

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

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| **Code assigned:** | **2020.016B** |  |
| **Short title:** Create one new family (*Autolykiviridae*) of non-tailed dsDNA bacterial viruses in the double jelly roll fold major capsid lineage | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| Bacterial and Archaeal Viruses Subcommittee |

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

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| n/a |

**Authority to use the name of a living person**

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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 | July 2020 |
| 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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| 2020.016B.R.Autolykiviridae.xlsx |

**Abstract**

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| We propose the creation of a new family of non-tailed dsDNA bacterial viruses named the *Autolykiviridae*, including two new genera and 5 new species, in the realm *Varidnaviria*, kingdom *Bamfordvirae*, phylum *Preplasmiviricota*, and class *Tectiliviricetes*. |

**Text of proposal**

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| |  | | --- | | We propose the creation of a new family named the *Autolykiviridae* (after the character from Greek mythology, Autolykos, who was storied as being difficult to catch), including two new genera and 5 new species.  The *Autolykiviridae* are non-tailed dsDNA bacterial viruses (Fig. 1a) and encode a double jelly roll fold major capsid protein and a FtsK-HerA superfamily packaging ATPase, as well as a protein primed DNA polymerase (pDNApol) (Fig. 1b). These features place this family within the realm *Varidnaviria*, kingdom *Bamfordvirae*, phylum *Preplasmiviricota*, and class *Tectiliviricetes*.  Phylogenetic analyses considering viruses within the *Tectiliviricetes* show that the viruses of the *Autolykiviridae* embody a distinct combination of different features of viruses of currently described families within the class (Fig. 2). In their morphogenetic module (MCP and ATPase) the *Autolykiviridae* are most closely related to the *Corticoviridae* (Fig. 2a-d)[1, 2], yet unlike the *Corticoviridae* they contain a pDNApol-based replication apparatus like the *Tectiviridae* (Fig. 2e,f). In genome length the *Autolykiviridae* are also more similar to the *Corticoviridae* (which have approximately 10 kbp genome lengths) than they are to the *Tectiviridae* (approximately 15 kbp), however in their linear genome topology they are like the *Tectiviridae* (also linear) and unlike the *Corticoviridae* (circular).  Autolykivirid virion and genome properties indicate that they contain lipid membranes within their capsids (like other members of the *Tectiliviricetes*) and terminal proteins covalently bound to their genomes (like the tectivirids). Electron micrographs show features consistent with the presence of lipid membranes within autolykivirid capsids, their virions have lower buoyant densities relative to tailed virus virions in iodixanol density gradients, and their infectivity is reduced by exposure to chloroform[1]. DNA extraction protocols that do not use proteases yield lower recoveries of autolykivirid genomes, which is consistent with their having terminal proteins covalently bound to their genome termini and with the presence of predicted pDNApol and putative terminal protein genes in their genomes[1].  All currently described autolykivirids were isolated on coastal marine heterotrophic bacteria in the genus *Vibrio*, and host range assays against multiple species within the bacterial family Vibrionaceae revealed that some species of autolykivirids are capable of replicating in at least 6 bacterial species[1].  Demarcation of proposed genera and species within the *Autolykiviridae* is based on whole genome nucleotide sequence identity thresholds of 50% and 95%, respectively (Fig. 3). On this basis we propose the creation of the genus *Paulavirus* (basis of name: a euphonious name independent of viral family name), containing the 4 new species *Paulavirus viph1008o*, *Paulavirus viph1020o, Paulavirus viph1080o, and Paulavirus viph1044o,* and the new genus *Livvievirus* (basis of name: a euphonious name independent of viral family name), containing the 1 new species *Livvievirus viph1249a*; these groups are described below.  New genus *Paulavirus*, (Fig. 3, groups A-D), containing new species *Paulavirus viph1008o, Paulavirus viph1020o, Paulavirus viph1080o,* and *Paulavirus viph1044o.*  New species *Paulavirus viph1008o* (Fig. 3, group A) – these viruses (7) were isolated on *Vibrio lentus*, *V. cyclitrophicus*, and *V. splendidus* hosts and in an assay against >250 potential hosts in the Vibrionaceae were shown to kill hosts in up to 6 species, with some members able to kill hosts in both the *Vibrio* and the *Enterovibrio*. Notably, though they kill broadly in the sense that they kill hosts in multiple species, these phages kill only specific host strains and show extensive overlap in their killing profiles.  New species *Paulavirus viph1020o* (Fig. 3, group B) – this virus (1) was isolated on a *V. tasmaniensis* strain and in an assay against >250 potential hosts in the Vibrionaceae was found to kill one additional V*. lentus* strain. The host of isolation was not killed by any other autolykivirids, whereas the *V. lentus* strain was.  New species *Paulavirus viph1080o* (Fig. 3, group C) – these viruses (2) were isolated on *V. kanaloae* and *V. lentus* host strains and in an assay against >250 potential hosts in the Vibrionaceae were found to kill hosts in 5 *Vibrio* species and have largely overlapping host ranges with each other and with autolykivirids of the species *Paulavirus viph1008o* and *Paulavirus viph1044o*.  New species *Paulavirus viph1044o* (Fig. 3, group D) – these viruses (9) were isolated on *V. lentus* and *Vibrio sp. F12* host strains and in an assay against >250 potential hosts in the Vibrionaceae were found to kill hosts in 4 *Vibrio* species and have largely overlapping host ranges with each other and with autolykivirids of the species *Paulavirus viph1008o* and *Paulavirus viph1080o*.  New genus *Livvievirus*, containing new species *Livvievirus viph1249a.*  New species *Livvievirus viph1249a* (Fig. 3, group E) – this virus (1) was isolated on a *V. cyclitrophicus* host and in an assay against >250 potential hosts in the Vibrionaceae was found to kill no other strains hosts, it also did not overlap in host range with any other autolykivirids. | |

