Bacterial Viruses Subcommittee and Archaeal Viruses Subcommittee of the ICTV: update of taxonomy changes in 2021

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Abstract

In this article, we – the Bacterial Viruses Subcommittee and the Archaeal Viruses Subcommittee of the International Committee on Taxonomy of Viruses (ICTV) – summarise the results of our activities for the period March 2020 – March 2021. We report the division of the former Bacterial and Archaeal Viruses Subcommittee in two separate Subcommittees, welcome new members, a new Subcommittee Chair and Vice Chair, and give an overview of the new taxa that were proposed in 2020, approved by the Executive Committee and ratified by vote in 2021. In particular, a new realm, three orders, 15 families, 31 subfamilies, 734 genera and 1845 species were newly created or redefined (moved/promoted).

Changes in Subcommittee structure and membership

Bacteriophage and archaeal virus taxonomy has been formally under the auspices of the ICTV Bacterial and Archaeal Viruses Subcommittee, which, at its inception in 1966, was named the Viruses of Prokaryotes Subcommittee, led by David E. Bradley (https://talk.ictvonline.org/information/w/ictv-history). Given the revived interest in bacterial and archaeal viruses and recent enormous increase in the number of characterized isolates and need for creation of numerous taxa to classify them, the Executive Committee (EC) voted on the creation of two separate Subcommittees (EC51, July 2019), formally starting their mandates after EC52 (October 2020). The new Bacterial Viruses Subcommittee is chaired by Evelien Adriaenssens, supported by Dann Turner as the Vice Chair, and the new Archaeal Viruses Subcommittee is chaired by Mart Krupovic. Both Chairs were elected for three-year terms ending in 2023. As a result, this taxonomy update summarises both bacterial and archaeal virus proposals for the last time, reflecting the fact that proposals were submitted prior to the formal reorganisation of the original Subcommittee.

In the new Bacterial Viruses Subcommittee, we continue our structure of Study Groups (SGs), regional representatives and general members. We would like to welcome new members Jesca Nakavuma (Uganda), Alejandro Reyes (Colombia), Cristina Moraru (Germany), Susan Lehman (USA), Cédric Lood (Belgium) and Andrey Shkoporov (Ireland) and would like to thank those who have left the Subcommittee for their service.

In the framework of the Bacterial and Archaeal Viruses Subcommittee, all taxonomic proposals dealing with archaeal viruses were handled by a single SG. The new
Archaeal Viruses Subcommittee currently includes 11 SGs (Table 1), each created for a three-year term. Of note, the *Halopanivirales* SG, chaired by Hanna M. Oksanen (Finland), oversees the taxonomy of evolutionarily related viruses of the order *Halopanivirales*, which includes two families of viruses infecting archaea (*Sphaerolipoviridae* and *Simuloviridae*) and one family of bacteriophages (*Mat- sushitaviridae*). Thus, the latter SG bridges the two Subcommittees. Additional SGs will be created in the near future, in particular, to develop the taxonomy of archaeal members of the class *Caudoviricetes*; only a handful of isolated representatives of this highly diverse and expansive group of archaeal viruses are currently classified.

**Taxonomy update**

We had a record year of submissions of taxonomy proposals in 2020, with 188 proposals submitted, of which all but one were approved and ratified (Supplementary Table S1). The changes at each of the taxonomic ranks in use for bacterial and archaeal viruses are summarised in Table 2. We

