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Genomic Analysis of Novel Bacteriophage ProphiA311-1

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*Mycobacterium abscessus* is a ubiquitous bacterial pathogen found in the environment that causes pulmonary and disseminated infections, especially in patients who have cystic fibrosis or an immunodeficiency. Bacteriophages are viruses that can infect *M. abscessus* and become prophages upon integration into the bacterial genome. The prophages can encode for defensive mechanisms that protect the bacteria from environmental stressors, and infection by other bacteriophages. Not much is known about the prophages found in *M. abscessus*, but analysis of their genomes and the mechanisms they use to protect bacteria can help advance treatment against infections. ProphiA311-1 is a prophage extracted from the *M. abscessus* clinical isolate A311 using Phaster. ProphiA311-1 was analyzed and annotated using multiple bioinformatic tools. The prophage genome is 61,507 bps in length, containing 89 genes and no tRNAs. This prophage is part of cluster MabL phages, which only contains four prophages to date that share similarities in the structural and replication regions. Some of the most notable features of prophiA311-1 include a WhiB1 transcription factor located at gp28, and a forward-oriented WXG-100 family polymorphic toxin system (gp85 – gp87) similar to that found in MabE2 prophage, prophiGD91-4. Gp85 encodes an Esx1-like protein and the downstream polymorphic toxin with an N-terminal WXG-100 motif and C-terminal peptidoglycan endopeptidase RipA toxin. gp87 is an orpham and likely encodes the cognate immunity protein. Prophi311-1 also encodes two orpham proteins, gp83 and 84, that align to WXG-100 family protein and a colicin toxin protein.