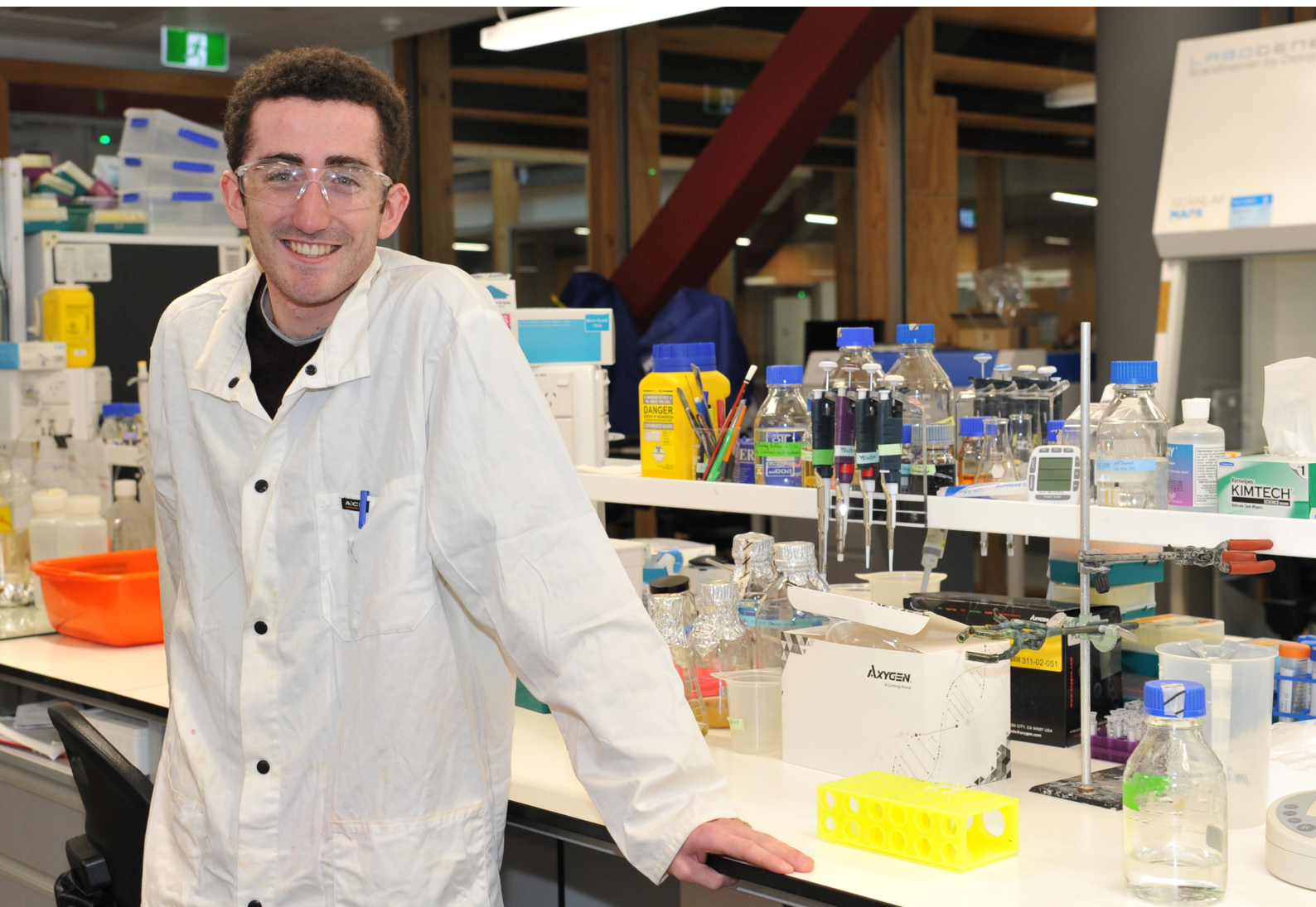


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Whaowhia te kete mātauranga

Fill the basket of knowledge



Mick Adriaansens

PhD - BEL, Herbold

Metagenomic survey of Aotearoa/New Zealand salterns: When does the microbiome embrace a halophilic lifestyle?

Salt is a major limiting factor for life. However, extreme microbes called halophiles can live in high salt environments. Common high salt environments are man-made (often pink) salt pools called salterns. Salterns are large shallow pools in arid landscapes which evaporate seawater until the water is saturated, and the salt crystalizes out. Seawater and salterns microbiomes were found to share little to no species, with halophiles only present at high salinity salterns. However, we know little about how extreme halophilic microbiomes came to be.

To answer these questions, we compared the metagenomic DNA from the different salt lakes, starting with ocean water and sampling salt lakes each increasing in salinity. We used this to infer when certain traits and microbes emerged in relation to salinity.

We linked our results to global observations from salt lakes across the world. Genetic adaptations in the New Zealand saltern exactly match global patterns. We observed a turning point for salinity resistance genes at 14% (w/v) salinity, with the New Zealand saltern microbiome composition changing above this turn point. Novel species were detected and interesting transitions in microbiome were observed impacted by the turning point observed. Above 14% salinity, we observe that halophiles emerge in the microbiome, and as salinity increases, slowly start to dominate the microbiome. My research provides an in-depth view of the microbiome of oceanic salinity to saturation level salinity, answering how and when extreme halophiles emerge.

