

Poster Board Number	Title	Presenting author	Affiliation	Country
PS1.05.180	<i>Addition of Blautia pseudococcoides as a potential alternative hydrogen sink and its effect on rumen function in vitro</i>	Rich Duong		United States of America
PS1.05.181	<i>A Feedback-Controlled Fed-Batch Reactor Platform for Reproducible In Vitro Rumen Simulation</i>	Noelia Rubio	Number 8 Bio	Australia
PS1.05.182	<i>A multi-omic meta-analysis of rumen microbial responses to methane-mitigating feeding strategies in cattle</i>	Velma Aho	Norwegian University of Life Sciences	Norway
PS1.05.183	<i>Arsenophonus-mediated folate augmentation enhances insecticide susceptibility of Nilaparvata lugens</i>	Hu Wan	Huazhong Agricultural University	China
PS1.05.184	<i>Bacterial culture-based analysis of the Tuatara gut reveals functional roles of the core genus chryseobacterium</i>	Tabitha Caldwell	The University of Auckland	New Zealand
PS1.05.185	<i>Behavioural manipulation by parasitic nematodes is associated with microbiome composition</i>	Priscila Salloum	University of Auckland	New Zealand
PS1.05.186	<i>Behavioural Phase Transitions in the Migratory Locust, Locusta migratoria, are Related to Changes in Gut Microbiome Composition</i>	Jaeha Kim		Japan
PS1.05.187	<i>Benchmarking and Optimizing Long-read Microbial Functional Profiles for Rumen Methane Prediction in Sheep</i>	Yuhao Li		Australia
PS1.05.188	<i>Beneficial Effects of Bifidobacterium animalis against Bacterial Vaginosis Induced by Gardnerella vaginalis</i>	Juyoun Kang		Korea, Republic of
PS1.05.189	<i>Beyond methanogen inhibition: novel mechanisms and functional niche displacement in Asparagopsis-mediated methane reduction</i>	Sharon Huws		United Kingdom

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PS1.05.190	<i>Cellulose degradation capability of three Parabasalia flagellates in the gut of Reticulitermes aculabialis</i>	Hong Yang	School of Life Sciences, Central China Normal University	China
PS1.05.191	<i>Characterising the Bacterial Microbiome in Australian Stingless Bee Brood Food and Pollen</i>	Jasmin Li		Australia
PS1.05.192	<i>Codiversification, cophylogeny and metabolic complementary of deep-sea glass sponge holobiont to endure harsh environmental limitations</i>	Kwok-Lun HUI	Hong Kong University of Science and Technology	Hong Kong
PS1.05.193	<i>Comparative analysis of adhesin-like proteins from Methanobacteriales species from the rumen and human gut</i>	Henning Seedorf	Bioeconomy Science Institute - AgResearch Group, Grasslands Research Centre	Singapore
PS1.05.194	<i>Comparative Analysis of Gut Microbiota and Host Phenotypic Characteristics Across Enterotype-like Clusters in Cynomolgus and Rhesus Macaques</i>	Kyuyoung Shim		Korea, Republic of
PS1.05.195	<i>Comparative genomics of rumen and human Ruminococcus bromii reveals conserved starch specialisation with lineage-specific adaptations</i>	Sophia Escobar-Correas	Ecosciences Precint	Australia
PS1.05.196	<i>Corals select and structure distinct and diverse fungal communities across tissues and skeletons</i>	Ming Sheng Ng		Singapore
PS1.05.197	<i>Core genera of the gut microbiome of rainbow trout and the first butyrate-producing bacterium isolated from fish gut representing a novel genus in the family Fusobacteriaceae, Piscibacter tructae</i>	Mio Takeuchi		Japan
PS1.05.198	<i>Cross-Species Comparative Metagenomics of the Vulture Gut Multi-Kingdom Microbiome</i>	Zakie Hage		Canada
PS1.05.199	<i>Culture-independent characterization of Planctomycetota class SZUA-567 inhabiting the koala gut</i>	Zeran Li	University of Queensland	Australia

