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70 years

NZMS2025 
CONFERENCE

ROTORUA 17-20 NOVEMBER

Programme and Abstracts

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Plenary Speakers



Gavin Lear – Microbial Ecology and Evolution

Gavin is President of the New Zealand Microbiology Society and a leading researcher in microbial ecology, employing modern molecular tools to conduct a wide range of investigations across microbial ecology, biotechnology, and environmental science. His work focuses on the complex interactions among microbial communities and the diverse environments they inhabit. A central aim of his research is to use microbial responses to environmental disturbances such as plastic pollution as quantitative indicators of human impact on New Zealand's fragile soil, freshwater, and marine ecosystems.



Anna-Louise Reysenbach - Microbial Ecology & Evolution

Anna-Louise is an extremophile microbiologist at Portland State University, USA, where she is an emeritus professor. Anna-Louise is one of the foremost experts on deep-sea vent microbiology and high temperature terrestrial hot springs (including those in NZ). Her extensive research in this area includes the discovery and cultivation of novel thermophilic archaea, the ecology of hydrothermal and geothermal systems, and global patterns in hydrothermal vent biodiversity.



Sam Abraham - One Health

Professor Sam Abraham is a microbiologist and the Director of the Centre for Biosecurity and One Health at Murdoch University's Harry Butler Institute. He founded the Antimicrobial Resistance and Infectious Diseases (AMRID) Laboratory, where his research focuses on antimicrobial resistance (AMR) in zoonotic pathogens that can be transmitted between animals and humans. Prof. Abraham's work is pivotal in understanding and mitigating the spread of AMR, which poses a significant global health threat. His research integrates a One Health approach, recognizing the interconnectedness of human, animal, and environmental health in combating infectious diseases.



Carolina Tropini - Human and Medical Microbiology

Carolina is a human gut microbiologist and Assistant Professor at the University of British Columbia, where she is also a Paul Allen Distinguished Investigator, a Johnson & Johnson Women in STEM2D Scholar in the field of Engineering, a CIFAR Fellow in the Human & the Microbiome Program and a Michael Smith Foundation for Health Research Scholar. Carolina's research investigates the microbial response to perturbations during disease, such as inflammatory bowel disease, and the spatial organisation of microorganisms in the gut.



David Hayman - Animal-Microbe Interactions

David is an epizootic epidemiologist at Massey University, Palmerston North, where he holds the Percival Carmine Chair in Epidemiology and Public Health and Professor of Infectious Disease Ecology. He is also co-Director of the Molecular Epidemiology and Public Health Laboratory (mEpiLab), and his research focus is on human infectious disease and microbial transmission, and includes the identification of transmissions between wild and domestic animals and humans and pathogen reservoirs.

NZMS 2025 Orator



Mike Taylor - Microbial Ecology

Mike is a microbial ecologist at the University of Auckland. His research specialises in host-microbiome associations. He has considerable expertise in a range of host-microbiome systems, including those involving sponges, humans, animals and even insects. Mike's research contributes to our understanding of the diversity across these systems, the roles of microbiomes in human health (e.g., diet and respiratory illness), and has implication for the management of endangered animal species. Notably, recent research from Mike's group has also illustrated the extraordinary novelty of the microbiomes of a number of endangered or at-risk animal species, including the kākāpō and tuatara.

Invited Speakers

Steve Flint

Food Microbiology/Safety
Massey University

Augusto Barbosa

Human Microbiology and Parasitology
University of Auckland

Jemma Geoghegan

Animal-Microbe Interactions and Virology
University of Otago

Nikki Freed

Bioinformatics
Auckland Genomics, University of Auckland

Christine Voisey

Plant-Microbe Interactions
Bioeconomy Science Institute

Craig Herbold

Microbial Ecology and Evolution
University of Canterbury

Ian Dickie

Mycology
University of Canterbury

Robin MacDiarmid

Virology
Bioeconomy Science Institute/University of
Auckland

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SCIENCE



Programme

Day 1 – Monday 17th November

Time	Rutherford	Batten 2
14:00	<i>Registration opens in the Exhibition Foyer</i>	
15:00		Student Oral Competition (3-minute talks)
17:00	<i>Welcome Reception in the Exhibition Foyer</i>	
18:00	Opening Remarks – Kim Handley and Syrie Hermans	
18:15	Opening Plenary – Gavin Lear When small things matter: how microbes adapt to our polluted planet	
19:10	End of Day 1	

Day 2 – Tuesday 18th November

Time	Rutherford	Batten 2
08:00	<i>Registration Desk and Trade Exhibits Open in the Exhibition Foyer</i>	
08:35	Mihi whakatau – Selwyn Insley	
08:45	Plenary 1 – Anna-Louise Reysenbach The microbial diversity and ecology of high temperature ecosystems <i>Chaired by Carlo Carere and Matt Stott</i>	
	Session 1: Microbial Ecology and Evolution <i>Chairs: Carlo Carere and Matt Stott</i>	Session 2: Food and Public Health Microbiology <i>Chair: Brent Seale</i>
09:45	Jean Power A genus in the bacterial phylum Aquificota appears to be endemic to Aotearoa-New Zealand	Invited - Steve Flint Biofilm Development and Control in the Food Industry – Key outcomes from the Massey University Research Team 2015-2025
10:00	Paul Battersby Genomic adaptations of ammonia oxidising microbes in diverse geothermal hot springs	
10:15	<i>Morning Tea in the Exhibition Foyer – NZMS 70th Birthday Cake</i>	
	Session 1: Microbial Ecology and Evolution <i>Chairs: Carlo Carere and Matt Stott</i>	Session 2: Food and Public Health Microbiology <i>Chair: Stephen On</i>
10:45	Meghan Marshall The Physiological, Metabolic, and Transcriptomic Responses of the Endemic Thermophilic Bacterial Genus <i>Venenivibrio</i> to Environmental Stress	Kevin Keener Inactivation of <i>Aspergillus flavus</i> and Aflatoxin B1 on Inoculated Raw Peanuts with High Voltage Atmospheric Cold Plasma
11:00	Nicholas Dragone Isolation of thermophilic plastic degrading bacteria from hot springs of Aotearoa New Zealand	

Time	Rutherford	Batten 2
11:15	Jacob Scadden The evolution and adaptation of the bacterial flagellar filament	Srinithi Muthuraman The air-liquid interface: a focal point for EPS overproduction and biofilm architecture.
11:30	Mick Adriaansens The taxonomic distribution of the Cation Proton Antiporter; the most prevalent and abundant Na ⁺ /H ⁺ antiporter across all taxa	Krishna Pant Friends Under Flow: <i>Listeria</i> stress adaptation in single and dual species biofilm
11:45	Sarah Manners Exploring Microbial Metabolism of Volatile Sulfur Compounds in Geothermal Hot Springs	Julie Warren Rapid Commercial Sterility Testing of UHT Dairy Products: Method Comparison and Optimisation
12:00	Yapeng Lai MtCLR-2 Regulates Cellulase Production via Mtegl2 and Mtbgl1 in <i>Myceliophthora thermophila</i>	Yuwei Zhang Into the blue: phylogenetic and phenotypic characterisation of <i>Vibrio vulnificus</i> isolates from New Zealand shellfish
12:05	<i>Lunch in Atlas Restaurant</i>	
13:00	Plenary 2 – Sam Abraham Robotic Antimicrobial Susceptibility Platform (RASP): Transforming AMR Surveillance through Automation and Scale <i>Chaired by Brent Seale</i>	
	Session 1: Microbial Ecology and Evolution <i>Chair: Kim Handley</i>	Session 2: Human and Medical Microbiology <i>Chair: David Broderick</i>
14:00	Invited - Craig Herbold Twenty Years on the Ice: Unveiling the Microbial Mysteries of Mt. Erebus	Invited - Augusto Barbosa Microbial competition-cooperation as opposing ecological drivers reshaping the human vaginal microbiome
14:30	Kelsey McKenzie Local diversity in a global context: microbial communities in Aotearoa-New Zealand hydrocarbon reservoirs and their impacts on hydrogen geostorage	Zoe King Investigating the Fibrotic Phenotype of Liver Cells during <i>Bartonella</i> Infection.
14:45	Karen Houghton National patterns of diversity and metabolism of microbial communities in groundwater ecosystems	Valter Almeida Metagenomic analysis of <i>Campylobacter</i> at a wildlife–livestock–human interface in Uganda reveals novel species associated with human disease
15:00	Janani Rajpirathap Evolutionary Insights into Cyanophycin Genes in Toxic and Non-Toxic <i>Microcoleus</i> Strains	Sarah Hannah Integrating Genomics and Epidemiology to Investigate the 2018 W:CC11 Meningococcal Outbreak in New Zealand
15:15	Sophie van Hamelsveld Enrichment and characterisation of cable bacteria from a New Zealand estuary and their potential application in denitrifying bioreactors	
15:30	<i>Afternoon tea in the Exhibition Foyer</i>	

Time	Rutherford	Batten 2
	Session 1: Plant-Microorganism Interactions <i>Chair: Darryl Herron</i>	Session 2: Human and Medical Microbiology <i>Chair: Kristi Biswas</i>
16:00	Manpreet Dhami Invisible Influencers – How flower yeasts mediate pollinator behaviour?	Richard Cannon Importance of the membrane environment for fungal drug efflux pump function
16:15	Hanareia Ehau-Taumaunu Within site and geographic location of Maire Tawake (<i>Syzygium maire</i>) are significant contributors to its leaf microbiome	Nicholas Heng Staphylococcin YAS1, a new antibiotic bacteriocin produced by <i>Staphylococcus aureus</i>
16:30	Natalie Graham Host genetic influences on the root microbiomes of conifers	David Broderick Unravelling the complexity of <i>Staphylococcus aureus</i> in Chronic Rhinosinusitis
16:45	Sarah Addison Microbiomes on the move: Interspecific selection and local adaptation drive <i>Pinus radiata</i> root microbiome symbiosis.	Megan Koschany Re-evaluating postoperative antibiotic use in Chronic Rhinosinusitis: A microbiome perspective
17:00	Jewel Roch Illuminating the microbiomes of native New Zealand mosses using 16S rRNA gene sequencing	Riya Balia Development of an ex vivo porcine wound infection model to evaluate antibiofilm therapies
17:05	Folau Langi Yeast diversity associated with New Zealand Beech trees.	
17:15	<i>Poster Session 1 in Rutherford with refreshments in the Exhibition Foyer</i>	
18:15	<i>End of Day 2 (Student Function @ 19:00 - Our Backyard Pub)</i>	

Day 3 – Wednesday 19th November

Time	Rutherford	Batten 2
08:15	<i>Registration Desk and Trade Exhibits Open in the Exhibition Foyer</i>	
08:45	Plenary 3 – Carolina Tropini The role of the gut environment in shaping the intestinal microbiota and disease outcomes <i>Chaired by Carmen Hoffbeck</i>	
	Session 1: Microbial Ecology and Evolution <i>Chair: Syrie Hermans</i>	Session 2: Food and Public Health Microbiology <i>Chair: Brent Seale</i>
09:45	Invited – Ian Dickie The myco-biology of plant invasion: co-invasions, novel associations, enemy accumulation and pathogen spillover	Jens Andre Hammerl Population dynamics in a biofloc aquaculture: ‘What happens in an aquaculture stays in an aquaculture’
10:00		Graham Fletcher International development programme achieves dramatic improvements in the microbiological safety of eaten-raw vegetables in Cambodia
10:15	<i>Morning tea in the Exhibition Foyer</i>	

Time	Rutherford	Batten 2
	Session 1: Microbial Ecology and Evolution <i>Chair: Syrie Hermans</i>	Session 2: Food and Public Health Microbiology <i>Chair: Steve Flint and Graham Fletcher</i>
10:45	Marcus Francis Genetic divergence of non-toxic and toxic <i>Microcoleus</i> leading to vitamin auxotrophy	Xiaodong Guo Phenotype and Elastic Light Scatter Characteristics of Clinical and Environmental Strains of <i>Vibrio Parahaemolyticus</i> from New Zealand
11:00	Nilukshi Muthuthanthrige Variation in soil microbial composition and functional potential with <i>Pinus radiata</i> stand age	Sana Bari A Probabilistic Approach to the Analysis of Elastic Light Scatter Profiles for the Identification of Foodborne Bacteria
11:15	Ziva Louisson Microbial trait and community shifts at the forest-grassland edge	Thi-Van Nguyen Unveiling the biofilm control potential of bacteriocin produced by <i>Pediococcus acidilactici</i> PaN4 and nisin.
11:30	Freya Newton Elevated CO ₂ and Grazing Restructure Microbial Networks in Grasslands: Trade-offs of Connectivity and Modularity	Aline Parolin Calarga Characterisation of mobile elements of <i>Campylobacter jejuni</i> and coli in New Zealand
11:45	Barry Palmer Microbes, Metals, Mud & Metagenomics. Heavy metal contaminants as environmental drivers of AMR in agricultural soil.	Stephen On What's this?! Identification challenges for taxonomically complex bacteria – the <i>Vibrio</i> exemplar that revealed new aquacultural pathogens in New Zealand
12:00	<i>Lunch break (not provided)</i>	
13:15	Plenary 4 – David Hayman Pathogen transmission and gut microbiomes at the human, animal, and environmental interface in Uganda <i>Chaired by Richard Cannon</i>	
	Session 1: Animal-Microorganism Interactions <i>Danielle Middleton</i>	Session 2: Human and Medical Microbiology <i>Chair: David Broderick</i>
14:15	Invited - Jemma Geoghegan Exploring Aotearoa's Virosphere	Invited – Nikki Freed Genetic and epigenetic dynamics of streptomycin resistance revealed by experimental evolution and direct RNA sequencing
14:45	Heather Hendrickson Phage-Based Biocontrol of American Foulbrood in Honeybees: The ABAtE Project	Le Tuong Van Vo Antimicrobial Peptide-Coated Dermal Substitute Eradicates Infection by Targeting Polymicrobial Biofilms and Immunomodulation in Wound Infection Models
15:00	Jieyun Wu Moving beyond taxonomic descriptions: dietary-dependent microbiota-metabolome interactions reveal often-overlooked impacts of artificial diets on laboratory-reared caterpillars	Mathilda Saunders Exploring the potential of vitamin B12-antibiotic conjugates to combat antimicrobial resistance in Gram-negative bacteria of WHO critical concern.

Time	Rutherford	Batten 2
15:15	Carmen Hoffbeck Response of the tuatara gut microbiome to dietary manipulation and captivity	Keely Oldham Identification of novel inhibitors targeting serine acetyltransferase from <i>Neisseria gonorrhoeae</i>
15:30	Amber Kanis The Role Of Kākāpō Nest Mycobiota in Shaping <i>Aspergillus spp.</i> Abundance and Pathogenic Potential	Saurab Munshi Exploring the Metabolic Secrets of <i>Haemophilus influenzae</i> : Does Ribose Utilization Contribute to Its Virulence and Persistence?
15:45	<i>Afternoon tea in the Exhibition Foyer</i>	
16:15	Student Oral Competition Finalists <i>Chaired by Manpreet Dhani</i>	
17:15	<i>Poster Session 2 in Rutherford with refreshments in the Exhibition Foyer</i>	
18:15	<i>End of Day 3 (Conference Dinner @ 19:00 - Stratosphere)</i>	

Day 4 – Thursday 20th November

Time	Rutherford	Batten 2
09:00	<i>Registration Desk and Trade Exhibits Open in the Exhibition Foyer</i>	
	Session 1: Animal-Microorganism Interactions <i>Chair: Heather Hendrickson</i>	Session 2: Plant-Microorganism Interactions <i>Chair: Ian Dickie</i>
09:00	Stephen On Prevalence and distribution of <i>Bifidobacterium animalis</i> subsp. <i>animalis</i> in domestic and production animals in Canterbury, New Zealand	Invited - Christine Voisey How plant-microbe partnerships have shaped agriculture
09:15	Samantha Stevenson Diet and digestive strategy shape the hindgut microbiome in New Zealand marine herbivorous fish	
09:30	Amali Thrimawithana Role of temperature on the gut microbiota in the marine teleost snapper (<i>Chrysophrys auratus</i> , tāmure) in captivity and the wild	Bevan Weir Global diversity analysis of plant-associated <i>Pseudophthomyces</i> fungi associated with facial eczema in livestock
09:45	Stephen Archer Rumen adapted for future feeds to improve animal health and performance	Mahnoor Hayat Soil Microbial Responses to Organic Inputs Under Pathogen Stress: Implications for Disease Suppression
10:00	Sinisa Vidovic Integrated microbiome-proteome analysis identifies key factors associated with the low abundance of <i>Vibrio parahaemolyticus</i> in green-lipped mussels (<i>Perna canaliculus</i>)	Darryl Herron How sterile is “sterile”? Exploring the microbiome of tissue-cultured plants
10:15	Aymee Lewis Lighting the Way: Bioluminescent Huakita for Feed Visibility.	
10:20	<i>Morning tea in the Exhibition Foyer</i>	

Time	Rutherford	Batten 2
10:50	Invited - Robin MacDiarmid Botrytis cinerea for global mycovirus study: what do you need? <i>Chaired by Bevan Weir</i>	
11:20	NZMS Orator – Mike Taylor Love and other relationships: animals and the microbes they live with <i>Chaired by Manpreet Dhani</i>	
12:20	Conference closing – Gavin Lear	
12:30	<i>End of Conference</i>	









Poster Presentations

Posters are displayed in the Rutherford Room

● Food & Public Health
 ● Ecology & Evolution
 ● Human & Medical
 ● Plant-Microorganism
● Biotechnology
 ● Eukaryotes

	Poster	Presenter	Topic	Title
Poster Session 1 - Tuesday	1	Nikolai Pavlov	●	Can <i>Thermus</i> revolutionize plastic bioremediation like it transformed molecular biology?
	3	Thilina Herath	●	Enteropathogenic <i>E. coli</i> Subverts Host Exocytosis to Promote Pedestal Formation
	5	Yining He	●	Plasma-Activated Water for <i>Controlling Listeria monocytogenes</i> Biofilm: Effect on Viable Cells and Extracellular Polymeric Substances Matrix
	7	Kirill Bogdanov	●	Fungal communities in New Zealand pasture soils show stronger response to historical rainfall patterns than prokaryotes
	9	Bolin Li	●	Preliminary metagenomics evaluation of biofilm microbiota on raw milk bulk tanks
	11	Max Pizarro	●	<i>Tenacibaculum maritimum</i> in Aotearoa-New Zealand salmon industry presents a problem for the future of aquaculture
	13	Hansani Senarath Pathirana	●	Influence of seawater based medium on biofilm robustness in <i>Vibrio parahaemolyticus</i> : implications for seafood safety
	17	Kevin Keener	●	Sterilization of <i>Bacillus atrophaeus</i> (BA) spores on surgical stainless-steel scalpels using high voltage atmospheric cold plasma (HVACP) treatment
	19	Dinendra Dhanapala	●	Isolation And Characterization Of Novel <i>Acidithiobacillus</i> Strains From The Taupo Volcanic Zone (TVZ)

Poster Session 1 - Tuesday	21	Krishna Kansagra	●	Metabolites from endophytic fungi
	1	Megan Addison	●	Inducing single-cell morphology in naturally aggregating rumen <i>Methanosarcina</i> species
	25	Hazel Clemens	●	Geothermal springs as a novel platform for antibiotic discovery
	27	Nicola Jones	●	Specific Synbiotic Sugars Stimulate <i>Streptococcus salivarius</i> BLIS K12 and BLIS M18 Lantibiotic Production to Expand Bacterial Inhibition Range and Potency
	29	Stella Colquhoun	●	Investigating the in vivo efficacy of a novel antimicrobial agent
	31	Shuguang Zhang	●	Thriving without oxygen: Anaerobic culture at Callaghan Innovation
	33	Callum Lambert	●	Scaling science: From flask to factory
Poster Session 2 - Wednesday	2	Pasan Sepala Dahanayake	●	Enteropathogenic <i>Escherichia coli</i> (EPEC) exploits the host exocyst complex to augment pedestal formation
	4	Sanjay Biswas	●	Comparison of Biofire Film Array Blood Culture ID Panel with Conventional Methods of Identification of Pathogens and Antimicrobial Resistant Genes in Cancer Patients
	6	Emily Caldelari-Hume	●	Do mutations in <i>nuoG</i> impact the growth of the mouse gut pathogen <i>Citrobacter rodentium</i>
	8	Kirill Bogdanov	●	Microbial soil carbon sequestration under distinct precipitation patterns
	10	Dilushi Polegodage	●	Evaluation of the Synergistic Antibiofilm Activity of Nisin and Lysozyme against <i>Listeria monocytogenes</i> on Stainless Steel Surfaces
	12	Yapeng Lai	●	The transcription factor MtCLR-2 regulates cellulase production by directly modulating the expression of Mtegl2 and Mtbgl1 in <i>Myceliophthora thermophila</i>
	14	Nadija Palinich	●	Optimising elite athletic performance through the gut microbiome
	16	Bailey Dickson	●	Lysozymes as microbiome modulators: Molecular insights into <i>Trichomonas vaginalis</i> -bacteria interactions
	18	Mitankumar Vitthani	●	Forest Plant Root Endophytes:

Poster Session 2 - Wednesday	2	Carissa Huynh		The B12 Backdoor: Exploiting the B12-Uptake Pathway for Antibiotic Delivery
	22	Stella Pearless		Evolutionary Dynamics of rsmG-Mediated Streptomycin Resistance Revealed by Nanopore RNA Sequencing
	24	Kizzie Amoore		Decoding Microbial Dynamics on Seaweed: Implications for Process Optimisation and Quality Control
	26	Bevan Weir		International Collection of Microorganisms from Plants (ICMP)
	28	Marcus Francis		Genetic divergence of non-toxic and toxic <i>Microcoleus</i> leading to vitamin auxotrophy
	30	Shiroma Lenaduwa		Root endophytes from the kauri companion plant
	32	Josie Mainwaring		Peptones derived from protein-rich by-product streams for microbial fermentation
	34	Shivangi Singh		Creating the World's First ISO 17025-Accredited Remote Microbiological Testing Service

Abstracts – Plenaries

Gavin Lear

When small things matter: how microbes adapt to our polluted planet

Microbial communities are highly responsive to environmental change, yet their potential as indicators of ecosystem health and sustainability remains underexploited. My research examines microbial DNA as a tool for assessing ecological status across aquatic and terrestrial environments in Aotearoa New Zealand. Our analyses of DNA sequence data using machine learning models can provide accurate predictions of key land-use and soil properties, such as pH, bulk density, and microporosity. Collectively, our studies underscore the predictive value of microbial data as a tool for monitoring ecosystem health and assessing production potential, with implications for evaluating carbon cycling and methane mitigation.

Our recent work has focused on the interactions between microbes and marine plastics. We developed PlasticDB, a curated database of microorganisms and enzymes linked to plastic degradation, enabling genomic screening and functional prediction. Experimental deployments of plastics in marine environments confirmed rapid microbial colonisation but negligible polymer breakdown, suggesting that microbial responses to environmental plastics are driven by plastic leachates rather than solid polymers.

