

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

**Part 1a: Details of taxonomy proposals**

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| **Title:**  | Create a new phylum ‘Commensaviricota’ for the kingdom *Shotokuvirae* and family *Anelloviridae* |
| **Code assigned:**  | 2024.012D.N.v1.Shotokuvirae\_newphylum |

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| **Author(s), affiliation and email address(es):**  |
| **Name**  | **Affiliation**  | **Email address**  | **Corresponding author(s)** X |
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**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:**  |
| Animal DNA Viruses and Retroviruses | **X** | Bacterial viruses |  |
| Animal minus-strand and dsRNA viruses |  | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses |  | Plant viruses |  |
| Archaeal viruses |  | General - |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:**  |
| *Anelloviridae* SG |

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| **Optional – complete only if formally voted on by an ICTV Study Group:**  |
| **Study Group** | **Number of members** |
| **Votes in support** | **Votes against** | **No vote** |
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| **Submission date:** |  24/06/2024 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required |  |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J - Reject |  |
| W - Withdrawn |  |

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| **Comments from the Executive Committee:** |
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**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:**  |
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| **Revision date:** |  DD/MM/YYYY |

**Part 3:** **TAXONOMIC PROPOSAL**

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| **Name of accompanying Excel module:**  |
| 2024.012D.N.v1.1.Shotokuvirae\_newphylum.xlsx |

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| **Taxonomic changes proposed:**  |
| Establish new taxon |  | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

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| **Is any taxon name used here derived from that of a living person:**  |  **N** |
| **Taxon name** | **Person from whom the name is derived** | **Attached X** |
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| **Abstract of Taxonomy Proposal:**  |
| *Taxonomic rank(s) affected*: *Monodnaviria*, *Shotokuvirae**Description of current taxonomy*: Currently, kingdom *Shotokuvirae* includes 2 phyla, with eukaryotic ssDNA and related dsDNA viruses classified into phyla *Cressdnaviricota* and *Cossaviricota*, respectively. *Anelloviridae* is the only family of eukaryotic ssDNA viruses not assigned to the realm *Monodnaviria.**Proposed* *taxonomic change(s):* Move family *Anelloviridae* into a new order, within a new class and a new phylum ‘*Commensaviricota*’ within the kingdom *Shotokuvirae*. The intermediate taxa between the phylum and family, will be order ‘*Sanitavirales*’ and a class ‘*Cardeaviricetes*’.*Justification*:Sequence and structural comparisons suggest that anelloviruses have evolved from a circovirus-like ancestor through gradual augmentation of the capsid protein and loss of the Rep protein genes. |

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| * **Text of Taxonomy proposal:**
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| *Taxonomic rank(s) affected*: *Monodnaviria*, *Shotokuvirae**Description of current taxonomy*: Currently, kingdom *Shotokuvirae* includes 2 phyla, with eukaryotic ssDNA and related dsDNA viruses classified into phyla *Cressdnaviricota* and *Cossaviricota*, respectively. *Anelloviridae* is the only family of eukaryotic ssDNA viruses not assigned to the realm *Monodnaviria.**Proposed* *taxonomic change(s)*: Move family *Anelloviridae* into a new order, within a new class and a new phylum ‘*Commensaviricota*’ within the kingdom *Shotokuvirae*. The intermediate taxa between the phylum and family, will be order ‘*Sanitavirales*’ and a class ‘*Cardeaviricetes*’. *Demarcation criteria:*Not applicable.*Justification*: Anelloviruses are highly prevalent in diverse mammals, including humans, but so far have not been linked to any disease and are considered to be part of the ‘healthy virome’. These viruses have small circular single-stranded DNA (ssDNA) genomes and encode several proteins with no detectable sequence similarity to proteins of other known viruses. Consequently, in the absence of an identifiable Rep or a capsid protein typical of other eukaryotic ssDNA viruses, *Anelloviridae* is the only family of eukaryote-infecting viruses with circular ssDNA genomes currently not included in the phylum *Cressdnaviricota* of the realm *Monodnaviria* (Koonin et al., 2020). Although anelloviruses appear not to encode a homolog of the typical Rep of the HUH endonuclease superfamily, recent sequence and structure-based comparisons showed that ORF1 orthologs from all *Anelloviridae* genera adopt a jelly-roll fold typical of cressdnaviricot capsid proteins, establishing an evolutionary link to other eukaryotic ssDNA viruses, specifically, circoviruses (Butkovic et al., 2023). In particular, searches queried with the ORF1 sequence of torque teno virus 1 (TTV1; NP\_817122) against the PDB and viral protein profile databases using HHsearch yielded a highly significant hit (Probability=95.8) to the CP of a bat circovirus (PDB id: 6RPO). Importantly, the aligned regions encompassed nearly the entirety of the circovirus CP but only ~30% of the anellovirus protein, highlighting the disparity in their respective sizes (233 versus 770 aa). Significant hits were also obtained with ORF1 sequences from viruses of other anellovirus genera (Butkovic et al., 2023).Circovirus CPs contain an N-terminal arginine-rich region involved in DNA-binding (Sarker et al., 2016) and a single jelly-roll (SJR) domain comprising 8 antiparallel β-strands (B through I), which form 2 juxtaposed β-sheets, BIDG and CHEF (Fig. 1a). The anellovirus ORF1 protein also contains an arginine-rich N-terminal region similar to that of circovirus CPs. Structural modeling of representative ORF1 protein sequences from each of the established *Anelloviridae* genera with AlphaFold2 (Jumper et al., 2021) confirmed that in all ORF1 protein homologs, the arginine-rich domain is followed by the conserved SJR domain (Fig. 1b, 1c). Comparison of the ORF1 structural models from anelloviruses belonging to different genera explained their remarkable size variation and evolution of ORF1 proteins. It was found that the SJR domain shared with the circovirus CPs represents a conserved part of the proteins. The variation in ORF1 size (and sequence) could be attributed to a specific insertion (Projection domain) within a loop connecting the β-strands H and I (Fig. 2). Thus, it was proposed that anelloviruses evolved from a circovirus-like ancestor through a gradual augmentation of the Projection domain.Given the shared evolutionary history between anelloviruses and other members of the *Cressdnaviricota*, in particular, we propose that anelloviruses should be included into the realm *Monodnaviria*, as a separate new phylum within the kingdom *Shotokuvirae*, alongside *Cressdnaviricota* and *Cossaviricota*. We propose assigning *Anelloviridae* to the order ‘*Sanitavirales*’ (after Latin *sanitas* for health, referring to anelloviruses being part of the healthy human virome), within class ‘*Cardeaviricetes*’ (after Cardea, Roman goddess of health) and phylum ‘*Commensaviricota*’, referring to the commensal lifestyle of anelloviruses.  |

