Australian Academy of Science

THE MICROBIOME

Exploring the role of microorganisms in ecosystem processes and health

PROGRAM ADELAIDE, 29 NOVEMBER – 1 DECEMBER

CONTENTS

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FOREWORD

The Academy has hosted the Theo Murphy Australian Frontiers of Science symposium since 2003, bringing together the very best young Australian scientists to discuss emerging technologies, new opportunities and exciting cutting-edge advances in their fields.

The health and functioning of the planet is intrinsically linked to microbiology—from maintenance of human health to microbes as drivers of global biogeochemical cycles. This area has seen rapid growth due to recent developments in molecular methodologies that are enabling scientists to document the incredible diversity and previously unrecognised ecological functions.

This year, 70 outstanding early- and mid-career researchers from diverse fields will come together to consider the contributions and transformations that this explosion of information may have in their areas of research. This meeting will focus broadly on three themes: the living environment, the human microbiome and studying microbiomes.

The 2016 Theo Murphy Australian Frontiers of Science symposium is generously supported by the Theo Murphy (Australia) Fund courtesy of the Royal Society of London. The Academy is delighted to have this funding available to enable some of Australia's brightest young scientists to engage in fresh thinking and to develop networks that will enrich their careers.

Professor Andrew Holmes AM PresAA FRS FTSE
President, Australian Academy of Science

SYMPOSIUM ORGANISERS

Organising committee

Dr David Briskey
Health CRN Research Fellow, School of Human Movement and Nutrition Sciences, University of Queensland

Associate Professor Kathryn Holt
Academic, Biochemistry and Molecular Biology, University of Melbourne

Professor Emma Johnston
Pro Vice-Chancellor (Research), Evolution and Ecology Research Centre, UNSW Australia

Associate Professor Lutz Krause
Principal Research Fellow, Diamantina Institute Faculty of Medicine, University of Queensland

Associate Professor Jeff Powell
Associate Professor, Hawkesbury Institute for the Environment, Western Sydney University

Dr Carly Rosewarne
Microbial Ecologist, Health and Biosecurity, CSIRO

Dr Laura Weyrich
ARC Postdoctoral Research Associate, Genetics and Evolution, University of Adelaide

Oversight committee

Professor Anthony Linnane
Managing Director, Centre for Molecular Biology and Medicine

Professor Jim McCluskey
Deputy Vice-Chancellor (Research), University of Melbourne

Professor Marilyn Renfree
Professor of Zoology, University of Melbourne

Professor Luis Vitetta
Director of Medical Research, Medlab Clinical, University of Sydney

Academy secretariat

Dr Sandra Gardam
Early- and Mid-Career Researcher Project Officer, Australian Academy of Science

Mr Ray Kellett
Events Administrator

Ms Sarah Tynan
Content Producer, Nova: science for curious minds

PROGRAM

Day one—Tuesday 29 November

5.00 pm	**Registration and poster setup**
5.30 pm	**Welcome to country** Uncle Lewis Yerloburka O'Brien
5.40 pm	**Introduction of opening addressee** Professor David Day FAA, Matthew Flinders Distinguished Professor, Flinders University
5.45 pm	**Official opening** Dr Leanna Read, Chief Scientist of South Australia
5.55 pm	**Introduction of keynote speaker** Professor David Day FAA, Matthew Flinders Distinguished Professor, Flinders University
6.00 pm	**Keynote:** *The challenge of the microbiome in human health and disease* Professor Luis Vitetta, Medlab Clinical Ltd
6.30 pm	**Cocktail reception and poster session**
8.30 pm	**Cocktail reception concludes**

Day two—Wednesday 30 November

8.30 am	**Welcome and general introduction** Professor Anthony Linnane, Centre for Molecular Biology and Medicine
Session 1: Overview of Microbiome environments **Chair: Professor Emma Johnston**	
8.40 am	*The evolutionary history of human microbiota, and its impacts on human health today* Dr Laura Weyrich, Adelaide University
9.00 am	*Sediment, soil and sea: microbes as proxies for ecosystem health* Dr Katherine Dafforn, UNSW Australia
9.20 am	*Host-microbiome interactions: plotting the course of human health* Associate Professor Geriant Rogers, South Australian Health and Medical Research Institute
9.40 am	**Group discussion**
10.10 am	MORNING TEA
Session 2: Metabolic conditions and gastrointestinal microbiome **Chair: Dr David Briskey**	
10.40 am	*The role of gut bacteria in Crohn's Disease* Dr Claire O'Brien, Australian National University
11.00 am	*Exploring the interrelationships between diet, the gut system and metabolic health* Dr Yan Yan Lam, University of Sydney
11.20 am	*Life in the small intestine: the forgotten microbiome?* Dr Erin Shanahan, University of Queensland

11.40 am	**Group discussion**
12.10 pm	LUNCH
Session 3: Monitoring microbiomes for desirable outcomes **Chair: Dr Carly Rosewarne**	
1.10 pm	*Beneficial responses of the rumen microbiome to reducing methane emissions* Dr Gonzalo Martinez Fernandez, CSIRO
1.30 pm	*An ecogenomic and systems-biology approach to understanding microbial bioremediation* Dr Tom Jeffries, Western Sydney University
1.50 pm	*The microbiome of mercury-contaminated environments* Dr John Moreau, University of Melbourne
2.10 pm	*Breaking bad: the role of microbial dysbiosis and opportunistic pathogens in marine diseases* Dr Suhelen Egan, UNSW Australia
2.30 pm	**Group discussion**
3.00 pm	AFTERNOON TEA
Session 4: Studying microbiomes **Chair: Associate Professor Kathryn Holt**	
3.30 pm	*The bioinformatics of the human microbiome* Associate Professor Lutz Krause, University of Queensland
3.50 pm	*Computational modelling and simulation techniques to investigate the gut bacterial ecosystems response to diet* Dr Mark Read, University of Sydney
4.10 pm	*Multivariate dimension reduction methods for microbiome data analysis* Dr Kim-Anh Lê Cao, University of Queensland
4.30 pm	**Group discussion**
5.00 pm	**Keynote:** *The structure, dynamics and diversity of natural microbial communities through genome-resolved metagenomics* Professor Jillian Banfield, University of California, Berkley
5.30 pm	END OF DAY 2
6.45 pm	Coach departs for dinner venue
7.00 pm	**Pre-dinner wine tasting**
7.30 pm	**Dinner at National Wine Centre of Australia** Dinner speaker: Dr Kristin Alford, Director, Science Creativity Education Studio, University of South Australia
10.00 pm	Coaches return to hotel

Day three—Thursday 1 December

Session 5: Allergy, skin and respiratory microbiome
Co-Chairs: Dr Laura Weyrich and Dr David Briskey

8.30 am	*Characterising the skin microbiome of diabetic skin and chronic wounds* Dr Catherine Burke, University of Technology Sydney
8.50 am	*Administration of probiotics that shift the intestinal microbiome to improve inflammatory biomarkers in adults with pre-diabetes and type 2 diabetes mellitus* Ms Talia Palacios, University of Sydney
9.10 am	*Role of the infant respiratory microbiome in the development of asthma and allergy* Associate Professor Kathryn Holt, University of Melbourne
9.30 am	**Group discussion**
10.00 am	MORNING TEA

Session 6: Microbial processes in non-human ecosystems
Chair: Associate Professor Jeff Powell

10.20 am	*The bleached coral microbiome: a case for whole system dysbiosis?* Dr Tracy Ainsworth, James Cook University
10.40 am	*Into the wild: integration of human-derived microorganisms in wildlife* Associate Professor Michelle Power, Macquarie University
11.00 am	*Antarctic soils and plant microbiomes* Dr Paul Dennis, University of Queensland
11.20 am	**Group discussion**
11.50 am	LUNCH

Session 7: Metagenomics analytical tools and methods
Chair: Associate Professor Lutz Krause

12.50 pm	*Beyond -omics: What happens when we've sequenced everything?* Dr Páraic Ó Cuív, University of Queensland

1.10 pm	*Environmental microbiomes (soil, marine) and efforts to move beyond survey work to where genomic approaches are coupled with ecosystem data to model assemblages* Dr Mark Brown, UNSW Australia
1.30 pm	*Five oceans, thousands of sailboats, trillions of microbes: citizen science and the ocean data bottleneck* Associate Professor Fredrico Lauro, UNSW Australia, Nanyang Technological University, Indigo V Expeditions
1.50 pm	**Group discussion**
2.20 pm	AFTERNOON TEA

Session 8: Non-gut human microbiota
Chair: Dr Laura Weyrich

2.40 pm	*Translocation and dissemination of intestinal bacteria after stroke: the role of gut mucosal microbiota and* Akkermansia muciniphila Dr Dragana Stanley, Central Queensland University
3.00 pm	*Using twins to study how genetic and environmental factors influence the developing oral microbiota and drive disease* Dr Christina Adler, University of Sydney
3.20 pm	*A natural history of the actinic keratosis microbiome in immunocompetent men* Dr David Wood, University of Queensland
3.40 pm	**Group discussion**
4.10 pm	**Closing remarks** Associate Professor Jeff Powell
4.30 pm	Coaches depart

OPENING SPEAKER

Dr Leanna Read FTSE
Chief Scientist of South Australia

Dr Leanna Read is the fourth Chief Scientist for South Australia. She is a renowned biotechnology expert and brings a wealth of executive, board and investment experience in technology-based businesses.

Leanna is currently the chair of the Cooperative Research Centre for Cell Therapy Manufacturing and member of the SA Economic Development Board, the Council for the University of South Australia and a member of BioAngels, which supports early-stage life sciences businesses.

She is a Fellow of the Australian Academy of Technology and Engineering and Board Director of Biosensis Pty Ltd. She has led a number of successful research and commercial ventures, including the Cooperative Research Centre for Tissue Growth and Repair, widely considered to be one of the most successful commercially focused CRCs. She was also the founding Managing Director and CEO of Adelaide biotechnology company, TGR BioSciences from 2001 to 2012.

A physiologist by training, Leanna has published over 90 scientific papers and been awarded an Honorary Doctorate from the University of South Australia. She has received a number of awards, including the 2006 South Australian of the Year (Science and Technology) and the 2011 Central Region winner of the EY Entrepreneur of the Year in the technology category.

DINNER SPEAKER

Dr Kristin Alford
Director, Science Creativity Education (SciCEd) Studio, University of South Australia

Kristin is a futurist and the inaugural Director of the Science Creativity Education (Sci.C.Ed) Studio. This new cultural institution at the University of South Australia opens in 2018 and aims to inspire young adults about the role and potential of science in creating futures.

Prior to this role, Kristin was the founding director of foresight agency Bridge8, facilitating futures and engagement on water sustainability, nanotechnology, health, advanced manufacturing, clean technologies and climate futures for clients including the Australian Government, the South Australian Government and local councils, as well as businesses, arts organisations and not-for-profits.

Kristin has had various careers in engineering, human resources, strategy and product development for companies including BHP Billiton, Ansett-Air New Zealand, the Royal Agricultural Society of Victoria and Nanotechnology Victoria. She holds a PhD in process engineering and a masters degree in strategic foresight. She is a graduate of the Australian Institute of Company Directors, a Fellow of the Governor's Leadership Foundation and a sessional lecturer at the University of Adelaide. She was a co-organiser and facilitator for *Negotiating our Future: Towards Australia in 2050* with the Australian Academy of Science.

PRESENTATION ABSTRACTS

Keynote presentations

The challenge of the microbiome in human health and disease

PROFESSOR LUIS VITETTA

University of Sydney and Medlab Clinical Ltd

Bacteria comprise the earliest form of independent life on this planet. Bacterial development has included co-operative symbiosis with plants and animals. A fusion event of two prokaryotes evolutionarily gave rise to the eukaryote cell in which mitochondria may be envisaged as a genetically functional mosaic, a relic from one of the prokaryote cells. The discovery of bacterial inhibitors such chloramphenicol and others has been exploited to highlight mitochondria as arising from a bacterial progenitor. As such the evolution of human life has been complexly connected to bacterial activity. This is embodied, by the appearance of mitochondria in eukaryotes (alphaproteobacteria contribution), a significant endosymbiotic evolutionary event. During the 20th century there was an increasing dependency on anti-microbials as mainline therapy against bacterial infections. The intestinal microbiome plays an essential role in human health and development as opposed to it being a toxic collection of micro-organisms. The gastrointestinal tract microbiome is comprised of a complex cohort of commensal and potentially pathogenic bacteria. Microbial interactions in the intestines provide the necessary cues for the development of regulated signals that promote immunological tolerance, metabolic regulation and stability, and other factors, which may then help control local and extra-intestinal end organ physiology.

The structure, dynamics and diversity of natural microbial communities through genome-resolved metagenomics

PROFESSOR JILL BANFIELD

University of California, Berkeley

Genome-resolved metagenomics studies provide comprehensive insights regarding natural microbial communities that can be achieved no other way. Recent bioinformatics advances now enable the application of this approach to the most complex of ecosystems, including soils, aquifers and sediments. These environments host a vast diversity of little known or previously unknown groups of bacteria and archaea, the genomes of which have contributed to a major reconfiguring of the tree of life. Apparent from metabolic analyses based on these genomes are critical interdependencies that have the potential to directly impact biogeochemical cycling processes. These include obligate symbioses as well as handoffs of metabolic products that link collections of organisms into dynamic redox pathway-based networks.

Each session will last 1.5 hours and include time for interactive discussion with all meeting participants.

Session 1: Overview of microbiome environments

Chair: Professor Emma Johnston

The evolutionary history of human microbiota, and its impacts on human health today

DR LAURA WEYRICH

Adelaide University

Interpreting the evolutionary history of microbial communities within the human body (microbiota) is critical to clearly understand how microbiota-associated diseases arose in modern humans. DNA sequencing of preserved dental plaque (calculus) from ancient hominin skeletons now provides a unique opportunity to examine the evolution of microbiota and disease through time. We utilised a shotgun sequencing approach to obtain ancient microbial DNA from the dental calculus of European Neandertals; European, America, Asian and African humans; and great apes to examine how these diverse microbial communities have adapted to shifts in lifestyle, diet, and environment over the past 40,000 years. We reconstruct the first oral microbiota of an extinct species (Neandertals), and reveal nearly 200 bacterial species shared within ancient hominins. This analysis highlighted marked alterations in oral microbiota as different hunter-gatherer communities on different continents altered their diet, and when individuals move from hunting-gathering to farming practices.

Overall, we observe significant shifts in the human oral microbiota linked to meat, carbohydrate (sugar), and lactose consumption through time in different environments. Lastly, we find marked alterations in microbiota when European colonialists arrived in foreign lands, revealing microbiota alterations that are linked to past human interactions. Together, these data provide the first record of human microbiota evolution in real-time, and a means to understand why certain bacterial communities are now linked to disease in a modern world.

Sediment, soil and sea: microbes as proxies for ecosystem health

DR KATHERINE DAFFORN
UNSW Australia

Ecological observation of global change processes is dependent on matching the scale and quality of biological data with associated geophysical and geochemical driver information. Until recently, the scale and quality of biological observation on natural assemblages has often failed to match data generated through physical or chemical platforms due to constraints of cost and taxonomic resolution. With the advent of next-generation sequencing platforms, creating 'big data' scale structural and functional observations of biological assemblages across a wide range of groups is now a reality. I will draw insight from a variety of studies to illustrate the potential benefits and drawbacks of this new data source for enhancing our observation of ecological change compared with traditional methods. I focus on a key habitat—estuaries—which are among the most threatened by human change processes. Results suggest that molecular approaches are now sufficiently advanced to provide not just equivalent information to that collected using traditional morphological approaches, but rather an order of magnitude bigger, better, and faster data with which to address pressing ecological questions.