Collectively, these findings underscore the utility of microbial communities as sensitive indicators of environmental health and as predictive tools for soil and water quality assessment. Advances in nucleic acid sequencing and AI-driven modelling position microbial methods as attractive tools to support sustainable land management and pollution mitigation strategies, while also highlighting critical knowledge gaps in microbial adaptation to synthetic pollutants.

Anna-Louise Reysenbach

The microbial diversity and ecology of high temperature ecosystems

Over the past decades, terrestrial and deep-sea hot springs have continually challenged our understanding of the extent and limits of life. Studying these ecosystems has helped define and greatly expand the Tree of Life, and sparked our imagination of the origins of life in our solar system. In my talk I will demonstrate how using a combination of cultivation-dependent and molecular ecological approaches we have greatly increased the genomic biodiversity of Archaea and Bacteria. Further, using the deep-sea Brothers volcano north of New Zealand as a natural laboratory, we have shown that geological dynamics of high temperature ecosystems influence the diversity and assembly of microbial communities. Finally, I will come full circle and land back here at Tikitere, to show why it is important to cultivate some of these unusual hot spring thermophiles.

Robotic Antimicrobial Susceptibility Platform (RASP): Transforming AMR Surveillance through Automation and Scale

Effective antimicrobial resistance (AMR) surveillance in food-producing animals demands analytical capacity that far exceeds the limits of traditional microbiological workflows. To meet this challenge, the Robotic Antimicrobial Susceptibility Platform (RASP) was developed as an integrated, high-throughput system that unites sample processing, bacterial isolation, phenotypic and genotypic characterization, and real-time data analytics within a single automated pipeline. Built on a foundation of CLSI and ISO 20776-1:2019 compliance, RASP combines precision liquid-handling robotics, automated broth microdilution, MALDI-TOF identification, and next-generation sequencing to deliver scalable, reproducible, and standards-aligned AMR surveillance at unprecedented speed and depth.

The platform enables the processing and antimicrobial profiling of thousands of *Escherichia coli* and other indicator or pathogenic isolates per week, while supporting multi-pathogen applications across *Enterococcus*, *Campylobacter*, *Staphylococcus*, and *Salmonella*. Comparative validation against human-performed microdilution assays demonstrated 97% concordance and consistency within one doubling dilution across replicates, while achieving over tenfold gains in throughput and major reductions in labour and cost.

Large-scale RASP deployments in Australian poultry and pig industries illustrate its impact. In poultry, RASP enabled high-resolution quantification of resistance carriage across caecal samples and genomic tracing of fluoroquinolone-resistant *E. coli* lineages (ST354) likely introduced via international sources. In pigs, longitudinal RASP surveillance spanning over 900 samples from ten herds revealed dynamic temporal trends—persistence of ampicillin and tetracycline resistance, a decline in aminoglycoside resistance, and the emergence of extended-spectrum β -lactamase (ESBL) plasmids (*bla* CTX-M-1-Inc11) across genetically diverse *E. coli*. These insights demonstrate RASP's unique capacity to detect early warning signals of emerging AMR threats and to inform targeted interventions.

Beyond its surveillance role, RASP underpins a new ecosystem of integrated diagnostic and research tools for food safety, vaccine development, phage therapy, and drug discovery. By combining robotics, genomics, and advanced analytics, RASP represents a major step toward a unified, One Health-aligned framework for scalable, data-driven antimicrobial stewardship in animal and human health systems.

The role of the gut environment in shaping the intestinal microbiota and disease outcomes

In the intricate ecosystems of the human gut, physical forces profoundly shape the diverse consortium of microbes residing within, a subject of increasing interest in human biology and potential microbiota therapies. Despite advances in characterizing these microbial communities and their connections to health, the fundamental physical responses of this ecosystem—crucial for understanding disease impacts and therapeutic interventions—have been understudied. Diseases affect the gut's physical environment, altering osmolality through malabsorption, increasing temperature via fever and cancer, and modifying pH in bowel diseases. Moreover, the gut hosts highly diverse microbial populations within localized niches, each defined by unique physical conditions.

Our interdisciplinary research bridges ecology, microbiology, and biophysics to elucidate how changes in the gut microenvironment, driven by factors like drugs and diseases, influence microbiota dynamics and bacterial pathogenesis across the gut's biogeography. Our findings demonstrate that physical disruptions can significantly alter microbial function, enhancing bacterial pathogenesis or causing the loss of specialized commensals, with broad implications for host health. This work highlights the critical role of physical factors in microbial ecology, providing a foundation for novel microbiota therapies informed by the gut's physical landscape.

Pathogen transmission and gut microbiomes at the human, animal, and environmental interface in Uganda.

Gut microbiomes play a vital role in health and are shaped by diet, environment, and interactions with other species. Understanding microbial host-switching, including pathogen transmission, is key to mitigating health risks in human, domestic, and wildlife populations. This study examines human-animal contact networks and health within communities around Bwindi Impenetrable National Park (BINP), Uganda, integrating ethnographic, epidemiological, ecological, and molecular approaches.

A survey of 100 participants collected background data, self-reported health diaries, and stool samples for metagenomic analysis. Contact networks included humans, domestic, peri-domestic, and wild animals, identified through questionnaires and diaries. Ethnographic fieldwork provided insights into local perspectives on human-animal interactions. Over 2,400 bacterial metagenome-assembled genomes from ~600 human, livestock, and mountain gorilla microbiomes were analyzed to assess microbial sharing.

Participants frequently reported illness symptoms, with tiredness and headaches most common. Human-to-human contacts were most frequent, but direct interactions with livestock and peri-domestic animals were also high. While wildlife encounters were primarily observational, direct contact, including with gorillas, was reported. Gorillas engaged mainly in intra-species interactions but had contact with five other species, including humans and domestic animals. Shared bacteria, including antibiotic resistance genes, were detected across species, with community members reporting using antimicrobials against which microbes had resistance. *Campylobacter* is typically a zoonotic pathogen from livestock and poultry in high income countries, yet metagenomic analyses identified novel *Campylobacter* strains in asymptomatic people and other microbes absent in populations consuming industrialized diets.

Overall, the BINP community experiences frequent illness in an environment conducive to pathogen transmission. While infection sharing occurs, microbiomes remain largely host-specific, with commensal genera potentially pathogenic in other settings. These findings underscore the need for One Health approaches to address the complex interplay between human, animal, and environmental health, and highlight inequities in under-researched tropical regions.

Abstracts – Invited Speakers

Biofilm Development and Control in the Food Industry – Key outcomes from the Massey University Research Team 2015-2025.

Steve Flint (Massey University), Jon Palmer (Massey University)

Aim: This presentation provides an overview of some of the investigations from the Massey University Food Microbiology Biofilm research team from 2015-2025.

Methods: Methods used in the research specific biofilm culture methods such as Communicable Disease Centre (CDC) reactors, molecular techniques such as Q-PCR for gene expression, epifluorescence microscopy for biofilm morphology and biochemical analysis for metabolic assays such as enzyme production.

Results: Specific factors involved in biofilm formation include abiotic factors such as temperature, total solids and turbulence and divalent cations, in particular calcium. Biological factors include, gene expression, biofilm morphology and bacterial fingerprints. The microbial activity influenced by biofilm formation includes enzyme production, spore formation and toxin production. While most research has focused on single species, the interaction between different species in a biofilm is providing new challenges. Ultimately, the understanding around biofilm formation should lead to control strategies. Those showing most promise include enzyme cleaning and stress response on biological surfaces.

Conclusion: Factors having the greatest influence on biofilms across the food industry are temperature and di-valent cations. Interactions between different are also likely to be important.

Twenty Years on the Ice: Unveiling the Microbial Mysteries of Mt. Erebus

Craig Herbold (University of Canterbury)

Aim: Over the past two decades, studies on the microbial communities of Mt. Erebus, Antarctica's southernmost active volcano, have revealed unique microbial communities thriving in extreme environments. This talk will synthesise the findings thus far, beginning with insights from early small-scale studies and continuing with more recent regional studies.

Methods: The talk will primarily draw on data derived from amplicon-based surveys as well as that from shotgun metagenomic approaches.

Results: The geothermally heated soil environments of Mt. Erebus are diverse in physicochemical and thermal properties, resulting in stark contrasts in microbial assemblages. Exposed sites are warmest, with high numbers of cyanobacteria and complex community assemblages that are strongly correlated with pH and other soil parameters such as carbon, nitrogen, and sulfur content. The subsurface of some exposed sites appear to be dominated by a few heterotrophic organisms that appear to coexist through specialisation on different carbon sources. Ice caves host simpler communities dominated by organisms that may have novel RubisCO gene variants, suggesting that CO₂ fixation via the Calvin-Benson-Bassham cycle may be a key metabolic strategy in these dimly-lit, chemically reducing environments.

Conclusion: Together, these studies illuminate the unique evolutionary trajectories and functional adaptations of Mt. Erebus's microbial life, from fumarolic soils to subglacial ice caves. The talk will conclude with a forward-looking perspective on emerging technologies such as long-read sequencing, in situ metabolomics, and spatially resolved transcriptomics, which if carefully leveraged would deepen our understanding of these ecosystems and potentially their relevance to astrobiology and biotechnology.

Microbial competition-cooperation as opposing ecological drivers reshaping the human vaginal microbiome

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Aim: The human vagina represents a dynamic microbial ecosystem where host and microorganisms across kingdoms interact and shape community structure-function. With just over a decade of research, our studies are showing how microbial interactions in this important mucosal niche - involving the most prevalent non-viral sexually transmitted pathogen *Trichomonas vaginalis* and bacterial members of the vaginal microbiome - contribute to health and disease.

Methods: We employed co-culture and competition assays with *T. vaginalis*, lactobacilli, and BV-associated anaerobes; omics & gene-expression profiling; genetic modification; enzymatic assays; and epithelial cell barrier-integrity and adhesion models.

Results: *T. vaginalis* is strongly correlated to microbial shifts from *Lactobacillus* dominance to anaerobe-rich communities resembling bacterial vaginosis (BV). Our studies move from correlation to causation. The protozoan *T. vaginalis* not only thrives under these conditions but also actively participates in community remodeling through functional traits gained via horizontal gene transfer. The parasite acquired bacterial peptidoglycan hydrolases, enabling it to target lactobacilli and disrupt community structure. While *T. vaginalis* and host-protective lactobacilli exhibit competitive traits, the parasite engages in cooperative interactions with BV-associated anaerobes, enhancing dispersal and adhesion to host substrates. Moreover, *T. vaginalis* and BV-associated anaerobes thrive together in conditions non-permissive in isolation. Their co-growth is supported by a metabolic shunt toward amino acid catabolism, with activation of the arginine dihydrolase pathway and polyamine biosynthesis.

Conclusion: Collectively, our findings exemplify competition-cooperation as opposing ecological drivers reshaping a microbiome with the vaginal microbiome emerging as a valuable experimental system to examine cross-kingdom interactions, genetic and ecological feedback loops that impact on host-associated microbial ecosystems.

The myco-biology of plant invasion: co-invasions, novel associations, enemy accumulation and pathogen spillover

Ian Dickie (University of Canterbury)

Aim: Aotearoa NZ is one of the most invaded countries on Earth, with more invasive than native plant species. Invasive plants are frequently considered to experience 'enemy release', where reduced pathogen loads in the introduced range contribute to their success, while a lack of co-evolved mutualists is believed to limit success. I will discuss how 20 years of research into the mutualists and pathogens of exotic and invasive plants calls into question some of these long-held beliefs.

Methods: Using techniques ranging from DNA barcoding to large-scale experimental mesocosms and computer models, I will discuss how fungal communities shape plant invasions in Aotearoa, including examples from wilding pines and other species.

Results: Contrary to expectation, we show that ectomycorrhizal trees overcome symbiont limitation by co-invasion of co-evolved mutualists. Conversely, invasive plants show little sign of enemy release. Instead we find that the r-selected traits of invasive plants contribute to higher pathogen loads in exotic plants compared to natives. Despite high enemy loads, successful invasive plants can remain dominant due to high growth rates rather than lack of damage. Consequently, generalist herbivore and pathogen populations are amplified by invasives and can spillover onto native plants. Where this occurs, the generalist enemies of invasive plants may instead be hidden allies that amplify invader success and impacts.

Conclusion: Fungal mutualists and pathogens are key components of invasive plant success and impacts. Established frameworks seem to mischaracterize the role of fungal co-invasion and novel associations in driving plant invasions.

Exploring Aotearoa's Virosphere.

Jemma L. Geoghegan (University of Otago)

Aim: Aotearoa is a unique place to study viral evolution. Separated from Gondwana over 80 million years ago, many native hosts have lived in isolation, likely harbouring novel and highly divergent viruses. This fauna provides a natural experiment to evaluate the genetic and ecological parameters that shape viral evolution. The coexistence of native and invasive species, with a well-documented history of introductions, also presents an opportunity to determine the factors that drive viral host-jumping across ecological timescales.

Methods: We used metatranscriptomics to characterise viromes across a broad range of animal hosts, including birds, fish, reptiles, and mammals. This unbiased sequencing approach enabled the detection of both known and novel viruses, and facilitated assessments of viral diversity, evolutionary relationships and ecological associations.

Results: We identified hundreds novel and highly divergent viruses, greatly expanding the known virosphere of Aotearoa. Viral communities reflected host ecology and life history traits, while phylogenetic analyses revealed repeated host-jumping across species boundaries. Introduced hosts harboured viruses closely related to those in their native home range as well as native species, suggesting introductions have influenced viral transmission dynamics.

Conclusion: Metatranscriptomics provides powerful insights into hidden viral diversity and the ecological drivers of host-virus associations. By revealing potential disease-causing viruses and the conditions that promote host-jumping, our work advances understanding of viral emergence and underscores the importance of continued viral surveillance of Aotearoa's unique fauna.

Genetic and epigenetic dynamics of streptomycin resistance revealed by experimental evolution and direct RNA sequencing

Nikki Freed (University of Auckland), Stella Pearless (University of Auckland) and Olin Silander (University of Auckland)

Aim: The evolution of antibiotic resistance remains a pressing problem in microbiology and medicine. We aimed to investigate the genetic and epigenetic mechanisms underlying streptomycin resistance using experimental evolution and direct RNA sequencing

Methods: We conducted a large-scale experimental evolution study using over 40 genetically diverse, environmental isolates of *Escherichia coli* exposed to increasing concentrations of streptomycin. To identify the genetic changes that arose, we tracked genetic mutations across lineages. To directly assess RNA methylation, we applied native direct RNA sequencing using Oxford Nanopore sequencing to both resistant and ancestral strains.

Results: Across the evolving populations, we observed repeated mutations in *rsmG*, a methyltransferase responsible for methylation of the 16S rRNA. These mutations were associated with altered RNA modification profiles, consistent with known impacts of rRNA methylation on streptomycin resistance. Direct RNA sequencing revealed differences in methylation patterns between resistant and ancestral strains, providing insight into the epigenetic contributions to resistance.

Conclusion: Our findings demonstrate the value of combining experimental evolution with direct RNA modification profiling to uncover mechanisms of antibiotic resistance. This approach not only sheds light on the mutational spectrum of *rsmG* and its effects on rRNA methylation but also illustrates the broader potential of direct RNA sequencing for applications ranging from understanding resistance to mRNA vaccine characterisation and transcript isoform discovery.

How Plant-Microbe Partnerships have Shaped Agriculture

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Aim: When early European settlers brought forage grass seed to New Zealand, they unknowingly carried with them a mutualistic fungal endophyte, *Epichloë*, that would transform pastoral agriculture. Selective grass breeding for resistance to insect pests inadvertently selected for traits associated with ryegrass staggers in livestock, a debilitating neurological disorder characterized by tremors and collapse. Decades of scientific investigation eventually revealed the presence of the endophyte in the seed and forage and confirmed that *Epichloë* alkaloids caused insect resistance and animal health issues. This discovery initiated a search for animal-safe, insect-active strains and became one of the most successful commercial examples of a symbiosis for agricultural impact.

Methods/Results: Multidisciplinary approaches have now created novel *Epichloë*/grass associations for improved livestock productivity and health, pasture persistence and wild-life deterrence, and the hunt for strains with new functionality continues. *Epichloë* grass seed products are on the market nationally and internationally, and one strain alone (AR37) is estimated will contribute NZ\$3.6 billion over 20 years to the New Zealand economy through enhanced insect protection and animal productivity. More recently, the host range of *Epichloë* endophytes has been extended to arable crops such as rye and wheat, and a CRISPR-Cas9 gene editing platform has been developed to manipulate *Epichloë* secondary metabolite pathways and alter the safety and functionality of commercial strains.

Conclusion: The *Epichloë* story provides a blueprint for next generation endophyte technologies and offers the potential to deliver sustainable solutions to drought, nutrient deficiency and pest challenges, both within and beyond agriculture.

***Botrytis cinerea* for global mycovirus study: what do you need?**

Robin MacDiarmid (Bioeconomy Science Institute- PFR group), Saadiah Arshed (Bioeconomy Science Institute- PFR group), Cinthy Jimenez-Silva (University of Auckland), Karmun Chooi (Bioeconomy Science Institute- PFR group), and Bevan Weir (Bioeconomy Science Institute- MWLCR group)

Aim: With a vast and diverse range of fungi that probably act as hosts to countless mycoviruses that together have pleiotropic biological impacts, we propose the comprehensive study of a single fungus, *Botrytis cinerea*, as a model system for mycovirology. We aim to convince you of the power of mycoviruses, why they matter, and how you can embrace them as part of your research, whether on *B. cinerea* or other fungi.

Methods: We identified the need to have a model system for mycovirus research, reviewed the qualities of potential model fungi that might be used to study mycoviruses, and determined the steps required to develop *B. cinerea* as a model to understand the biology, evolution and epidemiology of mycoviruses. Now we are socializing the potential of *B. cinerea* as a model, and enquiring about tools and information that you may need to advance your understanding and/or use of a fungus and its virome.

Results: Mycovirus research has occurred at pace in fungal hosts, revealing complex viromes that contain RNA and DNA mycoviruses with single or double-stranded genomes, which are either encapsidated or apparently naked within their host. Some mycoviruses confer hypovirulence to their otherwise pathogenic fungal host, while others increase pathogenicity. Many mycoviruses seemingly have neutral or undetermined effects on their host but some patterns of combined infections are becoming apparent. Combinations of mycoviruses infect single isolates of fungi (e.g. 25 distinct mycovirus species in a single isolate), with virus-free status being a rare event. To understand the diversity and impact of mycoviruses on fungi, we need to focus on a single fungal species. While seven key fungi have a history of mycovirus research, each of these hosts has one or more drawbacks for use as an international model for mycovirus research compared with *B. cinerea*. *B. cinerea* has highly tractable characteristics: it is easy to culture; has a worldwide distribution; infects a wide range of host plants; can be transformed and gene-edited; and has an existing depth of biological resources including annotated genomes, transcriptomes, and isolates with gene knockouts. We recently published this review* in which we described the biological tools and processes that would enhance progress e.g. infectious virus clones with trackable markers, coupled with virus or host mutants. A single repository of *B. cinerea* isolates/information comprising metadata on virome constituents, host growth habit and pathogenicity could act as a powerful resource for mycologists and mycovirologists worldwide.

Conclusion: A model system is powerful when it is used by multiple researchers to address many experimental questions. How might you use information about mycoviruses of *B. cinerea* or to translate the findings to your fungus of interest? What tools, information or collaborations

do you require to assist your exploration of the mycovirome, its biology and profound impact on fungal epidemiology?

*Khalifa, Mahmoud E., María A. Ayllón, Lorena Rodríguez Coy, Kim M. Plummer, Anthony R. Gendall, Kar Mun Chooi, Jan AL Van Kan, and Robin M. MacDiarmid. "Mycologists and Virologists Align: Proposing *Botrytis cinerea* for Global Mycovirus Studies." *Viruses* 16, no. 9 (2024): 1483.

Abstracts – Oral Presentations

A genus in the bacterial phylum Aquificota appears to be endemic to Aotearoa-New Zealand

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Aim:

Allopatric speciation has been difficult to examine among microorganisms, with prior reports of endemism restricted to sub-genus level taxa. Previous microbial community analysis via 16S rRNA gene sequencing of 925 geothermal springs from the Taupō Volcanic Zone (TVZ), Aotearoa-New Zealand, revealed widespread distribution and abundance of a single bacterial genus across 686 of these ecosystems (pH 1.2-9.6 and 17.4-99.8 °C). Here, we present evidence to suggest that this genus, *Venenivibrio* (phylum Aquificota), is endemic to Aotearoa-New Zealand.

Methods & Results:

A specific environmental niche that increases habitat isolation was identified, with maximal read abundance of *Venenivibrio* occurring at pH 4-6, 50-70 °C, and low oxidation-reduction potentials. This was further highlighted by genomic and culture-based analyses of the only characterised species for the genus, *Venenivibrio stagnispumantis* CP.B2T, which confirmed a chemolithoautotrophic metabolism dependent on hydrogen oxidation. While similarity between *Venenivibrio* populations illustrated that dispersal is not limited across the TVZ, extensive amplicon, metagenomic, and phylogenomic analyses of global microbial communities from DNA sequence databases indicates *Venenivibrio* is geographically restricted to the Aotearoa-New Zealand archipelago.

Conclusion:

We conclude that geographic isolation, complemented by physicochemical constraints, has resulted in the establishment of an endemic bacterial genus in Aotearoa-New Zealand.

Genomic adaptations of ammonia oxidising microbes in diverse geothermal hot springs

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The microbial mediated nitrogen cycle is one of the most fundamental biogeochemical processes in all ecosystems, including geothermal hot springs. Nitrification is the oxidation of ammonium to nitrite (step one) and then finally nitrate (step two) in oxic environments. Chemolithoautotrophic ammonia oxidation can be undertaken by a narrow range of archaea (in the Thermoproteota) and bacteria (in the Pseudomonadota), typically via collaborations between prokaryotes each capable of only one step in the pathway. The recently discovered complete ammonia oxidising bacteria, (comammox from the bacterial *Nitrospira* genus) has shifted the view of nitrification as they can oxidise both ammonia and nitrite. Geothermal environments can be extremely high in ammonium, yet nitrification is understudied in these systems. To determine how this ammonium is utilised and transformed by prokaryotes in these systems we generated 1594 genomes and 14 metatranscriptomes from 46 samples collected from a variety of geothermal springs in New Zealand and Yellowstone National Park (USA) (pH 2.5-9.44, temperature 22-77°C). We show that nitrification is conducted by ammonia oxidising archaea and comammox bacteria in diverse geothermal hot springs, although counterintuitively they were generally associated with springs with low levels of ammonia. Nitrifiers were identified in springs with temperatures up to 77°C. These nitrifiers are therefore high temperature adapted even though results show they are phylogenetically similar to nitrifiers found in non-thermal environments. Ongoing genomic analyses aim to demonstrate the metabolic diversity and thermal adaptations that allow nitrifiers to survive in these thermal environments.

