**Session Proposal**

# Session Title

One carbon metabolism in terrestrial ecosystems

# Session Organizers

Jingjing Peng, China Agricultural University, jingjing.peng@cau.edu.cn

Werner liesack, Max Planck Institute for Terrestrial Microbiology, liesack@mpi-marburg.mpg.de

Lei Cheng, Biogas Institute of Ministry of Agriculture and Rural Affairs, chenglei@caas.cn

Diana Z. Sousa, Wageningen University and Research, diana.sousa@wur.nl

# Session Description

 Microbial transformations of one-carbon (C1) compounds, including methane (CH4), carbon dioxide (CO2), carbon monoxide (CO), methanol (CH3OH), and formate, are integral to the functioning of terrestrial ecosystems, influencing both greenhouse gas dynamics and carbon sequestration. This session will delve into the microbial mechanisms driving the production, transformation, and consumption of C1 compounds in soils, with a particular emphasis on methanogenesis, methanotrophy, methylotrophy, CO oxidation, and carbon mineralization. The session aims to highlight the role of soil microbial communities in mediating these processes and their responses to environmental changes. We welcome innovative contributions that explore: the diversity, physiology, and ecological functions of C1-metabolizing microorganisms; environmental and physicochemical factors shaping C1 metabolic pathways; cross-domain interactions, including virus-host dynamics within C1 cycling; synthetic microbial consortia and their potential for C1 compound conversion; and cutting-edge strategies such as single-cell technologies, meta-omics, stable isotope tracing, and machine learning to unravel the complexities of soil C1 metabolism. This session provides a dynamic platform for interdisciplinary dialogue among microbiologists, soil biogeochemists, systems biologists, and environmental modelers. By bridging molecular-level insights with ecosystem-scale processes, we aim to advance understanding of how microbial C1 metabolism influences terrestrial carbon fluxes and how this knowledge can be applied to inform climate strategies, enhance carbon use efficiency, and support terrestrial sustainability in the context of climate change. We encourage submissions that link molecular mechanisms to ecosystem-level processes and explore the implications of microbial C1 metabolism for climate change mitigation, carbon management, and agricultural sustainability.

