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2024 SEA Symposium Abstract

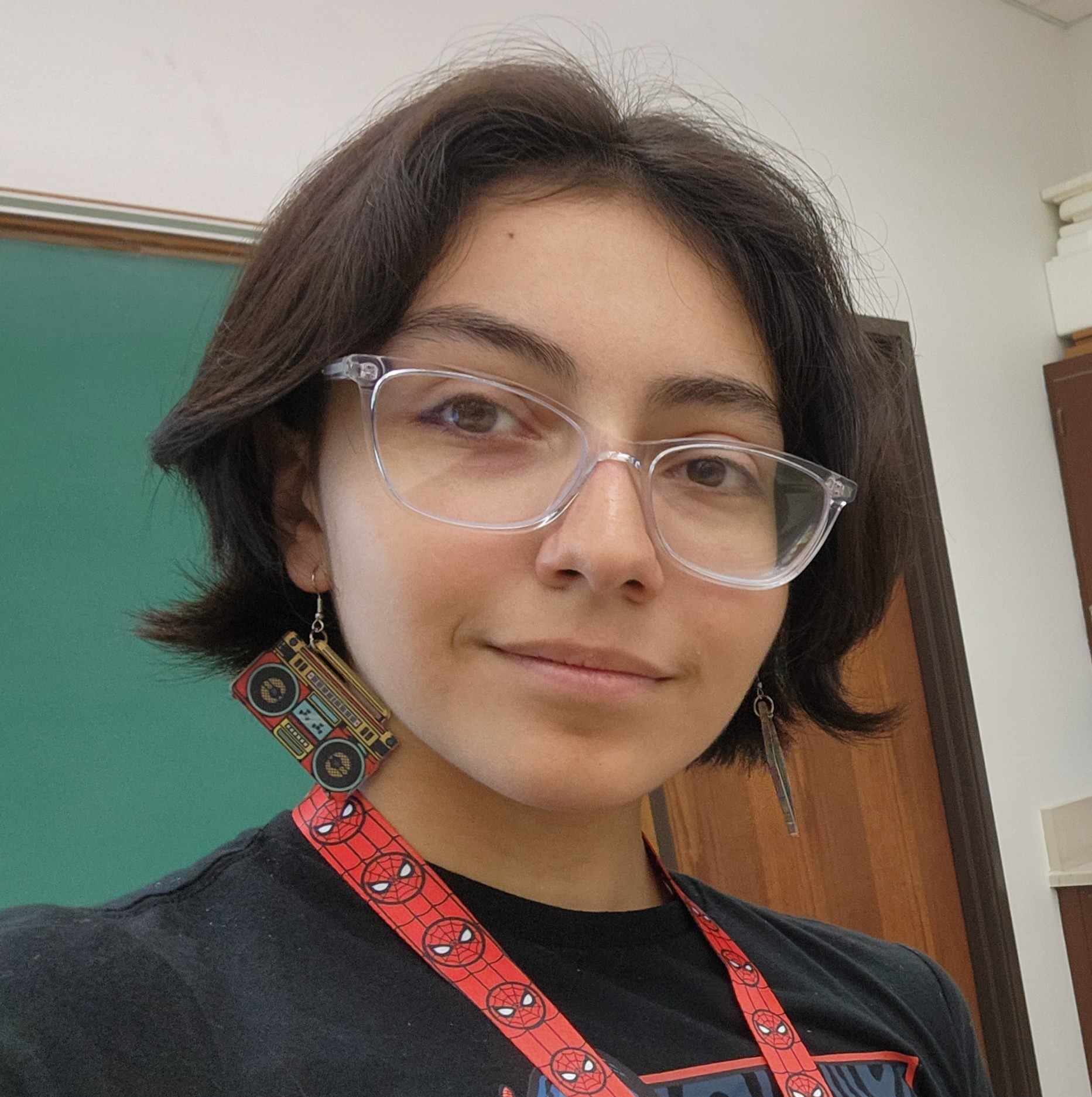
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Isolation, Characterization, and Genome Annotation of North Texas Streptomyces baarnensis bacteriophages ElGato, Jevington, and Samora

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Bacteriophages, also known as phages, are viruses that infect bacteria. *Streptomyces baarnensis* NRRL B-2842 was the host bacterium used in this study, which resulted in the isolation of three bacteriophages: ElGato, Jevington, and Samora. All three were taken from soil samples from Denton, TX. The plaques for ElGato and Jevington were clear and circular. Jevington's plaques ranged from 0.25mm to 0.5mm in diameter, whereas ElGato's plaques were an average of 1mm in size. The plaques for Samora were cloudy with an average diameter of 0.5mm. They also each have a temperate life cycle. Jevington and Samora tested positive for lysogeny. These phages were sequenced at the Pittsburgh Bacteriophage Institute using the Illumina Sequencing Method. ElGato, Jevington, and Samora are all in different subclusters: BD3, BD2, and BB1 respectively. ElGato’s genome is 48,922bp, Jevington’s 50,941bp, and Samora the smallest at 41,794bp. All three genomes have 3’ sticky overhangs with 11bp for ElGato (CGGTACGTGAT) and Jevington (CGCCACGTCTT) and 10bp for Samora (CCCGGCCCCA). The three bacteriophages have similar GC contents, with ElGato having 65.9%, Jevington having 67.6%, and Samora having 62.7%. The genomes were annotated using bioinformatics tools including PECAAN, GeneMark and Glimmer, HHPred, NCBI and PhagesDB BLAST, Phamerator, Starterator, and Deep TMHMM using the principles outlined in the Phage Genomics Guide published as part of the HHMI SEA-PHAGES program. ElGato has 79 ORFs , Jevington has 86 ORFs, and Samora has 60 ORFs. Jevington and Samora both have 1 tRNA.