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GREENHOUSE GAS AS A NUTRIENT: METHANOTROPHIC ACTIVITY IN SOILS OF HYDROTHERMAL SYSTEMS

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Abstract

Methane is the most abundant hydrocarbon in the atmosphere and a significant contributor to the radiative forcing with a global warming potential about 21 times that of CO₂. Methane is released to the atmosphere by a wide number of sources, both natural and anthropogenic, with the latter being twice as large as the former. Significant amounts of geological methane, produced within the Earth's crust (e.g. volcanic/geothermal areas), are currently released into the atmosphere (48 Tg CH₄/y).

Microbial oxidation in soils by methanotrophic bacteria contributes to the removal of CH₄ from the atmosphere for about 3-9%. Methanotrophs belong to the Gamma- and Alpha-proteobacteria and to the recently discovered acidophilic Verrucomicrobia.

Evidence of methanotrophic activity also in soils of volcanic/geothermal areas has been recently revealed, notwithstanding their harsh environmental conditions (high temperatures, low pH, high concentrations of H₂S and NH₃).

The purpose of our study was to verify the methanotrophic potential and the bacterial diversity of the soils of the main geothermal area of Pantelleria island (Italy).

Close to the fumarolic area (Le Favare) the mean detected temperature is about 90 °C at 30 cm of depth and the mean measured pH of the soil is about 4.8.

Laboratory incubation experiments with soil samples collected at the main exhalative area showed methane consumption values of up to 9500 ng/g of dry soil per hour while soils collected outside the geothermal area consumed less than 6 ng/g/h. Geothermal soils showed their maximum methane consumption in the shallowest part of the soil profile (0-3 cm). Furthermore they showed the maximum consumption at about 37°C, showing a still recognizable consumption (>20 ng/g/h) at 80°C. These results can be considered a clear evidence of the presence of methanotrophs.

In order to evaluate the bacterial diversity, soil metagenomic DNA was extracted from Le Favare and analysed using a Temporal Temperature Gradient Electrophoresis (TTGE) analysis of the amplified Bacterial 16S rRNA gene. The amplification of metagenomic DNA with primers targeting Proteobacterial and Verrucomicrobial MMO (methane monooxygenase) genes is in progress. Enrichment cultures on a mineral medium in a CH₄-enriched (25%) atmosphere led to the isolation of different strains that are under characterization.
