

Poster Board Number	Title	Presenting author	Affiliation	Country
PS3.22.375	<i>A communal catalogue of host-informed phytopathogenic bacteria and their global biogeographical distribution</i>	Pengfa Li	Fujian Agriculture & Forestry University	China
PS3.22.376	<i>Agricultural management shapes soil viral community assembly across spatial, temporal and fertility gradients</i>	Hannah Goemann	University of California, Davis	United States of America
PS3.22.377	<i>Bacterial cheating in soils: a microscale ecological process that is globally widespread</i>	Yingyi Fu		China
PS3.22.378	<i>Biogeography and life cycle characterization of soil actinophages</i>	Sadaf Khan	Aarhus University	Denmark
PS3.22.379	<i>Biome identity and soil thresholds shape global alpha diversity of root-colonising arbuscular mycorrhizal fungi</i>	Yun Chen	Griffith University	Australia
PS3.22.380	<i>Bloom or Bust: How is the base of our marine ecosystems responding to a changing climate?</i>	Kirsty Smith	Cawthron Institute	New Zealand
PS3.22.381	<i>Building a FAIR data framework for a Global Atlas of Prokaryotic Diversity</i>	Varsha Kale	Aalborg University	Denmark
PS3.22.382	<i>Charting bacterial diversity and functional shifts across lotic and lentic habitats in a boreal oligotrophic lake network</i>	Sofia Papadopoulou	Uppsala University	Sweden
PS3.22.383	<i>CheckAMG and PhAuxDB enable ecosystem-scale discovery and pangenomic classification of auxiliary viral genes</i>	James C. Kosmopoulos	University of Wisconsin, Madison	United States of America
PS3.22.384	<i>Climate and host-tree attributes differentially shape fungal phylogenetic diversity and structure in global deadwood</i>	Jia-Yun Zou		Germany
PS3.22.385	<i>Climatic Drivers of Global Fungal Sporocarp Richness from Community Science Data</i>	Phoebe Hagberg	University of California, Irvine	United States of America
PS3.22.386	<i>Connecting microbial species distributions with functional potential across global ecosystems using mOTUs</i>	Marija Dmitrijeva	Swiss Institute of Bioinformatics	Switzerland
PS3.22.387	<i>Core and Tissue-defined Taxa Across Spatially Distributed <i>Leptospermum scoparium</i></i>	Amali Thrimawithana	New Zealand Institute for Bioeconomy Science Limited, University of Auckland	New Zealand

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PS3.22.388	<i>Defining the impact of marine heatwaves on the diversity and function of pelagic microbes</i>	Apoorva Prabhu	Sydney Institute of Marine Science	Australia
PS3.22.389	<i>Density dependent interactions alter competitive outcomes for Streptomyces in soil</i>	Evangeline Wang		United States of America
PS3.22.390	<i>Discovery and niche differentiation of Candidatus Nitrosomaritimum, an overlooked genus of ammonia-oxidizing archaea in anoxic coastal wetland sediments</i>	Ze Zhao	Westlake University	China
PS3.22.391	<i>Distribution of salinity resistance genes across water-based microbiomes</i>	Mick Adriaansens	University of Canterbury	Netherlands
PS3.22.392	<i>Diversity of halophilous Apiospora associated with intertidal Cyperaceae and Poaceae in Korea</i>	Minseo Cho	Korea University	Korea, Republic of
PS3.22.393	<i>DNA viruses are constrained by ecological niche and exhibit environmental adaptations in common with prokaryote hosts</i>	Michael Hoggard	University of Auckland	New Zealand
PS3.22.394	<i>Does spatial distribution of human fungal pathogens align with reported clinical cases?</i>	Etienne Richy	Czech Academy of Sciences	Czechia
PS3.22.395	<i>Effect of recent climatic anomalies on soil mycobiome composition</i>	Johana Kaiserová		Czechia
PS3.22.396	<i>Evaluation of metabarcoding performance in detecting morphologically identified foliar fungal pathogens</i>	Mariam Saadani	Martin Luther University Halle-Wittenberg	Germany
PS3.22.397	<i>Exploring Aotearoa New Zealand's yeast diversity</i>	Sarah J Knight	University of Auckland	New Zealand
PS3.22.398	<i>Extreme drought homogenizes soil microbial communities across central USA grasslands</i>	Tianjiao Dai		China
PS3.22.399	<i>Forests microbiomes are too slow to adapt to climate change</i>	Petr Baldrian	Institute of Microbiology of the ASCR	Czechia
PS3.22.400	<i>From host-coupled to function-driven: cyanophages reshape viral communities along a latitudinal gradient</i>	Kang Eun Kim	Korea Institute of Ocean Science & Technology	Korea, Republic of

