

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

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| **Code assigned:** | ***2023.005D*** |  |
| **Short title:** Create 16 new species and 4 new genera in the family *Anelloviridae* | | |

**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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**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** |
| Anelloviridae SG | 7 |  |  |
|  |  |  |  |

**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 | 2 Dec 2022 |
| 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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| 2023.005D.N.v2.Anelloviride\_4ngen\_16nsp.xlsx |

**Abstract**

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| In order to classify human anellovirid sequences that don’t belong to the three classical human infecting genera (*Alpha*-, *Beta*-, *Gammatorquevirus*), we propose the establishment of 16 new species together with 4 new genera in the *Anelloviridae* family.  This includes:   * 6 new species in the exiting *Hetorquevirus* genus:  1. *Hetorquevirus hominid3* 2. *Hetorquevirus hominid4* 3. *Hetorquevirus hominid5* 4. *Hetorquevirus hominid6* 5. *Hetorquevirus hominid7* 6. *Hetorquevirus hominid8*  * 2 new species in the new proposed genus *Yodtorquevirus*:  1. *Yodtorquevirus* *hominid9* 2. *Yodtorquevirus* *hominid10*  * 1 new species in new proposed genus *Lamedtorquevirus*:  1. *Lamedtorquevirus* *hominid11*  * 3 new species in new proposed genus *Memtorquevirus*:  1. *Memtorquevirus hominid12* 2. *Memtorquevirus hominid13* 3. *Memtorquevirus hominid14*  * 4 new species in the new proposed genus *Samektorquevirus*:  1. *Samektorquevirus hominid15* 2. *Samektorquevirus hominid16* 3. *Samektorquevirus hominid17* 4. *Samektorquevirus hominid18* |

**Text of proposal**

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| |  | | --- | | Currently, ORF1-codding sequences are used to classify *Anelloviridae*, with a species demarcation threshold at >69% pairwise nucleotide identity, whereas genera demarcation is based on phylogeny [1]. Human infecting anelloviruses have been assigned to genera *Alphatorquevirus*, *Betatorquevirus*, *Gammatorquevirus* andmore recently to *Hetorquevirus*.  For this proposal, all anellovirus sequences with complete ORF1-coding sequence available in GenBank from genera known to infect primates were considered for analysis. Representative amino acid sequences were selected for *Alphatorquevirus*, *Betatorquevirus* and *Gammatorquevirus* using CD-HIT (50% amino acid identity) [2, 3].The 502 remaining sequences were aligned and trimmed using MAFFT [4]. Then, evolutionary analysis was done using Maximum Likelihood method LG+G+I+F model [5] (best fitting model; 100 bootstrap) and phylogenetic tree was generated by MEGA X [6]. In addition, pairwise nucleotide identity were used to determine species assignation.  Novel genera and species were named using the Phoenician alphabet and binomial names, respectively, according to the International Committee on Taxonomy of Viruses (ICTV) recommendations [7, 8].  Our analysis reveal 6 new species (total number of sequences = 102) in the exiting *Hetorquevirus* genus (*Hetorquevirus hominid3, Hetorquevirus hominid4*, *Hetorquevirus hominid5*, *Hetorquevirus hominid6*, *Hetorquevirus hominid7* and *Hetorquevirus hominid8),* 2 new species (total number of sequences = 17) in the new proposed genus *Yodtorquevirus* (*Yodtorquevirus* *hominid9* and *Yodtorquevirus* *hominid10),* 1 new species (total number of sequences = 33) in the new proposed genus *Lamedtorquevirus* (*Lamedtorquevirus* *hominid11)*, 3 new species (total number of sequences = 55) in the new proposed genus *Memtorquevirus* (*Memtorquevirus hominid12,* *Memtorquevirus hominid13* and *Memtorquevirus hominid14)* and 4 new species (total number of sequences = 123) in the new proposed genus *Samektorquevirus* (*Samektorquevirus hominid15*, *Samektorquevirus hominid16*, *Samektorquevirus hominid17* and *Samektorquevirus hominid18)*.  Bootstrap values reported in the phylogenetic tree further support the genera demarcations and the analysis of the pairwise identity matrix of the ORF1 nucleotide sequences confirms the species demarcations. | |

**Supporting evidence**

A screenshot of a computer

Description automatically generated with medium confidence

Figure 1: Phylogenetic analysis of the ORF1 product of the *Anelloviridae* family members. The tree shows Alpha-, Beta-, Gamma-, Omega- and Hetorqueviruses, rooted with Epsilon- and Zetatorqueviruses [AB041960 and AB041961, respectively]. Novel genera are displayed in colours. Bootstrap values (100 replicates) and evolutionary distances are reported.

**A picture containing pattern, rectangle, screenshot, colorfulness

Description automatically generated**

Figure 2: Pairwise identity matrix of the ORF1 nucleotide sequences of representative members from *He-*, *Yod-*, *Lamed-*, *Mem-* and *Samektorquevirus*.

**References**

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