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2021 SEA Symposium Abstract

University of Maine, Honors College

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Characterization of prophiG122-2 from clinical Mycobacterium abscessus strain G122: a novel cluster A1 prophage

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Mycobacterium abscessus causes severe respiratory, skin, and mucosal infections, particularly in immunocompromised and cystic fibrosis patients. Infections are difficult to treat because M. abscessus is typically multi-drug resistant. Most mycobacteria carry integrated viral genomes, or prophages, within their genomes and these are hypothesized to play a role in pathogen fitness. Yet little is known about the prophages of M. abscessus. Studying the gene content of these genomes could reveal how they affect bacterial fitness, virulence, and resistance to treatment. The novel prophage prophiG122-2 is one of two prophage genomes identified in the clinical M. abscessus strain G122 using Phaster. The prophiG122-2 genome was annotated by determining gene starts and functions. ProphiG122-2 is one of 14 genomes belonging to Cluster MabA1. The genome is 61,077 base pairs in length, has a GC content of 59.7% and encodes 111 genes. When compared to other genomes in cluster MabA1, prophiG122-2 shares the same tyrosine integrase and a majority of the genes in the structural region, however it has a unique immunity repressor that is not present in other genomes. ProphiG122-2 also encodes a BrnT/BrnA toxin/antitoxin cassette and a polymorphic toxin system with Type VII secretion system motifs. The polymorphic toxin cassette includes a 114-amino acid Esx-1-like protein, a polymorphic toxin with no identifiable toxin motif, and a likely immunity protein.