

Taxonomy of prokaryotic viruses: 2016 update from the ICTV bacterial and archaeal viruses subcommittee

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The prokaryotic virus community is represented at the International Committee on Taxonomy of Viruses (ICTV) by the Bacterial and Archaeal Viruses Subcommittee. Since our last report [8], the committee composition has changed, and a large number of taxonomic proposals (TaxoProps) were submitted to the ICTV Executive Committee (EC) for approval.

1. **New appointments.** The committee has been enlarged through the additions of Drs. J. Rodney Brister

(Chair—Molecular Typing), Ho Bin Jang (Member), Petar Knezevic (Chair—ICTV *Inoviridae* Study Group), Hanna M. Oksanen (Chair—ICTV *Corticoviridae* Study Group), and Minna M. Poranen (Chair—ICTV *Cystoviridae* Study Group). In addition, Dr. Mart Krupovic has taken over the Chairmanship of the ICTV *Plasmaviridae* Study Group.

2. **Future of the order *Caudovirales*.** With the dramatic increase in the number of characterized tailed bacterial

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and archaeal viruses, it is becoming increasingly clear that the order *Caudovirales* (and the three included families *Myoviridae*, *Siphoviridae* and *Podoviridae*) can no longer sustain the huge genetic diversity within this virus group [5] and has to be adequately reorganized. Indeed, taxonomic hurdles with this and some other expansive groups of viruses, prompted ICTV to explore the possibility of introducing additional taxonomic levels. Initial ideas and plans were presented to the microbial viruses community at the 2016 EMBO conference “Viruses of Microbes IV” (Liverpool, UK). Currently, the Bacterial and Archaeal Viruses Subcommittee is examining the consistency of the order *Caudovirales* on the example of a diverse group of phages currently classified in the subfamily *Spounavirinae* [2, 6, 7, 9, 12]. We applied a range of complementary DNA and protein sequence analysis tools as well as phylogenetic methods to the analysis of 93 *Bacillus*, *Enterococcus*, *Listeria*, and *Staphylococcus* phages with large genomes (≈ 110 – 160 kb). A manuscript describing our findings is in preparation, and the appropriate TaxoProps will be submitted.

3. **Taxonomy of prokaryotic viruses found in GenBank.** Genome sequences of prokaryotic viruses are accumulating in public sequence databases, such as GenBank, at an increasing rate. Oftentimes, these sequences are being deposited without or with only minimal taxonomy descriptions. To appropriately

classify these viruses, the Subcommittee adopted a holistic approach with the first-line discriminator being DNA sequence identity (calculated using NCBI BLASTN [3, 10] or Gegenees BLASTN [1]) of the genome in question to those of previously classified viruses. Next, overall protein identity was calculated using Gegenees TBLASTX for large datasets and CoreGenes 3.5 [11] for smaller sets. Lastly, phylogenetic analyses of one to three conserved phage proteins, often including the large subunit of the terminase and major capsid proteins or DNA-replication-associated proteins, were carried out using maximum-likelihood method as implemented at Phylogeny.fr [4]. The changes described here were formalized and submitted in more than 80 ICTV TaxoProps for consideration by the ICTV EC (<http://www.ictvonline.org>). One new archaeal virus family (*Tristromaviridae*), six new bacteriophage subfamilies (*Ounavirinae* [*Salmonella* phage FelixO1], *Sepvirinae* [*Escherichia* phage 933 W], *Arquatrovirinae* [*Streptomyces* phage R4], *Bclasvirinae* [*Mycobacterium* phage Acadian], *Mclasvirinae* [*Mycobacterium* phage Pipefish] and *Pclasvirinae* [*Mycobacterium* phage Fishburne]), and 88 new genera including 249 species are covered in these proposals (Table 1). These proposals were submitted to the ICTV EC in 2016 for approval. In addition, another 70 phages and one archaeal virus belonging to existing genera were

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Table 1 Taxonomy proposals (TaxoProps) describing new taxa (families, subfamilies, genera) submitted to the ICTV Executive Committee in 2016

