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Identifying and Characterizing Bacteriophages: Deenasa and Devonte

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Bacteriophages (phages) are viruses that have the potential to infect bacteria. Phages can be used for medical treatment, research advancement, phage therapy, ecology, and many other scientific endeavors. Through the isolation and characterization of mycobacteriophages from soil samples collected on the Howard University campus, this project's goal is to investigate the diversity of phages. Deenasa and Devonte were two of the phages sampled from the soil on Howard University’s campus and the bacterial host used was Mycobacterium smegmatis MC2 155. This host is significant due to its similar genus to Mycobacterium tuberculosis, which causes the tuberculosis disease. The purpose of phage research is to expand the diverse catalog of phages that have been discovered at Howard University along with other phage discoveries. The phage samples were put through isolation and purification, high-titer lysates were generated from which phage DNA was isolated. The genomes were sequenced at the Pittsburgh Bacteriophage Institute, on the MiSeq platform (Illumina Sequencing). The phages Deenasa and Devonte are a part of the B3 sub cluster. Deenasa contains 69,888 base pairs and has a 67.5% G+C content. Devonte contains 68,301 base pairs with a 67.6% G+C content. Phage genome annotation is currently on going where PECAAN and DNAMaster and been used for that purpose. The study of bacteriophages will advance our understanding of the evolutionary mechanisms by which bacteriophages have grown to be so diverse and will benefit from the acquisition and understanding of genomic information from a wide variety of clusters, including those that are currently underrepresented.  
  
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