

Poster Board Number	Title	Presenting author	Affiliation	Country
PS1.01.001	<i>A comparison of the microbiome of apple fruit skin and lenticels from orchards with historic high and low bull's eye rot infections</i>	Irene Patricia Shamini Pushparajah	New Zealand Institute for Bioeconomy Science Limited	New Zealand
PS1.01.002	<i>Adaptive Strategies of Rhizosphere Microbiomes Under Saline-Alkali Stress and High-Throughput Isolation of Functional Strains From Salt-Alkali-Tolerant Plants</i>	Qing He		China
PS1.01.003	<i>Advancing duckweed microbiome engineering for improving biomass productivity by application of predatory bacteria</i>	Tomomi Sugiyama		Japan
PS1.01.004	<i>Agroforestry promotes time-dependent recovery of microbial diversity and carbon cycling in Amazonian soils</i>	Guilherme Lucio Martins	University of Sao Paulo	Brazil
PS1.01.005	<i>A Halophyte-Derived Endophyte Restructures the Rhizosphere Microbiome and Enhances Salt Tolerance in Non-Halophytic Plants</i>	YUXIN PENG	Korea Research Institute of Bioscience and Biotechnology	Korea, Republic of
PS1.01.006	<i>A microbial index for predicting soil health: rethinking the role of microbial diversity</i>	Giovana Slanzon		United States of America
PS1.01.007	<i>Application of potassic rock dust alters edaphic filtering of fungal genera in the soybean rhizosphere</i>	Amanda Oliveira	University of São Paulo	Brazil
PS1.01.008	<i>A Preliminary Study on the Microecological Mechanisms of the Synergistic Chemical-Biological Control of Fusarium Wilt and Root-Knot Nematode Disease in Cucumber</i>	Xiaohong Lu		China
PS1.01.009	<i>Artificial selection of rhizosphere microbiomes reveals strong temporal dynamics and weak heritability of plant growth</i>	Abdulkabir Omeiza Abdulmalik		Germany
PS1.01.010	<i>Assessing the vertical variation in grapevine trunk fungal communities for the development of robust mycobiome sampling strategies</i>	Beatrice Fulton	Bioeconomy Science Institute	New Zealand

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PS1.01.011	<i>A synthetic microbial community with a microbial stimulator promotes tomato growth</i>	Ju Hui Kim		Korea, Republic of
PS1.01.012	<i>A Traceable and Biosafe Endophyte Selection Pipeline for Enhancing Stress Resilience in Medicinal Plants</i>	Kiaan Grobler	North-west university	South Africa
PS1.01.013	<i>Azospirillum-mediated associative nitrogen fixation compensates for low nitrogen use efficiency in domesticated rapeseed</i>	Zhen Zhang	Huazhong Agricultural University	China
PS1.01.014	<i>Bacteria isolated from biodiverse Mediterranean island habitats yield a large array of biopesticidal metabolites against mosquito larvae</i>	Martyn Wood	Foundation for Research and Technology Hellas	Greece
PS1.01.015	<i>Bacterial consortia shape growth responses of tropical forages Urochloa decumbens and Megathyrsus maximus</i>	Igor Souza	Federal University of Rio de Janeiro	Brazil
PS1.01.016	<i>Bacterial metabolism of host-specific secondary metabolites</i>	Mikiko Karasawa	University of Basel	Switzerland
PS1.01.017	<i>Beyond biomass: Microbial VOCs drive root architectural changes and rhizosphere microbiome restructuring</i>	Vaishnavi Padaki		United States of America
PS1.01.018	<i>Biocontrol of Cucumber Powdery Mildew by a Pseudonocardia Consortium</i>	Sook-Min Kwon	Kyungpook National University	Korea, Republic of
PS1.01.019	<i>Burkholderia strain B23 promotes citrus growth by restructuring rhizosphere bacterial and fungal communities</i>	yunzeng Zhang	Yangzhou University	China
PS1.01.020	<i>Characterization of Rhs Effectors in the T6SS of Pseudomonas kribbensis XP1-6 and Their Contribution to Biocontrol efficacy</i>	TE EN CHEN		Taiwan, Province of China

