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The Bobb family grows up

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Several strains of Bacillus pumilus are hosts for a number of phages isolated at James Madison University. B. pumilus SAFR32 emerged as the host where the biggest variety of phages were discovered, and the Bobb family are among these. The phages were discovered over a period of two years, and shortly after that, two closely related cousins were reported from China and and Germany. The founding member of the group, Bobb, was published in GenBank several years ago. The genomes of others in this group, Shifty23, Maclean, Pinkman, Gadheer, and Marcel have been used for a number of years as “practice” genomes for Viral Genomics classes, before the class would go on to annotate more recently discovered phages including those that been found by students in that current class. We have more completely annotated Shifty23 in our class and are on the cusp of having finalized all the members of this family. Our six phages range from 152,843 to 156557 bp long with a GC content of 41%, similar to that of their host. All have long inverted repeats (1886 to 3104 bp) at the genome ends, identified by a pileup of reads adjacent to the repeated area, and have an average of 231 genes. Typically, 60 genes could be identified confidently with a function. Eight to ten of these were membrane proteins with otherwise unidentified functions. The genomes contain 6-8 tRNA genes. Bacillus phages often have a DNA polymerase gene that is present in two segments in the genome, divided by a frame shift or the presence of an intron or other identified gene. Four of the Bobb famiy members have a split DNA polymerase gene, the genetic details of which are being investigated. These phages appear to have a 4-member lysis cassette, including the typical endolysin and holin, still being characterized. Two genomes have an insert of a second domain in the DNA helicase gene, and two others have a separate helicase located in a different region of the chromosome. The ribonucleoside diphosphate reductase genes for the two subunits vary in size and arrangement. All of these interesting genomic features are under investigation.  
  
The Bobb family is one of three clusters of phages isolated on B. pumilus strains. Additional phages falling into these clusters are among our more recent discoveries.