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Annotation and Comparative Analysis of Gordonia phage Miskis (Cluster CQ)

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Gordonia phage Miskis is a temperate phage that was isolated via an enrichment protocol using the Gordonia terrae host. The Miskis genome is 92,098 base pairs in length, has a 3’ 10-base overhang, and has a GC content of 62.1%. As expected, a nucleotide BLAST of its full genome indicated its closest matches as other members of the CQ cluster of Gordonia phages (e.g., ClubL, Norvs, PhinkBoden, Cucurbita, and Toniann). Of the 186 preliminary open reading frames identified in its genome, 46 code for functional gene products, 10 are orphams, 8 code for tRNAs, and the remaining 122 code for hypothetical proteins of no known function. Many of the orphams (e.g., GP 1 and GP 11) will be removed from the final annotation due to significant overlap issues or lack of coding potential. The Miskis genome is read from both the + and – strands, and begins with a short stretch of 8 reverse genes, transitions to an extended stretch of primarily forward genes (GP10-148) which contains the 8 tRNA genes and 3 reverse genes, before returning to the minus strand for the remainder of the genome. With the exception of GP16 (HNH endonuclease) and the 8 tRNA genes located together between GPs 21 and 31, all earlier genes represent hypothetical proteins. Most functional genes are found between GP 32 – GP80 and include terminase, portal, minor and major capsid, scaffolding, capsid decoration, head-to-tail adaptor and stopper, tail terminator, tail assembly chaperone, tapemeasure, lysin A , holin, tyrosine integrase, and immunity repressor proteins. The Miskis genome Phamerator map shows a high degree of homology with the other CQ cluster phages with minor areas of differences extending towards the right arm of the genome (e.g., GP 74-79; GP 112-115; GP 122).