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PS1.01.021	<i>Characterization of T6SS effectors and the role of the VasX-like toxin PK_1102 in interbacterial competition of Pseudomonas kribbensis XP1-6</i>	NAI-CHUN LIN	National Taiwan University	Taiwan, Province of China
PS1.01.022	<i>Comammox Nitrospira drive low-N₂O nitrification in acidic agricultural soils across China</i>	Ping Han	City University of Hong Kong	Hong Kong
PS1.01.023	<i>Compartment and management shape the Eucalyptus bacteriome in Brazilian forest systems</i>	Millena Araujo Salles	Federal University of Rio de Janeiro	Brazil
PS1.01.024	<i>Contribution of Sorghum bicolor Genotype to Rhizosphere Microbiome Composition</i>	Victoria White		United States of America
PS1.01.025	<i>Could Microbes be the Architects of Improved Soil Structure Under Miscanthus x giganteus?</i>	Phillip de Lorimier	Iowa State University	United States of America
PS1.01.026	<i>Cover crop legacy shapes soybean root exudation through soil microbiome structuring</i>	Caio César Gomes Freitas	University of São Paulo - Luiz de Queiroz College of Agriculture	Brazil
PS1.01.027	<i>Culture Media as Ecological Filters Shaping the Cultivable Plant-Associated Fungal Microbiome</i>	Sook-Young Park	Sunchon National University	Korea, Republic of
PS1.01.028	<i>Different remediation treatments enhance soil health through shaping microbial communities in saline-sodic soils</i>	Fan Zhu	Hunan Agricultural University	China
PS1.01.029	<i>Differential root exudates between resistant and susceptible cucumber cultivars enhance the plants resistance to Fusarium wilt through recruitment of beneficial microbiota</i>	Rongjun Guo	Chinese Academy of Agricultural Sciences	China
PS1.01.030	<i>Dissecting and engineering metabolic competition among phyllosphere bacteria for pathogen suppression</i>	Paul Kramer y Rosado	ETH Zürich	Switzerland

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PS1.01.031	<i>Diversity of endophytic Mucoromycota fungi colonizing Zea mays in a white clover living mulch system</i>	Katsuharu Saito	Shinshu University	Japan
PS1.01.032	<i>Do fungi play a role in sustainably producing Miscanthus as a bioenergy feedstock?</i>	Lorien Radmer		United States of America
PS1.01.033	<i>Do Microbial Communities Affect the Efficacy of Phage-Based Biocontrol?</i>	Mada Triandala Sibero	University of Otago	New Zealand
PS1.01.034	<i>Ecological and Evolutionary Insights into the Occidiofungin Gene Cluster in Burkholderia</i>	Jinyan Yu	Yangzhou University	China
PS1.01.035	<i>Effects of heavy metals on the structure and function of rhizosphere microbial communities of Panax quinquefolius L. with different cultivation years</i>	Caixia Wang	Shandong Medical and Pharmaceutical University, Yantai, Shandong Province, China	China
PS1.01.036	<i>Enhancing plant-associated synthetic communities through open metabolic niche filling</i>	Aster Liu		Germany
PS1.01.037	<i>Environmental signals distinctly regulate cyclic lipopeptide production in Pseudomonas fluorescence spp. through LuxR regulators</i>	Johanna Helene Zech		Denmark
PS1.01.038	<i>Epichloë endophytes buffer drought-driven disruption of ryegrass-associated bacterial communities</i>	Sandeep Kumar	Bioeconomy Science Institute	New Zealand
PS1.01.039	<i>Exopolysaccharide producing endophytic fungus mitigates ROS and biofilters sodium to boost oil yield in Canola</i>	Aneesa Nayab	Women University Mardan	Pakistan
PS1.01.040	<i>Exploring bacteria associated with Athelia rolfsii sclerotia</i>	FITRA PARLINDO	Tokyo University of Agriculture and Technology (TUAT)	Japan

