CONSIDER FOR TALK

9th Annual SEA-PHAGES Symposium Abstract

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GingkoMaracino: Tiny Virus, Big Prospects

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The Mycobacterium genus is home to human pathogens such as Mycobacterium leprae (leprosy) and Mycobacterium tuberculosis (Tuberculosis). Given the rise of antibiotic-resistance, focus has shifted to finding alternative therapies for these debilitating and often fatal diseases. Bioinformatic analysis has provided us with the tools to annotate and understand the genomes of mycobacteriophages. These tools have facilitated the search for novel genetic systems and have allowed bio-prospecting for the discovery of phages useful in treatment of these diseases. DNA master was used to annotate the genome of Mycobacteriophage GingkoMaracino. Comparative analysis software such as the PhagesDB Blast feature, Phamerator and predictive software like HHPred allowed for the identification of homologous traits with known viruses. This has revealed a plethora of interesting properties for mycobacteriophage GingkoMaracino: an endolysin system exclusive to cluster A phages, a mechanism responsible for capsid formation involving the interaction of a V-ATPase scaffolding protein with a terminase and portal protein system, phage attachment sites homologous to corresponding bacterial attachment sites of Mycobacterium tuberculosis, homology of tail proteins and GP5 region thought to be involved with phage adsorption into tuberculosis, a repressor-stoperator system which controls the switch between lytic and lysogenic behavior, and a hypothetical pathway to lysis. GingkoMaracino also encodes an exonuclease whose gene product could be utilized in creating gene knockouts, point mutations, deletions, and insertions in Mycobacterium tuberculosis. Collectively, this evidence suggests that mycobacteriophage GingkoMaracino has potential for use in the treatment and molecular manipulation of Mycobacterium tuberculosis.