Abstract

A Comprehensive Population Based Comparative Genomic Analysis of the Legionella Pangenome

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A comparative genomic analysis of the Legionella genus’ pangenome was done to elucidate the level and significance of mutation and recombination within the selected population. It was found that recombination occurred less frequently then mutation, but it had a much greater effect on the pangenome’s genetic change. Additionally, a variety of phylogenetic trees were created, showing strain and clade associated genetic clustering. This was the most complete study of the Legionella genus’ pangenome to date, utilizing 43 genomes with 35 strains being newly sequenced for this analysis.