



Taxonomy of prokaryotic viruses: 2018-2019 update from the ICTV Bacterial and Archaeal Viruses Subcommittee

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Abstract

This article is a summary of the activities of the ICTV's Bacterial and Archaeal Viruses Subcommittee for the years 2018 and 2019. Highlights include the creation of a new order, 10 families, 22 subfamilies, 424 genera and 964 species. Some of our concerns about the ICTV's ability to adjust to and incorporate new DNA- and protein-based taxonomic tools are discussed.

Introduction

The prokaryotic virus community is represented in the International Committee on Taxonomy of Viruses (ICTV) by the Bacterial and Archaeal Viruses Subcommittee. Since our last report [1], the committee composition has changed, and over 200 taxonomic proposals (TaxoProps) were submitted to the ICTV Executive Committee (EC) for evaluation and approval. Below, we summarize these new developments.

Changes in subcommittee membership

In an effort to increase the geographical diversity of members, we appointed representatives from Australia (İ. Kurtböke), Canada (L. Goodridge), Georgia (N. Chanishvili), India (B.L. Sarkar), Russia (V.V. Morozova) and Ukraine (A. Kushkina). Lamentably, Nicola Petty has had to withdraw from our committee.

Taxonomic updates

Over the past two years, our subcommittee has proposed the creation of a new order (*Tubulavirales*), ten new families (*Autographiviridae*, *Chaseviridae*, *Demereciviridae*, *Drexleriviridae*, *Finnlakeviridae*, *Halspiviridae*, *Herelleviridae*, *Ovaliviridae*, *Plectroviridae*, *Thaspiviridae*), 22 new subfamilies, 424 new genera and 964 new species. In previous versions of this update, we listed each of the new taxa, but this is not practical with the introduction of almost 500 new genera. Instead, we briefly introduce the new order and each of the new families below.

Tubulavirales

The new bacteriophage order *Tubulavirales* comprises the rearranged family *Inoviridae* (five existing genera and 18 new genera) and the new family *Plectroviridae* (two existing genera and one new genus). The members of the order *Tubulavirales* possess (+)ssDNA genomes and have a unique morphology, visible as flexible filaments or rigid rods, due to helical symmetry of the capsid. This combination of particle morphology and genome type is unique among viruses, with the exception of representatives of archaeal viruses from the family *Spiraviridae*, which, however, are substantially different in virion organization and gene content [2]. The

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genomes of the new order members contain from 4 to 15 ORFs and are similarly organized, with a modular organization. These phages infect Gram-positive, Gram-negative or cell-wall-less bacteria. A prominent characteristic of this order is that its member viruses enter neither typical lytic nor lysogenic cycles. Instead, virions are released from cells by extrusion, causing a chronic infection without killing the host. The phages belonging to the rearranged family *Inoviridae* infect Gram-negative and Gram-positive bacteria, and virions appear as long and flexible filaments. The members of the new family *Plectroviridae*, previously classified as members of the family *Inoviridae*, infect cell-wall-less bacteria and exhibit the morphology of rigid rods.

Autographiviridae

In 2008, Lavigne et al. [3] re-examined the taxonomy of the family *Podoviridae* and, based on shared protein homologs, defined three genera of T7-like phages within a single subfamily, the *Autographivirinae*. The defining characteristic of the subfamily was the presence of a virion-encoded RNA polymerase (RNAP) from which the subfamily derived its name; “auto” and “graphein” derived from the Greek, meaning “self-writing” or “self-transcribing”. The defining morphological characteristics of all these viruses is that they possess a small (ca. 60 nm in diameter) isometric head attached to a short tail. Their genomes are composed of a linear terminally redundant dsDNA of approximately 41 kb, and all encode a large (> 100 kDa) single-subunit RNA polymerase, which is responsible for middle and late transcription. Further common characteristics of these phages include conservation of gene arrangement and apparently genus-specific lysis cassettes and RNAP specificity loops. A new analysis of these viruses reveals nine subfamilies and 132 genera whose members infect bacteria of the classes Betaproteobacteria and Gammaproteobacteria, and the phylum Cyanobacteria. Many of the genera are undersampled and further analyses are required to demonstrate that the new family is not polyphyletic. It is anticipated that further revisions will be necessary in the future.

