The Taxonomy of Bacterial & Archaeal Viruses: An Update from the International Committee on Taxonomy of Viruses

Rob Lavigne**, Takashi Yamada, Johannes Wittmann, Finn K. Vogensen, Mathew B. Sullivan, Janis Rumnieks, David Prangishvili, Jens H. Kuhn, Mart Krupovic, Andrew M. Kropinski*, Jochen Klumpp, Annika Gillis, Francois Enault, Rob A. Edwards, Bas E. Dutilh, Siobain Duffy, Martha R.C. Clokie, Jakub Barylski, Hans-Wolfgang Ackermann, Evelien M. Adriaenssens**

* Submitting author: Departments of Food Science, Molecular and Cellular Biology, and Pathobiology, University of Guelph, Guelph, Ontario, Canada.

** Presenting authors

INTRODUCTION

Over the last several years the Bacterial and Archaeal Viruses Subcommittee (BAVS; http://www.ictv.global/subcommittee.asp?se=5&committee=56) of the International Committee on Taxonomy of Viruses (ICTV) has made significant progress in classifying phages into taxa. The work of Adriaenssens et al [1] on the *Siphoviridae* resulted in the creation of 39 new genera, comprising 216 phage species, and added 62 species to two previously defined genera (*Phic3unalikevirus*; *L5likevirus*). These proposals have been accepted by ICTV and can be viewed at http://www.ictv.global/virusTaxonomy.asp. Below we have summarized the achievements during the last year:

ITEM 1 - Voted to eliminate the infill "*like*" from the genus taxon name.

Comment: The naming of phage taxa has been an evolving process with genera name changing from "P22-like virus" which was always considered to be a stop-gap measure, to *P22likevirus*. The latter convention is problematic since it was only applied to members of the Caudovirales, and the like was unnecessary since all genera contain species which are alike. It is important to realize that "viruses are real physical entities produced by biological evolution and genetics, whereas virus species and higher taxa are abstract concepts produced by rational thought and logic." (ICTV).

After much discussion which centred upon renaming all genera using a system equivalent to *Alphabaculovirus*, *Betabaculovirus* etc., but it was concluded that name recognition was of primary importance, so in most cases the infill like was simply removed resulting in *P22likevirus* becoming *P22virus*.

ITEM 2 - Voted to discontinue the use of *Phi* in the naming of new genera.

Comment: Since some people believe the *Phi* in its various forms (phi, φ,Φ) indicate that what follows is a phage, we were faced with numerous potential genera with the prefix *Phi*. It was voted that, unless there was sufficient historical precedent, Phi would no longer be added to the names of genera. Indeed, we would like to actively discourage phage scientists from using any Greek letter when naming their virus.

ITEM 3 - Voted to replace *phage* in the taxon name with virus.

Comment: *Pseudomonas phage phiKMV* is the name of the taxon which includes *Pseudomonas* phage ΦKMV. The use of the word phage suggests that phages are fundamentally different from other viruses, which they are not. Therefore, in an effort to align the taxa names of phages with those of other viruses the word phage will be replaced with virus, yielding, in this case *Pseudomonas virus phiKMV.*

ITEM 4 - Voted to largely eliminate hyphens from the names of taxa.

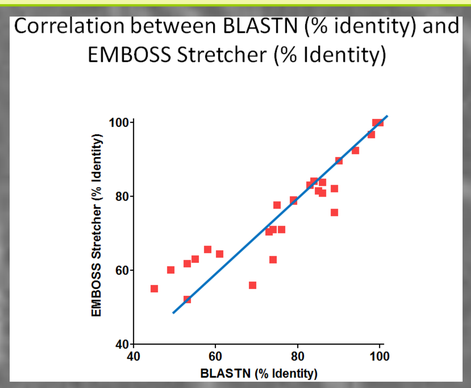
Comment: This is in keeping with ICTV policy i.e. *Yersinia phage L-413C* becomes *Yersinia virus L413C*. The exception is where the hyphen appears in a number string thus *Thermus phage P23*45 becomes *Thermus virus P23-45* (its correct name).

ITEM 5 - Voted to include the isolation host name in the taxon name.

Comment: Where *Enterobacteria* or *Pseudomonad* had appeared in the taxon name, it will be replaced with the isolation host genus name. Therefore, *Enterobacteria phage T7* will become *Escherichia virus T7*. Host species names are eliminated from the taxon name.

ITEM 6 - Investigated the use of DNA-DNA sequence relatedness in the classification of phages.