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PS1.05.200	<i>Development of a Strain Library for the Global Methane Hub Genetic Toolkits Project</i>	Sophia Sanguedolce	University of Illinois, Urbana-Champaign	United States of America
PS1.05.201	<i>Development of Genetic Toolkits for Five Dominant Rumen Bacteria to Enable Targeted Microbiome Engineering for Reduced Methane Emissions</i>	Rhiannon Cecil	BiomEdit, Inc.	United States of America
PS1.05.202	<i>Development of genetic tools for rumen bacteria and methanogens</i>	Sam Mahoney-Kurpe	Bioeconomy Science Institute - AgResearch Group, Grasslands Research Centre	New Zealand
PS1.05.203	<i>Diet and nutritional strategy shape the hindgut microbiome in marine herbivorous fish</i>	Samantha Stevenson	University of Auckland	New Zealand
PS1.05.204	<i>Dietary Latilactobacillus curvatus CACC879 Reduces Fecal Odor by Modulating Gut Microbiota and Organic Acids in Finishing Pigs</i>	YANGSEON KIM		Korea, Republic of
PS1.05.205	<i>Different vertical transmission patterns of coral-associated bacteria between brooding and broadcast-spawning corals</i>	Jia-Ho Shiu		Taiwan, Province of China
PS1.05.206	<i>Disentangling a Holobiont: Role of microbes in the ecology and evolution of the jewel wasp, Nasonia</i>	Anjali Rana	Indian Institute of Science Education and Research Mohali, India	India
PS1.05.207	<i>Distribution patterns of Escherichia coli phage genera in the porcine gut</i>	Xuelin Zhu		China
PS1.05.208	<i>Diversity and Host Dependence in the Gut Microbiota of Marine Fish from an Annual Variation Perspective</i>	Masaya Fujino		Japan
PS1.05.209	<i>Diversity of Bee Microbiomes</i>	Zoë Wilson		United States of America

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PS1.05.210	<i>Early-life assembly of gut microbiota in Ficedula flycatchers: insights from a cross-fostering experiment</i>	Ester Martinez Renau	Uppsala University	Sweden
PS1.05.211	<i>Ecological characterization of the rumen RNA virome and its implications for feed efficiency in ruminants</i>	Fabio Lima	University of California Davis	United States of America
PS1.05.212	<i>Environmental drivers of a toxic trait? linking pond physicochemical profiles to shifts in the newt microbiome and tetrodotoxin levels</i>	Andres Brunetti	Department of Insect Symbiosis, Max Planck Institute for Chemical Ecology, Jena	Germany
PS1.05.213	<i>Establishing Novel Molecular Tools for Rumen Microbes</i>	Marla Josephine Jeckstiess		Germany
PS1.05.214	<i>Evaluation of Methane Mitigation Potential and Microbial Community Shifts by Halophytes in Rumen Fermentation</i>	Eun Bi Jang		Korea, Republic of
PS1.05.215	<i>Evolutionary dynamics of the transition to an intestinal lifestyle in Methanobacteriota</i>	Evgenii Protasov	Max Planck Institute for Terrestrial Microbiology	Germany
PS1.05.216	<i>Exendin-4-associated remodeling of gut microbiome assembly and intestinal lipid-responsive transcription in diet-induced obesity</i>	Jin-Kyung Hong	Chonnam National University	Korea, Republic of
PS1.05.217	<i>Exploring the RNA virus populations of the rumen and saliva of cattle</i>	Rosalind Gilbert	Ecosciences Precint	Australia
PS1.05.218	<i>Extrinsic and intrinsic factors differentially shape the fish gut microbiome</i>	Gyeong Hak Han	University of Science & Technology	Korea, Republic of
PS1.05.219	<i>Facial eczema tolerant and susceptible pasture-grazed rams have similar rumen microbial communities</i>	Christina D. Moon	Bioeconomy Science Institute Maiangi Taiao	New Zealand

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PS1.05.220	<i>Feeding beef ruminants red seaweed reduces methane emissions due to a rumen microbiome modulation</i>	Kayley Barnes		United Kingdom
PS1.05.221	<i>First Characterization of RNA Viruses and DNA Viral Activity in Corals Affected by White Plague Disease</i>	Shara Sookhoo	UC Berkeley	United States of America
PS1.05.222	<i>Fumarate Supplementation and its Effect on the Hydrogen Metabolism of the Rumen Microbiome and Rumen Co-cultures under Inhibition of Methanogenesis</i>	Pedro Romero		United States of America
PS1.05.223	<i>Functional gene-guided enrichment plus in situ microsphere cultivation enables isolation of new ureolytic bacteria from the rumen</i>	Shengguo Zhao	Chinese Academy of Agricultural Sciences	China
PS1.05.224	<i>Genetic Toolkit for Five Rumen Methanogens</i>	Biswarup Mukhopadhyay	Virginia Tech	United States of America
PS1.05.225	<i>Genomic Insights into Lactate Cross-Feeding in the Rumen</i>	Joshua N. Joseph		New Zealand
PS1.05.226	<i>High-throughput cultivation of the rumen microbiome reveals novel prokaryotes involved in host fermentation and metabolism</i>	Elise Henderson		Australia
PS1.05.227	<i>Housing and Early-Life Disease Shape Gut Microbiome Development in Pre-Weaned Dairy Calves</i>	Victoria Talbott	Colorado State University	United States of America
PS1.05.228	<i>Identifying biomarkers of Alzheimer's disease through a comparative analysis of mouse and human microbiomes</i>	Gina Faraci	University of California, Irvine	United States of America
PS1.05.229	<i>Identifying prognostic biomarkers for post weaning diarrhea (PWD) in piglets using combinatorial predictive models</i>	Mohak Gujare	Wageningen University	Netherlands

