

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

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| **Code assigned:** | ***2023.002F*** |  |
| **Short title:** Rename four species and create one new species in the genus *Trichomonasvirus* | | |
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**Author(s) and email address(es)**

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

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| *Totiviridae* SG |

**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** |
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**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)** |
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**Submission dates**

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| Date first submitted to SC Chair | 17 May 2023 |
| Date of this revision (if different to above) | 10 October 2023 |

**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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| 2023.002F.v2.Trichomonasvirus\_1nsp\_spren.xlsx |

**Abstract**

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| Genus *Trichomonasvirus* (family *Totiviridae*, order *Ghabrivirales*, etc.) currently comprises four species. To abide by the new binomial nomenclature policy, we propose to rename these species. In addition, we have recently reported trichomonasvirus strains that define a discrete phylogenetic clade relative to strains assigned to other species within the genus, and we therefore also propose to create a new species to accommodate these distinctive strains. |

**Text of proposal**

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| |  | | --- | | Members of genus *Trichomonasvirus* share a typical genome organization with other members of family *Totiviridae*: a single dsRNA molecule encompassing two long open reading frames (ORFs) on the genomic plus strand, the upstream ORF encoding the capsid protein (CP) and the downstream ORF encoding the RNA-dependent RNA polymerase (RdRP) (Goodman et al., 2011a, b; Wickner et al., 2011). Different members within the family show variability in the mechanism by which the downstream ORF is translated, including a ribosomal frameshifting mechanism or a stop/restart mechanism. The trichomonasviruses employ a ribosomal frameshifting mechanism: –2 frameshifting for members of species *Trichomonas vaginalis virus 1* and –1 frameshifting for members of the other three current species (Goodman et al., 2011a, b; Manny et al., 2022; Parent et al., 2013).  To abide by the new binomial nomenclature policy, we propose to change the names of the four current species in genus *Trichomonasvirus* from *Trichomonas vaginalis virus 1*, *Trichomonas vaginalis virus 2*, *Trichomonas vaginalis virus 3*, and *Trichomonas vaginalis virus 4* to *Trichomonasvirus* *vagiprimus*, *Trichomonasvirus* *vagisecundus*, *Trichomonas-virus* *vagitertius*, and *Trichomonasvirus* *vagiquartus*, respectively. We feel that since serial numbering is used in the current species names, continuing that format in the new names is reasonable. The choice of using ordinal rather than cardinal numbers in Latin reflects the historical order in which the first strain of each respective species was reported (first, second, etc.). We have additionally added the suffix “*vagi-*” to each epithet, not only to reflect the host species epithet “*vaginalis*”, but also out of consideration that (a) the strains representing all four current species were identified from lab-cultured isolates of *T. vaginalis* such that the host species of these strains is more or less definitively known and (b) yet-to-be-discovered viruses defining future new species in this genus might be derived from different host species, for example, *Trichomonas tenax*, which could also be reflected in the future virus species names.  In addition, we have recently reported six newly sequenced trichomonasvirus strains, also derived from lab-cultured isolates of *T. vaginalis*, that define a distinct phylogenetic clade relative to other members of the genus (Manny et al., 2022) (Fig. 1). Yet other strains belonging to this clade are in the process of being reported (Manny et al., manuscript in preparation). The common name we have chosen to use for members of this clade is Trichomonas vaginalis virus 5 (TVV5). Among the original set of six strains, the sequences for two, TVV5-NYCD15(NYU) and TVV5-NYCE32(NYU) (GenBank accessions BK063445.1 and BK063446.1), are coding complete, respectively spanning 5022 and 5026 bp, and the sequence of a third, TVV5-NYCC37(NYU) (GenBank accession BK063444.1), is coding complete (5015 bp) except for two internal gaps. The three strains for which partial sequences have been reported to date are TVV5-NYCA04(NYU), TVV5-NYCG31(NYU), and TVV5-SD2\_11591\*(NYU) (GenBank accessions BK063443.1, BK063447.1, and BK063448.1). We propose here that this clade of viruses should be recognized to represent a new species in genus *Trichomonasvirus*, and in line with the proposal for binomial nomenclature, we propose the name *Trichomonasvirus* *vagiquintus* for this new, fifth species.  