Complete genome sequence of new virulent actinophages belonging to *Streptomyces flavovirens*

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Complete genome sequence of new virulent actinophages belongi to *Streptomyces flavovirens*

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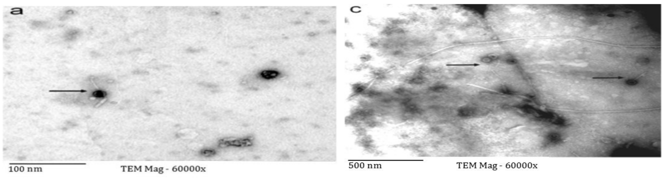
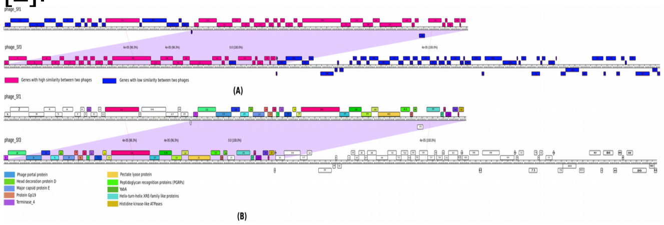
Introduction

We report biological and physiochemical features and use NGS to provide the complete annotated genomes for two new strains (Sf1 and Sf3) of the virulent phage *Streptomyces flavovirens*, isolated from Egyptian soil samples.

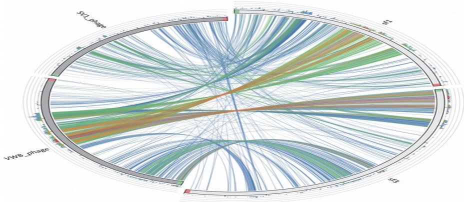


Results

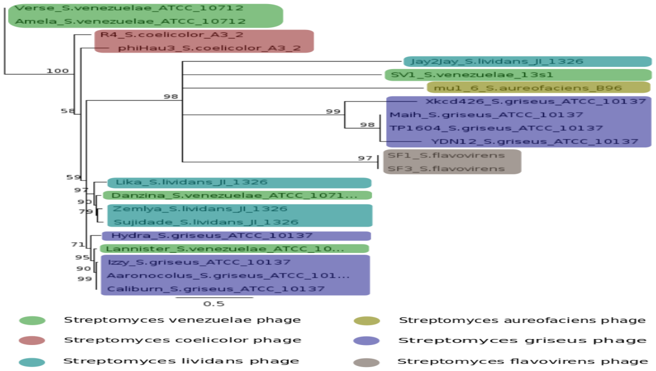
The one-step growth experiment was performed as described by Dowding (1973) [1]. Genomic DNA was isolated and sequencing libraries were prepared. Libraries were sequenced on an Ion Torrent PGM semiconductor sequencer (Life Technologies, Carlsbad, USA). Raw reads were assembled using the gsAssembler (Roche Applied Science, Indianapolis, IN). Open reading frames (ORFs) were identified and annotated using DNA Master (J. G. Lawrence) software [2].



A comparison map among the sequenced phages and closely related phages (VWB and SV1) was generated by Circoletto [3].



The phylogenetic tree of Major Capsid Protein (MCP) genes constructed with Geneious software version (R8) based on the Neighbor-Joining (NJ) algorithm.



Conclusion

The *S. flavovirens* phages (Sf1 and Sf3) show high adsorption rates (82 and 85 %, respectively), indicating a strong specificity to their host, and their burst sizes were 1.95 and 2.49 virions per mL. The phage genomes are parts of a singleton cluster with sizes of 43,150 bp and 60,934 bp, respectively. the assignment of possible functions to 19 and 28 putative ORFs were identified, which included phage structural proteins, lysis components and metabolic proteins. Comparative genomic analysis revealed significant homology between the two phages and the closest Streptomyces phage (VWB phages). However, the phylogenetic analysis highlighted that the isolated phages belong to the BG Streptomyces phage group but are clearly separated, representing a novel sub-cluster.

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