

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

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| **Code assigned:** | **2020.007D** |  |
| **Short title:** Create four new genera (*Quwivirus*, *Patagivirus*, *Bossavirus*, *Manticavirus*) including five new species and two previously unassigned species, and one new species in the genus *Varicellovirus* (*Herpesvirales*: *Herpesviridae*) |

**Author(s) and email address(es)**

|  |  |
| --- | --- |
| Gatherer D, Benkő M, Brandt CR, Bryant NA, das Neves CG, Dastjerdi A, Depledge DP, Doszpoly A, 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, Davison AJ | d.gatherer@lancaster.ac.uk; maribenko@gmail.com; crbrandt@wisc.edu; neil.bryant@aht.org.uk; carlos.dasneves@vetinst.no; akbar.dastjerdi@apha.gov.uk ; daniel.depledge@nyulangone.org; andor.doszpoly@gmail.com; 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; dss1@cdc.gov ; stephen.spatz@ars.usda.gov ; j.p.stewart@liverpool.ac.uk; moriah@psu.edu; trimpert.jakob@fu-berlin.de ; pvaz@unimelb.edu.au; tbwaltzek@ufl.edu; andrew.davison@glasgow.ac.uk |

**Author(s) institutional address(es) (optional)**

|  |
| --- |
| Lancaster University, Lancaster, United Kingdom [DG]Centre for Agricultural Research, Budapest, Hungary [MB, AD2]University of Wisconsin-Madison, Madison, WI, USA [CRB]Animal Health Trust, Newmarket, United Kingdom [NAB]Norwegian Veterinary Institute, Oslo, Norway (CGdN)Animal and Plant Health Agency-Weybridge, Addlestone, United Kingdom [AD1]NYU Grossman School of Medicine, New York, NY, USA [DPD]Virokine Therapeutics Ltd, London, United Kingdom [UAG]University of Melbourne, Parkville, VIC, Australia [CAH, PV]Gifu Pharmaceutical University, Gifu, Japan [NI]University of Illinois at Champaign-Urbana, Urbana, IL, USA [KWJ]University of Delhi, New Delhi, India [RK]Institut Pasteur, Paris, France [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, MI, USA [PEP]Centers for Disease Control and Prevention, Atlanta, GA, USA [DSS]US Department of Agriculture, Athens, GA, USA [SJS]University of Liverpool, Liverpool, United Kingdom [JPS]Pennsylvania State University, University Park, PA, USA [MLS]Freie Universität Berlin, Berlin, Germany [JT]University of Florida, Gainesville, Florida, USA [TBW]University of Glasgow, Glasgow, UK [AJD] |

**Corresponding author**

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| --- |
| Andrew Davison (andrew.davison@glasgow.ac.uk) |

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

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| *Herpesvirales* SG |

**ICTV study group comments and response of proposer**

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| The authors are all the members of the *Herpesvirales* Study Group plus CGdN |

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

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| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
| *Bossavirus* | Dr. Greg Bossart | N; the person is no longer living but agreement was nonetheless obtained by TBW from his widow |

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | August 12, 2020 |
| Date of this revision (if different to above) | August 20, 2020 |

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

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

**Name of accompanying Excel module**

2020.007D.N.v1.Herpesviridae\_4gen\_6sp.xslx

**Abstract**

These proposals are made on the basis of a previous phylogenetic analysis of a concatenation of the encoded amino acid sequences of six well-conserved viral genes. They involve creating species *Cervid alphaherpesvirus 3* in genus *Varicellovirus* in subfamily *Alphaherpesvirinae*, species *Miniopterid betaherpesvirus 1* in new genus *Quwivirus* in subfamily *Betaherpesvirinae,* species *Vespertilionid gammaherpesvirus 3* in new genus *Patagivirus* insubfamily *Gammaherpesvirinae*, species *Delphinid gammaherpesvirus 1* in new genus *Bossavirus* in subfamily *Gammaherpesvirinae*, and species *Phascolarctid gammaherpesvirus 1* and *Vombatid gammaherpesvirus 1* in new genus *Manticavirus* in subfamily *Gammaherpesvirinae*. They also involve moving existing unassigned species *Caviid betaherpesvirus 2* and *Tupaiid betaherpesvirus 1* into new genus *Quwivirus*.

**Text of proposal**

**Introduction**

# Previously, we proposed (see [here](https://talk.ictvonline.org/files/ictv_official_taxonomy_updates_since_the_8th_report/m/animal-dna-viruses-and-retroviruses/8056)) the classification of 18 new species in existing genera in family *Herpesviridae* and the placement of one existing species into an existing genus. In the phylogenetic trees supporting these proposals, several viruses were included for which the sequence data had not been released. We now propose the classification of some of these viruses.

**Species demarcation criteria**

The criteria for the order *Herpesvirales* are outlined in the 9th ICTV Report as follows.