| Study Group                | Member               | Country   |
|----------------------------|----------------------|-----------|
| *Bicaudaviridae* SG       | Mart Krupovic*       | France    |
|                           | Li Huang             | China     |
|                           | Mark J. Young        | USA       |
|                           | Virginija Cvirkaite-Krupovic | France |
| *Desulfurococcaceae viruses* SG | Tomohiro Mochizuki* | Japan     |
|                           | Mart Krupovic        | France    |
| *Fuselloviridae* SG       | Kenneth M. Stedman*  | USA       |
|                           | Mart Krupovic        | France    |
| *Halopanivirales* SG      | Hanna M. Oksanen*    | Finland   |
|                           | Mike Dyall-Smith     | Australia |
|                           | Shishen Du           | China     |
|                           | Matti Jalasvuori     | Finland   |
| *Halspiridae* SG          | Mike Dyall-Smith*    | Australia |
|                           | Hanna M. Oksanen     | Finland   |
| *Ovaliviridae* SG         | Li Huang*            | China     |
| *Pleolipoviridae* SG      | Hanna M. Oksanen*    | Finland   |
|                           | Mike Dyall-Smith     | Australia |
|                           | Ying Liu             | France    |
| *Portogloboviridae* SG    | Mart Krupovic*       | France    |
|                           | Ying Liu             | France    |
| *Thaspiridae* SG          | Sung-Keun Rhee*      | Republic of Korea |
|                           | Mart Krupovic        | France    |
| *Tokiviricetes* SG        | Mart Krupovic*       | France    |
|                           | Tomohiro Mochizuki   | Japan     |
|                           | Xu Peng              | Denmark   |
|                           | Diana P. Baquero     | France    |
| *Turriviridae* SG         | Mark J. Young*       | USA       |

*Study Group Chair

| Species | Genus | Subfamily | Family | Order | Class | Phylum | Kingdom | Realm |
|---------|-------|-----------|--------|-------|-------|--------|---------|-------|
| Abolished | 20    | 2         | 0      | 0     | 0     | 0      | 0       | 0     |
| New      | 1775  | 700       | 28     | 14    | 2     | 1      | 1       | 1     |
| Moved or promoted (and/or renamed) | 70    | 34        | 3      | 1     | 1     | 0      | 0       | 0     |
| Renamed  | 33    | 8         | 0      | 1     | 1     | 1      | 0       | 0     |

**Table 1** Composition of the archaeal viruses subcommittee

**Table 2** Summary of taxonomic changes for bacterial and archaeal viruses for Master Species List 36, ratified March 2021
created a record 1775 new species, 700 new genera, 28 new subfamilies, 14 new families and two new orders and also created one new realm containing one new kingdom, one new phylum and one new class. Given the large numbers of proposals and taxa that were created, moved or renamed, it becomes unfeasible to describe all the changes in detail; however, we urge interested readers to consult Supplementary Table S1 and the associated proposals from the ICTV website (https://talk.ictvonline.org/files/ictv_official_taxonomy_updates_since_the_8th_report/m/prokaryote-official). Instead, below we provide a brief overview of the most notable changes.

The new realm Adnaviria, a new megataxon of archaean filamentous viruses

Recently, the taxonomic framework of the ICTV has been expanded from five to 15 ranks, with the highest-level rank, realm, being equivalent to the domain rank used for cellular organisms [1]. Until recently, four such realms had been established for classification of viruses infecting hosts from different domains of life [2, 3]. This year, a new realm, Adnaviria, was created for classification of archaean filamentous viruses with dsDNA genomes that adopt the A-form conformation within their virions [4, 5]. The realm includes three families, Tristromaviridae, Rudiviridae and Lipothrixviridae, which are evolutionarily related to each other, but not to any other known group of viruses. The families Rudiviridae and Lipothrixviridae were already grouped together in the order Ligamenvirales [6], and a single-family order, Primavirales, has now been created for the family Tristromaviridae. The two orders are unified in the class Primavirales [6], and a single-family order, Tristromaviridae, has now been created for the family Tristromaviridae. The two orders are unified in the class Primavirales [6].

Class Caudoviricetes, order Caudovirales

We delineated three new families of short-tailed phages with small genomes that were formerly assigned to the family Podoviridae. The family Salasmaviridae, named in honour of Margarita Salas Falgueras, comprises the existing subfamily Picovirinae, which includes the classical bacillus phage φ29 and a range of related Bacillus-infecting phages with genomes between 18 and 27 kb in size. The family Rountreeviridae, named in honour of Phyllis Margaret Rountree, groups Enterococcus-infecting phages with genomes between 17 and 19 kb in size, whereas the family Guelinviridae, named after Antonina Guelin, groups Clostridium-infecting phages with genome sizes between 16 and 19 kb.

