DO NOT CONSIDER FOR TALK

2023 SEA Symposium Abstract

College of St. Scholastica

Duluth MN

Corresponding Faculty Member: Daniel Westholm (dwesthol@css.edu)

Determination of gene function in mycobacteriophage Brusacoram

Campbell E Jugovich, Julia L Carlson, Hannah R Garcia, Riley Leslie, Carter J Meints, Jaden L Meyer, Ellie J Peddle, Jack Perala, Harrison S Reinke, Madison M Salmela, Hoau Thao, Laila Zemar

Cluster P1 mycobacteriophage Brusacoram has a 47,618 base pair genome containing 78 putative protein coding genes, 46 of which have no known function. Previous RNAseq and tandem mass spectrometry experiments have confirmed the expression of the majority of these genes, including those with no known function. Through participation in the SEA-GENES program, we are in the process of elucidating the role Brusacoram genes with no known function may play in host cell infection. In the SEA-GENES project, Brusacoram genes are first PCR amplified and cloned into the pExTra expression vector for use in a series of phenotypic assays. To date, we have successfully PCR amplified nearly all 78 Brusacoram genes and cloned 51 into pExTra constructs. We have then employed these constructs in phenotypic assays to determine cytotoxic or homotypic defense effects of Brusacoram gene expression in Mycobacterium smegmatis. In these assays, we have identified 18 genes that exhibit varying levels of cytotoxicity. No genes that exhibit defense against phage infection have been identified, although our dataset is incomplete. Currently, we are conducting a project examining the effect toxic gene expression has on cell morphology. We are transforming M. smegmatis with toxic and non-toxic Brusacoram genes, then acid fast staining the cells and examining under 1000x magnification. Results will be presented in the poster.