

Microbial dimethylsulfide (DMS) degradation along the anoxic sediments of the Medway Estuary, UK

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Methane is a potent greenhouse gas however, its production pathways have not been fully explored. One potentially significant production pathway is the microbial degradation of dimethylsulfide (DMS), a highly abundant organosulfur compound. Early studies showed that DMS is degraded by methanogens in anoxic sediments and by sulfate-reducing bacteria (SRB) when sulfate is available, potentially limiting the amount of methane production in saline sediments. However, we have limited knowledge about this process and underlying microbial populations. Tidal estuaries are ideal ecosystems to study DMS degradation as they exhibit a salinity (hence sulfate) gradient. Here, we explored the potential for DMS-dependent methane production and the diversity of DMS-degrading methanogens and SRB in estuarine sediments.

We incubated freshwater, brackish, and marine sediments from the Medway Estuary, UK, using DMS, and analysed the methanogen and SRB diversities by sequencing their functional genes (*mcrA* and *dsrB*). 61-67% (mol/mol) of DMS degraded to methane despite salinity differences between the sediments.

Methanomethylovorans (66%±8%), *Methanolobus* (73%±11%), and *Methanococoides* (98%±1%) were dominant in freshwater, brackish, and marine incubations, respectively. Reductive bacterial type *dsrAB*, Deltaproteobacteria, and uncultured SRB were the prevalent SRB in the freshwater (55%±8%), brackish (43%±7%), and marine incubations (31%±7%), respectively.

Our results demonstrated that DMS leads to significant methane production in anoxic sediments regardless of sulfate availability. Additionally, different methanogens degrade DMS along the estuarine salinity gradient. The above suggests an interaction with SRB and niche-differentiation of DMS-degrading methanogens in estuarine sediments.