

Title: Microbial competition for copper can enhance greenhouse gas emissions

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Project Goals: It is the general goal of this project to determine how microbial competition for copper affects net greenhouse gas emissions, specifically methane and nitrous oxide.

Abstract Text: Copper is an important trace nutrient for both methanotrophs and denitrifiers as it controls the activity and expression of key metabolic enzymes involved in methane consumption and nitrous oxide production, i.e., the methane monooxygenase (MMO) and nitrous oxide (N₂O) reductase (NosZ). Considering that methanotrophs and denitrifiers can co-exist in many environments, significant competition for copper can occur between these microbes. To collect copper, some methanotrophs secrete a copper-binding compound named methanobactin (MB) that has very high affinity for copper. MB is secreted into the environment, and after binding copper, is re-internalized via a specific TonB-dependent transporter (TBDT). *Methylosinus trichosporium* OB3b has two such MB uptake systems - one for uptake of its own MB (MB-OB3b), and another for uptake of MB from other methanotrophs, e.g., MB of *Methylocystis* sp. SB2 (MB-SB2). Interestingly, expression of the TBDT for MB-SB2 uptake in *M. trichosporium* OB3b is induced by MB-SB2, suggesting that some methanotrophs actively “steal” MB from other microbes. Moreover, both TBDTs are involved in regulating the expression of alternative MMOs in *M. trichosporium* OB3b. Active uptake of both forms of MB and the corresponding metabolic regulation thus exerts not only strong control on overall methane consumption by *M. trichosporium* OB3b, but also the activity of other methanotrophs. Interestingly, however, copper bound to MB is unavailable to denitrifiers as they lack the TBDT required for uptake. As a result, in the presence of MB or MB-expressing methanotrophs, complete conversion of nitrate to dinitrogen by denitrifying bacteria does not occur. Rather, as copper is unavailable to these microbes in the presence of MB, NosZ expression and activity is substantially reduced, significantly increasing N₂O emissions. Interestingly, MB-OB3b and MB-SB2 differentially affected copper uptake, *nosZ* expression and N₂O production by multiple denitrifiers. This study provides critical information for enhanced understanding of microbial copper competition that are important for the development of better predictive models of net greenhouse gas emission that are significantly controlled by microbial activity.

References/Publications

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