The Physiological, Metabolic, and Transcriptomic Responses of the Endemic Thermophilic Bacterial Genus *Venenivibrio* to Environmental Stress

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Aim

Venenivibrio is a thermophilic bacterial genus that dominates Aotearoa-New Zealand geothermal springs, yet has been found nowhere else globally. This apparent country-wide endemism of a microbial genus is novel. Currently, the conditions that define the growth and survival of *Venenivibrio* are poorly understood, therefore, I aim to characterize the response of *Venenivibrio* to various environmental stressors to identify conditions that limit its global dispersal.

Methods

To determine the mechanisms behind its endemism, *Venenivibrio stagnispumantis* has been grown in a chemostat under varying temperature, pH, and redox conditions. Changes in biomass abundance have been quantified by optical density, cell counts, and qPCR; with corresponding consumption of H₂, O₂, and CO₂ measured via gas chromatography; and differential gene expression determined using RNA sequencing.

Results

Despite previous characterizations as a 'strict microaerophile', chemostat experiments indicate *V. stagnispumantis* can grow both aerobically and anaerobically. This highlights the limitations of performing characterization experiments in batch cultures, in which conditions change rapidly and are often unable to be monitored and controlled. Thus, the experiments performed here in a chemostat better represent hot spring conditions, with constant influx and outflux of compounds.

Furthermore, the RNA sequencing results reveal significant regulation of key genes involved in *V. stagnispumantis* metabolism and stress responses when compared to baseline 'optimal' growth conditions.

Conclusion

These results have provided insights into the physiology, metabolism, and transcriptome of *Venenivibrio*, and will allow for identification of conditions that may limit the dispersal of this 'microbial kiwi'.

Isolation of thermophilic plastic degrading bacteria from hot springs of Aotearoa New Zealand

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Aim: Geothermal springs are distinct environments that harbor diverse populations of microorganisms with unique functional adaptations and metabolic capabilities. For example, recent research has suggested that Aotearoa-New Zealand's geothermal springs contain numerous microorganisms who may be capable of metabolizing plastic. But why would geothermal organisms have this capability? Does this mean in situ hot spring communities degrade introduced plastic? Can we isolate these putative degraders and show they can degrade plastic in vitro?

Methods: To address these questions, we first incubated polyethylene terephthalate, polylactic acid, and polyhydroxybutyrate (PHB) substrates in springs of varying conditions to search for signs of microbial plastic degradation. We then characterized the microorganisms that grew on our substrates with cultivation-independent sequencing methods to evaluate how plastics influence microbial communities. Finally, we used targeted microbial culturing and whole genome sequencing to determine whether any putative degraders could degrade plastics, and annotate any plastic degrading genes.

Results: We confirmed that plastic degrading bacteria can be found in Aotearoa-New Zealand's geothermal springs. Unsurprisingly, microbially produced polymers and biopolymers were more susceptible to microbial degradation than petrochemical polymers. We were able to isolate two thermophilic bacterial strains –*Cupriavidus* sp. and *Rubrobacter* sp., that were shown to degrade PHB in vitro.

Conclusions: While we found evidence that certain organisms may use plastics as a source of carbon, our results suggest that the primary use of plastics by geothermal microbial communities appears to be as substrates for biofilm formation by non-plastic degrading taxa.

The evolution and adaptation of the bacterial flagellar filament

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Aim: Understanding the evolution of the flagellar filament protein, flagellin, is important to elucidate the diversity observed within this protein and its adaptation in various environments to provide motility.

Methods: 210 flagellin protein sequences from representative species were aligned using MUSCLE and generated a phylogenetic tree using RAxML. A further 254 bacterial genomes isolated from high temperature environments were analysed, flagellin sequences identified and examined in conjunction with genomic metadata. We then designed and engineered two outer domain *E. coli* FliC deleted mutants and 11 outer domain chimeras. FliC variants were cloned into expression vectors and tested for motility in a fliC disrupted *E. coli* strain. Motility was analysed using swim plate and free-swimming assays. Filaments were stained with crystal violet and imaged using light microscopy.

Results: Phylogenetic analysis of representative flagellin sequences found that 63% of flagellins from bacteria isolated from animals contained outer domains. Analysis of flagellins found in thermophilic bacteria identified that 47% of genomes contained two or more copies of the flagellin gene and the largest outer domains were found in bacteria which grow at 62°C. We subsequently tested the interchangeability of the flagellin outer domains, of which 2 of the 11 chimeras, alongside outer domain deleted variants, were able to provide motility.

Conclusions: This study provides evidence that there is adaption of flagellin outer domains in different environments. We show that the outer domains are not necessary for motility in *E. coli* K-12 and that rational engineering of outer domains can provide motility, highlighting the possibility of horizontal gene transfer and subsequent adaption to niches.

The taxonomic distribution of the Cation Proton Antiporter; the most prevalent and abundant Na⁺/H⁺ antiporter across all taxa

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Aim

Most organisms are constrained by narrow pH and salinity ranges, yet life thrives even in extreme environments. This adaptability is thought to be enabled by Na⁺/H⁺ antiporters, which regulate the concentration of proton and sodium ions across cell membranes. Despite their importance, little is known about their distribution and evolutionary history. This study aimed to address this knowledge gap by detecting Na⁺/H⁺ antiporters homologs and classifying them based on inferred phylogeny.

Methods

Comprehensive databases of two antiporter families, the Ion-Transporter (IT) and the Cation Proton Antiporter (CPA), were constructed using homology searches against species-representative proteomes from the Genome Taxonomy Database for Archaea and Bacteria, supplemented by Eukarya proteomes. The prevalence and quantity of IT and CPA were assessed across taxonomic ranks, and phylogenetic inference was used to define distinct clades of interest.

Results

CPA was found to be the most common antiporter, present in 80% of screened prokaryotes and 97% of eukaryotes. CPA count was found to be higher in gene count per genome compared to IT, with clear variations between taxonomic groups. The inferred CPA phylogeny defines novel clades and supports multiple bacterial origins of Eukarya CPAs.

Conclusion

This study provides the most detailed view of antiporter distribution to date. Their broad distribution reinforces the importance of both superfamilies and enables more informed inferences about prokaryotic lifestyle. Further work will explore the environmental relevance of individual clades and possession of CPA in multi-copy by some taxonomic groups.

Exploring Microbial Metabolism of Volatile Sulfur Compounds in Geothermal Hot Springs

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Aim

My research aims to investigate the complex microbial processes that underpin an underrepresented subset of the sulfur cycle, known as volatile sulfur compounds (VSCs). We look to investigate VSC formation and consumption in geothermal hot springs.

Methods

Our research utilizes a range of chemical, biochemical, microbiological and bioinformatic tools to paint a picture of how sulfur is metabolized in hot springs in the Taupō Volcanic Zone. We have identified abundant VSCs in hot springs via HS-SPME GC-MS. Through species enrichment and isolation, we have extracted and sequenced the DNA of several species from these environments. Microbial genomic analyses have identified several enzymes of interest which bind VSCs, and microbial community context is provided through 16S rRNA amplicon and metagenomic data.

Results

We have determined the key VSCs present in these hot springs, the microbial species that thrive in these environments, and the biological pathways that allow them to do so. Bioinformatic analyses and species characterization of the microbes within these springs will confirm the presence and activity of sulfur utilizing microbial species, with the goal of understanding how these microorganisms metabolize VSCs.

Conclusion

VSCs are an understudied subset of sulfur compounds found within geothermal environments, yet they contribute significantly to several biological processes. In this research we have produced a survey of the VSCs found in hot springs and identified the key microbes within their communities which thrive off these compounds. We have investigated the VSC utilization pathway, with several enzymes identified showing potential for biotechnological applications.

Local diversity in a global context: microbial communities in Aotearoa-New Zealand hydrocarbon reservoirs and their impacts on hydrogen geostorage

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Aim:

To facilitate Carbon Net Zero by 2050 in Aotearoa-New Zealand (A-NZ), this research is investigating the feasibility of storing hydrogen gas in local depleted hydrocarbon reservoirs (HCRs). Hydrogen-oxidising microorganisms play a key role in these systems as they can interact with stored gases and have potential to deplete stored hydrogen in HCRs. This presentation will report the first study on the microbiome of A-NZ HCRs to determine native microbial interactions with stored hydrogen, as well as a comparison to global HCR microbial communities.

Methods:

Using culture-independent techniques, microbial communities of seven oil and gas wells in the Taranaki region were studied. Firstly, both 16S rRNA gene amplicon and shotgun metagenomic sequencing were performed to determine; (a) the relative abundance of microorganisms found in A-NZ HCRs, and (b) the metabolic capabilities of these communities. Secondly, a meta-analysis of both local and global HCR microbial communities was conducted by analysing publicly available 16S rRNA genomic data.

Results:

The 16S rRNA gene amplicon data indicated that A-NZ HCRs contain microorganisms capable of oxidising hydrogen. Interestingly, there was a distinct difference in hydrogen oxidisers between reservoir types, which was further supported by metagenomic analysis. Differences were also observed between local and global HCR microbial communities.

Conclusion:

Hydrogen-oxidising microorganisms found in A-NZ HCRs will impact efforts to store hydrogen underground. Due to dissimilar local and global microbial communities found by this study, it is imperative that future research focuses on local sites to inform implementation and management strategies of A-NZ's green hydrogen economy.

National patterns of diversity and metabolism of microbial communities in groundwater ecosystems

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Aim: To investigate how subsurface geochemistry influences microbial diversity and metabolic potential in New Zealand aquifers.

Methods: We collected 39 samples from 33 aquifers nationwide and performed shotgun metagenomics.

Results: We recovered 494 metagenome-assembled genomes (MAGs), which clustered into three groups based on hydrochemistry and geography. Distance-based redundancy analysis (dbRDA) showed that MAG distribution strongly correlated with nitrate, sulfate, and potassium concentrations.

Cluster A was characterized by anoxic, reducing conditions and signs of land-use impact (elevated Na, Cl, SO₄, Ca, Mg). It showed the highest microbial diversity, with many uncultured taxa, and dominant genera including *Rhodoferrax* and *Aquabacterium*. Many MAGs encoded cytochrome c oxidase, usually associated with aerobic respiration.

Clusters B1 and B2 reflected more oxidizing conditions, with lower NH₄ and manganese but higher NO₃.

Cluster B1, mainly from Marlborough, Tasman, Canterbury, and Otago, featured common groundwater genera like *Phenyllobacterium*, *Aquabacterium*, and *Novosphingobium*. MAGs commonly encoded *cbb*₃-type cytochrome c, nitrate reduction, and sulfur oxidation pathways.

Cluster B2, representing geothermal regions (Waikato, Bay of Plenty) and some northern sites (Auckland, Northland), had lower pH, higher temperatures, and more SiO₂. Communities included both groundwater taxa and uncultured groups (e.g. *Patescibacteria*, *Omnitrophota*), with MAGs enriched in nitrogen-fixation pathways.

Conclusion: Aquifer geochemistry strongly shapes microbial communities and their metabolic functions across New Zealand, reflecting local adaptation to redox, nutrient, and thermal conditions.

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Aims: *Microcoleus* is a filamentous cyanobacterial genus commonly found in freshwater habitats where it can form thick biofilms comprising toxic and non-toxic strains. Strains cannot fix atmospheric nitrogen (are non-diazotrophic) and employ diverse strategies to scavenge nutrients and thrive in low-nutrient environments. One of the features distinguishing toxic and non-toxic strains is the number of cyanophycin genes (*cphAB*) present. The encoded enzymes synthesise (*CphA*) and degrade (*CphB*) cyanophycin (nitrogen-rich intracellular storage granules) and facilitate excess uptake and storage of nitrogen. Toxic strains typically possess a single putative copy of *cphAB*, while non-toxic strains carry two - one sharing high sequence similarity with the copy in toxic strains. We sought to confirm if *Microcoleus* can produce cyanophycin granules, as genomically predicted. We also investigated the evolutionary origin of the different *cphAB* copies.

Methods: Cyanophycin production was confirmed through electron and light microscopy. Phylogenetic trees were constructed using the protein sequences of toxic and non-toxic *Microcoleus* strains and other representative cyanobacteria.

Results: Analysis of *cphA* sequences shared by toxic and non-toxic strains showed they clustered with those from other non-diazotrophic cyanobacteria, with results highlighting the evolutionary divergence of cyanophycin genes based on cyanobacterial nitrogen-fixing capacity. The second *cphA* copy in non-toxic strains was divergent from non-diazotroph and diazotroph clades.

Expected impact: Ongoing work aims to determine whether this novel copy functions to produce and degrade cyanophycin, and whether, by harbouring a second copy, non-toxic strains better withstand periods of environmental nitrogen deprivation.

Enrichment and characterisation of cable bacteria from a New Zealand estuary and their potential application in denitrifying bioreactors

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Aim

Cable bacteria (family Desulfobulbaceae) are filamentous microorganisms capable of long-distance electron transport, facilitating redox reactions in aquatic sediment. Filaments orient across oxygen gradients, coupling hydrogen sulfide oxidation in anoxic zones with oxygen reduction in oxic layers. These bacteria influence biogeochemical cycling and may enhance denitrification. This study aimed to confirm the presence of cable bacteria in New Zealand estuarine environments, characterise their morphology and phylogeny, and assess their potential integration into sulfur-driven denitrifying bioreactors.

Methods

Sediment samples were collected from a Canterbury estuary and incubated in stabilised columns to enrich cable bacteria. Custom-built slides enabled visualisation of filaments using compound and phase contrast microscopy. DNA was extracted from enriched columns and underwent 16S rRNA gene amplicon sequencing to assess diversity.

Results

Filaments exceeding 5000 µm were observed 4–8 weeks post-enrichment, displaying gliding motility across oxic-anoxic boundaries. Microscopy confirmed morphological features consistent with cable bacteria, including intracellular polyphosphate granules, thought to enhance oxidative stress tolerance. Sequencing revealed multiple clades within the genera *Candidatus Electrothrix* and their relatives *Desulfobulbus*, suggesting cryptic species diversity.

Conclusion

This study provides the first confirmed isolation of cable bacteria from New Zealand sediments. Ongoing work aims to determine whether these isolates are endemic and to evaluate their integration into bioreactors to enhance denitrification.

Genetic divergence of non-toxic and toxic *Microcoleus* leading to vitamin auxotrophy

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Aims:

Microcoleus autumnalis is a filamentous cyanobacterium found in freshwaters worldwide. It is well known for producing anatoxins, which pose health risks to animals and humans. Our group previously identified genetic differences between toxic and non-toxic strains, including predicted thiamine (vitamin B1) auxotrophy. This study tested the predicted thiamine auxotrophy in laboratory conditions, and as *Microcoleus* cultures are non-axenic, investigated the thiamine biosynthesis capacities of co-cultured bacteria.

Methods:

Genomes of 4 toxic and 10 non-toxic *Microcoleus* strains and associated bacteria were analysed, including 4 newly generated genomes from long read data with improved completeness. To confirm thiamine auxotrophy, *Microcoleus* were grown with and without thiamine forms (thiamine hydrochloride, thiamine monophosphate and thiamine diphosphate).

Results:

Analysis of newly generated *Microcoleus* genomes confirmed that toxic strains lack key genes for the biosynthesis of thiamine, while all non-toxic strains encode complete biosynthesis pathways. Despite predicted thiamine auxotrophy in toxic strains, laboratory experiments showed no difference in growth of *Microcoleus* in media lacking thiamine, or in the presence of thiamine where thiamine was rapidly taken up by cells or absorbed onto biomass. However, analysis of the community members found alongside the toxic strains demonstrated that some have complete biosynthesis pathways and may be able to share thiamine. Generation of axenic cultures of *Microcoleus* is underway to further evaluate thiamine auxotrophy.

Conclusion:

This study provides insights into the genetic differences between toxic and non-toxic *Microcoleus* and suggests that community members may be important for proliferation of toxic strains.

Variation in soil microbial composition and functional potential with *Pinus radiata* stand age

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Soil microbes are key to understanding the mechanisms driving variation in forest biogeochemical processes. *Pinus* plantations have become widespread across New Zealand, yet changes in soil microbial communities and their potential functions over forest development remain poorly understood. This study aimed to investigate microbial community dynamics and functional shifts across different stand development stages in Kaingaroa Forest.

Soil samples were collected from four stand age categories: just planted (<1 year), young (2–10 years), mid-old (11–20 years), and old (>20 years). Microbial communities were analysed using 16S rRNA gene and ITS amplicon sequencing, along with shotgun metagenomics. Multivariate analyses assessed compositional patterns, and fungal functional traits were inferred using FUNGuild.

Bacterial community composition remained relatively stable across stand ages, with Pseudomonadota, Acidobacteriota, and Planctomycetota consistently dominant. In contrast, fungal communities showed strong successional shifts: Ascomycota dominated in younger stands but were gradually replaced by Basidiomycota in older stands. Both bacterial and fungal communities differed significantly among stand stages (PERMANOVA: $p < 0.001$). Fungal communities showed greater separation between younger and older stands and higher within-group variability (PERMDISP: $p = 0.010$), suggesting increased heterogeneity across stages. Functional annotation using FUNGuild revealed that saprotrophic fungi were dominant in early stages, while symbiotrophic fungi, including those with ectomycorrhizal traits, increased with forest age.

Stand development in *Pinus radiata* drives distinct shifts in fungal and bacterial communities, with implications for ecosystem function and forest management.

Microbial trait and community shifts at the forest–grassland edge

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Background: Trees at forest edges tend to grow larger than those in the interior, likely due to increased light, nitrogen deposition, and other resource inputs. This enhanced growth may increase belowground carbon through root exudates and litter inputs.

Aim: Our research explores how integrating clusters of trees into pastoral landscapes can enhance soil carbon stocks through edge-driven resource availability and ecosystem complementarity. We aim to identify key microbial processes that regulate soil carbon cycling at forest edges.

Methods: Through applying shotgun metagenomic sequencing alongside detailed abiotic and biotic metadata, we have generated high-resolution mapping of soil microbial communities spanning seven tree types across forest-to-grassland transects (n=105). We have applied a genome-to-trait pipeline (microTrait) to identify shifts in genome traits along the land use gradient.

Results: Microbial community composition and functional potential differed significantly among tree functional groups and sampling locations ($P < 0.001$), with a strong interaction between the two, indicating context-dependent microbial responses across the landscape gradient. The forest edge is emerging as an ecotone, including at the genomic level, where estimated traits such as growth rate and optimum growth temperature exhibit intermediate values relative to forest interior and grassland soils.

Conclusion: We aim to explore how these microbial traits and functions can be incorporated into a process-based ecosystem model to help inform carbon cycling predictions. By quantifying microbial trait–environment linkages, this research seeks to reduce uncertainty in landscape-scale carbon predictions and improve the empirical basis for national greenhouse gas accounting.

Elevated CO₂ and Grazing Restructure Microbial Networks in Grasslands: Trade-offs of Connectivity and Modularity

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Aim: How do elevated CO₂ and grazing interact to shape the stability and resilience of grassland soil microbial communities? Here I share results from a unique 23-year field experiment combining Free Air CO₂ enrichment (FACE) with active sheep grazing.

Methods: Using 16S and ITS sequencing and network analysis, we mapped changes in bacterial-fungal co-occurrence patterns across ambient and elevated CO₂ as well as grazing treatments.

Results: Elevated CO₂ increased network complexity, creating more interconnected communities but at the cost of modularity suggesting greater vulnerability to disturbance. In contrast, grazing boosted modularity, but reduced overall network complexity, suggesting a payoff of efficient resource exchange via decreased connectedness. Critically, combining both drivers produced an intermediate network that balanced complexity and modularity, but also heightened the dependence on nitrogen cycling bacteria shown by increased node connectivity and a steeper decline in network robustness following targeted node removal.

Conclusion: These findings highlight the trade-off between efficient resource exchange and ecosystem resilience, underscoring the need for integrated management strategies that support both microbial function and stability in grasslands under rising atmospheric CO₂.

Microbes, Metals, Mud & Metagenomics: Heavy metal contaminants as environmental drivers of AMR in agricultural soil.

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Aim

Environmental drivers selecting for the development and maintenance of antimicrobial resistance (AMR) are of increasing concern. Association of heavy metal (cadmium, Cd; zinc, Zn) contamination of agricultural soil and antibiotic resistance (ABR) at sites in the Waikato and Wellington regions were investigated.

Methods

Soils from 3 contaminated sites and one uncontaminated site in Waikato; and a farm airstrip near Wellington were sampled for the presence and proportion of total aerobic heterotrophic bacteria with metal resistance (HMR) (Cd, Zn and mercury, Hg - a positive control). Soil microcosm experiments determined the range of Cd, Zn or Hg concentrations that were associated with elevated numbers of ABR bacteria.

Antibiotic sensitivity, 16SrDNA and horizontal gene transfer analyses were employed to investigate co-selection for HMR and ABR in Waikato, Wellington airstrip and microcosm soil samples.

Results

Higher levels of bacterial resistance to Cd, Zn, Hg and 5 representative antibiotics correlated with higher levels of Cd or Zn in soil. Bacterial community structures were altered in soils with high HM levels. Cd resistance genes were transferred from donor bacterial isolates to recipients, and transconjugants were also resistant to Zn, Hg and a range of antibiotics. 16S rDNA next-generation sequencing profiling of Wellington airstrip and microcosm samples found changes in HM-exposed bacterial communities. The bacterial phyla Acidobacteria & Chloroflexi differed most in abundance between airstrip subsite samples ($p < 0.05$). The proportion of Acidobacteria in the Hg-spiked microcosms was reduced compared to control microcosms.

Conclusion

Much remains unknown about interactions of metals and ABR in soil, but these and other approaches can help illuminate them.

Inactivation of *Aspergillus flavus* and Aflatoxin B1 on Inoculated Raw Peanuts with High Voltage Atmospheric Cold Plasma

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Peanuts are susceptible to contamination with *Aspergillus* spp. mold, which may lead to generation of aflatoxin, a serious food safety issue. *A. flavus* is the primary mold that produces aflatoxin B1 (AFB1). High voltage atmospheric cold plasma (HVACP) is an emerging non-thermal technology with short treatment time, low energy consumption, that leaves no chemical residue on the food. In this study, 10 g peanut samples were inoculated with *A. flavus* spores and AFB1 toxin. Subsequently, samples were treated with HVACP using air as the working gas at 90 kV and a power of 160 W for several treatment times (2, 5, and 10 min), relative humidities (RH 5, 40, and 80%), and post-treatment storage times (0, 4, and 24 h) with a direct exposure mode. A reduction of 2.20 log CFU/sample of *A. flavus* spores was observed for the peanut treated for 5 min. A reduction of 3.0 log cfu/sample of *A. flavus* was obtained with HVACP treatment for 10 min at 80% RH and post-treatment time of 24 h. AFB1 toxin on peanuts was reduced by 71.3% and 84.5% by HVACP treatment of 2 min and 10 min, respectively. The gas chemistry during HVACP treatment measured by optical absorption spectroscopy quantified the concentrations of the reactive gas species (O₃, NO₂, H₂O₂+N₂O₅, NO₃) in the plasma and reached a maximum concentration of 1,715 ppm for O₃ at a treatment time of 7 min, and concentrations of 1338, 654, and 201 ppm for NO₂, H₂O₂+N₂O₅, and NO₃ after 10 min, respectively. At higher humidity (40% RH and 80% RH), the generation rate for hydroxyl radical (OH) and atomic O increased leading to greater decontamination rates of *A. flavus* spores and AFB1 toxin. Results indicate that HVACP is a promising technology to effectively inactivate *A. flavus* and reduce AFB1 on raw peanut kernels.