Mackenzie Aitken

PhD - BSA, Dobson

Solving the permeabilization problem: Investigating how bacteriophage enzyme PAX crosses the bacterial outer membrane

Antimicrobial resistance is a global issue, with rising antibiotic-resistant bacteria, such as the opportunistic Gram-negative pathogen *Pseudomonas aeruginosa*, posing challenges in the healthcare sector due to increased costs and patient morbidity and mortality. Treatment of this bacterium is difficult, partly due to its outer membrane providing a barrier to antibiotic entry. This has seen research shift to alternative antimicrobial compounds. One potential candidate are endolysins: proteins used by bacterial viruses (bacteriophages) to cleave the cell wall of their host bacteria, killing the organism and releasing progeny viruses. A handful of these endolysins have an innate ability to kill Gram-negative bacteria, such as *P. aeruginosa* when externally applied. While their mechanism of cell-wall cleavage is understood, their ability to cross the outer membrane to access the cell wall substrate is currently unknown. Here, we utilise a mixture of *in vitro* and *in vivo* assays to investigate how the endolysin PAX may cross the outer membrane. We show that PAX is unable to permeabilise liposomal membranes that mimic eukaryotic membranes and bacterial inner membranes. Additionally, further *in vivo* experiments with bacteria demonstrated PAX's ability to permeabilise the bacterial outer membrane, suggesting suitability as a foundational characterisation assay. Overall, this work has enabled us to begin investigating what parts of PAX are utilised to cross the outer membrane, and how these parts could be engineered to enhance PAX's antimicrobial ability.

Maddie Barrett

MSc - BSA, Garrill

The biomechanics of stress recovery in *Phytophthora* zoospores

Oomycetes include some of the most successful plant pathogens, with *Phytophthora* species capable of surviving and recovering from environmental stress. This ability allows them to persist and continue infecting host plants as conditions change. They pose significant threats to natural ecosystems through infection of a wide range of hosts, including many native plants in New Zealand, such as Kauri. Despite their ability to recover following environmental stress, the mechanisms underlying this process are not well understood, although rapid remodelling of the cell wall is thought to play a role. I investigated how osmotic stress alters the mechanical properties of encysted *Phytophthora* zoospores and whether cell wall synthesis contributes to these responses.

I used micropipette aspiration to measure Young's modulus as an indication of stiffness in encysted *P. nicotianae* and *P. cinnamomi* zoospores exposed to osmotic stress. I also examined the effects of the cell wall synthesis inhibitor iprovalicarb on Young's modulus. Osmotic stress produced concentration and time-dependent changes in Young's modulus over a 1–2 hours recovery period. Iprovalicarb treatment also altered Young's modulus, with results consistent with a reduction in cell wall stiffness. These findings suggest that encysted *Phytophthora* zoospores undergo dynamic changes in their mechanical properties following environmental stress.

Holly Bates

BSc(Hons), Osborne

Prenatal cannabidiol (CBD) exposure and hippocampal gene expression in rat offspring

Cannabidiol (CBD), a non-intoxicating component of cannabis, is increasingly used for therapeutic purposes, including during pregnancy to alleviate symptoms such as nausea and anxiety. Human epidemiological studies have linked prenatal cannabis exposure to adverse neurodevelopmental outcomes; however, limited evidence on prenatal CBD exposure means its effects during pregnancy remain unclear. Additionally, the long-term effects of prenatal CBD exposure on offspring brain development remain poorly understood, particularly when separated from co-exposures such as tetrahydrocannabinol (THC), tobacco and alcohol. The use of animal models can help define the risk profile for prenatal CBD exposure.

I investigated whether prenatal CBD exposure in a rodent model was associated with changes in hippocampal gene expression. The hippocampus is important for learning, memory and emotional regulation and is particularly sensitive to disruption during development. I examined key genes involved in synaptic function and the endocannabinoid system, which regulates brain development and function. I used pre-collected hippocampal tissue from CBD-exposed and control offspring. I also optimised and troubleshooted a workflow for DNA methylation analysis.

I found that prenatal CBD exposure was associated with reduced relative expression of *Bdnf* (brain-derived neurotrophic factor). *Syp* (synaptophysin) showed a similar pattern, although this was sensitive to sample exclusion. No clear differences were detected in *Gad1*, *Htr1a*, *Cnr1* and *Cnr2*. DNA methylation analysis required optimisation of DNA extraction, bisulfite conversion and downstream PCR, highlighting methodological challenges associated with analysing limited developmental brain tissue.

Together, these findings contribute to understanding the molecular effects of prenatal CBD exposure and provide a foundation for further investigation of associated epigenetic changes.

Kyla Brown

BSc(Hons), Garrill

Investigating the effect of iron-chelating deferasirox and antimalarial drug chloroquine on tumour burden and level of tissue iron in an ID8 tumour model

Ovarian cancer is frequently diagnosed at an advanced stage, when treatment is difficult. Growing resistance to chemotherapy highlights the need for more effective drug treatments to slow progression.

I investigated the anti-cancer activity of two repurposed drugs (deferasirox and chloroquine) used in combination, using an ID8 tumour mouse model, which reflects the pattern of ovarian cancer progression seen in humans. Neither drug significantly reduced tumour burden when used alone, but I hypothesised that combining them would be effective because each drug targets the limitation of the other drug. I had two aims which were first to assess systemic safety by measuring tissue iron content, and the second to determine whether the treatments affected tumour burden.

