

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

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| **Code assigned:** | **2022.001D** |  |
| **Short title:** Abolish 6 species and rename 1 family, 4 genera and 124 species in the order *Herpesvirales* | | |

**Authors and email addresses**

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| --- | --- |
| Benkő M, Brandt CR, Bryant NA, Dastjerdi A, Davison AJ, Depledge DP, Doszpoly A, Gatherer D, Gompels UA, Hartley CA, Inoue N, Jarosinski KW, Kaul R, Lacoste V, Norberg P, Origgi FC, Orton RJ, Pellett PE, Schmid DS, Spatz SJ, Stewart JP, Szpara ML, Trimpert J, Vaz P, Waltzek TB | benko.maria@atk.hu; crbrandt@wisc.edu; nab29@cam.ac.uk; akbar.dastjerdi@apha.gov.uk; andrew.davison@glasgow.ac.uk; depledge.daniel@mh-hannover.de; doszpoly.andor@atk.hu; d.gatherer@lancaster.ac.uk; uagompels@virokine.com; carolah@unimelb.edu.au; inoue@gifu-pu.ac.jp; kj4@illinois.edu; rkaul@south.du.ac.in; vincent.lacoste@pasteur.fr; peter.norberg@microbio.gu.se; francesco.origgi@vetsuisse.unibe.ch; richard.orton@glasgow.ac.uk; ppellett@med.wayne.edu; scott.schmid@live.com; stephen.spatz@usda.gov; j.p.stewart@liverpool.ac.uk; moriah@psu.edu; trimpert.jakob@fu-berlin.de; pvaz@unimelb.edu.au; tomwaltzek@gmail.com |

**Authors’ institutional affiliations**

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| --- |
| Veterinary Medical Research Institute, Eötvös Loránd Research Network, Budapest, Hungary [MB, AD2]  University of Wisconsin-Madison, Madison, Wisconsin, USA [CRB]  University of Cambridge, Cambridge, UK [NAB]  Animal and Plant Health Agency-Weybridge, Addlestone, Surrey, UK [AD1]  Institute of Virology, Hannover Medical School, Hannover, Germany [DPD]  Lancaster University, Lancaster, United Kingdom [DG]  Virokine Therapeutics, London BioScience Innovation Centre, Royal Veterinary College, London, UK [UAG]  The University of Melbourne, Parkville, Victoria, Australia [CAH, PV]  Gifu Pharmaceutical University, Gifu, Japan [NI]  University of Illinois at Urbana-Champaign, Urbana, Illinois, USA [KWJ]  University of Delhi, New Delhi, India [RK]  Institut Pasteur de Madagascar, Antananarivo, Madagascar [VL]  University of Gothenburg, Gothenburg, Sweden [PN]  University of Bern, Bern, Switzerland [FCO]  University of Glasgow, Glasgow, United Kingdom [RJO, AJD]  Wayne State University School of Medicine, Detroit, Michigan, USA [PEP]  Centers for Disease Control and Prevention, Atlanta, Georgia, USA [DSS] (previous affiliation)  US National Poultry Research Center, Athens, Georgia, USA [SJS]  University of Liverpool, Liverpool, UK [JPS]  Pennsylvania State University, Pennsylvania, USA [MLS]  Freie Universität Berlin, Berlin, Germany [JT]  University of Florida, Gainesville, Florida, USA [TBW] (previous affiliation) |

**Corresponding author**

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| Andrew Davison |

**List the ICTV Study Group(s) that have seen this proposal**

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| *Herpesvirales* |

**ICTV Study Group comments and response of proposer**

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| The authors are the *Herpesvirales* Study Group |

**ICTV Study Group votes on proposal**

|  |  |  |  |
| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes in support** | **Votes against** | **No vote** |
| *Herpesvirales* | 24 | 0 | 1 |

**Authority to use the name of a living person**

|  |  |
| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | 20 May 2022 |
| Date of this revision (if different from above) |  |

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

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2022.001D.N.v1.Herpesvirales\_1renfam\_4rengen\_124rensp\_6absp.xlsx |

**Abstract**

These proposals are to change the name of the family *Herpesviridae* to *Orthoherpesviridae*, abolish 6 species in this family that are not assigned to genera, rename 4 genera in the family *Alloherpesviridae*, and rename 124 species in the order *Herpesvirales*.

