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Uncovering the Soil Bacteriophage AksarBAT: Isolation, Purification, and Characterization

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Bacteriophages (phages) are viruses that infect bacteria, playing an essential role in bacterial genomics and offering valuable applications in medicine and biotechnology.   
  
As part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science (SEA-PHAGES) program at Metropolitan Community College (MCC) in collaboration with the Howard Hughes Medical Institute (HHMI), a novel bacteriophage named AksarBAT was isolated and characterized. Soil samples were collected from the Omaha area and subjected to enrichment and purification assays to obtain a viable phage. AksarBAT was isolated using *Gordonia rubripertincta* as the host bacteria and was identified as a Siphoviridae phage belonging to the DR cluster. Transmission Electron Microscopy (TEM) conducted at the University of Nebraska Medical Center (UNMC) revealed its characteristic morphology. The EM imaging showed that AksarBAT has a capsid diameter of ~60nm and a tail length of ~300nm. The phage genome was sequenced using Illumina NextSeq 1000 technology at the University of Pittsburgh. The sequencing data has been uploaded to PhagesDB.org, and preliminary genome analysis suggests a lytic life cycle. This phage genome contains 60,906 base pairs, has a GC content of 68.1%, and has 86 annotated genes.   
  
Our current research efforts are focused on annotating the genome for submission to GenBank and investigating potential unique gene functions that contribute to our understanding of phage diversity. The annotation of the AksarBAT genome is currently in progress, utilizing bioinformatics tools, including DNA Master, NCBI BLAST, PECAAN, and Phamerator maps. Some of the features these tools incorporate are GeneMarkS, Glimmer, and Starterator to aid in the process. Regarding synteny in relation to AksarBAT, the most closely related phage appears to be NHagos, which is another lytic phage from the DR cluster.