

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

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| **Code assigned:** | **2022.004D** |  |
| **Short title:** Create five new species in genus *Alphabaculovirus* and one new species in genus *Gammabaculovirus* (*Lefavirales*:*Baculoviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| The authors are the Baculoviridae and Nudiviridae Study Group. |

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

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**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| Baculoviridae and Nudiviridae Study Group |  |  |  |

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

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| **Is any taxon name used here derived from that of a living person (Y/N)** | No |

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | 02 May 2022 |
| Date of this revision (if different to above) |  |

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

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2022.004D.N.v2.Baculoviridae\_6nsp.xlsx |

**Abstract**

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| We propose the creation of five new species in the genus *Alphabaculovirus* and one new species in the genus *Gammabaculovirus*, of the family *Baculoviridae* (*Naldaviricetes*: *Lefavirales*). Analyses of fully-sequenced genomes for isolates of the proposed species indicate that the exemplar viruses meet the criteria for assignment to new species. |

**Text of proposal**

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| |  | | --- | | Analyses of new and previously published baculovirus genome sequences support the creation of six new species in the family *Baculoviridae*, including five species in the genus *Alphabaculovirus* and one species in the genus *Gammabaculovirus*. Isolates of the proposed species can be classified as belonging to these genera on the basis of the following criteria:  • host species of the insect order Lepidoptera for members of *Alphabaculovirus* or Hymenoptera for members of *Gammabaculovirus*;  • circular double-stranded DNA genome ranging in size from 80 to 180 kbp with a gene content characteristic of other alphabaculoviruses or gammabaculoviruses;  • relationships to other alpha- or gammabaculoviruses as inferred by molecular phylogeny;  • occlusion bodies formed within the nucleus, with a characteristic shape and size;  • rod-shaped virions consisting of enveloped nucleocapsids, with multiple virions contained in each occlusion body.  A species demarcation criterion for baculoviruses has been developed based on pairwise nucleotide distances estimated with the Kimura-2-parameter (K2P) substitution model. Initially, this criterion employed pairwise alignments of three conserved genes [8]. Pairwise K2P distances of >0.050 substitutions/site indicated that the viruses being compared belonged to different species, while distances <0.015 indicated that they belonged to the same species. For K2P distances between these two cutoff points, additional evidence was required to support the classification of the isolates being compared into different species. A modified version of the criterion based on a larger group of complete baculovirus genome sequences later was developed using concatenated pairwise nucleotide alignments of all 38 core genes of the family *Baculoviridae* [14]. While the core gene-based criterion largely confirmed the species assignments based on the three-loci criterion, the cutoff points for species demarcation were modified to be <0.021 (same species) and >0.072 (different species) substitutions/site, with additional evidence required for species assignments when pairwise distances fall between these two cutoff points.  A parallel taxonomic proposal describes the formation of binomial species names for members of family *Baculoviridae*. In short, the specific epithet is formed by a contraction of the first 2-4 letters of the host’s genus name followed by the epithet of the host in the genitive form. For example, the name of the species for the alphabaculovirus Autographa californica multiple nucleopolyhedrovirus is *Alphabaculovirus aucalifornicae*. This format has been used for the formation of species names for the proposed species.  The following new species are proposed:  1) ***Alphabaculovirus raous***  **Exemplar isolate:** Rachiplusia ou multiple nucleopolyhedrovirus R1 (RoMNPV-R1; AY145471)  RoMNPV is a Group I alphabaculovirus, and thus encodes a homolog of the GP64 envelope protein (Figure 1). Isolates of this species have been identified from both the gray looper/mint looper, *Rachiplusia* *ou*, and the celery looper, *Anagrapha falcifera* [2]*.* Analysis of the genome sequence of the exemplar isolate RoMNPV-R1 indicated that it was highly similar to the genome sequence of Autographa californica multiple nucleopolyhedrovirus (AcMNPV) [3], and K2P distances between RoMNPV and AcMNPV fell between the 0.015 and 0.050 cutoff points for two of three loci (*lef-8* and *lef-9*), but greatly exceeded the 0.050 cutoff point for the *polh* locus [8]. It was later discovered that part of the *polh* gene sequence of the AcMNPV lineage had been acquired by homologous recombination with the *polh* gene of a distantly related Group II alphabaculovirus [7]. Jehle et al. [8] cited additional features distinguishing RoMNPV and AcMNPV in support of their assignment into separate species. Later analysis with pairwise core gene alignments also produced K2P distances between AcMNPV and RoMNPV that fell between the cutoff points of the modified core gene criterion, and the authors again assigned RoMNPV-R1 to a separate species [14]. Isolates of RoMNPV form a separate and distinct clade from viruses of the AcMNPV clade in molecular phylogenies [4], and a separate analysis of species assignments using a phylogenetic-species-concept approach based on the multi-rate Poisson tree processes (mPTP) model also classified AcMNPV and RoMNPV isolates into separate species [13].  **Etymology:** According to BugGuide.Net, the origin of “ou” in the host species name is obscure. “Ou” may refer to a ligature of the letters “o” and “u” that may be descriptive of the wing scale pattern in host moths, so the genitive “ous” was used for the virus specific epithet.  2) ***Alphabaculovirus alterchrincludentis***  **Exemplar isolate:** Chrysodeixis includens nucleopolyhedrovirus #1 (ChinNPV #1; MK746083)  ChinNPV#1 and the other alphabaculoviruses in this proposal are Group II alphabaculoviruses, and thus do not possess homologs of the GP64 envelope protein (Figure 2). Other alphabaculoviruses have been previously isolated from the soybean looper, *Chrysodeixis includens*, but molecular phylogeny and K2P nucleotide distances clearly indicate that ChinNPV#1 represents a second different, previously undescribed species from this host [5].  **Etymology:** The specific epithet for this species has the prefix *alter* to indicate that this is the second distinct species with isolates originating from *C. includens*. The earlier identified species is called *Alphabaculovirus alterchrincludentis.*  3) ***Alphabaculovirus erankerariae***  **Exemplar virus:** Erannis ankeraria nucleopolyhedrovirus wlcb (EranNPV-wlcb; OK091173)  K2P distances in pairwise alignments with EranNPV exceeded the species demarcation cutoff points for both the three-loci and core gene criteria, indicating that EranNPV represents a previously undescribed species [10].  **Etymology:** The nominative “-aria” from the host specific epithet takes the genitive “-ariae”.  4) ***Alphabaculovirus olmendosae***  **Exemplar virus:** Olene mendosa nucleopolyhedrovirus 435 (OlmeNPV-435; MZ766431)  Analysis of the OlmeNPV-435 genome indicate that it is most closely related to isolates of *Alphabaculovirus lyxylinae*, but pairwise nucleotide distances exceed 0.050 for the three-loci criterion and 0.072 for the core gene criterion, indicating that OlmeNPV-435 represents a separate species [6].  **Etymology:** The host epithet “mendosa” is the single feminine nominative for an adjective meaning “full of faults”, “erroneous”, or “prone to error” and takes the genitive “mendosae”.  5) ***Alphabaculovirus travishnous***  **Exemplar virus**: Trabala vishnou gigantina nucleopolyhedrovirus wuqi (TrviNPV-wuqi; MW645368)  Pairwise distances between TrviNPV-wuqi and the alphabaculoviruses most closely related to it exceeded the species demarcation cutoff point for the core gene criterion, indicating that TrviNPV-wuqi represented a novel alphabaculovirus species [11].  **Eytmology:** The host epithet “vishnou” is French for the Hindu god Vishnu, possibly representing the widespread distribution of this moth in India. The genitive “vishnous” was used for forming the viral specific epithet.  6) ***Gammabaculovirus neabietis***  **Exemplar virus**: Neodiprion abietis nucleopolyhedrovirus (NeabNPV; DQ317692)  Unlike the other baculoviruses in this proposal, NeabNPV is a virus of genus *Gammabaculovirus* [1](Figure 3). NeabNPV genome analysis failed to identify a homolog of the core gene *p6.9*, but examination of the genome sequence revealed a short (21-codon) ORF in a conserved position for *p6.9* ORFs of other baculoviruses encoding a polypeptide with a high lysine and serine content, which is characteristic of P6.9 proteins. Pairwise distances in core gene alignments between NeabNPV and other gammabaculoviruses greatly exceed the 0.072 substitutions/site cutoff point for species demarcation under the core gene criterion, indicating that NeabNPV represents a novel gammabaculovirus species [14].  **Etymology:** The host epithet “abietis” is already the genitive of “abies”, meaning “fir” and referring to the balsam fir trees attacked by the larval stage of the host insect. | |

