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College of St. Scholastica

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

Lysogeny investigations in Cluster F1 Phages LittleShirley and Guppsters

Emma Alley, Lexi Hill, Mya Hoaglum, Maggie Lamppa, Khailee Pack, Hailey Pageau, Cale Prosen, Kylie Richards, Kendra Royer, Emily Slettedahl, Ian Strusz, Lydia Wiita, Jillian Zeidler

The College of St. Scholastica isolated, purified, and sequenced two Cluster F1 mycobacteriophages LittleShirley and Guppsters, which both infect *Mycobacterium smegmatis* mc2155. Genomic sequencing revealed genome lengths of 58611 and 54835 and preliminary annotations identified 111 and 98 protein coding genes in LittleShirley and Guppsters, respectively. During annotation, we identified tyrosine integrases, immunity repressors and antirepressors, agreeing with the temperate assignment of the cluster. Currently, we are in the process of identifying stoperator consensus sequences and their location on the genome with DNA Master, modeling repressor and antirepressor 3-dimensional protein structures with AlphaFold, and locating attP and attB sites with BLAST. In addition, we are investigating gaps in sequence homology between our phages and others in the subcluster with Dotplots and whole genome BLAST searches.