Dimethylsulphide (DMS) and methylated amines (such as trimethylamine, TMA) are climate active trace gases emitted from the oceans. Unlike greenhouse gases, such as carbon dioxide and methane, DMS and TMA are important in aerosol formation, subsequent formation of cloud condensation nuclei and cloud droplets in the remote marine atmosphere, therefore potentially acting as climate cooling gases.

Surface oceanic waters are the major sink of marine trace gases before they can reach the atmosphere. Microorganisms inhabiting the surface oceans can utilize these compounds as carbon/nitrogen/sulfur sources, thereby affecting their biogeochemical cycles in the marine environment. However, little is known of the marine microbes involved in these biogeochemical cycles, let alone the regulation of metabolism of these climate-active trace gases.

Using a model marine bacterium, *Ruegeria pomeroyi*, we have recently revealed the presence of a unique antisense RNA in the regulation of DMS/TMA metabolism in this bacterium (Lidbury et al 2016). *R. pomeroyi* can utilize TMA as a sole nitrogen source. It can also oxidise DMS, but only if TMA is present. This regulation is achieved through a non-coding RNA (also known as genetic dark matter), *fmoR*, encoded in the antisense strand of the flavin-containing TMA monoxygenase (Tmm), which was previously characterized by our groups. This dual regulation of DMS co-metabolism by TMA and *fmoR* has important environmental significance since both DMS and TMA are common metabolites resulting from degradation of osmolytes in a wide range of marine phytoplankton, providing an essential link between marine productivity and marine trace gas emission through ecologically important marine heterotrophs (such as *Ruegeria pomeroyi*). Unlike many other non-coding RNAs in bacterial genomes whose biological functionality remains difficult to ascertain, this project provides a unique opportunity to investigate the role of *fmoR* in regulating the co-metabolism of two globally important oceanic climate active gases.

**Aims and Methodology:**
The overall aim of this project is therefore to understand the regulation of TMA/DMS co-metabolism by *fmoR* in order to establish a comprehensive model of the role of *fmoR* in regulating trace gas metabolism in *R. pomeroyi*. 
Growth of *R. pomeroyi* will be achieved using both defined synthetic medium as well as nutrient broth. DMS/TMA will be quantified by gas chromatography and ion-exchange chromatography respectively. Metabolites of DMS/TMA catabolism will be identified and quantified using LC/MS.

**Training and skills:**
The Supervisory team has an excellent record in PhD supervision. The last two PhD students completed from the Chen group has published 4 and 3 first-authored papers respectively, including 2 in *PNAS*, 1 in the *ISME Journal*, 3 in *Environmental Microbiology* and 1 in the *FEBS Journal*.

The project is based on our recent published observation of a novel antisense RNA in a model marine bacterium which can co-metabolize both DMA and TMA (Lidbury et al 2016), therefore providing a unique opportunity to use contemporary bioinformatics with biology.

This exciting project provides cutting-edge training on genome-wide bioinformatic identification of novel regulatory RNAs. It will also provide excellent training in wider aspects of marine microbiology, biogeochemistry and molecular biology using cutting edge biochemical, molecular and ‘omic approaches’, as well as in a variety of analytical techniques currently available in the Chen/Schäfer group, including gas chromatography, ion-exchange chromatography, liquid chromatography-mass spectrometry.

**Partners and collaboration (including CASE):**
The Chen and Schäfer groups at Warwick have pioneered research of microbial-mediated climate-active gas cycles in the marine environment, particularly DMS and methylated amines. Current research in the groups is funded by NERC, BBSRC and the Gordon and Betty Moore Foundation.

Dr Chen’s group: [http://www2.warwick.ac.uk/fac/sci/lifesci/people/ychen](http://www2.warwick.ac.uk/fac/sci/lifesci/people/ychen)

Dr Schäfer’s group: [http://www2.warwick.ac.uk/fac/sci/lifesci/people/hschaefer](http://www2.warwick.ac.uk/fac/sci/lifesci/people/hschaefer)

**Possible timeline:**
**Year 1:** Identification and bioinformatics characterization of the antisense RNA, *fmoR* mapping by 5’ and 3’ rapid amplification of cDNA ends (RACE).

**Training on analytic methods including gas chromatography, ion-exchange chromatography and mass spectrometry.**

**Year 2:** Experimental confirmation of the anti-sense RNA through RNA-seq and qRT-PCR. Characterization of *fmoR* expression in TMA and DMS co-metabolism.

**Year 3:** Establishment of a comprehensive model of regulation through antisense RNA and transcriptional regulators in TMA/DMS cometabolism.

**Further reading:**
Chen et al (2011) 'Bacterial flavin-containing monooxygenase is trimethylamine monooxygenase', *Proceedings of The National Academy Of Sciences*, 108 (43), 17791 - 17796


**Further details:**
**Applicants** from the UK or the EU are eligible. Applicants should hold a BSc and/or MSc degree in relevant subjects.

**Informal enquires** can be made to Dr Yin Chen (y.chen.25@warwick.ac.uk, 00 44 24765 28976) or Dr Hendrik Schäfer (H.schaefer@warwick.ac.uk, 00 44 24765 75052).