



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

Evelien M. Adriaenssens¹ · Johannes Wittmann² · Jens H. Kuhn³ · Dann Turner⁴ · Matthew B. Sullivan⁵ · Bas E. Dutilh^{6,7} · Ho Bin Jang⁵ · Leonardo J. van Zyl⁸ · Jochen Klumpp⁹ · Malgorzata Lobočka¹⁰ · Andrea I. Moreno Switt¹¹ · Janis Rumnieks¹² · Robert A. Edwards¹³ · Jumpei Uchiyama¹⁴ · Poliane Alfenas-Zerbini¹⁵ · Nicola K. Petty¹⁶ · Andrew M. Kropinski¹⁷ · Jakub Barylski¹⁸ · Annika Gillis¹⁹ · Martha R. C. Clokie²⁰ · David Prangishvili²¹ · Rob Lavigne²² · Ramy Karam Aziz²³ · Siobain Duffy²⁴ · Mart Krupovic²¹ · Minna M. Poranen²⁵ · Petar Knezevic²⁶ · Francois Enault²⁷ · Yigang Tong²⁸ · Hanna M. Oksanen²⁵ · J. Rodney Brister²⁹

Received: 1 December 2017 / Accepted: 15 January 2018 / Published online: 22 January 2018
© Springer-Verlag GmbH Austria, part of Springer Nature 2018

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

Handling Editor: Sead Sabanadzovic.

Electronic supplementary material The online version of this article (<https://doi.org/10.1007/s00705-018-3723-z>) contains supplementary material, which is available to authorized users.

✉ Andrew M. Kropinski
Phage.Canada@gmail.com

¹ Institute of Integrative Biology, University of Liverpool, Liverpool L69 7ZB, United Kingdom

² Leibniz-Institut DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, 38124 Braunschweig, Germany

³ Integrated Research Facility at Fort Detrick, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Fort Detrick, Frederick, MD 21702, USA

⁴ Faculty of Health and Applied Sciences, UWE Bristol, Frenchay Campus, Bristol BS16 1QY, United Kingdom

⁵ Department of Microbiology, The Ohio State University, Columbus, OH 43210, USA

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

⁷ Centre for Molecular and Biomolecular Informatics, Radboud University Medical Centre, Nijmegen, The Netherlands

⁸ Department of Biotechnology, Institute for Microbial Biotechnology and Metagenomics (IMBM), University of the Western Cape, Bellville, Cape Town, 7535, South Africa

⁹ Institute of Food, Nutrition and Health, ETH Zurich, 8092 Zurich, Switzerland

¹⁰ Department of Microbial Biochemistry, Institute of Biochemistry and Biophysics of the Polish Academy of Sciences, 02-106, Warsaw, Poland

¹¹ Faculty of Ecology and Natural Resources School, Universidad Andres Bello, 8370146 Santiago, Chile

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

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

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).

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

¹⁴ School of Veterinary Medicine, Azabu University, Fuchinobe 1-7-71, Chuo-ku Sagamihara-shi, Kanagawa 252-0206, Japan

¹⁵ Laboratory of Industrial Microbiology, Instituto de Biotecnologia Aplicada à Agropecuária, Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil

¹⁶ The ithree institute, University of Technology Sydney, Sydney, NSW 2007, Australia

¹⁷ Departments of Food Science, and Pathobiology, University of Guelph, 50 Stone Rd E, Guelph, ON N1G 2W1, Canada

¹⁸ Department of Molecular Virology, Institute of Experimental Biology, Adam Mickiewicz University, Poznan, Poland

¹⁹ Laboratory of Food and Environmental Microbiology, Université Catholique de Louvain, 1348 Louvain-la-Neuve, Belgium

²⁰ Department of Infection, Immunity and Inflammation, University of Leicester, Leicester LE1 9HN, United Kingdom

²¹ Unit of Molecular Biology of the Gene in Extremophiles, Department of Microbiology, Institut Pasteur, 75015 Paris, France

²² Laboratory of Gene Technology, KU Leuven, 3001 Leuven, Belgium

²³ Department of Microbiology and Immunology, Faculty of Pharmacy, Cairo University, Qasr El-Ainy St, 11562 Cairo, Egypt

