DO NOT CONSIDER FOR TALK

2025 SEA Symposium Abstract

University of Louisiana at Monroe

Monroe LA

Corresponding Faculty Member: Ann Findley (afindley@ulm.edu)

Annotation and Comparative Analysis of Gordonia phages Talon44 (Cluster DJ) and Warrior24 (Cluster A15)

Jacob Buckley, Parker Coleman, Alexander Erwin, Trinity Hatten, Tova Husers, Karlee Lange, Cade Martin, Connor McVoy, Mariah Richardson, Temisan Taire, Savannah West, Jackson Ponarski, Arieus Shidiskis, Allison Litwin, Angela Boateng, Mallory H Benedetto, Ann M Findley

Talon44 and Warrior24 were isolated via an enrichment protocol using the *Gordonia terrae* 3612 host. The Talon44 genome is 60,184 base pairs in length, has a 3’ 9-base overhang, and a GC content of 51.0%. As expected, a nucleotide BLAST of its full genome indicated its closest matches as other members of the DJ cluster of Gordonia phages (e.g., Perkunas, Captrips, Avazak). The DJ cluster contains phages isolated on both the *G. terrae* and *G. rubripertincta* hosts. Interestingly, the DJ phages that show the highest degree of similarity with Talon44 were isolated from *G. rubripertincta*. Of the 96 preliminary open reading frames identified in its genome, 23 code for functional gene products while the remaining 73 code for hypothetical proteins of no known function. Talon44 is a lytic phage whose genome is read exclusively from the + strand. Structural genes found on the left-arm of the genome include the holin, portal, terminase, tail terminator, and major capsid protease fusion proteins. Functional genes found on the right-arm of the genome include the DNA helicase, DNA primase/polymerase, and Cas4 exonuclease. The Warrior24 genome is 52,847 base pairs in length, has a 3’ 10-base overhang and a GC content of 62.1%. As expected, a nucleotide BLAST of its full genome indicated its closest matches as other members of the A15 cluster of Gordonia phages (e.g., Oofda, Waits, Remus). Of the 106 preliminary open reading frames identified in its genome, 4 code for tRNAs, 39 code for functional gene products while the remaining 60 code for hypothetical proteins of no known function. Warrior 24 is a temperate phage whose genome is read from both the + and – strands, with a long stretch of forward genes (GP1-40) followed by an extended stretch of reverse genes (GP41-102) for the remainder of the genome. The left-arm, forward-facing structural genes include the portal, scaffolding, capsid maturation protease, terminase, tail assembly chaperone, and lysin A proteins. The right-arm, reverse facing functional genes include DNA polymerase I, ThyX-like thymidylate synthase, ribonucleotide reductase, metallophosphoesterase, DNA primase, serine hydrolase, endonuclease VII, Cas4 exonuclease, and immunity repressor.