

Abstract

The amount of data obtained by barcoding of prokaryotic 16S rDNA from natural habitats is increasing exponentially. Thus, methods enabling us to extract useful information from these data are of increasing importance. In this thesis microbial communities from water, sludge and drilling dust were analyzed by 16S rDNA sequencing in three geologically well described sedimentary aquifers in Bohemian Massif. The main goal of this research was to establish how different analytical approaches can be useful in interpretation of groundwater biogeochemical processes. Three approaches were used: First, taxonomy and metabolic traits of the most abundant microorganisms were assessed. Second, ordination methods showing metabolic and taxonomic variability between communities were used. Last the analysis of phylogenetic dissimilarity using UniFrac metrics was performed. When analyzing individual localities separately, the shift in microbial community composition corresponds with the change of environmental conditions. The unconstrained ordination method based on the variability in metabolic traits indicated, that sludge samples are more informative than water samples when asking which electron donor is used in microbial communities. On the other hand, unconstrained ordination methods were useless when the variability in operational taxonomic units (OTUs) between samples was calculated, since microbial communities share usually only small portion of OTUs. The phylogenetic dissimilarity analysis in combination with the other two methods provided new information regarding the aquifer conditions. This method can capture changes in phylogenetic microbial community composition before and after a borehole was drilled, or differences between environments with various degree of energy source limitation. A combination of these methods can provide significantly more information about trophic relations in hydrogeological wells than chemical analysis or traditional microbiological approaches.

Key words: microbial communities, Illumina, beta diversity, 16S rDNA, groundwater, aquifer, microbial metabolism, biogeochemical cycles, UniFrac