I compared iron concentrations in heart, liver, kidney, and spleen samples across treatment groups using a biochemical iron assay. To assess tumour burden, I sectioned, stained, and imaged abdominal wall and diaphragm tissue, then measured tumour thickness. I found that iron concentrations in iron-rich organs did not differ significantly between any treatment group and the controls ($P > 0.05$), suggesting that neither drug disrupted systemic iron and that both are systemically safe. I also found that the combination treatment significantly reduced tumour burden compared with controls ($P < 0.05$). These findings show that the combination treatment of deferasirox and chloroquine is safe and effective at reducing tumour burden in ID8 tumours. They support further study in human models and potential clinical use to slow ovarian cancer progression.

AG Camara

PhD - BEL, Prebble

Over 2000 years of fungal community change on Te Pātaka o Rākaihautū: Evidence from fossil spores

The pre-settlement history of fungal communities in Aotearoa New Zealand, including fungal pathogens, remains poorly documented despite their major role as ecosystem drivers. Through this PhD project, I investigate how human arrival and associated anthropogenic change, including introduced species, have impacted past and present fungal communities using palynology and molecular analyses. I developed and characterized a fungal spore record spanning ~2000 years and over 90 morphotypes from a peat core taken from Hickory Bay on Te Pātaka o Rākaihautū (Banks Peninsula). Fungal community composition, overall spore concentration, and fungal richness all changed through time. Specifically, overall spore concentration and fungal richness declined sharply between 175 and 130 cm depth. These initial findings indicate substantial fungal community change over the past ~2000 years on Te Pātaka. Ongoing chronological and compositional analysis will determine whether these shifts align with periods of anthropogenic disturbance, climate variation, or natural cyclical processes, with implications for establishing baselines to inform restoration and biosecurity efforts.

Francesco Cannone

PhD - BSA, Nelson

The spider dilemma: Understanding *Helpis minitabunda* diet

Jumping spiders actively hunt their prey and can adopt specific hunting strategies for prey in their diet. We observed individuals of *Helpis minitabunda* hunting other jumping spiders, while adopting specific techniques to approach them. A similar strategy is observed in the jumping spider genus *Portia*, where their specialization on hunting dangerous prey, like spiders, has led them to develop complex behaviours.

The tendency of *Helpis* to hunt other spiders suggests that they could be a useful model for investigating the evolution of complex behaviours in jumping spiders. Before considering the implications of this hunting behaviour, it was necessary to assess how strong *Helpis*' preference was towards spiders, since they seem to also survive well on a diet of flies. *Helpis*' diet preference was therefore assessed through a choice test. *Helpis* spiders were presented with two videos at the same time, one with an individual of *Musca domestica* walking on one side of a Y-shaped apparatus and the other showing a jumping spider, *Maratus griseus*. The gaze direction and relative position of *Helpis* spiders were assessed relative to the stimuli across trials. Despite a limited number of successful trials, preliminary results seem to show that *Helpis minitabunda* have no preference between spiders and flies, which is rare (most jumping spiders avoid hunting other spiders). This might imply that they are not specialised on a spider diet like *Portia* is, but their interest might still be strong enough to justify a comparison between the behaviours of the two spider groups in future experiments.

Lisa Chahine

MSc - SDC, Cameron

Are zebras just stripy horses?

Sociality is a profound but often unappreciated aspect of an animal's experience, affecting survival, reproductive success, and wellbeing. Despite its significance, there is a lack of understanding surrounding the evolution of sociality outside of the maternal-infant role, and the role domestication may play in domestic or feral species. Equids are highly social and some live in long-term stable groups with unrelated individuals, including feral horses and wild zebras, providing a unique circumstance to explore this knowledge gap. As such, I investigate equids as a model to explore the evolution of sociality. My research uses Hartmann's mountain zebra (HMZ, *Equus zebra hartmannae*), a vulnerable species lacking adequate research, and New Zealand's feral horse, the Kaimanawa (*Equus caballus*), to explore whether shared evolutionary history has a greater influence on sociality than domestication. To do this I studied the behaviour of two populations of HMZ in South Africa and compared their behaviour to similar data previously collected on Kaimanawa. The results differ significantly to those previously described in literature. I found that Hartmann's mountain zebra and Kaimanawa have similar social behaviour through multiple comparisons, however, female HMZ are more social with each other than female Kaimanawa. These results highlight the importance of re-investigating accepted notions in scientific literature. Importantly, they also provide testable hypotheses and several future research opportunities to aid in deciphering the evolutionary motivation of sociality outside of the maternal-infant role.

Jiayi Chen

PhD - BSA, Osborne

Adrenalectomy improves glucose metabolism in the mdx mouse model of Duchenne muscular dystrophy

Duchenne muscular dystrophy (DMD) is an X-linked disorder characterised by progressive loss of muscle contractility, leading to premature loss of ambulation, and cardiac failure. Glucocorticoids are the primary treatment for patients with DMD for improving motor function, but they cause severe side effects such as adrenal insufficiency. Chronic glucocorticoid treatment could cause complete loss of adrenal function, so this study assessed the impact of adrenal ablation on DMD pathophysiology.

Twenty male mdx mice (model of DMD) were adrenalectomized at 8 weeks of age and I assessed their pathophysiology and skeletal muscle histopathology at 12, 24 and 48 weeks of age, which correspond to different stages of DMD progression.

