

Poster Board Number	Title	Presenting author	Affiliation	Country
PS3.20.231	<i>Absolute Viral Abundance from Multi-Omic Data Reveal the Scale of Viral Contributions to Biogeochemically Relevant Host Metabolism Across Marine Ecological Provinces</i>	Jelani Williams	University of Southern California	United States of America
PS3.20.232	<i>Active and depth-stratified viral communities mediate microbial and biogeochemical dynamics in hadal sediments of the Mariana Trench</i>	Yuanchao Zhan		China
PS3.20.233	<i>A depth- and size fraction-resolved analysis of microbial and viral communities in the ocean water column</i>	Marguerite Langwig	University of Wisconsin-Madison	United States of America
PS3.20.234	<i>Algal DMSP production shapes phycosphere microbial communities and organic sulfur metabolism</i>	Xiao-Hua Zhang	Ocean University of China	China
PS3.20.235	<i>Are we burying our heads in the benthos? Rethinking water column metabarcoding as a proxy for benthic Gambierdiscus monitoring</i>	Jacqui Stuart		New Zealand
PS3.20.236	<i>Assimilation of dimethylsulfoniopropionate(DMSP)-Derived Sulfur by Marine Cyanobacteria</i>	yayun zhao		United Kingdom
PS3.20.237	<i>A widespread microbial pathway for the remineralization of archaeal and bacterial glycerol-phosphates in the ocean</i>	Mingyu Li	University of Warwick	United Kingdom
PS3.20.238	<i>Bathymetric structuring of the global hadal trench microbiome</i>	Yen-Ting Chen	University of Southern Denmark	Denmark
PS3.20.239	<i>Bloom-forming anoxygenic phototrophs heavily invest in anti-phage defense</i>	Roo Weed		United States of America
PS3.20.240	<i>Changes in Energy Metabolisms of Auxiliary Metabolic Genes of Bacteriophages in Temperate Coastal Ecosystem</i>	Seung Won Jung	Korea Institute of Ocean Science & Technology	Korea, Republic of
PS3.20.241	<i>Charting the Arabian Gulf Microbiome: Insights into Biogeochemistry and Climate Adaptation</i>	Thomas Grevesse		United Arab Emirates
PS3.20.242	<i>Chemolithoautotrophic carbon fixation in deep sea sponges</i>	Vanessa Fraser		Australia
PS3.20.243	<i>Combining quantitative eDNA metabarcoding and qPCR to explore the influence of fish and prokaryotic communities on coastal cetacean distribution</i>	Lin Xiaqi	The Hong Kong University of Science and Technology	Hong Kong

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PS3.20.244	<i>Comparative secretomics reveal the diversity of extracellular carbohydrate metabolism in Symbiodiniaceae</i>	Yuxin Liu	The University of Tokyo	Japan
PS3.20.245	<i>Consistent but not the same: following the phenology and succession of phytoplankton blooms in the context of an archipelago using an Imaging Flow CytoBot (IFCB)</i>	Deo Florence Onda	University of the Philippines Diliman	Philippines
PS3.20.246	<i>Contrasting differences in bacterial community stability and succession under acidic vs alkaline conditions</i>	mingjie Li		China
PS3.20.247	<i>Crocospaera spp. are important unicellular nitrogen-fixers in the Western Tropical South Pacific</i>	Caitlyn Parente		United States of America
PS3.20.248	<i>Cryptic microbial hydrocarbon cycling in the ocean</i>	Alicia Talavera	University of Essex	United Kingdom
PS3.20.249	<i>Cultivation and genomic insight into the first representative of UBA868, a globally distributed marine lineage</i>	Rajeev Meora	Inha University	Korea, Republic of
PS3.20.250	<i>Cultivation of Thiovulum reveals extreme motility, emergent collective behavior, and bioenergetic limits of bacterial life</i>	George Schaible	Montana State University	United States of America
PS3.20.251	<i>Decoding Nutrient Dynamics: Building Mathematical Models of the Microbial Loop from Laboratory Experiments</i>	Kaitlin Lesco	New York University, Abu Dhabi (NYUAD)	United Arab Emirates
PS3.20.252	<i>Depth-Driven Ecology and Metabolic Specialization of Marine Chloroflexi (SAR202 Lineages) Across the Global Ocean</i>	Chunqi Jiang	The University of Tokyo	Japan
PS3.20.253	<i>Dissolved oxygen concentrations influence microbial diversity and dominant players in an oxygen minimum zone</i>	Kaitlin Dombroski		United States of America
PS3.20.254	<i>Ecological Roles of Chemolithoautotrophic Bacteria in Carbon Sequestration Processes of Unvegetated Korean Tidal Flats</i>	Sang Hyun Lee		Korea, Republic of
PS3.20.255	<i>Enhancing coral larval settlement and restoration through new microbial technologies</i>	Morgan Farrell		United States of America
PS3.20.256	<i>Ephemeral coupling of dissolved organic matter and bacterioplankton in a land-ocean continuum: seasonal switching between substrate and chemical limitation</i>	Yunjie Ma	Southern University of Science and Technology	China

