

Copper homeostasis in *Methylococcus capsulatus*.

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Methylococcus capsulatus (Bath) is a methanotrophic bacterium, able to utilize methane as sole carbon and energy source. *M. capsulatus* and some other methanotrophs express two forms of methane monooxygenase (MMO), depending on the amount of bio-available copper. When no copper is present or the bacteria is grown under low copper-to-biomass ratios, a cytoplasmic, or soluble, methane monooxygenase (sMMO) is expressed, while a membrane-associated, or particulate, methane monooxygenase (pMMO) is found at higher copper-to-biomass ratios (5). The sMMO enzyme system is irreversibly inhibited by copper ions, whilst the pMMO enzyme is a copper-iron enzyme complex. The morphology of *M. capsulatus* is also altered under the different growth conditions. The University of Bergen has in collaboration with The Institute for Genomic Research (TIGR) sequenced the complete genome of *M. capsulatus* (URL: <http://www.tigr.org>).

The unique morphologically and phenotypic changes of this bacteria on response to copper, makes it an interesting model system for exploring the role of copper in biology.

Based on the annotation of the *M. capsulatus* genome, we have tried to get an *in silico* overview over the different apparatus found that can import, sequester and export copper. Together with results from micro-array analyses and RNA- and protein-expression studies, we attempt to describe the copper homeostasis in *M. capsulatus*.

Results from our efforts to describe the role of copper in *M. capsulatus*, will be shown and discussed.