The air-liquid interface: a focal point for EPS overproduction and biofilm architecture.

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The air-liquid interface promotes the formation of biofilms by pseudomonads and other bacteria. Bacteria move to the air-liquid interface by a mechanism called aero taxis. The air-liquid interface provides bacteria with higher nutrients and increased access to oxygen. This study explored the importance of air-liquid interface biofilm formation of psychotropic pseudomonads, which are known to affect the quality of food products. The pseudomonad isolates 3SM (*Pseudomonas lundensis*) and 20SM (*Pseudomonas cedrina*) were allowed to form biofilms in a CDC reactor under continuous flow of nutrients at 4°C. The coupon holders were lifted about 2.5 cm to create an air-liquid interface, which resulted in an air-liquid interface and liquid-liquid interface biofilm formation in the same reactor. The cell counts, extracellular polymeric substances matrix (EPS), biofilm architecture, the gene expression of EPS producing genes (*algK*, *pslA*, *bcsA*, *pelD*), and the biofilm EPS footprints after cleaning were compared between the air-liquid and liquid-liquid interface biofilm cells. The biofilms formed at the air-liquid interface produced significantly ($p < 0.05$) higher cell counts (7.26 -7.47 logCFU/cm²) and EPS quantity (75 -80 µg/10⁸ cells). The air-liquid interface biofilm formation resulted in higher expression of the *algK* and *bcsA* genes compared to the liquid-liquid interface. The biofilm footprints left after cleaning with NaOH were significantly ($p < 0.05$) higher in the air-liquid interface. These results suggest the role of the air-liquid interface in the EPS overproduction

Friends Under Flow: Listeria stress adaptation in single and dual species biofilm

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While the impact of stress on *L. monocytogenes* associated with food processing has been recognised in planktonic conditions, the available research overlooks the response of this pathogen in the multi-species biofilm, commonly found in food processing and manufacture. The objective of this study was to understand the effect of shear stress on *L. monocytogenes* in single and dual-species (with *P. fluorescens*) biofilm formed in a continuous turbulent flow system. In the single-species biofilm, *L. monocytogenes* was able to form a biofilm under the turbulent flow with cell concentration reaching 5.1 log CFU/cm² after 48 h, where filamentous cells (27.7 µm in length) were observed. In contrast, there were no visible filaments in the dual-species biofilm, and *L. monocytogenes* cell concentration was significantly higher ($p < 0.001$) at 8.7 log CFU/cm². The cells harvested from single-species *L. monocytogenes* biofilm formed under turbulent flow showed significantly ($p < 0.001$) lower motility and higher adhesion compared with cells harvested from planktonic and static conditions. Gene expression analysis showed significant ($p < 0.001$) downregulation of *motB* (motility), *sigB* (stress), and cell division (*ftsX* and *ftsW*), and upregulation of *mpl* (adhesion) and *rodA* (rod shape), indicating *L. monocytogenes* adaptation to shear stress. This study provides fundamental information on the multi-species biofilm formation by *L. monocytogenes* under stress.

Rapid Commercial Sterility Testing of UHT Dairy Products: Method Comparison and Optimisation

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Aim

The purpose of this research was to evaluate and compare two rapid commercial sterility testing approaches—a widely available ATP bioluminescence technique and a newly developed flow cytometry method—against the standard plate count protocol for detecting low numbers of obligate thermophiles in UHT dairy products. The study also assessed how reducing pre-incubation times would influence these methods' performance.

Methods

Five UHT dairy product types were deliberately contaminated with low numbers of obligate thermophiles. Traditional plate counts, ATP bioluminescence, and flow cytometry were conducted after varying pre-incubation times (6–48 hours). For whipping cream, enhanced sample preparation (mixing with cation chelator, centrifugation, etc.) was used for better accuracy.

Results

For UHT milk, pre-incubation times of 6–24 hours greatly improved ATP bioluminescence agreement with plate counts (>95%), versus just 50% at 48 hours. Flow cytometry also achieved >95% agreement with plate counts for UHT milk at all tested times, peaking at 24 hours. Neither rapid method matched the plate count method for in-house cream or medical beverage products. Enhanced preparation and gating for whipping cream improved flow cytometry agreement (>95%) at all times, while the ATP method had lower agreement.

Conclusion

Shorter pre-incubation times for UHT milk substantially enhance rapid testing, especially with the ATP bioluminescence method. Optimised flow cytometry works for whipping cream, but traditional plate counts remain necessary for in-house cream and medical beverages. Results may inform regulators and future industry standards.

Into the blue: phylogenetic and phenotypic characterisation of *Vibrio vulnificus* isolates from New Zealand shellfish

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Aim: *Vibrio vulnificus* is an opportunistic pathogen that can cause serious systemic disease and gastrointestinal illness in humans. Its isolation from NZ shellfish in recent years has been hypothesised to be related to warmer climatic conditions. Here we characterise the molecular epidemiology of NZ shellfish isolates, and compare the results with certain phenotypic characters to assess the epidemicity potential of different phylotypes.

Methods: Multi-locus sequence typing (MLST) was undertaken on 29 *V. vulnificus* isolates recovered from NZ Pacific oysters, compared with extant data from clinical strains and subjected to phylogenetic analysis. Phenotypic assays like antibiotic resistance, biofilm formation, motility and Elastic Light Scatter (ELS) profiling were also performed to evaluate any correlation between phylogenetic types.

Results: Nine MLST profiles were determined among the NZ shellfish isolates, including seven novel profiles. Phylogenetic analysis placed all strains into two broad clades which distinctly polarized vcg type-C and type-E. vcg-E isolates of the seven novel MLST profiles were further allocated into two branches, each contained extant clinical isolates. All strains examined demonstrated similar results in biofilm formation assays and ELS profiling.

Conclusions: This study is the first to examine phylogenetic relationships among *V. vulnificus* isolates of NZ origin. Although reports of human cases are rare in this country, a phylogenetic relationship was seen between environmental and clinical isolates. Phenotypic analyses so far indicate that *V. vulnificus* is relatively homogenous, in contrast with its genetic diversity. The seriousness of the known sequelae infers that caution should be exercised in every case where this organism is detected.

Population dynamics in a biofloc aquaculture: ‘What happens in an aquaculture stays in an aquaculture’

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Aim: The genus *Vibrio* has the potential to exert a considerable influence on the field of aquaculture. While some species are classified as pathogenic to fish and seafood, other species, have the potential to cause (extra)intestinal infections in humans. To mitigate the risk of public health threats posed by aquaculture products, it is essential to gain a deeper understanding of the prevalence and impact of human pathogenic *Vibrio* species.

Methods: The isolates were characterized by phenotypic and genotypic methods. WGS analysis was conducted to determine the population structure and to assess the impact of the isolates regarding virulence and resistance determinants.

Results: As part of a qualitative *Vibrio* monitoring of a German biofloc aquaculture in 2022, the diversity of *V. parahaemolyticus* over a period of one year was determined by SfiI-macrorestriction profiling. A further investigation was conducted 16 months after the last monitoring sampling in order to provide a comparison. In total, 214 strains of *V. parahaemolyticus*, originating from twelve shrimp and two water samples from one aquaculture basin, were investigated. Overall, the strains exhibited minimal variability in their SfiI-PFGE profiles across all sampling approaches, with 22 subclade clusters assigned to one clone, indicating the persistence of the predominant clonal type. In addition, AST, plasmid characterisation and WGS was conducted to characterized the strain diversity. The observed differences between strains were mainly attributed to the presence of plasmids, which were identified in some of the strains.

Conclusion: The study provides an overview about *Vibrio* spp. occurrence and insight into the impact of *V. parahaemolyticus* on human health and the persistence of a predominant clone.

International development programme achieves dramatic improvements in the microbiological safety of eaten-raw vegetables in Cambodia

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Aim

Cambodia Quality Horticulture (CQH), an 8-year programme, supported the Cambodian horticulture sector by meeting market demand for high-quality safe produce.

Methods

With NZ Ministry of Foreign Affairs funding, Plant & Food Research collaborated with AsureQuality and Cambodian partners: General Directorate of Agriculture, Royal University of Agriculture, Pasteur Institute du Cambodge and critically, vegetable growers and suppliers. The food safety team took a whole supply chain approach, developing and providing training and interventions along the chain: farm, transport, packhouse and retailer. Interventions included stopping on-farm washing, improving composting, water treatment, introducing packhouse washing systems and critically, training ~1000 farmers, Commune Agriculture Offices and supply chain actors to reinforce the importance of food safety, prevent cross-contamination and maintain hygiene. Improved postharvest practices included introducing reusable crates, off-ground handling, cold storage and traceability tools.

Results

An initial 2017 survey found high contamination: 13% of eaten-raw vegetable samples carried Salmonella, 29% exceeded safe Escherichia coli limits ($\geq 100/g$) and >50% contained human parasites. Results were impressive: Salmonella was eliminated throughout the supply chains; E. coli was eliminated on vegetables in fields; non-compliant E. coli vegetables were reduced by >80% at retail.

Impact

CQH left a strong legacy of improved awareness, strengthened systems and practical innovations. Partners demonstrated significant progress in food safety and postharvest handling, attributing reduced typhoid in their communities to improved hygiene practices. CQH established a solid foundation for a safer, more resilient Cambodian horticulture sector.

Phenotype and Elastic Light Scatter Characteristics of Clinical and Environmental Strains of *Vibrio parahaemolyticus* from New Zealand

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Aims: *Vibrio parahaemolyticus* is a leading cause of seafood-associated bacterial gastroenteritis, however not all strains are pathogenic. We compare the virulence potential of representative, phylogenetically characterized, clinical and environmental New Zealand isolates by assessing key phenotypic traits.

Methods: strains were examined for features including motility (swimming and swarming), protease and lipase activities, hemolysis, and halotolerance. Elastic Light Scatter (ELS) analysis was used to examine bacterial colony ultrastructure.

Results: Compared to clinical strains, environmental strains demonstrated wider halotolerance, and hemolytic activity was more frequently observed, despite absence of the common genetic markers (tdh/trh). ELS analysis identified two distinct clusters (ELS-1, ELS-2), one of which comprised environmental strains only; however, ELS-2 contained all clinical strains and several environmental strains, that tended to demonstrate more pronounced swarming motility than ELS-1 strains ($p < 0.05$). ELS-2-environmental strains also showed elevated swimming motility at 37 °C.

Conclusions: certain New Zealand isolates of *V. parahaemolyticus* from shellfish display key virulence traits and environmental adaptability, with wider implications for food and water safety. Hemolytic activity is exhibited independent of the tdh or trh genes, indicating alternative pathways. ELS, combined with phenotypic profiling, may be a powerful tool for rapid screening and risk assessment of potentially pathogenic *V. parahaemolyticus* strains.

A Probabilistic Approach to the Analysis of Elastic Light Scatter Profiles for the Identification of Foodborne Bacteria

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Aim

Elastic Light Scatter (ELS) profiling is a unique non-invasive technique for the rapid analysis and identification of bacterial colonies grown on agar. Colonies are inspected using a laser; the resulting light-scatter images have been shown to be species-specific. We examined a probabilistic approach to the analysis of ELS profiles for the identification of foodborne bacteria as an alternate method.

Methods

We analyzed 1,700 colonies representing 49 strains across 17 food-related bacterial species. Each of three ELS-derived feature sets (proprietary Patsekin elements, Zernike moments, pseudo-Zernike moments) were included, yielding a total of 2,254 features. Each individual feature was binarized using an adaptive threshold set at 50% of its maximum value, a strategy that preserved meaningful differences across feature types of varied scale. A species-level identification matrix was constructed by summarizing positively expressed features across colonies, and representative species profiles were generated for comparison.

Results

The framework accurately identified all represented species, with each group aligning closely with its own median profile. Importantly, test species not included in the database (*Arcobacter bilvalviorum*, *A. faecis*, *A. ellisi*) were correctly tagged as unknown based on a combined analysis of probabilistic scores and taxonomic distances, even when profiles shared partial similarity.

Conclusion

This strategy reduced the chance of strain misidentification, which can be critical in a clinical context. We believe this is the first study to apply a probabilistic identification approach to ELS data, allowing for both classification and rejection of non-database matches. These results may facilitate wider adoption of ELS in routine laboratory settings.

Unveiling the biofilm control potential of bacteriocin produced by *Pediococcus acidilactici* PaN4 and nisin.

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Introduction:

Bacteriocins are ribosomally synthesized antimicrobial peptides. Although their effects on planktonic bacteria are well-documented, their biofilm control mechanisms remain unclear.

Aim:

This study compared the antibacterial and antibiofilm properties of PaN4 bacteriocin preparations with those of commercial nisin, with implications for their use in biofilm control.

Methods:

This study compared two PaN4-derived bacteriocin preparations, cell-free supernatant (CFS-PaN4) and crude bacteriocin (CBac-PaN4), with nisin (Nisaplin). CFS-PaN4 was obtained by anaerobic culturing of PaN4 and collecting CFS with adjusted pH. CBac-PaN4 was prepared from CFS-PaN4 by aluminum sulfate precipitation, centrifugation, dialysis, and sterile filtration. Antibacterial activity was assessed using agar well-diffusion and inhibition assays against selected pathogens. The efficacy of antibiofilms on *L. monocytogenes* LmM4 biofilms on stainless steel. Preliminary characterization of CBac-PaN4 was also determined.

Results:

Nisin and bacteriocin produced by PaN4 show dose-dependent antibacterial activity against various pathogens. Bacteriocin treatment effectively prevented and disrupted the formation of LmM4 biofilms on stainless steel. Bacteriocin preparations have a protein concentration >10 mg/mL and a bacteriocin molecular weight >10 kDa. The pediocin gene was detected in *Pediococcus acidilactici* PaN4.

Conclusion:

Bacteriocin produced by PaN4 and nisin exhibit antibacterial and antibiofilm properties. Despite the presence of the pediocin-producing gene, the unusually high molecular weight of bacteriocin PaN4 that it may differ from typical pediocin.

Characterisation of mobile elements of *Campylobacter jejuni* and coli in New Zealand

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This research aimed to investigate the diversity, mobility, and potential functional roles of plasmids in *Campylobacter jejuni* and *Campylobacter coli* isolates from New Zealand using genomic analysis.

Methods: 64 *Campylobacter* genomes were analysed using long-read sequencing technology. These isolates were selected from a larger dataset of 1208 New Zealand isolates, using a plasmid-typing scheme based on relaxases, replicons, single-strand DNA binding proteins, and virulence markers (unpublished database developed by van der Graaf-van Bloois, L.B.). Comparative analyses of plasmid sequences were done using Clinker and Roary.

Results: Plasmid contigs were found in 48 isolates, totalling 77 plasmid contigs, including all five previously reported *Campylobacter* plasmid categories: megaplasmids, pVir, pTet, medium-size, and small plasmids. According to the plasmid-typing system used, three dominant plasmid types were identified. These plasmid groups were present in both species, with no association with specific hosts or sequence types, indicating plasmid mobility across different *Campylobacter* populations. The conjugation genes of two dominant plasmid subtypes shared >80% similarity to previously described conjugation genes in *C. jejuni* reference strain 81-176 pVir. These conjugation genes in *C. jejuni* 81-176 were classified as T4SS homologues and associated with host invasion. Additionally, amongst the conjugative plasmids detected, one was a pTet.

Conclusion: Our findings highlight extensive plasmid mobility across *C. coli* and *C. jejuni* populations in New Zealand. The observed prevalence of plasmids harbouring T4SS homologues reinforces the need for further studies to understand the role, evolution, and public health implications of *Campylobacter* plasmids.

What's this?! Identification challenges for taxonomically complex bacteria – the *Vibrio* exemplar that revealed new aquacultural pathogens in New Zealand

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Aim: to identify two NZ shellfish isolates presumptively identified as *Vibrio vulnificus*, from a genus containing over 150 species.

Methods: the API20E kit was used for biochemical phenotyping and Elastic Light Scatter (ELS) profiles were determined for strains of *V. parahaemolyticus*, *V. vulnificus* and the two unidentified strains. 16S rRNA gene sequences were determined and compared with similar data in NCBI using BLAST. Whole-genome sequencing of the strains was undertaken using an efficient in-house pipeline and compared to all comparable data in Genbank for distinct *Vibrio* species using digital DNA-DNA hybridisation.

Results: The API20E kit either misidentified, or failed to identify the strains depending on the database used. Comparisons of the 16S rRNA gene sequence was unable to confidently distinguish them from over 50 exemplars of other *Vibrio* spp. or *Allocatenococcus thioocyli*. Elastic light scatter analysis showed clear differences between each of the novel isolates and reference strains of *V. parahaemolyticus* and *V. vulnificus*, but limits of the in-house database, and the taxonomic scope required, precluded identification. DNA-DNA hybridisations modelled with 150 *Vibrio* spp. identified the strains as either *V. campbellii*, or one most closely resembling *V. rotiferianus*.

Conclusions: The limitations and challenges of methods for identifying microbes belonging to complex taxonomic groups are evident, and an effective strategy presented. Since *V. campbellii* and *V. rotiferianus* are aquacultural pathogens, this finding is of significance to this industry in New Zealand.

Investigating the Fibrotic Phenotype of Liver Cells during *Bartonella* Infection.

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Aim

Bartonella henselae is a prevalent, global bacterial pathogen that is the etiological agent for cat-scratch disease and is transmitted to people by bites and scratches from infected domestic cats. However, more severe manifestations occur in many patients. This includes bacterial colonisation of the liver, which can result in the formation of blood-filled cysts, known as bacillary peliosis. Multiple lines of evidence indicate that *Bartonella* promotes liver fibrosis as an important step in cyst formation. The aim of this project is to characterize the interactions between *B. henselae* and human liver cells, with a focus on fibrotic pathway markers.

Methods

The immortalised human hepatic stellate cell line, LX-2, was infected with *B. henselae* clinical isolates. The intracellular survival and replication of *B. henselae* inside hepatic stellate cells was assessed. Markers of cellular fibrosis, including cytokines and collagen, were evaluated by ELISAs, staining, and immunofluorescence.

Results (if applicable)

Co-incubation of *B. henselae* with LX-2 cells led to exponential uptake of bacterial cells by host cells, upregulation of markers associated with liver fibrosis, including collagen I production, and secretion of TGF- β . This was only observed in the presence of live bacteria. These findings suggest that factors produced by live bacteria promote the activation of fibrotic markers.

Conclusion (or expected impact)

Colonisation of the liver is predicted to have important clinical significance for the survival and spread of the *Bartonella* bacterium through the body. The results of this study provide insight into the mechanisms of cyst formation in the liver and provide new understanding into how the bacterium influences host cellular processes to drive disease.

Metagenomic analysis of *Campylobacter* at a wildlife–livestock–human interface in Uganda reveals novel species associated with human disease

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Aim:

To investigate *Campylobacter* diversity and prevalence at a high-intensity human–animal interface in Buhoma, Uganda, and assess the clinical relevance of human-associated species.

Methods

We analysed 553 gut microbiomes from mountain gorillas (n=200), cattle (n=83), goats (n=73), and humans (n=197) collected in Buhoma, Uganda. DNA was extracted and subjected to Illumina shotgun sequencing. Metagenome-assembled genomes (MAGs) were reconstructed, dereplicated, and classified using GTDB-Tk. Phylogenetic and functional analyses of *Campylobacter* were performed, and its abundance was compared across host groups. Clinical associations in humans were assessed via genome coverage, read-based mapping, and statistical analyses in R.

Results

We assembled 44 *Campylobacter* MAGs representing seven species, including five putative novel taxa. Mountain gorillas harboured three of these novel species, while livestock carried *C. vicugnae* (goats) and *C. sp017646085* (cattle). Human gut microbiomes revealed *Candidatus Campylobacter infans*, which was not associated with disease, and *C. sp900539255*, which was significantly enriched in clinical samples (p=0.001). Functional profiling revealed sulphur and nitrogen metabolic pathways unique to *C. sp900539255*. Phylogenetics revealed human-associated species clustered closer to non-human primate–derived species than to those from livestock. Antimicrobial resistance genes, including *blaOXA-471_1*, were detected in *Ca. C. infans* MAGs.

Conclusion

Campylobacter diversity is high at the human–animal interface in Buhoma, with novel species identified, including one significantly associated with human clinical samples. Expanding reference databases is critical for accurate surveillance and improved public health interventions.

Integrating Genomics and Epidemiology to Investigate the 2018 W:CC11 Meningococcal Outbreak in New Zealand

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Background: In 2018, Aotearoa New Zealand experienced a meningococcal outbreak caused by *Neisseria meningitidis* W:CC11, with Northland most affected. A prior study identified three W:CC11 strains in New Zealand, including one not widely seen internationally.

Aim: To integrate genomic and epidemiological data to understand who was affected, how the strain emerged, and the impact of the targeted MenACWY vaccination campaign.

Methods: All 95 MenW:CC11 cases with isolates were analysed using genomic sequences from Public Health and Forensic Science (formally ESR) and epidemiological data from EpiSurv. Emergence times were estimated via Bayesian phylogenetics (BEAST2). International comparisons were carried out via maximum likelihood analysis using publicly available genomes from PubMLST. Demographic analysis was conducted using EpiTools and EpiR in RStudio. Vaccination data was supplied by Te Whatu Ora.

Results: The three strains showed distinct geographic patterns: the UK strain in Counties Manukau, the 2013-UK strain in the South Island, and the 2015 strain in Northland, which drove the 2018 outbreak. All strains disproportionately affected Pacific People and Māori, especially those under 5 or over 60 in the most deprived areas. The 2015 strain likely resulted from a single importation in late 2015 - early 2016, followed by local expansion. This expansion clade included 57 of 65 New Zealand 2015 isolates and showed limited international mixing.

Conclusion: The outbreak was driven by a locally expanding strain not widely seen internationally. Identifying affected groups, evaluating vaccine impact, and tracing importation pathways highlight the importance of integrating genomic and epidemiological surveillance to inform future outbreak preparedness.

Importance of the membrane environment for fungal drug efflux pump function

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Membrane proteins (MPs) are responsible for vital cell functions and many are important drug targets. Dysfunctional MPs cause several human diseases and their overexpression frequently causes drug resistance in microbial pathogens and in human cancer cells. The drug resistance of the major human fungal pathogen *Candida albicans* is caused by the overexpression of MP Cdr1. Structure-directed drug design can overcome MP-mediated resistance, but this relies on correct MP structures. It is evident that MP structure and function depend on the complex composition and architecture of biological membranes. Aim: To investigate the effect of membrane composition on MP function. Methods: We generated a mutant of *Saccharomyces cerevisiae* that expresses the human homologue of *C. albicans* Cdr1, ABCB1, at a similar level to the parental strain but with increased pump activity. Results: Whole genome sequencing of the mutant identified mutations in ABCB1 (2), ergosterol [ERG25 (1)] and sphingolipid [CSG2 (1)] biosynthesis genes, and stop codons in VPS4, involved in protein trafficking and ergosterol metabolism, and CHD1, a chromatin remodeller and global regulator of transcription. Lipids were extracted from plasma membrane fractions of yeast cells and identified and quantified by liquid chromatography and mass spectroscopy. Although the membrane fractions contained surprisingly low levels of phosphatidyl serine and sphingolipids, there was an increased phospholipid to ergosterol ratio in the mutant with increased pump activity, which may affect membrane fluidity. There was also an increase in saturated, and a decrease in mono-unsaturated, free fatty acids in the mutant strain. Conclusion: This study shows that membrane fluidity and composition affect the function of efflux pumps.