**Supporting evidence**

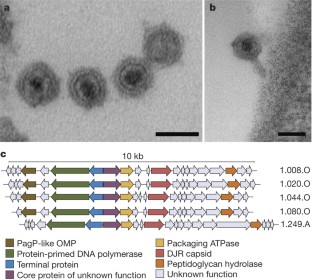


Figure 1. a, Thin-section electron microscopy of autolykivirid plaques shows non-tailed virions with inner cores similar to those of the lipid-bilayer-containing non-tailed corticovirus PM2 b, Rare virions show a tectivirus-like tail-tube-like structure when adjacent to cell membrane. Scale bars, 50 nm. c, Alignment of five genomes representing autolykivirid diversity, open reading frames are represented by block arrows. The linear 10-kb autolykivirid genomes have inverted terminal repeats. *Material reproduced with modifications from Nature*[1] *with default author permissions:* Kauffman, K., Hussain, F., Yang, J. *et al.* A major lineage of non-tailed dsDNA viruses as unrecognized killers of marine bacteria. *Nature* 554, 118–122 (2018).

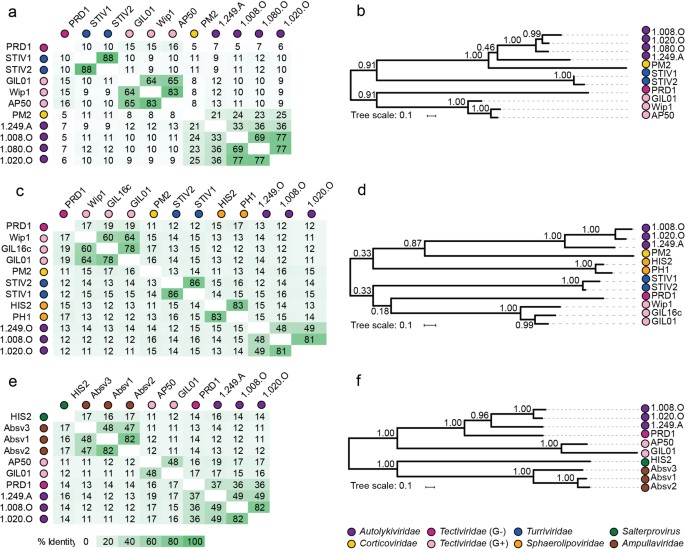


Figure 2. Autolykiviruses are most similar to the corticovirus PM2 in their major capsid protein, poorly resolved in their packaging ATPase, and most similar to the tectivirids in their protein-primed DNA polymerase. Pairwise identities and phylogenies of the protein sequences of the DJR major capsid protein (a and b), packaging ATPase (c and d) and protein primed DNA polymerase (e and f). Members of the *Tectiviridae* infecting Gram-positive and Gram-negative hosts are shown separately as G+ and G−, respectively. All alignments were performed using the ETE3 Toolkit with workflow eggNOG41. All trees are maximum-likelihood trees with aLRT branch supports. *Material reproduced with modifications from Nature*[1] *with default author permissions:* Kauffman, K., Hussain, F., Yang, J. *et al.* A major lineage of non-tailed dsDNA viruses as unrecognized killers of marine bacteria. *Nature* 554, 118–122 (2018).