A herpesvirus may be classified as a species if it has distinct epidemiological or biological characteristics and a distinct genome that represents an independent replicating lineage. Sequence information is required for formal recognition of new herpesvirus species. Replicating lineages of herpesviruses are now identified primarily on the basis of information derived from genomic sequences. Sequence information sufficient to demonstrate that a novel virus represents a replicating lineage distinct from known herpesvirus species is taken as evidence that the virus in question exists in nature, occupies a distinct ecological niche and thus can be recognized as a herpesvirus species. For some well-studied genes, there are levels of sequence difference beyond which there are no instances in which the viruses in question do not have distinct epidemiological and biological properties; such viruses can be reliably recognized as species on the basis of limited sequence information. There are also closely related viruses that have relatively small differences in the sequences of individual genes, but genetic differences extend across the respective genomes in a manner indicative of them representing independent replicating lineages. These viruses also have distinct epidemiological and biological characteristics (e.g. host identity, pathogenic and epidemiological properties, and the lack of occurrence of natural recombinants) and thus meet the definition of herpesvirus species.

**Phylogenetic analysis**

For using phylogenetic analysis to advance herpesvirus taxonomy, the Study Group does not mandate complete genome sequences, does not set a dependence on any particular gene or group of genes, or even that the sequence of any particular gene should be complete, and does not specify genetic distance thresholds for differentiating taxa. As in our previous proposals, the phylogenetic analysis in these proposals are based on a concatenation of the encoded amino acid sequences of six well-conserved viral genes. These genes encode uracil-DNA glycosylase, helicase-primase helicase subunit, DNA packaging terminase subunit 1, major capsid protein, envelope glycoprotein B and DNA polymerase catalytic subunit. An amino acid sequence alignment was generated using Protein Align in MOE (<https://www.chemcomp.com/>), and phylogenetic trees were constructed in MEGA (1). A neighbour-joining phylogenetic tree (2) using Poissondistances (3) was constructed with 100 bootstrap replicates (4) to assess clade confidence. The three unrooted trees shown below concern viruses in subfamilies *Alphaherpesvirinae*, *Betaherpesvirinae* and *Gammaherpesvirinae* of family *Herpesviridae*. The connection of these subfamilies in the family has been demonstrated in the literature (5) and is not reproduced here. The names of the existing genera into which viruses fall are shown on the right in black font, and those of proposed genera in orange font. Bootstrap values of ≥70 are indicated.

The rule-of-thumb applied to previous proposals is that the evolutionary distance between each virus to be classified and its closest classified relative should be more than that between the most closely related viruses that have already been classified into the family *Herpesviridae*. However, other factors, such as host species, may also be taken into account.

**Species names**

A herpesvirus species name consists of three elements. The first is derived from a taxon of the host that in its natural setting harbors the virus. The default taxon employed is that of family, and, except for the species of humans, it ends in ‘-id’. Exceptions are viral species from the family Bovidae, which are designated by host subfamily or genus, and nonhuman primates (host genus); these names end in ‘-ine’. The second element is the word ‘alphaherpesvirus’, ‘betaherpesvirus’ or ‘gammaherpesvirus’, depending on the subfamily to which the virus belongs. The third element is a numeral, in two cases followed by a letter. It is important to register that the numeral is intended solely to provide a unique identifier. It does not imply the existence of a complete or continuous series, or any particular relationship between viruses in difference series that carry the same numeral, and is chosen as much as is possible to avoid confusion in relation to the numerals used in virus names in the literature.

A virus may have several names in the literature, and these may have been used inconsistently. To avoid confusion, the short forms of virus names in this proposal are related to the species names and commence with the following alternatives.

Al alcelaphine

An anatid

Ao aotine

At ateline

Bo bovine

Bu bubaline

Ca canid

Cd caviid

Ce cercopithecine

Ch chelonid

Cl callitrichine

Co columbid

Cr cricetid

Cv cervid

De delphinid

El elephantid

Eq equid

Fe felid

Ga gallid

Hu human

Le leporid

Ma macropodid

Mc macacine

Md mandrilline

Me meleagrid

Mn miniopterid

Mo monodontid

Ms mustelid

Mu murid

Ov ovine

Pa papiine

Pc phascolarctid

Ph phocid

Pn panine

Ps psittacid

Pt pteropodid

Sa saimiriine

Sp spheniscid

Su suid

Te testudinid

Tu tupaiid

Ve vespertilionid

Vo vombatid

These two letters are followed by three more to indicate the subfamily (AHV, *Alphaherpesvirinae*; BHV, *Betaherpesvirinae*; and GHV, *Gammaherpesvirinae*), and finally by a numeral (and a further letter in two cases). Thus, the abbreviation of the virus name corresponds to the existing or proposed species name (e.g. BoAHV5, *Bovine alphaherpesvirus 5*).

