

Poster

Analysis of the presence of cell division proteins and its associated processes in two phyla lacking FtsZ, Planctomycetes and Chlamydiae



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ABSTRACT

Motivation:

Planctomycetes is a Gram-negative bacterial phylum that has been the subject of study on numerous occasions for its unique characteristics. In the past they were considered as an intermediate evolutionary step between Prokaryotes and Eukaryotes. 16S rRNA testing pointed to the phylum Chlamydiae as its closest relative, both are part of the PVC superphylum and share a common ancestor as well as some of those unique features.

These two clades of bacteria divide cellularly by a non-ftsZ-dependent division process, instead most members of these phyla divide cellularly by budding or by a binary fission-like process. These types of cell division alternative models are not fully understood yet due to the complexity of their components and the number of interactions between them. The study of the differences that these alternative models show compared to the conventional ones, and its associated mechanisms, could be useful to understand the evolutionary dynamics of cell division phenomenon and its role in a transcendental zone of the bacterial phylogenetic tree.

Methods: Through Blastp, it was performed a massive analysis of the protein sequences related to the cell division components and its associated processes in two phyla, Planctomycetes and Chlamydiae. Due to the data size, Python scripts were coded to allow filtering and editing the information of the files obtained on the analysis. A phylogenetic mapping of the taxonomic distribution (presence/absence) of the proteins under study will also be carried out.

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