31st Meeting of SIMGBM
Società Italiana di Microbiologia Generale e Biotecnologie Microbiche

MICROBIOLOGY 2015

SEPTEMBER 23 - 26
PALAZZO DEI CONGRESSI
RAVENNA

www.simgbm.it

integrated approach based on chemical, isotopic and microbiological analyses was developed to assess different parameters at laboratory scale and, therefore to pinpoint the source of contamination, to evaluate the occurrence of specific biodegradation processes and to identify microorganisms which are involved in.
In this respect, microcosms with groundwater and sediments from the above-mentioned site were set up and incubated under aerobic condition for 60 days. Biostimulated microcosms were also prepared adding nutrients, mainly nitrogen and phosphate. Moreover, heat-killed microcosms were set up and referred to as abiotic controls.
Concerning the biotransformation process, MCB (≈ 110 µg mL^{-1}) was generally completely removed in microcosms enriched with N and P within only 7 days, while a slower degradation kinetics was observed in the other microcosms (80% removed within 60 days). These results confirmed that a natural attenuation could occur at the contaminated site under specific oxidative conditions. However, the degradation process could be limited by the depletion of nutrients. Compound Specific ^{13}C Isotope Analysis (CSIA) confirmed a negligible isotope fractionation under oxidative conditions as already reported in previous studies. Thus, isotopic fingerprinting based on chlorine isotopes fractionation was planned (analysis still in progress). High-throughput sequencing (Illumina) analysis and quantitative PCR were also performed to gain insights into the structure of the microbial community and to quantify the copy number of possible taxonomic and functional biomarkers, which can be coupled with isotopic fingerprints for a complete assessment of biodegradation processes *in situ*.

B42. *Clostridium perfringens* as a "worst case" faecal indicator in soils and sediments

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Faecal Indicator Bacteria (FIB), such as *Escherichia coli*, are used to estimate faecal pollution in different environments. In the last years, several studies showed that a low correlation between the FIBs' abundance and pathogens might occur. Here we investigate *Clostridium perfringens* spores as a potential indicator of faecal contamination. *C. perfringens* is an anaerobic bacteria normally found in gut microbiome. In hostile conditions, this organism stops growing and produces spores, resistant forms able to survive in the environment for long time (months). Therefore, it is possible to consider the presence of spores of *Clostridium perfringens* as "the worst possible case": the presence of *C. perfringens* spores could suggest the occurrence of other persistent faecal pathogens. Aims of this study were i) to validate the ISS F004B method, recently developed by the "Istituto Superiore di Sanità" (ISS) for the quantification of *C. perfingens* spores, through interlaboratorial tests; ii) quantify the *C. perfringens* spores in soils and sediments showing different levels of pollution. The abundance of *C. perfringens* was hence measured in i) sediments deriving from the dredging of channels exposed to faecal contamination and biologically treated, ii) soils from different land uses not impacted by faecal contamination, iii) sludges from sewage plants, iv) compost and v) manures.
In the ISS F004B method spores are detected with a thermal shock that allows both the germination of spores and inactivation of the vegetative cells. Two selective media (mCP agar and TSC agar) are used for the bacteria isolation.
To validate the method, 12 common samples in duplicates were analyses in 3 different laboratories. No significant differences were observed among the values produced by the three laboratories.The concentrations of *C. perfringens* spores (ca. 20,000 cfu/g_{dw}) in sediments were higher than those in soils (ca. 400 cfu/g_{dw}) and lower than those in sludges (over 50,000 cfu/g_{dw}). Compost samples did not show the presence of spores while manures displayed a quantity of spores similar to those of the sediments (6,000 cfu/g_{dw}).

B43. Ground tire biodesulfurization process: microbial community characterization and properties of compounds containing biodesulfurized material

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The aim of the present study was to test bioreactor-based ground tire (GTR) biodesulfurization processes using two different strains: i) *Gordonia desulfuricans* 213E, a strain described in a biodesulfurization process patent and ii) *Rhodococcus* sp. AF21875, a strain isolated from tire factory wastewater. The latter strain was found to use dibenzothiophene (DBT) over sulfate as a preferred sulfur source, generating 2-hydroxybiphenyl through the desulfurization pathway encoded by the *dsz* operon. Pathways for assimilatory sulfate reduction and cysteine biosynthesis have been detected by whole genome shotgun sequencing and analysis. In addition, *tau*ABCD and *ssu*EADCB genes were annotated, along with a putative plasmid harboring the *dsz*ABC genes. Since the GTR material used was not sterile, automated ribosomal inter-genic spacer analysis (ARISA) and Illumina sequencing of 16S rRNA gene amplicons were used to analyze samples collected from the bioreactors over time to detect the persistence of the inoculated bacteria within the autochthonous communities, and to compare communities in the bioreactors inoculated with the different strains. Furthermore, the abundance of total bacteria (16S rRNA) and biodesulfurization potential (*dsz*A) were estimated using qPCR. ARISA showed that *G. desulfuricans* 213E was able to persist, while analysis of the bioreactor containing AF21875 was confounded due to the presence of matching ARISA fragments in the untreated GTR. In the bioreactors, a high abundance of genus *Gordonia* and *Rhodococcus* was observed, respectively. Both bioreactors showed an increase of *dsz*A copy numbers over time. The desulfurized GTR from each bioreactor was blended with fresh natural rubber in order to test if devulcanized rubber can be used for compounding and revulcanization. The results showed that the both biological process led to an increase of the mechanical and rheological properties of vulcanizates containing biodesulfurized GTRs compared to the untreated GRT.

B44. Distribution of laminar macrocolonies of *Nostoc* cf. *commune* around the Arctic

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The cyanobacterium *Nostoc commune* forms large curled laminar macrocolonies that develop on top of various substrates saturated with water, like grass, mosses, sand, gravel, and even road asphalt. The identity of these macrocolonies, whether each of them is made up of a clonal *Nostoc* population or, alternatively, more cyanobacterial strains, even not all of them belonging to the same species, are harboured in the same lamina, still needs to be definitely clarified.
In favourable conditions, a number of laminae can rapidly grow on a wide area, even exceeding the dimension of a football playground. Apparently, each lamina, up to the dimension of a small handkerchief, is separated from the others nearby, but by inspecting at a short distance, gelatinous ramifications can be seen that creep into the substrate or vegetation, and a marked boundary of the macrocolony cannot be defined. This raises the question whether a single or multiple populations colonize the same area. Because the species *Nostoc commune* is considered to be ubiquitous, an investigation on the degree of its intra-specific diversity among far away locations and different habitats is worth to be done. The task would be relatively simple because macrocolonies of *Nostoc* cf. *commune* (morphologically similar to the species *N. commune*) are easily picked