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Annotation and Comparative Analysis of Gordonia Phages Flatwoods (Cluster DE1), Francois (Cluster DI) and PullumCavea (Cluster DC1)

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Flatwoods, Francois, and PullumCavea were isolated via an enrichment protocol using the Gordonia terrae host. The Flatwoods genome is circularly permuted, is 57,123 base pairs in length, and has a GC content of 68.2%. As expected, a nucleotide BLAST of its full genome indicated its closest matches as other members of the DE1 cluster of Gordonia phages (e.g., Baddon, Kroos, Bizzy, Ribeye, Tangerine). Of the 85 preliminary open reading frames identified in its genome, 24 code for functional gene products while the remaining 61code for hypothetical proteins of no known function. The Flatwoods genome is read exclusively from the + strand. The Francois genome is 50,499 base pairs in length, has a 3’ 10-base pair overhang, and has a GC content of 67.4%. As expected, a nucleotide BLAST of its full genome indicated its closest matches as other member of the DI cluster of Gordonia phages (e.g., Bock, Mulch, Parada, Brylie, WheatThin). Of the 77 preliminary open reading frames identified in its genome, 34 code for functional gene products while the remaining 43 code for hypothetical proteins of no known function. The PullumCavea genome is circularly permutated, is 58,535 base pairs in length, and has a GC content of 67.9%. As expected, a nucleotide BLAST of its full genome indicated its closest matches to other members of the DC1 cluster of Gordonia phages (e.g., Phlop, Wizard). Of the 91 preliminary open reading frames identified in its genome, 30 code for functional gene products while the remaining 61 code for hypothetical proteins of no known function. Two of these phages, Flatwoods and PullumCavea, are similar to previous ULM isolates. Using pBLAST and the Phamerator visualization tool, we have begun a comparative analysis of Flatwoods with Baddon (both DE1 isolates) and PullumCavea with Phlop (both DC1 isolates). Although a whole genome BLAST of Flatwoods indicates Baddon as its closest match, individual pBLAST analysis of Flatwoods gene products show only two top no known function matches with Baddon. The whole genome BLAST of PullumCavea indicates Phlop as its closest match and pBLAST analysis reveals 8 functional and 20 no known function gene product top hits with Phlop. However, PullumCavea shares more individual gene product top hits with another Gordonia DC1 phage (Wizard – 17 functional and 24 no known function).