



Category: Metagenomics

Partial Scholarship Award Winner

# Genomic Resource and Genome Guided Comparison of Twenty Type Strains of the Genus *Methylobacterium*

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## Abstract

Bacteria of the genus *Methylobacterium* are widespread in diverse habitats ranging from soil, water and plant (phyllosphere, rhizosphere and endosphere). In the present study, we in house generated genomic data resource of six type strains along with fourteen database genomes of the *Methylobacterium* genus to carry out phylogenomic, taxonomic, comparative and ecological studies of this genus. Overall, the genus shows high diversity and genetic variation primarily due to its ability to acquire genetic material from diverse sources through horizontal gene transfer. As majority of species identified in this study are plant associated with their genomes equipped with methylotrophy and photosynthesis related gene along with genes for plant probiotic traits. Most of the species genomes are equipped with genes for adaptation and defense for UV radiation, oxidative stress and desiccation. The genus has an open pan-genome and we predicted the role of gain/loss of prophages and CRISPR elements in diversity and evolution. Our genomic resource with annotation and analysis provides a platform for interspecies genomic comparisons in the genus *Methylobacterium*, and to unravel their natural genome diversity and to study how natural selection shapes their genome with the adaptive mechanisms which allow them to acquire diverse habitat lifestyles. This type strains genomic data display power of Next Generation Sequencing in rapidly creating resource paving the way for studies on phylogeny and taxonomy as well as for basic and applied research for this important genus.

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