Host-microbiome interactions: plotting the course of human health

ASSOCIATE PROFESSOR GERIANT ROGERS
South Australian Health and Medical Research Institute

The links between host-microbiome interactions in early life and long-term health outcomes are becoming increasingly clear. Disruption of these developmental processes has been implicated in a range of conditions, particularly those with a chronic inflammatory component. The importance of appropriate interactions with resident microbiota during infancy is highlighted by emerging evidence that microbiome-level differences contribute substantially to the efficacy of neonatal vaccinations, with clear implications for clinical practice and antimicrobial stewardship. More widely, the use of novel interventions that aim to support early-life microbiome development show promise as a means to reduce the risks of long-term metabolic and immune dysregulation. Our emerging understanding of these processes, and the ways in which we might manage them for clinical benefit, will be discussed.

Session 2: Metabolic conditions and gastrointestinal microbiome

Chair: Dr David Briskey

The role of gut bacteria in Crohn's Disease

DR CLAIRE O'BRIEN
Australian National University

Crohn's disease (CD) is a relapsing inflammatory disorder of the gut, which is thought to result from an inappropriate immune response to luminal bacteria, in a genetically susceptible individual. The association of CD with microbes is complex, with no single organism being identified as causal. The composition and function of the microbiome is altered in CD, with the majority of studies reporting reduced diversity and bacterial community imbalance (dysbiosis). I will provide an overview of evidence supporting the role of microbes in CD; findings to-date; and how my current research seeks to further elucidate the role of microbes in CD.

Exploring the interrelationships between diet, the gut system and metabolic health

DR YAN YAN LAM
University of Sydney

There is a growing body of literature that suggests that the gut, in particular its microbes, is integral to metabolic health. While many diseases have been associated with a state of dysbiosis, the drivers of the alternations in microbiota and the extent to which these changes are causes, or consequences of metabolic sequelae is unclear. We hypothesised that dietary factors could modify gut health, primarily via changes in the gut microbes, and subsequently impact on systemic functions. We conducted a series of rodent studies that investigated the role of the gut in metabolic dysfunctions in the context of diet-induced obesity. Recently we completed the clinical phase of a cross-sectional study looking at gut permeability, diet and glucose homeostasis in humans, with the aim of informing on potential gut-specific intervention trials to improve metabolic wellbeing.

Life in the small intestine: the forgotten microbiome?

DR ERIN SHANAHAN
University of Queensland

Studies of the gastrointestinal microbiome typically focus on the large bowel and luminal contents such as the stool. However, it is likely that the mucosa-associated microbiota (MAM), in close proximity to host tissues, is critically important in the host-microbe interactions linked to health and disease. While the largest surface area of the gut is that of the small intestine, the microbiome of this difficult to sample region remains poorly understood. Our studies have investigated the MAM in the small intestine in functional dyspepsia, a functional gut disorder associated with low level inflammation. We reveal a potential role for the microbiota in driving dyspeptic symptoms in these patients. Furthermore, studies in patients with chronic liver disease have revealed alterations to the small intestinal MAM and links to gut permeability. Using culture-based methods, we have isolated mucosal bacteria from duodenal biopsies, and are investigating survival in the duodenal niche, along with host-microbe interactions. An improved understanding of the small intestinal microbiome will enable investigation of the interplay between microbes, inflammation and gut permeability that drives chronic gastrointestinal disorders.

Session 3: Monitoring microbiomes for desirable outcomes

Chair: Dr Carly Rosewarne

Beneficial responses of the rumen microbiome to reducing methane emissions

DR GONZALO MARTINEZ FERNANDEZ
CSIRO

Methane is the principal enteric greenhouse gas emitted from ruminant livestock, representing between 7 and 18% of total anthropogenic emissions. Methane also represents an energy loss from digested feed (estimated between 2–12% of gross energy intake). While dietary manipulation and improved feeding systems can reduce methane emissions, a better understanding of the rumen microorganisms involved will provide knowledge for interventions which improve rumen efficiency and decrease the amount of greenhouse gases from ruminant livestock.

Several studies have demonstrated how rumen microbiome can be manipulated to decrease methane emissions or redirect the metabolic hydrogen excess to alternative energy-pathways when methanogenesis is inhibited. Several strategies have been tested: from the use of dietary supplements that promoted microbial groups which use the excess of hydrogen in the rumen (such as degradation of phenolic compounds in the rumen by *Coproccocus* spp.); the promotion of propionic producers microorganisms (such as *Prevotella* spp.) which appear to consume the metabolic hydrogen, producing propionate which is a major gluconeogenic precursor; or the use of synthetic compounds (such as 3-nitrooxypropanol) which specifically inhibit methanogens targeting the methyl-coenzyme M reductase enzyme in the methanogenesis pathway.

An ecogenomic and systems-biology approach to understanding microbial bioremediation

DR TOM JEFFRIES
Western Sydney University

The growing extent of contaminated land and water due to industrialisation is a major global concern and the remediation of contaminated sites is a key sustainability goal. Organophosphate (OP) compounds represent a major environmental contaminant due to their role as a nerve agent and widespread application as pesticides. In addition to acute toxicity to humans, which results in over a million poisonings annually, chronic exposure to these compounds may lead to long term neurological and developmental effects. Microbial bioremediation of toxic compounds often suffers from a lack of understanding of the types and roles of degrading bacteria within the context of the diverse community and ecological drivers present in the system. New genomic technologies are leading to a more holistic understanding which synthesises information regarding the organisms present, functional gene abundances and environmental variables. Using OP compounds as an example, we applied ecogenomic approaches and network analysis to link key taxa to OP degrading genes within a wider metabolic network to elucidate the consequences of organophosphate pesticide on microbial function and degradation.

The microbiome of mercury-contaminated environments

DR JOHN MOREAU
University of Melbourne

Methylmercury is a potent microbially-produced neurotoxin found globally in flooded sediments, waterways, estuaries, and seawater. Although global atmospheric mercury emissions have been declining, global temperature increases could result in increased enzymatic conversion of previously deposited mercury to methylmercury. After over a half-century of research into its mechanism of formation, the key functional

PRESENTATION ABSTRACTS

genes involved in the transformation of Hg^{2+} to CH_3Hg^+ were only discovered within the last several years. However, we still do not understand the geographical or phylogenetic distribution of these genes, their evolution, their expression or relationship to metabolism and physiology, or their impacts on environmental biogeochemical mercury cycling. This presentation will review what we know, what we think we know, and what we don't know, as well as show some data from our recent finding of methylmercury formation by a major marine bacterium in supposedly 'pristine' Antarctic waters.

Breaking bad: the role of microbial dysbiosis and opportunistic pathogens in marine diseases

DR SUHELEN EGAN
UNSW Australia

While symbiotic interactions with microorganisms are essential for many marine plants and animals, we now also know that some microorganisms can be responsible for negative outcomes, such as disease of the host. A major challenge, however, is to link specific microbial pathogens to particular disease events or phenotypes. To overcome this challenge, we are using a combined approach of ecology, microbiology and molecular biology to understand the cause of a model disease, the bleaching of the red macroalga *Delisea pulchra*. I will provide an overview of some of our recent work in this area, including the discovery of multiple pathogens that are capable of causing bleaching of *D. pulchra*. Genomic analysis of these bacterial pathogens has identified common mechanisms for host interaction and virulence, such as colonisation factors, extracellular enzymes and stress resistance. Many of these virulence factors appear widespread in environmental bacteria and may respond to environmental change in a multitude of ways resulting in otherwise harmless symbionts to opportunistically 'break bad' and cause disease.

Session 4: Studying microbiomes

Chair: Associate Professor Kathryn Holt

The bioinformatics of the human microbiome

ASSOCIATE PROFESSOR LUTZ KRAUSE
University of Queensland

Newly developed molecular methods based on the high-throughput sequencing of bacterial DNA have become powerful tools for characterising the composition and diversity of entire microbial communities. These technological advances enable microbiologists to monitor microbial communities over time and to examine the effects of environmental perturbations on community composition. This presentation will provide an overview of available software packages and statistical methods for studying the human microbiome by next-generation sequencing.

Computational modelling and simulation techniques to investigate the gut bacterial ecosystems response to diet

DR MARK READ
University of Sydney

Diet is a driving factor of the gut microbiome composition, and both are linked to a host of diseases. However, determining how diet shapes the microbiome is complicated by their respective complexities: the microbiome, constituting thousands of functionally redundant, pleiotropic, cross-feeding species; dietary intake determined by macronutrient distribution (protein:carbohydrate:fat), energy density and temporal intake pattern. We adopt an ecological perspective to the microbiome, and employ computational agent-based simulation as a powerful tool to rapidly perform thousands of experiments. The core concept underpinning our simulation is the determination of a cell's most growth-limiting nutrient: carbon or nitrogen. The microbiome community is conceptualised in terms of functional guilds, defined by their diet- or host-derived carbohydrate and protein substrates. Host mucin secretion and nutrient absorption dynamics have been estimated, the remaining dietary nutrients being supplied to a one dimensional simulated gut environment that houses bacteria. Each bacteria cell agent internalises nutrients from its environment in accordance with its guild membership and an optimal target 5.2:1 carbon:nitrogen ratio. Nutrient-rich cells exhibit a higher probability of division, nutrient-poor cells undergo higher rates of death. We explore

the methods and challenges of verifying simulation-based predictions of dietary impacts on the microbiome.

Multivariate dimension reduction methods for microbiome data analysis

DR KIM-ANH LÊ CAO
University of Queensland

Culture independent techniques, such as shotgun metagenomics and 16S rRNA amplicon sequencing, have dramatically changed the way we can examine microbial communities. However, statistical methods are limited in their scope to identifying and comparing bacteria driving changes in their ecosystem. This is partly due to the inherent properties of microbiome data, including sparse counts, the compositional nature of data and the fact that microbial communities modulate and influence biological systems as a whole. We have developed mixMC, a multivariate data analysis framework to identify specific associations between Microbial Communities and their type of habitat. mixMC accounts for the compositional nature of 16S data and enables detection of subtle differences when high inter-subject variability is present due to microbial sampling performed repeatedly on the same subjects but in multiple habitats. Through data dimension reduction the multivariate methods provide insightful graphical visualisations to characterise each type of environment in a detailed manner. We will illustrate the added value of using multivariate methodologies to fully characterise and compare microbial communities.

Session 5: Allergy, skin and respiratory microbiome

Co-Chairs: Dr Laura Weyrich and Dr David Briskey

Characterising the skin microbiome of diabetic skin and chronic wounds

DR CATHERINE BURKE
University of Technology Sydney

Type II diabetes is a chronic health condition which is associated with skin conditions including chronic foot ulcers and an increased incidence of skin infections. The skin microbiome (microbes living on skin) is thought to play important roles in skin defense and immune functioning. Diabetes affects the skin environment, and this may perturb skin microbiome with

possible implications for skin infections and wound healing. This study examined the skin and wound microbiome in 10 type II diabetic subjects with chronic foot ulcers over a time course of 12 weeks, sampling from both skin and wounds, with the skin microbiome compared to a control group. The diabetic skin microbiome showed reduced diversity compared to healthy controls, and chronic wounds were colonised by skin taxa, along with different profiles of microbes in individual patients.

A novel probiotic for glucose management: A randomised double-blind placebo controlled pilot study

MS TALIA PALACIOS
University of Sydney

Type 2 diabetes mellitus (T2DM) is characterised by a persistent low-grade inflammatory response associated with the development of insulin resistance. Variations in the type, diversity and metabolic capacity of gastrointestinal (GI) microbial communities have been shown to alter these metabolic and inflammatory pathways by shifting energy balance and storage and promoting metabolic endotoxaemia. The aim of our study was to assess the therapeutic effect of a novel probiotic on glucose metabolism in adults diagnosed with prediabetes and early T2DM.

Sixty adults with a BMI ≥25 kg/m2 and diagnosed with pre-diabetes or T2DM (within the previous 12 months) were enrolled in a double-blind controlled clinical trial and randomised to a multi-strain probiotic or placebo for 12 weeks. Both groups received lifestyle advice. Measurements and samples were collected at baseline and 12 weeks after treatment. Outcome measures include fasting plasma glucose, 2-hour glucose tolerance, insulin, lipids, inflammatory markers, GI permeability, and faecal microbial and metabolomics profiles.

The primary outcome of fasting blood glucose will be reported, as well as secondary outcomes including insulin sensitivity, lipid profiles and inflammatory and permeability markers. Intentional manipulation of GI microbial profiles may be useful for regulating T2DM and its associated metabolic disorders.

Role of the infant respiratory microbiome in the development of asthma and allergy

ASSOCIATE PROFESSOR KATHRYN HOLT
University of Melbourne

In the past decade, respiratory infections during infancy have been recognised as an important factor driving the development of asthma during childhood. In addition, bacterial colonisation of the airways has been shown to influence viral infection and asthma development. We set out to characterise the bacterial composition of the nasopharyngeal microbiome (NPM) in a birth cohort of 234 individuals at high risk of allergy, which was previously established to investigate the role of respiratory infection in asthma development. The

nasopharyngeal microbiome was relatively simple in structure, with most children initially colonised two months of age by *Staphylococcus*, *Corynebacterium* or *Streptococcus*; then becoming colonised by *Moraxella* or *Alloiococcus* by one to two years of age and increasing in bacterial diversity up to age five. Early asymptomatic colonisation with *Streptococcus* (~two months) was significantly associated with the development of allergic asthma by age five.

Lower respiratory tract illness during infancy (first year of life), particularly febrile episodes, were significantly associated with asthma at age five. Symptomatic respiratory illnesses were characterised by detection of well-known viruses (HRV, RSV) but also *Streptococcus*, *Haemophilus* or *Moraxella*. Interestingly, during infancy but not later, these genera were also associated with symptom severity including progression to lower respiratory tract and presence of fever.

Session 6: Microbial processes in non-human ecosystems

Chair: Associate Professor Jeff Powell

The Bleached Coral Microbiome: A case for whole system dysbiosis?

DR TRACY AINSWORTH
James Cook University

Increased sea surface temperature (SST) anomalies in recent decades have contributed to wide-spread reports of mass coral bleaching and coral disease outbreaks following bleaching events. Greater anthropogenic CO_2 emissions into the atmosphere over the last century and the associated ocean acidification (OA, decreased surface ocean pH) are also predicted to influence coral survival and reef community structure into the future. I will discuss the case for a whole system dysbiosis under climate change regimes predicted to occur within the coming decades. This includes a discussion of how the interaction of increasing sea surface temperature and decreasing ocean pH impact bacterial colonisation of bleached tissues and the likely follow on effects to coral survival of bleaching conditions. The capacity to maintain normal (healthy) microbiomes during and following coral bleaching potentially contributes to corals' capacity to recover, survive and minimise subsequent disease outbreaks.

