Geophysical Research Abstracts,
Vol. 11, EGU2009-7598-1, 2009
EGU General Assembly 2009

Denitrification gene expression in clay-soil bacterial community

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Our contribution in the Italian research project SOILSINK was focused on microbial denitrification gene expression in Mediterranean agricultural soils. In ecosystems with high inputs of nitrogen, such as agricultural soils, denitrification causes a net loss of nitrogen since nitrate is reduced to gaseous forms, which are released into the atmosphere. Moreover, incomplete denitrification can lead to emission of nitrous oxide, a potent greenhouse gas which contributes to global warming and destruction of ozone layer. A critical role in denitrification is played by microorganisms and the ability to denitrify is widespread among a variety of phylogenetically unrelated organisms.

Data reported here are referred to wheat cultivation in a clay-rich soil under different environmental impact management (Agugliano, AN, Italy).

We analysed the RNA directly extracted from soil to provide information on in situ activities of specific populations. The expression of genes coding for two nitrate reductases (narG and napA), two nitrite reductases (nirS and nirK), two nitric oxide reductases (cnorB and qnorB) and nitrous oxide reductase (nosZ) was analyzed by reverse transcription (RT)-nested PCR. Only napA, nirS, nirK, qnorB and nosZ were detected and fragments sequenced showed high similarity with the corresponding gene sequences deposited in GenBank database. These results suggest the suitability of the method for the qualitative detection of denitrifying bacteria in environmental samples and they offered us the possibility to perform the denaturing gradient gel electrophoresis (DGGE) analyzes for denitrification genes..

Earlier conclusions showed nirK gene is more widely distributed in soil environment than nirS gene. The results concerning the nosZ expression indicated that microbial activity was clearly present only in no-tilled and no-fertilized soils.