Comparative genomics of six Pseudomonas phages isolated from composting

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Abstract

Bacteriophages (or simply phages) are viruses that infect bacterial cells and are the most abundant and, potentially, the most diverse biological entities on Earth. More than 1023 infections by phages are expected to occur every second. The dynamics of phage-host populations presents complex relationships and is thought to contribute to bacterial abundance and diversity as well as to environment homeostasis. In the billion years that phages co-existed with their bacterial hosts, phages have evolved highly diverse proteins that either inhibit or adapt bacterial metabolic processes to their own benefit. Since their discovery, in the early 20th century, phages and their proteins have been exploited as valuable molecular biology and biotechnology tools. Phages have been also considered potential antibacterial agents, and their use to reduce or eliminate bacterial infections is known as phage therapy. Phages might be a treatment option for?antibiotic resistant?bacteria. Phages that are lytic and that are not capable of displaying lysogeny are preferred for phage therapy purposes. In a previous work from our group, composting samples from the Sao Paulo Zoo Park were screened for phages infecting Pseudomonas aeruginosa PA14. Six phages were isolated and had their genome sequenced. One of them (ZC01) was shown to be from Siphoviridae Yu-A like genus and the other two (ZC03 and ZC08) were similar to each other and shown to be novel Podoviridae phages. All three phages are lytic and have the ability to degrade P. aeruginosa PA14 biofilm, and as such they can be promising candidates for antimicrobial application. In the present work, we extend this prior study by analyzing the three remaining phages (ZC04, ZC06 and ZC07). All three were predicted to belong to the Podoviridae family. Phylogenetic trees were generated based on multiple alignment of the terL marker gene using MAFFT, followed by alignment curation with GUIDANCE2 and maximum likelihood computation using RAxML. This analysis shows that phages ZC03, ZC08, ZC04, ZC06 and ZC07 are phylogenetically close. ZC06 and ZC07 are closer to each other than to others and their genomes have 99% similarity. The genomes of ZC04 and ZC03 have 97% similarity. Differences in these five genomes include INDELS that resulted in truncation of at least one CDS in ZC04. Other genomic differences that might have functional implications will be discussed.

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