**Taxonomic proposals**

The creation of the following species and genera is supported by the phylogenetic trees presented at the foot of this section. Where they exist, the papers that report the sequence data used for the analysis are cited. The key is as follows.

 Classified into species and genus; data in tree published; taxonomic changes not proposed

 Classified into species and genus; data in tree not published; taxonomic changes not proposed

 Classified into species but not genus; **classification proposed**

 Not classified; data in tree published; **classification proposed**

 Not classified and identities not shown; data in tree not published; classification not proposed

1. To create the new species *Cervid alphaherpesvirus 3* in genus *Varicellovirus* in subfamily *Alphaherpesvirinae*. The virus (elk herpesvirus) infects the elk or wapiti (*Cervus canadensis*), whereas its closest relative (red deer herpesvirus in species *Cervid alphaherpesvirus 1*) infects the red deer (*Cervus elaphus*). Earlier studies indicated that the host species diverged about 7 million years ago (6) and that there is sufficient genetic and antigenic divergence between the viruses to justify their classification in separate species (7). The concatenated nucleotide sequences of the six genes differ by 1.35% (*p*-distance in MEGA). This is less than the difference (2.92%) between BoAHV5 and BuAHV1, which are in a sister group and are presently the most closely related alphaherpesviruses classified into different species. These latter viruses originate from different host genera (cattle, *Bos taurus*,and water buffalo, *Bubalus bubalis*) rather than different host species, and are estimated to have diverged about 12.3 million years ago (CI: 8.8-16.1 million years ago; <http://www.timetree.org/>).
2. To assign the existing species *Caviid betaherpesvirus 2* as the type species of new genus *Quwivirus* in subfamily *Betaherpesvirinae* (8). The virus (guinea pig cytomegalovirus) infects the guinea pig (*Cavia porcellus*). “Quwi” is the Quechua name for the guinea pig.
3. To assign the existing species *Tupaiid betaherpesvirus 1* to new genus *Quwivirus* (9). The virus (tupaia herpesvirus) infects the northern treeshrew (*Tupaia belangeri*).
4. To create the new species *Miniopterid betaherpesvirus 1* and assign it to new genus *Quwivirus* (10). The virus (Miniopterus schreibersii herpesvirus) infects the common bent-wing bat (*Miniopterus schreibersii*). The new genus would contain three rather distantly related viruses and will possibly be divided when further members are discovered. The most appropriate step at present for ensuring that these species are assigned to genera, while avoiding the unnecessary creation of names, is to assign them to the same genus.
5. To create the new species *Vespertilionid gammaherpesvirus 3* and assign it as the type species of new genus *Patagivirus* insubfamily *Gammaherpesvirinae* (11). This virus (Eptesicus fuscus gammaherpesvirus) infects the big brown bat (*Eptesicus fuscus*). “Patagi” is from patagium, which is the skin forming the surface of the wing in bats. The numeral 3 is assigned because the numeral 2 is reserved for the species to which another bat herpesvirus (Myotis ricketti herpesvirus 2) will be assigned in future.
6. To create the new species *Delphinid gammaherpesvirus 1* and assign it as the type species of new genus *Bossavirus* in subfamily *Gammaherpesvirinae* (12). The virus (common bottlenose dolphin gammaherpesvirus 1) infects the common bottlenose dolphin (*Tursiops truncatus*). “Bossa” is from the name of Dr Gregory D Bossart, senior vice president and chief veterinary officer at Georgia Aquarium and expert in marine mammals (particularly dolphins) and their diseases, who died in 2019 (see [here](https://www.aazv.org/page/Bossart)).
7. To create the new species *Phascolarctid gammaherpesvirus 1* and assign it as the type species of the new genus *Manticavirus* in subfamily *Gammaherpesvirinae* (13). The virus (phascolarctid gammaherpesvirus 1) infects the koala (*Phascolarctos cinereus*). “Mantica” is the Latin for a small bag, sack or travelling bag and is given in reference to the marsupial pouch.
8. To create the new species *Vombatid gammaherpesvirus 1* in new genus *Manticavirus* (13). The virus (vombatid gammaherpesvirus 1) infects the common wombat (*Vombatus ursinus*).

Several established species will still lack assignment to genera. These are *Chelonid alphaherpesvirus 6*, which is assigned to subfamily *Alphaherpesvirinae*, *Equid gammaherpesvirus 7*, *Phocid gammaherpesvirus 2* and *Saguinine gammaherpesvirus 1*, which are assigned to subfamily *Gammaherpesvirinae*, and *Iguanid herpesvirus 2*, which is not assigned to a subfamily. Insufficient sequence data are available for assignments on the basis used above, and a suitable course of action will be determined in future.

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****Phylogeny of viruses in subfamily *Alphaherpesvirinae***

****Phylogeny of viruses in subfamily *Betaherpesvirinae***

****Phylogeny of viruses in subfamily *Gammaherpesvirinae***