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Characterization of a novel cluster MabN prophage genome discovered in the genome of pathogenic Mycobacterium chelonae isolate

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Non-tuberculosis mycobacteria (NTM) are highly abundant in the environment with high human-pathogen contact. They cause pulmonary and disseminating soft tissue infections in immunocompromised patients, including patients with cystic fibrosis (CF). Bacteria of the Mycobacterium abscessus/chelonae (Mab-chel) complex pose an immediate global health risk due to their sharp increase in antibiotic resistance and poor treatment success rates. Prophages, integrated viral genomes, are common in Mab-chel strains and potentially increase the pathogen’s virulence and their resistance to phage and drug therapies. In this project we aim to characterize novel prophage genomes and understand how these genomes and their genome content potentially contribute to host virulence and drug resistance. An M. chelonae strain, MCKB10, was isolated from an unknown fish and submitted for sequencing. VirSorter was utilized to identify two prophage sequences in the bacterial genome. ProphiMCKB10-1 is a MabN prophage, closely related to prophiT36-2. ProphiMCKB10-1 has a 38,274-bp genome with 63.3% GC content, encodes 56 protein coding genes, and encodes no tRNAs. The left arm encodes a reverse-transcribed immunity repressor (gp1) followed by forward transcribed replication and early lytic genes. The right arm encodes structural and assembly genes. Within the forward transcribed replication genes is a reverse transcribed moron with a single transmembrane domain that could play a role in phage defense. Gp 52-56 encodes a Phage-encoded ESX-secreted toxin (PEST) system that includes a WXG100 family protein domain, a polymorphic toxin with no known toxin domain, and an LpqN-like immunity protein