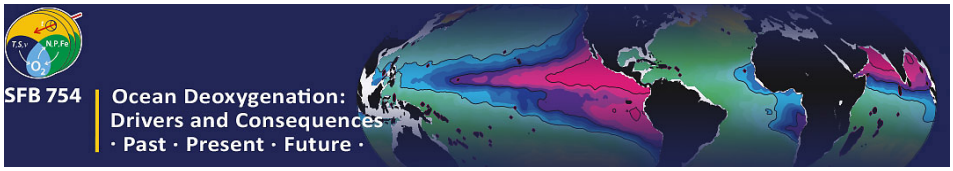

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Foraminifera as bacterial microniches in benthic biochemical processes?

Foraminifera are unicellular macroscopic eukaryotes found in a wide range of marine environments. Benthic species reach high abundance up to >500 individuals per square centimetre at sea floor sediments and exceed metazoan (i.e., animal) population density and biomass in certain habitats. Several foraminifera were reported to host a substantial amount of bacteria in their cytoplasm, either representing symbionts, food or just sharing the same habitat. Bacterial lineages are key players in marine biochemical cycles, especially in oxygen-depleted environments. However, the bulk of bacteria associated with foraminifera has never been characterized and has not been considered for benthic biochemical processes yet. Here we study metabolic pathways encoded in the genomes of bacteria associated with foraminifera and evaluate their contribution to biochemical cycles in oxygen-depleted sediments. From large-scale metagenome sequencing of the benthic foraminifera *Globobulimina* in a hypoxic fjord, we retrieved 26 draft genomes of foraminifera-associated organisms. Most of these genomes represent Gammaproteobacteria, while also Alphaproteobacteria and members of the phylum Bacteroidetes were identified. Their genetic content covered complete and partial metabolic pathways typically associated with oxygen-depleted environments and therefore were in line with the facultative anaerobic lifestyle of their foraminiferal host. Furthermore, multiple strains identified were related to bacteria previously found in host-association or as endosymbionts of marine eukaryotes. Several benthic foraminifera are capable to migrate deeper into sediments to avoid competition and to seek specific food sources. We hypothesize that foraminifera represent microniches for bacteria, bringing metabolic processes at the benthic interface into deeper sediment layers. Thus, our results expand the role of foraminifera in marine biochemical cycles by considering the bacterial community in their cells.

Position

Postdoc

Affiliation

Kiel University

Email Address

cwoehle@ifam.uni-kiel.de

Are you a SFB 754 / Future Ocean member?

Yes

Primary author(s) : Dr WOEHLE, Christian (Institute of Microbiology, Kiel University, 24118 Kiel, Germany.)

Co-author(s) : Dr ROY, Alexandra-Sophie (Institute of Microbiology, Kiel University, 24118 Kiel, Germany.); Dr GLOCK, Nicolaas (GEOMAR Helmholtz Centre for Ocean Research Kiel, 24148 Kiel, Germany.); WEIN, Tanita (Institute of Microbiology, Kiel University, 24118 Kiel, Germany.); Dr WEISSENBACH, Julia (Institute of Microbiology,

Kiel University, 24118 Kiel, Germany.); Prof. ROSENSTIEL, Philip (Institute of Clinical Molecular Biology, Kiel University, 24118 Kiel, Germany.); Dr HIEBENTHAL, Claas (GEOMAR Helmholtz Centre for Ocean Research Kiel, 24148 Kiel, Germany.); Dr MICHELS, Jan (Zoological Institute, Kiel University, 24118 Kiel, Germany.); Dr SCHÖNFELD, Joachim (GEOMAR Helmholtz Centre for Ocean Research Kiel, 24148 Kiel, Germany.); Prof. DAGAN, Tal (Institute of Microbiology, Kiel University, 24118 Kiel, Germany.)

Presenter(s): Dr WOEHLE, Christian (Institute of Microbiology, Kiel University, 24118 Kiel, Germany.)

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