

Tracking heterotrophic and autotrophic carbon cycling by magnetotactic bacteria in freshwater sediments using DNA stable isotope probing

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Magnetotactic bacteria (MTB) are diverse, widespread, motile prokaryotes which biomimic mineralize nanosize magnetic minerals, either magnetite or greigite, under highly conserved genetic control and have magnetotaxis to align their position in aquatic environment according to Earth's magnetic field. They play important roles on some geobiological cycle of important minerals such as iron, sulphur, nitrogen and carbon. Yet, to date, their importance in carbon cycle and carbon source in their natural environment have not been previously studied. In this study, we focused on freshwater benthic carbon cycling of MTB and total bacteria using DNA stable isotope probing (DNA-SIP) technique coupled with quantitative PCR (qPCR). Pond sediments from Unterlippach (Germany) were amended with ^{13}C -labelled sodium bicarbonate and ^{13}C -labelled organic matter, and incubated in the dark over a two week time period. Applying separate qPCR assays specific for total bacteria and MTB, respectively, allowed us to estimate the contribution of MTB to total heterotrophic and autotrophic carbon cycling via DNA-SIP. After one week, there was a slight degree of autotrophic activity which increased markedly after two weeks. Comparing total DNA to the qPCR data revealed that changes in the buoyant density of DNA was due mainly to autotrophic bacterial production. DNA-SIP also identified heterotrophic utilization of ^{13}C -labelled organic matter by MTB after 1 week. The qPCR data also allowed us to estimate uptake rates based on the incubation times for heterotrophic and autotrophic MTB. High-throughput DNA sequencing of 16S rRNA genes showed that most of the MTB involved in carbon cycling were related to the *Magnetococcus* genus. This study sheds light on the carbon sources for MTB in a natural environment and helps unravel their ecological role in the carbon cycle.