

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

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| **Code assigned:** | **2022.006D** |  |
| **Short title:** Create one new species in the genus *Chaphamaparvovirus*, and one new species in the genus *Dependoparvovirus*, in the family *Parvoviridae* | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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| Fabricio S. Campos |

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

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| *Parvoviridae* Study Group |

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

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| Dear Fabricio,  This is on behalf of your taxonomy proposal for two species within *Parvoviridae*. I would like to inform you that we have worked out a new species nomenclature, based on which you shall modify your proposal as follows:  Avian chapparvovirus to species Chaphamaparvovirus avian1  Avian adeno-associated virus 2 to Dependoparvovirus avian2  Please note the deadline is the 20th of May to submit proposals to the SC chair (Arvind Varsani, cc-ed).  Thank you for your contribution to parvovirus taxonomy.  Best regards,  Judit Penzes  Parvoviridae SG chair |

**ICTV Study Group votes on proposal**

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| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| *Parvoviridae* study group | 11 | 0 | 0 |
|  |  |  |  |

**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 |

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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 | 2nd May 2021 |
| Date of this revision (if different to above) | 27th May 2022 |

**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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| 2022.006D.N.v2.Parvoviridae\_2nsp.xlxs |

**Abstract**

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| We would like to propose the creation of two new species in *Parvoviridae*. Viruses related to subfamilies *Parvovirinae* and *Hamaparvovirinae* were detected in faeces samples from Brazilian wild animals. In the study, samples were grouped in two pools - Pool 1 with only birds (*Amazona aestiva* and *Sicalis flaveola*), and Pool 2 with mammals and birds (*Psittacara leucophthalmus*, *Didelphis albiventris*, *Sapajus libidinosus*, and *Galictis cuja*). Sequences of pool 1 were closely related to *Ambidensovirus*, *Iteradensovirus*, *Dependoparvovirus*, and *Chaphamaparvovirus* genera. For pool 2, just viruses closely related to *Dependoparvovirus* and *Chaphamaparvovirus* were detected. Phylogenetic analyses were performed using conserved NS1 protein amino acid sequence and shown low proximity (56.5%) to *Psittacine chaphamaparvovirus 1* and adeno-associated virus, corroborating with the detection of putative new viruses in faeces samples from Brazilian Cerrado fauna. |

**Text of proposal**

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| |  | | --- | | **1. One new species in the genus *Chaphamaparvovirus***  **1.1** **Creating species *Chaphamaparvovirus avian1***  Avian chapparvovirus BR\_DF10 can be considered a new species in the genus *Chaphamaparvovirus* for the following reasons:  a. Avian chapparvovirus BR\_DF10 (MN175612) has a 4,425 nt ssDNA genome with three genes, conserved NS1 and VP1 sequences, and putative NP (Table 1 and Figure 1A). Like others chaphamaparvoviruses, AvChPV-1 was found in faeces of animals [1,3-6, 8-10] and was found in pool 1, therefore it is associated to a neognath bird host [2]. In phylogenetic analysis using complete non-structural protein 1 (NS1) amino acid sequence, avian chapparvovirus shares a unique clade with Psittacara leucophthalmus chapparvovirusBR\_DF11(MN175613) (Figure 2) [2].  b. Avian chapparvovirus BR\_DF101 and the closest related virus, Psittacara leucophthalmus chapparvovirusBR\_DF11(MN175613) showed 56.5% amino acid identity (Table 1). NS1 amino acid sequence identity is used as demarcation criteria for species in *Parvoviridae* family, with 85.0% identity as threshold (taxonomy proposal 2019.010D). Thus, we would like to assign avian chapparvovirus into the proposed new species *Chaphamaparvovirus avian1* of the genus *Chaphamaparvovirus*.  **2. One new species in the genus *Dependoparvovirus***  **2.1** **Creating species *Dependoparvovirus avian2***  Avian adeno-associated virus BR\_DF12 can be considered a new species in the genus *Dependoparvovirus* for the following reasons:  a. Avian adeno-associated virus BR\_DF12 (MN175614) has a 4,642 nt ssDNA genome with four genes with non- and structural protein sequences (Table 1 and Figure 1B). It is a putative new representative of the genus *Dependoparvovirus*, that includes viruses that infect vertebrates, but replication in the cell usually depends on another virus, called helper, commonly adenoviruses, herpesviruses or papillomaviruses [7] In phylogenetic analysis using the conserved non-structural protein 1 (NS1) amino acid sequence, a demarcation criterion for the group, avian adeno-associated virus 2 occupies a unique branch near to others adeno-associated virus already known (Figure 3) [2].  b. The avian adeno-associated virus BR\_DF12 (MN175614) and the closely species related avian adeno-associated virus ATCC VR-865(AY186198) showed 42.6% amino acid identity (Table 1). NS1 amino acid sequence identity is used as demarcation criteria for species in *Parvoviridae* family, with 85% identity as threshold (taxonomy proposal 2019.010D). Thus, we would like to assign avian adeno-associated virus 2 into the proposed new species *Dependoparvovirus avian2* of the genus *Dependoparvovirus*. | |

**Supporting evidence**

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**Table 1.** Parvovirus-like contig ID identified from pool 1 and 2 used for phylogenetic analyses with their respective pairwise identities (Duarte et al., 2019).

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| --- | --- | --- | --- | --- | --- |
| Pool Number | Contig ID | GenBank accession number | Virus Name | Closely related virus | Pairwise identity (NS1 aa) |
| 1 | K1191463 | MN175612 | avian chapparvovirus BR\_DF10 | Psittacara leucophthalmus chapparvovirus BR\_DF11 | 56.5% |
| 1 | K1191997 | MN175614 | Avian adeno-associated virus BR\_DF12 | avian adeno-associated virus ATCC VR-865 | 42.6% |



**Figure 1**. Genome representation of two putative novel parvoviruses identified. A: Chaphamaparvovirus avian 1 (MN175612) with conserved NS1 and VP1 sequences, and putative NP (4,425 nt). B: Dependoparvovirus avian 2 (MN175614) with non- and structural protein sequences (4,642 nt) [2].



**Figure 2**. Bayesian tree based on complete non-structural protein 1 (NS1) amino acid sequences (769 aa) of 25 parvoviruses of the subfamily *Hamaparvovirinae*. The tree was built in BEAST v2.6.0 software using JTT substitution-rate matrix in accordance to ProtTest analysis. Posterior probability support values are shown. Chaphamaparvoviruses are in grey and the proposed Chaphamaparvovirus avian1 in red. GenBank accession numbers of the parvovirus sequences identified in this study are shown.



**Figure 3**. Bayesian tree based on complete non-structural protein 1 (NS1) amino acid sequences (662 aa) of 11 parvoviruses of the genus *Dependoparvovirus*. The tree was built in BEAST v2.6.0 software using JTT substitution-rate matrix in accordance to ProtTest analysis. Posterior probability support values are shown. The proposed Dependoparvovirus avian2 is in red. GenBank accession numbers of the parvovirus sequences identified in this study are shown.

**References**

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