

24 University, Utrecht, The Netherlands; ¹⁰Centre for Molecular and Biomolecular
25 Informatics, Radboud University Medical Centre, Nijmegen, The Netherlands;
26 ¹¹Departments of Computer Science and Biology, San Diego State University, San Diego,
27 CA 92182, USA; ¹²Laboratoire Microorganismes: Génome et Environnement, Clermont
28 Université, Université Blaise Pascal, Clermont-Ferrand, France; ¹³CNRS UMR 6023,
29 LMGE, Aubière, France; ¹⁴Department of Microbiology, The Ohio State University,
30 Columbus OH, 43210, USA; ¹⁵Institute of Food, Nutrition and Health, ETH Zurich, 8092
31 Zurich, Switzerland; ¹⁶Departments of Food Science, Molecular and Cellular Biology,
32 and Pathobiology, University of Guelph, Guelph, ON, N1G 2W1, Canada; ¹⁷Laboratory
33 of Gene Technology, KU Leuven, 3001 Leuven, Belgium; ¹⁸Department of Biosciences,
34 University of Helsinki, Helsinki, Finland; ¹⁹Latvian Biomedical Research and Study
35 Center, Riga, LV, 1067, Latvia; ²⁰Department of Food Science, University of
36 Copenhagen, 1958 Frederiksberg C, Denmark; ²¹Leibniz-Institut DSMZ-Deutsche
37 Sammlung von Mikroorganismen und Zellkulturen GmbH, 38124 Braunschweig,
38 Germany; ²² [Institute of Biotechnology](#), University of Helsinki, Helsinki, Finland;
39 ²³Laboratory of Food and Environmental Microbiology, Université catholique de
40 Louvain, 1348 Louvain-la-Neuve, Belgium; ²⁴Integrated Research Facility at Fort
41 Detrick, National Institute of Allergy and Infectious Diseases, National Institutes of
42 Health, Fort Detrick, Frederick, MD, 21702, USA

43

44 **ORCID**

45 Evelien M. Adriaenssens orcid.org/0000-0003-4826-5406

46 Bas E. Dutilh orcid.org/0000-0003-2329-7890

47 Rob Edwards orcid.org/0000-0001-8383-8949
48 Annika Gillis orcid.org/0000-0002-6735-3359
49 Andrew M. Kropinski orcid.org/0000-0002-6871-6799
50 Mart Krupovic orcid.org/0000-0001-5486-0098
51 Jens H. Kuhn orcid.org/0000-0002-7800-6045
52 Rob Lavigne orcid.org/0000-0001-7377-1314
53 Johannes Wittmann orcid.org/0000-0002-7275-9927

54

55 *Corresponding author: AMK: Departments of Food Science, Molecular and Cellular
56 Biology, and Pathobiology, University of Guelph, 50 Stone Rd E, Guelph, ON, N1G
57 2W1, Canada; Phone: +1 519-824-4120 x54519; Email: Phage.Canada@gmail.com

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61 The prokaryotic virus community is represented at the International Committee on
62 Taxonomy of Viruses (ICTV) by the Bacterial and Archaeal Viruses Subcommittee.
63 Since our last report [13], the committee composition has changed, and a large number of
64 taxonomic proposals (TaxoProps) were submitted to the ICTV Executive Committee
65 (EC) for approval.

66

67 1. **New appointments.** The committee has been enlarged through the additions of
68 Drs. J. Rodney Brister (Chair—Molecular Typing), Ho Bin Jang (Member), Petar
69 Knezevic (Chair—ICTV *Inoviridae* Study Group), Hanna M. Oksanen (Chair—
70 ICTV *Corticoviridae* Study Group), and Minna M. Poranen (Chair—ICTV
71 *Cystoviridae* Study Group). In addition, Dr. Mart Krupovic has taken over the
72 Chairmanship of the ICTV *Plasmaviridae* Study Group.

73

74 2. **Future of the order *Caudovirales*.** With dramatic increase in the number of
75 characterized tailed bacterial and archaeal viruses, it is becoming increasingly
76 clear that the order *Caudovirales* (and the three included families *Myoviridae*,
77 *Siphoviridae* and *Podoviridae*) can no longer sustain the huge genetic diversity
78 within this virus group [6] and has to be adequately reorganized. Indeed,
79 taxonomic hurdles with this and some other expansive groups of viruses,
80 prompted ICTV to explore the possibility of introducing additional taxonomic
81 levels. Initial ideas and plans were presented to the microbial viruses community
82 at the 2016 EMBO conference “Viruses of Microbes IV” (Liverpool, UK).
83 Currently, the Bacterial and Archaeal Viruses Subcommittee is examining the

84 consistency of the order *Caudovirales* on the example of a diverse group of
85 phages currently classified in the subfamily *Spounavirinae* [2,8,9,11,15]. We
86 applied a range of complementary DNA and protein sequence analysis tools as
87 well as phylogenetic methods to the analysis of 93 *Bacillus*, *Enterococcus*,
88 *Listeria*, and *Staphylococcus* phages with large genomes (\approx 110–160 kb). A
89 manuscript describing our findings is in preparation and the appropriate
90 TaxoProps will be submitted.