Staphylococcin YAS1, a new lantibiotic bacteriocin produced by *Staphylococcus aureus*

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Members of the genus *Staphylococcus* inhabit a variety of human body sites, notably the skin and nasal passages. Some species, such as *Staphylococcus aureus*, are not only known pathogens, causing infections such as folliculitis, cellulitis and food poisoning, but also prolific producers of proteinaceous antibiotics (bacteriocins). *Staphylococcus aureus* YAS1, initially isolated based on its potent inhibitory activity against *Micrococcus luteus*, was subsequently shown to produce a broad-spectrum antibacterial agent (inhibits >90% of >100 indicator strains comprising >25 species). The genome of *S. aureus* YAS1, which was sequenced completely using a hybrid Illumina+Nanopore sequencing strategy, comprises a 2,833,669-basepair chromosome and a 3,593-bp cryptic plasmid, and contains six rRNA operons, 60 tRNA genes and 2,675 putative coding sequences. Analysis of the YAS1 genome sequence using BAGEL4 and antiSMASH revealed the presence of a 9.6-kilobasepair 7-gene locus (designated scy), which encodes a putative two-peptide class II lantibiotic with significant similarities to the enterocin W and plantaricin W two-peptide bacteriocins produced by *Enterococcus faecalis* and *Lactibacillus plantarum*, respectively. The scy locus appears unusual in that there are two lanM-like genes encoding lantibiotic modification proteins, suggesting that each staphylococcin YAS1 precursor peptide is processed differently. Future functional genomic experiments may reveal the roles of the various genes in staphylococcin YAS1 biosynthesis.

Unravelling the complexity of *Staphylococcus aureus* in Chronic Rhinosinusitis

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Aim

Staphylococcus aureus is commonly isolated from patients with chronic rhinosinusitis (CRS), a persistent inflammatory condition. Despite antibiotics being first-line treatment, they often fail—likely due to biofilms. Since *S. aureus* also colonizes healthy individuals, we aimed to identify phenotypic and genotypic differences between isolates from CRS patients and healthy controls, and explore potential drivers of pathogenic adaptation.

Methods

Nasal swabs were collected monthly over three months from CRS patients with cystic fibrosis (CF, n=37) and healthy controls (n=12), supplemented with previously collected cross-sectional isolates from idiopathic CRS (n=14) and healthy controls (n=18). We assessed biofilm-forming capacity (BFC) with crystal violet staining, and minimum inhibitory (MIC) and biofilm eradication concentrations (MBEC) for doxycycline. Evolutionary assays exposed isolates to low-dose antibiotics in biofilm and planktonic conditions over two weeks to simulate CRS-like stress. Oxford Nanopore whole-genome sequencing on 80 isolates and 4 evolved lineages identified resistance and virulence genes.

Results

Phenotypically, MIC, MBEC, and BFC were similar between CRS and healthy isolates. Genomic data showed CRS/CF isolates had 5 virulence genes compared to 4 in healthy controls. Evolutionary assays revealed biofilm adaptation under CRS-like stress increased MIC values over 10-fold (<0.2->20 µg/mL). CRS isolates maintained BFC in planktonic culture, whereas healthy isolates showed a 96.8% absorbance drop.

Conclusion

Despite similar baseline traits, CRS-associated *S. aureus* isolates may have greater potential for pathogenic adaptation. Understanding evolutionary dynamics and biofilm resilience is key to developing effective, biofilm-targeted therapies.

Re-evaluating postoperative antibiotic use in Chronic Rhinosinusitis: A microbiome perspective

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Chronic rhinosinusitis (CRS) is highly prominent within Western societies. CRS refers to persistent and prolonged (greater than 12 weeks) inflammation of the sinonasal mucosa, leading to a series of symptoms, including facial heaviness, headache, and reduced sense of smell, all negatively impacting the quality of life. Endoscopic sinus surgery is a common treatment option, and antibiotics are commonly prescribed post-surgery despite limited evidence to support their efficacy. Inappropriate antibiotic use can disrupt natural bacterial communities, with negative effects on patients further exacerbated through the rise of antibiotic-resistant bacteria, which may promote secondary infection within individuals. This research investigated whether antibiotics are clinically beneficial for the recovery process post-endoscopic sinus surgery. A small-scale pilot study previously found no significant differences between antibiotics and the placebo in terms of patient outcomes and microbiome effects. This recent study built upon the results of the pilot study, using a larger cohort, across various hospitals in New Zealand to provide greater clarity on whether antibiotics are necessary. Here, we took a microbiological perspective to delve deeper into what was happening at the sinonasal microbiome level within these individuals, along with going to greater depth than the original pilot study, through the inclusion of immunological data. All to uncover whether antibiotics are necessary, or if it leaves individuals worse off, challenging long-standing beliefs about the unsupported use of antibiotics.

Development of an ex vivo porcine wound infection model to evaluate antibiofilm therapies

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Background: Biofilms delay healing and are highly resistant to antibiotic treatment and immune clearance. They are present in the majority of chronic wounds. Effective antibiofilm therapies are needed, but preclinical in vitro models often use abiotic surfaces that lack the biological and structural complexity of wound beds, limiting clinical applicability. Porcine skin explants provide a practical and physiologically relevant platform for evaluating antibiofilm therapies.

Aims: To develop an ex vivo porcine wound infection model that supports clinically relevant bacterial biofilms.

Methods: Skin explants from porcine belly (8 mm diameter) were wounded (3 mm wide × 1.5 mm deep) using dermal punches. Explants were sterilised with ethanol (70%), Riodine (50%, 70%), or chlorhexidine (1%, 2%, 4%) for 30 or 60 minutes. Residual contamination was assessed by monitoring microbial growth for 14 days, and tissue integrity was evaluated by haematoxylin and eosin staining. Explants sterilised using the optimal treatment were inoculated with *Pseudomonas aeruginosa* ATCC 25783 or *Staphylococcus aureus* ATCC 6538 and incubated for three days to allow biofilm formation. Biofilms were quantified by colony-forming unit enumeration and visualised using scanning electron microscopy.

Results: All sterilisation treatments preserved tissue architecture, but 4% chlorhexidine for 60 minutes achieved the longest microbial suppression (10 days). Experiments to grow biofilms are underway.

Discussion: Sterilisation removes endogenous microbes while preserving tissue integrity, enabling controlled colonisation by target bacterial species. Subsequent biofilm formation within wound beds will create a physiologically relevant platform for the future evaluation of antibiofilm therapies.

Antimicrobial Peptide-Coated Dermal Substitute Eradicates Infection by Targeting Polymicrobial Biofilms and Immunomodulation in Wound Infection Models

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Aim: Management of infection remains a major challenge in wound care, and the alarming rise of antimicrobial resistance (AMR) has intensified the need for the development of new therapeutics and wound healing strategies to tackle this overwhelming issue. The current work aims to develop a next-generation dermal substitute with antimicrobial properties, designed to achieve synergistic effects in infection control and wound healing promotion.

Methods: In this study, two AMPs, nisin and cathelicidin LL-37 were coated together onto a commercially available dermal substitute Novosorb® Biodegradable Temporising Matrix (BTM) to develop a next-generation antimicrobial dermal substitute (BTM-AMPs).

Results: In vitro results demonstrated strong antimicrobial activity of the BTM-AMPs, with an ability to eradicate mature polymicrobial biofilms consisting of common Gram-positive and Gram-negative pathogens. In a direct contact kill assay, BTM-AMPs showed a comparable efficacy to the commercially available antimicrobial matrix, Endoform®. Using an ex vivo bioluminescent biofilm model, BTM-AMPs reduced the burden of metabolically active bacteria by >50% after 6-hour treatment. Furthermore, BTM-AMPs exhibited strong anti-inflammatory properties by significantly reducing the level of pro-inflammatory TNF- α cytokine and increasing the phagocytotic activity of macrophages in vitro.

Conclusion: Overall, dual coating of Nisin and LL-37 onto BTM dermal substitute presents a promising approach for managing clinical infections and eradicating biofilms in chronic wounds.

Exploring the potential of vitamin B12-antibiotic conjugates to combat antimicrobial resistance in Gram-negative bacteria of WHO critical concern.

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Antimicrobial resistance is a significant global health risk, with priority bacteria (mostly Gram-negative) being identified for development of new antibiotics. More importantly, novel treatment approaches for currently available drugs are an ongoing research area.

We aim to develop a novel drug delivery method that utilises bacterial uptake of vitamin B12 (B12), an essential bacterial co-enzyme. Bacteria efficiently take up environmental B12/B12 analogues, therefore hijacking B12 uptake could circumvent the intrinsic resistance of the Gram-negative outer membrane - a key resistance mechanism. This “Trojan horse” principle has demonstrated previous success, with B12 conjugates demonstrating efficient intracellular transport of diverse substances. Clinical success has also been demonstrated, with approval of the siderophore-cephalosporin conjugate Cefiderocol.

A key part of this research was identifying the localisation of B12. B12-fluorophore localisation in *Escherichia coli* (*E. coli*) was assessed by separating cell compartments via fractionation. These conjugates were found in the combined outer membrane and periplasmic space fraction but absent from cytosol. Additional research is being done to better understand localisation to the outer membrane versus the periplasm. A range of B12-antibiotic conjugates were also synthesised and tested for activity using the minimum inhibitory concentration (MIC) assay in *E. coli*. Conjugates of Gram-positive drugs Rifampicin and Vancomycin were tested, but B12 conjugation did not result in efficacy. Further research is underway to determine if B12 conjugation enhances efficacy of Gram-negative antibiotics such as ampicillin.

These findings could restore and enhance antibiotic efficacy, significantly impacting global health.

Identification of novel inhibitors targeting serine acetyltransferase from *Neisseria gonorrhoeae*

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Aims: *Neisseria gonorrhoeae* is an obligate human pathogen and the causative agent of the sexually transmitted infection, gonorrhoea. Antimicrobial resistance has emerged at an alarming rate for *N. gonorrhoeae* and has reduced treatment to a sole antibiotic therapy. The biosynthesis of the amino acid L-cysteine has emerged as a promising target for antimicrobial development. Serine acetyltransferase (CysE) catalyzes the first step in cysteine biosynthesis and plays a central role in regulating intracellular cysteine levels. CysE is essential in *N. gonorrhoeae* and absent in humans, making it a promising target for antimicrobial intervention. This study aims to characterise and validate CysE as an antimicrobial target.

Methods: CysE enzymatic activity and inhibition were assessed via a spectrophotometric assay that monitored substrate depletion. Using X-ray crystallography, we determined the structure of CysE and used this to inform structure-based virtual inhibitor screening of commercially available compound libraries.

Results: CysE was shown to be enzymatically active and subject to competitive inhibition by the pathway end-product L-cysteine. Two crystal structures were resolved at 2.0 Å and 2.8 Å, with L-malate and L-serine bound, respectively. Structure-based virtual screening identified 28 candidate compounds, which were subsequently evaluated *in vitro*. One compound exhibited inhibitory activity against CysE with an IC₅₀ in the low micromolar range.

Conclusion: Collectively, we have identified the first inhibitor of CysE from *N. gonorrhoeae*. These findings represent the first attempt to target the cysteine biosynthesis pathway in *N. gonorrhoeae* and support further investigation of CysE as a therapeutic target.

Exploring the Metabolic Secrets of *Haemophilus influenzae*: Does Ribose Utilization Contribute to Its Virulence and Persistence?

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Aim: This study explored the role of ribose metabolism in *Haemophilus influenzae* (Hi) for its in-host survival and contribution to virulence, including Quorum Sensing (QS).

Methods: We investigated the growth, infections and virulence-related phenotypes of Hi2019 strain with mutations in ribose uptake (*rbsB*) and utilization (*rbsK*, *rpiA*).

Results: Ribose transport (*rbsB*) and phosphorylation (*rbsK*) are essential for ribose utilization. $\Delta rbsB$ and $\Delta rbsK$ strains also displayed impaired growth on nucleosides. $\Delta rbsK$ and $\Delta rpiA$ strains exhibited reduced anaerobic growth and increased NADH levels, indicating metabolic network alterations, while ATP production dropped minimally (~10%). In macrophage infection, intracellular survival of $\Delta rbsB$ and $\Delta rbsK$ strains decreased 2-fold, correlated with elevated TNF- α and IL-6 production. The *rbsB* mutation resulted in a 30% reduction in IL-8 production in infected 16HBE14 tissue cells. Interestingly, mutation of *rbsB* led to a 35% increase in biofilm formation, a key Hi virulence trait regulated by QS. *rbsB* is implicated in the uptake of the QS signal, autoinducer-2 (AI-2). AI-2 production by the $\Delta rbsB$ strain decreased ~25% over time in CDM medium and 16HBE14 infections. The $\Delta rbsB$ strain also showed a ~50% AI-2 reduction under 1 mM NCT-induced oxidative stress. While WT AI-2 production was unaffected by NCT. A mutation in *luxS*, encoding an AI-2-producing enzyme, resulted in no AI-2 production and increased biofilm formation, a phenotype also observed in the $\Delta rbsB$ strain. This suggests a functional link between AI-2 production and uptake.

Conclusion: While ribose utilization is not critical in most infection settings, the intriguing connection between ribose transport, pathogenicity, and QS warrants further investigation.

Invisible Influencers – How flower yeasts mediate pollinator behavior?

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Microbes inhabiting flowers can either attract or deter pollinators, yet the mechanisms underlying these interactions remain poorly understood. Certain nectar-inhabiting yeasts are especially appealing to honeybees and bumblebees. Here, we test whether yeast-mediated pollinator behavior is driven by (1) nutrients or (2) scent signals. We characterized amino acid and volatile profiles of multiple nectar yeasts using liquid chromatography and solid-phase microextraction coupled with gas chromatography–mass spectrometry, respectively, and paired these with behavioral assays of honeybee foraging. Highly attractive yeasts displayed distinct amino acid compositions and produced unique volatiles, though overall volatile profiles overlapped among species. Our results suggest that volatiles function as initial attractants, while yeast-derived nutrients likely determine honeybee foraging preferences.

Within-site and geographic location of Maire tawake (*Syzygium maire*) are significant contributors to its leaf microbiome

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Maire tawake (*Syzygium maire*) is an endemic swamp forest tree of the Myrtaceae plant family. In Aotearoa New Zealand it is the sole representative of the *Syzygium* genus and is uncommon due to land clearing, swamp draining, and extreme susceptibility to *Austropuccinia psidii*.

Aim

This research set out to characterise the epiphytic leaf microbiome of healthy Maire tawake trees and investigate how other species of neighbouring trees contribute to their microbiome.

Methods

Leaf samples were collected from the bottom canopy of focal Maire tawake at three geographically different locations across the country's North Island. Nine neighbouring plants at least 1 m above the ground floor within 5 m of the focal maire tawake were also sampled. Amplicons for 16S rRNA, 18S rRNA, and ITS1 regions were sequenced from microbial matter sonicated from the leaf phyllosphere, processed using DADA2, and analysed in R and Linux.

Results

Maire tawake leaf microbiomes host similar fungi, bacteria, and protists to their neighbouring plants. The shared core amplicon sequence variants (ASVs) between plant hosts were higher than unique host ASVs, whereas shared ASVs across geographic locations was lower. Within-site location explained the greatest microbiome variation for all samples, followed by geographic location. Differential abundance showed that several ASVs known to be plant pathogens, endophytes, and biocontrol agents were more or less abundant in maire tawake than other neighbouring trees. Neutral community modelling indicates that the fungal microbiomes are affected more by deterministic processes than bacteria and protists.

Impact

This is the first study of the Maire tawake leaf microbiome and lays the foundation for concurrent research into *A. psidii* and potential biocontrol applications.

Host genetic influences on the root microbiomes of conifers

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Conifers and other long-lived tree species with slow generational turnover have likely relied on the adaptive potential of their microbial partners to survive past environmental changes. Understanding these associations and how they influence tree fitness may hold opportunities for future survival, however, host-microbe relationships and the eco-evolutionary forces that have shaped them are poorly understood in most tree species.

AIM

We aimed to understand inter- and intraspecific host genetic influences on the bacterial and fungal tree-root microbiome. Using a phylosymbiosis framework, we analysed 23 conifer species for evidence of coevolution in root microbiome symbioses. We also explored the effect of intraspecific host genetics in *Pinus radiata* D. Don, sampling roots of 528 individuals from a structured breeding trial. Lastly, we examined heritability of microbial taxa within the *P. radiata* root microbiome.

RESULTS

We found strong evidence for phylosymbiosis between conifers and root microbiomes, evident to host genus-level. Unsurprisingly, host genetic effects within *P. radiata* were harder to detect but remained significant for the fungal root microbiome. Individual bacterial and microbial taxa with significant moderate heritability were identified; these were generally rare in occurrence and attributable to complex gene interactions in the host such as dominance and/or epistasis.

CONCLUSION

Our results demonstrate the importance of phylosymbiosis in the assembly of conifer root microbiomes. Modifying the relative abundance of certain microbial taxa through selective host breeding has potential, however, further investigation into the genetic mechanisms responsible and how these interact with each other and the environment is recommended.

Microbiomes on the move: Interspecific selection and local adaptation drive *Pinus radiata* root microbiome symbiosis.

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Aim

We investigated the microbiome of the widely grown conifer *Pinus radiata* to test how root microbiomes are shaped by evolutionary processes (e.g., interspecific selection) versus local environmental adaptation. *P. radiata* evolved in geographically isolated populations under long-term bioclimatic shifts. Its rapid global domestication has displaced it from endemic microbial associations, yet it thrives across diverse environments.

Methods

We sampled *P. radiata* in its endemic (USA and Mexico) and introduced (New Zealand and Australia) ranges. Microbial communities were characterised via Illumina MiSeq amplicon sequencing. Evolutionary influences were assessed by comparing endemic vs. introduced ranges, while local adaptation was examined via regional variation. Site-specific effects, including bulk soil microbiomes, were partitioned before evaluating the contributions of interspecific selection and local adaptation.

Results

Both bacterial and fungal root microbiomes were shaped by interspecific selection and local adaptation. For bacteria, local adaptation (15.8%) explained more variation than interspecific selection (11.2%); in fungi, both were comparable (19.8% vs. 19.3%). Soil communities had strong secondary effects on bacterial root composition (21.5%). Despite limited taxonomic overlap, a small set of core taxa was conserved across environments. Microbial networks were structurally conserved, but bacterial networks in introduced ranges were more connected, while fungal networks were more modular and flexible.

Conclusion

Root microbiomes are influenced by both local adaptation and evolutionary history. *P. radiata* succeeds globally by engaging microbiome assembly processes that draw on both its evolutionary legacy and adaptive flexibility.

Illuminating the microbiomes of native New Zealand mosses using 16S rRNA gene sequencing

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Mosses play vital ecological roles in water retention, nutrient cycling, and providing shelter for microfauna. Notably, certain moss species are consistently found in bird nests, even when they are not the most abundant mosses in the local environment. Recent research has identified six New Zealand mosses that are frequently incorporated into nests across diverse native and exotic bird taxa, yet the underlying drivers of this pattern remain unknown. One factor hitherto unexplored in New Zealand is the moss microbiome. This study aims to determine whether nest-associated mosses harbour distinct bacterial communities compared to morphologically similar non-nest mosses. We have collected a total of 108 moss samples, including four nest-associated and eight non-nest species, and are comparing bacterial communities in the two groups using 16S rRNA gene amplicon sequencing. We hypothesise that nest-associated mosses harbour distinct bacterial communities compared to non-nest mosses, as a first step toward understanding the potential role of moss microbiomes in avian nesting behaviour. As moss microbiomes in New Zealand remain unexplored, this study will offer new insights into plant-microbe-animal interactions, with potential implications for avian nesting ecology and biodiversity conservation.

Yeast diversity associated with New Zealand Beech trees.

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Yeast, single-celled fungi, play important roles in natural ecosystems, often acting as decomposers and nutrient cyclers. They are highly valued in industry due to their versatile roles in fermentation and bioprocessing. Due to our geographical isolation, New Zealand (NZ) has a high potential for endemism and yet little is known about the distinctiveness or diversity of yeast in our native environments. Internationally, unique species of yeast are known to associate with specific *Nothofagus* (Beech) species.

Aim: This research aims to evaluate the species diversity of yeast found associated with three species of NZ Beech and investigate if there is niche partitioning based on the species of tree.

Methods: Bark and soil samples were taken from three Beech tree species in Nelson Lakes National Park, NZ: Mountain beech (*Fuscospora cliffortioides*), Red beech (*Fuscospora fusca*) and Silver beech (*Lophozonia menziesii*). Yeast enriched from these samples are being identified using molecular methods and the species diversity will be compared between the three tree species.

Results: Preliminary species identifications using the 26S rRNA region suggest a diversity of yeast species have been isolated from the tree samples and species of *Saccharomyces*, *Lachancea*, *Torulaspora*, and *Hanseniaspora*.

Conclusion: New Zealand's native yeast diversity is largely unexplored and there is potential to discover new or endemic yeast species. Here the tree host species is investigated as a potential driver of yeast community differentiation, providing important ecological context to yeast diversity in NZ. These findings can contribute to the broader understanding and preservation of New Zealand's yeast biodiversity not only for conservation but for further biotechnological applications.

Global diversity analysis of plant-associated *Pseudopithomyces* fungi associated with facial eczema in livestock

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Aims

Facial eczema (FE) in ruminants is associated with the fungal toxin sporidesmin that can cause significant mortality in grazing livestock. Incidences are particularly severe in New Zealand but are reported worldwide. The syndrome has historically been attributed to *Pithomyces chartarum*, a species transferred to *Pseudopithomyces* in 2015, however the classification of many other *Pithomyces* species remains unresolved. In this study we investigate the taxonomy of *Pseudopithomyces* using modern species concepts and clarify which species make sporidesmin.

Methods

Fungal isolates were spore-purified from grass samples obtained from New Zealand farms in 2022, and from roadside collections in 2014, 2019, 2020 and 2021. International isolates, including all available types, and historic isolates deposited in the International Collection of Microorganisms from Plants (ICMP) were also evaluated. Phylogenetic analyses of the ITS region plus four concatenated protein coding genes distinguished 15 species in the genus, including new species and novel taxonomic combinations.

Results

Two species were recovered from pasture grass samples collected from the North and South Islands, with only one predominately associated with toxin production, that we describe as a new species.

