



UFZ-Kolloquium



20. Juni 2011, 15.00Uhr

Saal, Brückstr. 3a, Magdeburg

Klaus Jürgens, Leibniz Institute for Baltic Research, Rostock-Warnemünde
spricht zum Thema:

Microbial Ecology Of A Brackish Water Environment: Salinity And Redox Gradients Of The Baltic Sea

The Baltic Sea is one of the largest brackish water systems and characterized by a wide horizontal gradient in salinity but also by vertical redox gradients in the central basins. This makes it a fascinating aquatic ecosystem to study changes in the structure and function of microbial communities in relation to environmental gradients.

We recently obtained the first detailed bacterial inventory from 60 sampling stations distributed along the salinity gradient of the whole Baltic Sea, generated by using 454 pyrosequencing of partial 16S rRNA genes. Bacterial community composition altered at broad and finer-scale phylogenetic levels along the salinity gradient and a distinct bacterial brackish water community, comprising a diverse combination of freshwater and marine groups, along with populations unique to this environment, could be identified. In contrast to multicellular organisms, bacterial richness and diversity does not seem to be constrained by brackish water conditions. It is possible that the rapid adaptation rate of bacteria has enabled a variety of lineages to fill what for higher organisms remains a challenging and relatively unoccupied ecological niche. Experiments are in progress to elucidate whether and how these phylogenetic and functional genomic shifts affect microbially mediated ecosystem functions such as degradation of different organic compounds.

The oxic-anoxic transition zones in the central Baltic Sea are sites of important element transformations which impact the overall biogeochemical cycles (e.g., of N, S, C, trace metals) and are therefore relevant on an ecosystem scale. Furthermore, these environments can be considered as model systems for ancient oceans which were dominated by anoxia through much of the Earth's history. Recent studies in the central Baltic Sea redoxclines revealed the exceptional importance of relatively few, mostly chemoautotrophic prokaryotes which dominate microbial abundance and production in the pelagic redoxcline, and occupy key roles in transformations within the sulfur (H₂S oxidation) and nitrogen cycle (e.g., ammonia oxidation, denitrification). By applying techniques to link structure and function (e.g., MICRO-CARD-FISH, SIP-RNA), some of the responsible organisms could be identified. Insights into the adaptation of these organisms to the steep physico-chemical gradients were derived from gene expression patterns and genome analyses of an isolated key player. Despite these advances, we still largely miss a thorough understanding of the underlying regulating mechanisms, and of the interplay between hydrography (e.g., intermittent mixing events), redox driven energy generation, and development of microbial populations.

Falls Sie eine Videoübertragung nach Halle oder Leipzig gewünscht wird, bitte ich um eine E-Mail an hella.nietsch@ufz.de bis spätestens Freitag (17.6.), 12:00Uhr.