Taxonomy of prokaryotic viruses: 2017 update from the ICTV Bacterial and Archaeal Viruses Subcommittee.

Evelien M. Adriaenssens[1], Johannes Wittmann[2], Jens H. Kuhn[3], Dann Turner[4], Matthew B. Sullivan[5], Bas E. Dutilh[6,7], Ho Bin Jang[5], Leonardo J. van Zyl[8], Jochen Klumpp[9], Malgorzata Lobocka[10], Andrea I. Moreno Switt[11], Janis Rumnieks[12], Robert A. Edwards[13], Jumpei Uchiyama[14], Poliane Alfenas-Zerbini[15], Nicola K. Petty[16], Andrew M. Kropinski[17], Jakub Barylski[18], Annika Gillis[19], Martha R. C. Clokie[20], David Prangishvili[21], Rob Lavigne[22], Ramy Karam Aziz[23], Siobain Duffy[24], Mart Krupovic[21], Minna M. Poranen[25], Petar Knezevic[26], Francois Enault[27], Yigang Tong[28], Hanna M. Oksanen[25], J. Rodney Brister[29]

1 Institute of Integrative Biology, University of Liverpool, Liverpool L69 7ZB, United Kingdom. orcid.org/0000-0003-4826-5406

2 Leibniz-Institut DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, 38124 Braunschweig, Germany. orcid.org/0000-0002-7275-9927

3 Integrated Research Facility at Fort Detrick, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Fort Detrick, Frederick, MD 21702, USA. orcid.org/0000-0002-7800-6045

4 Faculty of Health and Applied Sciences (UWE Bristol), Frenchay Campus, Bristol, BS16 1QY, United Kingdom. orcid.org/0000-0002-0249-4513

5 Department of Microbiology, The Ohio State University, Columbus, OH 43210, USA. orcid.org/0000-0003-4040-9831

6 Theoretical Biology and Bioinformatics, Utrecht University, Utrecht, The Netherlands.

7 Centre for Molecular and Biomolecular Informatics, Radboud University Medical Centre, Nijmegen, The Netherlands. orcid.org/0000-0003-2329-7890

8 Institute for Microbial Biotechnology and Metagenomics (IMBM), Department of Biotechnology, University of the Western Cape, Bellville, Cape Town, 7535, South Africa. orcid.org/0000-0001-9364-8671

9 Institute of Food, Nutrition and Health, ETH Zurich, 8092, Zurich, Switzerland. orcid.org/0000-0003-3410-2702

10 Department of Microbial Biochemistry, Institute of Biochemistry and Biophysics of the Polish Academy of Sciences, 02-106 Warsaw, Poland. orcid.org/0000-0003-0679-5193

11 Faculty of Ecology and Natural Resources School, Universidad Andres Bello, 8370146 Santiago, Chile. Orcid.org/0000-0001-8231-9397

12 Latvian Biomedical Research and Study Center, Riga, LV-1067, Latvia.

13 Departments of Computer Science and Biology, San Diego State University, San Diego, CA, 92182, USA. orcid.org/0000-0001-8383-8949

14 School of Veterinary Medicine, Azabu University, Fuchinobe 1-7-71, Chuo-ku Sagamihara-shi, Kanagawa 252-0206, Japan. orcid.org/0000-0003-0846-0100

15 Laboratory of Industrial Microbiology, Instituto de Biotecnologia Aplicada à Agropecuária, Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil. orcid.org/0000-0002-8203-5244

16 The ithree institute, University of Technology Sydney, Sydney, NSW 2007, Australia. orchid,org/0000-0001-6528-9886

17 Departments of Food Science, and Pathobiology, University of Guelph, 50 Stone Rd E, Guelph, ON, N1G 2W1, Canada. Phage.Canada@gmail.com. orcid.org/0000-0002-6871-6799

18 Department of Molecular Virology, Institute of Experimental Biology, Adam Mickiewicz University, Poznan, Poland. orcid.org/0000-0001-6630-6932

