This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic\_Proposals\_Help\_2019.

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

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| --- | --- | --- | --- |
| **Code assigned:** | ***2019.021M*** | |  |
| **Short title:** Create one new genus with two speciesin the family *Artoviridae* | | | |
|  | | | |
| **Author(s) and email address(es):** | | | |
| List authors in a single line *Archives of Virology* citation format (e.g. Smith AB, Huang C-L, Santos, F) | | Provide email address for each author in a single line separated by semi-colons | |
| Økland AL, Nylund A | | [arnfinn.okland@uib.no](mailto:arnfinn.okland@uib.no); [are.nylund@uib.no](mailto:are.nylund@uib.no) | |
| **Corresponding author** | | | |
| Arnfinn Økland; [arnfinn.okland@uib.no](mailto:arnfinn.okland@uib.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 (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | **ICTV *Artoviridae* Study Group** | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | |
|  | | | |
|  | | | |
| Date first submitted to ICTV: | | | June 19, 2019 |
| Date of this revision (if different to above): | | |  |

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

**Part 3:** **PROPOSED TAXONOMY**

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| **Name of accompanying Excel module:** 2019.021M.A.v1.1newgenus\_Hexartovirus.xlsx |

**Supporting material:**

| additional material in support of this proposal | |
| --- | --- |
| Lepeophtheirus salmonis negative-stranded RNA virus 1 (LsNSRV-1) has been detected in salmon lice (*Lepeophtheirus salmonis* Krøyer, 1837) infesting farmed Atlantic salmon (*Salmo salar* Linnaeus, 1758). The virus has a prevalence of 97% in salmon lice collected from Norwegian salmon farming sites. *In situ* hybridization using genomic sense and mRNA sense hybridization probes detected viral RNA in nerve tissue, connective tissue, epithelial cells of the gut, subepidermal tissue, exocrine and cement glands, as well as the testis, vas deferens and spermatophore sac of male Atlantic salmon and the ovaries and oocytes of females. Viral RNA is detected in both the cytoplasm and the nucleoli of infected cells (1).The complete genome of LsNSRV-1 has been determined. The 12.4 kb genome encodes five putative proteins; three proteins of unknown function (ORFI, ORFII, and ORFIII), G protein and L protein (1).  Běihǎi barnacle virus 8 (BhBV-8), currently classified as a peropuvirus in the mononegaviral family *Artoviridae*, has been detected in *Amphibalanus rhizophorae* barnacles in Běihǎi, China. The virus was discovered in a large-scale meta-transcriptomic survey and its genome is the only knowledge we have of this virus. The 12.4 kb genome is reported to encode four putative protein; two proteins of unkown function (hypothetical protein 1 and hypothetical protein 2), putative glycoprotein and RNA-directed RNA polymerase (2).  Phylogenetic analysis of L protein amino acid sequences groups LsNSRV-1 and BhBV-8 in a monophyletic clade in the *Artoviridae* clade distinct from other peropuviruses (Figure 1).  We therefore propose the formation of the new genus *Hexartovirus* including the new species *Caligid hexartovirus* for LsNSRV-1 and the established species *Barnacle peropuvirus* (here proposed to be renamed *Balanid hexartovirus*) for BhBV-8.  The name *Hexartovirus* is derived from the crustacean class Hexanauplia and artovirus.  *Caligid hexartovirus* is designated as the type species of the genus as the virus assigned to it (LsNSRV-1) is the most described of the two hexartoviruses.  Caligid: members of the Caligidae (sea lice). Balanid: members of the Balanidae (certain barnacles).    Fig. 1 Phylogenetic position of LsNSRV-1 in relation to 73 other viruses from all genera of the 11 families of the order *Mononegavirales* and the family *Chuviridae* of the order *Jingchuvirales*. The currently assigned peropuviruses are marked blue whereas the proposed genus *Hexartovirus* is marked red. The 73 L-protein amino acid sequences were aligned using online MAFFT v7 and poorly aligned regions were removed using trimAl resulting in a sequence alignment of 565 amino acids. Phylogenetic trees were calculated using maximum-likelihood (ML) in MEGA 6 with the LG + G + I + F model and 1000 bootstrap replications. The branch lengths reflect the evolutionary distance and are represented as the number of amino acid substitutions in proportion to the scale bar | |
|  | |
| **References:** |
| 1. **Økland, A. L., Nylund, A., Øvergård, A. C., Skoge, R. H., & Kongshaug, H**. (2019). Genomic characterization, phylogenetic position and in situ localization of a novel putative mononegavirus in *Lepeophtheirus salmonis*. Archives of virology, 164(3), 675–689. doi:10.1007/s00705-018-04119-3 2. **Shi, M., Lin, X.-D., Tian, J.-H., Chen, L.-J., Chen, X., Li, C.-X., Qin, X.-C., Li, J., Cao, J.-P., Eden, J.-S., Buchmann, J., Wang, W., Xu, J., Holmes, E. C., & Zhang, Y.-Z.** (2016). Redefining the invertebrate RNA virosphere. Nature, 540, 539. doi:10.1038/nature20167 |