Project Title: Smelly sediment dwellers – identifying microbial populations driving DMSO reduction in anoxic sediments

Host University: University of Warwick

Themes: Organisms & Ecosystems

Supervisory team:

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Project Highlights:

- Identify uncharacterised microbes driving anaerobic organic matter degradation
- Master a wide range of cutting-edge environmental microbiology techniques
- Characterise the basis of DMSO reduction in sulfate reducing bacteria

Overview:

The organic volatile sulfur compound dimethylsulfide (DMS) has wide environmental significance. Often referred to as the ‘smell of the sea’, its emission to the atmosphere, mainly from marine sources, contributes significantly to the formation of atmospheric particles which affect radiative forcing and sulfur transport between the marine and terrestrial environments. Microorganisms have a major influence in controlling the amount of DMS that is emitted to the atmosphere as the production and degradation of DMS are linked to the activities of microorganisms. A complex and poorly understood interplay of various microbial processes is responsible for production of DMS, its conversion to dimethyloxide (DMSO) and its degradation by microorganisms (Schäfer et al 2011). This project will address the microbial cycling of DMS and DMSO by investigating the microbial populations that degrade DMSO in anoxic sediments as part of their respiratory metabolism. The main focus of this project will be on sediments in coastal marine ecosystems including salt marshes and intertidal mudflats.
In anaerobic respiration using DMSO as electron acceptor, DMSO is reduced to DMS by DMSO reductases (DMSOR). These enzymes belong to the class of molybdopterin oxidoreductases, which includes several groups of related enzymes. The biochemistry of DMSOR has been studied extensively, but their environmental distribution and the ecological significance of different types of DMSO reductases and the closely related (and functionally similar) trimethylamine N-oxide (TMAO) reductases are still poorly understood (Kappler and Schäfer, 2014). These enzymes carry out important transformations of the S- and N cycles respectively and effect organic matter degradation to CO$_2$, linking the cycling of carbon, nitrogen and sulfur. Previous studies have shown that DMSO is readily converted to DMS in marine sediments (Kiene and Capone 1986, Schäfer, unpublished data) and the ability of DMSO reduction has been demonstrated in a range of different organisms including, for example, sulfate reducing bacteria (Jonkers et al. 1996) Shewanella spp. and members of the marine Roseobacter clade (Gruender and Schäfer, unpublished results). The lack of knowledge about the identity of DMSO-reducing microorganisms and the role of different types of DMSOR in situ constitutes a fundamental gap of understanding of anaerobic degradation of organic matter in anoxic sediments.

The overarching aim is to identify DMSO reducing microorganisms, assess the primary substrates driving DMSO reduction, and establish which types of respiratory DMSO reductases are involved in DMSO/TMAO reduction.

**Figure 1:** Characteristic saltmarsh environment of the lower marsh at Stiffkey (at low tide) with tidal creeks and pools, illustrating a hotspot for organic sulfur cycling and DMSO reduction.

**Methodology:**

A combination of molecular environmental microbiology approaches will be used to identify the microorganisms and genes driving DMSO reduction in anoxic sediments. Work will primarily focus on marine and intertidal sediments of the coastal zone, but freshwater sediments can equally be included. Cultivation-dependent and cultivation-independent techniques will be used. Anaerobic microbiology cultivation will be carried out to enrich, isolate and characterise DMSO-reducing microorganisms, including genome sequencing. In parallel, cultivation of known DMSO-reducing strains will be carried out and the respiratory reductases involved in DMSO metabolism will be identified using molecular microbiology techniques. Primers for different types of DMSO reductases (dmsA, dorA/torA) will be optimised to assess the presence, diversity and expression of DMSO-reducing microorganisms in environmental samples using PCR-based methods and high throughput sequencing.
Training and skills:

Students will be awarded CENTA2 Training Credits (CTCs) for participation in CENTA2-provided and ‘free choice’ external training. One CTC equates to 1/2 day session and students must accrue 100 CTCs across the three years of their PhD.

You will receive training in cultivation and characterisation of anaerobic microorganisms, molecular microbiology techniques to study gene expression, PCR techniques including end-point, real time and reverse transcriptase PCR; cloning and sequencing, microbial community analysis using high throughput sequencing approaches, bioinformatics, genome analysis, as well as chemical analytical skills using ion- and gas chromatography.

Partners and collaboration:

We have an established network of collaborators at other universities in the UK and abroad which offers opportunities for joint experiments, exchange and research visits.

Possible timeline:

Year 1: environmental sampling, measurement of DMSO reduction activity in different sediment systems, enrichment and isolation

Year 2: Characterisation of DMSO and TMAO reduction in newly isolated and existing strains of Shewanella spp, sulfate-reducing bacteria and other DMSO reducing isolates; design/optimisation of PCR primers for different clades of DMSO reductase genes

Year 3: Metagenomic analysis of DMSO reducing organisms in environmental gradients

Further reading:


Further details:
If you would like to discuss any aspect of this project, please feel free to contact Hendrik Schäfer (H.Schaefer@warwick.ac.uk), Kevin Purdy (K.Purdy@warwick.ac.uk) or Yin Chen (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