Into the wild: integration of human-derived microorganisms in wildlife

ASSOCIATE PROFESSOR MICHELLE POWER
Macquarie University

Spill over of zoonotic pathogens from wildlife to humans is a primary threat to global health. In contrast, reverse pathogen transmission or zooanthroponosis, whereby pathogens move from humans into wildlife species remains largely unexplored. Globally, increasing urbanisation and habitat loss are driving wildlife species into urban and regional centres, creating a conduit for microbial traffic between humans, domestic animals and wildlife. In Australia, numerous wildlife species are well established in urban areas, for example flying foxes, possums and bandicoots. The close proximity of wildlife species to humans not only increases the risk of zooanthroponosis but also facilitates movement of non-pathogenic microbes to wildlife. Conservation management and translocation further establish routes for microbial traffic. Captive breeding for species recovery exposes wildlife to microorganisms not typically encountered in their wild habitats, and these microorganisms maybe spread to wild populations through translocation. This presentation will showcase some examples of integration of human-derived bacteria and protozoan parasites in wildlife species in urban areas, Antarctica and a conservation program. Case examples will include the detection of antibiotic resistant *Escherichia coli* and *Cryptosporidium* in numerous Australian wildlife species. The impacts of dissemination of human-derived microbes to wildlife and the implications for their microbiomes will be discussed.

Antarctic soils and plant microbiomes

DR PAUL DENNIS
University of Queensland

One of our research interests is to identify the environmental drivers of soil microbial diversity. This will help to improve predictions of how ecosystems are likely to respond to environmental change. We have been focusing on the ecology of soil microbial communities in the maritime Antarctic, which was until recently the most rapidly warming part of the southern hemisphere. Our work is highlighting that the diversity of bacterial and fungal communities is most strongly influenced by temperature. This suggests that these communities have been and will continue to undergo change.

We are also identifying ways to engineer the composition of plant microbiomes to reduce reliance on agrochemicals. These chemicals help to alleviate agricultural constraints, but rely on non-renewable resources and contribute to environmental degradation. Soils harbour a wide variety of microbial taxa that significantly enhance plant health and nutrition. These organisms could be used to more sustainably maintain, or enhance, global food security. Current approaches to engineer the composition of root microbiomes such as applications of

plant-growth-promoting microbial inoculants often fail under field conditions due to competition with native organisms. Likewise, attempts to modify microbial communities through changes in root exudation profiles are challenging because it is not clear which exudates recruit beneficial microbes and how these could be exuded in greater quantities without altering the levels of other compounds. We are currently searching for plant genes involved in microbial recruitment and using novel methods to decode the language of attraction between plant roots and microorganisms. Preliminary result from this work will be presented.

Session 7: Metagenomics analytical tools and methods

Chair: Associate Professor Lutz Krause

Beyond -omics: What happens when we've sequenced everything?

DR PÁRAIC Ó CUÍV
University of Queensland

The last decade has resulted in the establishment of the 'human microbiome' as a distinct field of research, enabled in large part by the rapid technological advances in DNA sequencing methods and computational analyses. These have advanced our awareness and appreciation of the extent of microbial 'dark matter' that exists in these communities, both in the form of 'not-yet-cultured' microbes as well as the genes that underpin their functional potential. However, recent analyses have revealed that the coverage of core gene content and functions has been saturated, suggesting that an increasingly greater effort will be needed to provide an even deeper insight into the gene repertoire of the microbiome. Additionally, despite the wealth of sequence data now available in the public databases, the overwhelming majority of gene products remain functionally uncharacterised. I will outline my efforts to develop new genetic tools and methodologies for fastidious gut bacteria that have the potential to transform our ability to functionally characterise the microbiota. Based on my observations, I contend the integration of new culture-dependent approaches and improved screening strategies, with directed genetic and -omic dissections will offer new opportunities to elucidate the relationship between the microbiota and host health.

Environmental microbiomes (soil, marine) and efforts to move beyond survey work to where genomic approaches are coupled with ecosystem data to model assemblages

DR MARK BROWN
University of New South Wales

Highly collaborative, continental scale projects are generating extensive molecular datasets describing microbial taxonomy, abundance and function in Australian biomes that equal (or sometimes exceed) those describing animal and plant distributions. Two such efforts include the Biomes of Australian Soil Environments (BASE) and the Australian Marine Microbiology Biodiversity Initiative. I will discuss these projects and how they are allowing us to use powerful statistical tools such as network models, structural equation models and species distribution models to explore the dynamics of unseen microbes inhabiting our vast country. Revealing how microbes interact with each other and their environment, and then relating this knowledge back to in situ measures of, for example, biogeochemical rates, will enable us to develop a mechanistic understanding of microbial impacts, predict their dynamics under future change scenarios and inform the development of next generation of environmental sensors.

Five oceans, thousands of sailboats, trillions of microbes: citizen science and the ocean data bottleneck

ASSOCIATE PROFESSOR FREDRICO LAURO
UNSW Australia, Nanyang Technological University, Indigo V Expeditions

The world's oceans contain an estimated 1.2×10^{29} microbes, which are the key drivers of marine biogeochemistry and the first responders to environmental change. Despite these important functions, our understanding of the marine microbiome is very rudimentary because modelling global biogeochemical cycles and microbial community dynamics requires the collection of high-density data both temporally and spatially. This cannot be achieved in a cost-effective way using traditional oceanography, where one day of sample collection can cost more than US$50,000, resulting in a seemingly insurmountable data collection bottleneck. This talk will summarise the results from the first two Indigo V Indian Ocean Expeditions, which used a sailing yacht rather a traditional oceanographic ship and showed how to drastically reduce the costs of sample acquisition, both in terms of resources and carbon footprint. The results from these expeditions include the discovery of distinct microbial communities in coral reefs and their responses to anthropogenic disturbances. It also provided a blueprint on how to overcome the data bottleneck by crowdsourcing the sample collection to thousands of private ocean-going vessels cruising the world's oceans every day. The outcomes of this project are expanding our view of the marine microbiome and its role in planetary health.

PRESENTATION ABSTRACTS

Session 8: Non-gut human microbiota

Chair: Dr Laura Weyrich

Translocation and dissemination of intestinal bacteria after stroke: the role of gut mucosal microbiota and *Akkermansia muciniphila*

DR DRAGANA STANLEY
Central Queensland University

Stroke is one of the leading causes of mortality worldwide. Although stroke causes neural deficits, the major cause of post-stroke death and complications is bacterial pneumonia. We recently provided evidence that a source of post-stroke lung infection after ischemic stroke is via bacterial translocation originating from the host small intestine. The observation that post-stroke lung infection was only apparent in mice born and raised as specific pathogen free, while germ-free raised mice did not develop pneumonia, supported this notion. In addition, histological and functional data suggested stroke-induced gut barrier permeability and epithelial dysfunction preceded the dissemination of orally-inoculated bacteria. We found significant differences in the mucosal microbiota composition at all taxonomic levels from the phylum to the species level between sham-operated and post-stroke mice. In fact, the dodenal mucosa was the most affected of all gut sections. *Akkermansia muciniphila* is the first cultured intestinal bacteria from the new phylum Verrucomicrobia and is emerging as a potential probiotic. It was found to play a major role in post-stroke mucosal events.

Using twins to study how genetic and environmental factors influence the developing oral microbiota and drive disease

DR CHRISTINA ADLER
University of Sydney

Children's oral health is in a dire state, with dental decay being the most common chronic disease. Our study is determining how an individuals' environment and their genetic makeup drive variation in the composition of the oral microbiota to produce childhood decay. We are doing this by genetically analysing dental plaque from an Australian twin cohort of approximately 400 individuals that have been followed longitudinally from three months to six–nine years of age. This is a collaborative project between the dental schools at Sydney and Adelaide universities, and involves scientists, dentists and research students. At a population level, we will use our findings to direct treatment approaches by discovering anti-caries agents among the oral microbiota. At a practitioner level, our study will inform the development of screening methods to identify high caries risk individuals.

A natural history of the actinic keratosis microbiome in immunocompetent men

DR DAVID WOOD
University of Queensland

Actinic keratosis (AK) is a condition where pre-malignant lesions develop on sun-damaged skin. Risk factors for AK include sun exposure, advancing age, fair complexion, and immunosuppression. Some AK lesions progress to cutaneous squamous cell carcinoma (cSCC). Mortality from cSCC is low, however it is the second most common cancer in Australia, and a substantial and rising burden.

Human skin hosts resident microbial populations, including viruses, fungi and bacteria. Human papillomaviruses are causative of cervical SCC, however evidence for viral activity remains inconclusive in cSCC. *Malassezia* yeasts have not been investigated in AK or cSCC pathology and only one PCR-based study has investigated bacterial involvement. To more thoroughly explore this, we longitudinally monitored the lesion microbiomes of 10 cSCC-prone immunocompetent men. We sought to identify differences between the lesion and non-lesional skin profiles, any taxa consistently associated with lesions, and how lesion microbiomes changed over time. Patient-specific analysis identified *Staphylococcus* taxa associated with both AK and cSCC, and antagonistic relationships of these taxa with other commensal skin microbes, including fungi. These findings indicate the personalised nature of AK pathology, and may aid in the treatment and prevention of cSCC lesions.

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Next step, colour for more biogas

Dr Sabrina Beckmann

UNSW Australia

Biogas emitted by microbes will be vital for meeting the world's future energy needs and helping reduce greenhouse gas emissions from the burning of other fossil fuels. We have discovered a new way to produce a tenfold increase in the amount of methane gas emitted by naturally occurring microbes living in coal seams and on renewable feedstocks such as food waste and by-products of municipal wastewater treatment. The discovery involves the addition of small amounts of a synthetic dye that forms previously unobserved needle-like crystals to help the methane-producing microbes grow faster. The tiny red crystals act as electron sponges, harvesting electrons from minerals and bacteria in the mixture and then transferring them with a lot of power to the methane-producing microbes, boosting their growth. It's simple: if the microbes grow faster, they fart more methane. This patented technology does not only change and invigorate the microbiome of methane-producing reservoirs but, more excitingly, promises new fundamental knowledge about how methane-producing microbes work and how to improve their gas-producing capabilities.

Microbes, contaminants, and molecular tools: functional sediment community responses to urban run-off

Ms Simone Birrer

UNSW Australia

Industry and agriculture have been major sources of toxic contaminants and organics for adjacent waterways. Due to increasing urbanisation of coastal areas, additional pollution is occurring as stormwater transports a complex mixture of contaminants. When contaminants reach estuarine waters, they generally bind to particles and concentrate on the sea floor, exposing sediment communities to high concentrations of toxicants. Sediment microbes provide a variety of ecosystem functions, and exposure to legacy contaminants and urban run-off can affect the function of these critical communities. To prioritise ecosystem management actions, we need to understand the nature and extent of the impact of multiple contaminants on sediment microbial communities. We investigated the differences in functioning of sediment communities adjacent to stormwater drains and at well-flushed reference sites within the same embayment. Proximity to stormwater drains was associated with significantly lower activity of signalling genes, suggesting that communication within the contaminated communities might be fractured. Furthermore, we found lower metabolic rates and disrupted nutrient cycling close to stormwater drains, potentially leading to overall lower productivity but higher production of greenhouse gases. Our results suggest that contaminants can lead to lower productivity, higher impact on climate change, and potentially lower remediation capacity of sediment communities.

Mine water genomics: improving the environmental legacy of open-cut mining

Dr Melanie Blanchette

Edith Cowen University

Mining alters catchments; large lakes may be created in a previously arid environment, rivers can be diverted, and discharge may flow in perpetuity. 'Mine water' is a substantial liability for communities, ecosystems, governments, and industry. I will present results from two case studies that use classical techniques in freshwater ecology to explore the aquatic microbiome in order to understand, monitor and rehabilitate mined catchments. Pit lakes are low in nutrients, which limits ecosystem development (and, therefore, water quality improvement). Using submerged 'litter bags' containing vegetation, in the first study I demonstrated that microbial assemblages on vegetation are significantly different among lakes, but also different from their respective 'background' soil communities, suggesting that addition of terrestrial vegetation to pit lakes may be a useful rehabilitation technique. Mine lakes are often acidic (pH 3-5). One strategy to improve lake water quality involves diverting a natural river through the lake. However, this has potential consequences downstream that need to be assessed. Using a large-scale 'transect' method to collect benthic and aquatic microbes at multiple riverine sites, results of my second study indicated that microbial relatedness (Unifrac distance) is sensitive enough to differentiate among rivers, as well as up- and downstream of pit lakes.

The placental and vaginal microbiomes of Papua New Guinean women and their association with pregnancy outcomes

Dr Phillipe Boeuf

Burnet Institute

The maternal mortality rate in Papua New Guinea is one of the highest in the world; 80 times that in Australia. Newborn and infant mortality is equally alarming and almost half of the children have stunted growth. Yet, the preventable causes of these adverse pregnancy outcomes are poorly known. The impact of the placental and vaginal microbiomes on pregnancy outcomes is starting to be unravelled but most studies have been conducted in developed countries. Very little is known about the placental

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and vaginal microbiomes in under-resourced settings and their association with pregnancy outcomes.

We have initiated the 'Healthy Mothers, Healthy Babies' program in which 700 Papua New Guinean pregnant women are recruited from their first antenatal clinic attendance, and followed-up, together with their baby, to 12 months after birth. This program aims to identify and quantify preventable causes adverse pregnancy outcomes, especially low birth weight and poor infant growth. We plan to investigate 1) the composition of the placental and vaginal microbiomes in Papua New Guinean women; 2) their modulators (especially maternal stressors); and 3) their association with pregnancy outcomes. This knowledge will guide the design of interventions aimed at improving pregnancy outcomes for Papua New Guinean women.

Wild wine: metagenomic analysis of microbial communities during wine fermentation
Dr Anthony Borneman
The Australian Wine Research Institution

Wine is a complex beverage, comprising thousands of metabolites that are produced by yeasts and bacteria acting on grape must. To ensure a robust and reliable fermentation, most wines are produced by inoculating grapes with commercial strains of wine yeast (*Saccharomyces cerevisiae*). However, there is a growing trend back to performing uninoculated or 'wild' fermentations, in which only those yeasts and bacteria that are naturally associated with the grapes or winery are relied on. Wild ferments show a far more complex progression of microbial species than inoculated wines and, accordingly, a more complex taste and aroma profile. Differences in these resident microflora between vineyards and wineries are therefore thought to have a key role in defining regional expression of wine characteristics.

In order to map the microflora of spontaneous fermentation, metagenomic techniques are being used to monitor the progression of microbial species in wild fermentations from around Australia. Both barcoding and shotgun metagenomics were used to assess community structure, with the isolation and sequencing of individual strains also being performed in order to aid the analysis. Notable differences between regions, vineyards and wineries were apparent and these can be broadly defined by the resulting microbial composition of the wild ferments.

Statin therapy causes microbiome alteration and gut dysbiosis in mice
Dr Jose A. Caparros-Martin
Curtin University

Statins are a group of highly prescribed therapeutics used as first-line agents to regulate serum cholesterol in patients at high risk of coronary vascular events. In this presentation, we describe for the first time profound changes in the composition of the commensal gut microbiota in mice receiving statins. This remodelling affected the diversity of the gut community, which became dominated by the family of Gram-negative bacteria Bacteroidales S24-7. Compared to the controls, the statin-associated intestinal microbiota was defined by a higher capacity to produce energy and by the depletion of genes encoding motility-related proteins. As it has been observed in patients, statin-treated mice trended to gain more weight than the control cohort and showed higher levels of blood glucose. Furthermore, statin treatment altered the size and composition of the bile acid pool in the intestine, which may explain the observed gut dysbiosis. Our study suggests that statin therapy affects the intestinal microflora by deregulating the bile acid metabolism and thus unbalancing the gut–liver axis. Since the demonstrated importance of the gut microbiota in host well-being, our work expands on the knowledge of the physiological consequences of taking statins and provides a new perspective to prevent their unintended metabolic effects.