Comment: DNA-DNA relatedness is the gold standard in the classification of bacteria, while we have previously used overall proteome similarity [1-3]. This has resulted in taxonomic lumping which has been pointed out by recent publications [4,5]. BLASTN is a good method for searching out close relatives and is superior to EMBOSS Stretcher to quantitatively compare the sequence identity of two viruses. There are a couple of problems with the latter program, the first being that the genomes must be colinear. The second and even more important point is that if one "aligns" coliphage T7 with randomly shuffled T7 DNA sequence (http://www.bioinformatics.org/sms2/shuffle_dna.html) one obtains a value of 47.6% identity. Therefore, below a certain threshold the values given by this program are meaningless. By comparison, a BLASTN search of this shuffled sequence specifically against "Enterobacteria phage T7" using BLASTN gives a score (Overall coverage x % identity) of 0, as desired. A graphical presentation of the correlation between the two techniques is given below. Most of the newer relationship programs including CLANS, GEGENEES, mVISTA etc are based upon BLASTN analyses.



ITEM 7 - Submitted over 50 TaxoProps to ICTV for consideration

Comment: The TaxoProp is the form in which proposals are made to ICTV (http://talk.ictvonline.org/files/ictv_documents/m/templates/default.aspx). BAVS proposed 1 new family (*Pleolipoviridae*, new archaeal virus family); 4 new subfamilies (*Guernseyvirinae* [*Salmonella* phage Jersey], *Vequintavirinae* [*Escherichia* phage rV5], *Tunavirinae* [*Escherichia* phage T1], *Bullavirinae* [*Escherichia* phage ΦX174]); plus 58 new genera and 232 species. Below we have listed some of the new genera:

Host genus	Phage Genus	Type phage	Phage Family
Bacillus	*Agatevirus*	Bacillus phage Agate	*Myoviridae*
	B4virus	Bacillus phage B4	*Myoviridae*
	Bastillevirus	Bacillus phage Bastille	*Myoviridae*
	Bc431virus	Bacillus phage Bc431	*Myoviridae*
	Cp51virus	Bacillus phage CP51	*Myoviridae*
	Nit1virus	Bacillus phage phiNIT1	*Myoviridae*
	Pagevirus	Bacillus phage Page	*Podoviridae*
	Sitaravirus	Bacillus phage Diva	*Siphoviridae*
	Slashvirus	Bacillus phage Slash	*Siphoviridae*
	Wphvirus	Bacillus phage W.Ph.	*Myoviridae*
Cellulophaga	*Cba41virus*	Cellulophaga phage	*Podoviridae*
	Cba181virus	Cellulophaga phage	*Siphoviridae*
	Cbastvirus	Cellulophaga phage	*Siphoviridae*
Pseudomonas	*Kpp10virus*	Pseudomonas phage KPP10	*Myoviridae*
	Pakpunavirus	Pseudomonas phage PAK_P1	*Myoviridae*
	Septima3virus	Pseudomonas phage 73	*Siphoviridae*

Listeria	*P70virus*	Listeria phage P70	*Myoviridae*
	P100virus	Listeria phage P100/A511	*Myoviridae*
	Psavirus	Listeria phage Psa	*Siphoviridae*
Staphylococcus	*Kayvirus*	Staphylococcus phage K	*Myoviridae*
	Sextaecvirus	Staphylococcus phage 6ec	*Siphoviridae*
	Silviavirus	Staphylococcus phage Romulus	*Myoviridae*
Escherichia	*T4virus*	Escherichia phage T4	*Myoviridae*
	*RB49virus**	Escherichia phage RB49	*Myoviridae*
	*RB69virus**	Escherichia phage RB69	*Myoviridae*
	*Js98virus **	Escherichia phage JS98	*Myoviridae*
Shigella	*Sp18virus **	Shigella phage SP18	*Myoviridae*
Salmonella	*S16virus **	Salmonella phage S16	*Myoviridae*
Enterobacter	*Cc31virus **	Enterobacter phage CC31	*Myoviridae*

* **new genera within the *Tevenvirinae***

REFERENCES

1: Adriaenssens EM, Edwards R, Nash JH, Mahadevan P, Seto D, Ackermann HW, Lavigne R, Kropinski AM. Integration of genomic and proteomic analyses in the classification of the *Siphoviridae* family. Virology. 2015;477:144-54.

2: Lavigne R, Seto D, Mahadevan P, Ackermann HW, Kropinski AM. Unifying classical and molecular taxonomic classification: analysis of the *Podoviridae* using BLASTP-based tools. Res Microbiol. 2008;159(5):406-14

.

3: Lavigne R, Darius P, Summer EJ, Seto D, Mahadevan P, Nilsson AS, Ackermann HW, Kropinski AM. Classification of *Myoviridae* bacteriophages using protein sequence similarity. BMC Microbiol. 2009;9:224.

4: Eriksson H, Maciejewska B, Latka A, Majkowska-Skrobek G, Hellstrand M, Melefors Ö, Wang JT, Kropinski AM, Drulis-Kawa Z, Nilsson AS. A suggested new bacteriophage genus, "Kp34likevirus", within the *Autographivirinae* subfamily of *Podoviridae*. Viruses. 2015;7(4):1804-22.

5. 1: Niu YD, McAllister TA, Nash JH, Kropinski AM, Stanford K. Four *Escherichia coli* O157:H7 phages: a new bacteriophage genus and taxonomic classification of T1-like phages. PLoS One. 2014;9(6):e100426.