I found that adrenalectomy attenuated glucose intolerance improved insulin production and did not impact the respiratory profile or body composition of mdx mice. Anxiety levels of adrenalectomised mdx mice did not differ from sham-operated mdx mice but they showed signs of lower anxiety after exogenous glucose administration. Adrenalectomy did not affect skeletal muscle strength, contractility kinetics, resistance to fatigue, fibrosis or degeneration, but it did lower thickness.

My findings suggest adrenal ablation improved indices of metabolic dysfunction in mdx mice but did not exacerbate characteristic DMD pathophysiology phenotypes.

Gavril Chong

MSc - BEL, Dobson

Finding the signals: Growing fish cells without the fish

A growing population, increasing environmental pressures, and the need for more sustainable food production are driving interest in alternative ways to produce food. Cellular agriculture is one such approach; growing and using cells outside of an animal to produce meat, fish, and other animal products directly, rather than raising and harvesting the whole animal. To do this, cells must be carefully guided into becoming the specific cell types needed using biological signals that tell them how to grow and develop. But what are these signals and how can we identify and produce them?

My project explores these questions using Chinook salmon as a case study. Most cellular agriculture research to date has focused on traditionally farmed land animals, but demand for fish and other aquatic foods is also rising, and fish cells may not follow the same rules as their mammalian counterparts. By looking at cells from different salmon tissues I will first get to know these cells on a basic level, discovering what they are, and how they grow. I'll then ask simpler questions, with potentially useful answers; what do these cells produce on their own, and could that tell us something about the signals that fish-based cellular agriculture will need?

Hazel Clemens

PhD - BEL, Stott

Isolating novel geothermal bacteria using fluorescence activated single-cell sorting

Fewer than 1% of microorganisms are readily culturable using conventional laboratory techniques, leaving much of microbial diversity accessible only through culture-independent approaches. Geothermal springs harbour unique and understudied bacterial lineages, many of which lack cultured representatives. Cultivating these microorganisms is therefore critical to enable our overall understanding of their evolution, ecosystem functional roles and the ability to harness these attributes for sustainable technologies and biomedical science. Fluorescence-activated cell sorting (FACS), a droplet-based flow cytometry technique that enables individual cells to be separated based on their optical and fluorescent properties, offers a promising approach for selectively isolating and cultivating previously uncultured microorganisms. In this study, I use FACS to isolate novel geothermal bacteria from diverse geothermal springs in the Taupō Volcanic Zone. I use bacterial-viability staining, along with size-based discrimination and single-cell sorting to deflect hundreds of droplets from geothermal samples onto selective media for cultivation. 93 bacterial isolates have been identified with 16S rRNA sequencing so far. These isolates span 21 unique genera, belonging to six different phyla. Whole genome investigation has so far yielded a previously uncultured genus from the family Burkholderiaceae and I expect more novel taxa as culturing efforts continue. My study shows the utility of this FACS technique as a new and effective way to culture previously uncultured microorganisms. This method can be used to complement popular molecular approaches to provide a better overall understanding of microbial communities and deliver new microbial cultures for biotechnology.

George Cox

PhD - BEL, Dickie

When fairies ring, invasive grasses pick up: The role of fungal fairy rings in facilitating plant invasion in the Canterbury high country

Grassland ecosystems are threatened by myriad invasive species, yet we currently have little understanding of if and how these ecosystems resist invasions. Fungal fairy rings in Aotearoa offer a unique opportunity to study how grassland ecosystems change across naturally replicated chronosequences. Fairy rings are circular patterns of vegetation and mushrooms formed by underground fungi expanding outwards at a consistent rate. These fungi act as ecosystem engineers, changing plant biomass and community composition at the ring edge. Anecdotal evidence also suggests fairy rings drive plant invasions. My PhD research aims to investigate the role of fungal fairy rings in the indigenous grasslands of Aotearoa and understand how plant and soil communities can recover from invasion.

I investigated plant community responses across 15 fungal fairy rings in the indigenous grasslands of the Mackenzie basin. Plots were established along a transect running from the middle of each fairy ring to beyond the outer reaches of the fungus, creating a chronosequence encompassing the ecosystem state before, during, and after fungal arrival.

My results indicate that fairy rings of *Lepista* sp. are driving ephemeral plant invasions in the Canterbury high country. At the fairy ring edges, the invasive grasses *Agrostis capillaris* and *Anthoxanthum odoratum* increased in biomass, while plant species diversity decreased. A strong recovery in species diversity and a reduction in invasive grass biomass was recorded in the 10 years after the fungal edge had passed. I am now investigating the below-ground mechanisms driving the fungal induced invasion and the subsequent ecosystem recovery.

Melvin Cubian

PhD - BEL, Dickie

Oomycete as hidden drivers of seed germination and survival along kanuka-grassland ecotone

The Janzen-Connell hypothesis predicts that the accumulation of soil pathogens like oomycetes near conspecific plants drives negative density-dependent seedling germination and survival, allowing other plant species to succeed. While oomycetes have been reported to be associated with early successional kānuka (*Kunzea ericoides*), it is unclear if Janzen-Connell predictions hold true in kānuka forests. I tested this prediction by sowing kānuka and mid-successional species fivefinger (*Pseudopanax arboreus*) into soils collected from inner kānuka forest, edge, and grassland habitats. Soils were subjected to three treatments: water, acetone carrier control, and oomycide (Mandipropamid). I hypothesised that germination and survival would be lower in the inner forest soils than edge or grassland soils, and that inner forest soils would have the greatest increase in germination and survival in oomycide, related to control groups (acetone and water). Germination proportion and seedling survival were modelled using generalized linear mixed models (binomial family, site as a random effect), with model selection via AICc.

