INTRODUCTION

Over the last several years the Bacterial and Archaeal Viruses Subcommittee (BAVS) has made significant progress in classifying phages in taxa. The work of Adriaenssens et al. [1] on the Siphoviridae resulted in the creation of three new genera, containing 216 phage species, and added 62 species to two previously defined genera (Plicananellovirus; L5 superviseus). 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 taxonomic name.

**Comment:** The naming of phage taxa has been an evolving process with genera name changing from “P2-like virus” which was considered to be a stop-gap measure, to P2-likeviruses. 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 P22-likeviruses becoming P22viruses.

**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 taxonomic name with virus.

**Comment:** Pseudomonas phage phiKMV is the name of the taxonomic 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 P2345 becomes Thermus virus P23-45 (its correct name).

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

**Comment:** Where Enterobacteria or Pseudomonad had appeared in the taxonomic 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 taxonomic 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 EMBASS Stretcher to quantitatively compare the sequence identity of two viruses. There are a couple of problems with the latter program, first the being that the genomes must be collinear. The second and even more important point is that if one “aligns” coliphage T7 with randomly shuffled T7 DNA sequence (http://www.bioinformatics.org/sgms/2/shuffled 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, GEGENERES, mVISTA etc are based upon BLASTN analyses.

**REFERENCES**


