

Poster Board Number	Title	Presenting author	Affiliation	Country
PS3.16.109	<i>Analysis of Metabolic Pathway Diversity of Marine Red Algae-associated Bacteria</i>	Hulya Bayburt	Chung Ang University	Korea, Republic of
PS3.16.110	<i>An endohyphal bacterium contributes to growth and metabolism of plant derived carbohydrates predominantly in light in an ubiquitous soil fungus</i>	Monika Schmoll		Austria
PS3.16.111	<i>A surgeonfish intestinal tract, the ideal environment for a giant bacterium such as <i>Epulopiscium viviparus</i></i>	Esther Angert	Cornell University	United States of America
PS3.16.112	<i>Blue dragon nudibranch recently observed in the Mediterranean does not acquire microbiome from its local prey</i>	Dafne Porcel Sanchis	Institute for integrative biology systems (UV-CSIC)	Spain
PS3.16.113	<i>Characterizing wild Fagaceae species associated ectomycorrhizal communities in Taiwan</i>	Yu-Ting Wu	National Pingtung University of Science and Technology	Taiwan, Province of China
PS3.16.114	<i>CRP links global transcriptional control to sRNA-mediated regulation of secondary metabolism in <i>Xenorhabdus doucetiae</i></i>	Agnieszka Nurek		Germany
PS3.16.115	<i>Deciphering coral-microalgae interactions using bulk-tissue and spatial lipidomics</i>	Mei-Chen Liu	University of Melbourne	Australia
PS3.16.116	<i>Diel Cross-Compartment Transcriptional Dynamics Reveal Regulatory Integration in the Nitroplast</i>	Yugo Tsunoda	RIKEN	Japan
PS3.16.117	<i>Dynamic Virus-Mediated Co-Adaptation in Complex Prokaryotic Communities under Environmental Stress Revealed by Temperature-Time Series</i>	Xinyue Kang		China
PS3.16.118	<i>Dynamics of the rhizosphere microbiome and bacterial facilitation of mycorrhizal symbiosis in <i>Gastrodia elata</i></i>	Yong Hoon Lee	Chungbuk National University	Korea, Republic of
PS3.16.119	<i>Ecological role of fungi comb to pangolin conservation</i>	Aprilia Ike Nurmalasari	National Pingtung University of Science and Technology	Taiwan, Province of China
PS3.16.120	<i>Effect of lignocelulosic substrates on the microbial community structure and the expression of genes involved in lignocellulose degradation in the hindgut of the termite, <i>Neotermes sugioi</i></i>	Gaku Tokuda	University of the Ryukyus	Japan

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PS3.16.121	<i>Elucidating the mechanisms of plant control over rhizosphere microbial homeostasis via immunometabolism feedback loops</i>	Chiao-Jung Han		Taiwan, Province of China
PS3.16.122	<i>Emiliania huxleyi uses coccoliths as a defence system against bacterial pathogens type IV secretion systems (T4SS)</i>	Nhi Nguyen	Nanyang Technological	Vietnam
PS3.16.123	<i>Endozoicomonas acroporae enhances coral thermal resilience through microbiome restructuring and cell-type-specific host stress modulation</i>	Chih-Ying Lu	Academia Sinica	Taiwan, Province of China
PS3.16.124	<i>Experimental validation of interspecific interactions in fungal endophyte communities</i>	Yu-Ling Huang	National Museum of Natural Science	Taiwan, Province of China
PS3.16.125	<i>Exploring phycosphere interactions: Microbial strategies to control toxic benthic cyanobacteria</i>	Jessica Moretto	University of Florida	United States of America
PS3.16.126	<i>First isolation of phages infecting the coral-associated bacterium Endozoicomonas montiporae: New insights for phage-host interactions in coral holobiont</i>	Mo Chen	Academia Sinica	Taiwan, Province of China
PS3.16.127	<i>Follow the lipids: insights into the ecology of symbiotic uncultured prokaryotes</i>	Feriel Bouderkha	University Duisburg-Essen	Germany
PS3.16.128	<i>Genetic basis underlying the endosymbiotic interface between sea slugs and Symbiodiniaceae</i>	Hideaki Mizobata	The University of Tokyo	Japan
PS3.16.129	<i>Genomic analysis of termite gut microbiomes: Functional profiles and dietary adaptations</i>	Anastasiia Ishchenko	Okinawa Institute of Science and Technology	Japan
PS3.16.130	<i>Genomic diversity and putative symbiotic islands in Lotus japonicus-nodulating rhizobia from New Zealand</i>	Damola Adejoro	Bioeconomy Science Institute	New Zealand
PS3.16.131	<i>Horizontal acquisition of a Lipopolysaccharides biosynthesis gene cluster shapes the symbiosis in Arsenophonus and insect</i>	Tingwei Cai	Huazhong Agricultural University	China
PS3.16.132	<i>Host-Driven Community Differentiation in Microalgal Microbiomes: Key Role of the Roseobacter Clade within Alphaproteobacteria</i>	Soo Hwan Jhin	Hanyang University	Korea, Republic of