19 Laboratory of Food and Environmental Microbiology, Université Catholique de Louvain, 1348, Louvain-la-Neuve, Belgium. orcid.org/0000-0002-6735-3359

20 Department of Infection, Immunity and Inflammation, University of Leicester, Leicester, LE1 9HN, United Kingdom. orcid.org/0000-0002-6069-8936

21 Unit of Molecular Biology of the Gene in Extremophiles, Department of Microbiology, Institut Pasteur, 75015, Paris, France. DP: orcid.org/0000-0002-0812-9699 ; MK: orcid.org/0000-0001-5486-0098

22 Laboratory of Gene Technology, KU Leuven, 3001, Leuven, Belgium. orcid.org/0000-0001-7377-1314

23 Department of Microbiology and Immunology, Faculty of Pharmacy, Cairo University, Qasr El-Ainy St., 11562 Cairo, Egypt. orcid.org/0000-0002-4448-7100

24 Department of Ecology, Evolution and Natural Resources, Rutgers University, New Brunswick, NJ, 08901, USA. orcid.org/0000-0003-0753-223X

25 Department of Biosciences, University of Helsinki, Helsinki, Finland. MMP: orcid.org/0000-0002-4775-3670; HMO: orcid.org/0000-0003-3047-8294

26 Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad, Novi Sad, Serbia. orcid.org/0000-0003-0353-3892

27 Université Clermont Auvergne, CNRS, LMGE, F-63000, Clermont-Ferrand, France. orcid.org/ 0000-0002-4968-3995

28 Beijing Institute of Microbiology and Epidemiology, State Key Laboratory of Pathogen and Biosecurity, Beijing, People's Republic of China. orcid.org/0000-0002-8503-8045

29 National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, MD, 20894, USA.

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 [5], the committee composition has changed, and a large number of taxonomic proposals (TaxoProps) were submitted to the ICTV Executive Committee (EC) for approval.

1. Changes in subcommittee membership. During the past year we have lost two members. Dr. Hans-Wolfgang Ackermann, a life member of the ICTV, the father of caudovirus taxonomy [1] and an electron microscopist extraordinaire [2-4], lamentably died and will be gravely missed. In addition, Dr. Jens H. Kuhn, who, in spite of protestations about not being a genuine phage biologist, proved invaluable to our discussions and preparation of TaxoProps and manuscripts, resigned from the Subcommittee. Both Hans and Jens are acknowledged for their significant contributions to prokaryotic virus taxonomy. Furthermore, a number of current members have new responsibilities; and, in an effort to increase the geographical diversity of members, we appointed representatives from South America, Africa, and Asia (Table 1).

Table 1. List of current subcommittee members who have new responsibilities (*), along with new members of the subcommittee.

Name	Country	Position
Evelien Adriaenssens*	United Kingdom	Chair, *Caudovirales* phage study group
Dann Turner	United Kingdom	Chair, *Acinetobacter* phage study group
Jakub Barylski*	Republic of Poland	Chair, *Bacillus* phage study group
Jochen Klumpp*	Swiss Confederation	Chair, *Listeria* phage study group
Małgorzata Łobocka	Republic of Poland	Chair, *Staphylococcus* phage study group
Poliane Alfenas-Zerbini	Brazil	Member
Ramy Aziz	Arab Republic of Egypt	Member
Andrea Moreno Switt	Republic of Chile	Member
Yigang Tong	People's Republic of China	Member
Leonardo van Zyl	Republic of South Africa	Member
Jumpei Uchiyama	Japan	Member
Nicola K. Petty	Australia	Member

