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Genome Comparison of two Novel Viruses, Biscayne and Bush, Isolated from Microbacterium foliorum

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Bacteriophages are a class of viruses known for inserting genetic material onto their host for replication, specifically a bacterium. After the bacteriophage’s successful completion of replication, the virus lyses the host and seeks a new target to infect. Two new bacteriophages, Bush and Biscayne, were isolated from soil samples from Miami, Fl. Both viruses belong to the family Siphoviridae, which contains double-stranded DNA phages. Both phages were isolated infecting the bacterium *Microbacterium foliorum*. These phages have differing genomes, both in number of genes and total nucleotide length. Bush contains a total of 67 genes and Biscayne a total of 25 genes. Despite the varying number of genes, they are both fully functional phages able to infect and create plaques. Bush is part of the cluster GA, and its genome’s length is 38,879 bp. Biscayne, however, is in the cluster EE and has a genome length of only 17,529 bp. Bioinformatic tools includingDNA Master, PhagesDB, HHpred, NCBI BLAST and Phamerator were used to compare both genomes and the function of each gene in the two phages. This comparison aims to determine why there is such a difference in the number of genes and genome length. Our finding indicates that genome size does not directly correlate with phage function. Biscayne had 19 genes with assigned functions and 5 hypothetical proteins, and Bush had 30 assigned functions and 34 hypothetical proteins. Despite their varied sizes there were multiple genes with functions that are conserved in both phages. In both, Biscayne and Bush, portal proteins, head-to-tail adaptors, major and minor tail proteins, tail assembly chaperones, Helix-turn-helix DNA binding domain, Holin, and HNH endonuclease were found and annotated. These are genes involved in the basic assembly and life cycle of the phage, and support the idea that phages do not necessarily need a big genome to function successfully in the environment. Biscayne is fully functional, even with its reduced number of genes compared to Bush. Bush has the largest genome size out of both, and more than 50% of its genes are annotated with an unknown function. It may seem that most of its proteins appear to be involved in non-essential functions for the phage