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Microbial diversity in marine sediments – what do we know about vertical, horizontal and temporal distribution patterns?

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This presentation will deal with the known, unknown and knowable factors influencing microbial diversity in the seabed. Investigations of animal diversity on the ocean floor have resulted in some general principles. For example, animal diversity is higher at bathyal compared to abyssal depths, at vents and seeps compared to surrounding regions, at habitats under medium disturbance compared to low and high disturbance, in oxygen rich compared to oxygen depleted habitats, in tropical compared to polar settings. We still do not know if any of these factors are relevant to explain variation of microbial diversity. Exploration of microbial diversity in the seabed so far has been mostly limited to comparisons of numbers of 16S rDNA sequences of various phylogenetic units, which is commonly used as “species richness” definition in microbial ecology, despite known problems with PCR biases (e.g. Bowman et al. 2003). This approach has at least helped to show that there are distinct differences in community composition between sites, and that certain microbial clusters appear endemic to certain habitats (e.g. to hydrate-containing sites (Inagaki et al. 2006); to hydrogen-rich hydrothermal vents (Reysenbach and Shock 2002)). A few works have also tackled the question of relative abundances of species using FISH or quantitative PCR to obtain in situ abundances of phylogenetic groups. Due to the considerable time and expertise needed to implement those methods, the amount of data available for statistical analyses has however been a limiting factor (e.g. Knittel et al. 2003; 2005; Bowman et al. 2005). Some of the first works in microbial ecology of the seabed showed a correlation of the abundance and activity of microbial communities with increasing water depth and decreasing flux of organic matter to the seabed (Deming and Baross 1993, Lochte 1992), or increasing sediment depth into the deep biosphere realm (Parkes et al. 1993), but it remains unknown if such trends are accompanied by significant changes in species richness or relative abundance of species. Biogeochemical investigations have established the image of the “electron tower” (the vertical sequence of electron donors and acceptors available for energy gain by microbes) as a main structuring factor of microbial metabolism. This concept has influenced most recent investigations of microbial diversity in the seabed, which concentrate on the distribution of functional groups in their potentially preferred sediment horizons (scales of cm to hundreds of m). On these scales, almost nothing is known about horizontal variation in microbial diversity, which may be caused by sediment mixing, small-scale variability introduced by animal burrows, seabed morphologies, etc. However, such investigations are important to test the applicability of ecological principles to microbial communities such as the taxa-area relationship (Horner-Devine et al. 2004). Furthermore, we do not have any knowledge about temporal variation of microbial diversity in the seabed, neither about seasonal patterns, nor succession of communities after disturbances. Using a combination of community fingerprinting techniques (e.g. Hewson et al. 2003, 2006) and multivariate gradient analyses, we show that it is now possible to identify the main factors at stake in very complex situations involving hundreds of genotypes, tens of environmental variables, along with vertical, horizontal and temporal information of the samples. Based on examples from our work on coastal sediments and from deep-sea ecosystems, which correlate community composition with habitat variability, this presentation will discuss emerging ecological trends of microbial diversity in the seabed.