Project Title | Revealing a cryptic organosulfur cycle in benthic marine environments using microbiology and metagenomics
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Host University | University of Warwick
Theme | Organisms & Ecosystems

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Project Highlights

- Microbiology of cycling of climatically active aerosol precursors and trace gases
- Apply metagenomics approaches to organosulfur cycling
- Investigate globally significant processes linking the nitrogen and sulfur cycles

Overview

Coastal saltmarshes are important environments for the cycling of organic matter. They are a source and sink for a number of atmospheric trace gases including volatile organic sulphur compounds such as dimethylsulfide (DMS) and methanethiol (MT), volatile amines, methyl halides and methane, which play diverse roles in atmospheric chemistry.

DMS is an organic sulfur gas that has been described as the ‘smell of the sea’. It is of biogeochemical significance as a precursor for secondary organic aerosols which play a role as cloud condensation nuclei and which affect the radiative balance of the Earth. It is also an important infochemical that has an effect on species interactions and the trophic web (Curson et al 2010). Approximately 300 million tons of DMS are produced annually, most of it in marine environments, but only a relatively small amount is emitted to the atmosphere, the majority being subject to microbial degradation (Schäfer et al 2011). Our previous work in the Stiffkey saltmarsh (Norfolk, UK) has identified methylotrophic bacterial populations that utilise DMS as a carbon and energy source (Pratscher et al., in prep). Another fate of DMS degradation is its oxidation to dimethylsulfoxide (DMSO). Bacterial groups that have been shown capable of DMS to DMSO oxidation include anoxygenic phototrophs such as *Rhodovulum sulfidophilum*, (using DMS dehydrogenase *ddhA*) (McDevitt et al 2002) and aerobic heterotrophs like *Ruegeria pomeroyi* which co-oxidatively convert DMS to DMSO using the enzyme trimethylamine monooxygenase (Tmm) dependent on the presence of methylated amines (Lidbury et al, 2015).

DMSO produced as described above is then available to act as a terminal electron acceptor for anaerobic respiration through the action of DMSO reductases which reduce DMSO to DMS (Satoh & Kurihara, 1987) and some also trimethylamine N-oxide (TMAO) to trimethylamine. Although the potential for DMSO (and TMAO) reduction in anoxic habitats is widely distributed, the identity of the organisms responsible for DMSO/TMAO reduction and the overall contribution of DMSO reduction to organic matter degradation remain poorly characterised.
Further, the production of DMS through the reduction of DMSO under anaerobic conditions could in turn regenerate the substrate for Tmm potentially constituting a full cycle of DMS to DMSO oxidation and DMSO to DMS reduction in surface sediments. This cycle may be driven by the spatially close interaction of DMS oxidising Tmm-containing bacteria in oxic sediment layers and DMSO-reducing bacteria in anoxic sediment layers.

The aim of this is to investigate how taxonomically and functionally diverse bacteria contribute to DMS/DMSO cycling in saltmarsh sediments, and how these contribute to organic carbon degradation under anaerobic conditions.

**Methodology**

You will use a combination of environmental sampling and laboratory experiments to assess diversity and activity of DMS and DMSO cycling microbial populations. Samples will be obtained from Stiffkey saltmarsh. You will use a variety of molecular approaches to characterise microbial community organisation and its ecological function. This will include DNA and RNA extraction and purification, PCR, sequencing using next generation platforms and bioinformatic analysis. You will also measure the processes such as DMS and DMSO degradation using gas chromatography as required.

**Training and skills**

CENTA students are required to complete 50 days training throughout their PhD including a 10-day placement. In the first year, students will be trained as a single cohort on environmental science, research methods and core skills. Throughout the PhD, training will progress from core skills sets to master classes specific to CENTA research themes. Discipline specific training opportunities in this project are based on the experimental approaches that will be used including microbial cultivation and characterisation, molecular microbial ecology techniques for analysis of microbial diversity and activity, including PCR based approaches, high-throughput amplicon sequencing for analysis of taxonomic and functional diversity as well as metagenomics approaches. You will also be trained in relevant analytical chemistry techniques such as ion and gas chromatography.
Partners and collaboration
There is ample potential for scientific exchange and collaboration with our network of collaborators throughout the UK and in Europe who study microbial trace gas metabolism, sulfur cycling, nitrogen cycling, and marine microbial ecology.

Possible timeline
Year 1: Assessment of potential to degrade DMS, TMA and DMSO under aerobic and anaerobic conditions in surface sediments and in the rhizosphere of saltmarsh vegetation. Characterisation of DMSO/TMAO-producing and -respiring bacteria from surface saltmarsh sediments by enrichment, isolation and physiological characterisation and genome sequencing. Analysis of taxonomic diversity of microbial communities using ribosomal marker genes and measurement of metabolic potential/process rates.

Years 2 & 3: Analysis of the functional diversity of microbial communities in the saltmarsh using analysis of functional genetic markers directly retrieved from saltmarsh sediment DNA (e.g tmm and DMSO reductase genes) by PCR analysis and/or metagenomics.

Further reading

Further details
If you would like to discuss about any aspect of this project, please feel free to contact Hendrik Schäfer or Yin Chen. Email: H.Schaefer@warwick.ac.uk or Yin.Chen.25@warwick.ac.uk
Further information and a link to the online application portal can be found at https://warwick.ac.uk/fac/sci/lifesci/study/pgr/apply