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Corresponding Faculty Member: Catherine Chia (cchia1@unl.edu)



Phoebe B Peña

Isolation of phage that infect Gordonia rubripertincta and annotation of Gibbous and Chikenjars

Phoebe B Peña, Lindsay R Birge, Layton D Bivans, Seth M Blakestad, Emma K Chesley, Elizabeth E Frank, Sarah Hoagland, Justin Hultquist, Ethan P Ramsey, Nicholas R Lee

The *Gordonia* genus includes species capable of transforming and degrading hydrocarbons, making them candidates for environmental and industrial biotechnology (Arenskötter, et al., 2004). Phages of *Gordonia* are potential genetic tools that can be used to study the genes coding for the metabolic enzymes of the bacteria. To bolster the numbers of identified phage that infect the genus *Gordonia* (currently ~ 1600), students used *Gordonia rubripertincta* NRRL B-1654 as the host in the Fall 2018 Virus Hunting course at UNL. By direct isolation, six phage were successfully acquired, archived and added to The Actinobacteriophage Database (phagesDB.org). All six phage are siphoviridae as judged by their morphology viewed by transmission electron microscopy, having tails ranging in length from 200 to 250 nm. Two genome sequences, Gibbous (45,810 bp; 60.5% GC) and Chikenjars (61,544 bp; 51.3% GC) were determined by Illumina Sequencing by the Pittsburgh Bacteriophage Institute. Auto-annotation using DNA Master predicted 69 genes in Gibbous (cluster CT) and 95 genes in Chikenjars (cluster DJ). An obvious difference between the phage genomes, based on the auto-annotation, was the presence of 24 reverse ORFs in Gibbous clustered largely in the right arm of its genome, while Chikenjars has only four small reverse ORFs that are isolated and dispersed through the genome. Phamerator analyses showed that the two phages shared no Phams although both had the requisite known proteins of tailed phages including terminase, HNH endonuclease, portal protein, capsid maturation protease, scaffolding protein, major and minor capsid proteins, endolysins, major and minor tail proteins, and tape measure protein. Very close relatives of Chikenjars, phages Duffington and Rickmore, (cluster DJ), were isolated in Idaho using *Gordonia terrae* 3612 as the host, raising the interesting questions of whether they can infect *G. rubripertincta* and if Chikenjars can infect *G. terrae*. Similarly, phages Cozz and Emalyn (cluster CT), identified using *G. terrae* as the host, are relatives of Gibbous. The same question arises as to whether the phages can cross infect the other *Gordonia* species. Annotation by the class group found support for functional assignments of 31 out of 69 genes (45%) for Gibbous. For Chikenjars, 19 out of 95 ( 20%) of the genes had credible support for functional predictions.