Chaseviridae

This taxon is named in honour of Martha Cowles Chase (1927–2003), who, together with Alfred Hershey, experimentally demonstrated that DNA rather than protein is the genetic material. The first isolated phage of this type is ϕ EcoM-GJ1 [4, 5]. Members of this family are myoviruses with isometric heads ~62 nm in diameter and contractile tails ~120 nm in length. The hosts belong to the genera *Escherichia*, *Erwinia*, *Pectobacterium*, *Shewanella* and *Aeromonas*, all members of the class Gammaproteobacteria. The genomes possess ~2600-bp direct terminal repeats, are

on average 54.2 kbp (46.5 mol% G + C) in length and encode about 77 proteins and, in some cases, a tRNA. Except where we have identified genera with two species, this group as a whole displays very little overall DNA sequence relatedness, presumably because the GC-content varies from 43.6 to 52.8 mol%. At the protein level, *Erwinia* phage vB_EamM-Y2 and *Shewanella* phage SppYZU05 share 34.8% homologs. Common proteins include the RNA polymerase, DNA polymerase, primase and exonuclease. vConTACT 2.0 [6, 7] clusters *Aeromonas* phage pAh6-C, *Escherichia* phage ϕ iEcoM-GJ1, *Erwinia* phage vB_EamM-Y2, *Pectobacterium* phage PM1, and *Shewanella* phage Spp001 into one cluster (VC 244_0). Our analysis suggests the presence of two subfamilies: one including the genera *Loessnervirus*, *Suwonvirus*, *Carltongylesvirus* and *Faunusvirus*, and the other including the genera *Yushanvirus* and *Pahsextavirus*.

Demerecviridae

This new family contains three new subfamilies (*Markadamsvirinae* [including the genera *Tequinavirus*, *Epseptimavirus*, and *Haartmanvirus*]; *Mccorquodalevirinae* [including the genera *Myunavirus* and *Hongcheonvirus*]; and *Ermolyevavirinae* [including the genera *Cetovirus*, *Vipunavirus*, and *Suttonboningtonvirus*]. The hosts for these phages are *Aeromonas*, *Escherichia*, *Klebsiella*, *Pectobacterium*, *Proteus*, *Providencia*, *Salmonella*, *Shigella*, *Vibrio*, and *Yersinia* species. The genome of coliphage T5 (AY543070.1) is 121.75 kbp in length, with a mol%GC content of 39.3 and encodes 162 proteins and 24 tRNAs. It is characterized by long (10,219-bp) direct terminal repeats. The average length of the genomes ranges from 106.2 to 122.8 kbp, but in most cases no evidence has been presented for terminal redundancy. The average mol%GC content varies from 39.1 to 45.2. This new family is named in honour of Milislav Demerec (1895–1966), the Croatian-American geneticist who pioneered the work on bacteriophages, and who, together with the Italian-American physicist Ugo Fano (1912–2001), first isolated *E. coli* phage T5 in 1945 from a mixture provided to them by Tony L. Rakietyen (Long Island College of Medicine, USA).

Drexelviriidae

When originally proposed in 1996, the “T1-like phages” included a single species, *Enterobacteria phage T1*. Since that time, numerous taxonomic changes have been introduced, with the genus name changing to “*T1likevirus*” to “*Tunlikevirus*” to “*T1virus*” and ultimately to “*Tunavirus*”. In 2015, the subfamily *Tunavirinae* was introduced, consisting of five genera: *Kp36virus*, *Rogue1virus*, *Rtpvirus*, *T1virus* and *Tlsvirus* [8]. In 2018, three additional genera were included: *Eclunavirus*, *Hanrivervirus* and *Sertoctavirus*,

