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Exploring the gene content of novel prophages identified in genomes of pathogenic non-tuberculosis mycobacteria

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Non-tuberculosis mycobacteria (NTM) are prevalent in the environment, highly drug resistant, and pose serious threats to human health—especially in immunocompromised individuals. The majority of NTM, such as Mycobaterium abscessus and M. chelonae, carry prophages (integrated bacteriophage genomes) which encode genes that are hypothesized to contribute to host fitness and pathogenicity. To better understand how prophages contribute to mycobacterial fitness, we identified and characterized prophage genomes from pathogenic M. chelonae strains isolated from infected fish. ProphiMCKB5-1 is a cluster MabD prophage, and has a 52,686-base-pair genome with 62% GC content. It has 84 predicted protein-coding genes, including a tyrosine integrase. ProphiMCKB1-4 is a cluster MabI prophage with a 76,080-bp genome that has relatively low GC content, 59.2%, compared to that of its bacterial host (~64%). It encodes 127 putative protein coding genes and 24 tRNAs. It encodes a serine integrase on the right arm of the genome. Both prophages encode a polymorphic toxin immunity system that includes a small WXG100 protein, a large polymorphic toxin with an N-terminus WXG100 domain, a C-terminus toxin domain, and an immunity protein that prevents self-intoxication. By annotating and studying mycobacterial prophages, we increase our understanding of their potential contributions to virulence and drug resistance, and create new opportunities to improve treatment of mycobacterial infections.