²⁴ Department of Ecology, Evolution and Natural Resources, Rutgers University, New Brunswick, NJ 08901, USA

²⁵ Department of Biosciences, University of Helsinki, Helsinki, Finland

²⁶ Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad, Novi Sad, Serbia

²⁷ Université Clermont Auvergne, CNRS, LMGE, 63000 Clermont-Ferrand, France

²⁸ Beijing Institute of Microbiology and Epidemiology, State Key Laboratory of Pathogen and Biosecurity, Beijing, People's Republic of China

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

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***
<i>Ackermannviridae</i>	<i>Aglimvirinae</i>	<i>Ag3virus</i>	<i>Shigella virus AG3</i>	1 (2)
<i>Ackermannviridae</i>	<i>Aglimvirinae</i>	<i>Limestonevirus</i>	<i>Dickeya virus Limestone</i>	1 (2)
<i>Ackermannviridae</i>	<i>Cvivirusinae</i>	<i>Cba120virus</i>	<i>Escherichia virus CBA120</i>	4 (9)
<i>Ackermannviridae</i>	<i>Cvivirusinae</i>	<i>Vi1virus*</i>	<i>Salmonella virus Vi1</i>	(5)
<i>Ackermannviridae</i>	unassigned	unassigned	<i>Erwinia virus Ea2809, Serratia virus MAM1, Serratia virus IME250, Klebsiella virus 0507KN21</i>	4
<i>Myoviridae*</i>		<i>Arvunavirus</i>	<i>Arthrobacter virus ArV1</i>	2
<i>Myoviridae*</i>		<i>Eah2virus</i>	<i>Erwinia virus Eah2</i>	2
<i>Myoviridae*</i>		<i>Machinavirus</i>	<i>Erwinia virus Machina</i>	1
<i>Myoviridae*</i>		<i>Ntreusvirus</i>	<i>Salmonella virus SPN3US</i>	1
<i>Myoviridae*</i>		<i>Svunavirus</i>	<i>Geobacillus virus GBSV1</i>	2
<i>Myoviridae*</i>	<i>Ampvirinae</i>	<i>Chippewavirus</i>	<i>Arthrobacter virus BarretLemon</i>	1
<i>Myoviridae*</i>	<i>Ampvirinae</i>	<i>Jawnskivirus</i>	<i>Arthrobacter virus Jawnski</i>	2
<i>Myoviridae*</i>	<i>Ampvirinae</i>	<i>Sonnyvirus</i>	<i>Arthrobacter virus Sonny</i>	3
<i>Podoviridae*</i>		<i>Dfl12virus</i>	<i>Dinoroseobacter virus DFL12phi1</i>	1
<i>Podoviridae*</i>		<i>Jwalphavirus</i>	<i>Achromobacter virus JWAAlpha</i>	2
<i>Podoviridae*</i>		<i>P22virus*</i>	<i>Salmonella virus P22</i>	1 (5)
<i>Podoviridae*</i>		<i>Sp58virus</i>	<i>Salmonella virus SP058</i>	3
