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

Code assigned:	***2015.019aM***	(to be completed by ICTV officers)

Short title: New species in the genus *Orthoreovirus*

Modules attached (modules 1 and 10 are required)	**1** ☒ **6** ☐	**2** X **7** ☐	**3** ☐ **8** ☐	**4** ☐ **9** ☐	**5** ☐ **10** ☒

Author(s):

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espen.rimstad@nmbu.no

List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at http://www.ictvonline.org/subcommittees.asp . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	Reoviridae Study Group

ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV: June 2015
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	***2015.019aM***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Orthoreovirus***
Subfamily:	***Spinareovirinae***
Family:	***Reoviridae***
Order:	***Unassigned***

Fill in all that apply.
- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Name of new species:	**Representative isolate:** (only 1 per species please)	**GenBank sequence accession number(s)**
Piscine orthoreovirus	MH050607	KR337473-KR337482

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.
- Further material in support of this proposal may be presented in the Appendix, Module 9

1. Piscine orthoreovirus (PRV) is associated with heart and skeletal muscle inflammation (HSMI) of farmed Atlantic salmon (*Salmo salar*) [1].

2. Piscine orthoreovirus has 10 genomic dsRNA segments. The sizes of the genomic segments are distributed in the classical orthoreoviral groups L1–3, M1–3 and S1–4 [2]. In general, amino acid identities between PRV and the members of genus *Orthoreovirus* are low for most gene segments, highest for the L-class gene segment (22-44%), and lower for M and S-classes (13-28%) [3]. The 3'-terminal nucleotide sequence (UCAUC-3') in the PRV gene segments is conserved and identical to both orthoreoviruses and aquareoviruses. The 5'-terminal nucleotide sequence (5'-GAUAAA/U) of PRV is unique, as are the analogue sequences for each of the individual species within the *Orthoreovirus* genus [3].

3. PRV encodes an outer-fiber protein, but PRV does not encode a fusion-associated small transmembrane (FAST) protein [4]. These properties differ from those of the majority of aquareoviruses, but are similar to those of aquareoviruses GCRV104 and GCRV-GD108 [5].

4. PRV has the following in common with the orthoreoviruses but not with the aquareoviruses: 10 versus 11 dsRNA segments; 47% GC-content, while that of aquareoviruses is 52–60%. Syncytia formation is not reported for PRV, in contrast to the majority of known aquareoviruses, but similar to GCRV-GD108 that seems not to induce syncytium formation in cell culture [6].

5. PRV is the first example among ortho- and aquareoviruses that encodes its outer-clamp protein on a bicistronic genome segment. PRV is also unique in that its outer-fiber protein is encoded on a monocistronic segment [4].

6. There are no indications of reassortment with aquareoviruses, although PRV and some aquareoviruses are present in the same econiche.

7. The only common criterion with aquareoviruses is perhaps the econiche – “fish”. However, “fish” consist of a large number of heterogenous species that live in very different environments and “fish” should not be regarded as a single econiche.

8. PRV infects and replicates in Atlantic salmon erythrocytes *in vivo* [7] and can be cultivated in Atlantic salmon erythrocytes *ex vivo* [8]. The amount of viral RNA plateaus after 2 weeks while the amount of viral proteins plateaus after 3 weeks of *ex vivo* cultivation.

9. There is no cell lysis accompanying virus replication in erythrocytes but a slow and steady release of virus [8].

10. PRV nucleotide and amino acid sequences from infected sea-farmed Atlantic salmon from Norway, western Canada and Chile have high identities , i.e. both in the range 97% of the S1 segment [9]. Although these samples were collected at vastly different geographical areas, the farmed Atlantic salmon all originated from Norway some generations ago.

11. The name piscine orthoreovirus will be in line with the naming tradition of orthoreoviruses, i.e. mammalian orthoreovirus (MRV) and avian orthoreovirus (ARV).

