Microbiological evidences of methanotrophic activity in the soils of the geother

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Methane plays an important role in the Earth's atmospheric chemistry and radiative balance being the second most important greenhouse gas after carbon dioxide. Methane is released to the atmosphere from several sources, both natural and anthropogenic, with the latter being twice as large as the former. It has recently been established that significant amounts of geological methane, produced within the Earth's crust, are currently released naturally into the atmosphere. Active or recent volcanic/geothermal areas represent one of these sources of geological methane.

Microbial oxidation in soils contributes for about 3-9% to the total removal of CH4 from the atmosphere. Recent studies evidenced methanotrophic activity also in soils of volcanic/geothermal areas withstanding their harsh environmental conditions (high temperatures, low pH and high concentrations of H_2S and NH_3).

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).

Laboratory incubation experiments with soil samples collected at the main exhalative area showed methane consumption values of up to 9500 ng per g of dry soil per hour while soils collected outside the geothermal area less than 6 ng/g/h. Geothermal soils showed their maximum methane consumption in the shallowest part of the soil profile (0-3 cm) mantaining high values (>100 ng/g/h) at least up to dephts of 15 cm. Furthermore they showed the maximum consumption at about 37°C, showing a still recognizable consumption (>20 ng/g/h) at 80°C, and a positive correlation with the methane concentration in the incubation atmosphere.

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 analyzed 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 CH_4-enriched (25%) atmosphere allowed to isolate different strains that are under characterization.

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