | 9 | EVA\_J6B4\_KC608038 | 62.3 | 62.8 | 62.3 | 61.4 | 60.1 | 59.9 | 59.9 | 59.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 10 | EVEX\_CV1153311\_FN557213 | 62.3 | 62.8 | 62.3 | 61.4 | 60.1 | 59.9 | 59.9 | 59.7 | 98.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 11 | EVEX\_C30\_JN639009 | 62.8 | 63.3 | 62.8 | 61.9 | 60.6 | 60.4 | 60.4 | 60.1 | 99.0 | 98.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 12 | EVEX\_DF25/04\_KC608037 | 62.6 | 63.1 | 62.6 | 61.6 | 60.4 | 60.1 | 60.1 | 59.9 | 99.3 | 99.0 | 99.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 13 | EVEX\_DK3545\_KC608034 | 62.8 | 63.3 | 62.8 | 61.9 | 60.9 | 60.6 | 60.6 | 60.4 | 98.8 | 98.3 | 99.3 | 99.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 14 | EVEX\_DK3631\_KC608035 | 62.8 | 63.3 | 62.8 | 61.9 | 60.9 | 60.6 | 60.6 | 60.4 | 99.0 | 98.5 | 99.5 | 99.3 | 99.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 15 | EVEX\_DK5743\_KC608036 | 62.8 | 63.3 | 62.8 | 61.9 | 60.9 | 60.6 | 60.6 | 60.4 | 98.8 | 98.3 | 99.3 | 99.0 | 100.0 | 99.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 16 | EVEX\_GG129\_JN639010 | 62.6 | 63.1 | 62.6 | 61.6 | 60.6 | 60.4 | 60.4 | 60.1 | 99.3 | 99.0 | 99.0 | 99.8 | 99.3 | 99.5 | 99.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 17 | EVEX\_GG184\_KC608033 | 62.6 | 63.1 | 62.6 | 61.6 | 60.6 | 60.4 | 60.4 | 60.1 | 99.3 | 99.0 | 99.0 | 99.8 | 99.3 | 99.5 | 99.3 | 100.0 |  |  |  |  |  |  |  |  |  |  |  |  |
| 18 | EVEX\_JP77\_JX827265 | 62.8 | 63.3 | 62.8 | 61.9 | 60.6 | 60.4 | 60.4 | 60.1 | 99.3 | 98.5 | 99.8 | 99.3 | 99.5 | 99.8 | 99.5 | 99.3 | 99.3 |  |  |  |  |  |  |  |  |  |  |  |
| *Cetarhavirus lagalorhynchus* | 19 | DRV\_KF958252 | 41.3 | 41.3 | 40.6 | 40.3 | 41.8 | 42.1 | 41.3 | 41.1 | 39.4 | 39.4 | 39.6 | 39.6 | 39.6 | 39.6 | 39.6 | 39.6 | 39.6 | 39.6 |  |  |  |  |  |  |  |  |  |  |
| *Cetarhavirus phocoena* | 20 | HPRV\_MN103537 | 42.3 | 42.8 | 42.8 | 42.8 | 44.3 | 44.0 | 43.0 | 43.3 | 43.5 | 43.8 | 43.8 | 43.8 | 43.8 | 43.8 | 43.8 | 43.8 | 43.8 | 43.8 | 68.2 |  |  |  |  |  |  |  |  |  |
| *Sinieperhavirus zoarces* | 21 | EPRV\_KR612230 | 41.1 | 40.8 | 41.6 | 40.8 | 40.8 | 40.6 | 40.1 | 40.3 | 39.1 | 39.1 | 39.6 | 39.4 | 39.6 | 39.6 | 39.6 | 39.4 | 39.4 | 39.6 | 48.7 | 46.2 |  |  |  |  |  |  |  |  |
| *Siniperhavirus chuatsi* | 22 | HSHV\_C1207\_KC519324 | 44.5 | 44.5 | 43.8 | 41.6 | 43.5 | 43.8 | 43.0 | 43.3 | 41.8 | 41.8 | 41.8 | 42.3 | 41.8 | 41.8 | 41.8 | 42.1 | 42.1 | 41.8 | 48.4 | 46.7 | 65.8 |  |  |  |  |  |  |  |
| 23 | HSHV\_SHVV19\_MW291462 | 44.5 | 44.5 | 43.8 | 41.6 | 43.3 | 43.5 | 42.8 | 43.0 | 41.8 | 41.8 | 41.8 | 42.3 | 41.8 | 41.8 | 41.8 | 42.1 | 42.1 | 41.8 | 48.2 | 46.5 | 66.0 | 99.3 |  |  |  |  |  |  |
| 24 | CrERV\_MH319839 | 43.8 | 43.8 | 43.3 | 42.3 | 43.3 | 43.5 | 42.8 | 43.0 | 42.5 | 42.5 | 42.5 | 42.8 | 42.5 | 42.5 | 42.5 | 42.8 | 42.8 | 42.5 | 48.2 | 46.5 | 66.3 | 96.3 | 95.6 |  |  |  |  |  |
