This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

For guidance, see the notes written in blue, below, and the help notes in file Taxonomic\_Proposals\_Help\_2018.

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

|  |  |  |  |
| --- | --- | --- | --- |
| **Code assigned:** | ***2018.010D*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  **1 new species in the genus *Dependoparvovirus*** | | | |
|  | | | |
| **Author(s):** | | | |
| Judit J. Penzes | | | |
| **Corresponding author with e-mail address:** | | | |
| Judit J. Penzes: Judit.penzes@ufl.edu | | | |
| **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) | | **Parvoviridae Study Group** | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | |
|  | | | |
|  | | | |
| Date first submitted to ICTV: | | | 5 June 2018 |
| Date of this revision (if different to above): | | | 20 June 2018 |

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

**Part 3:** **PROPOSED TAXONOMY**

|  |
| --- |
| **Name of accompanying Excel module: 2018.010D.N.v1.Dependoparvovirus\_sp** |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2017\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

| additional material in support of this proposal |
| --- |
| Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance. |

Genus *Dependoparvovirus* is one of the eight recognized genera comprising vertebrate-infecting subfamily *Parvovirinae* of the family *Parvoviridae*. The name *Dependoparvovirus* reflects a common feature of its members, i.e. their dependence on large DNA helper viruses (usually adeno- or herpesviruses) for efficient replication. However, the viruses causing the so-called Derzsy's disease in geese and Muscovy ducks are capable of autonomous replication even though they are members of the genus *Dependoparvovirus*. Based on the ability of autonomous replication of anseriform parvoviruses (PVs) and the basal phylogenetic position of reptilian dependoparvoviruses, a diapsid (common reptile−bird) origin of the genus has been proposed (Zadori et al., 1995; Penzes et al., 2015). Apart from members of the aforementioned dependoparvovirus (belonging to species *Anseriform dependoparvovirus 1*), dependoparvovirus infection has not been associated with pathogenicity. Members of the genus are prevalent in all major amniote vertebrate groups to date, with the exception of anapsid reptiles. Furthermore, of family *Parvoviridae*, dependoparvoviruses have been revealed to become endogenous viral elements (EVEs) most frequently by integration into vertebrate germlines, confirming the widespread pan-amniote occurrence of the genus. Dependoparvoviruses share similar transcription pattern and genome organization, including the presence of one *rep* and *cap* gene, expressing three or four viral replication proteins (Rep) and three or more capsid proteins (VP), respectively, from two or three promoters. A unique alternative ORF, encoding the assembly-associated protein with a scaffolding role is also present in adeno-associated viruses 1−12, however, this protein has not been proved to be essential for assembly in certain members. Currently there are seven recognized species, to which we propose adding one further new species to include the dependovirus of a squamate lizard, the inland bearded dragon (*Pogona vitticeps*), being the first hitherto recognized lizard parvovirus.

**Virus definition:**

Bearded dragon parvovirus in the newly proposed dependoparvovirus species meets the following virus definition, which has been in standard use by the Parvoviridae Study Group since 2014.

In order for an agent to be classified in the family *Parvoviridae*, it must be judged to be an authentic parvovirus on the basis of having been isolated and sequenced or, failing this, on the basis of having been sequenced in tissues, secretions, or excretions of unambiguous host origin, supported by evidence of its distribution in multiple individual hosts in a pattern that is compatible with dissemination by infection. The sequence must be in one piece, contain all the nonstructural (NS) and virus particle (VP) coding regions, and meet the size constraints and motif patterns typical of the family.

This definition is designed to allow the inclusion of viruses identified by virus discovery approaches, which typically lack reliable sequences from the telomeric hairpins, while avoiding viral sequence fragments integrated into host genomes or metagenomic data that lack clear host attribution.

**Taxon demarcation criteria**:

Throughout the *Parvovirinae*, viruses within a **genus** are required to be monophyletic and to encode NS1 proteins that are generally at least 30% identical to each other at the amino acid sequence level but less than 30% identical to those of other genera. Viruses within a **species** are generally required to encode NS1 proteins that show at least 85% amino acid sequence identity, while diverging by at least 15% from viruses in other species. Bearded dragon parvovirus in the candidate dependoparvovirus species proposed here meets these criteria.

As a second species demarcation criterion, this virus is from a host different from the hosts of the earlier described dependoviruses that became members of accepted species in the genus. The closest member was a snake adeno-associated virus (*Squamate dependoparvovirus 1*), while this is a lizard parvovirus.

An apparent capability of autonomous replication also separates this virus from all the other dependoparvoviruses (except members of the *Anseriform dependoparvovirus 1*).

Similarly, an anticipated pathogenicity separates the bearded dragon dependovirus from all other dependoparvoviruses (except members of the *Anseriform dependoparvovirus 1*). Moreover, bearded dragon parvovirus possesses the second longest ITR sequences of the genus at 257 nt (after anseriform dependoparvoviruses). This is significantly larger than the ones of snake adeno-associate virus, its closest relative (154 nt).

