

Poster Board Number	Title	Presenting author	Affiliation	Country
PS1.28.385	<i>Boosting Crop Resilience: Innovative Microbial Consortia Engineering for Sustainable Agriculture</i>	Mark Hurst		New Zealand
PS1.28.386	<i>Cascade changes of microbial interactions are one of major driving forces to induce community succession</i>	Reika Mimoto	Shizuoka University	Japan
PS1.28.387	<i>Comprehensive Elucidation of Bacterial Flora in Two Spider Mites and Identification of Potential Symbiotic Bacterial Strains</i>	Futaba Doi		Japan
PS1.28.388	<i>Construction of Synthetic Microbial Communities for Controlling Potato Common Scab</i>	Dan Wang	Guangdong Academy of Agricultural Sciences	China
PS1.28.389	<i>Cross-feeding dynamics and metabolic structure explain patterns of diversity in microbial communities</i>	Maria Rebolledo-Gomez		United States of America
PS1.28.390	<i>Deciphering the benzene activation mechanism in a methanogenic enrichment culture</i>	Rishika Puri		Canada
PS1.28.391	<i>Decoupling the effects of diet and time on the shrimp gut microbial consortia: diversity, composition and functional dynamics</i>	Jessica Taylor	Nanyang Technological University	Singapore
PS1.28.392	<i>Designing a synthetic consortium of gut commensals to restrict the intestinal growth of vancomycin-resistant enterococci</i>	Shannon O'Leary	Imperial College London	United Kingdom
PS1.28.393	<i>Design of a synthetic bacterial consortium to restrict the intestinal growth of carbapenem-resistant Enterobacteriaceae</i>	Julie A. K. McDonald		United Kingdom
PS1.28.394	<i>Discovery of anaerobic bacterial scavengers of dead cells</i>	Yuga Hirakata		Japan
PS1.28.395	<i>Disentangling the Environmental Controls and Dynamics of Cooperative Denitrification Using Synthetic and Enriched Microbial Communities</i>	Zachary Cooper		United States of America
PS1.28.396	<i>Ecological Adaptation of Microbial Communities Driven by Multiple Hurdles in White-Rot Fungal Fermentation</i>	Dongze Niu		China
PS1.28.397	<i>Emergence of alternative stable states in a synthetic human gut microbial community</i>	Bin Liu	Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences	China
PS1.28.398	<i>Empirical validation of keystone taxa in salinity-stressed SynComs reveal potential drivers of keystoneity</i>	Samiran Banerjee		United States of America
PS1.28.399	<i>Environmental acquisition of <i>Herbaspirillum</i> and its potential role in acaricide resistance in <i>Tetranychus urticae</i></i>	Kazuki Toyoda		Japan
PS1.28.400	<i>Extreme propionate enrichment reshapes anaerobic digestion communities and favors functionally redundant methanogenic potential</i>	TEODORO ESPINOSA-SOLARES	Universidad Autonoma Chapingo	Mexico
PS1.28.401	<i>Floral nectar microbiomes near hives host a honeybee signature</i>	Marion Donald		New Zealand
PS1.28.402	<i>From co-occurrence networks to synergistic communities: development of stable and protective vaginal synthetic communities</i>	Maline Victor	Korea University	Belgium
PS1.28.404	<i>Identification of a novel methanotroph, <i>Methylomonas radialis</i> sp. nov., and Enhanced Methane Oxidation in Coculture with Heterotrophic Bacteria</i>	Rina Shinjo	Nagoya University	Japan
PS1.28.405	<i>Incorporating microdiversity improves probiotic establishment in vitro</i>	Abigayle M.R. Simpson	University of California, Irvine	United States of America

