CONSIDER FOR TALK

2023 SEA Symposium Abstract

New York Institute of Technology

Old Westbury NY

Corresponding Faculty Member: Bryan Gibb (bgibb@nyit.edu)



Michael Kaczmarski



Mahir Rahman



Katie Chen



Sean Lee



Nigel Oommen

Phage Argan: A case study comparing Illumina and Nanopore sequencing of bacteriophage genomes

Michael Kaczmarski, Mahir Rahman, Katie Chen, Labiba Fairuj, William Hang, Alyssa Hillian, Sean Lee, Asweel Mehaboob, Rebecca Moses, Nigel Oommen, Kaylah Schultz, Muhammad Shamsi, Victor Vander, Yamini Patel, Srinidhi Gadula, Bryan Gibb

Next-generation sequencing technologies enable the rapid and cost-effective sequencing of genomes. The UPitt crew sequences SEA-PHAGE phages using an Illumina MiSeq sequencer, which does a fantastic job providing accurate genomes, however, Illumina sequencers are expensive and sequencing reactions become cost-effective only when performed on a large scale. Oxford Nanopore developed a different sequencing technology, which is cheaper to purchase and operate, making it attractive for use in undergraduate research projects. However, there are looming questions and concerns about the accuracy of Nanopore sequencing and whether this data is of sufficiently high quality to be used as the sole source of sequencing data when publishing bacteriophage genomes. We present a case study of bacteriophage Argan, isolated in Arthrobacter globiformis NRRL B-2880 from soil on Long Island New York by SEA-PHAGE students at New York Tech in Fall 2022. The genome of Argan was determined by Illumina MiSeq at UPitt and found to be 55 kilobases with ninety putative genes. Argan shares 82.88% gene content similarity with GantcherGoblin, placing it within cluster AU6. In an effort to explore the efficacy of Oxford Nanopore technology, the genome of Argan was also sequenced using a MinION and version R9 flowcells at New York Tech. The analysis comparing assembled genomes of Argan from the two sequencing methods is underway and will be presented in full at the SEA-PHAGE symposium.