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University of Evansville

Evansville IN

Corresponding Faculty Member: Joyce Stamm (joycestamm@twc.com)

Identifying the tail assembly chaperone programmed translational frameshift in BK cluster phages

Evan M Barr, Kelsey R Breneman, Audrey L Chambers, Kate N Clarke, Madelynn R Jacobs, Rafay Karim, Kylee M Peck, Caleb A Sager, Abigail K Sena, Jessica L Small, Daniel M Thompson, Forrest W Wade, Megan C Williams, Julie Merkle, Joyce Stamm

Emma1919 is a BK1 phage that infects the soil bacterium Streptomyces griseus. It was isolated from Ferdinand, IN by Elizabeth Miller and purified by Elizabeth Miller and Madeline Adamson. During our annotation of Emma1919, we noted that none of the annotated BK cluster phages showed a programmed translational frameshift in the tail assembly chaperone gene. Instead, these phages had been annotated with two adjacent tail assembly chaperone genes. We wondered if there was evidence for a programmed translational frameshift in Emma1919, or, alternatively, if all BK phages have two separate tail assembly proteins.

To address this question, we evaluated multiple lines of evidence in the region where the programmed translation would be: 1) the coding potential in Emma1919; 2) nucleotide conservation between Emma1919 and the closely related phage Gilson; and 3) the presence of a potential “slippery sequence” for a frameshift to occur. Through discussions with members of the SEA-PHAGES community in the the SEA-PHAGES Annotation Forum, we also examined multiple sequence alignments of all members of the relevant pham, which contain both BK and BE cluster phages. Together, the data indicate that the tail assembly chaperone genes in Emma1919 and the previously annotated BK cluster phages should be all annotated with a programmed translational frameshift.