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Reference List

[1] Finstad OW, Falk K, Lovoll M, Evensen O, Rimstad E. Immunohistochemical detection of piscine reovirus (PRV) in hearts of Atlantic salmon coincide with the course of heart and skeletal muscle inflammation (HSMI). Veterinary Research 2012;43.

[2] Palacios G, Lovoll M, Tengs T, et al. Heart and Skeletal Muscle Inflammation of Farmed Salmon Is Associated with Infection with a Novel Reovirus. Plos One 2010;5(7).

additional material in support of this proposal

References:

[3] Markussen T, Dahle MK, Tengs T, et al. Sequence Analysis of the Genome of Piscine Orthoreovirus (PRV) Associated with Heart and Skeletal Muscle Inflammation (HSMI) in Atlantic Salmon (Salmo salar). Plos One 2013;8(7).

[4] Key T, Read J, Nibert ML, Duncan R. Piscine reovirus encodes a cytotoxic, non-fusogenic, integral membrane protein and previously unrecognized virion outer-capsid proteins. Journal of General Virology 2013;94:1039-50.

[5] Nibert ML, Duncan R. Bioinformatics of Recent Aqua- and Orthoreovirus Isolates from Fish: Evolutionary Gain or Loss of FAST and Fiber Proteins and Taxonomic Implications. Plos One 2013;8(7).

[6] Ye X, Tian YY FAU - Deng G, Deng GC FAU - Chi Y, Chi YY FAU - Jiang X, Jiang XY. Complete genomic sequence of a reovirus isolated from grass carp in China.(1872-7492 (Electronic)).

[7] Finstad OW, Dahle MK, Lindholm TH, et al. Piscine orthoreovirus (PRV) infects Atlantic salmon erythrocytes. Veterinary Research 2014;45.

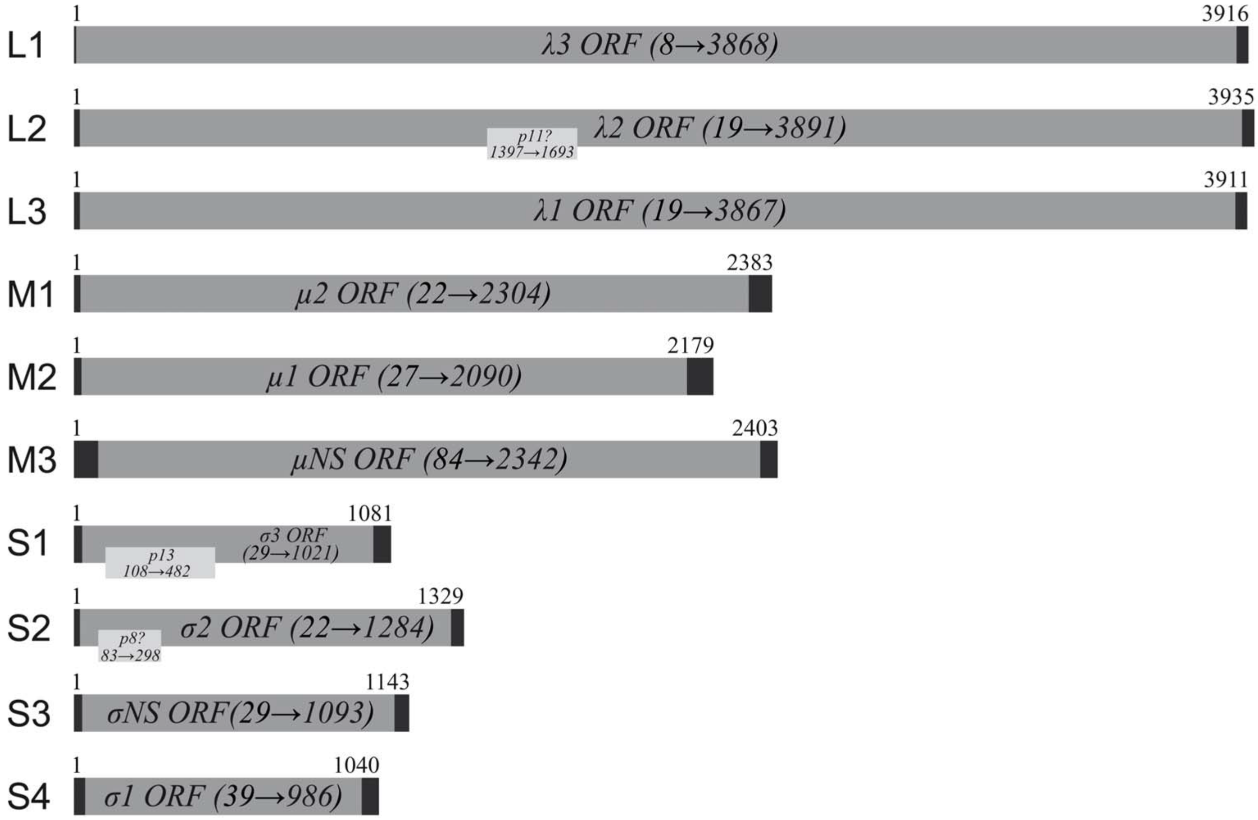
[8] Wessel O, Olsen CM, Rimstad E, Dahle MK. Piscine orthoreovirus (PRV) replicates in Atlantic salmon (Salmo salar L.) erythrocytes ex vivo. Veterinary Research 2015;46.

