May 14, 2015

Dear SMART member,

Please find attached the Hope College Fall 2014/Spring 2015 Mycobacteriophage Bella96 annotation file and author list. Bella96 is a Subcluster K1 phage with reasonably high identity to previously sequenced K1 phages. Below is a series of notes highlighting things we believe you should be aware of regarding the annotation.

**Additions:** We added two ORFs – gp41 and gp70.

**Deletions:** We deleted original ORF gp36 (as seen in draft phamerator map) and extended the start site of original ORF gp37 (now gp36) to cover the gap.

**Of Special Note:**

**gp96** – We believe the start sites in several other finished genomes should be reconsidered. Please see note for details.

There are two “novel” genes found only in K1 draft genomes. These are gp26 and gp78 in Bella96. Gp26 is embedded within minor tail proteins and is distributed among 4 draft K1 genomes only. Gp78 (gp77 in draft phamerator map) is in a cluster of 3 genes (gp77-79 in draft phamerator map; gp78-80 in DNA Master complete notes file) that are found only in genomes in K1+K5 (all draft genomes), K1 (all draft genomes; weak hits to some K1 complete genomes), and K1+K3 (K1 all draft genomes; K3 are not draft genomes), respectively. Interestingly, the middle gene, gp79, has the same distribution as gp26. The gp78 ORF has good homology to a gene from Segniliparus rugosus, a bacterium that harbors mycolic acids in its cell walls. This raises the possibility of host range expansion to this genus for these phages.

Thank you for your efforts on the QC process. Please let me know if you have any questions or concerns.

Sincerely,



Aaron A. Best, Ph.D.