

A novel Dhillonvirus phage bearing a unique open reading frame of intergeneric origin

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Abstract

Escherichia Coli (*E. coli*) is one of the most prevalent bacteria in the gut and plays an important role in the formation of the intestinal microbiome. In this study, *Escherichia* phage Ioannina, a novel member of *Caudoviricetes*, with high lytic activity against *E. coli* ATCC 25922, was isolated from hospital wastewater. *Escherichia* phage Ioannina was highly resistant to a broad range of temperatures and alkaline pH, but was sensitive to acidic pH. Whole genome sequencing of the phage, revealed that *Escherichia* phage Ioannina is a novel phage within the *Dhillonvirus* genus. Its genome is a 45,270 bp double-stranded DNA molecule that encodes 64 putative open reading frames (ORFs). The phylogenetic analysis of open reading frames, which diversified *Escherichia* phage Ioannina from other dhillonviruses, indicated that ORF31 (a putative tail fiber protein) presented higher similarity to representatives of other phage families. ORF31 was significantly more related to similar ORFs belonging to the *Kuravirus* and *Tunavirus* (*Drexelviriidae*) genera, indicating a possible recombination event.

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