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PS3.20.257	<i>Evaluating Extraction Methods for Marine Prokaryotic and Eukaryotic DNA in Coastal Sediment: Interactions Between Protocols and Sample Storage</i>	Ocean Rauszen	The Hong Kong University of Science and Technology	Hong Kong
PS3.20.258	<i>Exploring NCLDV Diversity and Infection Strategies in Coastal Ecosystems: Insights from the Pearl River Estuary</i>	Ruixian Sun	Department of Ocean Science, The Hong Kong University of Science and	China
PS3.20.259	<i>Exploring the symbiotic dance</i>	Amy Rose Birss	University of Sheffield, A* Genome Institute	Singapore
PS3.20.260	<i>Extreme Redox Environments Harbor Bioactive Actinomycetes: Evidence from the Mexican Tropical Pacific OMZ</i>	Alejandra Prieto-Davó	UNIVERSIDAD NACIONAL AUTÓNOMA DE MÉXICO, UNIDAD DE QUÍMICA,	Mexico
PS3.20.261	<i>Friends and foes: exploring the potential for coral mutualists and pathogens in macroalgal epibiomes</i>	Willow Dunster	University of California, Berkeley	United States of America
PS3.20.262	<i>From debris to destiny: how ocean plastics create new worlds - and new risks</i>	Olga Pantos	New Zealand Institute for Public Health and Forensic Science	New Zealand
PS3.20.263	<i>From Sediment to Host: Exploring Australian Benthic and Host-associated Microbial Eukaryotes Communities Using eDNA Metabarcoding</i>	Yuxuan Jiang	University of Technology Sydney	Australia
PS3.20.264	<i>Functional Characterization of the OR-C Family Reveals Expanded Respiratory Diversity Within the Cytochrome bd Superfamily</i>	Parker Ingram		United States of America
PS3.20.265	<i>Functional trade-offs between growth and prey diversity explain the global dominance of mixotrophic dinoflagellates</i>	Heechang Kang	Inha University	Korea, Republic of
PS3.20.266	<i>Genomic diversity and biogeography of six novel prasinoviruses infecting the cryptic Bathycoccus clade III isolated from Hong Kong coastal waters</i>	Yongqi Tang	The Hong Kong University of Science and Technology	China
PS3.20.267	<i>Harmful algae blooms drive microbial copiotrophy, but a lag in viral abundance</i>	Elizabeth Dinsdale	Flinders University	Australia
PS3.20.268	<i>Holobiont-Driven Bioethanol Production of Holopelagic Sargassum</i>	Katharina Paetz		Germany
PS3.20.269	<i>Impact of funnel accumulation on the ecological functions and evolution of hadal microorganisms</i>	Jiwen Liu		China