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PS1.01.041	<i>exploring endophytic microorganisms as biological agents in mitigating drought stress in soybean (Glycine max)</i>	Nqobile Ziqubu		Netherlands
PS1.01.042	<i>Exploring the root and soil microbiome of Lolium perenne under different nitrogen fertilization regimes</i>	Kritarth Seth	Bioeconomy Science Institute - AgResearch	New Zealand
PS1.01.043	<i>Fit for purpose: evaluation of agricultural bioinoculants across diverse production and application landscapes</i>	Lauren Hemara		Canada
PS1.01.044	<i>Flavonoid-mediated plant-microbiome interactions modulate mangrove growth</i>	Xiaoli Yu	Southern Marine Science and Engineering Guangdong Laboratory (Zhuhai)	China
PS1.01.045	<i>Flooding-Induced Oxygen Gradients Differentially Shape the Structure and Functional Potential of Rice Rhizosphere and Rhizoplane Microbiome</i>	Melania Migliore		Italy
PS1.01.046	<i>From cover to community: Strengthening soil microbial diversity and function in agriculture through the use of cover crops</i>	Anathi Sishuba		South Africa
PS1.01.047	<i>From Flowers to Fields: How Netting and Crop Diversification Drive Plant Microbiomes</i>	Natalia Ramirez Carrera	Swedish University of Agricultural Sciences	Sweden
PS1.01.048	<i>Functional Diversification of Alternative Sigma Factor Drives Ecological Adaptation in Plant-Associated Bacteria</i>	Arkaprabha China		India
PS1.01.049	<i>Fungal biomass affects microbial community structure via soil organic carbon accumulation across soil types</i>	Alberto Vinicius S. Rocha		Luxembourg
PS1.01.051	<i>Genomic potential and systemic impacts of inter-kingdom endophytic consortia on leaf ionomics and photosynthetic resilience in Solanum lycopersicum</i>	Dionné Viviers	North-West University	South Africa

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PS1.01.052	<i>Harnessing stress-alleviating microbiomes for improved drought tolerance in rice</i>	Cheng-Yen Chen	Temasek Life Science Laboratory	Singapore
PS1.01.053	<i>Host exudate recruits keystone microbiota to coordinate P uptake and ISR</i>	Lu Chang	华中农业大学	China
PS1.01.054	<i>Host genetics shapes microbiomes by tuning microbial enrichment</i>	Albina Khasanova	University of Texas at Austin	United States of America
PS1.01.055	<i>iChip-Based Recovery and Functional Profiling of Red Sea Mangrove Rhizosphere Bacteria</i>	Farah Alrammah		Saudi Arabia
PS1.01.056	<i>Identification of Novel Microbial Metabolites via Liquid Chromatography-Raman Spectroscopy: A Structure-Based Approach</i>	Takuma Kyotani	Waseda university	Japan
PS1.01.057	<i>Incredible, sporadic bacterial blooms over space and time in the rhizoplane of grassy plants</i>	James Tiedje	Michigan State University	United States of America
PS1.01.058	<i>Inheritance bottlenecks shape seed microbiome assembly</i>	Ahmed Abdelfattah	Leibniz Institute of Agricultural Engineering and Bio-economy e.v. ATB	Germany
PS1.01.059	<i>Integrating soil rhizobial diversity and host genomics to optimise biological nitrogen fixation in white clover</i>	Shengjing Shi	Bioeconomy Science Institute	New Zealand
PS1.01.060	<i>Interactive effects of earthworms and nematodes on soil microbial communities and plant-available phosphorus pools</i>	Lenin Apuri		Australia
PS1.01.061	<i>Iron redox-mediated plant-microbe interactions revealed by integrated field multi-omics and electrochemical sensing</i>	Shinichi Yamazaki	RIKEN	Japan

