May 15, 2015

RE: Mycobacteriophage JetBlade Genome Annotation

To the SEA-PHAGES submission/QC group:

We are pleased to pass along our annotated genome of JetBlade, an A4 subcluster phage isolated near the College of Idaho campus. We re-BLASTed all ORFs 5/14/2015 and have validated the genome in DNA Master. We are confident in the majority of our calls, as there are a considerable number of A4 phages available for comparison (we found Peaches and Bellus Terra to be very similar to our genome). Still, we would appreciate additional review on the regions below, which are referenced by their phamerator numbers and phams:

1. Phamerator gp22&23 (pham 9977), near ~15,100bp (a programmed translational frameshift similar to other A4 phages)
2. Phamerator gp33 (pham 3968), near ~27,000bp (we removed this predicted gene which overlaps a forward gene with more support)
3. The region ~27,000-~28,000. In this region many A4 genomes contain a gene (pham 1903) with a much longer ORF than our corresponding gene in this region. We therefore extended our predicted 1903 ORF to match other genomes as there is strong evidence for this gene call. With this change, we removed the ORF corresponding to phamerator gp36.
4. The region ~27,000-28000 (again). Many similar genomes contain a gene (pham 7833) that in our genome would be found at approximately 27900-27800 (reverse). We did not add a gene to this region but there is some support for it in our genome as well.
5. The region ~37000-38000. This region contains several overlapping ORFs (phams 9451, 4707, 1759) with support for each. We included each of these in our DNA master file, though not all similar phages (see Peaches) include each of them in their genomes.
6. The region ~37900-38400. Many similar genomes include a gene product in this region (pham 9262), between gp55 (pham 1759)and gp56 (pham 8280). We have added this ORF in our annotation.
7. Phamerator gp58 (pham 8541). We included this ORF but Peaches and other genomes leave it out.
8. Phamerator gp70 (pham 9112) and the gaps on either side. There are large gaps in some similar genomes (Bellus Terra) but not in others (Peaches)
9. The region ~45,200-45,400. Many similar genomes include an ORF in this region (pham 7657) that we have not included in our annotation.
10. The region 48800-48900. Many similar genomes include an ORF at this location (pham 8657), though many do not. We did not include this ORF in our annotation.

Thank you, and if you have any questions, please feel free to contact me by email (ldaniels@collegeofidaho.edu) or by phone (208-459-5893).

Sincerely,



R. Luke Daniels, Ph.D.

Assistant Professor of Biology

The College of Idaho