

Poster Board Number	Title	Presenting author	Affiliation	Country
PS3.21.313	<i>Active soil microbiomes are poorly represented in Genebank</i>	Carsten Suhr Jacobsen	Aarhus University	Denmark
PS3.21.314	<i>Amazonian Dark Earth as a Microbial Inoculum to Enhance Tree Growth and Soil Restoration in Degraded Tropical Systems</i>	Anderson Santos de Freitas	University of Sao Paulo	Brazil
PS3.21.315	<i>Antagonism or Synergy: Unraveling the intertwined relationship between Bacillus and Trichoderma against plant pathogens</i>	Jiyu Xie	Nanjing Agricultural University	China
PS3.21.316	<i>Beyond richness: reburns reshape soil fungal and bacterial communities in Mediterranean ecosystems</i>	Esbeiry Cordova-Ortiz	University of California, Riverside	United States of America
PS3.21.317	<i>Body-wrapping front flagella drive ultrafast swimming in bacterial zoospores</i>	Daisuke Nakane	The University of Electro-Communications	Japan
PS3.21.318	<i>Boom-bust or steady-state? Linking microbial community dynamics to carbon use efficiency through integrated long-read metagenomics</i>	Alessandro N. Garritano	University of Sydney	Australia
PS3.21.319	<i>Characterising the global extent of the Pinus radiata root microbiome</i>	Sarah Addison	Bioeconomy Science Institute	New Zealand
PS3.21.320	<i>Climate Gradients Structure Soil Microbial Genome Architecture and Functional Allocation Spectra Across Continental Australia</i>	Peipei Xue		Australia
PS3.21.321	<i>Compositional restructuring of rhizosphere microbial communities under plant invasion and nitrogen deposition</i>	Rakhi Palit		United States of America
PS3.21.322	<i>Convergent survival strategies but divergent metabolic capacities of bacterial communities along a Mollisol profile</i>	Xuefeng Zhu	Chinese Academy of Sciences	China
PS3.21.323	<i>What about the others? Transmission and infectivity implications of bacteria associated with the entomopathogenic nematode Heterorhabditis bacteriophora, beyond Photorhabdus</i>	Arletys Verdecia Mogena		Brazil
PS3.21.324	<i>Deciphering the flexibility of soil microbial biomass C/P stoichiometry</i>	Hao Cui	University of Sydney	Australia
PS3.21.325	<i>Decoding viral impacts in plant-rhizobacterial interactions</i>	Jonelle Basso	Lawrence Berkeley National Laboratory	United States of America
PS3.21.326	<i>Development of a distinctive lithotrophic iron-oxidizing bacterial community in rice rhizosphere</i>	Takeshi Watanabe	Nagoya University	Japan

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PS3.21.327	<i>Dissimilatory nitrate reduction to ammonium process sustains ammonium pool in deep soils</i>	Jun Shan	Institute of Soil Science, Chinese Academy of Sciences	China
PS3.21.328	<i>Ecological drivers of Mucoromycota: culture-dependent insights into abiotic and biotic filtering across South African biomes</i>	Alicia Kock		South Africa
PS3.21.329	<i>Ecological succession of bacterial communities on single sand grains</i>	Sebastian Silva	Max Planck Institute for Marine Microbiology	Germany
PS3.21.330	<i>Ecophysiology of two novel Ammonia Oxidizing Archaea enriched from a fen peatland</i>	Anna Burns		Germany
PS3.21.331	<i>Ecosystem-Specific Functional Differentiation of Cyanobacterial Carbon and Nitrogen Metabolism Revealed by Metagenomics</i>	Wenli Chen		China
PS3.21.332	<i>Environmental conditions mediate the recruitment of plant-associated microbes under disease and herbivory pressure</i>	Bastien Parisy		Finland
PS3.21.333	<i>Factors affecting the diversity of early diverging fungi and their associated endosymbiotic bacteria in South Africa</i>	Mmanoko Napo		South Africa
PS3.21.334	<i>Forest-to-pasture conversion increases microbial sensitivity to warming in Amazonian soils</i>	Jéssica Adriele Mandro	University of Sao Paulo	Brazil
PS3.21.335	<i>Fungal persistence and anaerobic activity in deep mangrove sediments</i>	Ying Chang	National University of Singapore	Singapore
PS3.21.336	<i>Future Precipitation Scenarios Unravel Strong Microbiome Responses and Bet-Hedging Strategies in a Mediterranean Oak Forest</i>	Ivan Aleksieienko	CEA BIAM	France
PS3.21.337	<i>Glacial retreat shapes huge phage evolution and virus-mediated sulfur oxidation during primary soil succession</i>	Hu Liao	Institute of Urban Environment, Chinese Academy of Sciences	China
PS3.21.338	<i>Harnessing community microgeography to interpret sample scale soil bacterial diversity</i>	Samuel Bickel	Graz University of Technology	Austria
PS3.21.339	<i>Heterogeneous distribution of nitrifier and denitrifier populations after manure application to soil</i>	Misato Toda		Denmark
PS3.21.340	<i>Host GIGANTEA function regulates the assembly and diversity of the Arabidopsis rhizosphere microbiome</i>	Sujin Lee	Gyeongsang National University	Korea, Republic of

