Tracking the dynamics of microbial communities inhabiting contaminated soils through the integrated use of electrochemical anaerobic reactors and genomic based modeling

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Introduction

Accidental oil spills and industrial discharges have resulted in pollution of the environment with monoaromatic hydrocarbons, such as benzene, toluene, ethylbenzene and xylene (BTEX). As a result, high concentrations of BTEX have been detected in soils, sediments and groundwater, and the cleanup of aromatic hydrocarbons polluted soils, has gained much attention in the last decades. Under anaerobic conditions, monoaromatic hydrocarbon degradation is a complex, multi-stage process, involving many microbial species. Soil microbial communities are highly heterogenic and complex and play essential roles in biogeochemical cycles. Generally, as a result of soil contamination, oxygen is rapidly depleted by aerobic respiration. Consequently, a gradient of redox zones is often developed, leading to prevalence of methanogens, especially near the source of the pollution. The methanogens act as the terminal members of the degradation and are critical for maintaining the process thermodynamically favorable by utilizing acetate and hydrogen produced in earlier stages of degradation and keeping their concentrations low. Although it is known that methanogenic hydrocarbon metabolism takes place in BTEX-contaminated environments, explicit syntrophic partnerships in such systems is far from being understood.
In this study, we developed a method for spatially dissecting the metabolic activity of complex soil microbial communities involved in BTEX biodegradation.

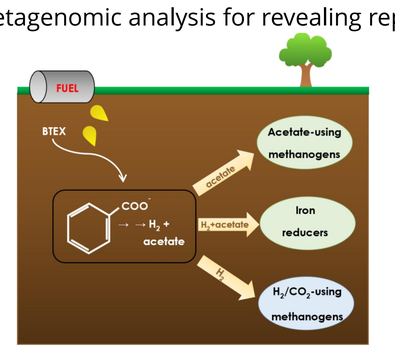
Objectives

1. Design and develop a successful three-chamber anaerobic system for analyzing the microbial removal of BETX from different types of soils.
2. Microbial community structure characterization in each of the three chambers.
3. Develop soil bioremediation schemes through metabolic modeling.

Methodology

1. Monitor reactors' operation (before and after BTEX-spiking) by measuring gas emissions (CH4, H2 and CO2), volatile fatty acids (VFAs) and BTEX degradation.
2. DNA extraction from each bioreactor and 16S amplicon sequencing to determine bacterial and archaeal diversity.
3. Metagenomic analysis for revealing representative species in each reactor chamber.

a



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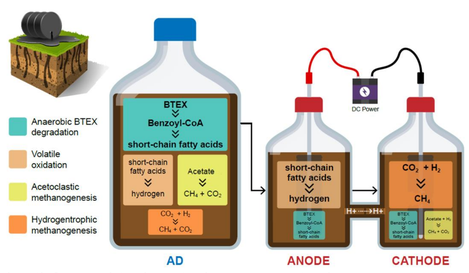
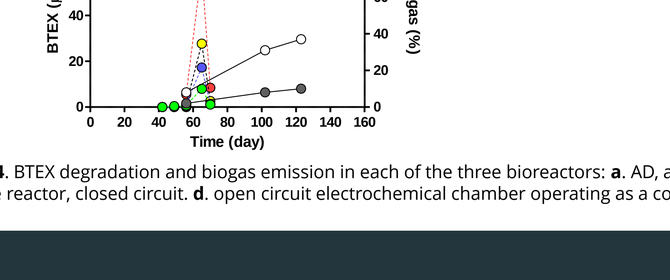


Figure 1. a. Schematic illustration of biodegradation processes in contaminated soil; **b**. Key biochemical processes in the reactor system

a



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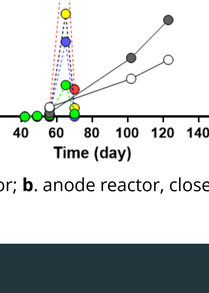

Figure 2. **a**. a picture of the three-chamber anaerobic systems currently operating at the Galilee Society Institute of Applied Research; **b**. experiment set-up.

Results – Monitoring reactor operation

Figure 4. BTEX degradation and biogas emission in each of the three bioreactors: **a**. AD, anaerobic digestor; **b**. anode reactor, closed circuit; **c**. cathode reactor, closed circuit. **d**. open circuit electrochemical chamber operating as a control.

