CONSIDER FOR TALK

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Morehouse College

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Corresponding Faculty Member: Larry Blumer (lblumer@morehouse.edu)

The discovery and annotation of mycobacteriophages BigPhil and Sotrice96

Cedric A Penn Jr., Antron Bristol, Voris M Bryant II, Dee-Andre' D Ferguson, Egyptian A Griffis, Gary M Hearst, Nick A Hicks, Phillip L Johnson, Mohamed A Kouyate, Andon R Mack, Antoine E Martin, Adam J McKinnon, Malakai Miller, Anthony L Moore, Akinola E Oladimeji, Justin J Owens, Chaz T Parks, Kirkland O Paulemont, Alexandra Peister, Lawrence S Blumer

Mycobacteriophages BigPhil and Sotrice96 were isolated from soil samples in or near Atlanta, Georgia, using *Mycobacterium smegmatis* as the host. BigPhil is a Cluster F1 virus 53,618bp long and Sotrice96 is a Cluster E virus 76,299bp long. The purpose of our research was to finalize draft annotations of both phages by manually confirming potential genes and identifying gene functions. Utilizing the annotation program, DNA Master, and guided by heuristic GeneMark output for both phages, we determined the most likely open reading frames to identify each gene in these two genomes. We also performed BLASTp searches, in GenBank, and used the Starterator application in the Phamerator program, to ascertain whether the start site designated for each gene aligned with other start sites of homologous genes, and the probability of these matches. Lastly, we utilized Phamerator, GenBank BLASTp searches, and HHPred searches to assign gene functions to these two phages. Both BigPhil and Sotrice96 have programmed translational frame shifts in the tail protein chaperone genes just upstream of the tapemeasure gene in each genome. In BigPhil, this was a +1 frameshift and in Sotrice96 this was a more common -1 frameshift. We confirmed 100 genes and no tRNA sequences in BigPhil. Sotrice96 has approximately 145 genes and two tRNA sequences. The BigPhil genome is very similar to the F1 mycobacterial phage Sparticus and Sotrice96 is very similar to the E mycobacterial phage Henry.