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Comparison of the Gordonia terrae CU3 Cluster Phage Dardanus with CU1 Cluster Members and the Singleton Phage Catfish

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During the 2017-18 academic year, ULM freshmen SEA PHAGES Program students isolated 24 novel bacteriophages using the Gordonia terrae host system. Gordonia phage Catfish was sequenced and determined to be a Singleton with no clear homology to any previously sequenced Gordonia phage. Catfish has 46,888 bp with a 3’ sticky overhang of eleven bases, 79 open reading frames, and a GC content of 65%. In functionally annotating the Catfish genome, highest BLAST hits for the entire genome and many of its functional open reading frames (ORFs) corresponded to members of the CU1 cluster of Gordonia terrae phages. We have since adopted Gordonia phage Dardanus for annotation (isolated by Florida Gulf Coast University). Dardanus, the sole member of the CU3 cluster of currently-sequenced Gordonia phages, has 43,143 bp, 74 ORFs, no tRNA genes, a GC content of 66%, and shares many of its functional ORFs with members of the CU1 cluster and Catfish. We provide a functional annotation of Dardanus and explore its relationship to CU1 cluster Gordonia phages and the Catfish singleton using the SplitsTree, Gepard DotPlot, and Phamerator visualization tools. Such analyses provide insight not only into the relationship between the Gordonia terrae phages but can point to extended comparisons between other Actinobacter phage group isolates.