Geophysical Research Abstracts, Vol. 8, 07244, 2006
SRef-ID: 1607-7962/gra/EGU06-A-07244

Methanotrophic population of a landfill cover soil - comparison of results from microbial diagnostic microarrays, PLFA and quinone measurements

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The atmospheric concentration of CH_4, an important greenhouse gas, has increased by a factor of 2.5 since the pre-industrial era. Thirteen percent of the global anthropogenic emissions derive from landfills. Microbial methane oxidation in the recultivation layer of landfill sites reduces CH_4 emissions from landfills. Understanding the microbial organisms involved helps to improve the design of an appropriate landfill cover. The samples for the study were collected from four different depths of 0.6 m deep lysimeters filled with a recultivation substrate (compost - gravel mixture) and vegetated with willow and poplar. The lysimeters were optionally fumigated with an artificial landfill gas (100 L CH_4 m^{-2} d^{-1}) and irrigated with landfill leachate or water for two years. The microbial methane oxidizing community was investigated by measurements of respiratory quinones, phospholipid fatty acids (PLFAs) and their δ^{13}C values and the use of oligonucleotide microarray targeting the particulate methane monooxygenase. The results obtained were compared and evaluated.

The microarray analysis clearly demonstrated the presence of comparable amounts of type Ia (strains of Methylomonas, Methylobacter, Methylomicrobium) and typ Ib (Methylocaldum, 501 group) to type II (Methylosinus, Methylocystis) methanotrophs under landfill gas fumigation and lower type I / type II ratio under water than landfill leachate irrigation. In correspondence, PLFA measurements showed an increase in 14:0, 16:1 isomers (present in type I methanotrophs) and 18:1 isomers (present in type II methanotrophs). Besides, the PLFA analysis showed a distinct depth dis-

tribution of the methanotrophic PLFAs depending on the type of methanotrophs and irrigation. Type I and Type II methanotrophic PLFAs correlated well with ubiquinone-8, generally found in β-proteobacteria but was also detected in strains of Methylomonas, Methylomicrobium, Methylobacter, Methylosinus and Methylocystis, and ubiquinone-10, present in α-proteobacteria, respectively. Measurement of the δ^{13}C values of the PLFAs confirmed incorporation of methane into type I methanotrophs, but not for type II bacteria. As the presence of obligate strains of type II methanotrophs was verified by the DNA analysis, this behaviour of type II bacteria was unexpected and has to be investigated in future research.