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The complete genome sequence of the Gordonia bacteriophage BiggityBass

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As the threat of antibiotic resistance increases, finding alternative treatments to bacterial infections has become more urgent. The potential of bacteriophages, a type of virus that infects bacteria, has recently gained interest in the scientific community to combat this issue. As part of HHMI’s SEA-PHAGES program, a cohort of undergraduate students from Arizona State University (ASU) annotated the genome of the bacteriophage BiggityBass. Genome annotations were completed using gene prediction programs such as DNAMaster, BLAST, Phamerator and PhagesDB. We discovered that the genome of BiggityBass contains 83 annotated genes. For 40 genes a putative function could be identifies using comparative data from closely-related bacteriophages in the DR cluster (e.g., AnClar, Sour, and Yago84), including minor tail proteins, lysin A proteins, lysin B proteins, and HNH endonucleases; no tRNAs were detected. Of the 43 genes with unknown functions, five were identified to be membrane proteins via SOSUI and TMHMM.