<i>Portogloboviridae</i>		<i>Alphaportoglobovirus</i>	<i>Sulfolobus alphaportoglobovirus 1</i>	1
<i>Siphoviridae*</i>		<i>Anatolevirus</i>	<i>Propionibacterium virus Anatole</i>	2
<i>Siphoviridae*</i>		<i>Attisvirus</i>	<i>Gordonia virus Attis</i>	1
<i>Siphoviridae*</i>		<i>Doucettevirus</i>	<i>Propionibacterium virus Doucette</i>	4
<i>Siphoviridae*</i>		<i>Hk97virus</i>	<i>Escherichia virus HK97*</i>	9 (11)
<i>Siphoviridae*</i>		<i>Lambdavirus*</i>	<i>Escherichia virus Lambda</i>	3 (4)
<i>Siphoviridae*</i>		<i>Pfr1virus</i>	<i>Propionibacterium virus PFR1</i>	1
<i>Siphoviridae*</i>		<i>Tp84virus</i>	<i>Geobacillus virus TP84</i>	1
<i>Siphoviridae*</i>		<i>Trigintaduovirus</i>	<i>Mycobacterium virus 32HC</i>	1
<i>Siphoviridae*</i>		<i>Wizardvirus</i>	<i>Gordonia virus Wizard</i>	2
<i>Siphoviridae*</i>	<i>Chebruvirinae</i>	<i>Brujita virus</i>	<i>Mycobacterium virus Brujita</i>	(2)
<i>Siphoviridae*</i>	<i>Chebruvirinae</i>	<i>Che9cvirus*</i>	<i>Mycobacterium virus Che9c</i>	1 (2)
<i>Siphoviridae*</i>	<i>Dclasvirinae</i>	<i>Hawkeyevirus</i>	<i>Mycobacterium virus Hawkeye</i>	1
<i>Siphoviridae*</i>	<i>Dclasvirinae</i>	<i>Plotvirus</i>	<i>Mycobacterium virus PLOT</i>	1
<i>Siphoviridae*</i>	<i>Mccleskeyvirinae</i>	<i>Lmd1 virus</i>	<i>Leuconostoc virus Lmd1</i>	6
<i>Siphoviridae*</i>	<i>Mccleskeyvirinae</i>	<i>Una4virus</i>	<i>Leuconostoc virus IA4</i>	6
<i>Siphoviridae*</i>	<i>Nclasvirinae</i>	<i>Buttersvirus</i>	<i>Mycobacterium virus Butters</i>	2
<i>Siphoviridae*</i>	<i>Nclasvirinae</i>	<i>Charlievirus</i>	<i>Mycobacterium virus Charlie</i>	2 (3)
<i>Siphoviridae*</i>	<i>Nclasvirinae</i>	<i>Redivirus</i>	<i>Mycobacterium virus Redi</i>	3 (4)
<i>Siphoviridae*</i>	<i>Nymbaxtervirinae</i>	<i>Baxtervirus</i>	<i>Gordonia virus BaxterFox</i>	2
<i>Siphoviridae*</i>	<i>Nymbaxtervirinae</i>	<i>Nymphadoravirus</i>	<i>Gordonia virus Nymphadora</i>	3
<i>Cystoviridae*</i>		<i>Cystovirus*</i>	<i>Pseudomonas virus phi6</i>	6 (7)
<i>Tectiviridae*</i>		<i>Alphatectivirus**</i>	<i>Pseudomonas virus PRD1</i>	1 (2)
<i>Tectiviridae*</i>		<i>Betatectivirus</i>	<i>Bacillus virus Bam35</i>	2 (4)

