June 25, 2015

Kheth

Thank you with the QC checking of this genome. It was pretty straightforward and we had 2 different class sections work on the annotations that were compared for the final file. The genome was very similar to several other B2 phages and they could be used as a guide.

Most of the starts lined up with prior annotations. There were a few that I would appreciate a second look.

ORFs that could use a second look:

ORF 20 – the best blast match I could fine is a 27:27 aa match to several phages.

ORF 49 – there was a very poor blast alignment found. There was a 56:65 alignment with Rosebush, a 56:60 alignment with Ares and TA17A, and a 56:51 aa alignment with Qyrzula. No other starts were useful. May just be a highly variable gene?

ORF53 – the best aa match was a 32:32 aa match to Rosebush. And the alignment was only for 64 aa, but the gene is 111 aa long.

ORF 84 – the 27:23 aa match was the best I could find. The start codon that the other phages used is not available in this phage. The other option is to make the start codon for kheth later, and just miss the first 25 aa of the other phage orfs. I don't know what the better option is.

ORF 87 – the best aa match I could do was a 22:22 aa match to rosebush and a 22:17 aa match to Qyrula. I’m not really confident in this call.

ORF 88 – 1:1 aa match to Rosebush, but rosebush is the only blast match.

Thanks for the help,

Alex