

Project Title	Quaternary and methylated amine cycle in coastal oceans: new genes, novel microbes and unexpected pathways
University (where student will register)	University of Warwick
Which institution will the student be based at?	As above
Theme (Max. 2 selections)	Climate & Environmental Sustainability <input type="checkbox"/> Organisms & Ecosystems <input checked="" type="checkbox"/> Dynamic Earth <input type="checkbox"/>
Key words	Environmental microbiology, climate change, omics
Supervisory team (including institution & email address)	PI: Yin Chen University of Warwick, y.chen.25@warwick.ac.uk Co-I: Kevin Purdy, University of Warwick, k.purdy@warwick.ac.uk

Project Highlights:

- **New genes and novel microbes**
- **Unexpected pathways**
- **World-leading supervisory team on climate-change microbiology**

Overview:

Quaternary amines such as glycine betaine and choline are ubiquitous in marine biota. Once released into the marine environment, the degradation of these compounds in marine ecosystems contributes significantly to the production of climate-active trace gases, the potent greenhouse gas methane and the volatile marine aerosol precursors methylated amines (**Fig. 1**)

Microbial amine cycles are of great importance in the coastal oceans. For example, coastal sediments are estimated to contribute to ~75% of the global oceanic methane emissions (8-13 Tg yr⁻¹). As much as 90% of the methane produced in salt marsh sediments (Oremland 1982), is derived from the degradation products of quaternary amines. Another study showed that the addition of quaternary amines to sediment microcosms markedly stimulated methane production and these compounds accounted for up to 60% of methane production in coastal marine sediments from Lowes Cove, USA (King 1984). Quaternary amine degradation also releases methylated amines (e.g trimethylamine) and these volatile compounds can not only be used directly by methanogens for methane production but also be released into the atmosphere. Recent studies have shown that methylated amines are important sources for marine aerosol formation, thereby contributing to the formation of cloud condensation nuclei and consequently may play an important role in the Earth's climate.

