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Isolation and Annotation of Novel Streptomyces Bacteriophages Shuckle and Axiom​

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Bacteriophage Shuckle and Bacteriophage Axiom were isolated and characterized as *Streptomyces lividans* infecting viruses under the SEA-PHAGES program at Washington University in St. Louis. This work adds to understanding the diversity of phages in hopes to further treatment research for antibiotic-resistant infections. Phages were isolated and amplified from soil samples from St. Louis, MO. Shuckle underwent four rounds of purification, with Axiom undergoing three. Both produced well-defined circular plaques. Shuckle’s DNA was extracted and sequenced to find a final genome length of 133,857bp, including a terminal repeat of 11,224bp starting at gene 210. Analysis suggests that Shuckle is a siphoviridae in the BE1 cluster. Shuckle has 230 protein-coding genes and 47 tRNA genes, including 9 genes considered to be ‘orphams,’ genes unlike any other phage genes seen. Axiom’s genome contains 51,703 base pairs, which code for 84 genes, including 3 orphams. Axiom is a temperate phage within the BD2 subcluster with characteristically unique genes at the end. The translation start codons for each gene have been validated by manual inspection. The functions of 65 genes have been assigned for phage Shuckle and 36 genes have been assigned for phage Axiom. Genes such as 7 and 108 in Shuckle and 27 and 28 in Axiom were studied in-depth due to weak evidence or conflicting phage annotations.