

# SFB 960-/BZR – Kolloquium

8. Juli 2014, 17.00 Uhr

BIO 5.2.38



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### ***Visualizing bottom up and top down control of bacterial populations in the ocean***

“Central steps of global biogeochemical cycles are catalyzed by marine Archaea and Bacteria. Molecular fingerprints have long indicated novel, often high microbial diversity, but fell short of quantifying specific population sizes. Fluorescence in situ hybridization (FISH) with rRNA-targeted oligonucleotide probes can today routinely provide such quantitative data on spatio-temporal distributions, and exact localizations. By catalyzed reporter deposition fluorescence in situ hybridization (CARD-FISH) abundant marine “key species” can even be accurately quantified in very oligotrophic environments. In combination with meta-genomics and meta-proteomics we can arrive at detailed mechanistic predictions (Teeling, Fuchs et al. Science 2012). These cultivation-independent molecular approaches are, however, always referring back to ground-truthed information obtained on pure cultures. For some relevant marine heterotrophic polymer-degrading bacteria we have recently obtained isolates, this includes representatives of the abundant marine class of Flavobacteria, e.g., “*Gramella forsetii*” (Phylum *Bacteroidetes*). The genome of “*G. forsetii*” shows characteristic adaptations to the degradation and uptake of polysaccharides which could explain deterministic substrate-driven successions of bacterioplankton clades during the breakdown of massive phytoplankton blooms. As much as these bottom-up effects are ruling the marine carbon cycle, also top-down effects such as protozoal grazing or viral lysis are of high importance in biogeochemical element cycling. To this end, a novel method termed phageFISH will be presented.”

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