This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

Code(s) assigned:	***2008.028-032V***	(to be completed by ICTV officers)

Short title: 3 species in genus Salmonivirus
(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

Modules attached (please check all that apply):	**1** ☐	**2** ☐	**3** ☐	**4** ☒	**5** ☒
	6 ☐	**7** ☐			

Author(s) with e-mail address(es) of the proposer:

Herpesvirales Study Group; P. Pellett, Chair; ppellett@med.wayne.edu

ICTV-EC or Study Group comments and response of the proposer:

MODULE 4: **NEW GENUS**

Code	***2008.028V***

To create a new genus assigned as follows:

Subfamily:	
Family:	***Alloherpesviridae***
Order:	***Herpesvirales***

Code	***2008.029V***

To name the new genus: *Salmonivirus*

Code	***2008.030V***

To assign the following as species in the new genus:

Salmonid herpesvirus 1
Salmonid herpesvirus 2
Salmonid herpesvirus 3

Code	***2008.031V***

To designate the following as the type species in the new genus:

Salmonid herpesvirus 1

Argument to justify the creation of a new genus:

Salmonid herpesvirus 1 is commonly known as herpesvirus salmonis and is a pathogen of rainbow trout. Salmonid herpesvirus 2 is commonly known as Oncorhynchus masou herpesvirus and is a pathogen of Pacific salmon. Salmonid herpesvirus 3 is the causative agent of epizootic epitheliotropic disease in lake trout. These three viruses are biologically distinct. They are unassigned in the family.

Partial genome sequence data show that the three viruses are distinct from each other and monophyletic. They are more distantly related to other classified fish herpesviruses, including ictalurid herpesvirus 1 (in the genus *Ictalurivirus*) and cyprinid herpesvirus 3 (in the species *Cyprinid herpesvirus 3*). DNA hybridization data showed that salmonid herpesvirus 1 shares at least 18 homologous genes with ictalurid herpesvirus 1 (Davison, 1998).

Origin of the new genus name:

Salmo, salmon

Argument to justify the choice of type species:

Salmonid herpesvirus 1 was the first to be described.

Species demarcation criteria in the genus:

Related herpesviruses are classified as distinct species if (a) their nucleotide sequences differ in a readily assayable and distinctive manner across the entire genome and (b) they occupy different ecological niches by virtue of their distinct epidemiology and pathogenesis or their distinct natural hosts. A paradigm is provided by HHV-1 and HHV-2, which differ in their sequence throughout the genome, tend to infect different epithelial surfaces and exhibit distinct epidemiological characteristics. These two viruses recombine readily in culture, but despite the fact that they can infect the same sites in the host, no recombinants have been isolated in nature, and the two viruses appear to have evolved independently for millions of years.

The three viruses appear to meet these criteria.

References:

Davison AJ. 1998. The genome of salmonid herpesvirus 1. J Virol 72:1974-82.
Kurobe T, Marcquenski S, Hedrick RP. 2009. Development of a polymerase chain reaction assay for improved diagnostics of the herpesvirus associated with epizootic epitheliotropic disease virus (EEDV) in lake trout (*Salvelinus namaycush*). Dis Aquat Org, in press.
Waltzek TB, Kelley GO, Alfaro, ME, Kurobe T, Davison AJ, Hedrick RP. 2009. Phylogenetic relationships in the family *Alloherpesviridae*. Dis Aquat Org, in press.

Accessions: salmonid herpesvirus 1, AF023673, ACD84543 and random sequences for which only the polypeptide translations have been published; salmonid herpesvirus 2, X70396, X81060, ACD84544; salmonid herpesvirus 3, ACD84548.

Annexes:

Figure 1. Amino acid sequence alignments of conceptual translation products of random salmonid herpesvirus 1 (SalHV-1) DNA sequences with their counterparts in the salmonid herpesvirus 2 (SalHV-2) genome and the channel catfish virus (CCV; ictalurid herpesvirus 1) gene 46 protein at residues 180 to 246 (a) and residues 759 to 837 (b) and the CCV ORF 62 protein at residues 345 to 401 (c). Residues conserved between SalHV-1 and SalHV-2 are indicated in the "con" line; those conserved between both viruses and CCV are indicated in the "CON" line. From Davison (1998).

