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Discovering genetic diversity with NapoleonB

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*Arthrobacter*, a type of bacteria commonly found in soil and sewage, has recently been used as a host for phage isolation by the SEA-PHAGES program. For this project, *Arthrobacter sp.* ATCC KY3901 was used to isolate *Arthrobacter* phage NapoleonB. This phage was used to explore genetic diversity of AM phages. NapoleonB was isolated using enriched media, and a DNA sample was sequenced by the Pittsburgh Bacteriophage Institute using Illumina sequencing. Genome, annotations were manually curated using tools such as DNA Master, NCBI databases, PhagesDB, HHpred, and Phamerator. After isolation and genome annotation, several questions regarding the uniqueness of NapoleonB and AM phages were raised in the form of %GC content, protein structure and mechanisms, unique repeats, and the potential for super-clustering. To test these questions and further explore NapoleonB’s genome, multiple sequence alignments were performed, phamerator maps were analyzed to determine any patterns in synteny, and NapoleonB’s holin and endolysin proteins were characterized through tertiary structure predicting computer programs such as Jmol and RaptorX. NapoleonB exhibits siphoviridae morphology and produces two distinct sizes of clear plaques with average diameters of 1.5 mm or 0.1 mm. Bioinformatic annotations indicated 100 potential genes, 73 with no known function and 25 with predicted functions within the 57,846 base pair genome. NapoleonB and other AM phages differ from other *Arthrobacter* phage clusters with significantly lower %GC. It was also noted that all phages in the cluster AM contain a putative holin protein that has previously been annotated as having no known function. Further examination of *Arthrobacter* phage lysin cassettes identified different types of conserved catalytic regions. This information provides examples of what makes NapoleonB and other AM phages unique among other clusters; it helps expand previous knowledge about phage diversity. Future bioinformatic work can address variations in %GC and potential super-clusters using models of horizontal gene transfer and comparative genomics.