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PS1.28.406	<i>Metabolic Interactions Enhance Polycaprolactone Degradation in a Marine Bacterial Consortium</i>	Dae Young Kwon	Korea university	Korea, Republic of
PS1.28.407	<i>Metabolic Rechannelling of Corynebacterium glutamicum for Efficient Uroporphyrin I Synthesis from Lignocellulosic Carbon Sources</i>	Sung Ok Han	Korea University	Korea, Republic of
PS1.28.408	<i>Microbial Interactions Shape the Establishment and Function of Synthetic Consortia for Soil Inoculations</i>	Ying Wang	Texas A&M University	United States of America
PS1.28.409	<i>Microbial succession during spontaneous fermentation of Brazilian stingless bee honey</i>	Gabriela Rodrigues Silva	University of Sao Paulo	Brazil
PS1.28.410	<i>Microbial trait with large body size facilitates ecosystem performance</i>	Qiang Lin	Chengdu Institute of Biology, Chinese Academy of Sciences	China
PS1.28.411	<i>Microbiome Analysis of a Biofilm Reactor Using Wood Pieces and Polyurethane Sponge for Mn(II) Oxidation</i>	Masataka Aoki	National Institute for Environmental Studies, Japan	Japan
PS1.28.412	<i>Nitrogen strategy drives emergent carbon-nitrogen co-fixation and cross-feeding in a phototrophic microbial community</i>	Minmin Pan	Helmholtz Centre for Environmental Research (UFZ)	Germany
PS1.28.413	<i>Phage-Driven Microbiome Engineering Reveals Drivers of Community Resilience in Salinity-Stressed Synthetic Microbial Communities</i>	Avery Folsom	North Dakota State University	United States of America
PS1.28.414	<i>Prokaryotic community structure and auxin biosynthesis in early developmental stages of farmed Atlantic Nori (Porphyra spp.)</i>	Rodrigo Costa	Instituto Superior Técnico, Universidade de Lisboa	Portugal
PS1.28.415	<i>Propionate degradation via electrochemical mechanisms using microbial fuel cells</i>	Takumi Higashi		Netherlands
PS1.28.416	<i>Purification and spectrophotometric characterization of cytochromes c that play a role in a deep-sea syntrophy</i>	Lauren Morgan	University of Nevada Las Vegas	United States of America
PS1.28.417	<i>Questiomycin A produced by Pseudomonas aurantiaca CM9 is a key biocontrol metabolite against crown gall disease</i>	Mengshuai Liu		China
PS1.28.418	<i>Reconstructing metabolic models of oral bacteria to investigate acidification and caries progression</i>	Dana Ofiteru	Newcastle University	United Kingdom
PS1.28.419	<i>Resource fluctuations modify coexistence in the Drosophila gut microbiome</i>	Yu-Pei Tseng		Australia
PS1.28.420	<i>Shewanella oneidensis promotes methanogenesis through cooperation in a synthetic consortium</i>	Xijia Cao		China
PS1.28.421	<i>Social interaction types drive community resistance in microbial consortia</i>	Yuqian Zhang		China
PS1.28.422	<i>STREAMS: Community-Driven Reporting Guidelines for Environmental, Non-human Host-associated, and Synthetic Microbiomes</i>	Julia Kelliher		United States of America
PS1.28.423	<i>Synergistic effects of microbial symbionts on fermentation profiles within South African traditional and craft beers</i>	Karabelo Macmillan Moloantoa	University of KwaZulu-Natal	South Africa
PS1.28.425	<i>Temperate phages regulate the ecological traits of microbial community in open ocean surface</i>	Long Wang		China

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PS1.28.426	<i>The effect of community diversity on bacterial spatial distributions in the phyllosphere</i>	Johannes Fuchs	Freie Universität Berlin	Germany
PS1.28.427	<i>Using a synthetic microbial community to investigate the role of bacterial host diversity in predicting phage coexistence</i>	Fiona Joy Wagner	UC Berkeley	United States of America
PS1.28.428	<i>Using synthetic communities to study microbial interactions in duckweed microbiomes</i>	Milla Similä		Finland