Feeding the Soil to Fight the Pathogen: Organic Amendments can Boost Microbial Defense in Potato and Lettuce

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Soilborne pathogens such as *Ralstonia solanacearum* (RS2) represent a major constraint to global horticultural production, causing bacterial wilt and severe yield losses in key crops including potato and lettuce. With limited natural resistance in most cultivars, sustainable management strategies are urgently needed. Here, we test whether different agricultural management and new microbial tools (Syncom) could enhance plant resistance and suppress bacterial infection by stimulating beneficial soil microbiomes. Pot and glasshouse experiments were conducted using compost, mineral fertilizer (NPK), microbial consortia (SynCom), and their combinations under both healthy and pathogen-challenged conditions. Compost-based treatments markedly improved plant growth, biomass, and yield compared with NPK or SynCom alone. Microbial community analyses revealed that compost and pathogen + compost (P+Compost) treatments increased bacterial and fungal diversity and enriched beneficial taxa, including Burkholderia, Streptomyces, Azospirillum, Trichoderma, and members of Serendipitaceae. Community composition differed significantly among treatments (PERMANOVA $R^2 = 0.37-0.60$, $P \leq 0.01$). Furthermore, co-occurrence network analysis revealed that RS2 decreased network complexity and connectivity as compared to healthy treated soil and roots. Together, these findings demonstrate that organic amendments could foster biologically active, disease-suppressive soils by promoting beneficial microbiomes. This work lays the groundwork for developing resilient, microbially informed disease management strategies, and future research will integrate meta transcriptomics and soil chemistry to elucidate the molecular pathways underpinning microbial-mediated disease suppression under changing environmental conditions.

How sterile is “sterile”? Exploring the microbiome of tissue-cultured plants

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New Zealand’s primary sector relies on the importation of diverse plant germplasm to meet the needs of growers and consumers. However, imported germplasm carries the risk of introducing unwanted pests and pathogens. While biosecurity measures are in place to mitigate these risks, they are often constrained by limited resources. Plant tissue culture, traditionally regarded as a sterile method for propagating plant material, may provide a safer means of importing germplasm into the country. To assess this potential, we investigated the microbial communities associated with tissue-cultured plants of *Pinus radiata* (radiata pine), *Vaccinium corymbosum* (blueberry), and *Humulus lupulus* (hops). A combination of culture-dependent methods and metabarcoding using the 16S and ITS markers was employed to characterize bacterial and fungal communities. Overall, microbial signals were low across all species. In hops and blueberry, fungi were detected in 8% and 5% of samples, while bacteria were detected in 6.5% of samples for both species. In *P. radiata* somatic embryogenic lines, bacterial isolates were primarily members of *Bacillus*, *Peribacillus*, and *Paenibacillus*, while fungal isolates included *Aspergillus* and *Chaetomium* species. Metabarcoding identified additional bacterial and fungal taxa, largely comprising plant-associated microbes. Notably, microbial communities differed between seed-derived and tissue-cultured material, with the number of sequences declining with as the time in tissue culture increased. Importantly, no primary plant pathogens were detected in any samples. These findings support the view that tissue-cultured plants represent a low biosecurity risk and could be a relatively safe pathway for importation of valued plants into New Zealand.

Phage-Based Biocontrol of American Foulbrood in Honeybees: The ABAtE Project

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AIM:

The European honeybee (*Apis mellifera*) is arguably the most economically valuable pollinator of crops worldwide. American Foulbrood (AFB) is a devastating disease of honeybee larvae caused by the bacterial pathogen *Paenibacillus larvae*. AFB is the most serious disease of honeybees and is found on every continent that has honeybees. The use of antibiotics or any substance to treat or mask AFB is prohibited under Australian and New Zealand law and infected hives must be destroyed. The ABAtE (Active Bacteriophages for AFB Elimination) project aims to discover and develop bacteriophages as a preventative measure against AFB. Previous work by Yost and colleagues in the USA has demonstrated that bacteriophages can protect hives against AFB infection when applied in advance of exposure (Yost et al., 2016).

METHODS:

A community science approach was used to undertake sampling over a short period of time and from these samples 26 novel *P. larvae* bacteriophages were discovered, sequenced, and annotated (Kok et al., 2023).

RESULTS:

This work describes the 93% host range coverage of *P. larvae* in New Zealand and the in vitro evaluation of phage cocktails, including evidence of potential phage-phage antagonism. I will also present phylogenetic data on these bacteriophages and how they have added to our understanding of the global distribution of *P. larvae* phages (Kok et al., 2025).

CONCLUSIONS:

This project is part of a larger MBIE-funded programme (Adaptable Phage Solutions) and provides the groundwork for an innovative approach to naturally protect beehives against AFB. The goal of the Adaptable Phage Solutions programme is to develop a platform for rapid development of phages to protect primary industries in New Zealand and around the world.

Moving beyond taxonomic descriptions: dietary-dependent microbiota-metabolome interactions reveal often-overlooked impacts of artificial diets on laboratory-reared caterpillars

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Aim

Mass rearing of insects on artificial diets has become essential for modern entomological research. While gut microbe is a dynamic component of insect physiology and development, mechanisms underlying microbe-host interactions remain poorly studied.

Methods

We examined how diet impacts gut microbiota and metabolome of *Spodoptera litura* fed three diets (cabbage, tobacco, artificial diet). Using 16S rRNA sequencing and metabolomics, combined with PICRUSt and MIMOSA2 (community metabolic model-based analysis), we identified key gut microbial taxa functionally contributing to metabolite variations and diet-induced changes in microbe-metabolome interactions.

Results

Diet significantly impacted microbial structure and metabolite abundance. We observed prevalent microbe-metabolome interactions across populations with distinct metabolite variations. Notably, dietary patterns in these interactions included a complete turnover of microbial taxa contributing to vitamin B metabolism between artificial-diet-fed and natural-plant-fed hosts, despite identical overall contributions of all taxa to this metabolism across diet groups. In artificial-diet-fed individuals, microbe-host interactions were predominantly related to amino acid metabolisms, likely due to high and diverse protein intake.

Conclusion

Our findings reveal overlooked impacts of artificial diets, affecting not only gut microbiomes or host metabolomes independently, but also microbe-insect interactions. This study highlights the importance of investigating microbial functions and metabolic interactions instead of focusing solely on taxonomic descriptions. These results emphasise carefully considering artificial diet effects when designing experiments or extrapolating laboratory findings to real-world scenarios.

Response of the tuatara gut microbiome to dietary manipulation and captivity

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The bacteria of a host's digestive tract play crucial roles in digestion and pathogen resistance. Hosts living in captivity often have more human interaction and antibiotic use, in addition to differences in diet and environment, compared to their wild counterparts. Consequently, wild and captive animals frequently harbour different bacterial communities. We tested whether diversity of diet provided in captivity shifts the gut bacteria of tuatara, an endemic New Zealand reptile, at three captive sites, and examined how the gut community of these tuatara compares to those in the wild. Dietary manipulation did not cause a strong overall shift in tuatara gut bacteria, but individual tuatara did experience bacterial shifts during manipulation, which subsequently reverted after manipulation. We found that *Bacteroides*, a genus common in most vertebrate guts but rare in tuatara, increased significantly in the gut during manipulation, then decreased post-manipulation. Finally, the gut bacteria of captive tuatara significantly differed from those of wild tuatara, though most of the dominant bacterial genera found in wild tuatara persisted in captive tuatara. This work represents a first investigation of the captive tuatara bacterial community and establishes the sensitivity of the gut community to dietary manipulation and captivity for this relict reptile.

The Role Of Kākāpō Nest Mycobiota in Shaping Aspergillus Spp. Abundance and Pathogenic Potential

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The critically endangered kākāpō (*Strigops habroptilus*), has faced two aspergillosis outbreaks in 2019 and 2022, affecting 21 and 7 individuals respectively.

Aim: We investigated how nest-associated environmental yeasts in kākāpō breeding sites influence the prevalence of *Aspergillus fumigatus*, the primary fungal pathogen responsible for aspergillosis.

Methods: We measured the abundance of viable *A. fumigatus* and yeast species in kākāpō nest soils and performed co-cultivation competition assays to confirm competitive dynamics between the two fungal types.

Results: The results show that almost half of nests with confirmed aspergillosis had no *Aspergillus* spp. counts and that there is an inverse relationship with yeasts species. The competition assays also confirmed that yeast isolates from kākāpō nest significantly suppressed *A. fumigatus* and *A. niger* ($p < 0.05$), although the mechanism of growth suppression remains unclear.

Conclusion: Our findings demonstrate a competitive dynamic between yeast species and *Aspergillus* spp. from kākāpō nests. Given that some of these yeasts have previously caused infection in kākāpō along with evidence that *Aspergillus*-yeast interactions can trigger the production of harmful secondary metabolites, further research is needed to clarify the role of nest-associated yeasts in kākāpō aspergillosis susceptibility.

Prevalence and distribution of *Bifidobacterium animalis* subsp. *animalis* in domestic and production animals in Canterbury, New Zealand

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Aim: *Bifidobacterium animalis* subsp. *animalis* was first described in 2004 and has been proposed as a microbiomic marker of positive health in certain animals, and thus has appeal for inclusion in some probiotic formulae. The prevalence of this organism is however poorly understood, with sources rarely investigated and no studies of the presence of the organism in New Zealand to our knowledge. We investigated the presence of the organism in a range of domestic and production animals in the Canterbury region.

Methods: Fifty-four samples from poultry feces (n=3) and intestine (n=22), pig intestine (n=16), rabbit (n=10)- and rat (n=3) feces, representing a variety of commercial and domestic sources, were examined for using each of two isolation protocols involving either a nonselective enrichment broth and selective agar; or selective enrichment and nonselective agar. Bacterial growth was screened for using a duplex PCR designed to detect both *Bifidobacterium animalis* subsp. *animalis* and *Bifidobacterium animalis* subsp. *lactis*. The PCR was validated against the type strains of these taxa.

Results: A total of 25 out of 54 samples examined (46.3%) tested positive for *Bifidobacterium animalis* subsp. *animalis*, of which 11 were from poultry intestines (from both conventionally reared and free range production systems), 12 from pigs and 2 from rats. None of the rabbits examined were found to harbour the organism.

Conclusion: This study indicates for the first time that *Bifidobacterium animalis* subsp. *animalis* is widely distributed among production- and domestic animals in the Canterbury region of New Zealand.

Diet and digestive strategy shape the hindgut microbiome in New Zealand marine herbivorous fish

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Aims: This study investigated differences in the functional and taxonomic compositions of the hindgut microbiota communities of four species of New Zealand herbivorous marine fish with diverse diets and digestive strategies.

Methods: Metagenomic data was used to compare how community-level functional differences were encoded within the microbiomes of the four fish species examined. MAGs were used to interrogate how the distribution of essential symbiotic functions encoded within the microbiome, differed across bacterial microbiota of the four host species.

Results: Host-specific trends in hindgut microbiome capacity to degrade a number seaweed-derived substrates were identified, particularly variations in the range and number carbohydrate degrading enzymes and enzymes families encoded across each host species microbiome. Members of the genera *Alistipes* and *Mailhella* were identified as key symbionts in some of the host fish species, with *Alistipes* MAGs demonstrating extensive carbohydrate-degrading abilities and *Mailhella* members encoded roles in dinitrogen fixation and biosynthesis of cobalamin and thiamine.

Conclusions: The study highlights the significant relationship between fish host dietary strategy, the extent to which the host relies on microbial fermentation to meet their energy needs, and functional capacity to degrade specific substrates from each host's diet. The MAGs indicated significant differences in the way carbohydrate-degrading capacities and other essential symbiotic functions like cobalamin and thiamine biosynthesis were distributed across different taxonomic groups of bacteria within the microbiome of each host fish species.

Role of temperature on the gut microbiota in the marine teleost snapper (*Chrysophrys auratus*, tāmure) in captivity and the wild

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The gut microbiome plays a crucial role in fish health and aquaculture sustainability, with environmental temperature generally being a key factor in shaping microbial community structure of the fish digestive system. We collected New Zealand snapper/tāmure (*Chrysophrys auratus*) to compared the gut microbiota of captive individuals exposed to contrasting thermal conditions (treatments: hot vs cold) with wild individuals collected along a latitudinal temperature gradient. Metagenomics and metatranscriptomics was then used to examine the diversity and potential strain variation of the gut microbiota. Currently there is minimal information on the gut microbiome of snapper, a carnivorous species, with no knowledge about how the wild gut microbiota compares to captive snapper reared for aquaculture production, or of the natural variation among individuals. Preliminary findings indicate a low level of microbiota complexity in snapper, with microbial alpha diversity remaining stable across varying temperatures and spatial locations that are 100 of kilometres apart. Across all conditions, *Bacillus* emerged as a key microbial member of the gut microbiome. Members of this genus were ubiquitous and present at high abundance (representing over 75% of the bacterial population on average). Further works aims to determine strain-level functional role of the gut taxa. To summarise, we will present results about the influence of temperature on microbial diversity and composition of snapper/tāmure

Rumen adapted for future feeds to improve animal health and performance.

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Aim

Microbiome-informed investigation to determine the influence of C₄ grass-dominated pastures on the rumen microbial community composition, diversity and functions in grazing ruminants.

Methods

In this study, we applied a metagenomic approach to investigate the ecosystem-level changes in rumen microorganisms in animals influenced by a C₄ grass fibre dominated pasture composition of Kikuyu (*Pennisetum clandestinum*). A total of 172 rumen samples were collected at three Northland farms (Broadwood, Te Kao and Dargaville) from Kikuyu (*Pennisetum clandestinum*)-adapted beef and dairy cattle. Metagenomic sequencing datasets were used to perform direct-profiling-based approach and construct metagenome-assembled genomes (MAGs). Wet chemistry analysis was also performed on freeze-dried representative pasture samples from each farm to determine the various plant composition characteristics.

Results

The chemical composition analysis determined that the Kikuyu samples did not have much neutral detergent fibre (NDF), and had low protein concentration. By integrating compositional and functional microbiome data from Kikuyu-fed animals across farms, we constructed high-quality MAGs and gene catalogues of anaerobic rumen microbes involved in fermentation and digestion of C₄ grasses.

Conclusion

Our microbiome, genome-inferred metagenomic analysis of rumen samples collected from Kikuyu-adapted ruminants has revealed the key microbiota species, functional pathways and enzymes responsible for biodegradation and metabolism of C₄ grasses in the rumen. This study provides a valuable microbial genomic resource to help future agricultural microbiome research aiming to improve animal production while facing nutritional challenges in a changing climate.

Integrated microbiome-proteome analysis identifies key factors associated with the low abundance of *Vibrio parahaemolyticus* in green-lipped mussels (*Perna canaliculus*)

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Aim

To determine the effect of abiotic and biotic factors and their interactions on the abundance of *V. parahaemolyticus* in its natural habitat/s.

Methods

16S RNA sequencing, comparative proteomics, qPCR - most probably number, algae quantitative and taxonomy identifications.

Results

Comparing 216 microbiomes of seawater, biofilms and mussels over one year, we found that the composition of mussel microbiota is not significantly influenced by the microbiomes of seawater and marine biofilms. Using an in-situ approach, our results showed that mussels with significantly low *V. parahaemolyticus* abundance have distinct microbiota, characterised by species of known vibriocidal status (e.g. *Pseudomonas* spp.) and species of unknown vibriocidal status (e.g. *Campylobacterota*, *Bacteroides massiliensis*, *Lancefieldella*, *Erysipelotrichales*, *Faecalibacterium*, and *Catenibacterium*). Examining proteomes of mussels with high and low *V. parahaemolyticus* abundance, we discovered the LMN domain-containing protein, which is constitutively induced only in mussels with low *V. parahaemolyticus* abundance regardless of mussel age or time of harvest. The LMN domain-containing protein showed significant interactions with a group of proteins involved in haemocyte differentiation and endosome biogenesis, key immunological processes in mussels.

Conclusion

This study provides novel insights into the complex diversity and interactions among marine microbiotas. The findings suggest that the low abundance of *V. parahaemolyticus* in mussels is a result of the distinct microbiota composition and proteome profile of mussels.

Lighting the Way: Bioluminescent Huakita for Feed Visibility.

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Introduction: *Artemia* sp. (brine shrimp) remain the most widely used live feed in larval aquaculture due to their ease of cultivation and nutrient loading. Yet, they are costly to produce, environmentally unsustainable, and not suitable for all ika (fish) species. Inert microdiets offer nutritionally complete alternatives but fail to trigger feeding in early-stage larvae due to their underdeveloped eyes. In *te taiao* (nature), bioluminescence functions as a highly effective visual tool, employed by organisms to attract prey and evade predators. In huakita (bacteria), bioluminescence is a genetically encoded trait that facilitates a range of ecological interactions, including host attraction and communication. We hypothesised that this trait could be harnessed to increase the visibility of larval fish feeding and elicit a strike-feeding response. Aim: To test whether hīnatore huakita (luminescent bacteria) can be used to enhance feed visibility and attractiveness of both live and inert feeds for larval ika. Methods: Luminous bacteria were tested in two experimental feed formats: live *Artemia* and an inert alginate-based microbead system. *Artemia* nauplii were inoculated by immersion and assessed for visible light emission, while alginate microbeads were produced by encapsulating the luminous bacteria in sodium alginate as it was dropped into CaCl₂. Luminescence was measured over time to determine signal duration. Results: Inoculated *Artemia* and encapsulated microbeads exhibited visible bioluminescence for several hours. Conclusion: Our data demonstrate the potential of bioluminescent huakita as a tool to enhance feed recognition and stimulate strike-feeding responses in larval ika, offering a novel alternative to conventional live feeds in early-stage aquaculture.

Abstracts – Poster Presentations

Microbial Ecology & Evolution

Can *Thermus* revolutionize plastic bioremediation like it transformed molecular biology?

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Plastic pollution has become a global issue, with debris being reported in various environments, including Arctic landscapes and the deepest parts of the Ocean. Despite the many environmental threats that plastics pose, the production of different plastic materials is still increasing and will continue its growth in the future, reaching 884 Mt in 2050 – double the current production volume.

Efficient plastic degradation typically occurs above 50 °C, limiting the applicability of most known microbial degraders and their enzymes. A well-known example is PETase, produced by *Ideonella sakaiensis*, which requires protein engineering to function effectively. We propose an alternative: exploring thermophilic microorganisms instead.

New Zealand's geothermal environments host a rich diversity of thermophiles whose potential in plastic bioremediation remains largely unexplored. We screened bacterial isolates from geothermal springs in Kuirau Park, Rotorua for potential abilities to degrade plastic polymers, specifically polystyrene (PS), polycaprolactone (PCL) and polyethylene terephthalate (PET). Our most notable isolate, *Thermus filiformis*, a species endemic to New Zealand, demonstrated signs of degradation of both PS and PCL, confirmed by halo formation and weight-loss assays. Genomic analysis revealed four candidate genes potentially involved in this process, including carboxylesterases and hydrolases. We now aim to heterologously express them and evaluate their activity against selected plastic substrates.

This work highlights the potential of thermophiles as a new frontier in plastic bioremediation, with *T. filiformis* offering promising leads for enzyme discovery and future applications.

Human and Medical Microbiology

Enteropathogenic *Escherichia coli* (EPEC) exploits the host exocyst complex to augment pedestal formation

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Enteropathogenic *Escherichia coli* (EPEC) is a leading cause of infantile diarrhea worldwide. Upon infection, EPEC uses its type III secretion system to inject effector proteins into the cytoplasm of the host cell. Tir, one of the major effectors inserted into the plasma membrane, triggers the assembly of actin filaments forming protrusive structures called "pedestals" on the apical cell surface. Apart from Tir, EPEC delivers ~25 additional effector proteins that contribute to pedestal formation and other events related to infection. Until now, actin filament assembly was the only host process known to contribute to pedestal formation. Here, we report that EPEC also exploits the host vesicular trafficking pathway of polarized exocytosis to enhance pedestal generation. Polarized exocytosis is facilitated by an octameric protein complex called the exocyst and the SNARE protein VAMP3. We found that depletion of exocyst proteins or VAMP3 using RNAi reduced the efficiency of pedestal formation. Moreover, by using an exocytic probe consisting of VAMP3 fused to EGFP, EPEC was found to stimulate exocytosis in pedestals. This upregulation of exocytosis required the effector protein EspH, which recruited the exocyst complex to sites of pedestal formation. Studies involving Airyscan super-resolution imaging revealed that deletion of the *espH* gene reduced the mean size of pedestals. Collectively, our results indicate that EPEC uses its effector EspH to exploit the host exocyst, thereby stimulating exocytosis that increases both the frequency of formation of pedestals and the size of these structures.

Human and Medical Microbiology

Enteropathogenic *E. coli* Subverts Host Exocytosis to Promote Pedestal Formation

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Enteropathogenic *E. coli* (EPEC) is a major cause of diarrhoea in children under five years of age. EPEC infection is characterized by formation of actin-rich structures known as "pedestals" underneath attached bacteria. Generation of pedestals is initiated by translocation of the bacterial effector protein Tir into host cells. Translocated Tir undergoes tyrosine phosphorylation, leading to activation of the host ARP2/3 complex and subsequent actin polymerization at bacterial adhesion sites. The resulting actin filaments provide a protrusive force to remodel the plasma membrane into a pedestal. We hypothesized that, in addition to manipulating actin dynamics, EPEC subverts host exocytosis to enhance pedestal formation. Exocytosis is mediated by an octameric human protein complex called the exocyst and also SNARE proteins. We found that exocytosis is stimulated at sites of EPEC pedestal formation. In addition, RNAi-mediated depletion of exocyst components or SNARE proteins in HeLa cells impaired pedestal formation. Importantly, co-depletion of the exocyst and ARP3 nearly abolished pedestal formation, indicating additive roles for exocytosis and actin polymerization. We also found that EPEC recruits the exocyst complex to pedestals. Screening of a collection of EPEC effector mutant strains revealed that the effector EspH is required for stimulation of exocytosis in pedestals. Compared to wild-type EPEC, the Δ espH strain produced shorter, thinner pedestals and failed to recruit the exocyst. Complementation of the mutant by expression of EspH on a plasmid rescued these defects. Together, our findings demonstrate that EspH-mediated stimulation of exocytosis works together with actin polymerization to optimize the efficiency of pedestal formation.

Human and Medical Microbiology

Comparison of Biofire Film Array Blood Culture ID Panel with Conventional Methods of Identification of Pathogens and Antimicrobial Resistant Genes in Cancer Patients

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AIM:This study aimed to assess the efficacy of BCID2 in identifying microorganisms and AMR genes directly from positive blood cultures and to determine its impact on turnaround time (TAT) compared with conventional culture methods of identification of pathogens and resistant genes.

METHODS: A total of 60472 samples from 19487 patients were received in 2024. All the blood samples were incubated in automated blood culture system for 5 days. Bottles flashed positive were processed on Blood agar, MaConkey agar and Chocolate agar plates. Identification and antibiotic susceptibility testing were performed on VITEK-2 system. BCID2 testing was performed according to the manufacturer's guidelines.