**Supporting evidence**

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**Figure 1.** Phylogeny showing the relationships of baculoviruses of the Group I clade of genus *Alphabaculovirus (Lefavirales: Baculoviridae*). Shown is a maximum likelihood tree inferred from the concatenated alignments of 38 baculovirus core gene amino acid sequences with RAxML [12] using the Le and Gascuel (LG) substitution model [9]. Reliability of the tree was assessed with 100 rapid bootstrap replicates, with bootstrap values shown for each node. Colored circles indicate exemplar viruses classified in genus *Alphabaculovirus* and are listed in the Virus Metadata Resource (<https://talk.ictvonline.org/taxonomy/vmr/>). Unclassified viruses are indicated by open circles. The exemplar virus for proposed species *Alphabaculovirus rous* is in bold type and indicated with an asterisk.

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**Figure 2.** Phylogeny showing the relationships of Group II baculoviruses of genus *Alphabaculovirus (Lefavirales: Baculoviridae*). Shown is a maximum likelihood tree inferred as described for Figure 1, with bootstrap values shown for each node. Branches for Group I alphabaculoviruses are collapsed. Colored circles indicate exemplar viruses classified in genus *Alphabaculovirus* (<https://talk.ictvonline.org/taxonomy/vmr/>) and unclassified viruses are indicated by open circles. The exemplar viruses for proposed species are in bold type and indicated with an asterisk.

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**Figure 3.** Phylogeny of the relationships of viruses in family *Baculoviridae* (*Lefavirales*). Shown is a maximum likelihood tree inferred as described for Figure 1, with bootstrap values shown for each node. Branches for viruses in the genera *Alphabaculovirus* and *Betabaculovirus* are collapsed. Colored circles indicate exemplar viruses classified in genera *Gammabaculovirus* and *Deltabaculovirus* (<https://talk.ictvonline.org/taxonomy/vmr/>) and the exemplar virus for proposed species *Gammabaculovirus abietis* is in bold type and indicated with an asterisk.

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