CONSIDER FOR TALK

7th Annual SEA-PHAGES Symposium Abstract

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Investigating Cluster O promoters at Gonzaga University

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In mycobacteriophage genomes, promoters can sometimes be predicted if they have similar sequences to mycobacterial SigA promoters, which conform to predicted consensus sequences. In the five cluster O phages, Corndog, FireCracker, YungJamal, Catdawg, and Dylan, 8 or 9 putative promoters were identified using bioinformatics (Cresawn *et. al*, 2015). However, since the promoters were identified *in silico*, biological confirmation is necessary. Upper division students at Gonzaga University amplified promoter sequences and directionally cloned them into a binary vector. Promoter activity was characterized by the cloned DNA’s ability to drive expression of the red fluorescent protein mCherry following transformation into *E. coli* and *M. smegmatis*. Although promoters PL1, PL2, PL3,and PL6 from various phages were successfully cloned, only PL4, PL5, and PR2 resulted in red *E. coli* and *M. smegmatis* colonies. This supports their role as mycobacteria strong phage promoters in vegetatively growing cells.