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PS1.01.062	<i>Isolation and molecular identification of rhizobia associated with nodules of the Colorín tree (Erythrina americana) in Mexican soils</i>	Yerely Villagra Ramirez	National Polytechnic Institute	Mexico
PS1.01.063	<i>Linking fungal diversity to soil health and sustainable crop production in black soils</i>	Teng Yang	Institute of Soil Science, Chinese Academy of Sciences	China
PS1.01.064	<i>Long-Term Organic Upland Management Drives Functional Convergence of Bacterial-Fungal Consortia for Root-Knot Nematode Suppression</i>	Ping-Hu Wu	National Pingtung University of Science and Technology	Taiwan, Province of China
PS1.01.065	<i>Manipulating soil microbiomes via plant-soil feedbacks to enhance the delivery of ecosystem services and sustainability in grazed grassland ecosystems</i>	Kate Orwin		New Zealand
PS1.01.066	<i>Metabolic reconstruction and functional analyses of violacein and polyhydroxybutyrate synthesis in Janthinobacterium sp. BmR6b isolated from the Chilean Southern Patagonia</i>	Michael Seeger Pfeiffer	Universidad Tecnica Federico Santa Maria	Chile
PS1.01.067	<i>Metatranscriptomic profiling of the crop residue-degrading microbiome informs soil carbon formation and disease management strategies</i>	Katia Taylor	CSIRO	Australia
PS1.01.068	<i>Microbial-Driven Humification of Sugarcane Leaf Residues in Lateritic Soils</i>	Xi-Mei Xue	Biology Centre (CAS)	China
PS1.01.069	<i>Microbially-informed strategies for the control of bacterial blotch</i>	Alex Vompe	The Pennsylvania State University	United States of America
PS1.01.070	<i>Microbiome in Steam Exploded Wood Fiber Used as Growth Media for Plants</i>	Marte Marie Fossum Ranvik	Norwegian University of Life Sciences (NMBU)	Norway
PS1.01.071	<i>Microbiome-Engineered Grapevines - A Novel Solution for healthy future vineyards</i>	Justine Larrouy	Bioeconomy Science Institute	New Zealand

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PS1.01.072	<i>Modulation of microbial interaction networks in the maize (Zea mays L.) crop and their impact on aflatoxin production</i>	Gerardo A. Ayil-Chan	El colegio de la frontera sur	Mexico
PS1.01.073	<i>Mycorrhizal fungi and deep-banded nutrient-rich amendments influence soil aggregation in a dispersive clay subsoil</i>	Helen Hayden	RMIT University	Australia
PS1.01.074	<i>Nitrogen fixation as an ecological indicator of methane oxidation potential in northern grassland soils</i>	Isaac Peetoom Heida	University of Alberta	Canada
PS1.01.075	<i>Pruning debris management has minimal impact on airborne fungal communities and grapevine trunk disease pathogens across European vineyards</i>	David Gramaje	Instituto de Ciencias de la Vid y del Vino (ICVV)	Spain
PS1.01.076	<i>Pruning intensity in grapevine reshapes microbial interactions without altering community composition</i>	Karen Andrea Corrales Adame		France
PS1.01.077	<i>Revealing mechanisms driving community invasion to facilitate microbiome engineering for crop health</i>	Leah Fulton	University of British Columbia	Canada
PS1.01.078	<i>Role of exopolysaccharide-producing rhizobacteria in enhancing salt stress tolerance in tomato (Solanum lycopersicum L.)</i>	Pei-Yu Tu		Taiwan, Province of China
PS1.01.079	<i>Root-derived low molecular weight organic acids modulate keystone microbial taxa impacting plant phosphorus acquisition</i>	Jie Zheng	Institute of Soil Science, Chinese Academy of Sciences	China
PS1.01.080	<i>Roots, Rhizosphere, and Resistance: Understanding Soil Communities in Sorghum halepense for Sustainable Weed Management</i>	Connor Purvis	Michigan State University	United States of America
PS1.01.081	<i>Screening Rhizobia from Semi-Arid regions for Sustainable and Climate-Resilient Lessertia frutescens cultivation</i>	Mokgadi Hlongwane	Tshwane University of Technology	South Africa