(a)

```
SalHV-2   CAVGGLLAALKENEIPAEWMVEMVRGTAYSCIMNYFGIGVPQAESTCWRQ
SalHV-1   CAIGGLLTALAKDSIPEDWMVDIVRGTTYSCIMTYLGVGVTQSDTPCWRQ
con       CA-GGLL-AL----IP--WMV--VRGT-YSCIM-Y-G-GV-Q----CWRQ
CCV       CAIATALTALYENKSVDARKLNILRGTSYTCLLGYLGIGELEPNSPCWTQ
CON       CA----L-AL--------------RGT-Y-C---Y-G-G-------CW-Q

SalHV-2   LGARCYTSMNQTEYCIS
SalHV-1   LGARCYLSLNQTRYCII
con       LGARCY-S-NQT-YCI-
CCV       LGPMCYGPLAEQVCVTA
CON       LG--CY-----------
```

(b)

```
SalHV-2   LAELSKTIPRYAIALNTYLPTTDILDHSAGFSAEDGIIEFIPKVTSVCAS
SalHV-1   LAVLDRRCTKTGVALNTYLPTTDPLDHSVGLNADNQLVEFIPKVTSSCVS
con       L--L---------ALNTYLPTTD-LDHS-G--A---L-EFIPKVTS-C-S
CCV       ITQATKVPSVFAIDINTFGVVNGSEYYVVGLEGTD.LVQYSPQVKQSCAF
CON       ---------------NT------------G-----------P-V---C--

SalHV-2   NNTDEVLRLNYIMLDSEFYFREP.IVRDEF
SalHV-1   NNKDALVRLNYIEVDSEFYFTEP.EVRETF
con       NN-D---RLNYI--DSEFYF-EP--VR--F
CCV       INTNETFNQTFITIDERFFFTGPRPVADGF
CON       -N---------I--D--F-F--P--V---F
```

(c)

```
SalHV-2   IYDKMLAVTTRMQYSSWFPEKHRMTEMFGSTNETREFRYHPDYKGTTKVH
SalHV-1   IYDKMLSVTTRMQYSSWFPEKHRMTEMFGSTNETREFRYHPDYKGTTKVH
con       IYDKML-VTTRMQYSSWFPEKHRMTEMFGSTNETREFRYHPDYKGTTKVH
CCV       LYDRVELVLHEIQHSPWYPEENRIVTIKGTT.ETREFIYDPAYKGTTRVH
CON       -YD----V----Q-S-W-PE--R-----G-T-ETREF-Y-P-YKGTT-VH

SalHV-2   FLSSSPL
SalHV-1   FLSSSPL
con       FLSSSPL
CCV       FLSSSPN
CON       FLSSSP-
```

Figure 2. Phylogram depicting relationships among fish and amphibian herpesviruses, based on the concatenated deduced partial amino acid sequences of the DNA polymerase and terminase genes. The quartet puzzling maximum likelihood tree was rooted with human herpesviruses 1 and 8 (HHV-1 and HHV-8) in the family *Herpesviridae*. The numbers above each node represent quartet puzzling probabilities (values >70 shown) of the maximum

likelihood analysis, and the numbers below represent posterior probabilities (values >90 shown) of the Bayesian analysis. The branch lengths are based on the number of inferred substitutions, as indicated by the scale. Adapted from Waltzek *et al.* (in press).

