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An analysis of Mycobacteriophage prophiA353-3

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*Mycobacterium abscessus* is an antibiotic resistant *Mycobacterium* that causes severe pulmonary infections in those who are immunocompromised, specifically those diagnosed with cystic fibrosis. This pathogen harbors prophages, the latent genomes of bacteriophage (viruses that infect bacteria exclusively), which may carry genes that act to make *M. abscessus* more resilient through mechanisms not currently well understood. Thus, further characterization of *M. abscessus* prophage is required to advance treatment strategies. By utilizing bioinformatic and genomic tools, we analyzed the genome of prophiA353-3, which was extracted from the genome of the *M. abscessus* clinical isolate A353 using Phaster. ProphiA353-3 is a cluster MabG mycobacteriophage whose genome is 55148 base pairs in length, containing 81 open reading frames and GC content of a 64.3%. The prophiA353-3 integrase, gp1, is adjacent to attL, and the immunity repressor is located at gp5. ProphiA353-3 harbors a polymorphic toxin cassette that is similar to those of other cluster MabG phage. Gp81 encodes an EsxG-like protein and a downstream polymorphic toxin with a C-terminal Tox-REase-5 domain and an N-terminal WXG-100 domain. Gp79 encodes the cognate immunity protein, Imm52. Further research into the mechanisms encoded by *M. abscessus* prophage genomes, especially in regard to polymorphic toxin systems and mechanisms that increase bacterial fitness, will increase understanding of their function and impact on human health.