Characterization and Genomic Analysis of Novel Acinetobacter baumannii Phages EAb3 and EAb7 for the Treatment of Multidrug-Resistant Infections

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Acinetobacter baumannii is a pathogenic bacterium associated with multi-drug resistant nosocomial infection that has been classified as an urgent threat by the CDC. Phage therapy is promising for resistant A. baumannii infections. Bacteriophages EAb3 and EAb7 were previously isolated on A. baumannii MRSN 3692; genomic and host-range analyses determined them to be similar but distinct novel phages in the Myoviridiae family. This study aimed to illuminate the characteristics of the phages through analysis of bacterial lysis, single-step growth curves, comparative genomics, and plaque morphology. The lytic properties of EAb3 and EAb7 were compared with an in vitro host growth dynamics assay. EAb3 and EAb7 multiplicities of infection (MOI) greater than 1 were found to cause near-immediate cell lysis, and even at MOI as low as .0001 were found to significantly decrease bacterial load. EAb7 decreased A. baumannii concentrations more quickly than EAb3, while EAb3 developed larger plaques than EAb7. Single-step growth analysis revealed phages EAb3 and EAb7 to have slow adsorption, a short latent period, and a relatively large burst size. 46 EAb3 genes and 49 EAb7 genes were assigned putative functions; the remaining 280 ORFs found were classified as hypothetical proteins. No potential lysogenic or toxin-encoding genes were found. EAb3 and EAb7 are promising candidates for further study; more work is needed to understand the relationships between plaque morphology, lysis dynamics, and lytic cycles for these phages. The microplate method for in vitro growth dynamics assays developed in this experiment should be considered for future use.

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