2. Changing the names of prokaryotic virus genera. A significant number of prokaryotic virus genera have either unpronounceable names (e.g., *Pocjvirus*, *Rdjlvirus*) or incorporated numerals (e.g., *T4virus*, *D3112virus*). In the first case, these names contravene The International Code of Virus Classification and Nomenclature (ICVCN, April 2017) Rule 3.12, which states “Names for taxa shall be easy to use and easy to remember. Euphonious names are preferred.” In the latter case, pronunciation is a problem. For example, is *D3112virus* pronounced “Dee+three thousand one hundred and twelve+virus” or “Dee+thirty one+twelve+virus” or “Dee+three+one+one+two+virus”? In addition, this nomenclature differs drastically from that for other virus taxa; and, would be incompatible with a Linnaean system of nomenclature [13]. We identified all prokaryotic taxon names that are problematic in the ICTV Master Species List (https://talk.ictvonline.org/files/master-species-lists/m/msl/6776) and suggested alternative names (Supplementary data file S1). These changes will be proposed officially at the next meeting of the ICTV EC in 2018.

3. Re-evaluation of the SPO1-like virus taxonomy. Over the past two years, members of the subcommittee have re-evaluated the taxonomy of a subset of myoviruses related to *Bacillus* phage SPO1. This group, made up of members of the subfamily *Spounavirinae* [10] and several genera of *Bacillus*-infecting viruses, was represented as a distinct module in various network analyses published recently [8, 9]. Using a combination of genomic, proteomics, and phylogenetic approaches, we have shown that this group of phages represents a new family, comprising five subfamilies and 13 genera [7]. We therefore suggest that these viruses be moved from their current taxonomic position in the family *Myoviridae* to a new family included in the order *Caudovirales*.

4. New taxa. Table 2 lists of all new taxa proposed at the ICTV EC49 meeting in Singapore in 2017. In total, two new families, eight new subfamilies, 34 new genera, and 91 new species were proposed. Two significant items are on this list. The first item is the introduction of two new families of prokaryotic viruses: *Ackermannviridae* and *Portogloboviridae*. With the acceptance of changes to ICVCN Rule 3.11, the second item is the application of the names of eminent phage scientists, specifically Hans-Wolfgang Ackermann (Université Laval) and Charles Shelton McCleskey (Louisiana State University) as prefixes for taxon name stems.

Table 2. Taxonomy proposals (TaxoProps) proposing new taxa (families, subfamilies, genera, species) submitted to the ICTV Executive Committee in 2017

Family	Subfamily	Genus	Type species	No. of species in genus***
Ackermannviridae	*Aglimvirinae*	*Ag3virus*	*Shigella virus AG3*	1 (2)
Ackermannviridae	*Aglimvirinae*	*Limestonevirus*	*Dickeya virus Limestone*	1 (2)
Ackermannviridae	*Cvivirinae*	*Cba120virus*	*Escherichia virus CBA120*	4 (9)
Ackermannviridae	*Cvivirinae*	*Vi1virus**	*Salmonella virus ViI*	(5)
Ackermannviridae	unassigned	unassigned	*Erwinia virus Ea2809, Serratia virus MAM1, Serratia virus IME250, Klebsiella virus 0507KN21*	4
*Myoviridae**		*Arvunavirus*	*Arthrobacter virus ArV1*	2
*Myoviridae**		*Eah2virus*	*Erwinia virus EaH2*	2
*Myoviridae**		*Machinavirus*	*Erwinia virus Machina*	1
*Myoviridae**		*Ntreusvirus*	*Salmonella virus SPN3US*	1
*Myoviridae**		*Svunavirus*	*Geobacillus virus GBSV1*	2
*Myoviridae**	*Ampvirinae*	*Chippewavirus*	*Arthrobacter virus BarretLemon*	1
*Myoviridae**	*Ampvirinae*	*Jawnskivirus*	*Arthrobacter virus Jawnski*	2
*Myoviridae**	*Ampvirinae*	*Sonnyvirus*	*Arthrobacter virus Sonny*	3
*Podoviridae**		*Dfl12virus*	*Dinoroseobacter virus DFL12phi1*	1
*Podoviridae**		*Jwalphavirus*	*Achromobacter virus*	2

