
Soil and phyllosphere microorganisms with potential impact on natural emissions of ozone-depleting chloromethane

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Abstract

Natural chloromethane (CH₃Cl) sources, mostly from vegetation, are responsible for 16% of the chlorine-dependent fraction of stratospheric ozone destruction with the phasing out of its anthropogenic emissions since the application of the Montreal Protocol in 1987. Atmospheric CH₃Cl emissions can be modulated by plant-associated microbial communities [1]. However, the taxonomical and metabolic diversity of the biotic CH₃Cl sink remains largely uncharacterized. Under laboratory conditions, CH₃Cl-degrading bacteria isolated from leaves and soils harbour the *cmu* pathway for chloromethane utilization [2]. Bacteria associated with CH₃Cl degradation in soils and plant leaves were identified by stable isotope probing [3] following incubation with ¹³C-labelled CH₃Cl. High through put sequencing of the heavy DNA targeted taxonomical and *cmu* genes as well as metagenomes.

In most experiments, detected taxa did not correspond to known *cmu*-containing bacteria [4],[5],[6]. In forest soil, taxa closely related to *Methylovirgula* and *Actinobacteria* were suggested to be associated with CH₃Cl degradation. Ongoing work on ¹³C-labeled metagenomes of CH₃Cl-degrading ferns and soils are expected to provide further information on one-carbon metabolism of the biological CH₃Cl sink in the phyllosphere and soil.

References.

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