Challenges in inferring 18S and 16S composition from metagenomic data
Dr Anthony Chariton
CSIRO

The advent of high-throughput sequencing is revolutionising the way we obtain ecological data. Currently the most common approach for obtaining DNA-diversity profiles is via the use of amplicon sequencing, also known as metabarcoding. While metabarcoding is a cost-effective and relatively rapid approach, a perceived major limitation is its inability to obtain reliable proportional abundance data. This is primarily due to the artefacts associated with PCR, a prerequiste of the technique. As a result, many researchers reduce the ambiguity of metabarcorded data by transforming read abundance to presence/absence. New metagenomic methods have recently become available which entirely circumvent the need for PCR. The potential to obtain unbias proportional abundance compositional data is a tantalising concept. However, before we jump into routinely using metagenomic data to make assumptions about ecological condition, it is pertinent to thoroughly understand the attributes associated with metagenomic compositional data, warts and all. Here we use an extensive data set obtained from estuarine sediments to explore the effects of sample depth; highlight the issues associated with the representiveness of 16S and 18S

communities extracted from metagenomes; air our concerns about this misconception of 'proportional metagenomic data'; and discuss how these attributes may influence ecological interpretation.

Exercise-induced gastrointestinal syndrome: does the intestinal microbiome have a role to play?
Dr Ricardo Costa
Monash University

Exertional stress is experienced by a number of occupational and recreational populations. Gastrointestinal perturbations and symptoms are a common feature of exertional stress, and can lead to debilitating exercise-induced gastrointestinal syndrome. The causes appear to be multi-factorial in origin, however stem from, 1) splanchnic hypoperfusion resulting in gut ischaemia, and 2) increased sympathetic drive resulting in alterations to gut motility. These primary causes can lead to gut injury, increased gut permeability, systemic endotoxaemia and cytokinaemia, impaired intestinal nutrient transporter activity and gastrointestinal transit. Such gut perturbations predisposes individuals to acute and chronic health implications, and if severe may lead to fatality (e.g. sepsis and systemic inflammatory response). Certain extrinsic and intrinsic factors, such as degree of exertional stress (intensity, duration, and mode), environmental conditions (heat), feeding tolerance, predisposition (established gastrointestinal disease), and non-steroidal anti-inflammatory drugs, have the ability to exacerbate disturbances to gut integrity, function, and symptoms in response to exertional stress. Considering evidence suggesting the gut microbiome alters in accordance with dietary and physical activity habits in healthy individuals, it is speculated that the composition of the intestinal microbiome (e.g. extent of dysbiosis) may influence the degree of exercise-induced gastrointestinal syndrome in response to exertional stress.

Identification of sorghum genotypes that differ in microbial recruitment
Dr Paul Dennis
University of Queensland

Plants recruit soil microorganisms that enhance host fitness. Fostering beneficial plant–microbe associations could help reduce the need for agrochemicals that exploit non-renewables and degrade ecosystems. Evidence suggests that genetic traits in plants influence the recruitment of microbes to roots so there is interest incorporating these traits into plant breeding programs. Here we characterised the diversity of bacterial, archaeal and fungal communities in the rhizospheres of 10 diverse sorghum genotypes. Our results highlight the existence of genetic variation in the ability of these sorghums to recruit microorganisms.

Near full-length 16S rRNA gene next-generation sequencing revealed *Asaia* as a prevalent larval midgut bacterium of wild and domesticated *Bactrocera tryoni*
Dr Ania Deutscher
NSW Department of Primary Industries

The Queensland fruit fly, *Bactrocera tryoni* (Diptera: Tephritidae), is a significant economic horticultural pest in Australia that can be managed by the sterile insect technique (SIT). SIT involves inundative releases of mass-reared sterile insects to reduce reproduction in a wild population of the same species. The performance of released sterile flies is critical to the success of SIT. However, very little is known about the gut bacteria of tephritid larvae and how they influence the quality of the adult fly. We utilised near full-length (>1300 bp) 16S rRNA gene amplicon sequencing on an Illumina MiSeq to analyse the low bacterial diversity of 56 individual *B. tryoni* larval midguts of three domesticated populations reared on artificial diets and two wild populations from peaches. The dominant genera detected in wild larvae belong to Acetobacteraceae, Enterobacteriaceae and Leuconostocaceae. A single bacterial genus, *Asaia*, was detected in all larvae except one, and was the predominant and often only genus detected in domesticated larvae. Larvae feeding on the same diet, whether whole fruit or artificial, shared similar gut bacteria. Further investigations into *B. tryoni* gut microbial ecology could lead to improved artificial diets enhancing the quality and performance of mass-reared *B. tryoni* for SIT approaches.

Microbiome and mobile antibiotic resistome in treated wastewater and in downstream environment
Dr Barbara Drigo
University of South Australia

Understanding the dynamics of antibiotic-resistant microorganisms in the urban water cycle is an increasingly important goal as antibiotic resistance is recognised as one of the greatest human health challenges of the 21st century. Urban wastewater is suspected to be a major hotspot for the evolution and propagation of antibiotic-resistant microorganisms back to the environment and consequently to humans. The mechanisms underlying this phenomenon are still unclear, but it is likely that the concomitant presence of antibiotics, metals and other pollutants in urban wastewater could trigger the co-selection and horizontal gene transfer of resistance genes. Here, we will give new insights into the relative efficacy and downstream effects of urban wastewater treatment on the survival and regrowth/transfer of antibiotic resistant microorganisms. To assess the abundance and expression profile of antibiotic-resistant bacteria and genes in urban waste water, we used a suite of high throughput molecular tools, including sequencing

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and digital droplet PCR. Our findings provided a baseline understanding of the prevalence of antibiotic resistance in wastewater influents and effluents. The efficacy of urban wastewater treatments on the survival and regrowth of antibiotic resistance is used to model and predict the fate of antibiotic resistance in complex environments.

Microbial succession patterns during plant residue decomposition

Dr Deirdre Gleeson

University of Western Australia

Microbial decomposition of soil organic matter varies with both organic matter quality and inherent soil properties, for example pH, and resident microbial communities and their functions. While the role of bacteria and fungi in organic matter decomposition has been the subject of numerous studies, the dynamics and functioning of the microorganisms involved remain under explored. In particular the succession and co-occurrence patterns of soil microbial communities during decomposition are poorly understood. Here we investigated, over the course of a six-month incubation experiment, the influence of soil pH and plant residue quality on the dynamics and successional patterns of the microbial decomposer communities and subsequent impact on soil carbon. We utilised a barcoded sequencing approach and network analysis of bacterial 16S rRNA and fungal ITS to determine the key microbial groups involved in residue decomposition. As soil microbial communities mediate organic matter decomposition through the actions of their enzymes we also assessed organic matter and plant residue decomposition processes by determining the abundance of some of the genes associated with this process, for example laccases involved in lignin decomposition and cellobiohydrolases involved in cellulose decomposition.

The diversity of gut bacteria: its interactions with sanitation and infectious disease

Dr Andrew Greenhill

Federation University of Australia

Considerable research has postulated that the gut microbiome impacts on human health, with particular focus on diseases that have seemingly become more common in high-income settings in recent generations. Loss of microbial lineages may contribute to the purported increased incidence of such diseases. An insight into changes that may have occurred since industrialisation can be gained by comparing gut microbial composition in industrialised populations to those living traditional lifestyles in non-industrialised settings. Our studies have demonstrated that rural Papua New Guineans with a high dependence on subsistence agriculture have a greater diversity of microbes in their gut than do individuals living in USA; findings supported by analyses of other datasets. Lack of

sanitation and hygiene is likely a key driver of this microbial diversity; but also a key factor in the high burden of infectious diseases in Papua New Guinea and other low-income settings. Interestingly, in sheep, increased gut microbiome diversity correlates with increased susceptibility to a gastrointestinal parasite: the significance of this finding for (monogastric) humans is unclear at this stage. We seek to better understand correlations between the gut microbiome and susceptibility to gastrointestinal pathogens in humans and animals, and the significance of microbial composition and diversity.

Unravelling the sugarcane microbiome to resolve the Yellow Canopy Syndrome in Australia

Dr Kelly Hamonts

Western Sydney University

Yellow Canopy Syndrome (YCS) is a largely undiagnosed condition impacting sugarcane crops in Australia, causing yield losses of more than 30% in severe cases. Since the first observation of YCS near Cairns in 2012, the condition has spread to all major cane growing areas and is a critical issue for the industry. Key YCS symptoms differ from leaf yellowing due to drought stress, phytotoxicity, insect attack, known diseases, nutrient deficiency or natural maturing. We aimed to determine the involvement of biotic interactions and soil nutritional health in YCS development. A microbiome-based approach using Illumina MiSeq and HiSeq was applied on >600 samples to reveal the complexity of organisms (bacteria, fungi, other eukaryotes, viruses) present in YCS-affected sugarcane plants and rhizosphere soil. Soil nutrient status and microbial enzyme activity were determined and did not significantly differ between affected and healthy fields. Bacterial (>25000 OTUs) and fungal (>11000 OTUs) assemblages of leaves, stalks, roots and rhizosphere soils differed between asymptomatic vs. symptomatic plants, as well as particular rhizosphere microbial functions. Community shifts with YCS appeared location- and variety-specific, and to date only few consistent bacterial and fungal signals and no consistent viral signal associated with YCS have emerged.

Conducting a microbiome study in a resource-poor setting

Dr Sarah Hanieh

University of Melbourne

Microbiome research is a rapidly evolving area and the human microbiome has been shown to be associated with numerous aspects of health and disease including nutritional status, behaviour and chronic diseases, which have significant implications for resource-poor settings. Quality of results rely heavily on optimal sample collection, storage and transit conditions which may impact on the yield and quality of DNA and risk of contamination. Collection of samples for microbiome analysis

requires careful planning and adherence to accepted protocols to ensure consistent and reproducible results. This may be challenging in a resource-poor setting where environmental conditions, maintenance of the cold-chain and other factors such as cultural influences may come into play. We conducted a study in a rural province of North Vietnam where stool samples were collected from children aged 36 months of age. We discuss factors to be considered in the design of studies for microbiome analysis conducted in resource-poor settings.

Into the deep: evaluation of bacterial community profiling and SourceTracker for assessment of faecal contamination of coastal waters.
Dr Rebekah Henry

Monash University

Faecal contamination of recreational waters is an increasing global health concern. Tracing the source of the contaminant is a vital step towards mitigation and disease prevention. Total 16S rRNA amplicon data for a specific environment and computational tools such as the Markov-Chain Monte Carlo based SourceTracker can be applied to microbial source tracking (MST) and attribution studies. The current study applied artificial and in-laboratory derived bacterial communities to define the potential and limitations associated with the use of SourceTracker, prior to its application for faecal source tracking. The results demonstrated that at minimum multiple model runs of the tool were required to identify potential false positive predictions. The calculation of relative standard deviations (RSDs) for each attributed source improved overall predictive confidence. In general, default parameter settings provided high sensitivity, specificity, accuracy and precision. Application of SourceTracker to recreational beach samples identified treated effluent (69% of samples) as a major source of human-derived faecal contamination. Site-specific sources were also identified. The results suggest that local sources of contamination have the greatest effect on recreational coastal water quality. As such, microbial community MST has the potential to become a powerful tool in the mitigation of microbial contamination of aquatic systems.

Assessment of immunomodulatory properties of methanogenic archaea *Methanobrevibacter* and *Methanosphaera* spp. on healthy human PBMC and a mouse macrophage cell line
Ms Emily Hoedt

University of Queensland

Thought originally to be commensals of the gut, methanogenic archaea are now demonstrating the ability to stimulate both the innate and adaptive immune system. We have assessed the immunogenic properties of both human and animal originating *Methanobrevibacter* and *Methanosphaera* strains using human peripheral blood mononuclear cells (PBMC) and a mouse macrophage cell line. We show that *Methanosphaera stadtmanae* cell preparations produce a stronger TNF-α response from PBMC than *Methanobrevibacter smithii*, as well as the other *Methanosphaera* isolates WGK6 and BMS, but ruminant *Methanobrevibacter ruminantium* cells produced the strongest TNF-α response. In subsequent studies a broader range of cytokines were measured using a multi-bead array and flow cytometry techniques from healthy PBMC. In these studies, *Methanobrevibacter smithii* was more immunogenic compared to *Methanosphaera stadtmanae*, but both types of cells induce a similar cytokine profile. Last, a murine macrophage cell line bearing a reporter gene activated by the NF-κB transcription system, further confirmed that cell preparations of all these archaea induce reporter gene activation via this important pathway of stress response. Collectively, the results suggest all these methanogens possess immunostimulatory properties that remain cell associated, and the findings are discussed with respect to gastrointestinal inflammation and also the development of anti-methanogen vaccines.

Microbial low pH Mn(II) oxidation in subsoils
Dr Qing Hu

CSIRO

Mn oxides are ubiquitous in natural environments ranging in a broad pH range. Microbial activity is believed the major force to mediate Mn oxides formation in neutral oxic environments. Diverse microorganisms, including prokaryotes and eukaryotes, are known to readily oxidise Mn(II) and precipitate Mn oxides at pH ~7 under oxic conditions. However, low pH Mn(II) oxidation poses a challenge to microbes because the reaction is thermodynamically unfavorable and the ability of Mn(II)-oxidising microorganisms to precipitate Mn oxides under acidic conditions were rarely studied. This study aimed to investigate indigenous low pH Mn(II) oxidisers at a heavy metal-contaminated oligotrophic Mn mineral deposit and adjacent subsoil ecosystems, especially focusing on their abundance, communities, key players, pH-dependent mechanisms, and environmental relevance.

A space for time approach to help understand future impacts of temperature on marine microbiomes
Dr Megan Huggett

Edith Cowan University

Future increases in oceanic temperature are predicted to occur globally. In general, environmental change will probably have strong impacts on native microbial communities and these impacts are likely to be complex, species-specific and difficult to predict. With respect to studying the effects of temperature on benthic marine habitats, the Western Australian

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coastline presents a unique opportunity: it is one of the last remaining areas of relatively pristine marine habitats in the world and has a well-defined temperature gradient due to the Leeuwin Current. Here, we examined in situ effects of temperature using a space for time sampling design along hundreds of kilometres of the WA coastline. Our analyses include microbiomes from a range of key marine organisms including a coralline alga, a sponge, a coral and an herbivorous fish. In all organisms there were strong beta diversity shifts among locations along the WA coastline. However, in general there were no substantial changes in alpha diversity between locations nor was alpha diversity high in locations at the edge of species ranges as may be expected under dysbiosis of host associated communities.

Epithelial secreted nutrients influence host–microbial interactions during inflammatory stress

Dr Simon Keely

University of Newcastle

The intestinal microbiota exists in symbiosis with the host mucosa, offering digestive function, protection and immune-regulation, while benefiting from host-secreted metabolites. Dysbiosis is associated with a wide range of chronic digestive diseases although it is unclear as to whether this is a consequence or initiating factor for disease pathology. Our work has focused on epithelial stress-responses during intestinal disease and we have identified changes to epithelial-derived metabolites during inflammation, particularly metabolites serving as microbial micronutrients for the microbiota. Hypothesising that these micronutrient changes could drive transcriptional responses in bacteria, we examined whether epithelial micronutrients secreted during inflammatory stress were sufficient to alter bacterial virulence. Incubation of *E. coli* and *P. aeruginosa* with cells subjected to inflammatory stress was sufficient to increase bacterial-epithelial adherence and led to changes in expression of bacterial universal stress proteins, key regulators of bacterial adhesion and motility. Importantly, cross-over experiments replenishing cells with fresh media before bacterial challenge attenuated these responses. In addition, incubation of commensal strains with faecal waters isolated from IBD patients led to significant changes in microbial gene expression. These results indicate that altered epithelial micronutrients during inflammation influences host–microbe interactions and may select for the survival of certain microbiota populations over others contributing to the 'disease-associated microbiota'.