			JWAlpha	
*Podoviridae**		*P22virus**	*Salmonella virus P22*	1 (5)
*Podoviridae**		*Sp58virus*	*Salmonella virus SP058*	3
Portogloboviridae		*Alphaportoglobovirus*	*Sulfolobus alphaportoglobovirus 1*	1
*Siphoviridae**		*Anatolevirus*	*Propionibacterium virus Anatole*	2
*Siphoviridae**		*Attisvirus*	*Gordonia virus Attis*	1
*Siphoviridae**		*Doucettevirus*	*Propionibacterium virus Doucette*	4
*Siphoviridae**		*Hk97virus*	*Escherichia virus HK97**	9 (11)
*Siphoviridae**		*Lambdavirus**	*Escherichia virus Lambda*	3 (4)
*Siphoviridae**		*Pfr1virus*	*Propionibacterium virus PFR1*	1
*Siphoviridae**		*Tp84virus*	*Geobacillus virus TP84*	1
*Siphoviridae**		*Trigintaduovirus*	*Mycobacterium virus 32HC*	1
*Siphoviridae**		*Wizardvirus*	*Gordonia virus Wizard*	2
*Siphoviridae**	*Chebruvirinae*	*Brujitavirus*	*Mycobacterium virus Brujita*	(2)
*Siphoviridae**	*Chebruvirinae*	*Che9cvirus**	*Mycobacterium virus Che9c*	1 (2)
*Siphoviridae**	*Dclasvirinae*	*Hawkeyevirus*	*Mycobacterium virus Hawkeye*	1
*Siphoviridae**	*Dclasvirinae*	*Plotvirus*	*Mycobacterium virus PLot*	1
*Siphoviridae**	*Mccleskeyvirinae*	*Lmd1virus*	*Leuconostoc virus Lmd1*	6
*Siphoviridae**	*Mccleskeyvirinae*	*Una4virus*	*Leuconostoc virus 1A4*	6
*Siphoviridae**	*Nclasvirinae*	*Buttersvirus*	*Mycobacterium virus Butters*	2
*Siphoviridae**	*Nclasvirinae*	*Charlievirus*	*Mycobacterium virus Charlie*	2 (3)
*Siphoviridae**	*Nclasvirinae*	*Redivirus*	*Mycobacterium virus Redi*	3 (4)
*Siphoviridae**	*Nymbaxtervirinae*	*Baxtervirus*	*Gordonia virus BaxterFox*	2
*Siphoviridae**	*Nymbaxtervirinae*	*Nymphadoravirus*	*Gordonia virus Nymphadora*	3
*Cystoviridae**		*Cystovirus**	*Pseudomonas virus phi6*	6 (7)
*Tectiviridae**		*Alphatectivirus***	*Pseudomonas virus*	1 (2)

			PRD1	
*Tectiviridae**		*Betatectivirus*	*Bacillus virus Bam35*	2 (4)

* taxon established, ** previously known as *Tectivirus,* *** Number in parenthesis indicates the total number of viral species in this genus.

5. Updates to taxonomy. As the readership may be aware, “Virus Taxonomy: The Classification and Nomenclature of Viruses - The Online (10th) Report of the ICTV” is freely accessible at http://ictv.global/report. We would like to acknowledge the hard work of Hanna M. Oksanen (*Corticoviridae*), Dennis H. Bamford (*Pleolipoviridae*), and Minna M. Poranen (*Cystoviridae*) for completing updates to their sections. The family *Pleolipoviridae* is now recognized as the first virus taxon in the newly established ICTV category for ssDNA/dsDNA Viruses. The summaries of the ICTV Report chapters are published in The Journal of General Virology [6, 11, 12].

Notes

Supplementary Table S1. Proposed new names for bacteriophage taxa which contravene ICVCN Rule 3.12 or contain numerals.

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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

The authors did not perform any studies with human participants or animals in this article.

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