[9] Kibenge MJ, Iwamoto T, Wang Y, Morton A, Godoy MG, Kibenge FS. Whole-genome analysis of piscine reovirus (PRV) shows PRV represents a new genus in family Reoviridae and its genome segment S1 sequences group it into two separate sub-genotypes. Virology Journal 2013;10.

Annex:

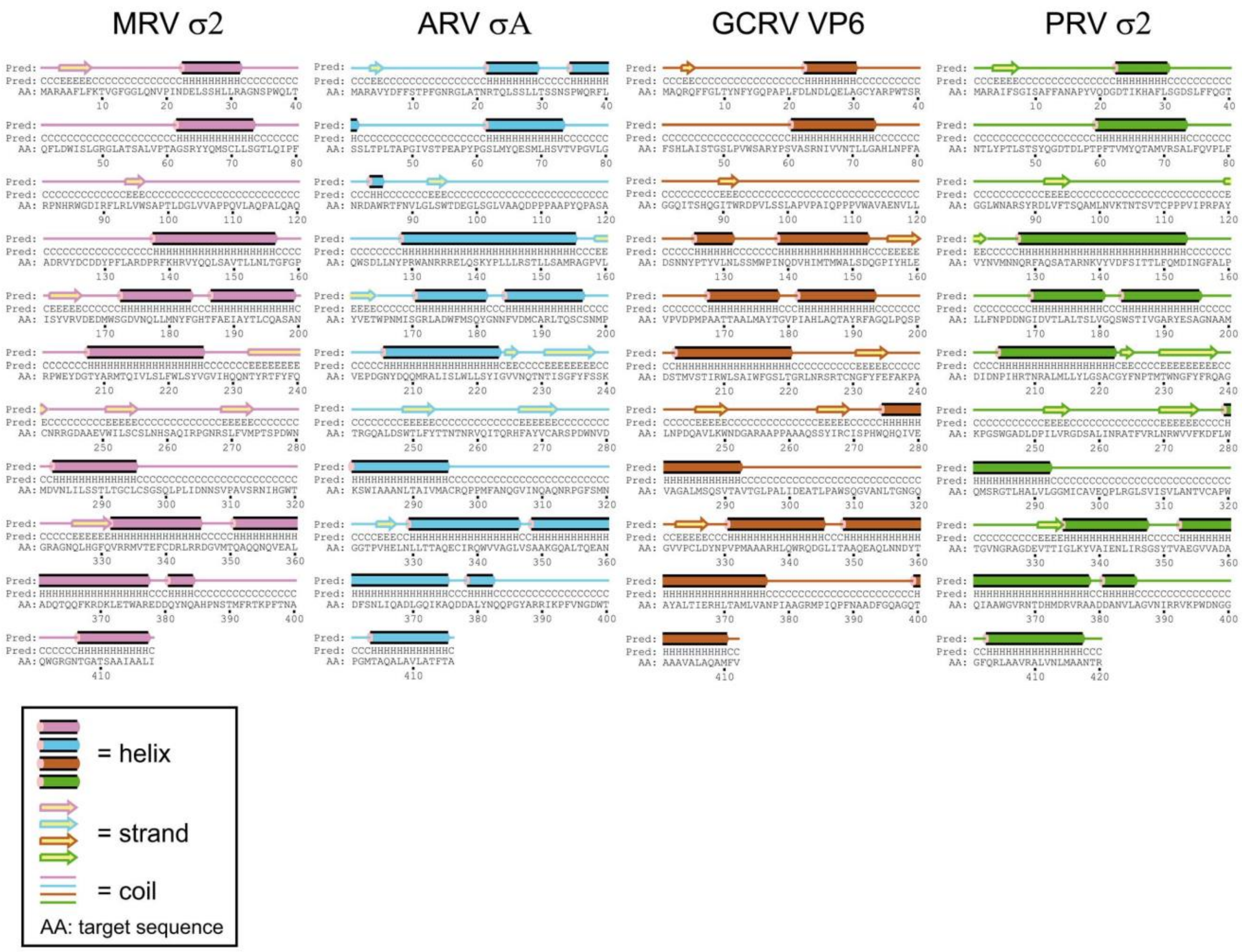
Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