# Format

Oral presentations

# Proposed Speakers

1. **Diana Z. Sousa**, Wageningen University and Research, diana.sousa@wur.nl, (a leading expert of anaerobic microbiology (methanogenesis). Her research interests are in the study of the metabolic pathways, microbes and microbial networks that anaerobically convert one-carbon molecules such as carbon monoxide, carbon dioxide, methane and methanol, and their application to produce chemicals. An example is her research on the design and development of synthetic co-cultures for the conversion of syngas to medium-chain fatty acids, alcohols and other low solubility added-value products. Other topics researched at her group include, syntrophy, methanogenesis, the microbial sulfur cycle and, more recently, electromicrobiology. She seeks a better understanding of microbial communities and microbial interactions, while searching for biotechnological applications of these communities in circular economy approaches.)
2. **Julia Vorholt**, ETH Zürich, jvorholt@ethz.ch (a leading expert of plant associated methylotrophy. She is interested in a systems-level understanding of the phyllosphere with the aim to identify organizing principles of bacterial community members. We developed a cultivation-independent metaproteogenomic approach and applied it to phyllosphere communities of different host plants in planta in order to get an unbiased view on the overall bacterial community composition and in particular to identify abundant proteins as a proxy for important protein function of community members in the habitat.)
3. **Marina G. Kalyuzhnaya,** mkalyuzh@u.washington.edu (a leading expert of methanotroph (high affinity methanotrophy). She hasexplored methane metabolism - a set of unique biochemical conversions that shapes global climate, balances the carbon cycle and provides endless possibilities for sustainable bio-catalysis. His current research interests lie in these interconnected areas: Describe the environmental distribution of methane metabolism, a core biological function that controls methane emission and thus global climate, using a system-wide perspective; Improve our understanding of subcellular organization of the microbial metabolic network; Develop microbial catalysts for conversion of flared/vented methane into green chemicals.)
4. **Colin Murrell**, University of East Angilia, J.C.Murrell@uea.ac.uk (a leading expert of aerobic methanotrophy. He has wide ranging research interests centered around the microbiology of atmospheric trace gases such as methane, isoprene, dimethyl sulfide, methyl halides and the metabolism of one carbon compounds (methanol, methylamines, methanesulfonate) in the terrestrial, aquatic and marine environment. His research over the past 35 years has resulted in around 350 publications and six edited books with funding from NERC, BBSRC, EU, Royal Society, British Council, The Gordon and Betty Moore Foundation, SGM, SfAM and recently an ERC Advanced Grant to work on the microbiology of the terrestrial isoprene cycle. )
5. **Kelly C. Wrighton**, Department of Soil and Crop Sciences, Colorado State University. wrighton@colostate.edu (a leading expert of virus-host interactions of carbon cycling. In her laboratory, computational systems biology approaches result in predictions of metabolic potential in both individual microorganisms and microbial communities. These insights underpin laboratory investigations targeting physical, chemical, and biological controllers on biogeochemical processes. She couples holistic and reductionist approaches to interrogate the interactions between organismal bioenergetics, interconnected community metabolism, and chemical processes)
6. **Yahai Lu**, College of Resources and Environment, Peking University, luyh@pku.edu.cn (a leading expert of methanogenesis in paddy soil. He has led numerous research projects, including those funded by the National Natural Science Foundation of China, the Ministry of Science and Technology’s 863 High-Tech Program, the 973 Major Basic Research Program, and collaborative projects with the Max Planck Society in Germany. His long-term research focuses on carbon cycling and microbial mechanisms in paddy soils. He has published over 100 SCI-indexed papers, which have been cited more than10,000 times in total.)
7. **Shungui Zhou**, College of Resources and Environment, Fujian Agriculture and Forestry University, sgzhou@soil.gd.cn (a leading expert of methane metabolism. He is Vice President of Fujian Agriculture and Forestry University. Professor Zhou’s research focuses on the fundamental theories and applications of soil microbial electrochemistry. He has led over 30 major research projects, including 10 grants from the National Natural Science Foundation of China (NSFC) (e.g., Distinguished Young Scholars, Excellent Young Scholars, Major Research Plan, Key Joint Fund, General Program, and Youth Program), as well as projects under the National 863 Program, National Science and Technology Support Program, and National Key R&D Program. He has published more than 200 SCI-indexed papers as the first or corresponding author, with over 15,000 citations and an H-index of 75. Since 2021, he has been consecutively listed as an ESI Highly Cited Researcher in China.)
8. **Lei Cheng**, Biogas Institute of Ministry of Agriculture and Rural Affairs, chenglei@caas.cn (a leading expert of methanogenesis. He has dedicated to advancing the study of anaerobic microbial resources and their applications. They developed cutting-edge platforms for the long-term preservation and high-throughput screening of anaerobic microorganisms, establishing China’s largest repository of anaerobic model species with over 900 strains. Their groundbreaking discovery of alkyl-type methanogenesis—a fifth methanogenic pathway where methanogenic archaea directly degrade long-chain alkanes to produce methane—has reshaped understanding of microbial methane production. By integrating culturomics, stable isotope tracing, and organic geochemistry, their research explores the metabolic processes and ecological roles of anaerobic life, with a focus on novel archaea, alkyl-type methanogenesis, and crude oil degradation. Additionally, they co-founded Sichuan Anaerobic Biotechnology Co., Ltd., pioneering the application of anaerobic microbial resources in human health.)
9. **Josh D Neufeld**, University of Waterloo, jneufeld@uwaterloo.ca, (a leading expert in environmental microbiologist. He thrives at the interface between method development, basic microbial ecology, and applied research, providing exceptional training opportunities for students and postdoctoral research fellows. In order to address important global challenges, his lab characterizes bacterial and archaeal communities in terrestrial, aquatic, and host-associated habitats. By developing and applying cultivation-dependent and molecular techniques, his team explores the “microbes that matter” to connect these microorganisms with the roles that they play in their communities and habitats. Current research projects include characterizing nitrifiers in engineered aquatic environments, exploring subsurface microbiology in relation to a deep geological repository for used nuclear fuel, and investigating bacteria from Boreal Shield lakes that have an impact on global biogeochemical cycling.)
10. **Ashish Malik**, School of Geosciences, The University of Edinburgh, ashish.malik@ed.ac.uk (He is a biogeochemist with extensive expertise in soil microbial processes and carbon cycling. Currently a lecturer at the University of Aberdeen, he has held prestigious postdoctoral and fellowship positions at renowned institutions such as the University of California, Max Planck Institute, and NERC Centre for Ecology & Hydrology. His research focuses on microbial contributions to soil carbon cycling, including methanogenesis and carbon mineralization, with significant implications for climate change, ecosystem functioning, and carbon sequestration. he has received several awards, including the Marie Skłodowska-Curie Fellowship, and has contributed to numerous influential publications in the field.)
11. **Marcela Hernández** García, University of East Angilia, Marcela.Hernandez@uea.ac.uk (She is an environmental microbiologist studying the diversity and function of soil microbiomes, in particular, the mechanisms of microbes involved in the oxidation of carbon monoxide and methane. She aims to identify and characterise the major players in biogeochemical cycling of the components of trace gases (for example carbon monoxide and methane) by using metagenomic approaches to determine which natural gases they use as carbon sources. She leads sampling campaigns in volcanoes in Chile and the US and incubate volcanic soils with labelled carbon and perform metagenomics to identify the active microbial communities and characterise their function in these soil deposits.)
12. **Luis Valentin Alvarado**, Luis.Valentin-Alvarado@monash.edu (His work focuses on how MGEs and microbial hosts interact and co-evolve through these enzymes, aiming to uncover new molecular mechanisms that govern microbial evolution and adaptation. This aligns with new projects in the Knott lab exploring the influence of MGEs on nucleic acid machineries in uncultivated microbes. Luis's research interests encompass ecosystem-scale genomics and enzyme function, with a particular emphasis on how uncultivated microbe contribute to biogeochemical cycles in subsurface ecosystems. He is intrigued by microbial enzymes that drive critical processes such as carbon cycling, hydrogen production, and epigenetic regulation. By applying advanced bioinformatics tools and conducting enzyme function studies, he generates complete genomes that shed light on metabolic networks and essential enzymes. His exploration of evolutionary conflicts with nucleic acid enzymes seeks to reveal how MGEs influence microbial evolution at both the genomic and enzymatic levels, uncovering new molecular mechanisms that shape ecosystem dynamics.)