CONSIDER FOR TALK

9th Annual SEA-PHAGES Symposium Abstract

Western Kentucky University

Bowling Green KY

Corresponding Faculty Member: Rodney King (rodney.king@wku.edu)



Megan E Dillingham



Dimond A Shelton

Characteristics of Gordonia Phage Getalong (DN) and Mycobacteriophages Wachhund (F1), Squiggle (B1), Drake55 (A2), Belladonna (K1), and Morpher26 (A4).

James K Anderson, Haley D Austin, Ethan A Brown, Margaret K Cook, Caleb W Curry, Megan E Dillingham, Alicia C Edds, Jaraan R Fernando, Callie A Freeman, Rukmini Ganesh, Clarissa V Gearner, Emily K Guernsey, Jacob C Harris, Olivia Hawkins, Morgan O Holt, Wren A Jenkins, Cydne C Kitchens, Chloe M Lindsey, Jack J Marquardt, Janki R Naidugari, Natalie B Ngong, Emily H Nguyen, Aidan E O'Brien, Deeya D Patel, Meghan T Perez, Dimond A Shelton, Tom J Shervin, Olivia C Simpson, Zachariah N Shone, Mason R Tomko, Tara N Watkins, Summer Wei, Emily M Xu, Brian Z Zhu, Amanda K Staples, Bobby L Gaffney, Rodney A King, Claire A Rinehart

One Gordonia phage was isolated using *Gordonia terrae* 3612 and five mycobacteriophages were isolated from *M. smegmatis* mc155. The annotations were done with the PECAAN program.
 The Gordonia phage named **Getalong** came from an enriched compost bin in Bowling Green, Kentucky. The Getalong genome is 56,157 bp long and has 100 protein-encoding genes and no tRNAs. There are 43 genes with assigned functions. Getalong is related to three DN cluster Gordonia draft phages- Asapag, Horus, and Phistory.
 **Wachhund** is an F1 cluster mycobacteriophage isolated from Cromwell, KY. The Wachhund genome is 54,513 base pairs long and has 98 predicted protein-encoding genes and no tRNAs. There are 47 genes with assigned functions. Wachhund is 97% identical to XFactor.
 **Squiggle** is a cluster B1 mycobacteriophage isolated from Bowling Green, KY. The Squiggle genome is 68,325 bp long and has 101 protein-encoding genes and no tRNAs. There are 44 genes with assigned functions. Squiggle is 99% identical to Mana at the nucleotide level. Squiggle varies from other B1 phages in the region from 46,700 to 48,700 bp. The genes in this region of Squiggle’s genome differ in pham type, length, and the number of genes compared to the corresponding region in other annotated B1 phage genomes. As typical of other B1 phages, Squiggle does not possess a frameshift within its tail assembly chaperone genes.
 **Drake55** is a cluster A2 mycobacteriophage isolated from Bowling Green, KY. The Drake55 genome is 52,719 bp long and encodes 96 proteins and 1 tRNA. There are 45 genes with assigned functions. Drake55 is 97% identical to Piro94, at the nucleotide level and is a top match, for most genes, at the protein level. Drake55 gene 34 is an orpham, with no known function.
 **Belladonna** is a cluster K1 mycobacteriophage isolated from Bowling Green, KY. The Belladonna genome is 59,708 bp long and encodes 94 proteins and 2 tRNAs. There are 44 genes with assigned functions. Belladonna is 99% identical to CREW at the nucleotide level. An added gene, Gene 68, is not found in other K1 phages except DrHayes, Emerson, SamuelLPlaqson, Urkel and Validus, all of which belong to pham 2971.
 **Morpher26** is a cluster A4 mycobacteriophage isolated from soil samples taken in Bowling Green, KY. The Morpher26 genome is 51,294 bp in length and encodes 85 proteins and no tRNAs. There are 49 genes that have been assigned functions. Morpher26 is most closely related to the A4 phage Wile both at the nucleotide level and at the protein level. All genes also match at the pham level between Morpher26 and Wile.