CONSIDER FOR TALK

10th Annual SEA Symposium Abstract

Kansas State University

Manhattan KS

Corresponding Faculty Member: Christopher Herren (cdherren@ksu.edu)



Ayanna M Castro-Ross

Flint Hills Phages – Netting the Jumping Gene of Pollywog and other F1 Mycobacteriophages

Ayanna M Castro-Ross, Lucas G Ernzen, Victoria D Dorman, Connor M Horn, Grant R Hughes, Benjamin D Hulsing, Ana C Martinez, Adrienne E Pohl, Martha Smith Caldas, Christopher D Herren

For 3 years, Kansas State University has been isolating mycobacteriophages from enriched soil samples in *Mycobacterium smegmatis* strain mc2155 at 37°C. This year’s project isolated Pollywog, an F1 subcluster mycobacteriophage. Currently there are 146 subcluster F1 phages that average 104 genes over 57,428 nucleotides with no encoded tRNA genes. Pollywog encodes 104 genes over 58,397 base pairs with no encoded tRNAs. In annotation of Pollywog, it was noticed that Pollywog encodes an appropriately located integrase gene (Y-int) for lysogeny and an additional transposase gene. It is currently not hypothesized that mycobacteriophages utilize transposase mechanisms for chromosomal integration, as seen in Mu phage infection (1), but instead rely on integrase and att sites to establish lysogeny (2). Upon further investigation, it was determined that a total of 21 subcluster F1 phages (14% of all F1 phages), but no other subcluster of mycobacteriophages, contain this Pham of transposase gene. Genomic location of transposase corresponds to one of 2 sites found in 20 of the 21 identified F1 phages and a third unique site found in only one of the F1 phages. In 11 of the F1 phages, transposase is found in the reverse orientation 0-1 gene 5’ to the usual integrase gene. In 9 other F1 phages, transposase in located in the reverse orientation immediately 3’ to the tapemeasure gene on the left arm of the genome. In a single F1 phage, transposase is located on the far right arm in the forward orientation. Phamerator, Clustal Omega and other gene alignment tools were used to both map the ends of the transposons in each of the identified F1 phages, including Pollywog, and to compare differences within the transposase genes themselves.

References:

(1) Rasila TS, Vihinen M, Paulin L, Haapa-Paananen S, Savilahti H (2012) Flexibility in MuA Transposase Family Protein Structures: Functional Mapping with Scanning Mutagenesis and Sequence Alignment of Protein Homologues. PLoS ONE 7(5): e37922. https://doi.org/10.1371/journal.pone.0037922

(2) Peña CE, Stoner J, Hatfull GF. Mycobacteriophage D29 integrase-mediated recombination: specificity of mycobacteriophage integration. Gene. 1998 Dec 28;225(1-2):143-51.