CONSIDER FOR TALK

7th Annual SEA-PHAGES Symposium Abstract

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TsarBomba, a multi-host sub-cluster forms deep inside Saratov, Russia

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*Bacillus cereus* group phage TsarBomba was isolated from soil samples collected from Saratova, Russia on *Bacillus thuringiensis* subsp. *Kurstaki*. The phage was characterized by plaque morphology, electron microscopy, and cluster analysis using primer extension prior to genomic sequencing by Illumina next-generation sequencing. TsarBomba was determined to have a genome of 162,486 bp in length, with 40.1% GC content, and 6,364 bp direct terminal repeats. Detailed examination of the genome revealed TsarBomba to contain 247 protein coding genes and 20 tRNA genes. Comparison of TsarBomba with other phages belonging to the proposed C cluster by genomic synteny and phylogenetic methods suggests the inclusion of a fourth sub-cluster containing *B. cereus* group phages BCP78, TsarBomba, Hobo, and IceQueen. Host range for TsarBomba was assessed experimentally with a cohort of *B. cereus* group hosts. TsarBomba was found to target all the tested *B. thuringiensis* strains, several *B. cereus* strains and a *B. anthracis* strain, but not more distantly related species, such as *B. pumilus*, *B. megaterium*, or *B. subtilis*. The ability of bacteriophages to infect different hosts depends largely on the ability of tail fibers to interact with specific membrane elements, enabling the assessment of host range through comparative phylogenies of housekeeping and membrane proteins in bacterial hosts. Codon usage bias has also been postulated as a putative determinant of host range, especially for bacteriophages harboring tRNA genes in their genomes. Analysis of the translational component of codon usage bias using the scnRCA index inferred from multiple hosts reveals that codon usage patterns have not changed significantly across the *Bacillus* genus and, therefore, should not have an impact on *B. cereus* group bacteriophage host range. Furthermore, comparison of codon usage bias among several *B. cereus* group phages harboring and not harboring tRNA genes suggests that codon usage patterns are not optimized among the former to exploit their genomic tRNA component.