This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

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.

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

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| **Code assigned:** | ***2017.012D*** | | | | (to be completed by ICTV officers) |
| **Short title**: 1 new species in the genus *Batrachovirus*, family *Alloherpesviridae,* order *Herpesvirales* | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Francesco C. Origgi | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Francesco C. Origgi, [Francesco.origgi@vetsuisse.unibe.ch](mailto:Francesco.origgi@vetsuisse.unibe.ch) | | | | | |
| **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) | | | **Herpesvirales Study Group** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
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| Date first submitted to ICTV: | | | | June 8, 2017 | |
| Date of this revision (if different to above): | | | | June 22, 2017 | |

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| **ICTV-EC comments and response of the proposer:** |
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**Part 2**: **PROPOSED TAXONOMY**

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| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet: 2017.012D.N.v1.Batrachovirus\_sp** |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

A new ranid herpesvirus, named ranid herpesvirus 3 (RHV3) has been identified in common frogs (*Rana temporaria*) in Switzerland. The virus is associated with a severe proliferative skin disease (proliferative-hyperplastic-dermatitis) characterized grossly by obvious gray patches corresponding histologically to prominently thickened portions of epidermis, expansion of the stratum spongiosum of the dermis and skin gland degeneration. Large numbers of eosinophilic to amphophilic intranuclear inclusions are observed in the affected skin. Electron microscopy revealed the presence of herpesvirus-like particles in the affected skin both intracellular and forming large extracellular clusters. Next generation sequencing allowed the sequencing of the RHV3 genome that is 207,914 nt long and it contains at least 186 open reading frames. At least 41 of the putative proteins encoded by the predicted ORFs share variable homology with proteins encoded by RHV1 and/or RHV2. Phylogenetic analyses (Maximum likelihood, figure 1) based on the amino acid sequences of the DNA polymerase and the terminase position the novel RHV3 unambiguously and with convincing bootstrap values together with the members of the genus *Batrachovirus*, family *Alloherpesviridae*. Furthermore RHV3 appears to be more closely related to RHV1 than RHV2.

On the basis of phylogenetic distance and genome organization differences, we propose to establish a new species for RHV3 in the genus *Batrachovirus*, family *Alloherpesviridae,* order *Herpesvirales*.

The name was formulated on the basis of the host (frog, Ranidae) and on the basis of the number of similar herpesviruses already known (ranid herpesvirus 1 and 2).

**Part 4:** **APPENDIX**: supporting material

| **References:** |
| --- |
| Origgi FC, Schmidt BR, Lohmann P, Otten P, Akdesir E, Gaschen V, Aguilar-Bultet L, Wahli T, Sattler U, Stoffel MH. Ranid herpesvirus 3 and proliferative dermatitis in free-ranging wild common frogs (*Rana temporaria*). Vet Pathol. 2017, 54(4):686-694 doi: 10.1177/0300985817705176. |

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| **Annex:**  This taxonomic proposal is based on the discovery of a new herpesvirus infecting common frogs.   * **Species demarcation criteria**: Although 41 of the the putative encoded proteins of RHV3 predicted genes identified in the RHV3 genome share variable homology with those encoded by RHV1 and RHV2, the highest homology, shown by ORF 100, is only 65%, which is consistent with being a different species. Furthermore the phylogenetic trees attached show unambiguously the differences between the new proposed species and the other known ranid herpesviruses. * **Supporting evidence**: The figure attached has been recently published in Veterinary Pathology. An authorization to publish the figure on the ICTV website will be requested. |

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Fig. 1. Maximum-likelihood analysis based on the amino acid sequences of the (“14”) DNA polymerase and the (“15”) terminase show the clear distinctness of ranid herpesvirus 3 from members of the official species *Ranid herpesvirus 1* and *Ranid herpesvirus 2* with an adequate phylogenetic distance to represent a new species but belonging to the same genus *Batrachovirus.* Bootstrap values are shown for 100 resamplings. All shown alloherpesviruses are representatives of separate accepted species. Testudinid herpesvirus 3 (TeHV3), an unclassified scutavirus, *Alphaherpesvirinae, Herpesviridae* is applied as outgroup.