Family	Subfamily	New genus	Type species	Number of new species in genus (total number of species in genus)
<i>Inoviridae</i>		<i>Fibrovirus</i>	<i>Vibrio virus fs1</i>	1 (2)
<i>Inoviridae</i>		<i>Habenivirus</i>	<i>Ralstonia virus RSM1</i>	3
<i>Inoviridae</i>		<i>Lineavirus</i>	<i>Salmonella virus Ike</i>	0 (2)
<i>Inoviridae</i>		<i>Saetivirus</i>	<i>Vibrio virus fs2</i>	1 (2)
<i>Inoviridae</i>		<i>Vespertiliovirus</i>	<i>Spiroplasma virus R8A2B</i>	1 (3)
<i>Myoviridae</i>	<i>Ounavirinae</i>	<i>Ea214virus</i>	<i>Erwinia virus Ea214</i>	1 (2)
<i>Myoviridae</i>	<i>Ounavirinae</i>	<i>Mooglevirus</i>	<i>Citrobacter virus Moogle</i>	2
<i>Myoviridae</i>	<i>Ounavirinae</i>	<i>Suspivirus</i>	<i>Escherichia virus SUSP1</i>	2
<i>Myoviridae</i>	<i>Spounavirinae</i>	<i>Tsarbombavirus</i>	<i>Bacillus virus TsarBomba</i>	2
<i>Myoviridae</i>	<i>Tevenvirinae</i>	<i>Jd18virus</i>	<i>Klebsiella virus JD18</i>	2
<i>Myoviridae</i>	<i>Tevenvirinae</i>	<i>Kp15virus</i>	<i>Klebsiella virus KP15</i>	5
<i>Myoviridae</i>	<i>Tevenvirinae</i>	<i>Moonvirus</i>	<i>Citrobacter virus Moon</i>	2
<i>Myoviridae</i>		<i>Abouovirus</i>	<i>Brevibacillus virus Abouo</i>	2
<i>Myoviridae</i>		<i>Agrican357virus</i>	<i>Erwinia virus Ea35-70</i>	5
<i>Myoviridae</i>		<i>Arv1virus</i>	<i>Arthobacter virus ArV1</i>	2
<i>Myoviridae</i>		<i>Elvirus</i>	<i>Pseudomonas virus EL</i>	0 (1)
<i>Myoviridae</i>		<i>Jimmervirus</i>	<i>Brevibacillus virus Jimmer</i>	2
<i>Myoviridae</i>		<i>M12virus</i>	<i>Sinorhizobium virus M12</i>	3
<i>Myoviridae</i>		<i>Marthavirus</i>	<i>Arthrobacter virus Martha</i>	4
<i>Myoviridae</i>		<i>Msw3virus</i>	<i>Edwardsiella virus MSW3</i>	2
<i>Myoviridae</i>		<i>Rsl2virus</i>	<i>Ralstonia virus RSL2</i>	2
<i>Myoviridae</i>		<i>Rslunavirus</i>	<i>Ralstonia virus RSL1</i>	1
<i>Myoviridae</i>		<i>Sep1virus</i>	<i>Staphylococcus virus SEP1</i>	2
<i>Myoviridae</i>		<i>Spn3virus</i>	<i>Salmonella virus SPN3US</i>	1
<i>Podoviridae</i>	<i>Autographivirinae</i>	<i>Fri1virus</i>	<i>Acinetobacter virus Fri1</i>	7