**Text of proposal**

We propose changing the name of the family *Herpesviridae* to *Orthoherpesviridae*. This would allow viruses in the current family *Herpesviridae* to be distinguished by a vernacular term (“orthoherpesviruses”) from those in the other two families (“alloherpesviruses” and “malacoherpesviruses”) and from those in the order *Herpesvirales* as a whole (“herpesviruses”).

We propose renaming 4 genera in the family *Alloherpesviridae*. Changing *Batrachovirus* to *Batravirus*, *Cyprinivirus* to *Cyvirus*, *Ictalurivirus* to *Ictavirus* and *Salmonivirus* to *Salmovirus* will lessen the implication that viruses in these genera are restricted to animals belonging to particular host taxa.

We propose abolishing 6 species in the family *Herpesviridae* (proposed family *Orthoherpesviridae*). These species (*Chelonid alphaherpesvirus 6*, *Cercopithecine gammaherpesvirus 14*, *Equid gammaherpesvirus 7*, *Phocid gammaherpesvirus 2*, *Saguinine gammaherpesvirus 1* and *Iguanid herpesvirus 2*) are either not currently classified into genera or lack identifying sequence information. It is possible that new information will allow the viruses concerned to be classified again in future.

We propose renaming 124 species in the order *Herpesvirales* using a binomial format as mandated by the ICTV. Current species names are trinomials. The first word is derived from a taxon of the host that in its natural setting harbours the virus. The default taxon is family, and the derived word ends in ‘*-id*’. Exceptions are species from humans (designated by ‘*Human’*), from the family Bovidae (designated by host subfamily or genus and ending in ‘*-ine*’) and from nonhuman primates (designated by host genus and also ending in ‘*-ine*’). In the family *Herpesviridae*, the second word is ‘*alphaherpesvirus’*, ‘*betaherpesvirus’* or ‘*gammaherpesvirus’*, depending on the subfamily to which the species belongs. In the families *Alloherpesviridae* and *Malacoherpesviridae*, the second word is ‘*herpesvirus*’. The third word is a numeral, or, in rare cases, a numeral followed by a capital letter. The numeral is intended solely to provide a unique identifier, and does not imply the existence of a complete or continuous series. These numerals are chosen to avoid confusion in relation to those used in virus names in the literature. An example of a current species name is *Gallid alphaherpesvirus 1*, of which infectious laryngotracheitis virus is a member.

In the proposed binomial format, the first word would be the name of the genus to which the species belongs. For the family *Herpesviridae* (proposed family *Orthoherpesviridae*), the second word (the species epithet) would be derived from the current species name contracted by changing the initiating upper case character to lower case and deleting the term ‘*herpesvirus’* and the two space characters. Thus, *Gallid alphaherpesvirus 1* would become *Iltovirus gallidalpha1*. We propose a similar approach for the families *Alloherpesviridae* and *Malacoherpesviridae*, except that a term from the virus family would be used instead of that for the virus subfamily, because these families lack subfamilies. Thus, *Ranid herpesvirus 1* would become *Batravirus ranidallo1* and *Ostreid herpesvirus 1* would become *Ostreavirus ostreidmalaco1*. We do not recommend the classification of herpesviruses identified in the absence of host information. However, if this were to become necessary, a generic species epithet (e.g. *incognitus*) followed by a number could be used.

Viruses in the order *Herpesvirales* often have multiple names, and there has been an increasing tendency to mirror species names in these names. For example, infectious laryngotracheitis virus is often referred to as gallid herpesvirus 1 or, since the previous change to species names, gallid alphaherpesvirus 1. We do not consider this to be problematic, because virus names and species names are readily differentiated by orthography (e.g. gallid alphaherpesvirus 1 is the virus name and *Gallid alphaherpesvirus 1* is the species name). However, the proposed change to a binomial format for species names would present an opportunity for the two categories of name to be kept distinct, with systematic virus names remaining as at present (essentially following the current rules for naming species), and these names being parsed into binomial species names. Thus, the systematic virus name would be gallid alphaherpesvirus 1 and the species name would be *Iltovirus gallidalpha1*.

We have taken a conservative approach to developing a binomial species nomenclature because we believe that it will allow the field to retain an accepted system for naming viruses that is easily implemented in naming species. Species names would then continue to convey the information that we consider to be important, especially to those who are unfamiliar with the wide range of viruses classified in the order *Herpesvirales*, namely on the virus host and the virus family or subfamily to which the species belongs, and retaining the distinguishing number assigned previously.