and the genera *Rogue1virus*, *T1virus* and *Kp36virus* were renamed *Rogunavirus*, *Tunavirus* and *Webervirus*, respectively. In total, 31 species have been classified. GenBank now contains the genome sequences of 84 T1 related phages, calling for re-examination of the relationships within the subfamily. The hosts belong predominantly to the genus *Escherichia*, but *Cronobacter*-, *Enterobacter*-, *Klebsiella*-, *Pantoea*- and *Shigella*-specific isolates have been isolated and sequenced as well. These hosts are all members of the class Gammaproteobacteria. The phage genomes are on average 48.9 kbp long (46.0 mol% G + C) and encode about 79 proteins and 0–2 tRNAs. This resulted in the addition of 12 new genera and three new subfamilies (*Tempevirinae* [including the genera *Tlsvirus*, *Hanrivervirus*, and *Warwickvirus*], *Rogunavirinae* [including the genera *Rogunavirus*, *Eastlansingvirus*, *Wilsonroadvirus*, and *Lindendrivevirus*], and *Braunvirinae* [including the genera *Rtpvirus*, *Shandongvirus*, *Loudonvirus*, and *Guelphvirus*]). This family is named in honour of Henry Drexler, who pioneered research on phage T1.

Finnlakeviridae

This new taxon was created for the new “Finnish lake” virus species *Flavobacterium virus FLiP* (in the new genus *Finnlakevirus*). FLiP is the sole member of this family and is the only known icosahedral single-stranded (ss) DNA bacteriophage with an internal membrane. FLiP and its host bacterium *Flavobacterium* sp. strain B330 were isolated from a boreal lake, Lake Jyväsjärvi, Jyväskylä, Finland [9]. The FLiP genome is a circular ssDNA molecule of 9,174 nucleotides. Nine of the 16 open reading frames have no significant sequence identity to other sequences in the databases. The diameter of the virion is 59 nm, and the vertices have elongated spike structures. The capsid (T=21) is formed by trimeric major capsid proteins with a double β -barrel fold. Network analysis of the major capsid protein sequences has shown that FLiP forms its own group among the bacterial and archaeal icosahedral viruses and related proviruses [10].

Halspiviridae

The spindle-shaped virus His1 has a linear double-stranded DNA genome of 14,464 bp with terminal inverted repeats and encodes a protein-primed family B DNA polymerase [11]. His1 infects the halophilic archaeon *Haloarcula hispanica* (phylum Euryarchaeota) [12] and was originally classified as a member of the unassigned genus *Salterprovirus* [11]. The major capsid protein of His1 shows sequence similarity to those of members of the family *Fuselloviridae*,

which infect hyperthermophilic acidophiles of the order Sulfolobales (phylum Crenarchaeota) [13, 14]. However, unlike His1, fuselloviruses have circular dsDNA genomes and do not encode their own DNA polymerases. Because His1 is sufficiently distinct from all other known cultured viruses, the genus *Salterprovirus* has been assigned to a separate new family, the *Halspiviridae* (hal- for halophilic, spi- for spindle-shaped). Furthermore, the species *His 1 virus* has been renamed “*Salterprovirus His1*”.

Herelleviridae

The family *Herelleviridae* was named after Félix d’Hérelle, celebrating the 100th anniversary of his discovery of bacteriophages [15]. Members of this family are large myoviruses with a virulent lifestyle that infect bacteria of the phylum Firmicutes. The family was extended from the subfamily *Spounavirinae*, with *Bacillus* phage SPO1 being the type member [16], and includes four other subfamilies: *Jasinkavirinae*, *Brockvirinae*, *Bastillevirinae* and *Twortvirinae*. All members of the family *Herelleviridae* share a set of core genes, including the terminase large subunit, major capsid protein, tail tube, tail sheath, and tail tape measure protein. They form a monophyletic clade within the tailed phages when using single and concatenated marker gene phylogenies [15], as well as when using GRAViTy [17], vCONTACT2 [6], and the phage proteomic tree approach [18]. Members of the same genus in this family share at least 50% nucleotide sequence identity over the entire genome, whereas members of the same subfamily share at least 25% translated genome sequence identity as determined with tBLASTx.