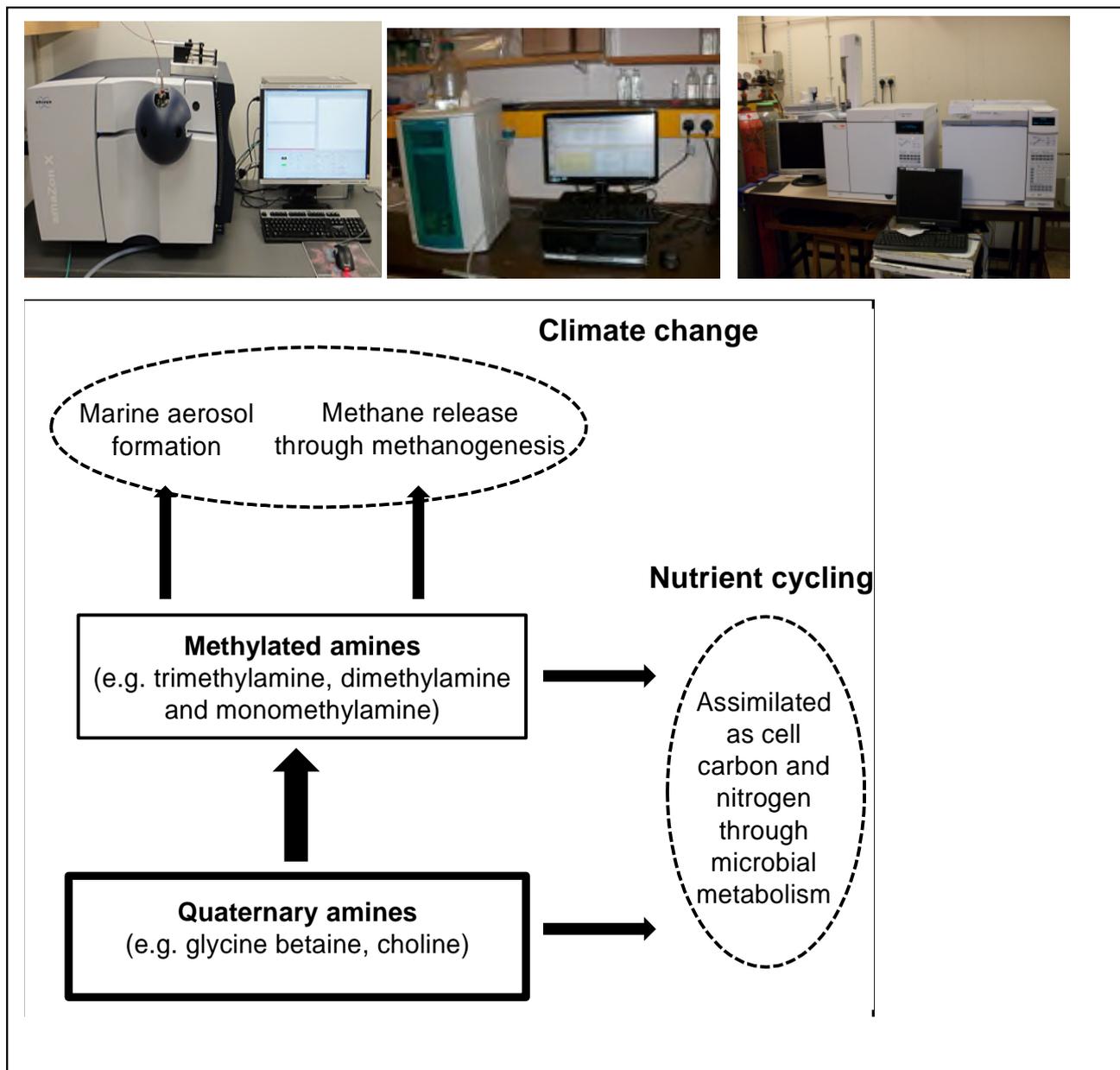


Figure 1 Top: key analytic instruments for quaternary amine and methylated amine analyses, including (left to right) liquid chromatography-mass spectrometry, ion-exchange chromatography, gas chromatography. Bottom: Environmental impact of quaternary and methylated amine cycles in the oceans.

Our knowledge on the microbial transformation of these important climate-active compounds is very limited. Neither the identity nor the metabolic pathways involved in their transformations has been firmly established. Over the past five years, our groups have started to uncover many new genes, novel microbes and unexpected pathways responsible for the degradation of quaternary amines and methylated amines, including a novel flavin containing monooxygenase that is ubiquitous in marine microbes (Chen et al 2011 PNAS), a novel choline-to-trimethylamine pathway for trimethylamine formation (Jameson et al., 2015, 2016), a new pathway for trimethylamine oxide degradation (Lidbury et al 2014 PNAS).

Methodology:

The overall aim of this project is therefore to continue discovering many as yet uncovered genes, enzymes and novel pathways for methylamine amine cycles in coastal oceans. Specifically, we aim to 1) determine the role of sulfate reducing bacteria in trimethylamine cycle, 2) characterise novel substrates for trimethylamine formation, and 3) determine the role of novel Archaea in methylamine metabolism.

Microcosms studies will be performed using costal sediment samples. Quaternary amines and methylamines will be quantified by gas chromatography, ion-exchange chromatography or HPLC mass spectrometry (MS). Metabolites of amine catabolism will be identified and quantified using HPLC-MS. The identity of microbes enriched in microcosms will be characterized by 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.

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*. This exciting project provides cutting-edge training on cutting edge bioinformatics. 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/Purdy group, including gas chromatography, ion-exchange chromatography, liquid chromatography-mass spectrometry.

Partners and collaboration (including CASE):

The Chen and Purdy groups at Warwick have pioneered research of microbial-mediated climate-active gas cycles in the marine environment, particularly methylated and quaternary amines. Current research in the groups is funded by NERC, BBSRC and the ERC. Chen's group: <http://www2.warwick.ac.uk/fac/sci/lifesci/people/ychen>

COVID-19 Resilience of the Project:

In unforeseen circumstances where wet lab work is not feasible due to COVID outbreak, the project will shift towards bioinformatic analyses of publicly available metagenome/metatranscriptomics datasets which can be used to reconstruct bacterial and archaeal genomes and mining for key functional genes and pathways for microbial amine metabolism. We will particularly focus on metagenomes/transcriptomes from marine sediments as this is where methylamine-dependent methanogenesis is likely to occur between the oxic/anoxic interphase.

Possible timeline:

Year 1: identify the role of sulfate reducing bacteria in methylamine amine metabolism.

Year 2: microcosm enrichment using a range of quaternary amine and methylamines, monitoring methane formation, high throughput sequencing and bioinformatics

Year 3: uncover novel enzymes and pathways in trimethylamine formation

Further reading:

Oremland RS et al. 1982 Methane production and simultaneous sulphate reduction in anoxic, salt marsh sediments. *Nature* 296:143-145.

King GM 1984 Metabolism of trimethylamine, choline, and glycine betaine by sulfate-reducing and methanogenic bacteria in marine sediments. *Appl Environ Microbiol* 48:719-725.

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

Lidbury et al (2014) 'Trimethylamine N-oxide metabolism by abundant marine heterotrophic bacteria', *Proceedings of The National Academy Of Sciences*, 111 (7), 2710 – 2715.

Jameson et al (2016a) Metagenomic data-mining reveals contrasting microbial populations responsible for trimethylamine formation in human gut and marine ecosystems. *Microbial Genomics*, 2(9): doi:10.1099/mgen.0.000080

Jameson et al (2016b) Anaerobic choline metabolism in microcompartments promotes growth and swarming of *Proteus mirabilis*. *Environmental Microbiology*, 18(9) 2886-2898.

Further details:

Applicants should hold a BSc and/or MSc degree in relevant subjects. Informal enquiries can be made to y.chen.25@warwick.ac.uk.