**Phylogenetic Tree:**

Phylogenetic analyses described here are based on the derived amino acid sequence of the complete viral replication protein encoding ORF, *rep*. The alignment was carried out by combining the M-coffee algorithm of the t-coffee web server with the MUSCLE and Clustal Omega v1.2.2 softwares. Gap removal and alignment editing was executed in Unipro UGENE. ProtTest was utilized for model selection, selecting the substitution model RtREV+I+G+F, α = 1.29, ρ inv = 0.03 the most suitable based on both the Akaike and Bayes information criteria. The maximum likelihood phylogenetic tree was constructed by implementing a previously built guide tree (distance matrix by JTT substitution rates, Fitch-Margoliash with global rearrangements to obtain the guide tree) in PhyML v3.1. The reliability of the topology was tested by bootstrapping of 100 repeats.

**Nomenclature:**

Following our standard binomial nomenclature for species in this family, proposed species are named for a host taxon and their genus affiliation, followed by a distinguishing numeral. Species with like names receive numerals that follow on from those of previously recognized species.

**Proposed new species:**

**Table 1: Proposed new species in genus *Dependoparvovirus***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Proposed new  species | Exemplar isolate | Accession # | Acronym | Ref-  erence |
| *Squamate dependoparvovirus 2* | bearded dragon parvovirus | KP733794 | BDPV | 1 |

***Squamate dependoparvovirus 2***

The derived amino acid sequence of the bearded dragon parvovirus rep ORF shares most identity with its homologue in serpentine adeno-associated virus 1 (SAAV) of *Squamate dependoparvovirus 1* (GenBank AY349010) (58 %) and not less than 34 % with all other members of the genus *Dependoparvovirus*. The VP protein sequence also displays the highest identity with that of SAAV (70 %), whilst this value is not lower than 56 % in case of other dependoparvoviruses. This virus requires classification in a new species because the above-mentioned identity values are less than 85%, showing bearded dragon parvovirus to be divergent from SAAV, its closest neighbor, according to the NS-based phylogeny inference (Figure 1). It is still, however, more than 30% identical to other members of genus *Dependoparvovirus*, hence the suggested taxonomic position.

**Figure 1. Phylogenetic tree showing the proposed taxonomy of members of the genus *Dependoparvovirus* in the context of the seven further genera of subfamily *Parvovirinae*.**

Bearded dragon parvovirus of the proposed new species, *Squamate dependoparvovirus 2* is underlined and highlighted in bold. Bootstrap values are positioned on the nodes, reaching from 1 to 100. Calculations were based on the complete derived amino acid sequence of the rep ORF (maximum-likelihood, RtREV+I+G+F, α = 1.29, ρ inv = 0.03).

0.5

canine parvovirus

**bearded dragon parvovirus**

rhesus macaque parvovirus

snake adeno-associated virus

California sealion adeno-associated virus

bat adeno-associated virus

canine minute virus

gray fox amdovirus

bovine adeno-associated virus

bovine hokovirus 1

human parvovirus 4 G1

porcine parvovirus 4

porcine parvovirus

adeno-associated virus 2

chicken parvovirus

bovine parvovirus

minute virus of mice

human parvovirus B19-Au

avian adeno-associated virus

*Eidolon helvum* parvovirus

duck parvovirus

chipmunk parvovirus

human bocavirus 3

turkey parvovirus

goose parvovirus

bovine parvovirus 2

adeno-associated virus 5

95

100

100

90

55

51

64

98

100

100

91

100

87

100

100

66

94

49

42

100

78

98

100

100

100

95

Aleutian mink disease virus

*Galliform aveparvovirus 1*

*Ungulate protroparvovirus 1*

*Carnivore protoparvovirus 1*

*Rodent protoparvovirus 1*

*Ungulate bocaparvovirus 1*

*Primate bocaparvovirus 1*

*Carnivore bocaparvovirus 1*

*Rodent erythroparvovirus 1*

*Primate erythroparvovirus 1*

*Primate erythroparvovirus 1*

*Chiropteran tetraparvovirus 1*

*Primate tetraparvovirus 1*

*Ungulate tetraparvovirus 1*

*Ungulate copiparvovirus 1*

*Ungulate copiparvovirus 2*

*Avian dependoparvovirus 1*

*Squamate dependoparvovirus 1*

*Anseriform dependoparvovirus 1*

*Adeno-associated dependoparvovirus A*

*Adeno-associated dependoparvovirus B*

*Pinniped dependoparvovirus 1*

*Carnivore amdoparvovirus 2*

*Protoparvovirus*

*Aveparvovirus*

*Bocaparvovirus*

*Erythroparvovirus*

*Tetraparvovirus*

*Copiparvovirus*

***Dependo-  
parvovirus***

***Squamate dependoparvovirus 2***

*Chiropteran dependoparvovirus 1*

*Amdo-parvovirus*

*Carnivore amdoparvovirus 1*

| **References:** |
| --- |
| 1. Pénzes JJ, Pham HT, Benkő M, Tijssen P: Novel parvoviruses in reptiles and genome sequence of a lizard parvovirus shed light on *Dependoparvovirus* genus evolution. J Gen Virol. 2015 96(9):2769-79.  2. Zádori Z, Stefancsik R, Rauch T, Kisary J: Analysis of the complete nucleotide sequences of goose and Muscovy duck parvoviruses indicates common ancestral origin with adeno-associated virus 2. Virology. 1995 212(2):562-73. |