



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

<b>Code assigned:</b>	<b>2009.005a-fV</b>	(to be completed by ICTV officers)			
<b>Short title:</b> Fish paramyxoviruses: one new species in new genus Aquaparamyxovirus (e.g. 6 new species in the genus <i>Zetavirus</i> )					
<b>Modules attached</b> (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/>	2 <input checked="" type="checkbox"/>	3 <input checked="" type="checkbox"/>	4 <input type="checkbox"/>	5 <input type="checkbox"/>
	6 <input type="checkbox"/>	7 <input type="checkbox"/>	8 <input type="checkbox"/>	9 <input checked="" type="checkbox"/>	

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

Gael Kurath (gkurath@usgs.gov)

Has this proposal has been seen and agreed by the relevant study group(s)?  
Please select answer in the box on the right

**Yes**

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

Date first submitted to ICTV:

May 10<sup>th</sup>, 2009

Date of this revision (if different to above):

MODULE 2: **NEW SPECIES**

**Part (a)** to create and name one or more new species.

If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	<b>2009.005aV</b>	(assigned by ICTV officers)
<b>To create 1 new species with the name(s):</b>		
<i>Atlantic salmon paramyxovirus</i>		

**Part (b)** assigning new species to higher taxa

All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	<b>2009.005bV</b>	(assigned by ICTV officers)
<b>To assign the species listed in section 2(a) as follows:</b>		
Genus:	<i>Aquaparamyxovirus (new)</i>	Fill in all that apply. <ul style="list-style-type: none"> <li>• If the higher taxon has yet to be created (in a later module, below) write "<b>(new)</b>" after its proposed name.</li> <li>• If no genus is specified, enter "<b>unassigned</b>" in the genus box.</li> </ul>
Subfamily:	<i>Paramyxovirinae</i>	
Family:	<i>Paramyxoviridae</i>	
Order:	<i>Mononegavirales</i>	

**Reasons to justify the creation and assignment of the new species:**

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

AsaPV is a paramyxovirus isolated from Atlantic salmon (*Salmo salar*). It replicates at low temperatures (6-21C) as expected for viruses from poikilothermic (cold-blooded) hosts. It has biological and molecular features consistent with being a member of the subfamily *Paramyxovirinae*, in the family *Paramyxoviridae*. It is distinct from all other paramyxovirus species in having fish hosts, low replication temperatures, and low levels of identity in nucleotide gene sequences and predicted amino acid protein sequences.

GenBank Numbers:

EU156171: full length genome sequence of AsaPV described in Falk et al., 2008.

EF646380: full length genome sequence of AsaPV described in Nylund et al., 2008.

MODULE 3: **NEW GENUS**

creating and naming a new genus

Code	<b>2009.005cV</b>	(assigned by ICTV officers)
<b>To create a new genus to contain the species listed below</b>		

Code	<b>2009.005dV</b>	(assigned by ICTV officers)
<b>To name the new genus: <i>Aquaparamyxovirus</i></b>		

assigning a new genus to higher taxa

Code	<b>2009.005eV</b>	(assigned by ICTV officers)
<b>To assign the new genus as follows:</b> Ideally, a genus should be placed within a higher taxon, but if not, write " <b>unassigned</b> " in the box below.		
Subfamily:	<i>Paramyxovirinae</i>	If any of these taxa has yet to be created (in module 4, 5 or 6) please write " <b>(new)</b> " after its proposed name.
Family:	<i>Paramyxoviridae</i>	
Order:	<i>Mononegavirales</i>	

assigning type species and other species to a new genus

Code	<b>2009.005fV</b>	(assigned by ICTV officers)
<b>To designate the following as the type species of the new genus</b>		
<i>Atlantic salmon paramyxovirus</i>		Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered
Code		(assigned by ICTV officers)
<b>To assign the following as additional species of the new genus:</b>		

**Reasons to justify the creation of a new genus:**

Additional material in support of this proposal may be presented in the Appendix, Module 9

AsaPV occupies a host niche in fish species and replicates at low temperatures: both of these features are distinct from known mammalian paramyxoviruses. Phylogenetic analyses indicate this species is on a long branch that is distinct from branches leading to known paramyxovirus genera or unassigned paramyxovirus species from mammalian hosts. See trees in module 9.

**Origin of the new genus name:**

"Aqua" to indicate aquatic animal host niche, and "paramyxovirus" for the family. Follows precedent of the established genera "*Aquareovirus*", and "*Aquabirnavirus*".

**Reasons to justify the choice of type species:**

The complete genome of AsaPV has been determined by two independent lab groups.

**Species demarcation criteria in the new genus:**

- If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences of new species

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

**References:**

Winton et al., 1985. *Fish Pathology* 20: 373-380.

First isolation of paramyxoviruses from fish. This described two isolates from Pacific salmon.

Kvellingstad et al., 2003. *Journal of General Virology* 84:2179-2189.

First isolation of ASPV in Norway, designation of the name ASPV, classical characterization and very nice electron micrographs.

Fridell et al., 2004. *Diseases of Aquatic Organisms* 59:11-15.

Partial L sequence of ASPV and first phylogenetic analyses.

Nylund et al., 2008. *Virology* 373:137-148, and

Falk et al., 2008 *Virus Research* 133:218-227.

Both of these papers describe full length genome sequence of ASPV, and they come to the same conclusions. Genome length is 16,965 nt (Nylund) or 16,968 nt (Falk).

**Annex:**

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders.

The use of Figures and Tables is strongly recommended.

**Atlantic salmon paramyxovirus (AsaPV)**

For AsaPV, analyses of the full length genome sequences of two isolates in Falk et al., 2008 and Nylund et al., 2008 provide the following information.

