

Reconstructing the phylogeny of Corynebacteriales while accounting for Horizontal Gene Transfer

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Abstract

Horizontal Gene Transfer (HGT) is a common mechanism in bacteria that affects the genomic content of extant organisms. However, most traditional methods for bacterial phylogeny reconstruction assume only vertical inheritance in the evolution of homologous genes. Here, we present a new method for bacterial phylogeny reconstruction that accounts for the presence of genes acquired by HGT in genomes. A gene tree-based method was devised to identify and correct putative transferred genes (PTG). The method is applied to the reconstruction of the phylogeny of the Order Corynebacteriales, the largest clade in the Phylum Actinobacteria.

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