CONSIDER FOR TALK

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Mycobacterium abscessus ProphageG72-1: no polymoprhic toxin but still in with the cluster MabD kin

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Mycobacterium abscessus causes pulmonary infections in immunocompromised, and cystic fibrosis patients. Typically, M. abscessus strains are highly drug-resistant and challenging to treat. Prophage (integrated viral genomes) are known to contribute to virulence and drug resistance in other bacterial pathogens yet the prophage of M. abscessus are not well described. We used the tool Phaster to identify two novel prophages in the genome of the clinical M. abscessus isolate G72 (QXAE01000001). ProphiG72-1 is a 50,824 base pair long genome with a GC content of 63.4% that codes for 86 genes. This prophage belongs to cluster MabD, which contains 5 other prophages. ProphiG72-1 encodes an immunity repressor (gp 5) which is shared by only one other prophage, prophiFVLQ01-2 of cluster MabD. ProphiG72-1 does not contain a toxin-antitoxin system but encodes a remnant of a polymorphic toxin system immediately adjacent to the right attachment site. ProphiG72-1 is the only prophage in MabD that does not have an intact Type VII secretion system polymorphic toxin gene. It does however encode an SUKH-family immunity protein that is paired with a putative polymorphic toxin in prophiFSQJ0-3. ProphiG72-1 also encodes a homing endonuclease gene that has been inserted into the open reading frame of a Cas4 exonuclease. Future research on the gene content of additional M. abscessus prophages could help us better understand how prophage may contribute to antibiotic resistance and increased virulence of their host.