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Characterization of AZ cluster phages JohnDoe, Cassia and ObiToo using Gepard DotPlot software

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Bacteriophages are viruses that infect bacterial cells. They can be found everywhere in nature and are recognized as the most abundant biological agent on the planet. In 2021, three new *Arthrobacter globiformis* bacteriophages - JohnDoe, Cassia, and ObiToo - which are assigned to the AZ cluster were discovered and isolated in Ottawa by students at the University of Ottawa. Phage JohnDoe was found in the soil near an in-ground pool. Cassia was found in the soil near a vegetable garden with fertilizer. ObiToo was found in the soil from a compost hole full of sauerkraut. These three bacteriophages belong to the *siphoviridae* family of double-stranded DNA viruses. In addition, we have isolated lysogens of all three bacteriophages confirming that they are temperate.

The DNA from all three phages was sequenced at the University of Pittsburgh by Illumina Sequencing. Functional annotations were done in early 2022 using PECAAN, GeneMark, Phamerator, HHpred, NCBI databases, PhagesDB, and Starterator. In our final submitted annotations, JohnDoe has 70 genes and a 67.6% GC content. ObiToo has 74 genes and a GC content percentage of 68.8%, while Cassia’s genome consists of 69 genes and has 68.4% GC content.

The aim of this project is to characterize these three new AZ phages by assessing the similarities in their nucleotide sequences using the Gepard Dot Plot software. Dot Plots can be used to provide a graphical representation of the similarity between two or multiple nucleotide sequences to demonstrate cluster relationships. Our preliminary results showed that phages Cassia and JohnDoe share more similarities than phages JohnDoe and ObiToo and than phages Cassia and ObiToo.

Further analysis of the data obtained using the Gepard Dot Plot will allow us to learn more about the AZ cluster of phages and the phages found in the Ottawa region. This data will also allow us to discover the unique features of each phage.