Microbial functional capacity is preserved within engineered soil formulations used in mine site restoration

Dr Deepak Kumaresan

University of Western Australia

Mining of mineral resources has been an integral part in the global history of social and economic development. Mine operators are legally obligated to restore the extraction site as specified by the local government's environmental regulation. Establishment of rehabilitated landforms using post-mining substrates (i.e. waste rocks, tailings) that typically exhibit extreme conditions can be a major issue during mine closure operations. Current mine rehabilitation strategies focus on the establishment of above-ground diversity (i.e 60-80% of the plant taxa in an adjacent reference site), which are the primary indicators for successful rehabilitation. Poor establishment of plant growth and diversity can lead to other complications such as impaired landform stability and accelerated erosion. Despite the wide acknowledgement on the impact of microbial functional diversity on overall soil health and plant diversity, no detailed attention has been paid to understand the role of microbes in mine rehabilitation strategies. Here we describe results from a pilot study that investigates the impact of different topsoil and tailings ratio on phylogenetic and functional composition of microbial communities and use them as both indicator and facilitator in rehabilitation of post-mining substrates.

The murine appendiceal microbiome is altered in spontaneous colitis and its pathological progression

Dr Dale Kunde

University of Tasmania

Inflammatory bowel disease (IBD) is a multifactorial disease that is extensively associated with stool microbiome changes (dysbiosis). Appendicitis and appendectomy limits subsequent colitis, clinically, and in animal models. We examined how the appendiceal and stool microbiome fared in our spontaneous colitic Winnie (Muc2-/-) mice model. Bacteriodetes was decreased in 15-week Winnie mice appendices compared to corresponding stool samples ($P < 0.01$). Proteobacteria was increased in appendices of Winnie mice compared to corresponding stool samples ($P < 0.05$). The Bacteroidetes family Rikenellaceae could be identified only in 15-week-old Winnie mice appendices. A higher quantity of Acetobacteraceae (Proteobacteria phylum) was present in 15-week Winnie mice when compared to 12-week Winnie mice ($P < 0.01$). Helicobacteraceae (Proteobacteria phylum), which is prominent in all Winnie mice, is absent in control mice. The presence of Helicobacteraceae (Proteobacteria phylum) only in colitic Winnie mice is consistent with reports of increased *Helicobacter* in IBD patients. *Bacteroides* (Bacteroidetes phylum) decreases may be

a reflection of reduced anti-inflammatory commensal species such as *B. fragilis*. Further research is warranted to expand and delineate the relationship between IBD and the appendix microbiome.

Evaluation of ddRAD-seq for reduced representation metagenome sequencing
Dr Michael Liu
University of Technology Sydney

Metagenomics is the direct analysis of the genome content of the microbial communities that exist in our environment. It provides access to the phylogenetic profile of the associated microbial community and generates novel hypotheses for microbial function. The large and rapid reduction in sequencing cost has dramatically accelerated the development of sequencing-based metagenomics and has been proposed by many scientists as a means to characterise the microbiome. Here we describe a novel approach by accessing the 'reduced representation' of a metagenomic library, including a complete laboratory protocol and analysis workflow. Our method borrows from recent developments in reduced-representation genome sequencing experiments known as restriction site associated DNA sequencing (RADSeq). The technique takes advantage of sequence specificity of restriction endonuclease to construct a set of sequences that are adjacent to the restriction site. This results in a reduced sequencing library whose smaller size is roughly proportional to the frequency of the restriction enzyme cut-site. The performance of such approach is explored here by applying the analysis on human gut microbiome samples. The results report and discuss the advantages and disadvantages of the approach, by comparing the phylogenetic and functional profiles between the 'reduced' metagenome and its full counterpart.

The Gut-Brain-Microbiome Axis: a SWOT analysis
Ms Amy Loughman
RMIT University

Mounting evidence from animal models documents the constant, bidirectional and homeostatic communication between gut microbiota and brain function. However there remains a dearth of large human studies. Amongst numerous strengths and opportunities in this exciting field of research, a number of significant challenges remain. These include undefined and evolving methodology, the multidisciplinary nature of the research and the premature adoption of findings in the public domain. Two projects described here seek to replicate findings from animal and small sample human studies. The first, at the National Institute of Mental Health in Bethesda, USA, aims to measure relationships between gut microbiota, known contributors to mental health (genetic, family and lifestyle factors), physical health indicators and biomarkers of disease, and mental health and migraine outcomes. The second, within the Barwon Infant Study, Geelong aims to evaluate the trajectories of prenatal and antenatal influences on early childhood behaviour.

The co-evolution of helminth parasites and the intestinal microbiome: implications for the immune-mediated disease
Dr Maria Lund
University of Technology Sydney

Over millennia of co-evolution, helminth parasites and intestinal microbiota have evolved elegant adaptations to live in harmony with one another, and with their mammalian host. The intestinal microbiota and helminth parasites exert influence on one another and, importantly, both the intestinal microbiota and helminth parasites exert significant influence on the host immune response. It is likely that this three-way interaction is required for immune homeostasis, and that disturbances in this complex relationship may lead to dysregulated immune responses and ultimately autoimmune/inflammatory disease. It has long been recognised that helminth parasite infection modulates the host immune response and can therefore prevent and/or ameliorate a variety of autoimmune/inflammatory disorders. Emerging evidence suggests that the therapeutic potential of helminth parasite infection may lie in the parasite's manipulation of intestinal microbial populations, which in turn contribute to the regulation of the host immune response. Understanding this intricate three-way relationship will allow us to identify novel strategies for the rebalancing of the immune system and, ultimately, the therapy of immune dysregulatory disorders.

The role of microbial diseases on the decline of dominant seaweed holobionts
Dr Esequiel Marzinelli
UNSW Australia

Emerging evidence from a wide diversity of systems increasingly shows that host-associated microorganisms are critically important for the normal development and functioning of eukaryotic hosts. Understanding the relationship between hosts and microbes is particularly crucial for habitat-forming holobionts that form the biogenic structure of ecosystems—such as trees and corals—because impacts on the interaction between these hosts and their associated microbiome can cascade throughout an entire ecosystem. Critically, such habitat-forming 'foundation' species are in global decline. On temperate rocky coasts, seaweeds are the dominant biogenic habitat, forming dense underwater forests that underpin coastal biodiversity and functioning. Disruptions to host–microbiome interactions via environmental change can lead to higher incidence and severity of disease, affecting the resilience of seaweed populations. We have identified putative disease

phenotypes of two key Australian seaweeds: the dominant kelp *Ecklonia radiata* and the fucoid *Phyllospora comosa*. Putative disease phenotypes were common and widespread, and in some cases greater in summer or on urbanised shorelines. Host-associated microbial communities characterised using 16S rRNA gene sequencing and metagenomics differed markedly between 'diseased' vs 'healthy' algae, even at a continental scale. Inoculation experiments have identified bacterial and fungal pathogens, which affected seaweed performance and survival, suggesting that microbial diseases may be an important process contributing to declines of seaweed forests. In the holobiont context, these results reinforce the idea that host–microbiome associations form a coherent biological entity, or holobiont, that must be studied together if we are to have an understanding of biological systems.

The ocean microbiome in a changing environment
Dr Allison McInnes

University of Technology Sydney

Marine systems cover 70% of Earth's surface and represent the largest ecosystem on Earth. The marine microbial community drives all of the biological processes from the surface to the deep sea, through carbon sequestration (from the atmosphere) and conversion of inorganic to organic carbon (representing the base of the food web). We present results from nine manipulative experiments carried out aboard the RV Investigator in June 2016 across a large latitudinal gradient. Sample water was incubated with ambient light at seven different temperatures to determine the community plasticity to thermal excursions. Flow cytometric analyses of live cells using natural and added fluorescent markers demonstrated marine microbes have varying tolerance to temperature excursions resulting in overall changes to community function of both carbon and nitrogen cycling.

Combinations of cereal soluble dietary fibres in porcine diets promote bacterial community diversity within the large intestine
Dr Deirdre Mikkelsen

University of Queensland

A diet with a range of complex dietary fibres, in terms of both the range of foods consumed and each food component's structural composition, is being recognised as profoundly affecting the gastro-intestinal bacterial community diversity. Here we investigated the effects of two cereal soluble dietary fibres (SDF), wheat-arabinoxylan (AX) and oat-mixed linkage glucans (MLG), on the porcine caecum (Cae) and distal colon (DC) bacterial communities. Five groups of six pigs were each fed one diet based on wheat starch (WS) only, or treatment diets in which some WS was replaced by 10% AX, or 10% MLG, a combination of 5% AX:5% MLG (AXMLG), or completely replaced with ground whole wheat. 16S rRNA gene amplicon 454 pyrosequencing of digesta, collected from the Cae and DC post-anaesthesia, revealed that the bacterial community composition significantly differed between the different SDF ($P < 0.001$), with distinct population shifts found for AX and MLG diets. Methods have also been developed to visualise bacterial associations with fluorescently-labelled dietary remnants. Ultimately, this approach will provide an understanding of the mechanisms by which complex cereal SDF containing diets may influence gut bacterial community diversity, an important part of their effects on human health.

The skin microbiome: a possible role in the progression of squamous skin cancer
Dr Katharina Noske

University of Queensland

In recent years, microbiomes of various tissues have received increased attention. Here, we propose a role of the skin microbiome in the progression of squamous cancers of the skin. It has been established that local immunity influences the progression of sun-damaged, pre-malignant areas, called actinic keratosis (AK), towards squamous cell carcinoma (SCC). We identified a different microbiome associated with lesional skin from AK and SCC patients compared with healthy skin. By cultivating the identified microbial species and treating different epithelial cell systems with microbial products, we aim to study the influence of the microbiome on immunoregulatory and inflammatory responses of skin cells. The insights gained from this study will promote a better understanding of how the skin microbiome contributes to the progression of skin cancer.

Climate change impact on crop productivity: legacy effect through plant-soil feedback
Dr Yui Osani

University of New England

Changes in crop productivity, resource allocation and nutrient uptake can impact soil nutrient availability, in both the short and long term, through changes in organic matter input into the soil. Projected changes in atmospheric concentrations of CO_2 and temperature have been shown to impact crop productivity. However, the short-term nature of most studies makes it difficult to assess the full extent of altered climate on crop productivity through plant–soil feedback, thus potentially limiting our ability to predict the long-term implications of these changes. Here, we examined the effects of elevated CO_2 (CE) and temperature (TE) on cotton productivity over two seasons to assess the legacy of these treatments through plant–soil feedback. TE increased cotton yield in both seasons; however, yield response to CE at ambient temperature (TA) was reversed from positive to negative in the second season. Nutrient analyses revealed nitrogen limitation under CETA, while

belowground carbon allocation, soil respiration and microbial biomass were increased by CE, suggesting increased microbial immobilisation of soil nitrogen. These results indicate that positive effects of CE on crop productivity may be dampened by negative plant–soil feedbacks that reduce nitrogen availability in the long term. Further research is needed to identify the underlying mechanism that drives such feedback effects.

Shifts in plankton community composition as indicators of enrichment processes in shelf waters of the Great Australian Bight (southern Australia)
Dr Nicole Patten
South Australian Research Development Institute

In the eastern Great Australian Bight, coastal upwelling processes occurring in the austral summer promote elevated phytoplankton biomass and primary production and support higher trophic levels (zooplankton through to small pelagic fish). Studies to date have focused on discrete plankton groups, with little known about how the plankton community as a whole responds to changing environmental conditions. Here, we investigated the size structure of planktonic communities from viruses through to meso-zooplankton during contrasting oceanographic conditions in July and October 2014 and February and April 2015. Significant shifts in the planktonic assemblage occurred between depths, stations and sampling times. Overall, picophytoplankton and nanoplankton dominated the phytoplankton community. The exception was in February (at station NRSKAI), when large phytoplankton (> 5 µm) dominated together with highest abundances of bacteria (but not viruses). Diatoms comprised the bulk of > 5 µm phytoplankton (> 85%), with this community shift linked to upwelled cold nutrient-rich water. Highest zooplankton abundances also occurred at this time, with an overall shift from a copepod/appendicularian community to a copepod/cladoceran/echinoderm-dominated community.

Icy Microbiomes
Dr Shane Powell
University of Tasmania

Microbial communities form a significant part of the Antarctic ecosystem from the sea-ice to the sediments and soils and are vital for many biogeochemical processes in the region. Once thought to be low in abundance and diversity, it is now known that Antarctic microbial communities are as diverse and numerous as any. We have shown that Antarctic soil and marine sediment bacterial communities are diverse and respond quickly to changes in their environment. This poster provides three examples of the importance of understanding the functions of the microbiome in cold regions: the important of denitrification to hydrocarbon biodegradation in Antarctic soils; the use of microbial genes as markers for ecotoxicological effects; and the impact of ocean acidification on bacterial and eukaryotic microbial communities.

The role of gut microbiota in the pathology of neuroinflammation and depression following methamphetamine use
Dr Monica Prakash
Victoria University

Methamphetamine (METH) is a potent psychostimulant and sympathomimetic drug that acts on the central nervous system. Accumulating evidence associates METH use with neuropsychiatric disorders, including depression. Depression is linked to activation of the immune response and the presence of pro-inflammatory cytokines and microbial products in the brain. METH use is also associated with increased intestinal permeability; a condition referred to as 'leaky gut'. Interestingly, increased intestinal permeability plays a role in the inflammatory pathophysiology of depression. Enteric microbial toxins and activated immune cells can 'leak' from the gut into the bloodstream and travel to the brain, causing inflammation that contributes to neuropsychiatric disorders.

We examined the complex interaction of the gastrointestinal, immune and nervous systems using an acute mouse model of METH use. Metabolic cages were used to monitor animal behaviour during treatment. Flow cytometry was used to examine changes in systemic immune cell populations and expression of neurotransmitter receptors following METH use. Changes in enteric neuron populations and innervation and tight junction proteins were examined by immunohistochemistry. Preliminary studies show that METH use induces changes in gut neuro-immune interactions and this may have implications for the development of neuropsychiatric disorders seen with METH use.

Searching for methanogen genomic needles in a rumen microbiome haystack
Dr Carly Rosewarne
CSIRO

Many surveys continue to be undertaken to catalogue the key microbes responsible for methane production in livestock ('who's there?'). We are missing the important functional genomic information required to support development of targeted approaches for reducing methane emissions. Through the use of novel methods to study the genetic potential and gene expression profiles of rumen methanogens, it has been possible to reveal novel mechanisms used to enable their survival and persistence under in vivo conditions.