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PS3.16.133	<i>Host-specific growth promotion by core microbiota in the harmful benthic dinoflagellate Prorocentrum lima</i>	Joo-Hwan Kim	Hanyang University	Korea, Republic of
PS3.16.134	<i>Isolating Microbiome Members from Marine Nematodes (Stilbonematinae)</i>	Max Binkowski		United States of America
PS3.16.135	<i>Life in glass houses: Deep-sea siliceous sponges harbor distinct and functionally diverse microbiomes</i>	Katherine Lane	Massachusetts Institute of Technology	United States of America
PS3.16.136	<i>Living at the Thermal Edge: Cultivation and Genomic Characterization of Coral Photosymbionts from the Persian/Arabian Gulf</i>	Janja Ceh	New York University, Abu Dhabi (NYUAD)	United Arab Emirates
PS3.16.137	<i>Meta-analysis of coral hologenomes highlights the diversity, lifestyle, and genome evolution of endosymbiotic dinoflagellates</i>	Hisatake Ishida		Australia
PS3.16.138	<i>Metabolic Interactions between Marine Red Algae and a Novel Blastopirellula strain J2-11 Promote Algal Growth and Stress Resilience</i>	Byeong Jun Choi	Chung-Ang University	Korea, Republic of
PS3.16.139	<i>Microbial oxidation of inorganic compounds contributes to the coral holobiont energy budget</i>	Jialing Zeng		Australia
PS3.16.140	<i>Natural product biodiscovery from the bacterial symbionts of Aotearoa New Zealand endemic insects</i>	Rory Little	Victoria University of Wellington	New Zealand
PS3.16.141	<i>Obligate intracellular symbiosis with a culturable and genetically manipulatable symbiont in an insect</i>	Kazutaka Takeshita	Akita Prefectural University	Japan
PS3.16.142	<i>Pelagic bobtail squids harbor bioluminescent symbionts with reduced genomes</i>	Arno Hagenbeek		Japan
PS3.16.143	<i>Physiological Responses of Chlorella vulgaris to Co-cultivation with Extracellular Carbonic Anhydrase-Encoding Bacteria</i>	Chaerin Park	Korea Institute of Geoscience and Mineral Resources	Korea, Republic of
PS3.16.144	<i>Proliferation of a bloom-forming phytoplankton via uptake of polyphosphate-accumulating bacteria under phosphate-limiting conditions</i>	Shoko Ueki		Japan

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PS3.16.145	<i>Resilient endophytic consortia drive vitamin B12 production in aquatic plants</i>	Rhishika Dutta		Israel
PS3.16.146	<i>Rhizobial denitrification decouples nodulation from ambient nitrogen</i>	Omri Finkel	Hebrew University	Israel
PS3.16.147	<i>Roles of natural products in nematode-bacteria symbiosis</i>	Michelle Anne Diano		Germany
PS3.16.148	<i>Signaling molecules and extracellular DNA elicit chemotactic and regulatory responses in surface-associated Roseobacteraceae</i>	Thorsten Brinkhoff		Germany
PS3.16.149	<i>Strain-specific roles of bacteriophages in growth regulation of ammonia-oxidizing bacteria</i>	Rino Isshiki	National Institute of Advanced Industrial Science and Technology	Japan
PS3.16.150	<i>Streptococcus mutans can uptake vitamin B2 via membrane vesicles</i>	Tamami Ito	University of Tsukuba	Japan
PS3.16.151	<i>Strigulaceae Genomes Provide Insight into Lichenization Beyond Lecanoromycetes</i>	Seung-Yoon Oh		Korea, Republic of
PS3.16.152	<i>The genomic basis of bacterial mechanisms promoting coral larval settlement</i>	Paul O'Brien	School of Chemistry and Molecular Biosciences, Australian Centre for	Australia
PS3.16.153	<i>Towards a framework for studying algal-bacterial co-cultures using infrared spectromicroscopy</i>	Julian M. Künkel	University of Duisburg-Essen	Germany
PS3.16.154	<i>Transstadial association of amoeba Naegleria australiensis and Legionella bacteria in Anopheles mosquitoes</i>	Artur Trzebny	Molecular Biology Techniques Laboratory, Faculty of Biology, Adam Mickiewicz University in	Poland
PS3.16.155	<i>Two novel symbiotic Mycoplasmatales discovered from deep-sea sea stars</i>	Yu Yoshida		Japan
PS3.16.156	<i>Uncovering the functional core of New Zealand seaweed microbiomes</i>	Chelsea Vickers		New Zealand

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PS3.16.157	<i>Widespread pleiotropy among axes of defense against a bacterial pathogen in C. elegans</i>	Michael Blazanin		Canada