<i>Podoviridae</i>	<i>Autographivirinae</i>	<i>Kp32virus</i>	<i>Klebsiella virus KP32</i>	6
<i>Podoviridae</i>	<i>Autographivirinae</i>	<i>Pradovirus</i>	<i>Xylella virus Prado</i>	3
<i>Podoviridae</i>	<i>Picovirinae</i>	<i>Cp1virus</i>	<i>Streptococcus virus Cp1</i>	1
<i>Podoviridae</i>	<i>Sepvirinae</i>	<i>Nona33virus</i>	<i>Escherichia virus 933 W</i>	5
<i>Podoviridae</i>	<i>Sepvirinae</i>	<i>Pocjvirus</i>	<i>Shigella virus POCJ13</i>	2
<i>Podoviridae</i>	<i>Sepvirinae</i>	<i>TL2011virus</i>	<i>Escherichia virus TL2011</i>	4
<i>Podoviridae</i>		<i>Ea92virus</i>	<i>Erwinia virus Ea9-2</i>	2
<i>Podoviridae</i>		<i>Kf1virus</i>	<i>Edwardsiella virus KF1</i>	1
<i>Podoviridae</i>		<i>Kpp25virus</i>	<i>Pseudomonas virus KPP25</i>	2
<i>Podoviridae</i>		<i>Luz7virus</i>	<i>Pseudomonas virus LUZ7</i>	2
<i>Podoviridae</i>		<i>Prtbvirus</i>	<i>Brucella virus Pr</i>	2
<i>Podoviridae</i>		<i>Una961virus</i>	<i>Helicobacter virus 1961P</i>	3
<i>Siphoviridae</i>	<i>Arquatrovirinae</i>	<i>Camvirus</i>	<i>Streptomyces virus phiCam</i>	2
<i>Siphoviridae</i>	<i>Arquatrovirinae</i>	<i>Likavirus</i>	<i>Streptomyces virus Lika</i>	9
<i>Siphoviridae</i>	<i>Arquatrovirinae</i>	<i>R4virus</i>	<i>Streptomyces virus R4</i>	2
<i>Siphoviridae</i>	<i>Bclavirinae</i>	<i>Acadianvirus</i>	<i>Mycobacterium virus Acadian</i>	2 (3)
<i>Siphoviridae</i>	<i>Bclavirinae</i>	<i>Coopervirus</i>	<i>Mycobacterium virus Cooper</i>	5 (10)
<i>Siphoviridae</i>	<i>Bclavirinae</i>	<i>Pipefishvirus</i>	<i>Mycobacterium virus Pipefish</i>	1 (4)
<i>Siphoviridae</i>	<i>Bclavirinae</i>	<i>Rosebushvirus</i>	<i>Mycobacterium virus Rosebush</i>	1 (2)
<i>Siphoviridae</i>	<i>Mclavirinae</i>	<i>Bongovirus</i>	<i>Mycobacterium virus Bongo</i>	0 (1)
<i>Siphoviridae</i>	<i>Pclavirinae</i>	<i>Fishburnevirus</i>	<i>Mycobacterium virus Fishburne</i>	4 (5)
<i>Siphoviridae</i>	<i>Pclavirinae</i>	<i>Phayoncevirus</i>	<i>Mycobacterium virus Phayonce</i>	1