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PS1.01.082	<i>Seeds mycobiome and entomopathogenic fungi as components of microbiome-based strategies for sustainable agriculture</i>	Magdalena Frac	Institute of Agrophysics, Polish Academy of Sciences	Poland
PS1.01.083	<i>Soil bacteriome diversity and composition of rooftop and surface gardens in urban and peri-urban areas of Bangladesh</i>	Md. Tanvir Rahman	Bangladesh Agricultural University	Bangladesh
PS1.01.084	<i>Soil disturbance and humic substances shape plant microbiome assembly and health</i>	Morten Streblov	Graz University of Technology	Austria
PS1.01.085	<i>Soil fertility context controls fungal-organic acid coupling and mineral nutrient mobilization in tropical rhizospheres amended with silicate rocks</i>	Rafael Lima Oliveira	Luiz de Queiroz College of Agriculture (ESALQ), University of São Paulo (USP)	Brazil
PS1.01.086	<i>Soil Microbiome Dynamics and Methane Emissions under Controlled Irrigation in Rice</i>	Kenny Lau		Singapore
PS1.01.087	<i>Soil microbiota synergistically inhibit co-infecting opportunistic plant pathogens</i>	Yonghua Li	Beijing Academy of Agriculture and Forestry Sciences	China
PS1.01.088	<i>Soil nutrient limitation controls trophic cascade effects of micro-food web-derived ecological functions in degraded agroecosystems</i>	Wende Yan		China
PS1.01.089	<i>Soil properties and rhizosphere specialization shape the structure and activity of the methanogenic community in rice paddies</i>	Luciana Pereira-Mora	Universidad de la República - Facultad de Química	Uruguay
PS1.01.090	<i>Such a big loser: spontaneous loss of almost one quarter of the <i>Paraburkholderia</i> <i>sabiae</i> genome</i>	Kim Bolli	University of Zürich	Switzerland
PS1.01.091	<i>Synergistic bioaugmentation and biostimulation by indigenous microorganisms enhance peanut (<i>Arachis hypogaea</i>) productivity in diesel and waste-oil contaminated soils</i>	TCHIAZE IFOUE Alice Virginie		Cameroon

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PS1.01.092	<i>The biotechnological potential of the citrus rhizosphere is constrained by its ecological dynamics</i>	Helena Lima		Brazil
PS1.01.093	<i>Trichoderma drives functional reassembly of root-associated microbiomes across New Zealand pastures</i>	Sereyboth Soth		New Zealand
PS1.01.094	<i>Understanding bacterial community assembly in the switchgrass rhizosphere using a synthetic community</i>	Nicole Geerdes		United States of America
PS1.01.095	<i>Understanding post-translational regulation in a wheat-Pseudomonas fluorescens model through tracking newly synthesised proteins</i>	Xiaoyu Liu		Australia
PS1.01.096	<i>Understanding the evolution of beneficial soil bacteria to identify the most effective strains for sustainable agriculture</i>	Bridget Watson	University of Otago	New Zealand
PS1.01.097	<i>Unraveling the Impacts of Bio- and Synthetic Pesticides on Potato Production</i>	Weitao Wang		New Zealand
PS1.01.098	<i>Unravelling the molecular evolution of plant-microbiome interactions in drylands</i>	Tingting Song	The Hebrew University of Jerusalem	Israel
PS1.01.099	<i>Using total RNA sequencing to assess the non-target effects of nitrification inhibitors nitrapyrin and DMPP on soil microbial communities</i>	Erkin Gozdereliler	Aarhus University	Denmark
PS1.01.100	<i>Water stress and rootstock genotype reshape the grapevine- associated microbiome: Insights into climate-resilient viticulture</i>	Kavindi E. Weerasinghe	University of Auckland, New Zealand	New Zealand
PS1.01.101	<i>Wounding stress increases bioactive metabolite concentrations in Plantago lanceolata and enriches the rhizosphere microbiota with beneficial taxa</i>	Daniel Bastias	BSI	New Zealand