

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

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| **Code assigned:** | **2021.001B** |  |
| **Short title:** Abolish the order *Caudovirales* and the families *Myoviridae*, *Siphoviridae* and *Podoviridae* (*Caudoviricetes*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| Bacterial Viruses Subcommittee |

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

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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 | May 2021 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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

**Name of accompanying Excel module**

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| 2021.001B.A.v1.abolish\_Caudovirales.xlsx |

**Abstract**

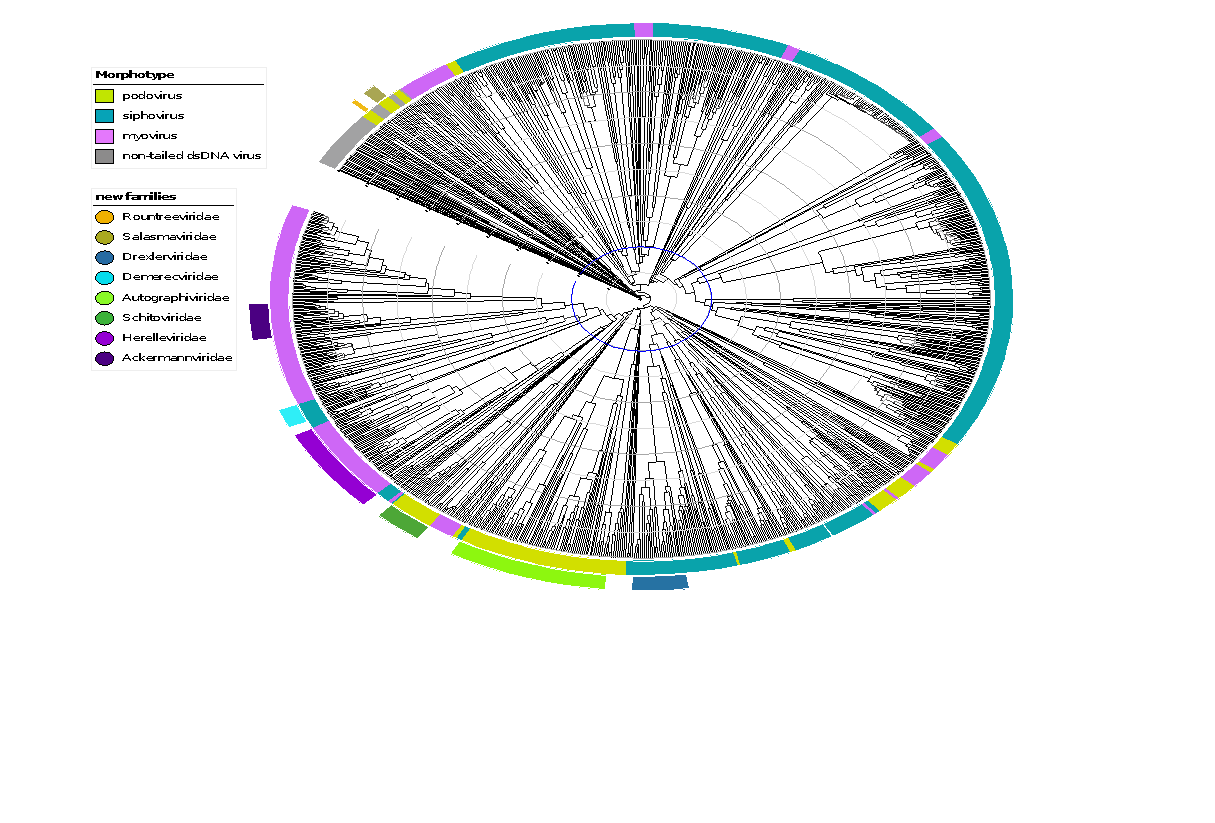
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| Here we propose to abolish the order *Caudovirales* keeping all underlying taxonomic ranks in the class *Caudoviricetes*. We also propose to abolish the morphology-based phage families *Myoviridae*, *Siphoviridae* and *Podoviridae* which have been repeatedly shown not to be monophyletic. |

**Text of proposal**

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| |  | | --- | | Once phage genome sequencing became more prevalent, it has been known since the early 2000’s that the families *Myoviridae*, *Siphoviridae* and *Podoviridae* are not monophyletic. Therefore, we propose to abolish these.  In our opinion piece in Viruses [1], we summarize the studies, methods and software tools that have shown this paraphyly before:   * The Phage Proteomic Tree [2] and its web server ViPTree [3]: tree dendrogram based on shared predicted protein content * The first reticulate network representation of phage genomes [4] * A bipartite network of shared genes [5] * vConTACT2, a weighted network of phage genome shared predict protein content [6] * GRAViTy, a method based on shared protein content and genome organization [7, 8] * A virus ﻿domain orthologous groups approach (VDOG) [9] * CCP77, a concatenated protein phylogeny of members of the order *Caudovirales* [10]   In the past couple of years, we have started to disentangle the phages comprising these families in favor of those created using genome-based relationships and metrics. In our Roadmap paper we suggest the following criteria for the establishment of a new family:   * ﻿The family is represented by a cohesive and monophyletic group in the main predicted proteome-based clustering tools (ViPTree, GRAViTy dendrogram, vCon- TACT2 network) * Members of the family share a significant number of orthologous genes (the number will depend on the genome sizes and number of coding sequences of members of the family). * If a family-level cluster shares orthologues with another family-level cluster, the family cluster needs to be monophyletic in a phylogenetic analysis of the shared orthologue(s).   We also propose to abolish the order *Caudovirales* and have its membership and the current structure automatically assigned to the class *Caudoviricetes*. This will open up the possibility to create new genome-based orders that better reflect the diversity of tailed bacteriophages. | |

