MICROBIAL COMMUNITY SHIFTS IN KEROSENE POLLUTED SOIL

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Results

Introduction

A major part of anthropogenic activities have as consequence release of petroleum and its derivates into various ecosystems. Thus, endogenous microbial communities show versatility and high adaptation capacity, being able to survive in most any new environmental condition. This study analyses for 80 days, the structural and metabolic shift of a soil microbial community following kerosene pollution. Metabolic profiles of the community at given time points were obtained using Biolog Ecoplates System, for utilization of 31 different carbon sources. Data from each plate was normalized by the average well color development (AWCD). Statistical analysis implied guild grouping and one-dimensional relative divergence metric (Weber and Legge, 2009). Structural studies addressed molecular level using Ribosomal Intergenic Spacer Analysis (RISA). Data analysis was performed on OTUs (Operational Taxonomic Units) on ITS (Internal transcribed spacer) phylotype (Böer et al., 2009). The highly complex 31dimensions data was compressed into 5 dimensions, and the total carbon source utilization percentage was divided in 5 guilds accordingly. Shifts in the % of carbon utilization for the 5 groups, in time, following pollution implied significant functional changes in the microbial community. Functional divergence expressed as Euclidean distance confirmed the drastic metabolic shift from the initial point. Moreover, the number of OTUs preceding pollution drastically decreased, thus suggesting a high taxonomical specialization within the microbial community. This study reveals an endogenous microbial community shift of the metabolic activities, confirmed also as a structural specialization, as an expression of the high adaptation potential of the microbial communities to new environmental conditions.

Methods

- A. Metabolic assay: Biolog Ecoplates
- **B. Molecular study:** Ribosomal Intergenic

Spacer Analysis (RISA)

Statistical data analysis



Fig. 1 The % of total carbon source utilization for each guild over the 80 days study period.

B. MOLECULAR STUDY Operational taxonomic units (OTUs) shift



Fig. 3 OTUs Turnover for 80 days. The line represents the number of OTUs for every sample. Bars show the % of OTUs shared (striped)/not shared (not striped) between a sample and the previous one.

A. METABOLIC ASSAY

b) Functional community divergence



Conclusions

- pollution.
- taxonomical level.

References

Weber K. P., Legge R. L., 2009. One-dimensional metric for tracking bacterial community divergence using sole carbon source utilization patterns. Journal of *microbiological methods*, 79(1), 55-61. Böer S. I., Hedtkamp S. I., Van Beusekom J. E., Fuhrman J. A., Boetius A., Ramette, A., 2009. Time-and sediment depth-related variations in bacterial diversity and community structure in subtidal sands. *The ISME journal*, 3(7), 780-791.





Fig.2 Community divergence obtained by Euclidean distance for 80 days following kerosene pollution (day 0).

Statistical processing of Biolog Ecoplates data captured the metabolic shift of the microbial community adaptation following kerosene

• After the pollution event it was observed a high functional community divergence between subsequent samples and the initial one.

Molecular profiles, represented by the number of detected OTUs and sample similarities, reflected the community specialization at