### Project Highlights:
- **Study a dynamic coastal environment**
- ‘**Metagenomics meets trace gas microbiology**’
- **Relevance to climate system and ozone depleting gases**

### Overview:
Coastal saltmarshes are highly productive ecosystems that can be found in many parts of the UK and Europe. They are a habitat for a range of specialised plant communities, provide birds with feeding and nesting areas and are beneficial due to provision of range of ecosystem services. Though relatively small in total area, saltmarshes are important environments for the cycling of organic matter. It has also been established previously that saltmarshes are a source and sink for a number of atmospheric trace gases including volatile organic sulphur compounds such as dimethylsulfide (DMS) and methanethiol (MT), methyl halides and methane important as climate active gases or ozone depleting compounds (Atkinson and Hall 1976; Oremland et al 1982; and reviews by Schäfer et al 2007; Schäfer et al 2010). In previous work funded by a NERC-responsive mode grant, we have identified bacterial populations in the Stiffkey saltmarsh (Norfolk, UK) involved in production and degradation of DMS using microbial ecology approaches ranging from enrichment and isolation of relevant microorganisms to stable isotope probing and metagenomics (Pratscher et al unpublished). Related work carried out by a NERC-funded PhD student is assessing the distribution and activity of DMS degrading microbial populations living in association with vegetation such as the cord grass *Spartina*, which is one of the few angiosperm species that are known to make dimethylsulfiniopropionate (DMSP), a precursor for DMS and other trace gases.

The aim of this PhD project will be to investigate the diversity and activity of microorganisms involved in cycling of a wider range of trace gases in the salt marsh environment in order to better understand the link between trace gas fluxes and microbial diversity in the saltmarsh.

![Figure 1: Characteristic saltmarsh environment of the lower marsh at Stiffkey (at low tide) with tidal creeks and pools, showing widespread Spartina anglica colonisation.](image-url)
Methodology:
You will use a combination of environmental sampling and laboratory experiments to assess diversity and activity of trace gas 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 rate of environmental processes such as trace gas degradation (DMS, methyl halides, methane) using gas chromatography as required.

You will receive training in a wide range of environmental microbiology approaches including assessment of metabolic potential of communities in environmental samples, DNA and RNA based assessment of community composition and function, processing and bioinformatic analysis of next generation high throughput sequencing data, metagenomics and related approaches, as well as analytical techniques such as gas and ion chromatography.

Training and skills:
CENTA students are required to complete 45 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 the student's projects and themes.

Partners and collaboration:
We have active collaborations with colleagues at the University of East Anglia with whom we have collaborated on microbial transformations of dimethylsulfide, methanethiol, methyl halides and methane and previously worked jointly in a NERC funded project on DMS and DMSP cycling in the salt marsh at Stiffkey using microbial ecology approaches. In addition to linking up with these partners, there are further opportunities to establish new links with colleagues elsewhere in the UK depending on the type of trace gas transformations that will become the key focus of the current project and thus provide relevant complementary expertise.

Possible timeline:
Year 1: Characterisation of the metabolic potential to degrade a range of trace gases (dimethylsulfide, methyl halides, methane) in both sediment and vegetation associated microbial communities found in the salt marsh; probing of functional diversity using specific marker genes and measurement of metabolic potential/process rates.
Year 2: More detailed analysis of microbial communities, focussing on specific trace gases and across ecological compartments (sediment, rhizosphere, phyllosphere) to investigate dynamics through seasonal cycles and in relation to changes in environmental conditions. SIP metagenomics or metatranscriptomic assessment of community function.
Year 3: Assessment of the diversity of trace gas cycling microbial communities at the landscape level.

Further reading:

Further details:
If you would like to discuss any aspects of this project or get additional information, we would love to hear from you. Please do get in touch with us.

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