Reproducibility of human gut microbiome analysis for a pregnancy-birth cohort study: impact of collection-storage method and sequencing laboratory

Dr Alexandra Jazmin Roth Schulze

Walter and Eliza Hall Institute of Medical Research

Environmental Determinants of Islet Autoimmunity (ENDIA) (endia.org.au) is a longitudinal study from early pregnancy of environment-gene interactions in 1,400 infants at risk for type 1 diabetes. To optimise analysis of the human gut microbiome in ENDIA and obtain insight into sources of variation, we undertook a quality control study on sequential stool samples from six healthy individuals. Four different collection-storage methods were compared, including immediate processing with a commercial kit (OMR-200) and storage in a home fridge or freezer, prior to transfer and -80°C storage within 24 hours. Sample aliquots were sent to two laboratories for DNA extraction and sequencing. The V4 region of the 16S rRNA gene was sequenced (MiSeq) in each laboratory with different library primers, and analysed using the QIIME pipeline and Greengenes database.

Variation in gut microbiome composition and diversity was dominated by differences between individuals, not by methods or day of collection. Differences in the abundance of taxa, including at the phylum level, were evident between the two laboratories. We conclude: 1) for practical purposes, home collection with storage and transport at 4°C within 24 hours is adequate for analysis of the gut microbiome; and 2) cohort samples should be analysed by the same method in one laboratory.

Microbial community assembly in industrial wastes: implications for enhanced bioremediation strategies

Dr Talitha Santini

University of Queensland

Tailings from mineral processing industries are challenging environments for microbial survival and growth, typically exhibiting extremes of pH (pH≤4 or pH≥9), high salinity and dissolved metals, and low organic carbon concentrations. Developing microbially-driven strategies for tailings remediation depends on understanding how succession proceeds over time in field-weathered tailings to avoid negative (competition, amensalism) interactions with existing communities. The extreme geochemical and physical properties of tailings compared with natural geological materials, and their spatial isolation from inoculant sources, necessitates tailings-specific investigations of microbial community establishment and successional processes. Here, I present results from an international study evaluating microbial community assembly across ten tailings sites during the first year after production.

Assembly in the tailings microbial communities during the first year after production was largely controlled by the arrival of extremophilic species through dispersal. Increases in microbial community diversity in tailings were significantly slower than observed in natural primary successional systems (e.g. post-wildfire soils, deglaciated till). Dispersal alone was insufficient to shift microbial community composition towards that of natural soils. Rehabilitation was only effective in shifting tailings microbial community compositions towards those of natural soils if chemical and physical properties of tailings (pH, salinity, moisture content) approximated those of the natural soils. Within tailings types, microbial community composition was substantially similar during the first year after production, supporting the development of microbially-assisted tailings bioremediation strategies.

Exploring the depths: examining microbial communities within Bundera Sinkhole, a unique Australian anchialine ecosystem

Dr Sasha Tetu

Macquarie University

Bundera sinkhole represents Australia's only deep anchialine environment: an inland oligohaline pool connected to the ocean via a lengthy subterranean cave. Such habitats generally contain a rich diversity of micro- and macroorganisms, many unique to anchialine environments, yet few studies have examined the microbial component of such systems in depth. The water column within the Bundera sinkhole was sampled at multiple depths, from 2 m down to 28 m, to collect biological material and measure chemical and physical parameters. We performed 16S rRNA gene amplicon and metagenomic sequencing to investigate the ecology, structure and metabolic capabilities of the residing microbial communities. Our results show that this environment supports a series of very distinct microbial assemblages at different depths. Community composition can be correlated with a number of different physicochemical parameters. Representatives of sulphur-oxidising, nitrifying and ammonia-oxidising organisms in samples below 8 m provide us with new insight into the variety of chemolithotrophic primary production mechanisms employed in this interesting ecosystem, the only known occurrence in the southern hemisphere.

Effects of ocean acidification on the marine microbial loop in Antarctic waters

Dr Karen Westwood

Australian Antarctic Division

The marine microbial loop is important in Antarctic waters for two reasons: a) it is the driver of the biological pump in the Southern Ocean where up to 12% of anthropogenic carbon dioxide emissions are absorbed, and b) it forms the base of the Antarctic food web, directly influencing krill and zooplankton populations, and subsequently higher trophic levels.

Anthropogenic carbon dioxide emissions are acidifying the upper ocean and microbial communities in polar regions are at increased risk of effects due to higher solubility in colder waters. Our research examines the shifts that may occur in the Antarctic marine microbial loop due to ocean acidification (OA) and demonstrates the importance of conducting community-level studies. OA may cause decreased primary and net community production and a shift to smaller phytoplankton species. This will potentially cause a decrease in the draw-down of atmospheric carbon dioxide, forming a positive feedback to climate change and exacerbating the problem. It may also be detrimental to krill populations given they have difficulty feeding on small cells. The threshold above which OA effects on the Antarctic marine microbial loop may become apparent is at carbon dioxide concentrations >780 ppm, thus there is some resilience in the system.

Translocation and dissemination of commensal bacteria in post-stroke infection
Dr Connie Wong

Monash University

Bacterial infection is highly prevalent in patients who have had a stroke. Despite the potential contribution of micro-aspiration in post-stroke pneumonia, we found that the majority of the microorganisms detected in the patients who developed infections after having a stroke were common commensal bacteria that normally reside in the intestinal tracts. In a mouse model of ischemic stroke, post-stroke infection was only observed in mice that were born and raised in specific-pathogen-free facilities; this was not seen in mice that were born and raised in germ-free facilities. Using high-throughput 16S rRNA gene amplicon sequencing and bioinformatics analyses, we provide evidence demonstrating that the source of the bacteria forming the microbial community in the lungs of post-stroke mice was indeed the host small intestine. Additionally, stroke-induced gut barrier permeability and dysfunction preceded the dissemination of orally inoculated bacteria to peripheral tissues. This study identifies a novel pathway in which stroke promotes the translocation and dissemination of selective strains of bacteria that originated from the host gut microbiota.

Quantifying and comparing diversity and co-occurrence patterns in microbial datasets
Dr Stephen Woodcock

University of Technology Sydney

The identification of trends, patterns and similarities in ecological datasets is a long-standing and well-studied problem in classical ecology. Despite the vast differences in community sizes and complexity, many of the techniques and indices used for microbial studies are simply those developed for macroscale organisms. Here, we examine some of the common techniques used to quantify and characterise microbial communities. We demonstrate that injudicious selection of diversity or similarity indices can greatly influence the conclusions drawn. Especially when datasets are further summarised—for example by using only presence/absence data—wildly contradictory results can be obtained by using different metrics.

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Dr Christina Adler
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Christina is an academic in the Faculty of Dentistry at Sydney University and her research focuses on understanding how the oral microbiome contributes to the maintenance of health and the development of oral disease. She was recently awarded an NHMRC project grant to apply genetic technologies to the significant public health problem of dental decay in childhood. Childhood decay is the most common chronic childhood disease in Australia. To address gaps in current knowledge, she is determining how an individual's environment and genetic makeup drive variation in the composition of the oral microbiome to produce childhood decay.

Dr Tracy Ainsworth
Research Fellow

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Tracy is a research fellow studying coral holobiont response to early thermal stress events, coral host-microbe interactions and coral symbioses in diverse environments. Her research aims to investigate the response of marine organisms to changes in the marine environment and to determine how host-microbe-environment interactions influence physiology, adaptation and acclimation. She has been a research fellow (APD 2008–11, Super Science 2011–14) in the ARC Centre of Excellence for Coral Reefs Studies. She received a PhD at the University of Queensland in 2008.

Professor Jill Banfield
Professor

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Jill was born in Armidale, NSW and obtained her degree at the Australian National University. She obtained her PhD at Johns Hopkins University, Baltimore USA. She has been located at the Faculty UW Madison, University of Tokyo, University of California and Lawrence Berkeley National Laboratory.

Dr Sabrina Beckmann
Research Associate

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Sabrina is a research associate at UNSW Australia. She was born in Germany and obtained her doctorate there. Her PhD focused on the microbial methane formation in abandoned coal mines. She moved to Australia in 2011 to invigorate methanogenic archaea and breathe new life into retired coal seam wells for energy production. Special research interests include the lifestyle of Archaea and methane in agricultural soils, pristine river sediments, bio waste, and in the deep biosphere of coal reservoirs.

Ms Simone Birrer
PhD Candidate

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Simone is a marine ecologist at UNSW Australia. Originally from Switzerland, Simone completed her BSc and MSc in biology at the Swiss Federal Institute of Technology in Zurich and came to Australia to venture into marine science. In her PhD, which she recently submitted, she performed in-situ experiments and conducted an extensive survey to investigate the impacts of anthropogenic contaminants on estuarine sediment microbes. Specifically, Simone uses modern molecular tools to elucidate the genetic mechanisms behind altered biogeochemical cycles.

Dr Melanie Blanchette
Research Fellow

Edith Cowan University

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Growing up next to a river, it was inevitable that Melanie would become a freshwater ecologist. Her research, while firmly in the aquatic sciences, is highly interdisciplinary, with a focus on the effect of mining activities on rivers. She believes harnessing new technologies is vital to improve environmental monitoring and assessment, and also incorporates classic techniques in freshwater ecology to explore the microbiome. As a Research Fellow at Edith Cowan University, she currently holds two Australian Competitive Grants from the Australian Coal Association Research Program exploring how genomics can improve the environmental legacy of mining.

Dr Philippe Boeuf
Senior Research Officer

Burnet Institute

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Philippe is a senior research officer and theme leader at Burnet Institute in Melbourne. During his PhD at the Pasteur Institute in Paris, and using a combination of lab-based and field research, he showed that severe anaemia and cerebral malaria, the two main forms of severe paediatric malaria, were associated with specific immune profiles. In 2005, he joined the lab of Professor Stephen Rogerson at the University of Melbourne and generated seminal data on mechanisms of disease in foetal growth restriction in malaria in pregnancy. This work should open the way to interventions to alleviate the burden of malaria in pregnancy. Since January 2015, he leads the maternal, placental and fetal health theme at Burnet Institute whilst continuing research into the immune mechanisms of protection against malaria.

Dr Anthony Borneman
Principal Research Scientist

Australian Wine Research Institute

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Anthony obtained his PhD in genetics from the University of Melbourne and then spent four years as a postdoctoral associate with Professor Michael Snyder at Yale University, applying omics technologies to study gene networks in yeast. Anthony is currently a Principle Research Scientist at the Australian Wine Research Institute. His research is focused on applying genomics, systems- and synthetic-biology to understand the genetic basis of phenotypic diversity in industrial microorganisms, with particular focus on the wine yeasts *Saccharomyces cerevisiae* and *Brettanomyces bruxellensis*.

Dr David Briskey
Member of the Organising Committee
Research Fellow

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David's primary research expertise is in biochemistry and biomedical research, with a focus on the role of microbiota on inflammation, oxidative stress and intestinal permeability. He is currently focused on linking the microbiota with chronic diseases. By combining knowledge of the microbiota with the pathogenesis of CKD and CVD he has hypothesised that the microbiota have the capability to affect CVD and CKD through regulation of NO and inflammation. Previously he has shown a probiotics supplementation in an animal model of non-alcoholic fatty liver disease is capable of altering intestinal epithelial permeability and reducing the severity of a chronic disease.

Dr Mark Brown
Senior Research Fellow

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Mark's research focuses on ecological dynamics and biogeochemical impacts of microbial assemblages across a range of biomes. During research at the University of Tasmania, University of Southern California, University of Hawaii, and UNSW Australia, Mark has undertaken four Antarctic expeditions and spent nearly a cumulative year at sea, while studying microbial life in coastal and open oceans, sea-ice, marine mammals, soils, lakes, caves and even (theoretically) in extraterrestrial systems. His is currently interested in how extensive, nationally collected microbial datasets can enable predictive capacities for microbial assemblage structure and function under changing environmental conditions.

Dr Catherine Burke
Lecturer

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Catherine is a microbial ecologist, with a primary interest in researching the human microbiome.

She received her PhD in 2010 from UNSW Australia for her study of microbial communities on marine algae. She moved to the University of Technology Sydney in 2010 to study the human microbiome, and collaborate with microbiologists, clinicians and bioinformaticians to examine the microbiome in depression, chronic rhinosinusitis, diabetes and pelvic inflammatory disease. She also has an interest in developing methods for long read DNA sequencing, and is passionate about teaching the human microbiome to undergraduate and research students.

Dr Jose A Caparros-Martin
Research Associate

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Jose completed his PhD at the Institute for Plant Molecular and Cell Biology (Valencia, Spain). Later, he took advantage of different state-of-the-art genetic techniques and bioinformatics, to find causative genes of different rare genetic disorders in humans. In 2015 he joined the WA Department of Health-funded Human Microbiome Research Centre at Curtin University. His main interest is in using a 'systems medicine' approach of integrating omics and bioinformatic approaches

PARTICIPANTS

to understand functional microbiomes and metagenomes and how they shape health and disease. His current work includes investigating the impact of statins on the intestinal microbiota and dysbiosis in mice.

Dr Anthony Chariton
Research Team Leader: Molecular Ecology and Toxicology

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Anthony's research focus is on the development, application and integration of omic technologies and traditional ecology for the monitoring and assessment of aquatic systems. His research is primarily in the area of estuarine ecology, with a focus on the effects on environmental contaminants on sedimentary environments. However, his research interests are broad and cover terrestrial ecology, risk assessment, ecotoxicology, network analysis, food-web ecology and biometry.

Dr Adam Collison
Lecturer

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Adam's research has focused upon identification of novel therapeutic targets and molecular biomarkers to assist in better identification and treatment of asthma and food allergy in order to address currently unmet clinical needs. Adam's current focus is on better understanding the early development of asthma and immunological learning from the developing gut microbiome through the first year of life to understand the mechanism underpinning the development of asthma in early childhood.

Dr Ricardo Costa
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Ricardo is a lecturer, researcher, and consultant in exercise physiology, metabolism and dietetics at Monash University's Department of Nutrition and Dietetics. Before joining Monash University in 2013, he was lecturer, researcher and course director at Coventry University, UK after completing his PhD in neuroendocrine and nutritional immunology at the University of Wales in 2010, while still active as a Community Dietitian for the Wirral NHS PCT-UK. His sporting and exercise experience extends academia; he was a professional triathlete/duathlete competing on the world and European circuit from 1994 to 2003.

Dr Katherine Dafforn
Senior Research Associate

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Katherine is a Senior Research Associate at the UNSW Australia and Co-Director of the Applied Marine and Estuarine Ecology Lab. Katherine's research focuses on understanding and mitigating human impacts on marine communities. She was one of the first to demonstrate that molecular tools can provide more sensitive indicators of ecosystem health than traditional monitoring techniques. Katherine is also enthusiastic about science communication. She has published in media outlets such as *The Conversation* and is an avid tweeter. She recently received a Young Tall Poppy Science Award for science excellence and community engagement.

Dr Paul Dennis
Lecturer

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Paul is a lecturer in soil and environmental sciences in the School of Agriculture and Food Sciences at the University of Queensland, and runs the school's Molecular Microbial Ecology group. His group aims to develop an understanding of the factors that determine the structure and function of biological communities at multiple spatio-temporal scales; develop strategies that facilitate manipulation of microbial communities for environmental and commercial purposes; and improve our ability to predict the consequences of environmental change on ecosystem structure, function and stability. The group is strongly multidisciplinary and draws on a wide range of expertise in ecology, statistics, bioinformatics, soil science, advanced imaging and molecular biology.