The new family Schitoviridae, named after Giancarlo Schito, is the formalisation of the group of N4-like phages defined by the presence of a large virion-associated RNA polymerase, described in more detail in reference [7].

The new family Zobellviridae, named after Claude Zobell, groups a set of globally distributed podoviruses associated with marine ecosystems first proposed by Bischoff and colleagues [8].

Class Leviricetes

Based on the investigation by Callanan and colleagues on the expansion of known ssRNA virus genomes [9], the family Leviricetes was elevated to the rank of class, named Leviricetes (replacing the class Allassoviricetes), and expanded to include two orders (Norzivirales and Timlovirales) and six new families: Fiersviridae (renamed from the original family Fiersviridae), Atkinsovirdae, Dainiridae, Solspiriridae, Blumerviridae and Steitzviridae. A detailed description of the new taxa will be published separately.

Class Tectiliviricetes, new family Autolykiviridae

The new family Autolykiviridae formalises the group of non-tailed dsDNA bacteriophages discovered and described by Kauffmann and colleagues [10], combining features of both corticoviruses and tectiviruses. This new family contains two new genera and five new species.

Order Halopanivirales, new families Matsushitaviridae and Simuloviridae

Until recently, the family Sphaerolipoviridae, which includes icosahedral tailless viruses with internal membranes, consisted of three genera, Alphasphaerolipovirus, Betasphaerolipovirus and Gammasphaerolipovirus. The first two of these genera included viruses infecting halophilic archaea, whereas the last one included phages infecting thermophilic bacteria [11]. Although viruses from the three genera are evolutionarily related [12], they display considerable sequence divergence. Thus, the genera Betasphaerolipovirus and Gammasphaerolipovirus have been renamed and moved from the Sphaerolipoviridae into new families, Simuloviridae and Matsushitaviridae (named after Isao Matsushita), respectively. The order Halopanivirales now contains a family of bacterial viruses, Matsushitaviridae, and two families of archaeal viruses, family Sphaerolipoviridae and Simuloviridae. As mentioned above, the order is under purview of a single Study Group, which is part of both the Archaeal Viruses SC and the Bacterial Viruses SC.

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**Order Tubulavirales, new family Paulinoviridae**

The new family *Paulinoviridae* addresses the challenge of defining family demarcation criteria for phages with small genomes, where members of the same family would share at least two orthologous proteins. Informed by prior work on a gene-content network of predicted filamentous prophage sequences [13], we moved the genera *Bifilivirus* and *Thomixivirus* from the family *Inoviridae* to the family *Paulinoviridae*.

**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](http://ictv.global/report), and summaries of the chapters on each virus family are published in the Journal of General Virology. In 2020, four new chapters on bacterial and archaeal viruses were produced by members of the Archaeal Viruses SC and Bacterial Viruses SC, namely, on the families *Herelleviridae* [14], *Spiraviridae* [15], *Ovaliviridae* [16] and *Finnlakeviridae* [17].

**Conclusion**

This past year has been extremely productive in terms of new bacterial and archaeal virus taxa described. It would not have been possible without an active pool of scientists, both within and outside the subcommittee and its study groups, who scour databases, perform analyses and submit proposals. We continue to encourage people to contact us to formalise new discoveries into the taxonomic framework and will keep reaching out to interested parties. Finally, we would like to acknowledge one person in particular, Prof Andrew Kropinski, the Subcommittee Chair from 2014–2020, who authored, co-authored and/or assisted with the majority of proposals that have been approved in the last decade.

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**Declarations**

**Conflict of interest** All authors are current or former members of the Bacterial and Archaeal Viruses Subcommittee, Bacterial Viruses Subcommittee and/or Archaeal Viruses Subcommittee of the International Committee on Taxonomy of Viruses (ICTV).

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