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Mab Cluster C prophages prophiA315 and prophiG190 provide Mycobacterium abscessus clinical isolates with Esx-like toxin systems.

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Infections caused by *Mycobacterium abscessus* target immunocompromised patients resulting in serious pulmonary and disseminated infections, particularly those with a history of cystic fibrosis. This pathogen is highly antibiotic resistant, making treatment of infections extremely difficult. Many bacterial pathogens host bacterial viruses, known as prophages, that have been inserted into the bacterial genome. These prophages often contribute to pathogenesis by encoding mechanisms to increase bacterial fitness, including pathogenicity and antibiotic resistance. However, there are gaps in knowledge about how *M. abscessus* prophages function to impact overall bacterial fitness. We identified two Mab Cluster C prophage genomes in the genomes of clinical *M. abscessus* isolates A315 and G190. Strain A315 carries only 1 prophage, prophiA315-1, with a genome of 50,949 base pairs, a GC content of 64.3%, and encodes 70 genes. ProphiG190-1 was also the only prophage found in *M. abscessus* strain G190 and has a genome of 53,071 base pairs in length with 78 open reading frames and a GC content of 64.1%. Both prophages encode an integration-dependent immunity repressor (gp1) next to attL and a Tyrosine integrase adjacent to attR. As with the 16 other MabC cluster prophage genomes, there is a polymorphic toxin cassette with Type VII secretion motifs located next to the right attachment sites. The cassette includes two small WXG100 family proteins, a large polymorphic toxin with a C-terminal ADP-ribosyltransferase motif, and a cognate immunity protein with a deaminase domain. Expression of prophage-encoded toxin systems may provide the pathogen with increased survival strategies.