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PS1.05.230	<i>Metabolic alterations of citrus residue fermented with complex microbiomes of Bacillus subtilis and Aspergillus niger at different time durations</i>	Hyejin Hyeon		South Korea
PS1.05.231	<i>Improved cultivation of rumen Methanobrevibacter species to enable genetic tool kit development and methane mitigation strategies</i>	William Whitman	University of Georgia	United States of America
PS1.05.232	<i>Insecticide Stress Regulates Spodoptera frugiperda Resistance Evolution via Remodeling Symbiotic Community and Chloride Ion Homeostasis</i>	Yunhua Zhang		China
PS1.05.233	<i>Integrating microscopy and multi-omic data to understand the role of microorganisms in a coral disease outbreak in the northwest Gulf of Mexico</i>	Carly Karrick		United States of America
PS1.05.234	<i>Isolation and validation of extracellular vesicles across Red Sea coral genera</i>	Vivian Hayde Aguilar Molina		Mexico
PS1.05.235	<i>Longitudinal Gut Microbiome Dynamics in a Diet-Induced NAFLD Model of Cynomolgus Macaques</i>	Jeonghwa Choi		Korea, Republic of
PS1.05.236	<i>Loss of enolase gene does not constrain growth of Butyrivibrio and Pseudobutyrvibrio species on glucose</i>	Kerri Reilly		New Zealand
PS1.05.237	<i>Cuticular microbiome of natural sexual and asexual populations of a facultatively parthenogenetic stick insect, Megacrania batesii</i>	Nathali Machado de Lima		Australia
PS1.05.238	<i>Metabolic strategies of ruminal Selenomonas strains: the effects of hydrogen on terminal electron acceptor use and fermentation end products</i>	Krsana Rajasekaran	Bioeconomy Science Institute	New Zealand
PS1.05.239	<i>Metagenome-based insights into protozoa-driven rumen communities and host performance</i>	Hongyu Duan		Australia

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PS1.05.240	<i>Metagenomic insights into rumens adapted to a climate-smart forage</i>	Nikola Palevich	Bioeconomy Science Institute Maiangi Taiao	New Zealand
PS1.05.241	<i>Microbial abundance and dynamic following rumen content exchange</i>	Adrian Omar Maynez Perez		Norway
PS1.05.242	<i>Microbial Interactions between Carrion Insect Symbiont Yarrowia lipolytica and Carrion Bacteria Staphylococcus aureus</i>	Wan-Hsuan Li		United States of America
PS1.05.243	<i>Microbial stages of life: Gut transplants uncover age-dependent microbiome shifts in Daphnia magna</i>	Emma Gouwy	KU Leuven	Belgium
PS1.05.244	<i>Microbiome-based tracking of diet shifts in ectotherms: a new approach to monitor effects of global changes on food webs?</i>	Paula Eterovick		Germany
PS1.05.245	<i>Mycobiota Remodeling Mediates DON-Induced Gut Dysbiosis in Piglets</i>	Hao-Yu Liu		China
PS1.05.246	<i>Proteomic and Microbiome Insights into Bacterial Regulation of Coral Metamorphosis and Settlement</i>	Yanying Zhang	Yantai University	China
PS1.05.247	<i>Rapid Identification of Meat-Associated Bacteria Using Matrix-Assisted Laser Desorption/Ionisation Time-of-Flight Mass Spectrometry (MALDI-ToF MS)</i>	Icaro Castro		United Kingdom
PS1.05.248	<i>Neobalantidium coli tracking in pig gut metagenomes reveals it is more than a tropical parasite</i>	Baris Erhan Ozdinc	Wageningen University	Netherlands
PS1.05.249	<i>Restriction-Enzyme Reduced Representation Sequencing Captures Greater Methane-Associated Rumen Microbiome Variation Than Shotgun Metagenomics or Metatranscriptomics</i>	Ben Perry	Bioeconomy Science Institute	New Zealand

