

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

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| **Code assigned:** | ***2023.013D*** |  |
| **Short title:** A new species in the genus *Gammapolyomavirus* (*Polyomaviridae*) |
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**Author(s) and email address(es)**

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

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**Corresponding author**

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| Enikő Fehér |

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

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**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** |
| ICTV *Polyomaviridae* Study Group | 7 |  | 3 (did not reply) |

**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)** | N |

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

**Submission dates**

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| Date first submitted to SC Chair | 3 May 2023 |
| 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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| 2023.013D.N.v2.Polyomaviridae\_1nsp.xlsx |

**Abstract**

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| A novel gammapolyomavirus (named cormorant polyomavirus [CoPyV]) has been detected in mixed organ samples (kidney, liver) of a great cormorant (*Phalacrocorax carbo*). The genome of the CoPyV is 5,133 bp long and has a genomic structure typical for other gammapolyomaviruses (GenBank accession number MZ666388). The genome contains putative ORFs encoding the large and small T antigens (LTA and STA, respectively), the viral proteins VP1, VP2 and VP3, and the ORF-X (Figure 1A). Each of the coding sequences shared a maximum of 66.6% aa pairwise identity with that of other gammapolyomaviruses. CoPyV is proposed as the first member of a novel species within the *Gammapolyomavirus* genus (Fehér et al., 2022) that has been tentatively named *Gammapolyomavirus phacarbo*. |

**Text of proposal**

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| The genomic structure of the CoPyV (Fehér et al., 2022; GenBank accession number MZ666388) (Figure 1A), as well as the phylogenetic analysis (Figure 1B) suggested that the CoPyV represents a novel species within the *Gammapolyomavirus* genus. The LTA aa sequence of the CoPyV showed 45.6–50.4% pairwise identity with that of other gammapolyomaviruses. The genetic distance >15% of the LTA nuceotide sequence meets the criterion set by the ICTV for species demarcation, thus CoPyV is proposed as member of a novel species tentatively named *Gammapolyomavirus phacarbo*. |

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**Supporting evidence**

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**Figure 1. (A)** Structure of the cormorant polyomavirus genome. **(B)** Maximum likelihood phylogenetic tree prepared using large T antigen aa sequences of representative polyomaviruses. The tree was generated by the PhyML software, GTR+G+I model and aLRT SH-like branch support (<80% support are hidden). The scale bar shows substitutions per site. The sequence of the Japanese eel endothelial cells-infecting virus was applied as the root. The proposed cormorant polyomavirus is labelled with blue triangle.

**References**

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