Methanogenesis and methanotrophy in Lake Kinneret (Israel)

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In this research we quantified the rate profiles of methane production (methanogenesis) and consumption (methanotrophy) in Lake Kinneret (Israel). This is by performing seasonal high resolution chemical and isotopic profiles in the lake water column and sediments' porewater and by modeling the data.

Water samples and sediments cores were collected from the lake every two months for 14 months and being analyzed for methane and its possible coupled species - sulfide, sulfate, oxygen, iron (II and III), alkalinity and dissolved inorganic carbon (DIC), as well as the stable isotopic composition of carbon in the DIC and methane. Sulfate reduction, methanogenesis and methanotrophy rate profiles were conducted based on the chemical and the isotope profiles.

The results show that anaerobic sulfate reduction dominants the upper 7 cm of the sediments, and dissolved iron (almost entirely Fe(II)) starts increasing as sulfide is depleted. Methane starts to accumulate when sulfate is almost depleted, where there might be an overlap between methanogenesis and sulfate reduction. Methane and the stable isotopic composition of carbon in the DIC porewater profiles imply that methanogenesis is restricted to a certain layer (5-12 cm depth). The obvious methanotrophy occurs at the thermocline, however our data and incubation experiments suggest the possibility for anaerobic methane oxidation in Lake Kinneret.

Genomics as a tool to analyze bioremediation potentials and functional diversification in subsurface environments

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Anaerobic subsurface environments such as anaerobic aquifers, terrestrial deep subsurface materials and marine sediments are inhabited by massive amounts of bacteria. Population analyses using molecular techniques have demonstrated diverse communities including many bacteria for which no physiological characterization and no ecological role is known. While population analyses mostly rely on sequencing of 16S rRNA genes, genome analyses of either single (isolated) strains or of full communities can contribute to the understanding of physiological characteristics because functional genes are identified.

As an example, a specific group of the bacterial phylum *Chloroflexi* was detected in many contaminated and non-contaminated subsurface environments but cultivation yet failed. The closest relatives of this group are bacteria of the genus *Dehalococcoides* that are physiologically characterized and the genome of three *Dehalococcoides* species is fully sequenced. *Dehalococcoides* species are strictly anaerobic bacteria that rely in their metabolism on halogenated compounds which are used for a respiratory process. Genome sequencing shows evolution of a wide range of respiratory proteins that enable growth with unusual substrates. Judged from the genomes, the bacteria rely on symbiotic partners in regard to buffering of redox conditions, cofactor production, hydrogen production, acetate production and nitrogen fixation. The presented genomes not only give a reference point to genomes of respiratory dehalogenating bacteria, they also allow comparative analysis and possibly comparative annotation of yet unknown genes identified by metagenomic approaches from other subsurface environments.

[1] Kube *et al*. (2005) *Nature Biotechnology* **23**,1269-1273.