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Isolation and Characterization of Fourteen Siphoviridae and Myoviridae Isolated from The Campus of Howard University

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Bacteriophages, or phages, may be utilized to study viral ecology, epidemiology, and enhance the development of therapeutics. In the current study, enrichment and direct culturing methods, in conjunction with host Mycobacterium smegmatis MC2155, were used to elucidate phage diversity in soil samples collected from the campus of Howard University. Over 100 phages were purified using standard isolation protocols. Subsequently, lysates were generated, and DNA was extracted. Fourteen genomes were sequenced (Pittsburgh Bacteriophage Institute), using Illumina Sequencing. This revealed that the sample phages belong to four clusters: A (phage Naji); B (phages Bishoperium, CamL, Mecca, Samaymay, Omniscient, QueenBeane and West99); C (Basquiat, Chargie21, Fludd, JustHall and Naija), and Q (DeepSoil15). The genome sizes range from 53,746 to 154,456 bp with G+C contents ranging from 63.5 to 68.9%. Morphotypes were identified as Siphoviridae and Myoviridae. Annotation of the genomes is currently underway. Additionally, all of phages in the 2017-2018 collection are undergoing assays to determine patterns of phage sensitivity/insensitivity—immunity using wildtype *M. smegmatis* MC2155 and lysogens generated from the collection.   
  
  
Key words: Mycobacteriophages, Soil, *Mycobacterium smegmatis*, Siphoviridae and Myoviridae