The figures are derived from the journal PLoS ONE. This journal is an open access journal that permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.



The organisation of PRV genomic segments.

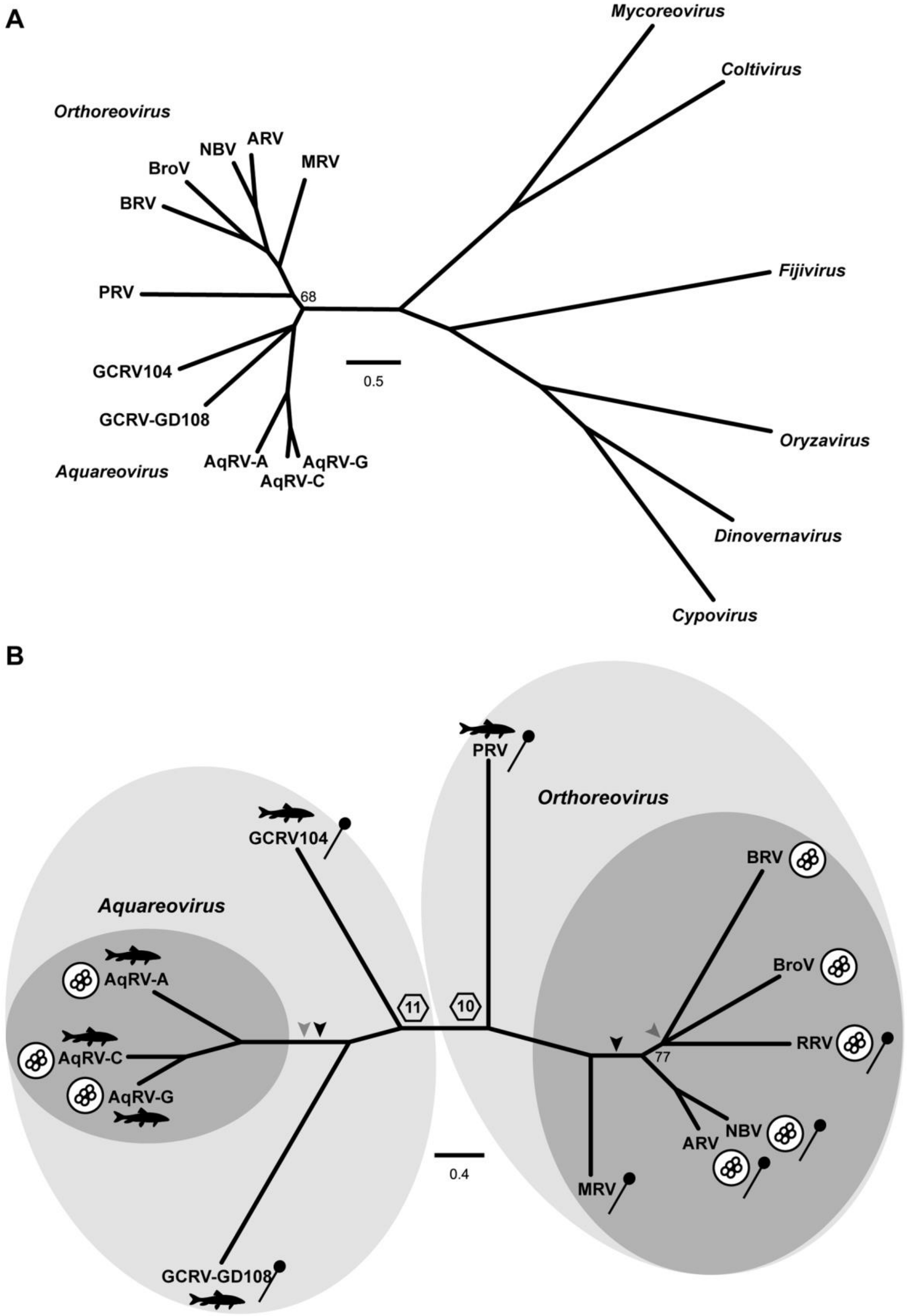
Source and credit: Markussen T, Løvoll M, Tengs T, Dahle MK, Wiik-Nielsen CR, Grove S, Lauksund RS, Finstad ØW, Robertsen B, Rimstad E.. (2013) Sequence Analysis of the Genome of Piscine Orthoreovirus (PRV) Associated with Heart and Skeletal Muscle Inflammation (HSMI) in Atlantic Salmon (Salmo salar). PLoS ONE 8(7): e70075. doi:10.1371/journal.pone.0070075



PSIPRED secondary structure predictions of PRV s2 (green) and the homologous proteins from the reovirus prototype strains MRV T3D (s2, pink), ARV-138 (sA, blue) and GCRV-873 (VP6, brown). doi:10.1371/journal.pone.0070075.g002

For PRV σ2, PSIPRED predicts a high a-helical content in its C-terminal region as for MRV and ARV, and the predicted pI of the PRV σ2 protein is close to that of the MRV- and ARV proteins

Source and credit: Markussen T, Løvoll M, Tengs T, Dahle MK, Wiik-Nielsen CR, Grove S, Lauksund RS, Finstad ØW, Robertsen B, Rimstad E. (2013) Sequence Analysis of the Genome of Piscine Orthoreovirus (PRV) Associated with Heart and Skeletal Muscle Inflammation (HSMI) in Atlantic Salmon (Salmo salar). PLoS ONE 8(7): e70075. doi:10.1371/journal.pone.0070075



Phylogenetic analyses of aqua- and orthoreovirus structural proteins.
doi:10.1371/journal.pone.0068607.g003

Source: Nibert ML, Duncan R (2013) Bioinformatics of Recent Aqua- and Orthoreovirus Isolates from Fish: Evolutionary Gain or Loss of FAST and Fiber Proteins and Taxonomic Implications. PLoS ONE 8(7): e68607. doi:10.1371/journal.pone.0068607.