RESULTS: 2568 blood samples showed growth of pathogens. 104 samples were processed for BCID2 panels. E.coli was most commonest isolate followed by Klebsiella pneumoniae , Neisseria meningitidis , Staphylococcus spp and Pseudomonas aeruginosa . CTX-M with NDM was the most common resistant genotype detected followed by CTX-M with NDM and OXA-48 like, NDM with OXA-48 like, NDM only and CTX-M with OXA-48 like, CTX-M only) and OXA-48 like only. Concordance in identification of organisms was seen in 88% isolates and concordance in resistant genotype and phenotypic sensitivity was seen in 91.7% isolates.

CONCLUSION: BioFire BCID2 panel is a reliable system for directly identifying pathogens and their AMR genes in positive blood cultures. BCID 2 provided an edge over conventional diagnostics in terms of ease of performing and timing of reporting results. Also, decrease in turnaround time and detection of antibiotic resistance gene may result in early initiation of appropriate antimicrobial therapy and shorter hospital stay.

Food & Public Health Microbiology

Plasma-Activated Water for Controlling *Listeria monocytogenes* Biofilm: Effect on Viable Cells and Extracellular Polymeric Substances Matrix

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Aim:

Plasma-activated water (PAW) has emerged as a promising approach for controlling microbial biofilms due to the presence of diverse reactive oxygen and nitrogen species (RONS). This study investigated the potential of PAW in controlling *Listeria monocytogenes* biofilms.

Method:

- PAW was generated by treating 25 mL of sterile distilled water (dH₂O) using a dielectric barrier discharge (DBD) system at 60 kV with ambient air as the feed gas.
- The concentrations (hydrogen peroxide, nitrite, and nitrate) in PAW were evaluated by spectrophotometry.
- *L. monocytogenes* biofilms were treated with PAW activated at 60 kV for 15 minutes, combined with 15 minutes of post-treatment.

The viable cell counts were determined using the bead vortex method, and the EPS matrix was visualized via fluorescence microscopy.

Result:

- The concentrations of hydrogen peroxide, nitrite ions, and nitrate ions significantly ($P \leq 0.05$) increased with activation time, reaching 9.49 ± 0.23 , 0.19 ± 0.01 , and 27.50 ± 0.55 mg/L after treating at 60 kV for 15 min, respectively. The pH decreased to 3.43 ± 0.01 .
- Biofilms treated with sterile dH₂O, 6.28 ± 0.18 , 6.24 ± 0.22 , and 6.38 ± 0.13 log CFU/cm² of viable cells were found in 2, 4, and 7-day biofilms, respectively. In contrast, groups treated with PAW had viable cell counts below the detection limit (2.47 log CFU/cm²).
- For controlled groups, the stronger fluorescence signals were found in the biofilm with longer incubation time, indicating the formation of the EPS matrix during the maturation. The lower fluorescence intensities were found in all PAW-treated groups, which represented PAW partially removing the EPS matrix.

Conclusion:

PAW is effective for controlling *L. monocytogenes* biofilm by reducing the viable cells and the EPS matrix.

Human and Medical Microbiology

Do mutations in *nuoG* impact the growth of the mouse gut pathogen *Citrobacter rodentium*

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Citrobacter rodentium is a gut bacterium that infects laboratory mice in a similar way to the human pathogenic bacteria Enteropathogenic *Escherichia coli* (EPEC) and Enterohaemorrhagic *E. coli* (EHEC). The Bioluminescent Superbugs Lab has previously investigated the in-host evolution of the bioluminescent *C. rodentium* derivative ICC180 during which a ‘hyper’-infectious phenotype emerged. Whole genome sequencing identified several fixed mutations in the hyper-infectious populations, including in *nuoG*, a gene involved in the bacterial equivalent of the electron transport chain.

Aim: This project aims to investigate the role of mutations in *nuoG* on the in vitro growth of *C. rodentium*.

Methods: We created a *nuoG* knockout strain in *C. rodentium* using the method developed by Edwards and colleagues. This involves homologous recombination with a suicide vector (pRE112), which uses chloramphenicol and sucrose as selection markers. We also created two *nuoG* complementation plasmids: one containing wild-type *nuoG* (pACYC*nuoG*-WT) and one containing the mutated *nuoG* from the hyper-infectious *C. rodentium* populations (pACYC*nuoG*-HI). We compared the in vitro growth of *C. rodentium* ICC180, the *nuoG* knockout strain (ICC180 Δ *nuoG*), and ICC180 Δ *nuoG* complemented with pACYC*nuoG*-WT or pACYC*nuoG*-HI, on different carbon sources, including acetate, glucose, and succinate.

Results: Preliminary results show that the carbon source affects the growth of *C. rodentium* ICC180 Δ *nuoG*, with this strain struggling to grow on tryptone media supplemented with sodium acetate.

Conclusion: Our data show that *nuoG* is important for the in vitro growth of *C. rodentium* ICC180 when acetate is used as a sole carbon source. The link of *nuoG* to in vivo hyper-infectivity in remains to be elucidated.

Microbial Ecology & Evolution

Fungal communities in New Zealand pasture soils show stronger response to historical rainfall patterns than prokaryotes

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Aim. Agricultural soils are considered likely storage sites for carbon making them a potential tool for climate change mitigation. To predict the effect of certain agricultural management on soil organic carbon (SOC), the mechanisms of C transformations in soil must be understood. The key to understanding C dynamics in soils is integrating the role of microbial communities since they control the net transformations of C in soils. In this study, we assessed the potential link between SOC and soil microbiomes for pasture soils in the South Island of New Zealand and the role of median annual precipitation (MAP) in controlling them.

Methods. A total of 48 soil samples were collected from 16 farms across the South Island representing a MAP gradient (500-5000 mm/year). 16S rRNA and ITS profiles were generated from DNA extracted from composite soil samples representing the top 0-10 cm. Physicochemical profiles were also created for all sites.

Results. Significant differences in fungal communities were observed, with strong grouping of sites based on MAP, where sites with < 1000 mm of rain a year clustered separately from higher rainfall areas, but similar clustering was absent for prokaryotes. This correlated with higher precipitation sites having lower % of SOC. However, prokaryotic communities demonstrated stronger clustering based on soil texture. Finally, C/N ratio was found to be one of the most significant drivers of fungal communities.

Conclusion. Our results suggest that fungal communities are more responsive to changes in precipitation and nutrients availability. This could indicate that under future scenarios, altered rainfall patterns in response to climate change could lead to significant shifts in microbiomes and SOC stocks.

Microbial Ecology & Evolution

Microbial soil carbon sequestration under distinct precipitation patterns

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Aim. Greenhouse gas emissions (GHG) challenge the modern world and future generations. One possible strategy for climate change mitigation is enhancing soil carbon (C) sequestration by promoting C uptake from the atmosphere and storing it in the form of soil organic matter to reduce increases in atmospheric CO₂ concentration. Yet, understanding of C turnover and the mechanisms controlling them is limited. Our study aims to explore the impact of historical rainfall patterns on C sequestration in pasture soils under background and urine patch conditions.

Methods. Soils from two sites representing low (550 mm/year) and high (3500) median annual precipitation (MAP) were used to create packed cores for lab incubations. Four treatments were applied: (i) control soil with only water, (ii) soil mixed with isotopically labelled roots (13.1 atom% ¹³C, 12.1 atom% ¹⁵N), (iii) soil mixed with synthetic urine, (iv) soil mixed with the labelled roots and urine. The samples were incubated on tension tables to maintain water-filled pore space at 30% and sampled over 2.5 months.

Results. Urine altered microbiomes in low MAP soil, but not in high one. Thus, prokaryotic species richness significantly decreased ($p < 0.05$) from 300 to 200 after urine addition, while fungi were not affected. Furthermore, low MAP soil showed higher TC accumulation (4 mg/g soil) and lower CO₂ emissions (7500 ppm) after urine addition, than high MAP soil (3 mg/g and up to 15000 ppm, respectively).

Conclusion. The preliminary results highlight the importance of precipitation, nutrient input, and microbial communities in soil C sequestration. Our findings can contribute to the development of novel sustainable techniques for land management that may reduce GHG emissions and favour soil fertility.

Food & Public Health Microbiology

Preliminary metagenomics evaluation of biofilm microbiota on raw milk bulk tanks

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Preliminary metagenomics evaluation of biofilm microbiota on raw milk bulk tanks

Background:

Raw milk has a complex microbiota due to multiple sources of bacterial contamination in the dairy farm environment. This diverse microbial community promotes the formation of multi-species biofilms on the surfaces of raw milk bulk tanks during on-farm storage. Such biofilm development can result in microbial accumulation during the early stages of milk collection, and possibly influencing milk quality.

Aim:

To investigate the microbial composition of multi-species biofilms formed on the surfaces of raw milk bulk tanks on a selected dairy farm, and to evaluate methods for their identification.

Methods:

Surfaces of two similar raw milk bulk tanks from the same farm were sampled in parallel. Microbial communities in biofilms were identified using 16S rRNA gene sequencing and metagenomic analysis, and compared with traditional culture-based methods based on Tryptic Soy Agar (TSA) and Milk Plate Count Agar (MPCA) culture plates. Isolates obtained from these plates were identified by MALDI-TOF mass spectrometry.

Results:

Metagenomic analysis provided more comprehensive microbial diversity, including unculturable strains, and showed better consistency between parallel samples compared to plate isolation. However, metagenomic data alone cannot show the absolute abundance of different genera across samples without the help of other methods such as numbers of cells using plate counts or flow cytometry assays.

Conclusion:

These preliminary results show that metagenomics analysis can add to information on bacteria that form part of the multi-species biofilms present on surfaces of raw milk bulk tanks.

Food & Public Health Microbiology

Evaluation of the Synergistic Antibiofilm Activity of Nisin and Lysozyme *against Listeria monocytogenes* on Stainless Steel Surfaces

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The formation of biofilms by *Listeria monocytogenes* on food contact surfaces like stainless steel enhances its survival and antimicrobial resistance, making it challenging to ensure food safety. This study investigated the synergistic effect of nisin and lysozyme, natural antimicrobials generally recognized as safe (GRAS), to eliminate mature, pre-formed biofilms of two different *L. monocytogenes* strains.

The synergistic interaction of nisin and lysozyme was studied to reduce *L. monocytogenes* biofilms grown for 48 hours on stainless steel coupons at 37 °C. Biofilms showed much higher resistance than planktonic state with; Minimum Biofilm Eradication Concentrations (MBECs) for the first isolate were 5000 µg/mL (MBECN) and 2500 µg/mL (MBECL). For the second isolate, MBECN was 2500 µg/mL with a similar MBECL.

A synergy between nisin and lysozyme was observed using the checkerboard method, as measured by the reduction in viable cells via plate counting. The optimal combination for reducing the biofilm cell count compared to the respective nisin and lysozyme single antimicrobial treatment for the first strain was MBECN/4 combined with either MBECL/4 or MBECL/8 within a 2-hour treatment at 37°C. The second strain's most effective combinations were MBECN/2 with MBECL/8 and MBECN/4 with MBECL/8. All optimal combinations showed the Fractional Inhibitory Concentration (FIC) index values below 0.5 within 2 hours, resulting in biofilm below detectable levels after a 24-hour treatment, confirming a potent synergy. These results indicate that combining nisin and lysozyme presents a promising biocontrol strategy for controlling mature *L. monocytogenes* biofilms with reduced antimicrobial concentrations.

Food & Public Health Microbiology

***Tenacibaculum maritimum* in Aotearoa-New Zealand salmon industry presents a problem for the future of aquaculture**

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Salmon farming is an important industry in New Zealand's aquaculture sector, bringing in around 300\$ million NZD in revenue annually providing thousands of jobs. *Tenacibaculum maritimum* is a devastating pathogen for salmon aquaculture globally and has been identified as a concern in New Zealand. The aquaculture sector is looking for alternatives to antibiotics leaving a gap for novel methods to arise. Aim: Analyse the genomes of *T. maritimum* isolated in New Zealand to evaluate potential strategies for biocontrol of this pathogen. Methods: Geneious was used to identify differences in strains's annotated genomes. Online web tools DefenceFinder and Padlock were used to identify anti-phage defence systems. TypeStrainGenomeServer was used to construct phylogenetic trees. PHASTEST was used to identify prophages the genomes. Results: 15 of the 31 obtained *T. maritimum* isolates found in New Zealand's Marlborough Sounds belong to one out of 10 representative sequence types and 26 strains cluster into one of three distinct clades showing a relatively homogenous group. Genomes present 21 different anti-phage defence systems as well as five different prophages integrated into their genome which suggests that it has encountered phages in the past and that it could be possible to isolate bacteriophages against it in New Zealand waters. I will describe my early efforts at discovering NZ phages against this pathogen. Conclusion: Tenacibaculosis is a relatively new challenge for the Salmon Aquaculture sector in New Zealand. The strains studied of *T. maritimum* show evidence that there are phages present and phages for *T. maritimum* have been found elsewhere. This suggests that there is potential for phage biocontrol of *T. maritimum* if future efforts at phage discovery are successful.

***Myceliophthora thermophila* cellulase production through Mtegl2 and Mtbgl1 expression modulated by MtCLR-2 transcription factor**Yapeng Lai ^{1,2}, Juan Wang ¹, Ning Xie ¹, Gang Liu ¹ and Donnabella C. Lacap-Bugler ²

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Aim: The thermophilic fungus *Myceliophthora thermophila* can secrete large amounts of lignocellulolytic enzymes, such as cellulases and xylanases, which are regulated by multiple transcription factors. However, the understanding of the regulatory mechanism of cellulase gene expression in *M. thermophila* is limited. Here, we characterized the function of MtCLR-2, an ortholog of the cellulolytic regulator CLR-2 first identified in *Neurospora crassa*.

Methods: The function of MtCLR-2 was investigated by CRISPR/Cas9 mediated gene deletion, overexpression, real-time quantitative reverse transcription PCR (RT-qPCR) analysis, electrophoretic mobility shift assays (EMSAs), and comparative transcriptomic analysis.

Results: Deletion of *Mtclr-2* significantly reduced cellulase activities, particularly affecting endoglucanase production, whereas overexpression of *Mtclr-2* led to the elevation in cellulase secretion when *M. thermophila* was grown on Avicel. RT-qPCR analysis found that disruption of *Mtclr-2* caused a decrease in transcript levels of the β -glucosidase gene *bgl1* (MYCTH_66804) and the endoglucanase gene *egl2* (MYCTH_86753) throughout the stages of growth in cellulose medium. Furthermore, electrophoretic mobility shift assays (EMSAs) demonstrated that MtCLR-2 directly binds to the promoter regions of *bgl1* and *egl2* in a zinc-dependent manner. The comparative transcriptomic analysis also showed that MtCLR-2 positively regulates the expression of ribosomal protein genes under cellulosic conditions.

Conclusions: These findings contribute to further understanding of the regulatory network governing cellulase gene expression and provide a potential target for boosting cellulase biosynthesis in *M. thermophila*.

Food & Public Health Microbiology

Influence of seawater based medium on biofilm robustness in *Vibrio parahaemolyticus*: implications for seafood safety

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Vibrio parahaemolyticus (VP) is a significant seafood-borne pathogen known for forming biofilms that persist in marine and seafood processing environments, posing food safety challenges.

Aim:

This study investigated the effect of seawater-based medium (SW3%) on extracellular polymeric substance (EPS) polysaccharide production in VP biofilms formed under air liquid-solid interface (ALI) and fully submerged (SM) conditions to understand biofilm persistence mechanisms.

Methods:

Biofilms were developed at 30°C for 24 h in standard tryptic soy broth with 3% NaCl (TSB) and in SW3%, composed of 50% seawater and 50% double-strength TSB with 2.5% NaCl. Two clinical and one oyster-isolated isolates were tested on partially submerged stainless-steel coupons to allow direct comparison of ALI and SM biofilms.

Results:

Viable cell counts and normalised EPS polysaccharide concentrations were measured.

Viable cell counts were higher in TSB (>5.5 log CFU/cm²), while normalized EPS polysaccharide levels were greater in SW3%, up to 10.369 µg/10⁴ cells compared to 1.094 µg/10⁴ cells in TSB. Submerged biofilms produced more polysaccharide but fewer viable cells than ALI biofilms across all isolates.

Conclusion:

Seawater constituents possibly Ca²⁺ and Mg²⁺ ions enhance EPS polysaccharide production in VP biofilms, particularly under submerged, conditions, contributing to biofilm robustness and persistence in seafood environments. Differences in EPS production between ALI and SM biofilms likely reflect bacterial adaptation to environmental conditions. Genetic analysis is needed to clarify underlying mechanisms. Further research should explain how ion regulation affects EPS production and the expression of polysaccharide biosynthesis genes to develop seafood safety strategies.

Human and Medical Microbiology

Optimising elite athletic performance through the gut microbiome

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The human gut encompasses a diverse community of microorganisms, collectively termed the gut microbiome, that play an essential role in host nutrition, pathogen defence, and host immune response. While factors such as age, antibiotic use, and diet are well-known to shape the gut microbiome, the impact of exercise is relatively unexplored. Preliminary evidence suggests that exercise cultivates a gut microbiome rich in health-associated bacteria and metabolites; however, the stress of prolonged and intensive exercise on the gut can lead to gastrointestinal issues. This study compares the gut microbiomes of two distinct athletic groups: elite endurance and sprint cyclists. The different physiological demands of each group are hypothesised to cause differences in the gut microbiome. Faecal samples and dietary data were collected from High Performance Sport New Zealand-affiliated cyclists during their routine training. These samples will be analysed using a multi-omic approach that combines shotgun metagenomics, metatranscriptomics, and metabolomics to profile the gut microbiome and assess its functions. Initial results will be presented. Differences in microbial composition and function are expected between the two groups, reflecting their respective physiological adaptations and training loads. This research should deliver valuable insights into optimising gut health for endurance and sprint athletes, providing a foundation for future research on the gut microbiome's role in athletic performance.

Food & Public Health Microbiology

Microbial gold diggers: A study of conditional synergy in multispecies biofilm

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Aim: Bacteria exist in varying nutrient conditions and complex microbial consortia. *Pseudomonas fluorescens*, *Staphylococcus aureus*, and *Listeria monocytogenes* are commonly occurring biofilm-formers, share a similar nutritional niche, and have been isolated from common surfaces in multispecies environments.

Methods: Biofilm properties, including biomass (O.D590 nm), cell concentration (log CFU/cm²), exopolysaccharide content (µg/cm²), and sanitizer tolerance (sodium hypochlorite), were observed under varying nutrient (full-strength TSB and 10% TSB) conditions on polystyrene surfaces for single and multispecies biofilm.

Results: The synergistic interactions between the bacteria in multispecies biofilm were found to be nutrient-dependent, with significantly higher ($p > 0.05$) biofilm formation, exopolysaccharide content, and sanitizer tolerance in high nutrient conditions (TSB) compared with low nutrient conditions (10% TSB). The cell concentrations in the biofilm (single and multispecies) were found to be comparable between TSB and 10% TSB. All three bacteria involved showed increased tolerance against sanitizers in the multispecies arrangement compared to their single-species counterparts, with significantly higher survival for *L. monocytogenes* (5.3 log CFU/cm²) in a multispecies biofilm compared to its single-species counterpart (2.3 log CFU/cm²). A positive correlation was observed between exopolysaccharide concentration and sanitizer tolerance.

Conclusion: This study highlights the importance of taking multiple bacteria and their growth environment into account when understanding sanitizer response, as it varies in multispecies biofilm setups and according to nutrient availability.

Human and Medical Microbiology

Lysozymes as microbiome modulators: Molecular insights into *Trichomonas vaginalis*-bacteria interactions

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Aim

The human vaginal microbiome is a complex ecosystem primarily dominated by lactobacilli, which maintain an acidic environment and inhibit pathogen colonization. However, when lactobacilli decline, anaerobic bacteria such as *Gardnerella vaginalis*, among others, may flourish as a polymicrobial condition known as bacterial vaginosis (BV). Coincidentally, the vaginal infection by the protozoan *Trichomonas vaginalis* (i.e., trichomoniasis) is accompanied by this dysbiotic BV-like microbiome, including *G. vaginalis*. However, the molecular effectors enabling these microbiome interactions and manipulation remain poorly understood. Our research investigates eleven predicted lysozymes encoded by *T. vaginalis*, hypothesizing that these enzymes facilitate microbial manipulation by degrading bacterial peptidoglycan, selectively targeting commensal lactobacilli.

Methods

We employed complementary approaches to overexpress these genes in *T. vaginalis* using epitope-tagged constructs, with Western blotting and on-going secretion assays to characterize their expression and localization. On-going experiments include ddPCR-based transcriptional profiling of lysozyme genes during bacterial co-culture, functional assays using recombinant lysozymes, and differential proteomic analysis of *T. vaginalis* in various microbiome contexts.

Results

Conditions for co-incubation assays with *Lactobacillus gasseri* and *G. vaginalis* reveal functional competition assays of parasite-bacteria interactions and how expressing lysozymes provide advantages to the parasite over one or another bacterium.

Conclusion (or expected impact)

Trichomoniasis is a reproductive disease with limited research into its mechanisms. Together, these approaches aim to identify candidate enzymes mediating microbiome disruption.

Human and Medical Microbiology

Sterilization of *Bacillus atrophaeus* (BA) spores on surgical stainless-steel scalpels using high voltage atmospheric cold plasma (HVACP) treatment

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Cold plasma (ACP) is the conversion of a gas, such as air, into a reactive gas at atmospheric pressure and temperature using a small amount of electricity. Specifically, an electric field is applied to the “working” gas (air) leading to the breakdown of diatomic oxygen, diatomic nitrogen, and water vapor into a mixture of radicals (e.g., atomic oxygen, atomic nitrogen, atomic hydrogen, hydroxyls), metastables (ozone, hydrogen peroxide), and ions (e.g., nitrate, nitrite, peroxyxynitrate). In a cold plasma process, approximately 5% or less of the working gas is ionized, but it can generate 1000’s of ppm of reactive gas species (RGS). High voltage atmospheric cold plasma (HVACP) is a special type of cold plasma treatment developed in our laboratory which has low energy consumption and requires short treatment times. The objective of this study was to evaluate the inactivation efficiency of *Bacillus atrophaeus* spores inoculated on stainless-steel scalpels with HVACP using room air (78% N₂ and 22% O₂) or MA65 (65% O₂, 30% CO₂, and 5% N₂) and their effects on the surface of scalpels. A five-minute HVACP eliminated all spores in the peptone solution, resulting in a greater than 5.39 log reductions for both working gases with 90% relative humidity and direct treatment. A 10 min direct treatment on scalpels resulted in 3.0 and 3.5 log spore reductions for air and MA65, respectively. HVACP treatment did not change the surface roughness or color of the scalpel blades. The results demonstrate the ability of HVACP to reduce a common biological indicator potentially leading to an alternative sterilization process compared to chemicals.