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| **References:**  |
| Butkovic A, Kraberger S, Smeele Z, Martin DP, Schmidlin K, Fontenele RS, Shero MR, Beltran RS, Kirkham AL, Aleamotu'a M, Burns JM, Koonin EV, Varsani A, Krupovic M. Evolution of anelloviruses from a circovirus-like ancestor through gradual augmentation of the jelly-roll capsid protein. Virus Evol. 2023; 9(1):vead035. doi: 10.1093/ve/vead035. PMID: 37325085Jumper J, Evans R, Pritzel A, Green T, Figurnov M, Ronneberger O, Tunyasuvunakool K, Bates R, Žídek A, Potapenko A, Bridgland A, Meyer C, Kohl SAA, Ballard AJ, Cowie A, Romera-Paredes B, Nikolov S, Jain R, Adler J, Back T, Petersen S, Reiman D, Clancy E, Zielinski M, Steinegger M, Pacholska M, Berghammer T, Bodenstein S, Silver D, Vinyals O, Senior AW, Kavukcuoglu K, Kohli P, Hassabis D. Highly accurate protein structure prediction with AlphaFold. Nature. 2021; 596(7873):583-589. doi: 10.1038/s41586-021-03819-2. PMID: 34265844Koonin EV, Dolja VV, Krupovic M, Varsani A, Wolf YI, Yutin N, Zerbini FM, Kuhn JH. Global Organization and Proposed Megataxonomy of the Virus World. Microbiol Mol Biol Rev. 2020; 84(2):e00061-19. doi: 10.1128/MMBR.00061-19. PMID: 32132243Sarker S, Terrón MC, Khandokar Y, Aragão D, Hardy JM, Radjainia M, Jiménez-Zaragoza M, de Pablo PJ, Coulibaly F, Luque D, Raidal SR, Forwood JK. Structural insights into the assembly and regulation of distinct viral capsid complexes. Nat Commun. 2016; 7:13014. doi: 10.1038/ncomms13014.PMID: 27698405   |

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| **Tables, Figures:**  |

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**Figure 1.** Structure of the circovirus jelly-roll capsid protein and structural model of anellovirus ORF1. A. Capsid protein of bat circovirus (BCV, family *Circoviridae*; PDB id: 6RPK) colored using the rainbow scheme from blue N-terminus to red C-terminus. The inset shows the schematic topology of the jelly-roll fold. The 8 -strands are labeled from B to I and form two antiparallel -sheets BIDG and CHEF. The location of the projection (P-)domain is shown as a grey rectangle. B. Structural model of ORF1 from torque teno virus 21 (TTV21, genus *Alphatorquevirus*; GenBank accession number: AAK27697). The jelly-roll domain shared with circoviruses is colored using the rainbow scheme, whereas the P-domain is shown in grey. C. The superposed structures of the BCV (green) and TTV21 (grey) structures.

**Figure 2.** Evolution of the anellovirus capsid protein by the projection domain augmentation. Examples of ORF1 structures with the circled projection domains inserted between strands H-I and arrow indicating additional smaller insertion between strands B-C are also shown. The anellovirus ORF1 proteins are numbered in the order of increasing size. The models are colored using the rainbow scheme, from blue N-terminus to red C-terminus.