

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

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| **Code assigned:** | **2022.002D** |  |
| **Short title:** **Create 9 new species in the family *Orthoherpesviridae* (*Herpesvirales*)** |

**Authors and email addresses**

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**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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| 2022.002D.N.v1.Herpesvirales\_9nsp.xlsx |

**Abstract**

These proposals are made on the basis of a phylogenetic analysis of six well-conserved viral genes. The proposed new species are: *Iltovirus cacatuidalpha2* and *Iltovirus psittacidalpha5* in genus *Iltovirus*, *Simplexvirus macropodidalpha4* and *Simplexvirus pteropodidalpha2* in genus *Simplexvirus*, and *Varicellovirus equidalpha6* in genus *Varicellovirus* (in subfamily *Alphaherpesvirinae*); *Proboscivirus elephantidbeta3* in genus *Proboscivirus* (in subfamily *Betaherpesvirinae*); and *Lymphocryptovirus macacinegamma13* in genus *Lymphocryptovirus*, *Percavirus rhinolophidgamma1* in genus *Percavirus*, and *Rhadinovirus colobinegamma1* in genus *Rhadinovirus* (in subfamily *Gammaherpesvirinae*).

**Text of proposal**

**Introduction**

# Previously, we proposed ([here](https://talk.ictvonline.org/files/ictv_official_taxonomy_updates_since_the_8th_report/m/animal-dna-viruses-and-retroviruses/8056) and [here](https://talk.ictvonline.org/files/ictv_official_taxonomy_updates_since_the_8th_report/m/animal-dna-viruses-and-retroviruses/11017)) the classification of new species in family *Herpesviridae* on the basis of a phylogenetic analysis of a concatenation of the encoded amino acid sequences of six well-conserved viral genes. We propose the classification of nine additional viruses on the same basis. This should be viewed as an extension of the accompanying proposals entitled “Abolish 6 species and rename 1 family, 4 genera and 124 species in the order *Herpesvirales*”, which include proposals to change the name of the family *Herpesviridae* to *Orthoherpesviridae* and proposals to implement a binomial nomenclature for species in the order *Herpesvirales*.

**Species demarcation criteria**

The criteria adopted by the Study Group are as follows.

Members of different herpesvirus species have distinct epidemiological or biological characteristics and distinct genomes that represent independent replicating lineages. Replicating lineages of herpesviruses are identified primarily on the basis of information derived from genome sequences. Moreover, sequence information sufficient to demonstrate that a novel virus represents a replicating lineage distinct from members of known species is taken as evidence that the virus in question exists in nature and thus can be recognised as a member of an additional species. For some well-studied genes, there are levels of sequence difference beyond which the viruses in question are presumed to have distinct epidemiological and biological properties; such viruses can be reliably recognised as members of different 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 these differences extend across the respective genomes in a manner indicating that they represent independent replicating lineages. These viruses also have distinct epidemiological and biological characteristics (e.g. host identity, pathogenic and epidemiological properties, and the absence or rarity of contemporary natural recombinants).

The Study Group has developed the following guidance on the role of sequence data.

At present, sequence data are used flexibly to support taxonomic proposals on the basis of phylogenetic grouping of viruses. Each case is considered on its merits and does not require the availability of a complete genome sequence, does not depend on any specified gene or group of genes, and does not specify genetic distance thresholds for differentiating taxa.

**Species names**

Until now, the Study Group has adopted the following scheme for naming species.

Species names in the family consist of three elements. The first is derived from the name of a taxon of the host that in its natural setting harbours the virus. The default taxon employed is that of family, and, except for herpesvirus species from humans, it ends in ‘*-id*’. Other exceptions are viral species from the family Bovidae, which are designated by host subfamily or genus, and from nonhuman primates, which are designated by 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, or, in two cases (*Human betaherpesvirus 6A* and *Human betaherpesvirus 6B*), a numeral followed by a letter. The numeral is intended solely to provide a unique identifier, rather than to imply the existence of a complete or continuous series, or any particular relationship between viruses in different series that carry the same numeral. These numbers have been chosen to avoid confusion in relation to the numerals used in virus names in the literature.

The accompanying proposals essentially maintain this scheme for deriving systematic virus names, which would then form the basis of binomial species names.

In the proposed binomial format, the first word would be the name of the genus to which the species belongs. For the family *Orthoherpesviridae*, the second word (the species epithet) would consist of the current species name contracted by changing the initiating upper case character to lower case, deleting space characters, and deleting ‘herpesvirus’. Thus, *Gallid alphaherpesvirus 1* would become *Iltovirus gallidalpha1*.

**Phylogenetic analysis**

An analysis was performed using MEGA 7 and MEGA X. Subfamily-specific alignments were made of the concatenated predicted amino acid sequences of six well-conserved genes (encoding uracil-DNA glycosylase, helicase-primase helicase subunit, DNA packaging terminase subunit 1, major capsid protein, envelope glycoprotein B and DNA polymerase catalytic subunit) for all classified herpesviruses for which these sequences are available. Neighbour-joining, midpoint-rooted trees were computed with 500 bootstrap replicates, and evolutionary distances were calculated in amino acid substitutions per site using the Poisson correction method. Systematic virus names that parallel the species names are shown. Genera with names are shown by brackets, and some are in collapsed format. The viruses proposed for classification are marked by red diamonds (♦).

