



Identification and enumeration of bacteria assimilating dimethylsulfoniopropionate (DMSP) in the North Atlantic and Gulf of Mexico

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ABSTRACT: The algal-derived compound dimethylsulfoniopropionate (DMSP), which is the precursor of the climatically active gas dimethylsulfide, is potentially an important source of carbon and sulfur to marine bacterioplankton. Currently, bacteria of the *Roseobacter* clade, a subgroup of α -proteobacteria, are hypothesized to be the key participants in the metabolism of DMSP. To test this hypothesis, we used a combination of microautoradiography and fluorescence in situ hybridization (Micro-FISH) to identify the bacteria assimilating ^{35}S DMSP in the Gulf of Mexico, the Gulf of Maine, and the Sargasso Sea. On average, half of the bacterial community assimilated DMSP in these environments. Members of the α -proteobacteria dominated DMSP assimilation, accounting for 35-40% of bacteria assimilating DMSP. *Cytophaga*-like bacteria and β -proteobacteria each accounted for 15-30% of DMSP-assimilating cells. The α -proteobacteria accounted for a greater fraction of the DMSP-assimilating community than expected based on their overall abundance, whereas *Cytophaga*-like bacteria were typically underrepresented in the DMSP-assimilating community. Members of the *Roseobacter* clade assimilated more DMSP on a per-cell basis than any other group, but they did not account for most of the DMSP assimilation, nor were they always present even when DMSP turnover was high. These results indicate that the biogeochemical flux of dissolved DMSP is mediated by a large and diverse group of heterotrophic bacteria.

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