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## Recent Work

### Title

The genome of obligate methylotroph *Methylobacillus flagellatus*

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**The Genome of Obligate Methylophile *Methylobacillus flagellatus***

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The complete genome of a model obligate methylophile, *M. flagellatus* (strain KT) was sequenced. The genome is represented by a single circular chromosome of approximately 3 Mbp potentially encoding a total of 2,766 proteins. Based on genome analysis as well as the results from previous genetic and mutational analyses, methylophily is enabled by methanol- and methylamine dehydrogenases, the tetrahydromethanopterin-linked formaldehyde oxidation pathway, the assimilatory and dissimilatory branches of the ribulose monophosphate cycle, and a formate dehydrogenase. Some of the methylophily genes are present in more than one (identical or non-identical) copy. The obligate dependence on single carbon compounds is likely due to the incomplete tricarboxylic acid cycle, as no genes potentially encoding alpha-ketoglutarate-, malate- or succinate dehydrogenases are identifiable. The genome of *M. flagellatus* was compared, in terms of methylophily functions, to the previously sequenced genomes of three methylophilic: *Methylobacterium extorquens* (Alphaproteobacterium, 7 Mbp), *Methylibium petroleophilum* (Betaproteobacterium, 4 Mbp), and *Methylococcus capsulatus* (Gammaproteobacterium, 3.3 Mbp). Strikingly, metabolically and/or phylogenetically, methylophily functions in *M. flagellatus* are more similar to the ones in *M. capsulatus* and *M. extorquens* than to the ones in the more closely related *M. petroleophilum*, providing the first genomic evidence of polyphyletic origin of methylophily in Betaproteobacteria.

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