Plant-Microorganism Interactions

Forest Plant Root Endophytes

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1. School of Science, Faculty of Health & Environmental Sciences, Auckland University of Technology

Endophytic microorganisms inhabiting plant tissues without inducing illness, are increasingly acknowledged for their advantageous contributions to plant host development, stress resilience, and overall ecosystem functionality. Despite their importance, the taxonomic diversity and evolutionary relationships of endophytes, particularly those associated with forest plant roots, remain underexplored. This study aims to characterise fungal and bacterial endophytes at the molecular level, advancing our understanding of plant-microbe interactions in native forest systems.

High-quality genomic DNA from pure endophyte isolates were extracted and PCR amplification was conducted targeting the internal transcribed spacer (ITS) region of fungi and the 16S rRNA gene of bacteria. Phylogenetic analysis of the DNA sequence data revealed association of the endophyte isolates to fungal and bacterial species known to have biocontrol properties against plant disease. Microbiological techniques and phylogenetic analysis provide a snapshot of the endophytic communities inhabiting forest plant roots. The findings contribute to broader ecological knowledge and may inform future applications in sustainable forestry, plant health management, and microbial conservation.

Microbial Ecology & Evolution

Isolation And Characterization Of Novel *Acidithiobacillus* Strains From The Taupo Volcanic Zone (TVZ)

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Aims

The geothermal systems of the Taupō Volcanic Zone (TVZ) in Aotearoa host diverse thermophilic and acidophilic microorganisms, with *Acidithiobacillus* being one of the most abundant bacterial genera. Despite finding *Acidithiobacillus* DNA at extreme temperatures up to 90°C, species of this genus have never been characterised at such temperatures. We aim to isolate, culture, and characterise novel *Acidithiobacillus* strains from the TVZ to determine their true thermal limits.

Methods

Samples were collected from TVZ hot springs with predicted high *Acidithiobacillus* abundance. Strains were enriched and isolated using selective media and characterised in terms of optimum temperature and pH, substrate use, oxygen requirements, carbon/nitrogen metabolism, and chemotaxonomic traits. To confirm species identity, 16S rRNA genes of isolates were sequenced, and community 16S rRNA amplicon data were analysed to understand microbial diversity and contextualize *Acidithiobacillus* abundance. Whole-genome sequencing will be used to resolve taxonomy, investigate metabolic potential, and predict Optimal Growth Temperatures (OGT).

Results

Samples from 16 springs (17–94 °C, pH 2–7) have yielded several candidates, with OGT at 45–55 °C. Initial 16S rRNA results indicate isolated strains with high sequence identity to the *Acidithiobacillus* genus, with potential novel lineages identified. Isolates have been cultured on elemental sulfur and tetrathionate, confirming their sulfur-oxidizing capacity.

Impact

This study will define the true OGT of TVZ *Acidithiobacillus* strains and compare this to genome-based OGT predictions. It highlights the value of culture-dependent methods, the importance of strain characterisation, and deepens understanding of microbial adaptation in the geothermal system.

Human and Medical Microbiology

The B12 Backdoor: Exploiting the B12-Uptake Pathway for Antibiotic Delivery

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The Btu pathway is a crucial mechanism for the import of cobalamin (vitamin B12) and its precursors in Gram-negative bacteria such as *Escherichia coli*. The first protein of this pathway, a transporter protein BtuB, initially binds cobalamin to transport it across the outer membrane of these cells into the periplasmic space. Since vitamin B12 is crucial for growth, this pathway could be exploited to transport cobalamin conjugates carrying antibiotics through the impermeable outer membrane, into the periplasm and eventually cytoplasm of antibiotic-resistant cells. For this to work, BtuB must be expressed. Previous literature shows that BtuB production undergoes both transcriptional and translational regulation. Therefore, the aim of this research is to investigate BtuB transcript and protein levels under various growth conditions to optimise the uptake of B12-antibiotic conjugates. By defining conditions that optimise BtuB expression, we aim to establish a foundation for future delivery of vitamin B12-antibiotic conjugates into Gram-negative pathogens. This work will provide proof-of-principle for exploiting nutrient uptake pathways to overcome barriers to antibiotic delivery and address the challenge of drug-resistant infections.

Plant-Microorganism Interactions

Metabolites from endophytic fungi

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A broad category of microorganisms known as endophytic fungi lives in plant tissues without appearing to harm their host. Because of their capacity to generate a diverse range of secondary metabolites with possible uses in biotechnology, agriculture, and medicine, these symbiotic organisms have attracted a lot of scientific interest. Many of these metabolites, which include polyketides, terpenoids, alkaloids, and peptides, have been shown to possess antimicrobial, antifungal, anticancer, and biocontrol qualities. The ability of fungal endophytes to adapt to particular plant microenvironments, which frequently leads to the synthesis of novel compounds that may not be present in free-living fungi, is what gives them biotechnological potential. The purpose of this study is to identify secondary metabolites from endophytic fungi that have been isolated from companion plant roots in a forest with known plant disease. Endophytic fungi isolates were grown in potato dextrose broth at 25 to 28°C for 14 days. Ethyl acetate was used to extract the metabolites from the culture broth and dried using anhydrous sodium sulphate and a rotary evaporator. High-Performance Liquid Chromatography (HPLC) was used to analyse the resultant crude extracts to determine their chemical profiles and compare them to established standards. The metabolites that may have antimicrobial or biocontrol properties can be assessed using different bioassays against known plant pathogens. The results of this study can be used in future research to determine the compounds; viability for managing agricultural pathogens.

Microbial Ecology & Evolution

Evolutionary Dynamics of rsmG-Mediated Streptomycin Resistance Revealed by Nanopore RNA Sequencing

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The rise of antimicrobial resistance poses an urgent and ongoing threat to human health. If we can predict when and how antibiotic resistance evolves, we may be able to proactively mitigate its emergence. To explore the predictability of resistance evolution, we conducted a large-scale laboratory evolution experiment selecting for streptomycin resistance across a diverse collection of independently evolving natural *Escherichia coli* isolates. We observed repeated evolution in rsmG, a well-characterized antibiotic resistance gene that encodes a methyltransferase responsible for methylating 16S rRNA. To assess the functional consequences of these mutations, we performed native direct RNA sequencing using Oxford Nanopore Sequencing on both resistant and ancestral strains. I will present our findings on the variability of methylation patterns shown by mutations in the rsmG gene and how changes in methylation inhibit the antimicrobial effects of streptomycin.

Microbial Ecology & Evolution

Inducing single-cell morphology in naturally aggregating rumen *Methanosarcina* species

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Background: Methanogenic archaea use hydrogen, formate and simple organic compounds to produce methane, a major greenhouse gas. Methanogens within the genus *Methanosarcina* can use acetate as their primary substrate and typically grow as large, irregular cell aggregates. Different methods have been reported to generate single cell populations of various *Methanosarcina* spp., enabling research into their physiology and making them genetically tractable to understand their gene functions. However, cellular functions and genetics of rumen *Methanosarcina* remain poorly understood due to limited information on their growth characteristics as single cells.

Aim: To develop methods to induce a single-cell morphology in two genomically different rumen *Methanosarcina* isolates.

Methods: Three approaches were tested to induce single-cell morphology in these isolates: sequential culturing in high salt (HS) medium with increasing NaCl concentrations (0.1–1.0 M), treatment with disaggregatase (Dag) enzyme in protoplast-stabilising buffer (PSB), and incubation in PSB alone.

Results: Sequential culturing of isolate 1 in HS medium containing 0.2 M NaCl produced a single-cell phenotype. In contrast, sequential culturing of isolate 2 in HS medium with up to 1 M NaCl only reduced the size of cell aggregates. Treatment of strain 2 with Dag disaggregated clumps and generated protoplasts. However, these cells were unable to be regenerated. Interestingly, incubation of isolate 2 in PSB alone converted ~80% of cell aggregates into single cells.

Conclusion: These findings show that a single cell morphology can be induced in two rumen *Methanosarcina* isolates. This will be applied to improving our understanding of cellular function and establishing genetic tools in rumen *Methanosarcina* spp.

Food & Public Health Microbiology

Decoding Microbial Dynamics on Seaweed: Implications for Process Optimisation and Quality Control

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AIM

My PhD research integrates microbial ecology and food technology analyses on *Undaria pinnatifida* (i.e., wakame) to scope quality and safety risks in an emerging market with sparse historical data. This investigation explored the influence of post-harvest storage conditions on the quality of fresh *U. pinnatifida*, where local harvesters reported highly variable outcomes that affect export viability.

METHODS

I characterised post-harvest microbial degradation by characterising temporal changes in fungal and bacterial amplicons, alongside food quality and metabolomic analyses. These analyses were integrated to highlight the potential mechanisms underlying fresh *U. pinnatifida* spoilage and the consequences of different storage conditions.

RESULTS

Microbial succession at different storage temperatures was linked to the indicators of sensory colour, texture and aroma in unprocessed *U. pinnatifida*. Food quality profiles of *U. pinnatifida* were created to highlight relevant biochemical transformations and potential mitigating factors.

IMPACT

Multi-omic methods are underutilised as a scoping tool for novel food systems, which typically struggle with quality and safety control during scale-up. The techniques from this study could be applied to other emerging food industries as an extension of traditional practices. Within the context of wakame products, this research was designed to benefit a range of stakeholders in New Zealand, from marine reforestation groups to commercial seaweed farmers, and to inform the standardisation of locally sourced *U. pinnatifida* products.

Human and Medical Microbiology

Geothermal springs as a novel platform for antibiotic discovery

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Aim:

The need for discovery and development of antibiotics is critical if we are to alleviate the current crisis of antimicrobial resistance. Most clinical antibiotics have been sourced from culturable bacteria and fungi; however, the majority of microbes have never been cultured, leaving their biosynthetic potential largely unknown. Geothermal springs harbour unique and understudied lineages of bacteria and archaea which metagenomic sequencing allows us to expose. This research aims to elucidate these hot spring communities and their potential as a resource for novel antibiotic compounds.

Methods:

Hotsprings harbouring unique genera from around the Taupō Volcanic Zone were sampled and DNA was extracted for metagenomic and 16S rRNA gene sequencing. Metagenomes were assembled then resulting scaffolds were analysed using the program antiSMASH to identify biosynthetic gene clusters (BGCs) and predict secondary metabolites. Metagenome assembled genomes (MAGs) were classified using GTDB-Tk and the BGCs were linked to their phylogenetic origin.

Results:

563 bacterial and archaeal MAGs were assembled from 18 hot spring samples. 33% of MAGs and 66% of ASVs remained unclassified at the genus level indicating an abundance of undescribed taxa. Hundreds of BGCs were identified, including diverse non-ribosomal peptide synthases and polyketide synthases from across a vast range of taxa.

Expected impact:

This research reveals that hot springs in the Taupō Volcanic Zone are an untapped resource for microbial biosynthetic diversity. We hope that BGCs from metagenomes such as these will be taken forward for expression and development of novel antibiotic compounds with clinical relevance.

Plant-Microorganism Interactions

International Collection of Microorganisms from Plants (ICMP)

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The International Collection of Microorganisms from Plants (ICMP) is New Zealand's national culture collection of living Bacteria, Fungi, and Chromists. The collection and associated databases considered 'Nationally Significant' by the government, and in part publicly funded.

The ICMP holds over 25,000 cultures predominantly from plant, soil, and water in the natural environment, as well as important reference and type cultures of the world's plant pathogenic fungi and bacteria.

All cultures are databased and available online at <https://SCD.LandcareResearch.co.nz> and a database of the names and biostatus of fungi and bacteria in Aotearoa can be found at <https://BiotaNZ.LandcareResearch.co.nz>. Cultures are available for a fee to cover retrieval costs.

New accessions into the collection are welcome and recommended when publishing papers on microbes to provide a stable permanent resource for future researchers.

The cultures are preserved under liquid nitrogen or in freeze dried ampoules. The ICMP containment and transitional facility conforms to enhanced PC2 Containment criteria, with generic permits to import quarantine and unwanted organisms into New Zealand.

Human and Medical Microbiology

Specific Synbiotic Sugars Stimulate *Streptococcus salivarius* BLIS K12 and BLIS M18 Lantibiotic Production to Expand Bacterial Inhibition Range and Potency

Liam K. Harold¹, Nicola C Jones¹, Sarah L. Barber¹, Abigail L. Voss¹, Rohit Jain¹, John R. Tagg¹ and John D.F. Hale¹

1. BLIS Technologies Ltd

Aim

To identify synbiotic sugars that enhance the antimicrobial activity of *Streptococcus salivarius* BLIS K12 and BLIS M18, thereby improving their potential health benefits.

Methods

Modified deferred antagonism assays were used to test whether nine different sugars enhanced the inhibitory effects of BLIS K12 and BLIS M18 against bacterial indicators. Raffinose and galactose were further assessed across a concentration gradient and against an expanded range of indicators. Growth curves were performed to determine whether the effects were growth-related. Reverse transcriptase quantitative PCR (RT-qPCR) was used to measure lantibiotic gene expression (*salA*, *salB*, *sal9*) in these BLIS strains grown on sugar-supplemented media.

Results

Raffinose and galactose most strongly enhanced BLIS antimicrobial activity compared with other sugars. Growth assays confirmed that these effects were not attributable to increased growth rate. Optimal concentrations were identified as 2.5% (w/v) raffinose and 0.5% (w/v) galactose, which yielded both the greatest inhibition zones and the broadest spectrum of inhibited bacterial species. RT-qPCR analysis demonstrated upregulation of lantibiotic genes *salA*, *salB*, and *sal9* in the presence of raffinose or galactose, correlating with enhanced antimicrobial activity.

Conclusion

Raffinose and galactose act as synbiotic sugars that significantly augment the inhibitory potency and spectrum of BLIS K12 and BLIS M18 by stimulating lantibiotic gene expression. These findings highlight the potential for targeted synbiotic formulations to improve probiotic performance across oral, gut, and skin applications.

Microbial Ecology & Evolution

Genetic divergence of non-toxic and toxic *Microcoleus* leading to vitamin auxotrophy

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³ Lincoln University, Christchurch, New Zealand

⁴ U.S. Geological Survey, California, USA

Aims:

Microcoleus autumnalis are filamentous cyanobacteria found in freshwaters worldwide. They are well known for producing anatoxins, which pose health risks to animals and humans. Our group previously identified genetic differences between toxic and non-toxic strains, including predicted thiamine (vitamin B1) auxotrophy. This study tested the predicted thiamine auxotrophy in laboratory conditions, and as *Microcoleus* cultures are non-axenic, investigated the thiamine biosynthesis capacities of co-cultured bacteria.

Methods:

Genomes of 4 toxic and 10 non-toxic *Microcoleus* strains and associated bacteria were analysed, including 4 newly generated genomes from long read data with improved completeness. To confirm thiamine auxotrophy, *Microcoleus* were grown with and without thiamine forms (thiamine HCl, thiamine monophosphate and thiamine diphosphate).

Results:

Analysis of newly generated *Microcoleus* genomes confirmed that toxic strains lack key genes for the biosynthesis of thiamine, while all non-toxic strains encode complete biosynthesis pathways. Despite predicted thiamine auxotrophy in toxic strains, laboratory experiments showed no difference in growth of *Microcoleus* in media lacking thiamine, or in the presence of thiamine, where thiamine was rapidly taken up by cells or absorbed onto biomass. However, analysis of the community members found alongside the toxic strains demonstrated that some have complete biosynthesis pathways and may be able to share thiamine. Generation of axenic cultures of *Microcoleus* is underway to further evaluate thiamine auxotrophy.

Conclusion:

This study provides insights into the genetic differences between toxic and non-toxic *Microcoleus*, and suggests that community members may be important for proliferation of toxic strains.

Human and Medical Microbiology

Investigating the in vivo efficacy of a novel antimicrobial agent

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Aim

Surgical site infections caused by *Staphylococcus aureus* are a major healthcare challenge. Prophylactic skin/nasal decolonisation reduces infection risks, however current approaches, such as mupirocin, pose risks of resistance, toxicity and limited efficacy. Quaternary ammonium compounds (QACs) are widely used for their antimicrobial properties in antiseptics, disinfectants and preservatives. However their toxicity, skin irritation and low biodegradability cause QACs use to be limited in the health sector. A novel QAC analogue, B3a, has been developed within our research team. B3a shows lower toxicity and higher in vitro efficacy against *S. aureus* biofilms compared to mupirocin and a parent compound DDAC.

This study aims to investigate the in vivo efficacy of B3a at clearing an established nasal infection of *S. aureus* (JSNZ strain) within a mouse model.

Methods

Minimum inhibitory concentration (MIC) and minimum biofilm eradication concentration (MBEC) assays will be determined for JSNZ. These values will be used to evaluate the in vivo efficacy in a mouse model. The dose effects (single vs. multiple) and short-term vs. long-term effects will be investigated. The mice will be treated intranasally with B3a, DDAC or saline diluent. Bacterial load will be measured through CFU counts from nasal and stool samples.

Results

MICS and MBECs for ATCC 6538 *S. aureus* is 2-4 μM for B3a, and is significantly lower than DDAC (8 μM) and mupirocin (>40 μM). MICS and MBECs for JSNZ are underway, with results expected to be similar to ATCC 6538. The protocol for the established nasal infection mouse model is currently being replicated.

Conclusion

The findings from this study suggest B3a is a promising topical agent for addressing challenges of decolonisation prior to surgery.

Plant-Microorganism Interactions

Root endophytes from the kauri companion plant

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Kauri (*Agathis australis*) is a culturally and ecologically significant conifer tree endemic to Aotearoa, New Zealand. It is currently threatened by a dieback disease caused by the soil-borne pathogen *Phytophthora agathidicida*. The nature of the plant-endophyte relationship is significant in plant growth, host resilience, physiology, and the defence system. This research explores the potential role of endophytes in supporting defence mechanisms, specifically in terms of kauri dieback disease. Identifying and characterising the endophytic fungi and bacteria associated with roots of cutty grass (*Carex geminata*) and kauri grass (*Astelia trinervia*), companion plants in kauri forest in diseased and non-diseased sites, is the key research aim of this study. These companion plants are closely associated with kauri and offer a promising model due to their abundance. There were 61 endophytes isolated from cutty grass roots and kauri grass roots using different media. Colony and cell morphology of the isolates were characterised and the isolates were identified to be putative *Fusarium*, *Penicillium*, *Trichoderma*, and *Aspergillus* species. The full 16S rRNA gene and internal transcribed spacer (ITS) region confirmed the phylogenetic delineations of the endophytes. Some of these isolates demonstrated antagonistic effects on *Phytophthora agathidicida* using a dual culture assay. The bioactive metabolites from these endophyte isolates will be extracted for further analysis. This research provides novel insight into mitigating plant pathogens in native forests and ecosystems using companion plants hence, preserving forest integrity.

Biotechnology

Scaling science: From flask to factory

Callum Lambert¹, Shuguang Zhang¹ and Stephanie Harvey¹

1. Cawthron Institute, Nelson, New Zealand

Scaling bioprocesses from laboratory to industrial production is critical for transforming innovative concepts into market-ready solutions. Callaghan Innovation's expertise can bridge the gap between your budding idea and commercial manufacturing. Our capabilities span flask-scale culture, media development, and custom bioreactor formats from 1 L to over 1000 L, supported by integrated analytics and downstream processing. By partnering with us, clients gain process refinement, economic insights, and accelerated product launch, ensuring robust, scalable solutions for biotechnology and fermentation-based industries. Through collaborative development and tailored bioprocess design, we enable businesses to overcome production challenges and achieve growth.

Biotechnology**Peptones derived from protein-rich by-product streams for microbial fermentation**Josie Mainwaring¹, Campbell Ellison¹, Stephanie Harvey¹ and Shuguang Zhang¹

1. Cawthron Institute, Nelson, New Zealand

Peptones are essential components of microbial media, providing the amino acids and nitrogen necessary for consistent growth and product yields in fermentation. However, conventional peptones are typically animal-derived and costly, limiting their sustainability at industrial scale. We are exploring whether protein hydrolysates derived from horticultural by-product streams could serve as sustainable peptone alternatives. Several of these hydrolysates support the growth of common fermentation bacteria and fungi comparably to—if not better than—commercial peptones, demonstrating strong potential for by-product-stream valorisation into high-performance fermentation feedstocks. Interestingly, fractions that have been stripped of bitter components consistently support better growth, suggesting that microbes share with us a distaste for the chemicals associated with bitterness. This ongoing work aims to transform by-products—which would otherwise go to waste—into scalable, industry-ready media components that advance New Zealand's circular bioeconomy goals and reduce reliance on animal-derived ingredients in fermentation.

Biotechnology

Thriving without oxygen: Anaerobic culture at Callaghan Innovation

Callum Lambert¹, Josie Mainwaring¹ and Stephanie Harvey¹

1. Cawthron Institute, Nelson, New Zealand

Anaerobic microorganisms play critical roles in ecosystems and industrial processes, yet their cultivation remains challenging due to oxygen sensitivity. At Callaghan Innovation, we have developed robust capabilities for strict anaerobic culture using specialised equipment, including a Coy Anaerobic Chamber, pressure-rated vessels, and degassing equipment for nitrogen or carbon dioxide degassing. These tools enable isolation, enrichment, scale-up, and downstream processing of anaerobes for applications in biotechnology, health, and sustainability. Our expertise supports media optimisation, troubleshooting, and product development across sectors such as pharmaceuticals, agriculture, and food. Collaborative projects, including gut microbiome studies with the University of Auckland, demonstrate the potential for novel metabolic pathways and innovative products. By unlocking anaerobic culture, we provide clients with unique opportunities to access otherwise inaccessible bioprocesses.

Biotechnology**Creating the World's First ISO 17025-Accredited Remote Microbiological Testing Service**Shivangi Singh^{1,2}

1.School of Biological Sciences, Victoria University of Wellington

2.Bactosure, Wellington, New Zealand

Aim:

Bactosure created the world's first ISO 17025-accredited remote microbiological testing service, enabling accredited *E. coli* and total coliform analysis at users' sites. The aim was to eliminate transport and cost barriers, delivering accredited results within 16 hours through a low-cost, user-friendly system suitable for remote and developing communities.

Methods:

A multidisciplinary "accreditation-by-design" approach integrated microbiology, regulatory science, human-centred design, software, electronic and mechanical engineering, and product design. Every ISO 17025 clause (impartiality, traceability, competence, and control) was treated as a design input. The device uses USEPA-approved Colitag reagent and continuously monitors chromogenic and fluorogenic changes using a proprietary machine learning algorithm. More than 40 automated optical, thermal, and diagnostic checks replicate or exceed traditional laboratory controls. Usability testing with operators aged > 70 years and no scientific background ensured under two minutes of handling and full guidance via a mobile app. Validation used hundreds of samples across four water types, comparing results to APHA Standard Methods 9223 B via Lin's Concordance Correlation Coefficient (CCC).

Results:

The method achieved CCC = 0.81 (*E. coli*) and 0.76 (total coliforms), demonstrating substantial and moderate agreement with the reference method. In January 2025, IANZ granted ISO 17025 accreditation for potable and non-potable water: the first globally recognised field-based testing service.

Conclusion:

Bactosure redefined laboratory accreditation through automation, inclusive design, and centralised oversight. The system proves that decentralised, user-operated testing can meet ISO 17025 standards and offers a replicable framework for extending accredited analytical services to any location worldwide.