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The Puritan and the Phloozy: Genomic insights into the lifestyles of Gordonia phages Jabberwocky and Schwartz33

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Six *Gordonia* phages with siphoviridae morphology were isolated from soils in Grand Rapids, Michigan, using *Gordonia terrae* 3612 as a host. Three were isolated via direct plating and three via enrichment. We obtained complete genome sequences from two, Jabberwocky (enrichment; 85 ORF’s; subcluster DE1) and Schwartz33 (direct; 89 ORF’s; cluster DJ). Jabberwocky is most closely related to Stultis (93.2% nucleotide identity) and Schwartz33 is most closely related to OhMyWard (68.4% nucleotide identity). Jabberwocky’s genome contained all of the expected ORF’s, but the genome of Schwartz33 was missing several, including tail assembly chaperones and scaffolding proteins. The genome of Schwartz33 also contained nineteen orphams, significantly more than others in this cluster (OhMyWard has
six orphams). Several of the orphams were found to have a function, including a capsid maturation protease, a deoxycytidylate deaminase, a ThyX thymidylate synthase, a DNA helicase, and two membrane proteins. This is the second year in a row our phages grouped within DE1 and DJ, so we compared Jabberwocky and Schwartz33 with our previously isolated phages Kroos and Tanis. Jabberwocky and Kroos have moderate synteny but are only 76.3% identical at the nucleotide level. Schwartz33 and Tanis also have moderate synteny but are only 62.4% identical at the nucleotide level. We also used information on phamdb.org to explore possible correlations of clusters DE1 and DJ with geographic location, soil type, and isolation date. No significant correlations were found. Jabberwocky had 37 phams unique to the DE1 subcluster. Of the remaining, most were clusters exclusive to *Gordonia* phages. This suggests that Jabberwocky’s genome has evolved from phages with a limited host range. In contrast, Schwartz33 contains 30 phams found exclusively in the DJ cluster, but only six phams were found solely in *Gordonia* phages. 30 phams were also found within the two *Rhodococcus* phages in cluster CC: Pepy6 and Poco6, 14 of which were found within the first ⅓ of the genome and are structural in nature. Schwartz33 also shared 20 phams with the BI cluster (*Streptomyces*); 21 phams with *Arthobacter* clusters AM, AU and AW; 18 with EL (*Microbacterium*); and at least one ORF within *Mycobacterium* clusters K, L and M. Of the phams found in multiple bacterial genera, 16 had AM, AU, AW, BI, CC and EL together in a single pham. This leads us to believe the evolutionary history of Schwartz33 draws on phages with a broad host range. The fact that Schwartz33 shared 30 phams with *Rhodococcus* phages, many identified as having a structural function, makes testing of DJ phages on a *Rhodococcus* host enticing.