DO NOT CONSIDER FOR TALK

2025 SEA Symposium Abstract

North Carolina A & T State University

Greensboro NC

Corresponding Faculty Member: Liesl Jeffers-Francis (ljeffers@ncat.edu)

GoldenEssence Unearthed: Cracking the Genetic Code of a Soil-Borne Bacterial Slayer

Makaila Ross, Areale Webb, D'Essence Jackson, Chenel Miller, Jaya McCain, Kennedy Batty, Marley Gordy, Saivian Waters, Ugonna C Morikwe, Liesl Jeffers-Francis

Bacteriophages (phages) are viruses that infect and replicate within bacterial hosts, playing crucial roles in microbial ecology and offering promising applications in biotechnology and phage therapy. As part of the SEA-PHAGES program at North Carolina Agricultural and Technical State University, the bacteriophage GoldenEssence was isolated from enriched soil samples collected in Greensboro, North Carolina (36.0726° N, 79.7920° W), using Arthrobacter globiformis B-2979 as the host. Isolation and purification were achieved through serial dilution and plaque assays. The phage exhibited clear plaques, consistent with a lytic life cycle, and was confirmed to have Siphoviridae morphology via electron microscopy.
GoldenEssence was named by biology student D’Essence Jackson, inspired by the personal connection to her name and the radiant warmth of the day the phage was discovered. The term “Golden” honors her grandmother’s nickname “Penny”—a shiny, copper-colored coin—and the plaque morphology’s scattered appearance evoked the sparkle of golden sunlight on a reflective surface. The phage’s genome, sequenced at the Pittsburgh Bacteriophage Institute, spans 184,165 base pairs with a GC content of 53% and belongs to the FC cluster of Actinobacteriophages. Annotation identified 282 genes, including 31 tRNAs. Functional analysis was performed using bioinformatic tools such as PECAAN, GeneMark, Starterator, BLASTp, HHpred, and Pharmerator, with an E-value cutoff of 10⁻⁴. A majority of the genes code for hypothetical proteins, while others are predicted to be involved in structural assembly, replication, and host cell lysis. Comparative analysis revealed several unique genomic features not present in closely related phages. This discovery adds to the expanding body of knowledge on phage diversity, evolution, and function. The isolation and genomic annotation of GoldenEssence highlight the power of undergraduate research in advancing our understanding of bacteriophage biology and its future applications in microbial control and therapeutic development.