Dr Ania Deutscher
Professional Officer

NSW Department of Primary Industries

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Ania is a molecular biologist at the NSW Department of Primary Industries, interested in host–microbe interactions ranging from microbe adherence mechanisms to their effect(s) on the host. Ania's current research focuses on using molecular methods, NGS and comparative genomics to understand the dynamics of the Queensland fruit fly (Qfly) gut microbiome, and the role of gut microbiota in fruit fly development, physiology and nutrition. Her goal is improving the performance of mass-reared Qflies for the sterile insect technique. Earlier research included characterising putative adhesins of the swine

pathogen *Mycoplasma hyopneumoniae* and identifying potential Pacific oyster bacterial pathogens.

Dr Barbara Drigo
Lecturer

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Barbara conducted her doctoral studies at the Netherlands Institute of Ecology and was awarded her PhD in 2009. Her PhD research used a number of interrelated methods in molecular microbial ecology to study the effects of climatic conditions on plant-soil-microbial interactions. She then became research fellow at Wageningen University, where she studied the correlation between disease suppressiveness and bio-control agents. Shortly after, she moved to the Hawkesbury Institute for the Environment, where she developed novel experimental systems to test microbial dynamics and functioning in response to environmental change. In August 2016 she commenced a new research role with the Future Industries Institute at the University of South Australia.

Dr Suhelen Egan
Researcher

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Suhelen has a PhD in microbiology from UNSW Australia and has been a teaching and research academic for the Centre for Marine Bio-Innovation, UNSW since 2003. She has published more than 40 papers in the field of marine microbial ecology and biotechnology and in 2014 was awarded an ARC Future Fellowship to study microbial symbioses of macroalgae. Her major research interests include understanding the role of bacteria in health and disease of marine organisms, with a particular focus on the microbiome of macroalgae. She also leads projects in the area of natural product discovery from marine systems.

Dr Deirdre Gleeson
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Dierdre's research spans both natural and managed ecosystems across terrestrial and aquatic environments where she studies the microbiomes of agricultural systems, contaminated landscapes, microbioliates (microbial mats and thrombolites) and seagrass and mangrove rhizospheres. Dierdre co-leads the Avon River Critical Zone Observatory (AR-CZO), the first CZO in the southern hemisphere, which focuses on ancient soils in a semiarid landscape. Her research contributions focus on how the diversity and function of microorganisms are impacted by their surrounding habitat at both micro scale and at landscape scale (e.g. management practices and climate) with particular emphasis on the use of next generation sequencing tools.

Dr Andrew Greenhill
Senior Lecturer in Microbiology

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Since obtaining his PhD from James Cook University in 2007, Andrew's research has focused on infectious diseases in resource-poor settings. From 2008 to 2012, Andrew held a senior research position at the Papua New Guinea Institute of Medical Research, an institute that has gained global recognition for research in infectious diseases of low-income populations. Andrew took up a position as senior lecturer at Monash University in 2012, and in 2014 transferred with his regional campus to become part of Australia's most recently formed university, Federation University. Andrew maintains an interest in gastrointestinal pathogens and their interactions with the gut microbiome.

Dr Kelly Hamonts
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Kelly is an environmental microbiologist with expertise in applying metagenomics and metatranscriptomics to study soil and plant microbiomes. She obtained a PhD in bioscience engineering from the University of Leuven, Belgium, before taking up post-doc positions at Lincoln University, New Zealand, and CSIRO Plant Industry, Canberra. She currently works at the Hawkesbury Institute for the Environment on a grant funded by Sugar Research Australia, applying a comprehensive microbiome-based approach to determine the involvement of biotic interactions and soil nutritional health in the development of Yellow Canopy Syndrome, a largely undiagnosed condition affecting sugarcane crops in Australia.

Dr Sarah Hanieh
Paediatric Infectious Disease Physician and Research Fellow

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Sarah is a paediatric infectious diseases physician and post-doctoral Research Fellow in the International and Immigrant Health Group in the Department of Medicine at the Doherty Institute. Sarah was awarded a PhD in medicine at the University of Melbourne in 2015 for her

work on maternal and early infant factors contributing to chronic undernutrition in infants in rural Vietnam. Her current research focuses on developing a predictive algorithm to identify infants at high risk of stunting in resource-constrained settings, and investigating the link between the gut microbiome and child undernutrition.

Dr Rebekah Henry
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Rebekah has worked in the field of molecular microbiology for 16 years. Her current position is as a research fellow in the Environmental and Public Health Microbiology laboratory at Monash University. Here she works alongside several industry partners to develop and apply bacterial community profiling methods to understand, model and track sources of faecal contamination in urban waterways for downstream target mitigation. She also investigates the use of metagenomics to understand microbial dynamics within stormwater and greywater treatment systems in order to design improved systems for field application.

Ms Emily Hoedt
PhD Candidate

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Emily has just submitted her PhD thesis as a student of the University of Queensland School of Chemistry and Molecular Biosciences, and was supervised by Mark Morrison, Phil Hugenholtz and Gene Tyson. Her PhD studies focus on functional and comparative studies of heterotrophic methanogens from different gut environments, supported by an Australian Postgraduate Award and a top-up scholarship from Meat and Livestock Australia.

Associate Professor Kathryn Holt
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Kat has a double degree BA/BSc from the University of Western Australia, majoring in biochemistry, applied statistics and philosophy; a master of epidemiology from the University of Melbourne; and a PhD in molecular biology from the University of Cambridge. She is currently an NHMRC Career Development Fellow in the University of Melbourne's Department of Biochemistry and Molecular Biology. Kat's research focus is microbial genomics, and she is a founding member and Deputy Director of the University of Melbourne's new Centre for Systems Genomics.

Dr Qing Hu
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Qing (Mongolian name Tsing Bohu) is a new OCE postdoc in Mineral Resources, CSIRO, supervised by Dr Ravi Anand. He also works with Professor Elizabeth Watkin of Curtin University. He took his PhD study in Professor Kirsten Kuesel's lab, Friedrich Schiller University Jena, Germany. His major is biological low pH Mn(II) oxidation in the subsoil of mining areas. His research in CSIRO will focus on gold and fungi.

Dr Megan Huggett
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Megan is broadly interested in the diversity and function of microbes in coastal ecosystems. Her research includes free-living microbes in seawater as well as microbes associated with corals, sponges, algae and herbivorous fish. She is particularly interested in how these microbial communities are impacted by environmental changes.

Dr Thomas Jefferies
Research Associate

Western Sydney University

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Thomas is a microbial ecologist with a wide range of expertise in molecular microbiology, bioinformatics and microbial biogeography. He obtained his PhD in 2012 from Flinders University and has conducted postdoctoral research at the University of Technology Sydney and the Hawkesbury Institute for the Environment at Western Sydney University. His research focuses on identifying drivers of microbial diversity patterns on varying scales in soil and aquatic ecosystems, utilising microbes for bioremediation, and employing citizen science to microbial ecology.

Professor Emma Johnston
Member of the Organising Committee
Pro Vice-Chancellor

UNSW Australia

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Emma is Pro Vice-Chancellor (Research) and Professor of marine ecology and ecotoxicology at the UNSW Australia. She investigates the ways in which human activities impact coastal ecosystems, from the tropics to the poles. In 2014 she was awarded the Australian Academy of Science's inaugural Nancy Millis Medal for Women in Science and in 2015 the Eureka Prize for the public communication of science. Emma is also a television presenter for the BBC/Foxtel series, Coast Australia, and Vice President of Science and Technology Australia. She contributes expert opinion to state, federal and international government agencies and consults with industry through the development and implementation of environmental monitoring programs.

Dr Simon Keely
Senior Lecturer

University of Newcastle

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Simon graduated with a PhD from University College Dublin and undertook postdoctoral training at the Mucosal Inflammation Program in University of Colorado Denver. He held junior faculty positions (Instructor and Senior Instructor) in the UCDenver School of Medicine and received a prestigious fellowship from the Crohn's and Colitis Foundation of America. Simon moved to the University of Newcastle in 2011 and is chief investigator of the HMRI Gastrointestinal Research Group. His work covers basic and translational science and is primarily focused on understanding inflammation and host–microbe interactions in the gastrointestinal tract, and how they contribute to chronic GI disease.

Associate Professor Lutz Krause
Member of the Organising Committee
Principal Research Fellow

University of Queensland

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Lutz undertook undergraduate studies in computer science at Bielefeld University. After completing his PhD in bioinformatics and genome research in 2008 he joined the Nestlé Research Center in Lausanne, where he studied the role of the gut microbiota in health and disease, in particular in obesity and diabetes. In 2010 he moved to Brisbane to take up the role of head of the Bioinformatics laboratory at QIMR Berghofer. In 2014 Lutz joined the UQ Diamantina Institute to pursue his research on the human microbiome, parasite genomics, cancer genetics and epigenetics of complex diseases.

Dr Deepak Kumaresan
Research Assistant Professor

University of Western Australia

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Deepak is an environmental microbiologist with an interest in linking microbial phylogeny to function and elucidating the eco-physiological mechanisms in microbial systems that underpin ecosystem services. Specifically, he works on two complementary research areas: eco-physiology of methylotrophic organisms that can use C-1 compounds such as methane or methylated amines; and plant–microbe interactions and their impact on soil fertility in agro-ecosystems and mine rehabilitation sites.

Dr Dale Kunde
Lecturer

University of Tasmania

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Dale is a professional clinical biochemist lecturing in the laboratory medicine degree at the University of Tasmania. He obtained his PhD in 2010. His research interests include the development of colorectal cancer as a consequence of inflammatory bowel diseases, including the effect of the dysbiosis in disease progression.

Dr Yan Lam
Research Fellow

University of Sydney

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Yan's initial training was in nutritional biochemistry followed by a professional qualification and practice in clinical dietetics. His broad research interest is to understand how diet impacts on health, with the ultimate aim of developing evidence-based nutritional advice to improve metabolic wellbeing. His recent research primarily focuses on investigating the role of dietary factors on gut parameters, specifically barrier function and bacterial profile, and how these influence clinical metabolic risk factors.

PARTICIPANTS

Dr Federico Lauro
Associate Professor

UNSW Australia, Nanyang Technological University, Indigo V Expeditions

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Federico was born and raised in Venice, Italy. He graduated from the University of Padua and obtained his PhD at Scripps Institution of Oceanography at the University of California in San Diego, California (UCSD). He is currently an Associate Professor at Nanyang Technological University, Adjunct Professor at UNSW Australia and Associate Chair at the Asian School of the Environment. He has pioneered skills in both experimental and computational sciences—in particular, deep-sea and Antarctic microbiology. Federico is an Explorer's Club fellow and winner of the 2015 Lowell Thomas Award.

Dr Kim-Anh Lê Cao
Group Leader Computational Biostatistics Methods

University of Queensland

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Kim-Anh was awarded her PhD in 2008 at Université de Toulouse, France. She then moved to Australia as a postdoctoral fellow at the University of Queensland. Kim-Anh is currently leading the Computational Biostatistics Methods group at the UQ Diamantina Institute and is the head of the UQDI Biostatistics facility that provides statistical support to researchers from her institute. Her research interests focus on the development of innovative statistical approaches for the analysis and the integration of large biological data sets for studies in cancer, and diseases involving the immune system including arthritis, chronic infections and diabetes. She has been teaching statistics to undergraduate and postgraduate (UQ Bioinformatics Master's program) students for four years. Together with the mixOmics team, Kim-Anh continues to develop methodologies to analyse complex biological studies.

Professor Anthony Linnane FAA
Chair of the Oversight Committee
Managing Director

Centre for Molecular Biology and Medicine

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Tony Linnane is an Emeritus Professor at Monash University and an Adjunct Professor at the School of Medicine at the University of Sydney. Since 1963, he has published some 330 full papers, numerous abstracts and has several international granted patents. His research has covered the areas of mitochondria, bowel cancer and microbiome. Tony has previously been involved in clinical trials on statin toxicity and bowel cancer diagnostics and is currently working on trials of a potential therapy for diabetes mellitus type 2 neuropathy. Previously he was Professor of Biochemistry at Monash University from 1965-1994 and Associate Dean of Medicine from 1973-76. He is the recipient of numerous accolades including the Lemberg Medal, Centenary Medal, and the Union of Biochemistry and Molecular Biology Distinguished Service Award 2000.

Dr Michael Liu
Research Associate

University of Technology Sydney

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Michael's research focuses on the interaction of bacteria with their environment, with a strong interest in understanding the human microbiome and how it can be used to improve human health in various ways (through analysis of multi-omics). He currently operates the Sequencing Core Facility at the UTS's ithree Institute. The facility is equipped with the knowledge, expertise and instrumentation to perform high-throughput whole genome sequencing analysis, integrated metagenomics/microbiomics data production and analysis. He holds a bachelor degree from UNSW Australia (2006) and a PhD in microbiology (2012). He went on to carry out postdoctoral research at UTS in 2012.

Ms Amy Loughman
Associate Lecturer

RMIT University

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Amy is an associate lecturer in psychology at RMIT University. She has recently finished writing her PhD at the University of Melbourne, and has undertaken research at the Murdoch Childrens Research Institute and the National Institutes of Health in the US. Clinically trained in neuropsychology, she is passionate about understanding the relationships between physical and mental health. A particular research interest of Amy's is the gut microbiome and the potential relevance that this 'forgotten organ' may have for understanding human health.

Dr Maria Lund
Postdoctoral Researcher

University of Technology Sydney

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Maria's research at UTS has examined the potential of parasite-derived molecules to modulate the immune response, in order to treat autoimmune/inflammatory disorders, and prevent transplant rejection. Her interest in the microbiome arose from observations that intestinal parasites have co-evolved with intestinal microbiota to exist in the same niche (and so likely exert effects on one another). Both the intestinal microbiome and helminth parasites greatly influence the host immune response. Her interest is in the cross-talk between the microbiome, the parasite and the host, and how this information may be harnessed for the treatment of immune disorders.

Dr Gonzalo Martinez Fernandez
Postdoctoral Scientist

CSIRO

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Gonzalo is a Postdoctoral Researcher at CSIRO Agriculture and Food within the Gut Microbial function research group, under the supervision of Dr Chris McSweeney. Gonzalo's research interests are focused on the study of the rumen physiology, microbial function and the effectiveness of different compounds on methane inhibition and rumen efficiency. He has been working on several projects studying how the rumen microbiota adapts to inhibition of methanogenesis and accumulation of hydrogen in the rumen, and also how these populations can be manipulated to improve rumen efficiency in cattle.

Dr Ezequiel Marzinelli
Senior Research Fellow

UNSW Australia

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Ezequiel (Ziggy) is a Senior Research Fellow at the Centre for Marine Bio-Innovation, UNSW. Ziggy is a marine ecologist who studies how interactions between macroorganisms and microbes affect seaweed forests in natural and urban environments, and uses this information to advise management practices, particularly ecological restoration.

Dr Allison McInnes
Research Fellow

University of Technology Sydney

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Allison is a biological oceanographer studying phytoplankton community (and associated microbial community) composition and function and incorporating this into understanding of biogeochemical cycles. She is particularly interested in the origin, transfer and fate of carbon in the marine environment and the role it plays in both climate change and fisheries production. She has utilised and developed techniques to elucidate microbial and phytoplankton community composition and function, allowing hypotheses of their effect on carbon cycling through diverse environments, from fjords to the open ocean.

Dr Deirdre Mikkelsen
Research Fellow

University of Queensland

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Deirdre has expertise in gut fermentation microbiology and molecular microbial ecology. She received her PhD in microbiology from the University of Queensland in 2005, worked at the Advanced Water Management Centre (UQ) before moving to the Centre for Nutrition and Food Sciences in 2006. Since then, she has worked on modelling plant cell walls of cereals and grasses, developing molecular microbiology techniques to investigate gut microbe – dietary fibre interactions, and investigating the fermentability of cell wall components. Deirdre is currently the Queensland branch treasurer of the Australian Society for Microbiology.

