# iFAST: The International Forum on Advanced Environmental Sciences and Technology

*A series of distinguished seminars by eminent scientists*

**8 a.m. CDT; 9 a.m. EDT; 1 p.m. GMT; 9 p.m. Beijing**

## Wednesday, June 16, 2021


**Colin Murrell**

University of East Anglia

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Colin Murrell has wide-ranging research interests centered around the bacterial metabolism of methane and other one carbon compounds, and more recently, the microbiology of the climate-active gas isoprene. He has pioneered work on the physiology, biochemistry, molecular biology, genetics and ecology of methanotrophs, and the development of molecular ecology techniques such as functional gene probing and DNA stable isotope probing. His research has resulted in ~350 publications, six edited books and around 60 Ph.D. graduates. Murrell was a founding member of the *ISME Journal* editorial board and is currently on the editorial board of *Environmental Microbiology*. He was president of ISME from 2016-2018 and currently serves on their executive advisory board. He has chaired Gordon Research Conferences on C1 metabolism and applied and environmental microbiology. Murrell is a member of EMBO and the European Academy of Microbiology. He is a current ERC Advanced Grant holder, serves as a member of the SAB of the Max Planck Institute for Terrestrial Microbiology, Marburg, and the governing council of the John Innes Centre.

## The role of bacteria in the biogeochemical cycling of isoprene, a much-neglected atmospheric trace gas

Isoprene (methyl isobutene) is a climate-active volatile organic compound that is released into the atmosphere in similar quantities to that of methane, making it one of the most abundant trace volatiles. Large amounts of isoprene are produced by trees, but also substantial amounts are released by microorganisms, including algae in the marine environment. The consequences on the climate are complex. Isoprene can indirectly act as a global warming gas but in the marine environment it is also thought to promote aerosol formation, thus promoting cooling through increased cloud formation. We have shown that aerobic isoprene degrading bacteria are widespread in the environment. *Rhodococcus* AD45 and *Variovorax* WS11, our model isoprene degraders, oxidize isoprene using a soluble di-iron center monooxygenase that is similar to soluble methane monooxygenase and has considerable potential as a biocatalyst for biotransformations and bioremediation. The physiology, biochemistry and molecular biology of isoprene degraders will be described, together with genome analysis, transcriptome analysis and regulatory mechanisms of isoprene degradation by bacteria. The distribution, diversity and activity of isoprene degraders in the environment has also been studied using functional gene probing, DNA-stable isotope probing, metagenomics, metatranscriptomics and metaproteomics. Results indicate that isoprene-degrading bacteria are widespread in soils, leaf surfaces and estuarine sediments and that they are likely to play a major role in the metabolism of isoprene before it escapes to the atmosphere. Focused metagenomics using DNA-SIP has facilitated capture of the genomes of new isoprene degraders. Concomitant cultivation studies have enabled the isolation and characterization, at the physiological and molecular level, of novel isoprene degraders, all of which use a common pathway, initiated by isoprene monooxygenase, to degrade isoprene.

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