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

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Nontuberculous mycobacteria, such as the Mycobacterium abscessus (Mab-chel) complex, causes pulmonary and soft tissue infections and continues to increase on a global scale for individuals with cystic fibrosis, immunosuppression, and otherwise healthy people. These bacteria are ubiquitous in the environment and can be found in showerheads, medical instruments, soil, water, and other commonly-used areas. Most clinical strains are highly or totally drug resistant making the treatment success rate lower than 50%. Integrated viral genomes, prophages, are common in Mab-chel strains and potentially increase virulence and antibiotic resistance. This study aims to characterize novel prophage genomes in Mab-chel genomes in order to grow our understanding of prophage genome diversity and gene content. The M. chelonae strain MCKB11-2 was isolated from an American Eel and the genome was submitted for Illumina sequencing. VirSorter was used to identify three prophage sequences in the bacterial genome. ProphiMCKB11-2 is a cluster MabN prophage and is closely related to prophiT36-2a. It has a 42,351-bp genome, 63.4% GC content, and encodes for 64 proteins and no tRNAs. Gp1 is a reverse-oriented immunity repressor. Directly following is a divergently transcribed helix-turn-helix DNA binding domain (gp2) followed by genes involved in DNA replication. The right arm encodes structural and assembly genes. Adjacent to the right attachment site are five reverse-transcribed genes including a tyrosine integrase and three genes that are part of a phage-encoded ESX-secreted toxin system. The toxin system includes a WXG100 protein, a polymorphic toxin with an unidentified toxin domain, and an unidentified immunity protein.