Comparisons of several additional features support recognition of TVV5 strains as members of a new species. In BLASTp searches, the following values were obtained, for the two TVV5 strains with coding-complete sequences (Manny et al., 2022), indicating low sequence identities (<50%) with members of the other species in genus *Trichomonasvirus*.  TVV5-NYCD15(NYU) CP: top identity score **34.86%** (query cover 84%) with TVV3 AED99803.1  TVV5-NYCE32(NYU) CP: top identity score **35.25%** (query cover 84%) with TVV4 YP\_009507837.1  TVV5-NYCD15(NYU) CP/RdRP: top identity score **39.84%** (query cover 89%) with TVV2 AED99808.1  TVV5-NYCE32(NYU) CP/RdRP: top identity score **39.99%** (query cover 89%) with TVV2 AED99808.1  These values are consistent with the species demarcation threshold of 50–60% that has been suggested for members of the different genera in family *Totiviridae* (Wickner et al., 2011) and has also been identified as reasonable for members of genus *Trichomonasvirus* in particular (ICTV proposals 2010.001a-dF and 2013.002a-cF; Goodman et al., 2011a, 2011b; Manny et al., 2022).  On the other hand, the two TVV5 strains with coding-complete sequences (Manny et al., 2022) share much higher sequence identity with one another, consistent with being members of the same discrete clade (Fig. 1).  Pairwise TVV5-NYCD15(NYU) vs. TVV5-NYCE32(NYU)  genome: identity **85.05%** (query cover 99%)  CP: identity **87.78%** (query cover 100%)  CP/RdRp: identity **90.37%** (query cover 100%)  These values are in turn consistent with observed intra-species identity scores of >70% for members within each of the other species in genus *Trichomonasvirus* (ICTV proposals 2010.001a-dF and 2013.002a-cF; Goodman et al., 2011a, 2011b; Manny et al., 2022).  Lastly, these two TVV5 strains are distinctive in having the longest sequences among all trichomonasviruses reported to date (Manny et al., 2022).  TVV5-NYCD15(NYU) genome: 5022 bp  TVV5-NYCE32(NYU) genome: 5026 bp  longest other genome: 4944 bp TVV4 HQ607520 (5’ and 3’ termini determined by RACE)  In fact, though not yet reported to either GenBank or a journal (or otherwise included in this proposal), we have recently determined the coding-complete sequences of seven additional TVV5 strains, including the terminal sequences of three of them by RACE. The lengths of those complete genomes are 5031, 5041, and 5049 bp. These sequences will be reported soon as part of a larger study.  The downstream ORF in the six TVV5 strains reported to date (Manny et al., 2022) consistently overlaps and is in the –1 frame relative to the upstream ORF, suggesting a –1 ribosomal frameshifting mechanism to allow translation of the CP/RdRP fusion protein. Within this region of overlap, the proposed slippery sequence GGGCCCC is found in all six of the TVV5 strains. As noted above, a –1 ribosomal frameshifting mechanism is also employed by TVV2, TVV3, and TVV4 strains, with slippery sequences GGGCCCC, GGGCCCU, and GGGCCCU, respectively (Goodman et al., 2011a, b).  In summary, by renaming the current four species and creating a new species, we propose that genus *Trichomonasvirus* should now comprise five species with names *Trichomonasvirus* *vagiprimus*, *Trichomonasvirus* *vagisecundus*, *Trichomonasvirus* *vagitertius*, *Trichomonasvirus* *vagiquartus*, and *Trichomonasvirus* vagiquintus. | |

**Supporting evidence**

**Fig. 1.** Coding-complete and partial nucleotide sequences from GenBank >600 bp long and assigned to genus *Trichomonasvirus* as of May 17, 2023, plus TVV5 sequences reported in Manny et al. (2022) and described in this proposal (total n = 68). Alignment with MAFFT-L-INS-i (https://mafft.cbrc.jp/alignment/server/). Maximum-likelihood phylogenetic analysis with IQ-TREE (“find best and apply” option for substitution model, 1000 ultrafast bootstraps) (https://www.hiv.lanl.gov/content/sequence/ IQTREE/iqtree.html). Best-fit model according to Bayesian information criterion, JTT+F+I+G4. Clades are color-coded and labeled with the abbreviated common names used for the strains in each clade (TVV1–TVV5) plus the proposed new epithet for each respective species. Strains of TVV1–TVV4 are labeled with the GenBank accession numbers of their nucleotide sequences.

**![A picture containing text, diagram, plan, map

Description automatically generated]()­**

**References**

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