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PS3.20.270	<i>Impact of heat stress and pathogen challenges on the spatial organization of the microbial community in the Pacific oyster (Magallana gigas)</i>	Parker Lund		Canada
PS3.20.271	<i>Intracellular and division-associated variability in marine bacterial surface properties: preliminary observations</i>	Yosuke Yamada	Japan Agency for Marine-Earth Science and Technology	Japan
PS3.20.272	<i>Investigation of a Light-Harvesting Antenna in Sodium Ion-Pumping Rhodopsin</i>	Keigi Ou		Japan
PS3.20.273	<i>Island-wide, multi-scale surveys around Moorea reveal strikingly stable bacterial communities linked to habitat and environmental factors</i>	Sho Kodera		United States of America
PS3.20.274	<i>Keystone taxa predict marine microbial community structure and ecosystem function</i>	Ewa Merz		United States of America
PS3.20.275	<i>Latitudinal Variability of Synechococcus Pigmentation in the Euphotic Layer of the Pacific Ocean</i>	Ayane Tanaka	Tokyo university of marine science and technology	Japan
PS3.20.276	<i>Light availability shapes the fitness and distribution of cyanobacterial viruses with distinct diel infection traits</i>	Qinglu Zeng	The Hong Kong University of Science and Technology	Hong Kong
PS3.20.277	<i>Marine Fungi as "Master Cyclers": Integrated Carbon, Nitrogen, and Phosphorus Dynamics Across the Oceanic Particle Size Continuum</i>	Zihao Zhao		Austria
PS3.20.278	<i>Metabarcoding reveals distinct microalgal community assemblages across remote Pacific regions</i>	Greta Gaiani	University of Technology Sydney	Australia
PS3.20.279	<i>Microbial abundance and depth shape evolutionary dynamics of sponge-microbiome symbiosis</i>	Cristina Diez Vives		Spain
PS3.20.280	<i>Microbial and molecular diversity shaping carbon storage in Miyara River mangroves, Ishigaki Island, Japan</i>	Masumi Hasegawa-Takano	JAMSTEC	Japan
PS3.20.282	<i>Microbial communities in marine sediments underlying the northern Benguela oxygen minimum zone</i>	Paige Payne	Florida State University	United States of America
PS3.20.283	<i>Microbial oceanography of seamounts in the high seas of the Eastern Indian Ocean</i>	Janelle Thompson	Nanyang Technological University	Singapore

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PS3.20.284	<i>Microeukaryotic community dynamics during macroalgal blooms in the intertidal zone of a tropical island</i>	Wenxue Wu	Hainan University	China
PS3.20.285	<i>Monsoons reshape taxonomic composition with stable core functions in primo-colonizers of marine plastic surfaces</i>	Ronan Baculi	University of the Philippines	Philippines
PS3.20.286	<i>Multi-marker eDNA metabarcoding uncovers uneven planktonic diversity and reveals underrepresentation of deep-sea protist lineages in reference databases</i>	Clement Coclet		United States of America
PS3.20.287	<i>New sulfur-containing diketopiperazine from marine-derived bacteria streptomyces rochei sp. 81 with potent carbonic anhydrase ii inhibition</i>	Ahmed AlRawahi	Sultan Qaboos University	Oman
PS3.20.288	<i>Oxygen gradients structure microbial communities in the Benguela Upwelling System, corresponding to changes in nitrogen transformation pathways in genomes recovered from low-oxygen waters</i>	Alexa Crossen		United States of America
PS3.20.289	<i>Responses of uninfected bacteria to dissolved organic matter released by infected bacteria</i>	Chen Yubing	The Hong Kong University of Science and Technology	Hong Kong
PS3.20.290	<i>Revealing the potential role of multiple archaeal lineages in nitrogen transformations in Saanich Inlet, British Columbia</i>	Emily Guidry	Florida State University	United States of America
PS3.20.291	<i>Revealing widespread DNA compartmentalization in filamentous giant sulfur bacteria (Beggiatoaceae)</i>	Philip Nosler	University of California Santa Barbara	United States of America
PS3.20.292	<i>River-ocean transition zones act as hotspots of hidden molecular diversity</i>	Maïa Henry	Friedrich Schiller University Jena	Germany
PS3.20.293	<i>RNA Viruses Implicated in the Decline of a Microalgal Bloom in Marine Mesocosms</i>	Daria Di Blasi	University of Southern California	United States of America
PS3.20.294	<i>Salinity-driven turnover of pico-sized chlorophytes across freshwater-marine interfaces using dual-platform 18S rRNA gene metabarcoding</i>	Yun-Chi Lin	National Taiwan Ocean University	Taiwan, Province of China
PS3.20.295	<i>Season and depth dependent population structure of the marine heterotrophic bacteria Vibrio splendidus in the Southern California Bight</i>	Danny Osorio		United States of America
PS3.20.296	<i>Seasonal dynamics and functional responses of particle-attached microbial communities over an annual cycle and their associations with phytoplankton blooms at Helgoland Roads</i>	Feng-Qing Wang	Max Planck Institute for Marine Microbiology	Germany