Molecular features of the AsaPV genome: Gene order is 3'-N-P/V/C/-M-F-HN-L-5'. P gene encodes P protein (and C and possibly SB) directly, and mRNA editing encodes V and W (and possibly X). Editing strategy is thus like respiroviruses and most other paramyxoviruses, and not like rubulaviruses and Fer-de-Lance virus (of reptiles). Genome molecular features and sequence identities with cognate genes indicate AsaPV is unlike any known paramyxovirus, but most similar to respiroviruses in many features. Phylogenetic analyses with all genes place AsaPV on a long branch separate from any known paramyxovirus, but with some affinity for the *Respirovirus* genus by some genes. Both papers note that AsaPV is distinct, but most closely related to respiroviruses.

Phylogenies: Nylund paper Fig. 4 shows trees for full length F and L proteins (amino acid sequences) of AsaPV and known paramyxoviruses from other genera. The Falk paper shows trees of full length N and L proteins (amino acid sequences) with other paramyxoviruses. In both papers the L tree shows AsaPV on a long branch that diverges from the branch leading to the established respiroviruses, with the branch point close to the trunk of the tree. The F and N trees have AsaPV as a more independent branch from the trunk of the tree (see Falk 2008 Figure 3 below).

Taxonomy of AsaPV: Both papers indicate that a new genus may be appropriate, but recognize that the closest neighbor to AsaPV is the genus *Respirovirus*.

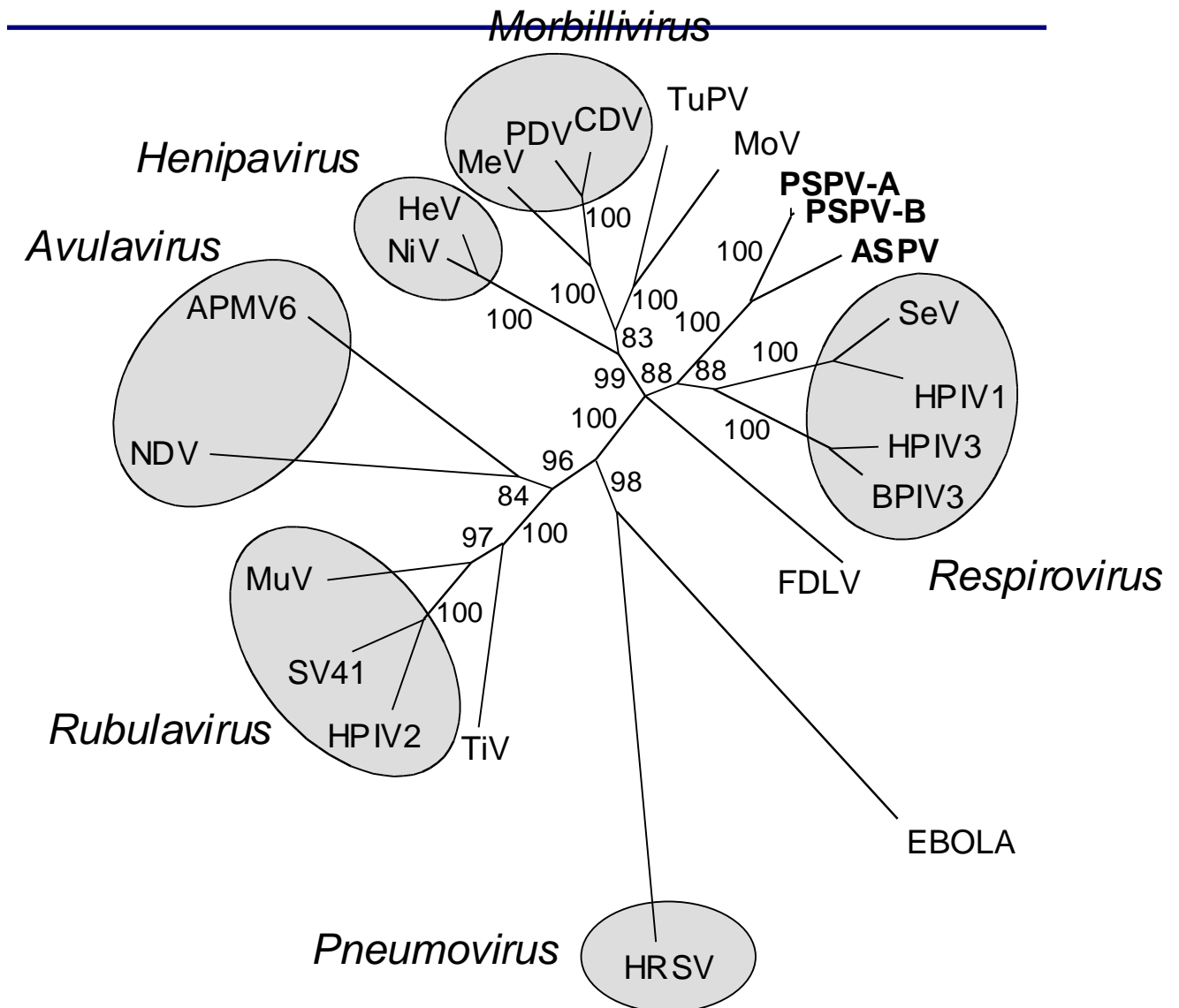
PLEASE SEE TREE BELOW



QuickTime™ and a  
TIFF (Uncompressed) decompressor  
are needed to see this picture.







Trees of partial L gene sequences (505nt) from Batts et al., 2008, *Journal of Aquatic Animal Health* 20:215-224, showing AsaPV and related paramyxoviruses from Pacific salmon on a branch distinct from other paramyxoviruses. Pacific salmon paramyxoviruses (PsaPV) may be either separate species or strains of AsaPV, so they are left unassigned until more genome sequence is available.