| 25 | MSRV\_MK397811 | 43.3 | 43.8 | 43.3 | 41.8 | 43.0 | 43.3 | 42.8 | 43.0 | 41.8 | 41.8 | 42.1 | 42.1 | 41.8 | 41.8 | 41.8 | 42.1 | 42.1 | 41.8 | 47.2 | 46.0 | 64.3 | 94.4 | 93.6 | 93.2 |  |  |  |  |
| 26 | SCRV\_DQ399789 | 43.5 | 44.0 | 43.3 | 41.8 | 43.0 | 43.3 | 42.3 | 42.5 | 41.3 | 41.3 | 41.8 | 41.6 | 41.6 | 41.6 | 41.6 | 41.6 | 41.6 | 41.6 | 48.2 | 46.2 | 65.3 | 96.6 | 95.8 | 95.8 | 95.6 |  |  |  |
| *Scophrhavirus maximus* | 27 | SMRV\_HQ003891 | 31.1 | 31.3 | 30.8 | 30.6 | 28.4 | 28.4 | 28.6 | 28.6 | 30.1 | 30.1 | 30.6 | 30.3 | 30.6 | 30.6 | 30.6 | 30.3 | 30.3 | 30.6 | 31.1 | 31.3 | 27.1 | 27.4 | 27.4 | 27.9 | 27.1 | 27.4 | # |  |
| *Scophrhavirus chanodychthys* | 28 | WhRCDRV\_MG600013 | 29.8 | 30.6 | 29.8 | 28.4 | 28.9 | 29.1 | 29.3 | 29.1 | 29.6 | 30.1 | 30.1 | 29.8 | 30.1 | 30.1 | 30.1 | 29.8 | 29.8 | 30.1 | 30.3 | 29.6 | 28.1 | 30.1 | 30.3 | 29.8 | 30.1 | 30.3 | 37.4 |  |

\*Existing species

**Table 3.** Percentage amino acid sequence identities (p-distances) estimated from a CLUSTAL W alignment of perhabdovirus, cetarhavirus, siniperhavirus and scophrhavirus G proteins.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Species** |  | Virus | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 |
| ***Perhabdovirus perca\**** | 1 | **PRV\_Dorson\_JX679246** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 2 | PRV\_16/121\_MN964000 | 96.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 3 | PRV\_P8350\_MN963998 | 98.2 | 96.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *Perhabdovirus leman* | 4 | LEMV\_18/193\_MN963996 | 83.1 | 82.0 | 83.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ***Perhabdovirus trutta\**** | 5 | **LTRV\_903/87\_AF434991** | 69.4 | 69.0 | 69.2 | 67.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 6 | STRV\_R6146\_MN963999 | 69.8 | 69.0 | 69.4 | 68.0 | 96.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 7 | STRV\_18/203\_MN963997 | 68.0 | 67.8 | 68.0 | 68.2 | 89.6 | 88.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 8 | STRV\_CH17\_MN510774 | 68.0 | 67.3 | 68.0 | 68.2 | 90.4 | 89.0 | 97.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ***Perhabdovirus anguilla\**** | 9 | EVA\_J6B4\_KC608038 | 53.9 | 53.7 | 53.3 | 52.2 | 52.4 | 52.0 | 53.1 | 52.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 10 | **EVEX\_CV1153311\_FN557213** | 54.1 | 53.3 | 53.5 | 52.0 | 52.7 | 52.4 | 52.4 | 52.4 | 96.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 11 | EVEX\_C30\_JN639009 | 54.1 | 53.3 | 53.5 | 52.0 | 52.4 | 52.2 | 52.2 | 52.2 | 96.7 | 99.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 12 | EVEX\_DF25/04\_KC608037 | 53.9 | 53.3 | 53.3 | 52.0 | 52.7 | 52.4 | 52.7 | 52.7 | 96.5 | 99.0 | 99.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 13 | EVEX\_DK3545\_KC608034 | 54.5 | 53.7 | 53.9 | 52.4 | 52.9 | 52.7 | 52.9 | 52.9 | 96.5 | 99.2 | 99.2 | 98.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 14 | **EVEX\_DK3631\_KC608035** | 54.5 | 53.7 | 53.9 | 52.2 | 52.4 | 52.2 | 52.2 | 52.2 | 96.1 | 97.8 | 97.8 | 97.3 | 98.