**Taxonomic proposals**

1. To create the new species *Iltovirus cacatuidalpha2* in genus *Iltovirus*, subfamily *Alphaherpesvirinae*. The virus was discovered in a little corella (*Cacatua sanguinea*). It was named cacatuid herpesvirus 2 and characterised as a potential member of genus *Iltovirus* [1]. Its systematic name is cacatuid alphaherpesvirus 2. The closest classified relative (psittacid alphaherpesvirus 1) infects psittacine birds.
2. To create the new species *Iltovirus psittacidalpha5* in genus *Iltovirus*,subfamily *Alphaherpesvirinae*. The virus was discovered in an Indian ringneck parrot (*Psittacula krameri*). It was named psittacid herpesvirus 5 or psittacid alphaherpesvirus 5 and characterised as a potential member of genus *Iltovirus* [2]. Its systematic name is psittacid alphaherpesvirus 5. The closest classified relatives (gallid alphaherpesvirus 1 and psittacid alphaherpesvirus 1) infect birds.
3. To create the new species *Simplexvirus macropodidalpha4* in genus *Simplexvirus*, subfamily *Alphaherpesvirinae*. The virus was discovered in an eastern grey kangaroo (*Macropus giganteus*). It was named macropodid alphaherpesvirus 4 (its systematic name) and characterised as a potential member of genus *Simplexvirus* [3]. The closest classified relative (macropodid alphaherpesvirus 2) infects the dorcopsis wallaby.
4. To create the new species *Simplexvirus pteropodidalpha2* in genus *Simplexvirus*,subfamily *Alphaherpesvirinae*. The virus was discovered in a Lyle's flying fox (*Pteropus lylei*). It was named *Pteropus lylei*-associated alphaherpesvirus and characterised as a potential member of genus *Simplexvirus* [4]. Its systematic name is pteropodid alphaherpesvirus 2. The closest classified relative (pteropodid alphaherpesvirus 1) infects a flying fox of unidentified species, with the small flying fox being the most closely related.
5. To create the new species *Varicellovirus equidalpha6 in genus Varicellovirus*,subfamily *Alphaherpesvirinae*. The virus was discovered in a donkey (*Equus asinus*). It was named asinine herpesvirus strain AsHV/Bari/2011/740 and characterised as a potential member of genus *Varicellovirus* [5]. Its systematic name is equid alphaherpesvirus 6. The discoverers reported that this virus has properties similar to those of a virus named in 1988 asinine herpesvirus 1 and later equid herpesvirus 6. However, neither this earlier virus nor associated sequence data are available. The closest classified relative (equid alphaherpevirus 3) infects the horse.
6. To create the new species *Proboscivirus elephantidbeta3* in genus *Proboscivirus*,subfamily *Betaherpesvirinae*. The virus was discovered in an African elephant (*Loxodonta africana*). It was named elephant endotheliotropic herpesvirus 3A and characterised as a potential member of genus *Proboscivirus* [GenBank accession no. MN373268.1]. Its systematic name is elephantid betaherpesvirus 3. The closest classified relative (elephantid betaherpesvirus 4) infects the Asian elephant.
7. To create the new species *Lymphocryptovirus macacinegamma13* in genus *Lymphocryptovirus*, subfamily *Gammaherpesvirinae*. The virus was discovered in a stump-tailed macaque (*Macaca arctoides*). It was named Macaca arctoides gammaherpesvirus 1 and characterised as a potential member of genus *Lymphocryptovirus* [6]. Its systematic name is macacine gammaherpesvirus 13. It is closely related to two classified viruses (macacine betaherpesviruses 4 and 10) that infect macaques in other species (rhesus macaque and cynomolgus macaque, respectively). Differences extend across the entire genomes.
8. To create the new species *Percavirus rhinolophidgamma1* in genus *Percavirus*, subfamily *Gammaherpesvirinae*. The virus was discovered in a greater horseshoe bat (*Rhinolophus ferrumequinum*). It was named Rhinolophus gammaherpesvirus 1 and characterised as a potential member of genus *Percavirus* [7]. Its systematic name is rhinolophid gammaherpesvirus 1. The closest classified relative (vespertilionid gammaherpesvirus 1) infects a bat, the cave myotis.
9. To create the new species *Rhadinovirus colobinegamma1* in genus *Rhadinovirus*,subfamily *Gammaherpesvirinae*. The virus was discovered in a mantled guereza (*Colobus guereza kikuyuensis*). It was named colobine gammaherpesvirus 1 (its systematic name) and characterised as a potential member of genus *Rhadinovirus* [8]. The closest classified relative (macacine gammaherpesvirus 8) infects the pig-tailed macaque.

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

*Mardivirus*

*Scutavirus*

*Varicellovirus*

*Iltovirus*

*Simplexvirus*

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

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*Cytomegalovirus*

*Quwivirus*

*Muromegalovirus*

*Roseolovirus*

*Proboscivirus*

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

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*Patagivirus*

*Manticavirus*

*Macavirus*

*Bossavirus*

*Percavirus*

*Rhadinovirus*

*Lymphocryptovirus*