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An APB on Mab Cluster C prophages prophiG73-1 and prophiA353-2: Armed and dangerous

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Mycobacterium abscessus is a ubiquitous non-tuberculosis Mycobacterium (NTM) that causes pulmonary and soft tissue infections in immunocompromised populations. It is highly drug resistant, resulting in a treatment success rate of 45.6%. Prophages (integrated viral genomes) increase bacterial fitness, pathogenicity, and antibiotic resistance in many pathogens, yet there are few studies on prophages of M. abscessus. Studying M. abscessus prophage genome content may help us better understand M. abscessus virulence and drug resistance and lead to improved therapies. We identified two cluster MabC prophage genomes in the genomes of clinical M. abscessus isolates A353 and G73. ProphiA353-2 in one of three prophages identified in the clinical strain of M. abscessus, A353. The genome is 52,643 bp long, encodes 76 genes, and has a GC content of 63.6%. Strain G73 carries only a single prophage, prophiG73-1, which has a genome length of 52,038 bp in length, a GC content of 63.4%, and encodes 75 genes. Like other 16 members of cluster MabC, both prophages encode an integration-dependent immunity repressor (gp1). Adjacent to the right attachment sites is a leftward transcribed polymorphic toxin system with Type VII secretion system motifs. The cassette includes two small WXG-100 family proteins, a large polymorphic toxin with a C-terminase GH-E nuclease motif, and a cognate immunity protein with an ankyrin repeat motif. Both prophages encode a reverse transcribed HicAB toxin/antitoxin pair that interrupts the lysis cassette. These toxin cassettes may arm the bacterial host with an improved ability to respond stress in the environment.