Contrary to Janzen-Connell predictions, kānuka germination was significantly higher in the inner forest soil, declining toward edge and grassland. Fivefinger showed a comparatively muted habitat response. Oomycide significantly increased kānuka germination relative to water, while the acetone carrier significantly reduced it; neither treatment significantly affected fivefinger. This oomycide benefit did not vary by habitat. Survival patterns partially diverged from germination trends across habitats.

These results do not support the Janzen-Connell negative density-dependence in kānuka and instead raise the possibility of a positive conspecific soil benefit. Preliminary findings have direct implications on future conservation strategies and highlight the need for long-term seedling experiment and field testing of oomycide.

Xinjue Cui

PhD - BEL, Chapman

Understanding relationships between semi-natural habitats and pollinating insects on Canterbury farms

Semi-natural habitats, such as hedgerows and field margins, often provide food and shelter for pollinating insects but vegetation beside a trap is only part of their environment. I am investigating whether surrounding habitats help explain why insect captures differ among sites with similar field boundaries.

I combine window-trap records from several sampling seasons on Canterbury farms, New Zealand, with fine-scale land-cover maps derived from aerial imagery. Mapping and classification are complete, but map accuracy has yet to be assessed. These maps allow comparisons of habitat cover within areas of different sizes around each sampling site.

Preliminary map summaries show that the average combined proportion of land covered by woody vegetation, New Zealand flax and non-crop herbaceous vegetation was lower when measured across larger areas around the sites. In one sampling season, the bee *Lasioglossum sordidum* accounted for over half of all insects captured across sites.

I am testing whether adding surrounding habitat information improves models that account for field-boundary type and sampling conditions. I will compare spatial scales and analyse the dominant bee species separately from other insect groups to check whether total counts mask different responses. This work will help assess which habitats and spatial scales need consideration when managing farmland for pollinating insects.

Amy Dellow

MSc - BSA, Herbold

Novel strategy for treating water system biofilms with bacteriophage encapsulating hydrogels

Safe drinking water is crucial for maintaining public health. Biofilms in water systems may threaten this safety by harbouring harmful antimicrobial resistant pathogens that can infect immunocompromised and elderly individuals. Currently, chemical disinfectants have limited effect on biofilms because of thick extracellular polymeric substances, limiting penetration. The objective of this research was to develop a method for targeting biofilms by encapsulating environmentally sourced bacteriophages capable of infecting *Klebsiella pneumoniae* into a hydrogel matrix. This hydrogel was developed for extrusion-based 3D bioprinting to control bacteriophage release and to mitigate bacterial biofilms. Currently the hydrogel has been extruded, and preliminary release experiments have allowed for fine tuning of the experimental design. 3D-printed hydrogels containing bacteriophages will be further tested for release over 48 hours to determine whether the system can release enough bacteriophage to maintain self-propagation. This project demonstrates the potential to develop innovative, long-lasting biofilm treatment strategies in water systems. Further work will define the release parameters of the hydrogel, improve printability, and investigate biofilm reduction using the 3D-printed bacteriophage-encapsulated hydrogels.

Deborah Anne Dimayacyac

PhD - BEL, Dickie

From nurseries to whenua: fungal and oomycete communities associated with nursery-grown and naturally regenerating kānuka (*Kunzea ericoides*)

Native plant restoration has been rapidly expanding across Aotearoa New Zealand to restore the whenua and support biodiversity. These restoration efforts rely on nursery-grown seedlings, potentially creating an overlooked pathway for the introduction of hitchhiking pathogens to restoration sites. Despite this, limited information exists on which fungal or oomycete communities accompany native planting stock, whether they persist post-planting, and if potentially pathogenic taxa affect other native plant species in the restoration scene in NZ. I am using *Kunzea ericoides* (kānuka), a widely propagated pioneering species in Canterbury, to investigate this nursery-to-restoration pathway. Here, I am addressing the pathway's first step by analysing whether communities differ between nursery-grown kānuka from those that are naturally regenerating. I sampled three plants from each 15 plant nurseries and 15 natural sites across Canterbury, collecting leaves, roots, and soil. Fungal and oomycete communities between these sites and substrates were analysed through eDNA metabarcoding and culture-based study. Culture-based sampling recovered 90 fungal and 19 oomycete isolates from nursery material, compared to 41 fungal and 14 oomycete isolates from natural sites. Sanger sequencing of cultures indicates differences in the oomycete and fungi assemblages between nursery and natural soils, with different taxa showing contrasting occurrence patterns across site types. These findings provide initial evidence that nurseries may influence the fungal and oomycete communities associated with native restoration plants. Ongoing metabarcoding analyses will determine whether these patterns extend across the broader fungal and oomycete communities across sites and substrates tested. These findings will establish baseline information to identify putative pathogens that are potentially transported with restoration stock. Future studies will track fungal and oomycete persistence following out-planting and test impacts of selected oomycete isolates on other native plant hosts.

