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Characterization of four novel prophages and their polymorphic toxin systems in the pathogenic Mycobacterium salmoniphilum

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Mycobacterium abscessus is a non-tuberculosis pathogenic bacterium that causes soft tissue and pulmonary infections in Cystic Fibrosis patients (CF) and is often completely drug resistant. Previous studies have shown that a significant portion of M. abscessus isolates carry prophages which are predicted to contribute to pathogenicity. To better understand the relationship between prophages and pathogenicity, we sequenced the genome of the fish pathogen, Mycobacterium salmoniphilum (MSKB-2), a close relative of M. abscessus. Using the program Phaster, we identified four novel prophages that share at least 35% gene content with M. abscessus prophages and therefore were assigned to Mab clusters. ProphiMSKB2-2, prophiMSKB2-3 and prophiMSKB2-4 have genome lengths of 61,691, 72,955 and 34,502 bp and were assigned to clusters MabE, MabK and MabN, respectively. ProphiMSKB2-1 is distinct from M. abscessus prophages already described, although nearly identical sequences exist in sequenced genomes of clinical M. abscessus isolates in GenBank. We recommend a novel cluster assignment to MabS. ProphiMSKB2-4 has a large deletion in its structural gene region and likely cannot form active phage particles. ProphiMSKB2-1, prophiMSKB2-2, and prophiMSKB2-4 encode polymorphic toxin systems which are predicted to contribute to bacterial virulence. In future research polymorphic toxin systems will be cloned in order to determine how these genes impact bacterial gene expression and potentially bacterial virulence.