creatures with an unpleasant smell and very corrosive for industrial facilities and equipments. Hydrogen sulfide removal with Physical or chemical processes are energetically costly and would add other contaminant to environment. Biological processes could be used as alternative for H_2S removal due to its lower energy consumption and environmental friendly technology.

We examined the optimization of H_2S removal by *Thiobacillus thioparaus* DSM5386 in flask and then designed and constructed a biotrickling filter(BTF) for this purpose. The various cultivation media were tested to select the best media for bacterial growth and removing H_2S. Then an experiment was done to optimize the media composition by using Taguchi experimental design (L-18). Then the flask results used in a Biotrickling Filter (BTF) consisted of cylindrical packed bed reactor made of glass, and 120 cm in height filled with crushed Lava Rock. The H_2S removal studied in various empty bed resistance times (10-60 sec), pollutant concentrations (20-85 ppm) and air flow rates (10-60lit/min).

The flask result showed that the optimized condition was pH 7.5, Temperature 30 °C and inoculum size 10% and optimized media also found. The experimental values (L-16) showed no interaction between factors. Experiments in BTF showed that in the range of 10-80 ppm H_2S concentration and EBRT 20-60 sec, the removal efficiency was 100%, but by decreasing the EBRT to 15 second, efficiency reached to 90%. A maximum elimination capacity of 31 $gH_2Sm^{-3}h^{-1}$ was observed with more than 95% removal efficiency.

A BTF using lava rock as the support was immobilized with *Thiobacillus thioparus* and had an acceptable level of performance during steady condition. Understanding the optimized condition for H_2S removal increased the efficiency of H_2S biodegradation.

doi:10.1016/j.jbiotec.2010.09.240

[P-E.219]

Propylene glycol-specific dehydrogenases as functional biomarkers for monitoring biodegradation in sites contaminated by de-icing chemicals

L. Cavalca [1,*], S. Ciccazzo [1], R. Scotti [2], M.A. Rao [2], M.L. Colarieti [3], G. Toscano [3]

[1] *DiSTAM, Università degli Studi di Milano, Italy*
[2] *DiSSPA, Università di Napoli Federico II, Italy*
[3] *DIC, Università di Napoli Federico II, Italy*
Keywords: Propylene glycol; soil contamination; biodegradation; ADH-IIG

The area under study at Gardermoen airport (Oslo, Norway) is a glacial contact formation with sand and gravels dominating near the ground surface. Due to the northern climate, every winter large amounts of de-icing chemicals, i.e. propylene glycol (PG) and potassium formate, are commonly used in the airport for the removal of snow and ice from airplanes and runways, respectively. Even though these contaminants are easily degradable by biotic or abiotic factors, they may still threaten groundwater, due to the system overloading.

The present study, performed within the FPVII European research project: "SoilCAM - Soil Contamination: Advanced integrated characterisation and time-lapse Monitoring", deals with the physic-chemical and microbiological characterization of the site and the development of suitable methods for monitoring PG biodegradation on site under reclamation. For this purpose, functional biomarkers were selected to evaluate their potential use in Real Time quantitative PCR (q-PCR) experiments directly on soil DNA. The soils are highly leached, with low biological and biochemical activities. Therefore, pollutant transfer to the groundwater occurs quickly and is virtually unhindered. Bacterial strains isolated from the soil were able to degrade PG in aerobic conditions at 4, 15 and 30 °C. The PG-degrading population was mainly composed by different species of *Pseudomonas*, as shown by denaturing gradient gel electrophoresis (DGGE) analysis on soil DNA. Gene probes for PG-specific alcohol dehydrogenase (ADH-IIG) detected the presence of such genes in the isolates. The deduced amino acid sequence of representative strains presented over 92% identities with PG-specific dehydrogenase-related proteins. ADH-IIG detected in soil DNA indicated that PG-degrading strains were present along the soil profile from 0 to 100 cm.

The application of q-PCR analysis on DNA from soil mesocosm experiments will confirm the suitability of ADH-IIG as biomarker for monitoring PG biodegradation in soil systems.

doi:10.1016/j.jbiotec.2010.09.241

[P-E.220]

Response of soil microbial communities to iron-porphyrin catalytic amendments

V. Ventorino [1,*], A. De Marco [2], O. Pepe [1], A. Virzo [2], A. Piccolo [3], G. Moschetti [4]

[1] *Department DSA, University of Naples "Federico II", Italy*
[2] *Department DBSF, University of Naples "Federico II", Italy*
[3] *Department DISSPAPA, University of Naples "Federico II", Italy*
[4] *Department S.EN.FI.MI.ZO., University of Palermo, Italy*
Keywords: microorganisms; soil carbon sequestration; iron-porphyrins

Intensive agricultural practices strongly increase CO_2 emission from soil. Synthetic metal-porphyrins were shown to significantly decreased CO_2 emission from soil due to an *in-situ* catalysis of oxidative polymerization of soil organic matter.

This research aimed to assess the effects of iron-porphyrin (POR) amendments on soil microbial communities in three arable soils under wheat and maize cropping located in Naples, Turin and Piacenza, characterized by different pedological and climatic conditions. Bulk-soil and rhizo-soil were sampled during 4 years and the microbial groups directly involved in organic matter (OM) mineralization and in key processes of the nitrogen cycle were examined. Moreover some microbial indicators of soil quality, i.e. microbial and fungal biomass, basal respiration, metabolic quotient (qCO_2), and coefficient of endogenous mineralization (CEM), were measured.

Unexpectedly, POR treatment in bulk-soil caused a significant increase in microbial groups directly implicated in OM mineralization, in respect to NOPOR control. Consistently CEM was higher in POR treatment than in control.

By contrast, the effect on rhizo-soil was different. In maize rhizosphere, POR treatment showed a significant decrease in microbial populations involved in the turn-over of OM as well as in fungal biomass, in respect to NOPOR. In wheat rhizosphere, there was no significant difference between POR and NOPOR treatments. However significantly higher CEM were found in POR rhizo-soil of Naples and Turin in the second and in the third experimental years, respectively. Finally, POR treatment did not significantly influence aerobic free-living N_2-fixing, ammonia-oxidizing and denitrifying bacterial populations. The iron-porphyrin significantly reduced fungal biomass and the ratio fungal C/microbial C, suggesting a higher sensitivity of fungi to POR or to POR end-products.

In conclusion, the effects of iron-porphyrin treatments on microbial communities are different in bulk- and rhizo-soil as well as in maize and wheat crop.