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

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The incidence of non-tuberculosis mycobacterial infections is increasing globally in patients with and without cystic fibrosis. Bacteria of the Mycobacterium abscessus/chelonae complex are one of the most frequently isolated and cause pulmonary, disseminating and soft tissue infections. Due to extensive or total drug resistance, treatment success rates are as low as 45%. Prophages, integrated viral genomes, are known to contribute to drug resistance through expression of prophage encoded ESX-secreted toxin (PEST) systems. This project aims to characterize novel prophage genomes and understand how diverse prophage genomes may contribute to mycobacterial virulence and drug resistance. A M. chelonae strain, MCKB6, was isolated from Coho Salmon and the genome was submitted for sequencing. Phaster was used to identify a single prophage sequence in the bacterial genome. ProphiMCKB6-1 is a cluster MabC (HC) prophage and is most closely related to prophiGD51-1. It has a 50,384-bp genome with 64.2% GC content and encodes 71 protein-coding genes and no tRNAs. Gp1 encodes a reverse-oriented integration-dependent immunity repressor and is followed by a divergently transcribed DNA binding domain protein (gp2). The right arm encodes structural and assembly genes that are highly conserved in cluster MabC genomes. A reverse oriented tyrosine integrase (gp71) is immediately adjacent to the right attachment site and downstream from this is a type 3 PEST system that includes two WXG100 proteins (gp68 and 69), a large polymorphic toxin with two WXG motifs and no identifiable toxin (gp67) and an immunity protein (gp66).