Ashlin Donaldson

MSc - SDC, Hetem

Hotspots of New Zealand fur seal road incidents in Kaikōura: Evaluating the effectiveness of motorcycle protection rails as a mitigation strategy

Identifying hotspots where a disproportionate number of wildlife-vehicle collisions occur, allows targeted mitigation, reducing the risk to wildlife and motorists.

Previous hotspots of incidents between New Zealand fur seal (*kekeno*: *Arctocephalus forsteri*) and vehicles on State Highway 1 (SH1) around Kaikōura, resulted in ~2 km of motorcycle protection railing (MPR) being installed in 2024, targeting hotspot areas. My research aims to evaluate the effectiveness of MPR as a mitigation strategy in reducing kekeno-road incidents.

Using data collected by the New Zealand Transport Agency (NZTA), I analysed the number and distribution of kekeno-road incidents. I also conducted systematic surveys along SH1 during the peak season (April to June 2026) to further quantify kekeno mortalities and assess whether incidents were being under-reported in NZTA records.

Kernel Density Estimation Plus identified eleven hotspots using NZTA data collected two years after MPR installation. The hotspots accounted for 79.5% of incidents and 2.8 km of SH1. Although incident numbers in the two years post MPR installation (79) were similar compared to prior (74), incidents in sections where MPR were installed decreased by 85.7% and total incident rates based on pup production numbers decreased by 47.1% (North Coast) and 57.1% (South Coast).

Systematic surveys identified sections of MPR uplift, allowing road access by pups, influencing mitigation effectiveness. The surveys also highlighted under-reporting of incidents by NZTA.

While further research is required, my findings suggest MPR is a promising mitigation measure for reducing kekeno-vehicle collisions on SH1 Kaikōura, and results support extending MPR coverage to further reduce collision risk

Malaika D'Souza

PhD - BEL, Kross

Pathogen transmission at the wildlife-livestock interface: Influences of biodiversity and agroecosystem management

In Aotearoa, backyard poultry production sites are commonly co-inhabited by wild passerine birds, which may maintain a complex network of pathogen introduction and re-introduction. *Campylobacter* and *Salmonella* spp. are widely circulating genera of enteropathogenic bacteria that infect a broad range of taxa and are important causes of gastroenteritis in people. Source attribution of infections involves collection of viable microbiological samples and is often time sensitive. *Salmonella* is implicated in mass mortality events in synanthropic and native wildlife and thus has been difficult to track in healthy populations. Contrastingly, there is sparse evidence for fatalities or clinical manifestation of *Campylobacter* spp. in wild animals and livestock. Therefore, the *Campylobacter* genus provides an interesting model to follow transmission mechanisms in similar bacteria. This wildlife-livestock pathogen transmission interface remains insufficiently surveilled in Aotearoa, with no information on baseline pathogen incidence. My PhD project is investigating possible routes of pathogen transmission in wild passerines. Using targeted sampling across sites in Canterbury, we aim to document pathogen diversity and identify key passerine species involved in transmission. We capture wild passerines using mist nets, collect cloacal swabs and then selectively culture for *Campylobacter* and *Salmonella* spp. We also use camera traps to quantify direct and indirect interactions between wild passerines and domestic chickens, helping identify species and behaviours associated with contamination and pathogen exposure. Preliminary results from samples collected from wild passerines and chickens show no *Salmonella* spp. incidence and a low incidence of *Campylobacter* spp. (2/40 samples). Camera trap data reveals direct contact between house sparrows and common starlings with chicken feed. Pathogen incidence, shared space-use and interaction data will help us analyse spillover-spillback mechanisms between wild and domesticated communities.

Nicolette Edmunds

PhD - SDC, Cameron

The common brushtail possum in the context of invasive species management across policies

Several invasive mammalian predators have been introduced to New Zealand by humans, both purposefully and accidentally, many of which are harmful to native biota. Purposeful introductions of the common brushtail possum to New Zealand began in the 1800s to develop a fur trade. In 1947, the New Zealand government began controlling possum numbers due to their invasiveness. Since then, New Zealand has established multiple conservational policies and government funded campaigns that involve possum control, most notably National Pest Management Strategy, and Predator Free 2050. I have completed a two-part comprehensive review of published literature on the common brushtail possum in New Zealand and Australia. The aim of this review was to gain an understanding of published literature about the common brushtail possum to identify how policies have impacted research, and what areas have been understudied, particularly regarding areas that could aid in future conservation management planning and possum control. I reviewed data by studying patterns in New Zealand as a whole, across New Zealand policies and comparing the last decade of New Zealand and Australian publications. I have identified topics of study that were lacking or missing between New Zealand and Australia, as well as patterns in key topics across policies. Interestingly, the number of papers written per 5-year period is not increasing significantly even though eradication is a current goal for New Zealand.

