



Numerical ecology allows linking microbial community structures and geochemical processes

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The first challenge in microbial ecology has been to obtain reliable data on the structure and dynamics of *in situ* microbial communities. From the 90's on, different powerful molecular profiling (fingerprinting) techniques have been developed and have been applied to all types of microbial habitats. The next challenge is now to proceed to the in-depth exploitation of these data and above all to link them with other data sets coming from the habitat structure, and from biological and geochemical processes. Plant ecologists have developed a collection of statistical tools since the 80's in a field called numerical ecology for the handling and representation of data obtained from field studies or generated in laboratory experiments. These tools allow establishing a connection between the communities and the inherent processes of the habitats. The application of these tools is either purely descriptive or can be formulated as a confirmation or rejection of causal hypothesis and development of new models. The majority of the methods are multivariate or multi-dimensional as they handle complete sets of samples which are defined by many observations and measurements. Generally, a community dataset, made of species occurrences or abundances, is considered the multivariate response to a combination of environmental and spatial variables.

Here we report the application of these statistical tools to the analysis of complex bacterial community structures sampled from tetrachloroethene (PCE) contaminated aquifers. PCE and the corresponding daughter molecules (trichloroethene, dichloroethene, and vinyl chloride) are among the most commonly observed groundwater contaminants. In reductive environments, these molecules are acting as terminal electron acceptors of a respiration chain in a process called dehalorespiration. In this example, bacterial community structures were resolved with a terminal restriction fragment length polymorphism (T-RFLP) analysis. The results of the T-RFLP analysis

clearly demonstrated a large heterogeneity of the community composition among all samples. Correlations with high probability values were obtained between the community structures and the geological settings of the wells, the chemical composition of the aquifer water (as well as the contaminant concentrations), showing the high adaptation degree of the communities to their environment. Important variables such as the presence of silt and clay particles could be highlighted, helping developing a conceptual model of the activity of the dehalorespiring guild in these contaminated aquifers.