Table 1 continued

Family	Subfamily	New genus	Type species	Number of new species in genus (total number of species in genus)
<i>Siphoviridae</i>		<i>Ab18virus</i>	<i>Pseudomonas virus Ab18</i>	3
<i>Siphoviridae</i>		<i>Amigovirus</i>	<i>Arthrobacter virus Amigo</i>	1
<i>Siphoviridae</i>		<i>Bennievirus</i>	<i>Arthrobacter virus Bennie</i>	9
<i>Siphoviridae</i>		<i>Bernal13virus</i>	<i>Mycobacterium virus Bernal13</i>	1
<i>Siphoviridae</i>		<i>Cronusvirus</i>	<i>Rhodobacter virus RcCronus</i>	1
<i>Siphoviridae</i>		<i>Decurrovirus</i>	<i>Arthrobacter virus Decurro</i>	1
<i>Siphoviridae</i>		<i>Demosthenesvirus</i>	<i>Gordonia virus Demosthenes</i>	3
<i>Siphoviridae</i>		<i>Eiauvirus</i>	<i>Edwardsiella virus eiAU</i>	1
<i>Siphoviridae</i>		<i>Gaiavirus</i>	<i>Mycobacterium virus Gaia</i>	1
<i>Siphoviridae</i>		<i>Gilesvirus</i>	<i>Mycobacterium virus Giles</i>	1
<i>Siphoviridae</i>		<i>Gordonvirus</i>	<i>Arthrobacter virus Gordon</i>	2
<i>Siphoviridae</i>		<i>Gordtnkvirus</i>	<i>Gordonia virus GordTnk2</i>	1
<i>Siphoviridae</i>		<i>Harrisonvirus</i>	<i>Paenibacillus virus Harrison</i>	1
<i>Siphoviridae</i>		<i>Jenstvirus</i>	<i>Brevibacillus virus Jenst</i>	1
<i>Siphoviridae</i>		<i>Jwxvirus</i>	<i>Achromobacter virus JWX</i>	2
<i>Siphoviridae</i>		<i>Kelleziovirus</i>	<i>Arthrobacter virus Kellezio</i>	2
<i>Siphoviridae</i>		<i>Laroyevirus</i>	<i>Arthrobacter virus Laroye</i>	1
<i>Siphoviridae</i>		<i>Marvinvirus</i>	<i>Mycobacterium virus Marvin</i>	2
<i>Siphoviridae</i>		<i>Mudcatvirus</i>	<i>Arthrobacter virus Mudcat</i>	2
<i>Siphoviridae</i>		<i>Np1virus</i>	<i>Pseudomonas virus NP1</i>	2
<i>Siphoviridae</i>		<i>P12002virus</i>	<i>Polaribacter virus P12002L</i>	2
<i>Siphoviridae</i>		<i>P12024virus</i>	<i>Nonlabens virus P12024S</i>	2
<i>Siphoviridae</i>		<i>Pa6virus</i>	<i>Propionibacterium virus PA6</i>	57
<i>Siphoviridae</i>		<i>PaMx74virus</i>	<i>Pseudomonas virus PaMx74</i>	2
<i>Siphoviridae</i>		<i>Patiencevirus</i>	<i>Mycobacterium virus Patience</i>	0 (1)
<i>Siphoviridae</i>		<i>Pepy6virus</i>	<i>Rhodococcus virus Pepy6</i>	2
<i>Siphoviridae</i>		<i>Pis4avirus</i>	<i>Aeromonas virus pIS4A</i>	1
<i>Siphoviridae</i>		<i>Rdjlvirus</i>	<i>Roseobacter virus RDJL1</i>	2
<i>Siphoviridae</i>		<i>Rer2virus</i>	<i>Rhodococcus virus RER2</i>	1
<i>Siphoviridae</i>		<i>Send513virus</i>	<i>Mycobacterium virus Send513</i>	2
<i>Siphoviridae</i>		<i>Smoothievirus</i>	<i>Gordonia virus Smoothie</i>	4
<i>Siphoviridae</i>		<i>Soupsvirus</i>	<i>Gordonia virus Soups</i>	1
<i>Siphoviridae</i>		<i>Tankvirus</i>	<i>Arthrobacter virus Tank</i>	1
<i>Siphoviridae</i>		<i>Tin2virus</i>	<i>Tsukamurella virus TIN2</i>	3
<i>Siphoviridae</i>		<i>Titanvirus</i>	<i>Rhodobacter virus RcTitan</i>	2
<i>Siphoviridae</i>		<i>Vegasvirus</i>	<i>Paenibacillus virus Vegas</i>	1
<i>Siphoviridae</i>		<i>Vendettavirus</i>	<i>Gordonia virus Vendetta</i>	1
<i>Siphoviridae</i>		<i>Wildcatvirus</i>	<i>Mycobacterium virus Wildcat</i>	1
<i>Siphoviridae</i>		<i>Woesvirus</i>	<i>Gordonia virus Woes</i>	3
<i>Siphoviridae</i>		<i>Ydn12virus</i>	<i>Streptomyces virus YDN12</i>	2
<i>Tristromaviridae</i>		<i>Alphatristromavirus</i>	<i>Pyrobaculum filamentous virus I</i>	1 (2)

classified. Of particular note is a fundamental reorganization of the family *Inoviridae* by Petar Knezevic, Chair of the *Inoviridae* Study Group, who has rearranged the two existing genera (*Inovirus* and *Plectrovirus*), created five new genera and 17 new species,

reassigned 12 previously approved species, and deleted 29 species.

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Compliance with ethical standards

The views and conclusions contained in this document are those of the authors and should not be interpreted as necessarily representing the official policies, either expressed or implied, of the US Department of Health and Human Services or of the institutions and companies affiliated with the authors.

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

Ethical approval This article does not contain any studies with human participants or animals performed by any of the authors.

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