Dr John Moreau
Senior Lecturer

University of Melbourne

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John earned his PhD in 2006 from the University of California–Berkeley, and then served as an NRC Fellow at the USGS until 2008, when he relocated to Australia to take up his current position. He leads the Melbourne Geomicrobiology Lab, which seeks to understand the ecology and evolution of microbe–metal interactions and their impacts on the environment.

Dr Katharina Noske
Postdoctoral Researcher

University of Queensland

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Katharina has a BSc in applied biology and a master's degree in molecular biology. She completed her PhD at the German Cancer Research Center in Heidelberg. She recently moved to Brisbane and is now a postdoctoral researcher in Ian Frazer's lab. Her research interests are skin and skin cancer.

Dr Páraic Ó Cuív
Research Fellow

University of Queensland

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Páraic is an expert in gut microbiology and has a long-standing interest in dissecting host–microbe interactions as they relate to the aetiology of chronic gut diseases. He received his PhD specialising in microbiology and bacterial genetics from Dublin City University, Ireland. Páraic isolated and characterised the genomes of the first fastidious gut bacteria to be isolated from Australian subjects in support of the International Human Microbiome Consortium. Now, as a research fellow at the University of Queensland Diamantina Institute, he combines genetic and functional omic approaches to identify and characterise novel immunomodulatory bacteria.

Dr Claire O'Brien
NHMRC Peter Doherty Biomedical Research Fellow

Australian National University

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Claire is an NHMRC Peter Doherty Biomedical Research Fellow at the Australian National University Medical School, based at Canberra Hospital. Claire's main research interests include host–microbiome interactions in Crohn's disease, understanding how perturbations of the gut microbiota relate to health and disease, and the genetics of *Escherichia coli*. Claire was awarded her PhD in 2012 for her work on the microbiological aspects of Crohn's disease. During her honours year she investigated the effect of diet and gut dynamics on the establishment and persistence of *E. coli*. Claire is a 'local champion' for Crohn's & Colitis Australia (CCA).

Dr Yui Osanai
Research Fellow

University of New England

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Yui is a post-doctoral research fellow at the University of New England, currently working on a project that aims to characterise the quantity, distribution and mechanisms of soil C and N turnover under contrasting cotton farming systems. Her research interests are focused on understanding nutrient cycling, soil microbial community and function under environmental changes (e.g. elevated CO_2, temperature and extreme weather events) and their interactions with plant communities.

Ms Talia Palacios
PhD Candidate

University of Sydney

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Talia is a PhD candidate at the Boden Institute of Obesity, Nutrition, Exercise and Eating Disorders, University of Sydney. She completed a bachelor degree in nutrition, a bachelor degree in psychology and a masters degree in dietetics at the University of San Francisco de Quito, Ecuador. Talia has 10 years of experience in clinical practice. Her current research area of interest is the relationship between the gut microbiome and obesity-related disorders. The aim of her PhD project is to evaluate the efficacy of an evidence-based multi-strain probiotic on metabolic biomarkers associated with type 2 diabetes.

Dr Nicole Patten
Microbial Ecologist

South Australian Research Development Institute

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Nicole is a microbial ecologist and biological oceanographer working at the South Australian Research and Development Institute. Her current research focuses primarily on the understanding of the influence of microbial and planktonic ecology, and their coupling with oceanographic processes, on ecosystem functioning and productivity. She has studied the spatial and temporal distributions of microorganisms and their roles in tropical through to temperate waters, with current work focused on coastal through to offshore waters of Southern Australia. Nicole has participated in numerous oceanographic voyages. Previous work as part of her PhD research involved studying viruses in coral reef ecosystems.
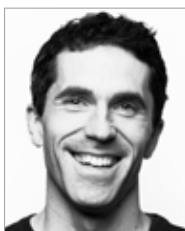
Associate Professor Jeff Powell
Member of the Organising Committee
Associate Professor

Western Sydney University

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Jeff is an Associate Professor of Ecological Bioinformatics and Deputy Leader for the Soil Biology and Genomics Theme within the Hawkesbury Institute for the Environment. He obtained his PhD from the University of Guelph, Canada and completed a postdoctoral fellowship at the Freie Universitaet Berlin before moving to Western Sydney University in 2011. Jeff is also an Editor-In-Chief of *Pedobiologia—Journal of Soil Ecology*.

Dr Shane Powell
Research Fellow

University of Tasmania

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Shane is a research fellow in the Tasmanian Institute of Agriculture at the University of Tasmania. After graduating with her PhD she was a visiting scholar at the University of Saskatchewan and worked for the (now) Department of Environment and Energy on microbial ecology of contaminated soils and sediments before taking up her current position. She is a molecular microbiologist who uses DNA-based methods to study the diversity and processes of microbial communities. Her current research is focused on microbiology in the food supply chain.

Associate Professor Michelle Power
Senior Lecturer

Macquarie University

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Michelle's research focuses on using symbiotic interactions to measure human impacts to fragile systems. The emphasis of her research was initially on protozoan parasites in single hosts, now her group uses multiple bacterial and parasitic targets to study systems. Within this framework her group addresses questions on emerging disease, wildlife health, co-evolution, adaptation, diversity, taxonomy and epidemiology. As a passionate teacher and postgraduate supervisor, Michelle seeks to engage undergraduate students through real-world research-orientated activities and ensure that her research students are well supported and mentored over the length of their study. Importantly, she still makes time among the diverse academic roles to get into the lab.

Dr Monica Prakash
Research Officer

Victoria University

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Monica's background is in immunology and cell biology, having completed a PhD in immunology at Monash University in 2013. Her doctoral thesis, 'The role of extracellular granzyme B in cytotoxic lymphocyte migration', demonstrated a novel role for the cytotoxic protease granzyme B in lymphocyte migration to target tissues during the viral immune response. Her current work uses animal models to examine how changes in intestinal permeability can cause gut proteins to leak into the bloodstream and enter the brain, causing inflammation. These studies incorporate expertise in immunology, neuroscience and gastrointestinal dysfunction and the complex interplay between these systems.

Dr Mark Read
Research Fellow

University of Sydney

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Mark is an interdisciplinary researcher spanning computer science and biology. He was awarded his PhD in 2012 by the University of York, UK, for work advancing the investigation of biological systems through simulation and statistics. He had a brief foray into swarm robotics whilst at York. He moved to the University of Sydney's Charles Perkins Centre in 2013 as an independent researcher. He has expanded into simulating the gut microbiota's response to diet, leukocyte motility patterns, and the application of machine learning to high throughput datasets in a clinical setting.

Associate Professor Geraint Rogers
Director of Microbiome Research

South Australian Health and Medical Research Institute

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Geraint is the Director of Microbiome Research at the South Australian Health and Medical Research Institute, Adelaide, and an Associate Professor at the Flinders University School of Medicine. Geraint leads a research group whose focus is the influence of host-microbiome interactions of human pathophysiology, with a particular interest in immune and metabolic regulation in chronic inflammatory conditions. He has a wide range of respiratory research interests, including early-life microbial determinants of long-term health, the role of the gut microbiome in respiratory and cardiometabolic disease outcomes, and the development of novel microbiome-targeted treatment strategies.

PARTICIPANTS

Dr Carly Rosewarne
Member of the Organising Committee
Research Scientist

CSIRO

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Carly works at CSIRO in Adelaide, where she provides capabilities in microbiology and metagenomics to understand the interplay between diet, gut microbiota and human health. She is currently focused on a collaborative project to investigate the efficacy of faecal microbiota transplantation for treatment of ulcerative colitis. Carly has developed novel approaches to study methane-producing microbes in the rumen of livestock, and in 2015 was awarded a Fulbright Professional Scholarship to further this research. She is a member of the Australian Academy of Science EMCR Forum Executive and is passionate about changing our national research environment through advocacy and engagement.

Dr Alexandra Roth Schulze
Postdoctoral Fellow

Walter and Eliza Hall Institute of Medical Research

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Alexandra obtained a degree in genomic sciences at the National Autonomous University of Mexico in 2010. This program integrates mathematics, bioinformatics and molecular biology. In December 2015, she was awarded a PhD degree in biochemistry and molecular genetics with the thesis 'Functional diversity and host-specificity of macroalgal surface-associated marine bacteria', which she conducted at UNSW Australia. She currently has a postdoctoral position at the Walter and Eliza Hall Institute investigating how gut and vaginal microbiomes contribute to or protect against islet autoimmunity and progression to Type I Diabetes.

Dr Talitha Santini
Senior Lecturer

University of Queensland

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Talitha is a Senior Lecturer in Environmental Management at the University of Queensland, and her research interests include geomicrobiology and microbial ecology, and soil formation and development. Her research addresses the interface between microbiology and Earth surface processes, focusing on the interactions between abiotic and biotic weathering processes acting upon bedrock to form soils and sediments, and how these interactions influence global biogeochemical cycles. Her research projects encompass both natural and engineered environmental systems, spanning timescales of decades to millennia, to understand their responses to global change and human-imposed perturbations such as agriculture and mining.

Dr Erin Shanahan
Research Fellow

Princess Alexandra Hospital — Translational Research Institute

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Erin gained a degree in science and university medal from the University of Sydney. This was followed by a PhD in molecular microbiology and bacterial pathogenesis in the Mycobacterial Research Laboratory, at the Centenary Institute, Sydney. She now works as a gastroenterology research fellow at Princess Alexandra Hospital and the University of Queensland. Her current research focus is on the role of the gut microbiota in the upper gastrointestinal tract, and through a combination of molecular and culture-based methods, is investigating host–microbe interactions in functional gastrointestinal disorders.

Dr Dragana Stanley
Senior Lecturer

Central Queensland University

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Dragana is a senior lecturer in molecular microbiology at Central Queensland University. She is an ARC DECRA fellow with strong research interest in the role of intestinal microbiota in health and performance. Her research projects span human and agricultural animals' health.

Dr Sasha Tetu
DECRA Fellow

Macquarie University

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Dr Sasha Tetu is a molecular microbiologist and DECRA Fellow at Macquarie University, Sydney. She obtained a PhD from the University of Sydney for research into the interactions of different mobile genetic elements within bacterial genomes. As a postdoctoral researcher she utilised a variety of omics techniques to better understand the biology of microorganisms involved in disease, and industrial and agricultural processes. Her current research efforts focus on understanding the genetic basis for microbial adaptation to environmental pressures and how environmental perturbations impact microbial communities.

PARTICIPANTS

Professor Luis Vitetta
Member of the Oversight Committee
Director of Medical Research

University of Sydney and Medlab Clinical Ltd

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Luis is currently Adjunct Professor at the University of Sydney, Sydney Medical School and Director of Medical Research at Medlab Clinical in Sydney. He is a clinical epidemiologist with expertise in conducting clinical trials with research interests in probiotics/prebiotics and the human microbiome, immune function, herbal medicines and nutrition. He is a graduate in biochemistry from Monash University and obtained his PhD from the University of Melbourne's Faculty of Medicine, Department of Surgery where he studied the epidemiological and aetiological factors of biliary disease. He has also studied medicine in his native Argentina.

Dr Karen Westwood
Scientist

Australian Antarctic Division

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Karen has worked as an aquatic microbial ecologist in a wide range of environments, from open ocean and coastal waters to estuaries and freshwater. Since completing her PhD in 2003 she has been employed at the Australian Antarctic Division. Her research focuses on the marine microbial loop in the Southern Ocean and Antarctic coastal waters, as part of the Southern Ocean Ecosystems and Change Program. The role of her group is to elucidate biogeochemical processes that drive the microbial loop, as well as to undertake long-term monitoring to detect change. Her group has also conducted extensive experimental work using minicosms to determine the effects of ocean acidification on microbial community structure. She has participated in eight marine science voyages and also spent six months on the Antarctic continent to undertake her research.

Dr Laura Weyrich
Member of the Organising Committee
ARC DECRA Fellow

University of Adelaide

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Laura obtained a PhD from The Penn State University, US, in 2012, and moved to Australia to lead the Ancient Metagenomics Research Group at the Australian Centre for Ancient DNA at the University of Adelaide in 2012. In 2015, Laura obtained a prestigious ARC DECRA fellowship, aimed at reconstructing the diversity of human microbiota around the world, especially in Indigenous people. During her career, she helped establish calcified dental plaque (calculus) as the only fossil record of human microbiota in existence, and was the first person to reconstruct the microbiome of an extinct hominid.

Dr Connie Wong
Research Fellow

Monash University

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Connie is a Heart Foundation Future Leader Fellow and currently leads a research team in the Centre for Inflammatory Diseases at Monash University. Her team uses cutting edge in vivo imaging techniques to directly visualise and study the immune processes involved in inflammation in both infectious and non-infectious models. Current work focuses on the mechanisms that underlie immune impairment after stroke and to identify strategies to strengthen the host immune defense against infection and modulate inflammation.

Dr David Wood
Postdoctoral Research Fellow

University of Queensland

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David completed his undergraduate studies at the Australian National University in 2003 and then worked as a bioinformatician until 2010 when he undertook a PhD in mammalian transcriptomics and genome informatics at the Queensland Centre for Medical Genomics under the supervision of Professor Sean Grimmond and Dr Nicole Cloonan. David is now a post-doctoral researcher supervised by Professor Phil Hugenholtz at the Australian Centre for Ecogenomics, UQ, studying host-associated clinical microbial ecology. He is engaged by genomics of all domains, the computational analysis of rich data sets, and has a habit of finding almost anything fascinating.

Dr Stephen Woodcock
Lecturer

University of Technology Sydney

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Stephen is an applied mathematician with a background in theoretical ecology and environmental engineering. His primary research interests are focused on modelling how natural and engineered ecosystems can provide important functions for mankind and the wider environment.

NOTES

ARE YOU A MEMBER OF THE EMCR FORUM?

The Australian Early- and Mid-Career Researcher (EMCR) Forum is the national voice of Australia's emerging scientists, representing researchers who are up to 15 years post-PhD (or other research higher degree), irrespective of their professional appointment.

The EMCR Forum examines critical issues including career structure, job security, funding, education, training and gender equity. It engages with early- and mid-career researchers (EMCRs) from around Australia and advises the Australian Academy of Science on issues relevant to EMCRs, to help inform its policy recommendations to government and develop its EMCR activities. It also liaises with other national organisations to positively contribute to both Australia's scientific research and the future careers of emerging research experts. The Forum provides a vital connection between Australia's most eminent scientists and tomorrow's future scientific leaders.

You can join the EMCR Forum as a member at any time and join your voice with thousands of other EMCRs around the country to create positive changes for your career. The EMCR Forum is run by an executive of 10 EMCRs and positions on the executive are advertised each year in October.

Why join?

- To stay informed about issues relevant to EMCRs and to voice your opinions and help create change

- To hear about awards, funding and educational opportunities for EMCRs

- To have the opportunity to attend EMCR-specific events held by the Australian Academy of Science such as Science Pathways, Theo Murphy High Flyers Think Tanks and Australian Frontiers of Science symposiums.

How to join?

- Find out more about the Forum and sign up online: www.science.org.au/emcr-forum

- Follow @EMCRForum on Twitter or Email us at emcr@science.org.au

- Talk to Carly Rosewarne, a member of the EMCR Forum executive, who is also a member of the organising committee for this event

- Talk to Sandra Gardam, the EMCR Project Officer at the Australian Academy of Science

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