Ovaliviridae

The new family *Ovaliviridae* (from the Latin *ovalis*, for oval) is represented by *Sulfolobus ellipsoid virus 1* (SEV1) [19], which harbors a linear double-stranded DNA genome of 23,219 bp and encodes 38 predicted proteins, most of which have no known function. SEV1 has been classified as the first representative of a new family because of its unique morphology, unusual architecture of the virion, and lack of gene content similarity to other characterized viruses. The virion of SEV1 contains a protein capsid with 16 regularly spaced striations and an 11-nm-thick envelope [19]. The virus acquires its envelope intracellularly and exits the host cell through hexagonal pyramidal portals that perforate the host cell envelope.

Sulfolobus ellipsoid virus 1 is designated as the type species of the genus *Alphaovalivirus*.

Thaspiviridae

The virions of *Nitrosopumilus* spindle-shaped virus 1 (NSV1) measure 64 ± 3 nm in diameter and 112 ± 6 nm in length, with a short tail at one pole [20]. This morphology is similar to that of fuselloviruses and the halspivirus His1 [13]. The genome of NSV1 is a linear dsDNA molecule of 27,548 bp, terminating with 176-bp-long inverted repeats. NSV1 encodes 48 predicted proteins, only one of which (protein-primed family B DNA polymerase) displays significant sequence similarity to the proteins of other known archaeal or bacterial viruses. NSV1 is the first and, thus far, the only virus isolated on ammonia-oxidising archaea of the phylum Thaumarchaeota [20]. NSV1 has been classified into the species *Nitmarvirus NSV1* within the genus *Nitmarvirus* (for *Nitrosopumilus maritimus* virus) and the new family *Thaspiviridae* (*Tha*- for *th*aumarchaeal, *spi*- for *sp*indle-shaped viruses).

Online (10th) Report of the ICTV

Virus Taxonomy: The Classification and Nomenclature of Viruses - The Online (10th) Report of the ICTV is freely accessible at <http://ictv.global/report>, and summaries of the chapters on each virus family are published in the Journal of General Virology. We would like to acknowledge the hard work of David Prangishvili and Mart Krupovic for contributing chapters on archaeal (*Ampullaviridae* [21], *Bicaudaviridae* [22], *Globuloviridae* [23], *Guttaviridae* [24], *Spiraviridae* [25], *Tristromaviridae* [26], and bacterial (*Plasmaviridae* [27]) viruses.

Final thoughts from the Chair, Professor Andrew Kropinski

I would hazard a guess that the Bacterial and Archaeal Viruses Subcommittee (BAVS) has changed the taxonomy of the viruses that are their responsibility over the past five years more than any other group within the ICTV at any point in history. This has resulted in a taxonomy which is much closer aligned to that of other viruses than ever before. To indicate how phage taxonomy has changed: In 2014, within the order *Caudovirales* there were three families, six subfamilies, 72 genera and 484 species. There are now 10 families, 35 subfamilies, 672 genera and 1976 species. The pace and volume of taxonomic changes over the last years may have introduced a period of confusion in the scientific literature. This transition period has been unavoidable but will create a more sustainable clarity in the long term. We

must do our best to guide the community through this transition period towards ‘stable ground’, which will in turn enable textbooks, education tools, databases etc. to follow through.

I would like to thank specifically four individuals: Hans Ackermann (aka Dr. Phage Electron Microscopy/ Dr. Comma), who in spite of misgivings about the direction that we were taking, was always supportive. Whenever I look at an electron micrograph of a phage, I ask myself “What would Hans think of this?” He is greatly missed. Jens Kuhn, who taught me what a taxon is, and who was always ready to support us and write long explanatory emails on the finer aspects of taxonomy, in spite of an extremely busy schedule. Igor Tolstoy from NCBI, who appears to operate without sleep and who sends me queries on deposited phage genomes which have enhanced our taxonomy. Evelien Adriaenssens, who became involved in phage taxonomy with me in 2012, and without whom we would have been far less productive. I know that our subcommittee will be in excellent hands when she takes over its leadership this year.

