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Ecogenomics of Microbes

The direction of gene transfer among pairs of genomes

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Microorganisms adapt rapidly to the environment and the exchange of DNA through events of horizontal gene transfer (HGT) represents a major mechanism for rapid evolution. This study focuses on evaluating the direction of some identified HGT events among pairs of microorganisms from different phyla. In this way, we can predict the origin and fate of DNA fragments which is of relevance to understand the evolutionary history of the microbial species. The pan-genome includes the known set of genes present within a taxon. The core genome represents the set of common genes within that taxon. By evaluating pairs of microorganisms (generally at the genus level), we could separate those shared genes belonging to the core genome in a genus and to the pan-genome in the other. Among the genes that are found in representatives of the two genera being compared, the ones that belong to the core genome of one of the genera will be considered to be originated from this genus while those genes only detected in a minor fraction of the representatives of a genome (i.e., belonging to the pan-genome of the genus) will be considered to be acquired in this second genus. We have been able to compare several pairs of taxa and to deduce that most of the shared genes, putatively acquired by HGT, are present in most species of one of the compared genera and sparsely found in the other and viceversa with the rest of shared genes. Thus, we can relatively easily define the origin of the HGT events involving those genes and pairs of taxa. The procedure comparing the genome sequences available from two different taxa will provide with valuable information to deduce the evolutionary history of specific taxa, its relevance to functional capabilities within these taxa and will decisively contribute to our understanding of the interactive relationships among microorganisms in the natural environment.

