DO NOT CONSIDER FOR TALK

2023 SEA Symposium Abstract

University of Colorado Boulder

Boulder CO

Corresponding Faculty Member: Christy Fillman (christy.fillman@Colorado.EDU)



Daniel M Debattista

Identifying the Unique Lysogenic Machinery In Cluster M Mycobacteriophage Auspice

Daniel M Debattista

Existing genome annotations of cluster M mycobacteriophages do not identify any repressor or excisionase genes, but previously conducted immunity assays determined that phage in this cluster are temperate in nature, observing both homoimmunity and phage release (Pope et al, 2014). This experimental evidence suggests that cluster M phages have repressor and excisonase genes that may be difficult to identify using bioinformatic analysis alone. The genes from mycobacteriophage Auspice that were selected as the best candidates for repressor were Auspice\_1 and Auspice\_2 acting as a complementary pair or Auspice\_12 working as a cro-adjacent repressor. Cro-adjacent repressors have been observed in a variety of phage genomes that have serine integrases at locations in the genome where the direction of transcription changes. Gene 12 in Auspice is the only gene in Auspice’s genome positioned this way, which could allow it to encode this type of repressor. Auspice\_127 was proposed to be a recombination directionality factor (RDF) due to its similarity to a metallophosphoesterase gene that acts as an RDF near a serine integrase in another phage genome. It was proposed that the functions of these candidates could be tested using immunity assays with and without the candidate genes inhibited to confirm their role in homoimmunity and phage release respectively.