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 15 | EVEX\_DK5743\_KC608036 | 53.5 | 52.7 | 52.9 | 51.4 | 51.8 | 51.6 | 51.6 | 51.6 | 95.9 | 98.8 | 99.2 | 98.2 | 98.4 | 96.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 16 | EVEX\_GG129\_JN639010 | 53.9 | 53.1 | 53.3 | 52.0 | 52.4 | 52.2 | 52.2 | 52.2 | 96.3 | 99.2 | 99.2 | 98.6 | 98.8 | 97.3 | 98.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 17 | EVEX\_GG184\_KC608033 | 53.9 | 53.1 | 53.3 | 52.0 | 52.4 | 52.2 | 52.2 | 52.2 | 96.5 | 99.4 | 99.4 | 98.8 | 99.0 | 97.6 | 98.6 | 99.8 |  |  |  |  |  |  |  |  |  |  |  |  |
| 18 | EVEX\_JP77\_JX827265 | 54.1 | 53.3 | 53.5 | 52.0 | 52.7 | 52.4 | 52.7 | 52.7 | 96.7 | 99.8 | 99.6 | 99.0 | 99.2 | 97.8 | 98.8 | 99.2 | 99.4 |  |  |  |  |  |  |  |  |  |  |  |
| *Cetarhavirus lagalorhynchus* | 19 | DRV\_KF958252 | 32.7 | 32.9 | 32.7 | 33.3 | 31.2 | 30.8 | 32.9 | 32.7 | 31.8 | 31.4 | 31.4 | 31.6 | 31.6 | 31.6 | 31.0 | 31.0 | 31.2 | 31.4 |  |  |  |  |  |  |  |  |  |  |
| *Cetarhavirus phocoena* | 20 | HPRV\_MN103537 | 33.5 | 33.7 | 33.3 | 33.7 | 31.6 | 31.6 | 32.0 | 32.0 | 33.1 | 32.7 | 32.7 | 32.9 | 32.7 | 32.4 | 32.2 | 32.4 | 32.4 | 32.7 | 43.9 |  |  |  |  |  |  |  |  |  |
| *Siniperhavirus zoarces* | 21 | EPRV\_KR612230 | 27.1 | 27.3 | 26.9 | 26.7 | 24.5 | 25.1 | 24.7 | 25.1 | 28.6 | 28.6 | 28.6 | 28.8 | 28.6 | 28.8 | 28.4 | 28.2 | 28.4 | 28.8 | 28.8 | 26.3 |  |  |  |  |  |  |  |  |
| *Siniperhavirus chuatsi* | 22 | HSHV\_C1207\_KC519324 | 26.9 | 26.9 | 26.7 | 27.3 | 26.9 | 27.3 | 26.5 | 26.3 | 27.3 | 27.6 | 27.6 | 27.8 | 27.8 | 28.0 | 27.3 | 27.3 | 27.6 | 27.6 | 30.6 | 29.6 | 49.6 |  |  |  |  |  |  |  |
| 23 | HSHV\_SHVV19\_MW291462 | 26.9 | 26.9 | 26.7 | 26.9 | 26.9 | 27.3 | 26.1 | 25.9 | 26.7 | 26.9 | 26.9 | 27.1 | 27.1 | 27.3 | 26.7 | 26.7 | 26.9 | 26.9 | 30.2 | 28.8 | 50.0 | 96.1 |  |  |  |  |  |  |
| 24 | CrERV\_MH319839 | 27.3 | 27.3 | 27.1 | 27.6 | 26.3 | 26.5 | 25.7 | 25.5 | 27.1 | 27.3 | 27.3 | 27.3 | 27.6 | 27.8 | 27.1 | 27.1 | 27.3 | 27.3 | 30.0 | 28.8 | 50.0 | 91.4 | 89.4 |  |  |  |  |  |
| 25 | MSRV\_MK397811 | 27.1 | 27.3 | 26.9 | 27.1 | 25.9 | 26.1 | 25.1 | 24.7 | 26.7 | 26.7 | 26.7 | 26.9 | 26.9 | 27.1 | 26.5 | 26.5 | 26.7 | 26.7 | 30.4 | 28.4 | 48.2 | 91.4 | 89.4 | 91.4 |  |  |  |  |
| 26 | SCRV\_DQ399789 | 27.8 | 27.8 | 27.6 | 27.6 | 26.1 | 26.3 | 25.1 | 24.9 | 26.7 | 26.9 | 26.9 | 27.1 | 27.1 | 27.3 | 26.7 | 26.7 | 26.9 | 26.9 | 30.8 | 28.0 | 48.8 | 93.7 | 91.6 | 93.3 | 94.9 |  |  |  |
| *Scophrhavirus maximus* | 27 | SMRV\_HQ003891 | 22.0 | 21.8 | 21.6 | 22.4 | 21.2 | 21.4 | 22.2 | 22.2 | 23.9 | 23.7 | 23.7 | 23.9 | 23.7 | 23.1 | 23.5 | 23.7 | 23.7 | 23.7 | 21.8 | 22.2 | 20.2 | 20.0 | 19.2 | 21.2 | 19.0 | 19.4 |  |  |
| *Scophrhavirus chanodychthys* | 28 | WhRCDRV\_MG600013 | 25.5 | 26.1 | 25.3 | 24.9 | 24.9 | 24.5 | 24.5 | 24.7 | 25.1 | 25.5 | 25.5 | 25.7 | 25.7 | 25.7 | 24.9 | 25.3 | 25.3 | 25.5 | 23.3 | 22.2 | 21.0 | 21.0 | 21.2 | 21.4 | 21.2 | 20.6 | 29.0 |  |

\*Existing species

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