Project Title | Microbial communities cycling organic sulfur compounds in Arctic sea ice
--- | ---
Host University | University of Warwick
Theme | Organisms & Ecosystems
Key words | Arctic, sea ice, microbiology, metagenomics, cryosphere, dimethylsulfide, dimethylsulfoniopropionate
Supervisory team | Dr Hendrik Schaefer, School of Life Sciences, University of Warwick
 | H.Schaefer@warwick.ac.uk
 | Dr Jonathan Todd, University of East Anglia, Norwich
 | Jonathan.Todd@uea.ac.uk
 | Dr Yin Chen, School of Life Sciences, University of Warwick
 | Yin.Chen.25@warwick.ac.uk

**Project Highlights**

- Explore Arctic microorganisms that affect atmospheric chemistry and climate
- Pioneer new methods to study microorganisms in sea ice
- Contribute to an international research programme investigating the Arctic Ocean

**Overview**

The Arctic is undergoing significant changes due to climate warming. Arctic ice cover has significant feedbacks and regulatory function for regional and global climate, but recently the extent of ice cover in the Arctic Ocean has fallen to record low levels (Notz and Stroeve 2016). Changes in the Arctic may also affect biological processes that lead to emission of biogenic volatile compounds into the atmosphere, which are precursors for secondary organic aerosols (SOA) that play important roles as particles for cloud formation and provide climate feedbacks (Carpenter et al 2012).

Dimethylsulfide (DMS) is an organosulfur gas with a role in SOA formation. The marine environment is the largest source for atmospheric DMS (Lana et al 2011). The amount of DMS that can be emitted to the atmosphere is linked to microbial activities driving its production and degradation. These complex pathways of organosulfur compound cycling are driven by a wide range of different enzymes and microbial groups (Figure 1). Most DMS is produced by enzymatic degradation of dimethylsulfoniopropionate (DMSP) by DMSP-lyases (Curson et al 2011). DMSP is an osmolyte produced in petagram quantities (Ksionzek et al 2016) per year by a range of phytoplankton, ice algae and, as shown by us, diverse marine bacteria (Curson et al 2017). The bacterial contribution to overall DMSP production is not well understood. DMS can be used as a carbon source by methylotrophic bacteria (Neufeld et al 2007, Schäfer 2007, Schäfer et al 2010) or as recently shown at Warwick, can be co-oxidised by heterotrophic bacteria to dimethylsulfoxide (DMSO) (Lidbury et al 2016). Both DMSP and DMS degradation can also involve the production of methanethiol (MT), which is degraded in bacteria by methanethiol oxidase (Eyice et al 2018), or which can be re-methylated to produce DMS (Carrión et al 2015). In 2019, we will participate in the multidisciplinary MOSAiC campaign (https://www.mosaic-expedition.org/), which will deploy an ice breaker in Arctic sea ice for an entire year to study the Arctic in unprecedented detail. MOSAiC is an opportunity to obtain samples from the Arctic and investigate sulfur cycling microorganisms in this ecosystem threatened by climate change.
Figure 1. Marine microbial organosulfur transformations, their importance and the key genes. MTHB methyltransferase (DsyB, DSYB & DSYD) are the key enzymes in DMSP synthesis. DMSP demethylation (dmdABCD) generates MT. DMSP lyases (ddd genes and Alma1) produce DMS. DMS is converted to MT via DMS monooxygenase (dmoA) or oxidised to DMSO via DMS dehydrogenase (ddhA) or trimethylamine monooxygenase (tmm). MT can be converted to DMS via methyltransferase (mddA) or degraded to H2S by methanethiol oxidase (mtoX). DMSP and DMS are key sources of carbon, sulfur and energy for marine microbes. DMSP and DMS are potent signal molecules. Atmospheric DMS is oxidised to sulfate aerosols that decrease the global radiation budget by scattering solar radiation back to space directly and indirectly by forming cloud condensation nuclei (CCN) that ‘cool’ the climate. The sulfate aerosols also return to land through wet and dry deposition: the major route for the transfer of biogenic sulfur from the oceans to land.

Methodology
You will use a wide range of experimental and analytical approaches, including microbiological, molecular biological and bioinformatic methods to isolate and characterise microorganisms and microbial communities from Arctic samples and experimental sea ice microcosms. Work may include physiological characterisation, genome sequencing and potentially genetic analysis of isolated microorganisms. You will analyse microbial community composition and function based on high throughput sequencing approaches (amplicon sequencing) as well as metagenomics of samples raised in the project. An exciting opportunity is the availability of an ice chamber at UEA, which will facilitate experimental work aimed at optimising approaches to study sea ice microorganisms. Traditionally, these involve slow melting of sea ice, which alters the chemical environment and potentially the physiological state of ice-dwelling microbes. Hence, methods that minimise such changes need to be developed, which could then be applied to study the response of ice microbes during freeze/thaw cycles, for instance.

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. Your project specific training will include a wide range of approaches as required and could include microbial cultivation and characterisation, bacterial genetics, biochemistry, genomics, and studying the diversity and metabolic potential of environmental microbial communities using high throughput sequencing methods and metagenomics. You will also be trained in relevant analytic chemistry techniques such as gas and ion chromatography.

Partners and collaboration (including CASE)
https://www.uea.ac.uk/environmental-sciences/sea-ice-chamber

Possible timeline
Year 1: Isolation and identification of organic sulfur cycling model organisms from Arctic Sea ice samples and brines and characterisation of their metabolic diversity, genome sequencing of isolates.
Year 2 & 3: Use of cultivation-independent techniques to investigate organic sulfur metabolism in microbial community samples from Arctic sea ice and sea water. Experimental work with the sea ice chamber at University of East Anglia: development and optimisation of new methods for analysis of sea ice microorganisms; microcosm experiments to assess changes in microbial organic sulfur cycling (diversity and activity) during freeze-thaw cycles;

Further reading

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