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

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.

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].

Acknowledgements The committee would like to thank Dr. Graham Hatfull (University of Pittsburgh) for permitting us to use Actinobacteriophage Database electron micrographs in 2017’s taxonomy proposals. The authors thank Laura Bollinger (National Institutes of Health/National Institute of Allergy and Infectious Diseases, Integrated Research Facility at Fort Detrick, Frederick, MD, USA) for editing this paper.

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.

Funding This work was funded in part through Battelle Memorial Institute’s prime contract with the US National Institute of Allergy and Infectious Diseases (NIAID) under Contract No. HHSN272200700016I (J.H.K.). B.E.D. was supported by the Netherlands Organization for Scientific Research (NWO), Vidi Grant 864.14.004. R.A.E was supported by grant MCB-1330800 from the National Science Foundation. J.R.B. was supported by the Intramural Research Program of the National Institutes of Health, National Library of Medicine. R.L. is a member of the phagebiotics research community, supported by

FWO Vlaanderen. M.M.P. was supported by the Academy of Finland (272507). A.G. was supported by the National Fund for Scientific Research (FNRS). H.M.O. was supported by University of Helsinki funding for Instruct-F1 research infrastructure.

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.

References

- Ackermann H-W (1998) Tailed bacteriophages: the order *Caudovirales*. *Adv Virus Res* 51:135–201
- Ackermann H-W (2007) 5500 Phages examined in the electron microscope. *Arch Virol* 152:227–243
- Ackermann HW (2012) Life in science: Hans-W. Ackermann. *Bacteriophage* 2:207
- Ackermann HW, Prangishvili D (2012) Prokaryote viruses studied by electron microscopy. *Arch Virol* 157:1843–1849
- Adriaenssens EM, Krupovic M, Knezevic P, Ackermann HW, Barylski J, Brister JR, Clokie MR, Duffy S, Dutilh BE, Edwards RA, Enault F, Jang HB, Klumpp J, Kropinski AM, Lavigne R, Poranen MM, Prangishvili D, Rumnieks J, Sullivan MB, Wittmann J, Oksanen HM, Gillis A, Kuhn JH (2017) Taxonomy of prokaryotic viruses: 2016 update from the ICTV bacterial and archaeal viruses subcommittee. *Arch Virol* 162:1153–1157
- Bamford DH, Pietila MK, Roine E, Atanasova NS, Dienstbier A, Oksanen HM, Ictv Report C (2017) ICTV Virus Taxonomy Profile: *Pleolipoviridae*. *J Gen Virol*. <https://doi.org/10.1099/jgv.0.000972> (Epub ahead of print)
- Barylski J, Enault F, Dutilh BE, Schuller MBP, Edwards RA, Gillis A, Klumpp J, Knezevic P, Krupovic M, Kuhn JH, Lavigne R, Oksanen HM, Sullivan MB, Wittmann J, Tolstoy I, Brister JR, Kropinski AM, Adriaenssens EM (2017) Genomic, proteomic, and phylogenetic analysis of spounaviruses indicates paraphyly of the order *Caudovirales*. bioRxiv preprint: <http://biorxiv.org/content/early/2017/11/16/220434.abstract>
- Bolduc B, Jang HB, Doucier G, You ZQ, Roux S, Sullivan MB (2017) vConTACT: an iVirus tool to classify double-stranded DNA viruses that infect Archaea and Bacteria. *PeerJ* 5:e3243
- Iranzo J, Krupovic M, Koonin EV (2016) The double-stranded DNA virosphere as a modular hierarchical network of gene sharing. *MBio* 7:e00978-16
- Klumpp J, Lavigne R, Loessner MJ, Ackermann HW (2010) The SPO1-related bacteriophages. *Arch Virol* 155:1547–1561
- Oksanen HM, Ictv Report C (2017) ICTV Virus Taxonomy Profile: *Corticoviridae*. *J Gen Virol* 98:888–889
- Poranen MM, Mantynen S, Ictv Report C (2017) ICTV virus taxonomy profile: *Cystoviridae*. *J Gen Virol* 98:2423–2424
- Postler TS, Clawson AN, Amarasinghe GK, Basler CF, Bavari S, Benko M, Blasdel KR, Briese T, Buchmeier MJ, Bukreyev A, Calisher CH, Chandran K, Charrel R, Clegg CS, Collins PL, Juan Carlos T, Derisi JL, Dietzgen RG, Dolnik O, Durrwald R, Dye JM, Easton AJ, Emonet S, Formenty P, Fouchier RAM, Ghedin E, Gonzalez JP, Harrach B, Hewson R, Horie M, Jiang D, Koberling G, Kondo H, Kropinski AM, Krupovic M, Kurath G, Lamb RA, Leroy EM, Lukashevich IS, Maisner A, Mushegian AR, Netesov SV, Nowotny N, Patterson JL, Payne SL, PaWeska JT,

Peters CJ, Radoshitzky SR, Rima BK, Romanowski V, Rubbenstroth D, Sabanadzovic S, Sanfacon H, Salvato MS, Schwemmler M, Smither SJ, Stenglein MD, Stone DM, Takada A, Tesh RB, Tomonaga K, Tordo N, Towner JS, Vasilakis N, Volchkov VE,

Wahl-Jensen V, Walker PJ, Wang LF, Varsani A, Whitfield AE, Zerbini FM, Kuhn JH (2017) Possibility and challenges of conversion of current virus species names to Linnaean binomials. *Syst Biol* 66:463–473