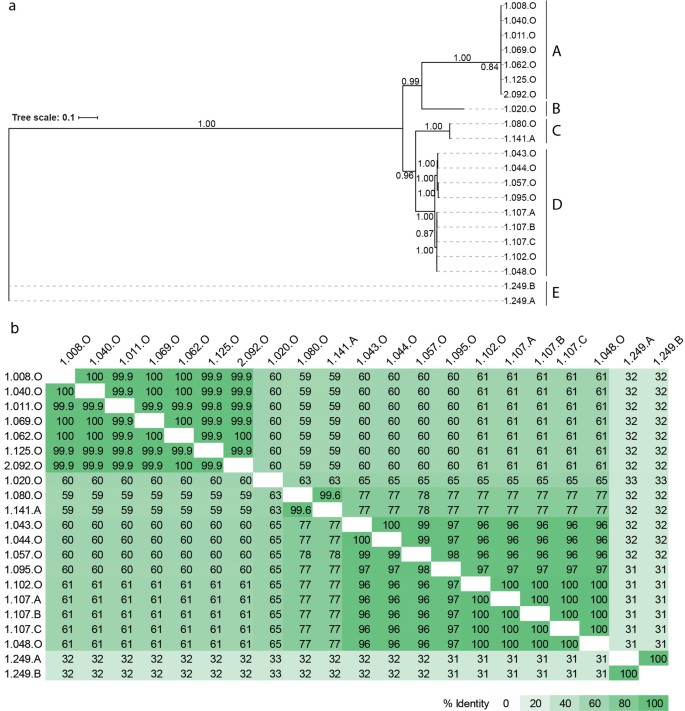


Figure 3. a, Maximum Likelihood phylogeny of whole-genome nucleotide alignments of 21 autolykivirids. Alignments were made with Clustal Omega and the phylogenetic tree was generated with PhyML-SMS with aLRT branch supports. Scale bar, substitutions per base. b, Percentage of whole-genome nucleotide identities among 21 autolykivirid genomes on the basis of the Clustal Omega alignment. Assumptions of 50% and 95% identity for genus and species classifications, respectively, suggest that these viruses represent two genera and five species. Two viruses with identical genomes were isolated at time points 39 days apart (1.048.O and 1.102.O), viruses with the same number and different letter suffixes represent lineages derived from a single plaque that gave rise to variable morphotypes during serial purification. *Material reproduced with modifications from Nature*[1] *with default author permissions:* Kauffman, K., Hussain, F., Yang, J. *et al.* A major lineage of non-tailed dsDNA viruses as unrecognized killers of marine bacteria. *Nature* 554, 118–122 (2018).

**References**

1. Kauffman KM, Hussain FA, Yang J, et al (2018) A major lineage of non-tailed dsDNA viruses as unrecognized killers of marine bacteria. Nature. PMID: 29364876 DOI: 10.1038/nature25474

2. Yutin N, Bäckström D, Ettema TJG, et al (2018) Vast diversity of prokaryotic virus genomes encoding double jelly-roll major capsid proteins uncovered by genomic and metagenomic sequence analysis. Virology Journal 15:67. PMID: 29636073 PMCID: PMC5894146 DOI: 10.1186/s12985-018-0974-y