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PS3.20.297	<i>Seasonal dynamics and potential interactions of free-living bacterioplankton during phytoplankton blooms at Helgoland Roads</i>	Pranita Mishra		Netherlands
PS3.20.298	<i>Seasonal productivity regimes restructure coastal microbial assemblages and pathogenic signatures along India's East coast</i>	Swarnaprava Behera	Centre for Marine Living Resources and Ecology, Ministry of Earth Science	India
PS3.20.299	<i>Seaweed-associated fungal communities are influenced by host species and location</i>	Angela Li		Australia
PS3.20.300	<i>Secretion of diverse and uncharacterized compounds by Cyanobacteria as a hidden source of marine organics</i>	Paula Prondzinsky	Japan Agency for Marine-Earth Science and Technology (JAMSTEC)	Japan
PS3.20.301	<i>Single-cell quantification reveals divergent mixotrophic strategies underlying niche partitioning in marine Synechococcus</i>	Qiang Zheng	Xiamen University	China
PS3.20.302	<i>Spatial distributions of deep-sea sediment microbiomes 12+ years after the Deepwater Horizon oil spill</i>	Jordan Heiman		United States of America
PS3.20.303	<i>Specialized bacterial degradation of sulfated glycans drives algal-microbe interactions</i>	Emma Marangon	Max Planck Institute for Marine Microbiology, Bremen	Germany
PS3.20.304	<i>Sub-daily virus sampling at the Bermuda Atlantic Time Series reveals diel and depth-structured population dynamics without community-level shifts</i>	Alfonso Carrillo	The Ohio State University	United States of America
PS3.20.305	<i>Substrate chemistry filters pioneer microbiomes and functions on reefs recovering from mass bleaching</i>	Joao Gabriel Duarte Rosado	King Abdullah University of Science and Technology (KAUST)	Saudi Arabia
PS3.20.306	<i>Temporal Dynamics and Core Microbial Taxa in Korean Intertidal Mudflat Sediments</i>	Yeonjae Yoo	Korea University	Korea, Republic of
PS3.20.307	<i>The marine microbiome of Papua New Guinea</i>	Golam Rabbani	National University of Singapore	Bangladesh
PS3.20.308	<i>The mechanisms associated with the suppression of Vibrio parahaemolyticus cells in green-lipped mussels (Perna canaliculus)</i>	Sinisa Vidovic	Massey University Manawatu	New Zealand
PS3.20.309	<i>Transcriptomic insights into intra-specific physiological differences in the marine dinoflagellate Prorocentrum cordatum</i>	Jeong-Ah Shin	Hanyang University	Korea, Republic of

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PS3.20.310	<i>Transcriptomic Reconstruction of a Marine Flavobacterium Harboring Microbial Rhodopsins</i>	Yurim Bae	Gyeongsang National University	Korea, Republic of
PS3.20.311	<i>Under the Sea: Seasonal Plant-Microbe Dynamics Regulate Recalcitrant Carbon Cycling in Zostera marina Meadows</i>	Gina Chaput	University of Massachusetts, Amherst	United States of America
PS3.20.312	<i>Variations of physico-chemical parameters in a mesocosm study cause disproportionate shifts in the microbial community composition of the sea-surface microlayer</i>	Isha Athale		Germany