Insights into phage endolysins

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Abstract

(Bacterio)phages are viruses that specifically infect bacteria, and thus are harmless to humans, animals, and plants. They are the most abundant microorganisms on the planet (estimated to be 1031 on Earth) in a ratio of 10 times more than bacteria (1). Consequently, even rare phage-induced events are frequent at the global level. Therefore, they have a staggering ecological impact on the bacterial population and in the evolution of bacterial genomic structure upon virus-host interactions, acting as agents in the recycling of organic matter and presenting a valuable tool in molecular biology and epidemiology. Regarding the diversity of phages, they can have different types of replication mechanisms, morphologies, nucleic acid composition and genome sizes. Over the last decade improvements on phages genome sequencing and progresses in genomic research have revealed information on open reading frames of proteins of interest (2).

Increasing interest has been given to phage (endo)lysins in molecular biology, biotechnology and medicine. Lysins are phage lytic enzymes that break down the peptidoglycan of the bacterial cell wall at the terminal stage of the phage reproduction cycle, in order to release the phage progeny with the consequent death of the bacterial cells (3).

The number of phage genomes deposited in GenBank has been increasing exponentially in the last years. However, no effort has been made so far to understand the relation between lysins and their phage family and host species, presenting challenges in their annotation, comparative analysis, and representation.

The almost 700 complete phage genomes deposited in the NCBI database were searched for the presence of lysins by making use of the Pfam (4) identified domains and BLAST comparison of putative or unidentified complete genome against known lysins. In approximately 5% of the phage genomes it was not possible to identify any lysin. The identified enzymes were used to construct a phylogenetic tree with Phylip (5), using Neighbor-Joining, Maximum Likelihood and Parsimony algorithms (6). From the resulting tree, we were able to present a phage-lysin characterization network analysis taking into account the lysin aminoacid sequence and the different phage classes (Family/Genus) and host species to study their evolutionary stories. Regarding the phage families, muramidases, amidases and peptidases are the largest type of lysins in *Myoviridae*, *Podoviridae* and *Siphoviridae* phages respectively. Grouped data will also be used to identify conserved domains among lysins of different phages which will play an important role in the annotation of the still unidentified lytic cassette of phages with sequenced genomes.

References

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