Future directions

In 2019, it was proposed to the ICTV Executive Committee that the Bacterial and Archaeal Viruses Subcommittee be split. This would result in the formation of the Archaeal Viruses Subcommittee and the Bacterial Viruses Subcommittee.

There is a movement within the ICTV towards a binomial system of viral nomenclature [28]. We therefore request that the phage community move away from giving their isolates names such as “*Escherichia* phage XYZ2020” and instead use a format similar to “*Escherichia* phage Fuddleduddle.” Using words (sensical or not) instead of an alphanumeric will facilitate the expected move to a Linnaean-like system for species names (i.e., if “*Escherichia* phage Fuddleduddle” is a member of the genus “*Twaddlevirus*”, then the new species for “*Escherichia* phage Fuddleduddle” could be called “*Twaddlevirus fuddleduddle*” (with apologies to Pierre Elliot Trudeau). Such a species name, I (AMK) believe, would be more acceptable to the bacteriophage community than the latinate “*Twaddlevirus fuddleduddlensis*”. This naming scheme also has the added benefit that it retains name recognition and better describes the isolate. In GenBank there are currently 426 complete genome sequences for “*Escherichia* phages”, which belong to numerous different families and genera; therefore, the prefix “*Escherichia virus*” has little additional utility in viral taxonomy. Furthermore, in the case of most virome-derived sequences, we do not know the host bacterium; therefore, the current-species naming convention (*host name* + *virus* + *species name*) will not work.

We have reached a stage where we need to see fundamental changes in the way Taxonomic Proposals are prepared and assessed. Every year, 400–600 complete phage genome sequences are deposited in the GenBank database, and it has become impossible to rapidly assess potentially new taxa, particularly if they contain numerous representatives. In simple terms, our current way to doing things is too complex and time-consuming. We need to take advantage of the bioinformatically competent ICTV members to develop and implement automated procedures for identification of virus isolates and their easy classification into species, genera, etc. and to generate appropriate documentation. We have recently seen the development of tools such as Pairwise Sequence Comparison (PASC [29]), Sequence Demarcation Tool (SDT [30]), Machine Learning with Digital Signal Processing (ML-DSP [31]), VICTOR [32], ClassiPhage [33], GRAViTy [17], ViPTree [34], vConTACT [6, 7], and the concatenated protein tree method of Low et al. [35], as well as the novel NCBI ORF finder-BLASTp-SymBets; [36] and BLASTN algorithms developed by Igor Tolstoy and Mathew Lueder, respectively. Until such systems are accepted by the ICTV and robust criteria are established to delineate families and subfamilies, phage taxonomy will always lag significantly behind submissions to NCBI, and our committees will not be able to taxonomically address the classification of prophages and metagenomically derived sequences. Environmental virome studies have indicated the existence of huge numbers of diverse and currently unclassified phages, whether it be in oceans, soils or the human gut [37–39]. The case is well illustrated by the families *Microviridae* and *Leviviridae*, which have received relatively little attention from the ICTV (i.e., two subfamilies, six genera and 21 species versus two genera and four species, respectively). Environmental studies have indicated that the family *Microviridae* contains at least five unclassified subfamilies [40–47]. Recently, Callanan et al. [48] predicted 331 species and 247 genera among the single-stranded RNA phages, potentially leading to a significant expansion of the family *Leviviridae*.

Until such a system is in place, we propose to work closely with NCBI to identify new phage species, genera, and subfamilies and to immediately provide names to NCBI. At the annual EC meeting, complete TaxoProps for the newly identified taxa would be presented to the ICTV.

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Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

Ethical approval The authors did not perform any studies with human participants or animals for this article.

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