Title
The genome of obligate methylotroph Methylobacillus flagellatus

Permalink
https://escholarship.org/uc/item/53s09404

Authors
Chistoserdova, L.
Lapidus, A.
Han, C.
et al.

Publication Date
2006-03-28
The Genome of Obligate Methylotroph *Methylobacillus flagellatus*

*Ludmila Chistoserdova*\(^1\), Alla Lapidus\(^2\), Cliff Han\(^3\), Lynne Goodwin\(^3\), Liz Saunders\(^3\), Tom Brettin\(^3\), Roxanne Tapia\(^3\), Paul Gilna\(^3\), Susan Lucas\(^2\), Paul M. Richardson\(^2\), and Mary E. Lidstrom\(^1\)

\(^1\)University of Washington, Seattle, WA, \(^2\)Joint Genome Institute, Production Genomics Facility, Walnut Creek, CA, \(^3\)Joint Genome Institute, Los Alamos National Laboratory, Los Alamos, NM

The complete genome of a model obligate methylotroph, *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, methylotrophy 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 methylotrophy 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 alphaketoglutarate-, malate- or succinate dehydrogenases are identifiable. The genome of *M. flagellatus* was compared, in terms of methylotrophy functions, to the previously sequenced genomes of three methylotrophs: *Methylobacterium extorquens* (Alphaproteobacterium, 7 Mbp), *Methylibium petroleophilum* (Betaproteobacterium, 4 Mbp), and *Methylococcus capsulatus* (Gammaproteobacterium, 3.3 Mbp). Strikingly, metabolically and/or phylogenetically, methylotrophy 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 methylotrophy in Betaproteobacteria.

This work was performed under the auspices of the US Department of Energy's Office of Science, Biological and Environmental Research Program, and by the University of California, Lawrence Livermore National Laboratory under Contract No. W-7405-Eng-48, Lawrence Berkeley National Laboratory under contract No. DE-AC02-05CH11231 and Los Alamos National Laboratory under contract No. DE-AC52-06NA25396.