Emma Godfrey

PhD - SDC, Cameron

Better safe than sultana: Risk sensitivity in common brushtail possums

Life is full of risks; some we are aware of, others less so, but each shapes our sensitivity to future interactions. Assessment and avoidance of risk may change based on life experience (learning), or due to innate behavioural differences ('personality'). Common brushtail possums (*Trichosurus vulpecula*) in Aotearoa New Zealand (NZ) can find themselves in risk-filled environments, with their responses influencing survival. Free from the natural predators of their native range, traps with rewarding treats act as artificial predation in NZ environments, thereby inducing a strong selection pressure for trap avoidance, either through selecting less trap-shy individuals (leaving the wary ones) or through experience-based learning. Populations across NZ experience different levels of this artificial predation pressure; some in intensively controlled sites, others in pockets free of predator control. But does this variation in environmental risk translate into variation in behaviour? Using giving-up densities (a risk-sensitivity measure), I examined possum interaction with artificial food patches across three areas differing in control intensity. Each population was offered two food patches containing sultanas: a 'safe' tray allowing visual scanning of the environment, and a 'risky' bucket with a head-sized hole, mimicking the physical risk traps pose. The number of sultanas uneaten measures perceived risk; higher residual amounts indicate greater caution. Results will establish whether possums exposed to greater control pressures show heightened caution towards risky patches, consistent with sensitivity to trap-like stimuli, or whether foraging behaviour remains unaffected by control intensity, with implications for how we can further understand trap avoidance

Jane Gosden

PhD - SDC, McIntosh

Aotearoa | New Zealand kettle hole tarns are small and ephemeral but high in plant diversity and need management aligned with their natural fragmentation

Kettle hole tarns that form ephemeral wetlands (hereafter kettles) are plant biodiversity hotspots. However, management is challenging because they are small (mean 0.56 ha), widely distributed in Te Waipounamu | the South Island, patchy in the landscape, found across a wide range of land tenures, and experience varied land uses. These are issues facing many wetlands worldwide. To better inform management of kettles, we investigated the shared environmental drivers that explain their plant and lichen (hereafter “plant”) communities. We surveyed plant communities from 15% of mapped kettles of Aotearoa. Specifically, we tested whether kettle plant communities cluster by geography, how different one kettle is from another, and identified environmental drivers of exotic plant cover, native plant richness and threatened plant richness. We found imperfect overlap between kettle plant communities and geographic location and strong differences in between kettle diversity (beta-diversity mean 0.84). Kettles with native-dominated terrestrial vegetation buffers, and wetter kettles, had less exotic plant cover. Additionally, we found evidence that some grazers, including Canada geese (*Branta canadensis*), are associated with higher native species richness and the presence of threatened plants. We recommend that kettle managers retain both native buffers and grazers (but not cows), maintain natural hydrological cycles and protect multiple rather than a few individual kettles at any given site. Our recommendations reflect a naturally fragmented ecosystem now found in a mixed-use landscape, including the presence of introduced herbivores, so highlight the importance of those contexts for ephemeral wetlands.

Aleshya Grant

BSc(Hons), Morris

Read it and weep: Characterisation of α -synuclein biomarkers in Parkinson's disease reflex tear fluid

Parkinson's Disease (PD) is currently diagnosed after motor symptoms appear, such as tremors, muscular rigidity, and slowness of movement. By this point, significant and irreversible nerve cell loss has already occurred. The protein α -synuclein (α -syn) is central to this disease. It is normally unstructured and monomeric, but in PD, it clumps into structures called oligomers and fibrils. Oligomers accumulate years before symptom onset, making them a promising target for early disease detection.

Seed amplification assay (SAA) is a sensitive oligomer detection method, mainly applied to cerebrospinal fluid. Collection requires an invasive lumbar puncture, unsuited for repeated testing. My research asks whether this assay can be optimised for tear fluid, a non-invasive and accessible alternative which can mirror the brain environment.

I aimed to increase the sensitivity and specificity of an established tear-based SAA protocol to match the diagnostic performance of its CSF-based counterpart. I explored three approaches: using histidine-tagged α -syn to produce a more sensitive assay, using immunoprecipitation to concentrate α -syn from tear samples, and characterising extracellular vesicles in tear fluid as an enriched α -syn source. The assay has been optimised through multiple rounds, identifying key variables impacting SAA performance. Extracellular vesicles have been successfully isolated, imaged and characterised by size and morphology, showing differences between control and PD samples.

My work provides novel insights into tear fluid and its extracellular vesicles, which are understudied in PD. Collectively, these findings are a valuable step towards improving tear-based PD diagnostics, offering an earlier and accessible alternative to current diagnostic methods.

Nathaniel Hearfield

PhD - BEL, Turnbull

Drought stress memory in radiata pines

Plant stress memory or “priming” is an emerging field of research with enormous potential for the agriculture sector. In short, plants previously exposed to biotic and abiotic stressors are quicker to respond to, are more tolerant to, and recover faster from subsequent stress periods than naïve plants. This PhD project aims to characterise the relationship between changing drought stress and the subsequent effects on photosynthesis in young radiata pine (*Pinus radiata*) trees grown under greenhouse conditions. A year-long drought trial was carried out on trees from two clonal lines which were exposed to a series of drought-recovery cycles. Statistical analyses of the changes in photosynthetic rate of trees undergoing drought stress demonstrated that primed plants were able to maintain higher photosynthetic rates compared to naïve trees and recovered faster upon rehydration. Needle tissue collected throughout the experiment is being analysed for differential gene expression to identify genes linked to the drought response, allowing for further molecular analyses of the epigenetic environment around these genes, and the quantification of signalling molecules and osmoprotectants produced during the drought response. The identification of inheritable genetic markers for improved drought tolerance and resistance may provide considerable benefits for breeders selecting for hardier genotypes in a changing global climate.