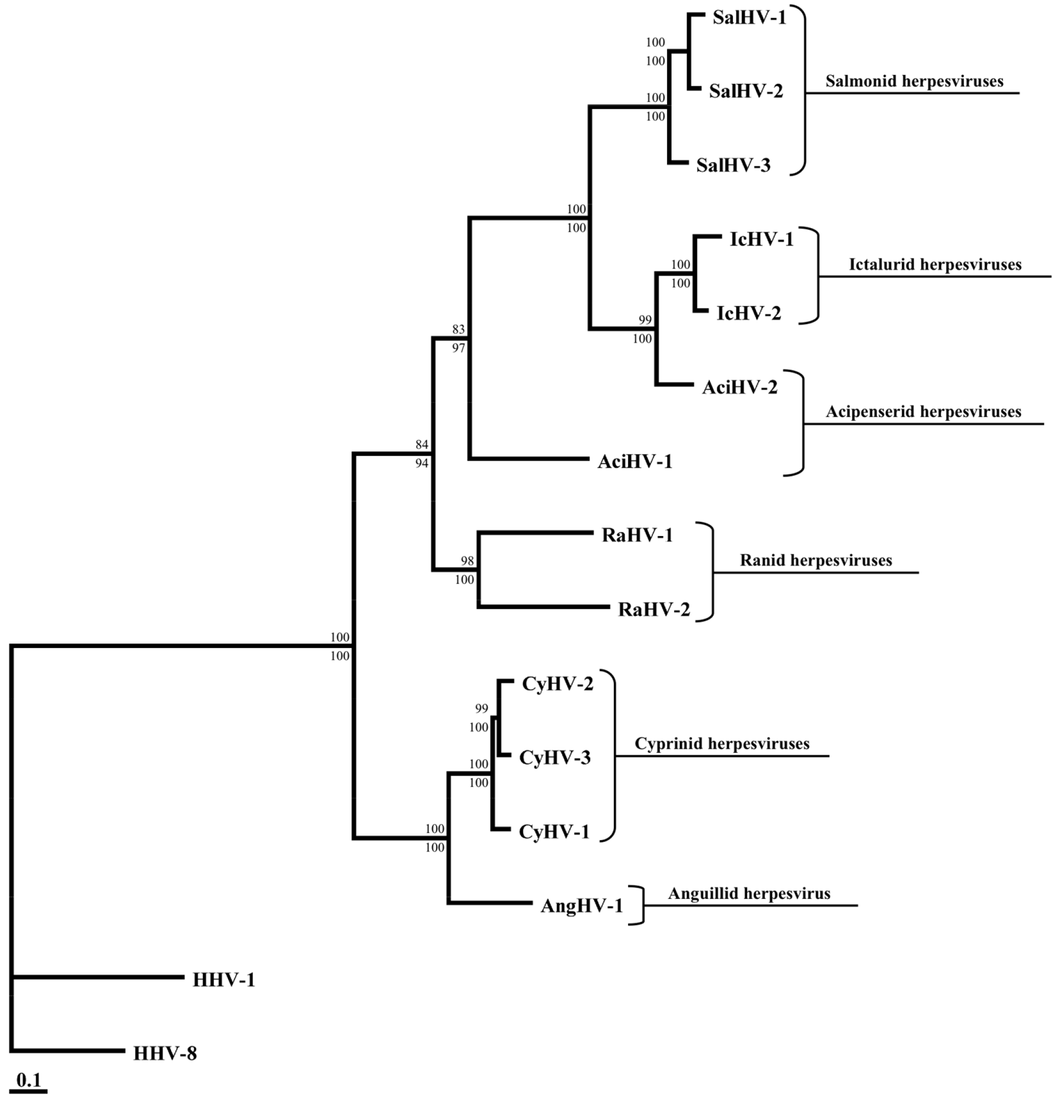

Figure 3. DNA alignment of parts of the terminase genes from SalHV-1, SalHV-2 and SalHV-3. The nucleotides that are identical to those in SalHV-3 are shown by dots. Adapted from Kurobe *et al.* (in press).

```
SalHV3  CTCACCTCCATCACTAGTCTGATCCCCCTCATGCTGGTCGCCGGGCGAAAGCAGATCCAC 95
SalHV1  .....A...........C..C..T..G..G.....C.....T..C............... 94
SalHV2  ........G..T..C.....C.....TT.G.....C.....T..T..G............ 420

SalHV3 ATTTCTTCCCACGTGGCCAAATCTTGGATTAACAACGTGGGCGACATTATCGACGAAACA 155
SalHV1 ..C.....G..T...........G.....G........T........C..A........T 154
SalHV2 ..C.....G.....T..G...........G........T..G.....C..A..T...G.T 480
```

```
SalHV3  ACGGGGGAGCCGGCGTTTCATGTTATCTCTCAGAAGTTTAAATGCGGTGCGCACATGCAC 215
SalHV1  ..C..A.....T.................C..............T.C...T..T...... 214
SalHV2  ..T.....A..T.................C.....A........T.C...T..T...... 540

SalHV3  CTACCAGGTCTGACGTGTCCCTGTGAAGCAGTCTACTGCCCCAGTCACATAGATATGAAC 275
SalHV1  .....CA....C..T............T.T...........A...........C...... 274
SalHV2  ..T..TA....C..T..C.....C........G.....T..A.....T............ 600

SalHV3  CCCGCTACGCAGGCCCTGCTCAGCTGTGTGGCCCCCGGGGGAGAAATGGAGATCACAGGT 335
SalHV1  ..T..A..A.....T.....T..T........A..T..T..C........A..A..C... 334
SalHV2  ..G..A..T...........T........C..A..A..T..T...........A..T..C 660

SalHV3  GGCACCGGTGACTTGGGTAATCTGGTGTCGGACTCGACCTTCCCCTTCCCAGATGAGACG 395
SalHV1  .....G..G..TC.C...G..A....T.....GAAT.T.ACA..T...A..ACA..ACTC 394
SalHV2  ..A..A..C...C....AG....A..C..A..AA.A.T.AC...T...A..AC....... 720

SalHV3 GTGCACAAGATAATGAACGATGTGATTGATATCAATGACCCGGGCGCCGAAGTTTCGGCT 455
SalHV1 A.T......G.T......A.......C...G...CC.CTT...AT..T.....G..T..C 454
SalHV2 A.T..T..A.........A.C...G.G..C....CA..T..TAAGA.G..G..G..A..A 780

SalHV3  TTCTACATTGCCATTGACCCCACCTATTCTTCCGGCAGCCAATCGTCAATG 506
SalHV1  ........C........T..A..A..CAG......A..T.TG.....CC.. 505
SalHV2  ..T...........C.....A..A...AG......A...TT......TT.. 831
```

MODULE 5: **NEW SPECIES**

Code	***2008.032V***

To create 3 new species assigned as follows:

Genus:	***Salmonivirus***
Subfamily:	
Family:	***Alloherpesviridae***
Order:	***Herpesvirales***

Name(s) of proposed new species:

Salmonid herpesvirus 1
Salmonid herpesvirus 2
Salmonid herpesvirus 3

Argument to justify the creation of the new species:

See module 4 above.

References:

Annexes: