Annotation notes and comments on phage Mana

I. Positional annotation issues:

Genes 3364..3918 and 3965..4411 are divergent. As annotated, there is a small gap of 46 base pairs. However, the corresponding genes in at least the ten most similar phages (Morgushi, Vortex, Squid, Lasso, Puhltonio, TallGRassMM, Serendipity, UncleHowie, Oosterbaan, and Hertubise) were all annotated the same way with a 46 base pair gap between these divergent genes.

Reverse strand gene 55079..54723 could also have been annotated 55160..54723. This second gene call would have had a smaller gap. However, it has a worse Shine-Dalgarno score, does not match the gene calls predicted by GeneMark or glimmer, and is not the suggested start on starterator.

II. Functional annotation issues:

Using a phamerator map that compared phage Mana to phage Oosterbaan and phage Puhltonio, Mana 6360..8933 was annotated as “portal.” Additionally, using HHpred, Mana 4441..6360 was annotated as “portal” (98.9%, p=5x10^-9). However, the presence of two adjacent portal genes is very unlikely so after contacting the Hatfull lab, Mana 6360..8933 was annotated as “capsid morphogenesis protein (Mu F-like)” from the 14 phages in the pham annotated as this, and Mana 4441..6360 was kept as “portal.”

HHpred was also used to annotate Mana reverse gene 38910..38695 as “HTH DNA binding domain” (99.4%, p=2x10^-13). No other members of the pham had been functionally annotated.

III. tRNA comments

The entire phage sequence was checked for tRNAs using a tRNA scan and Aragorn and there were no tRNAs found in the genome.

IV. Other (large gaps with no genes justified)

Mana had one grey hole, 55551..56006. However, there was no evidence for a gene in this region. There is little to no coding potential in this region and BLAST searches of the region gave no significant results.