Unraveling the insights into phage endolysin association

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In view of the abundacy of phages (1), even rare phage-induced events are frequent at the global level. 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. Th focus on 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, to release the phage progeny with the consequent death of the bacterial cells (3). Despite the increasing number of genomes in Genbank, 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/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 aa 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 unidentified lytic cassette of sequenced phages.

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