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PS3.22.401	<i>Functional Diversity of Multi-kingdom Microbial Communities Across Geographic and Environmental Gradients</i>	Allie J Hall	University of Hawaii at Manoa	United States of America
PS3.22.402	<i>Genome-resolved metagenomics reveals high taxonomic novelty and metabolic adaptations in the deep peat microbiome across climate zones</i>	Simon Cheung	University of Bristol	United Kingdom
PS3.22.404	<i>Global biogeography of microbes driving ocean ecological status under climate change</i>	Zhenyan Zhang	Shaoxing University	China
PS3.22.405	<i>Global deadwood microbial diversity in forests is jointly shaped by land-use change and climate</i>	Shamik Roy		Germany
PS3.22.406	<i>Global diversity and biogeography of eukaryotic populations in activated sludge from wastewater treatment plants</i>	Yue Huang	University of Hong Kong	Hong Kong
PS3.22.407	<i>GlobalBacteria: A comprehensive global atlas of bacterial community composition</i>	Tomáš Větrovský		Czechia
PS3.22.408	<i>Halophyte-Driven Differences in Blue Carbon Sequestration and Associated Microbial Communities in Coastal Mesocosms</i>	Hyeongsu Shin	Korea University	Korea, Republic of
PS3.22.409	<i>Hierarchical mode of evolution in freshwater SAR11 driven by species dispersal and lake history</i>	Clafy Fernandes	Biology Centre CAS	Czechia
PS3.22.410	<i>Hook, line, and swimmer: Evolution of the bacterial flagellar hook protein across environmental niches</i>	Divyangi Pandit	University of New South Wales	Australia
PS3.22.411	<i>Invasive plants are linked to decoupling between taxonomic and functional diversity in the soil microbiome: a global meta-analysis</i>	Isha Pokhrel		United States of America
PS3.22.412	<i>Is everything everywhere? A global metagenomic analysis of microbial dominance and prevalence</i>	Jasmin Patel	University of the Witwatersrand	South Africa
PS3.22.413	<i>Isolation and Characterization of Diverse Viruses Infecting Ammonia-Oxidizing Archaea in Marine Environments</i>	Jong-Geol Kim	wonkwang university	Korea, Republic of
PS3.22.414	<i>Lake Malawi endemism and diversity revealed by a global freshwater metagenomic survey</i>	Kent Pham	Institute of Hydrobiology, Biology Centre, Academy of Sciences of the Czech	Czechia