Results – 16S Amplicon sequencing

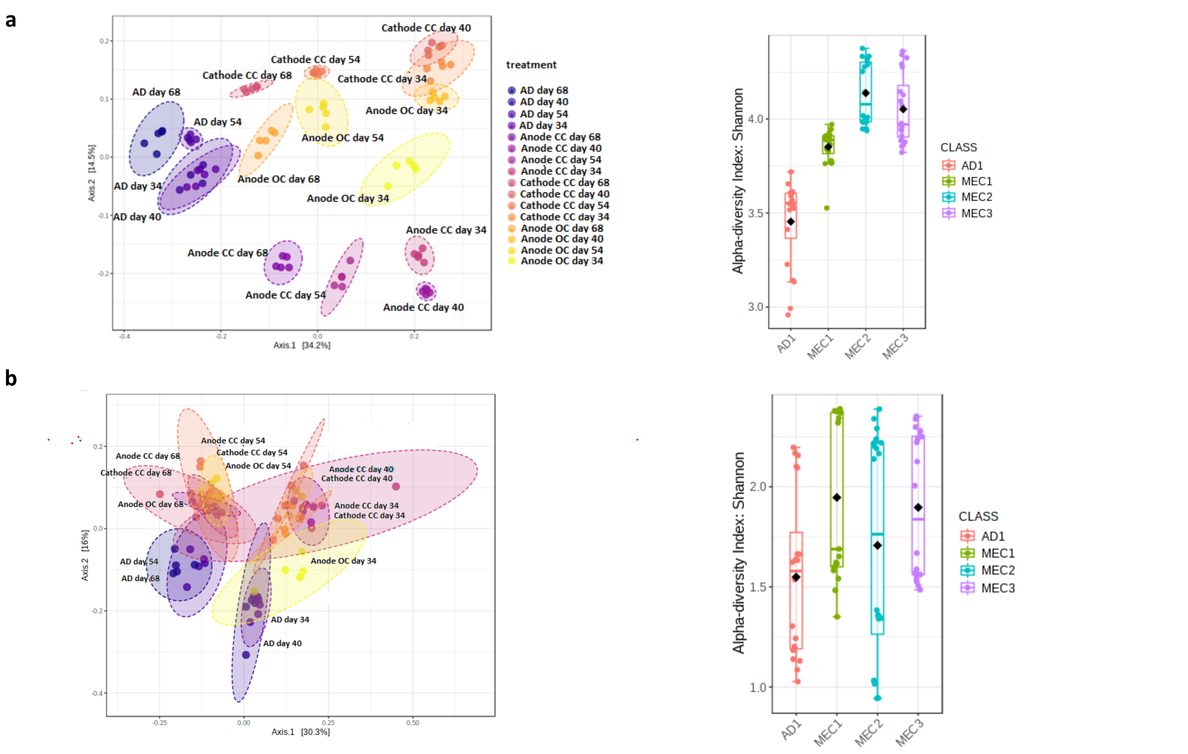

Figure 5. Alpha diversity (Shannon index) and Beta diversity (Bray-Curtis dissimilarity distance) of the three-chamber system: **a**. Bacteria; **b**. Archaea.

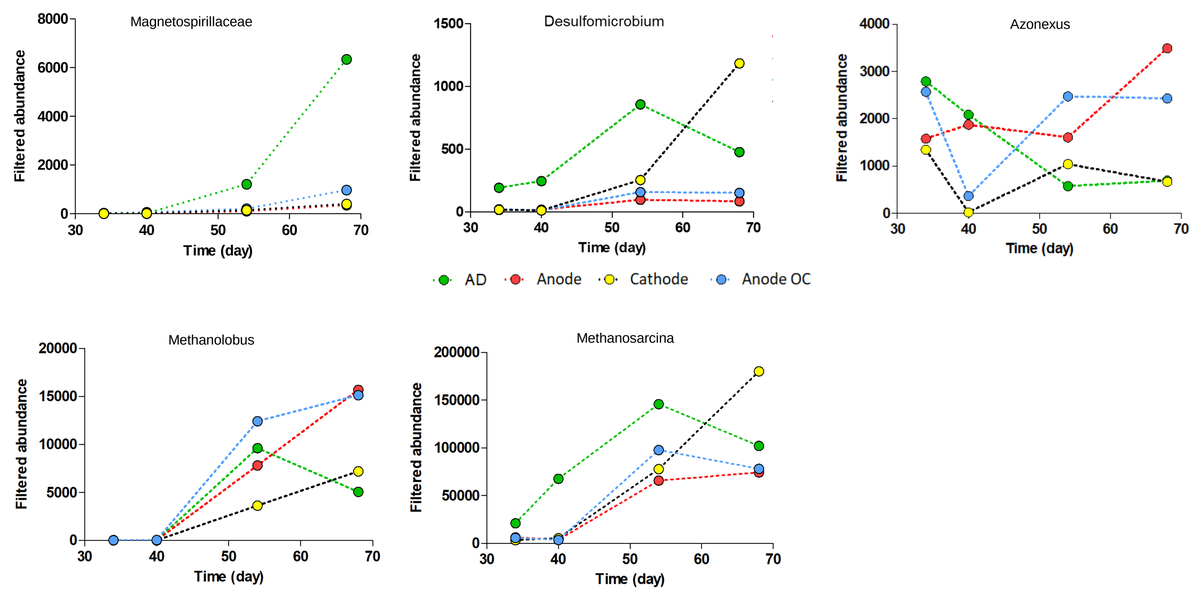

Figure 6. Normalized abundances of three representative bacteria and two representative archaea found significantly different among the different treatments using LEfSe.

Summary

1. The three bioreactors show different patterns of biogas emissions, indicating different bacterial and methanogenic communities were enriched.
2. While bacterial community diversity changed both temporally and by reactor-type, archaeal diversity changed only temporally (before vs. after BTEX-spiking).
3. Representative differentially abundant bacteria include: BTEX degraders and anode-associated organisms.
4. Representative differentially abundant archaea were mainly identified as methanogens.

Further research plans

1. Revealing the mechanisms underlying the high-performance in the three-chamber-reactor by combining community ecology with metabolic modeling. Conductance of multiple computational simulations will allow predicting optimal conditions for gaining a better control on the pollutant degradation efficiency at each metabolic stage.
2. Testing the prediction-based optimal conditions in the three-chamber experimental system.

Acknowledgements

I thank Prof. Zeev Ronen for his help in designing batch anaerobic experiments with soil microbial communities, and Dr. Maya Lalzar for her help with the bioinformatic analysis.