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PS3.21.341	<i>Illuminating soil virus-host interactions and their role in regulating nitrification</i>	Christina Hazard	Université Claude Bernard Lyon 1	France
PS3.21.342	<i>Integrating ITS and ef1 $\pm$ amplicon data to characterise Fusarium communities and their impacts in pasture ecosystems</i>	Sarah van Amsterdam		New Zealand
PS3.21.343	<i>Legacy effects from management determine viral community composition in greenhouse soils, but priority effects dominate after autoclaving</i>	Grant Gogul	University of California, Davis	United States of America
PS3.21.344	<i>Metaproteomics of shifting microbial community nutrient allocations in greening Arctic tundra soils</i>	Jacob R Waldbauer	University of Chicago	United States of America
PS3.21.345	<i>Metatranscriptomics and ^{13}C-quantitative stable isotope probing analysis in acidic soil reveal that acid resistance strategies affect bacterial growth rates</i>	Hannah Butler Robbins		United States of America
PS3.21.346	<i>Microbe-compound networks reveal soil organic matter and community sub-structure across soil depth</i>	Sean Darcy	University of Vienna	Austria
PS3.21.347	<i>Microbial body size structures the soil multifunctionality potential during ecosystem restoration</i>	Lingjuan LI		China
PS3.21.348	<i>Microbial coalescence under drought drives non-neutral and predictable assembly across tropical humid and dryland soils</i>	Danilo Silva		Brazil
PS3.21.349	<i>Microbial regulation of soil pore structure governs carbon dioxide diffusion across diverse land management systems</i>	Adriana Torres Ballesteros		United Kingdom
PS3.21.350	<i>Mobilisable plasmids carrying phosphorus-acquisition genes reveal adaptive potential of soil microbiomes under nutrient limitation</i>	Bangxiao Zheng	Xiamen University of Technology	China
PS3.21.351	<i>Natural geothermal gradients as a tool to study the effects of combined climate stressors on soil microbial communities</i>	Nicholas Joachim Finlay Robinson	Lincoln University	New Zealand
PS3.21.352	<i>Near-Natural Broadleaf Admixture Rewires Soil Microbial Networks and Shifts Soil Multifunctionality in Coniferous Plantations</i>	Chen Ning	Central South University of Forestry and Technology	China
PS3.21.353	<i>Nematode predation affects soil fungal community assembly with implications for carbon accumulation at the soil aggregate level</i>	Xiaoyue Wang	Institute of Soil Science (CAS)	China
PS3.21.354	<i>Nitrogen availability drives ecological dynamics and parallel evolution in synthetic root-associated bacterial communities</i>	Atharva Bhide	Monash University	Australia

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PS3.21.355	<i>Quorum sensing based interspecies signaling shifts gene regulation in response to competitive interactions</i>	Eryk Yarkosky		United States of America
PS3.21.356	<i>Seasonal drought reroutes Amazon soil microbiomes, with greater susceptibility in terra firme forests</i>	Jessica Finck	Max Planck Institute for Biogeochemistry	Germany
PS3.21.357	<i>Seasonal variation drives differential responses of soil bacterial and fungal diversity along elevational gradients</i>	Ruiqi Wang		China
PS3.21.358	<i>Sediment Microbial Functional Profiling across Three Mangrove plant root structure</i>	Jeeranan Khomampai		Taiwan, Province of China
PS3.21.359	<i>Site-Specific Effects of Long-Term Organic Fertilizer Application on Nitrogen-Cycling Functional Gene</i>	Kanade Fujiwara		Japan
PS3.21.360	<i>Soil Fungal Mediation of Lodgepole Pine Regeneration Following Mountain Pine Beetle Disturbance</i>	Julie Fowler		United States of America
PS3.21.361	<i>Soil microbial responses to copper fungicide exposure in pine forest soils</i>	Nilukshi Muthuthanthrige	Auckland University of Technology	New Zealand
PS3.21.362	<i>Soil viromes in agricultural systems: effects on microbiome assembly, function and crop production</i>	Jinjun Kan	Stroud Water Research Center	United States of America
PS3.21.363	<i>Substrate preferences of a denitrifying bacterial co-culture under varying O₂ and pH conditions</i>	Sara Altenburg		United States of America
PS3.21.364	<i>Surviving the extremes: characterizing soil and rock-inhabiting fungi in Saudi Arabia</i>	Israel Mani	University of Tartu	Estonia
PS3.21.365	<i>Temporal dynamics of the phoD gene, acid phosphatase activity, soil amino acid production and foliar P under different P doses in maize rhizosphere</i>	Simone Raposo Cotta	University of Sao Paulo	Brazil
PS3.21.366	<i>The anaerobic story: Methane cycling in winter-flooded rice paddy soil under oxygen-limited conditions</i>	Yongliang Mo	China West Normal University	China
PS3.21.367	<i>The effect of host population size and drought on the rhizosphere microbiome of Plantago lanceolata</i>	Jasmi Näsäkkälä	University of Helsinki	Finland
PS3.21.368	<i>The role of treethrow forms in soil carbon storage: Soil microbial community contribution</i>	Vendula Brabcova	Institute of Microbiology of the ASCR	Czechia

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PS3.21.369	<i>The soil habitat as a lens for microbial trait-based ecology: implications for soil health</i>	Berenice Della Porta		Australia
PS3.21.370	<i>Trace gas oxidation supports sub-surface microbial communities across Namib Desert fog and aridity gradients</i>	Dana Tribbia	University of New South Wales	Australia
PS3.21.371	<i>Tree Diversity, Mycorrhizal Type, and Shared Soil-Root Fungal Taxa Drive Tree Species Coexistence and Resilience in Subtropical Forests</i>	Thomas McNeil		Canada
PS3.21.372	<i>Understanding how multi-species communities dampen microbial antagonism</i>	Sarah Connery		United Kingdom
PS3.21.373	<i>Vegetation and carbon form regulate microbial trait shifts and trade-offs across forest-grassland transitions</i>	Ziva Louisson		New Zealand
PS3.21.374	<i>Warming and dominant plant removal restructure microbial biomass and diversity across alpine shrublands and meadows globally</i>	Julie Deslippe	Victoria University of Wellington	New Zealand