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PS3.22.415	<i>Long-term phage-host dynamics: viral modulation of bacterial community structure in Lake Mendota over a 20-year time series</i>	Shradha Sharma	Indian Institute of Technology, Madras	India
PS3.22.416	<i>Making Microbes Matter</i>	Ben Allen	Newcastle University	United Kingdom
PS3.22.417	<i>Mapping the phylogenetic diversity of non-ribosomal peptide synthetase-independent siderophore (NIS) synthetases at global scale</i>	Vincent Hervé	Université Paris Saclay, INRAE, AgroParisTech, UMR SayFood	France
PS3.22.418	<i>Mapping the Pinus radiata microbiome</i>	Kathryn Wigley	Bioeconomy Science Institute	New Zealand
PS3.22.419	<i>Microbial collections of the Bioeconomy Science Institute Maiangi Taiao - a major repository of Aotearoa New Zealand's biodiversity and economically important microbes</i>	Nigel Bell	Bioeconomy Research Institute	New Zealand
PS3.22.420	<i>Microbial Community Dynamics and Isotopic Connectivity Across the Mangrove-Seagrass-Coral Reef Continuum in Corumbau, Brazil</i>	Daniele Olmedo	Federal University of Rio de Janeiro	Brazil
PS3.22.421	<i>Microbiology among sea ice crystals</i>	Salvatore Campanile	Victoria University of Wellington	New Zealand
PS3.22.422	<i>Microorganisms outweigh minerals and climatic factors in governing the preservation of soil organic carbon</i>	Qiaoyun Huang	Huazhong Agricultural University	China
PS3.22.423	<i>Multi-scale climatic drivers govern food microbiome assembly</i>	Lijie Zhang		China
PS3.22.424	<i>Petroleum-associated Genome Database - PaGeD: An Interactive Web Platform of genes and genomes related to the oil supply chain K.</i>	Kelly Johanna Hidalgo Martinez	UNICAMP	Brazil
PS3.22.426	<i>Powering biogeography with Sandpiper 2</i>	Benjamin Woodcroft	Centre for Microbiome Research, Queensland University of Technology	Australia
PS3.22.427	<i>Selective filtering of microbial genomes in atmospheric aerosols revealed by genome-resolved metagenomics</i>	Jungsoo Park	Simon Fraser University	Canada
PS3.22.428	<i>Similar gradients, different drivers: Soil bacterial diversity at global scales</i>	Sailee Sakhalkar		Czechia

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PS3.22.429	<i>Soil microbial diversity is associated with lower prevalence of human bacterial pathogens across global soils</i>	Chao Xiong	University of Western Australia	Australia
PS3.22.430	<i>Structural patterns of sponge-associated bacterial communities in the Southeastern Pacific and Antarctica revealed by full-length 16S rRNA sequencing</i>	Philippe Andre Loustau Salazar		Chile
PS3.22.431	<i>Substrate uptake patterns and functional redundancy of size fractionated microbiomes from two mid Atlantic estuaries</i>	Barbara Campbell	Clemson University	United States of America
PS3.22.432	<i>Temperature-dependent biogeography of biosynthetic gene clusters across global ocean data</i>	Marco Gabrielli	ETH Zurich	Switzerland
PS3.22.433	<i>The impact of selection and dispersal on the phyllosphere microbiome differs by plant species within an ecosystem</i>	Natalie Cokel		United States of America
PS3.22.434	<i>Thermal history and host genetics drive microbiome composition in <i>Exaiptasia diaphana</i> along the Eastern Coast of Florida</i>	Mara Schwiesow		United States of America
PS3.22.435	<i>Traditional Hawaiian Fishponds Hold Hidden Bacterial Diversity that Challenge Concordance of 16SrRNA gene and ANI Identification</i>	Joerg Graf	University of Hawai'i at Mānoa	United States of America
PS3.22.436	<i>Trajectories of Fungal and Bacterial Primary Succession in Surface Films Across Contrasting Climatic Zones</i>	Nhu H	University of Hawai'i at Manoa	United States of America
PS3.22.437	<i>Trophic gradients shape genome size, functional potential, and metabolic interactions in prokaryotic communities across global biomes</i>	Huaxin Lei		China
PS3.22.438	<i>Understanding ecological functions and host feedback in microbiome community assembly</i>	Jessie Wang	University of Toronto	Canada
PS3.22.439	<i>Unraveling microbial diversity in Swedish lakes with drones</i>	Eric Capo		Sweden
PS3.22.440	<i>Weaving Communities of Inquiry from Microbes to Society: the Biocode and Ethnocode of Moorea</i>	Neil Davies	University of California, Berkeley	French Polynesia
PS3.22.441	<i>Wildfire Smoke Transports Viable Microorganisms and Functional Genetic Potential Across Atmospheric Interface</i>	Atena Sadat Sombolestani	University of Calgary	Canada

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PS3.22.442	<i>Zinc availability shapes the niche expansion and toxic potency of a major harmful alga</i>	Qiong Zhang		Hong Kong