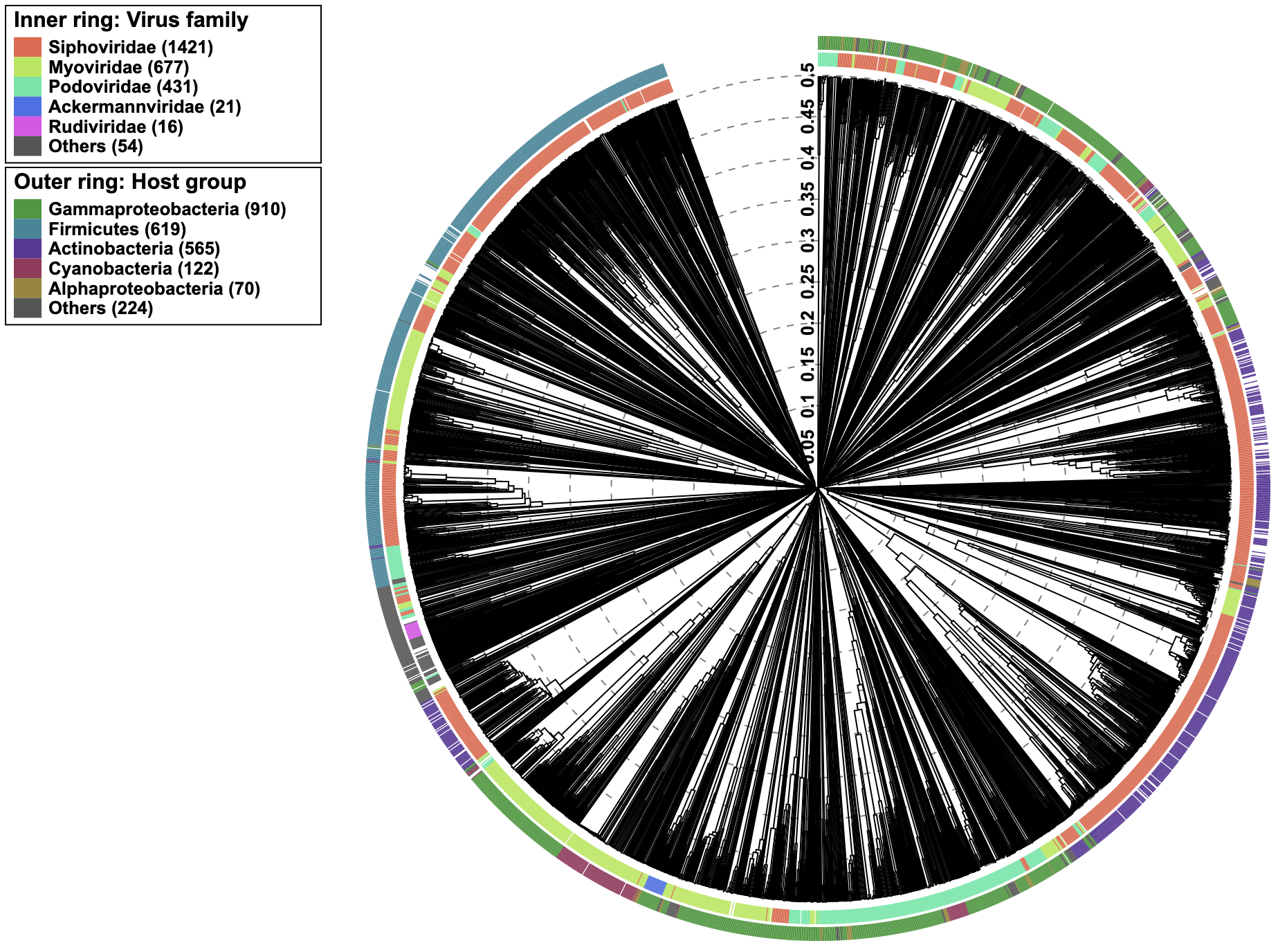
**Supporting evidence**

**GRAViTy**: The GRAViTy dendrogram shows the current morphotypes consistent with the morphology-based families on the inner ring and the families as of MSL35 on the outer ring. The composite generalized Jaccard distance (0-1) between two genomes is indicated by circles from the node to the center, where 0 is identical and 1 is no shared genome content. ﻿The Jaccard distance of 0.8, unifying the majority of eukaryotic virus families is indicated in blue for illustration purposes.

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*Figure 1: GRAViTy dendrogram, copyright the authors of Turner et al, 2021, Viruses* [1]*.*

**Phage Proteomic Tree – VipTree:** The latest iteration of VipTree (version 1.9, RefSeq release 93) shows that neither the morphology-based families, nor the order *Caudovirales*, are monophyletic. In this case, archaeal viruses (designated “*Rudiviridae*” or “others”) are interspersed within the tree because at the root of the tree, no groups of viruses share any protein orthologues.

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*Figure 2: VipTree dendrogram, genome.jp/viptree* [3]

**vConTACT2:** The network-based representation by vConTACT2 [6] shows that there are many groups of dsDNA bacterial and archaeal viruses that share little or no orthologous proteins.

**Network representation of prokaryotic virus diversity with nodes represented by circles coloured by genome-based family, connected with edges that represent shared protein content. **

*Figure 3: vConTACT2 network of all dsDNA bacterial and archaeal virus complete genomes based on the INPHARED pipeline* [11]*, image copyright the authors of Turner et al, 2021, Viruses* [1]*.*

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