

Metagenomics reveal dominance of sulfur cycle related bacteria inside benthic foraminifera

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Foraminifera are unicellular eukaryotes widespread in marine environments, known to play an important role in the benthic nitrogen and carbon cycles [1, 2]. They harbor a variety of endobionts, the role of which remains enigmatic. Here, we focus on the sulfur cycle related microbial communities inside benthic foraminifera.

Living foraminifera (*Ammonia* sp., *Elphidium* sp. and *Haynesina* sp.) were isolated from the top 10 cm of sediment retrieved from intertidal mudflats in the Wadden Sea. MiSeq sequencing of the bacterial 16S rRNA gene from within individual foraminiferal cells and from the surrounding sediments showed similarities between foraminiferal and sediment communities but different relative abundances. Sulfur oxidizing bacteria (e.g. *Sulfurovum* sp.) displayed a much higher abundance inside foraminifera, suggesting a selective uptake of such prokaryotes by foraminiferal cells.

Sequencing of the adenosine 5'-phosphosulfate reductase gene (*aprA*) revealed bacteria inside the foraminiferal cells mainly belonging to sulfur-oxidizing Gammaproteobacteria and sulfate-reducing Deltaproteobacteria. The observed *aprA* community variance was correlated with foraminiferal species and depth-related changes of sulfur porewater concentration. The phylogenetic positions and particular roles of these endobionts are currently under investigation.

- [1] Moodley et al. (2002) *Mar. Ecol. Prog. Ser.* **236**, 23-29.
[2] Piña-Ochoa et al. (2010) *PNAS* **107**, 1148–1153.