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PS1.05.250	<i>Rumen ciliates modulate methane emissions in ruminants</i>	Fei Xie	Nanjing Agricultural University	China
PS1.05.251	<i>Rumen microbial atlases of cattle from Sub-Saharan Africa and South Asia and their associations with methane emissions and productivity</i>	Dwi Susanti		United States of America
PS1.05.253	<i>Rumen Microbiome Structure and Functional Potential in Indigenous Goats Under Low-Input Systems</i>	Sinalo Mani		South Africa
PS1.05.254	<i>Ruminal lactate metabolism in low and high methane yield sheep</i>	Graeme Attwood	Bioeconomy Science Institute - AgResearch Group, Grasslands Research Centre	New Zealand
PS1.05.255	<i>Segment Resolved Metabolic Modelling Reveals Context-Dependent Function in the Black Solider Fly Gut Microbiome</i>	Matthew Morgan	Commonwealth Scientific and Industrial Research Organization (CSIRO)	Australia
PS1.05.256	<i>Short-term gut microbiota dynamics in the Western deer mouse, <i>Peromyscus sonoriensis</i></i>	Ashley Beck		United States of America
PS1.05.257	<i>Signatures and likely sources of the male pregnancy microbiome in wild bay pipefish (<i>Syngnathus leptorhynchus</i>)</i>	Elyse Barker		United States of America
PS1.05.258	<i>Single-cell viromics unveils active infection and novel viral-host interactions in the rumen microbiome</i>	Jinghong Xu	Zhejiang University	China
PS1.05.259	<i>Skin mucus microbiome of manta ray (<i>Mobula alfredi</i>): optimizing DNA extraction, storage, and revealing microbial traits as a non invasive health indicator</i>	QIU SHUTING	The Hong Kong University of Science and Technology	Hong Kong
PS1.05.260	<i>Snowshoe hare gut microbial responses to dietary toxins</i>	Bahareh Sorouri	University of Alaska Fairbanks	United States of America

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PS1.05.261	<i>Social Environment Shapes Gut Microbiome of Sailfin Mollies (Poecilia latipinna)</i>	Ian Sander	Ohio Wesleyan University	United States of America
PS1.05.262	<i>Species-level faecal microbiota development from suckling to 25 days postweaning in piglets</i>	Kevin Steven Jerez Bogota		Denmark
PS1.05.263	<i>Structural farm security scoring and gut microbiome assembly in breeding pigs</i>	Seung-Muk Yu	Chonnam National University	Korea, Republic of
PS1.05.264	<i>Targeting microbiota leverage points reshapes host xenobiotic tolerance and resistance evolution</i>	Shun He	Huazhong Agricultural University	China
PS1.05.265	<i>The effect of repeated exposure to hypoxia and warming on the eastern oyster microbiome</i>	Jade Fiorilla		United States of America
PS1.05.266	<i>The gut microbiome in monarch butterflies links plant-associated microbes to insect host specialization</i>	Luis Servín-Garcidueñas	Escuela Nacional de Estudios Superiores Unidad Morelia, UNAM	Mexico
PS1.05.267	<i>The Role of Coral Microbiomes in Resistance to Stony Coral Tissue Loss Disease</i>	Brooke Sienkiewicz		United States of America
PS1.05.268	<i>The role of the gut microbiota and the fat body in the health of honeybees</i>	Elien Van Der Straeten	KU Leuven	Belgium
PS1.05.269	<i>Time-series full-length 16S profiling identifies specific gut bacteria that could be linked to the suppression of Citrobacter rodentium infection</i>	Hiroaki Masuoka	Laboratory for Symbiotic Microbiome Sciences, RIKEN Center for Integrative Medical Sciences	Japan
PS1.05.270	<i>Tuna microbiome : a mosaic of microbial niches and hidden viral reservoirs</i>	Elsa Gadoin	University of California Santa Barbara	United States of America

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PS1.05.271	<i>Unravelling the feline and canine microbiome</i>	Yun-Wen Lim	Massey University	New Zealand
PS1.05.272	<i>Unveiling the ecological role of the beehive microbiome</i>	Kerry Barnard	University of Surrey	United Kingdom