91 **3. Taxonomy of prokaryotic viruses found in GenBank.** Genomes of prokaryotic
92 viruses are accumulating in public sequence databases, such as GenBank, at an
93 increasing rate. Oftentimes, these genomes are being deposited without or with
94 only minimal taxonomy descriptions. To appropriately classify these viruses, the
95 Subcommittee adopted a holistic approach with the first line discriminator being
96 DNA sequence identity (calculated using NCBI BLASTN [3, 12] or Gegenees
97 BLASTN [1]) of the genome in question to those of previously classified viruses.
98 Next, overall protein identity was calculated using Gegenees TBLASTX for large
99 datasets and CoreGenes 3.5 [14] for smaller sets. Lastly, phylogenetic analyses of
100 one to three conserved phage proteins, often including the large subunit of the
101 terminase and major capsid proteins or DNA replication-associated proteins, were
102 carried out using maximum likelihood method as implemented at Phylogeny.fr
103 [5]. The changes described here were formalized and submitted in more than 80
104 ICTV TaxoProps for consideration by the ICTV EC (<http://www.ictvonline.org>).
105 One new archaeal virus family (*Tristromaviridae*), six new bacteriophage
106 subfamilies (*Ounavirinae* [*Salmonella* phage FelixO1], *Sepvirinae* [*Escherichia*

107 phage 933W], *Arquatrovirinae* [*Streptomyces* phage R4], *Bclasvirinae*
108 [*Mycobacterium* phage Acadian], *Mclasvirinae* [*Mycobacterium* phage Pipefish]
109 and *Pclasvirinae* [*Mycobacterium* phage Fishburne]), and 88 new genera
110 including 249 species are covered in these proposals (Table 1). These proposals
111 were submitted to the ICTV EC in 2016 for approval. In addition, another 70
112 phages and one archaeal virus belonging to existing genera were classified. Of
113 particular note is a fundamental reorganization of the *Inoviridae* by Petar
114 Knezevic, Chair of the *Inoviridae* Study Group, who has rearranged the two
115 existing genera (*Inovirus* and *Plectovirus*); created five new genera and 17 new
116 species; reassigned 12 previously approved species; and deleted 29 species.

117 Table 1. Taxonomy proposals (TaxoProps) describing new taxa (families, subfamilies, genera) submitted to the ICTV Executive
 118 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 ArVI</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 SEPI</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 933W</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>Bclasvirinae</i>	<i>Acadianvirus</i>	<i>Mycobacterium virus Acadian</i>	2 (3)

<i>Siphoviridae</i>	<i>Bclasvirinae</i>	<i>Coopervirus</i>	<i>Mycobacterium virus Cooper</i>	5 (10)
<i>Siphoviridae</i>	<i>Bclasvirinae</i>	<i>Pipefishvirus</i>	<i>Mycobacterium virus Pipefish</i>	1 (4)
<i>Siphoviridae</i>	<i>Bclasvirinae</i>	<i>Rosebushvirus</i>	<i>Mycobacterium virus Rosebush</i>	1 (2)
<i>Siphoviridae</i>	<i>Mclasvirinae</i>	<i>Bongovirus</i>	<i>Mycobacterium virus Bongo</i>	0 (1)
<i>Siphoviridae</i>	<i>Pclasvirinae</i>	<i>Fishburnevirus</i>	<i>Mycobacterium virus Fishburne</i>	4 (5)
<i>Siphoviridae</i>	<i>Pclasvirinae</i>	<i>Phayoncevirus</i>	<i>Mycobacterium virus Phayonce</i>	1
<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>Kelleziavirus</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>PI2002virus</i>	<i>Polaribacter virus PI2002L</i>	2
<i>Siphoviridae</i>		<i>PI2024virus</i>	<i>Nonlabens virus PI2024S</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 1</i>	1 (2)

119 **COMPLIANCE WITH ETHICAL STANDARDS**

120 The views and conclusions contained in this document are those of the authors and
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139 **Conflict of interest**

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

141 **Ethical approval**

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