

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

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| **Code assigned:** | **2021.007D** |  |
| **Short title:**  Create two new genera (*Etapolyomavirus* and *Thetapolyomavirus*) and rename all 117 species in the family (*Sepolyvirales*: *Polyomaviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| SG *Polyomaviridae* |

**ICTV study group comments and response of proposer**

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| NA |

**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)** |  |

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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 | 26th May 2021 |
| 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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| 2021.007D.A.v1.Polyomaviridae\_2ngen\_117rensp.xlsx |

**Abstract**

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| We propose the creation of two new genera which will accommodate the last 5 recognized species yet unassigned to any genus. Following the decision to move to binomial species names, we propose new names for the 117 species in the family. |

**Text of proposal**

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| |  | | --- | | 1. **Creation of the genera *Etapolyomavirus* and *Thetapolyomavirus***   Out of the 117 currently recognized polyomavirus species, 5 does not currently belong to any genus. Viruses belonging to these 5 species all infect fish. In phylogenetic analyses of LTAg amino acid sequences (**Fig. 1**), these 5 species form two deep-branching lineages: a) the first lineage only comprises *Rhynchobatus djiddensis polyomavirus 1*, whose members infect a cartilaginous fish, b) the second lineage corresponds to a well-supported clade comprising the four other species, whose members all infect bony fish (*Centropristis striata polyomavirus 1*; *Sparus aurata polyomavirus 1*; *Trematomus bernacchii polyomavirus 1*; *Trematomus pennellii polyomavirus 1*). We propose to create the genera *Etapolyomavirus* and *Thetapolyomavirus* (whose names are derived from the Greek letters following zeta, which was used for the last genus creation in the family). *Rhynchobatus djiddensis polyomavirus 1* is assigned to the genus *Etapolyomavirus*. *Centropristis striata polyomavirus 1,* *Sparus aurata polyomavirus 1,* *Trematomus bernacchii polyomavirus 1 and* *Trematomus pennellii polyomavirus 1* are assigned to the genus *Thetapolyomavirus.*   1. **Renaming of all species in the family**   Following the recent decision to universally apply a binomial system for virus species nomenclature, we propose new names for the 117 currently recognized polyomavirus species (detailed in Taxonomic\_Proposals\_Polyomaviridae\_2021.v2.xlsx). Building on the current species names which were derived from host species names, we determined Latinized species epithets by: i) identifying the genitive form of the host genus name, ii) if (i) was not possible, by concatenating the first syllable of the host genus name and the the host species epithet. New species name were then formed as follows: <Genus\_name> <Newly\_formed\_species\_epithet>. | |

**Supporting evidence**

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**Figure 1. Maximum likelihood tree reconstructed with PhyML v3.1 based on an alignment of large T amino acid sequences.** Model of amino acid substitution (determined with smart model selection): LG+I+G+F. Branch support values: Shimodaira-Hasegawa-like approximate likelihood ratio tests (SH-like aLRT), grey branches: <0.9 SH-like aLRT. Scale in amino acid substitution per site.