Rich Iyagbaye

PhD - SDC, Thomsen

Species traits and environmental conditions determine the strength of facilitation cascades

Facilitation cascades (FCs) are ecologically important indirect species interactions, yet the factors determining their strength remain poorly understood. Species traits and environmental conditions can influence FCs, but their relative importance and interactive effects have rarely been quantified. Here, I tested the hypothesis that different traits and environmental conditions vary in their effects on FC strength, and that trait-by-condition interactions modify these effects. Seaweed species with different traits and epiphyte loads were collected across seasons and tidal elevations, and their associated small invertebrate communities were measured. FCs were calculated and compared by standardizing invertebrate counts both by host biomass and by the total (combined) host and epiphyte biomass, because both approaches have been reported in the literature.

FC strength varied substantially among traits and environmental conditions, supporting my hypothesis. Based on total biomass-standardised counts, FCs were strongest when epiphyte biomass was high, host morphology was simple (and epiphyte morphology complex), and during summer, whereas patterns across tidal elevations were less consistent. Many two-way interactions were detected, but three- and four-way high order interactions were few. The significant interactions indicated that FCs were strongest under conditions associated with higher baseline invertebrate abundances. However, predictor rankings and interaction patterns differed when FCs were calculated from host-only standardised counts, highlighting the importance of clearly reporting analytical approaches.

These findings demonstrate that FC strength is jointly shaped by species traits and environmental conditions. The structural complexity of the host seaweeds and their epiphytes appear to provide benign habitats with ample food, predator refugia and strong buffering of intertidal thermal stress. Future studies should test the generality of these patterns across species, environmental gradients, ecosystems, habitats, and biogeographic regions.

Sophie Jamieson

BSc(Hons), Meisrimler

Exploring the Potential Interaction Between NTL9 and KIN10

Plants rely on signalling networks to coordinate responses to abiotic and biotic stress, and transcription factors (TFs) regulate stress-responsive genes. Membrane-bound NAC TFs are activated following translocation from the endoplasmic reticulum (ER) to the nucleus. NTL9 is a membrane-associated NAC TF associated with abiotic and immune signalling in *Arabidopsis thaliana*, with its activity thought to be regulated primarily at the protein level. However, the upstream mechanisms controlling NTL9 remain poorly understood. The SNF1-related protein kinase 1 (SnRK1) catalytic subunit KIN10 is an energy-sensing kinase that coordinates stress responses. KIN10 has been shown to phosphorylate and regulate TFs including SPEECHLESS (SPCH) and AHL14. SnRK1 is known to interact with NAC TFs, suggesting KIN10 as a potential regulator of NTL9.

To investigate this potential interaction, NTL9 and KIN10 were cloned with an N-terminal RFP (red fluorescent protein) and a C-terminal GFP (green fluorescent protein) tag, respectively. Constructs were transiently expressed using *Agrobacterium*-mediated expression in *Nicotiana benthamiana* followed by confocal microscopy. Accordingly, NTL9 primarily localised to the ER and nuclear envelope, while KIN10 was predominantly cytosolic. Western blot analyses confirmed protein expression and stability in planta. Further, following co-expression, confocal microscopy showed that NTL9 and KIN10 co-localised, primarily around the nucleus. Co-immunoprecipitation (Co-IP) analysis was used to study the interaction between these proteins; however, the results require further experimental validation.

These findings provide new insight into the previously uncharacterised relationship between KIN10 and NTL9. This research expands our understanding of membrane-bound NAC TF regulation and how plants coordinate stress and immune signalling responses.

Olivia Janes

PhD - SDC, Steeves

Genetic incompatibility in threatened species: Can we mitigate what we struggle to define or measure?

Understanding the genetic causes of early reproductive failure in threatened species is essential for making informed management decisions. Early reproductive failure is often attributed to individual infertility; however, many of these failures arise not from infertile individuals but from genetically incompatible pairings. Yet, it is often unclear what is meant by “genetic incompatibility” or how it should be measured, limiting our ability to assess its contribution to early reproductive failure.

I present a systematic review demonstrating that genetic incompatibility remains poorly defined and under-explored, particularly in a conservation context. I show that the term is used inconsistently and has been applied to early reproductive failure caused by a range of underlying mechanisms. Furthermore, I show that the approaches used to measure genetic incompatibility may be insufficient to determine causation. I argue that establishing a clear framework for defining and measuring genetic incompatibility is therefore critical for understanding its role in early reproductive failure and for developing effective management strategies to mitigate it.

Ashleigh Johns

PhD - BSA, Dobson

Mechanism of sialic acid transcriptional regulation by CRP in *Haemophilus influenzae*

Protein-DNA interactions are essential in cells. These interactions include transcriptional regulator proteins. Transcriptional regulators facilitate many important cellular functions, including regulating gene expression and assisting with molecular responses to internal and external signals.

One of the largest groups is the cyclic AMP receptor protein (CRP) superfamily in bacteria, and these regulate many different genes. *HiCRP*, from *Haemophilus influenzae*, contributes to controlling the expression of genes required for the uptake and utilisation of an alternative carbohydrate, sialic acid. Sialic acids scavenged from human hosts are often used by pathogenic bacteria, like *H. influenzae*, as an energy source and to disguise themselves from the host's immune system, using the sialic acids as an outer "coat". Most protein genes involved in the sialic acid pathways are in the *nan-siaPQM* operons.

Previous work proposes that in *H. influenzae*, *HiCRP* regulates these two operons in tandem with another transcriptional regulator protein *HiNanR*. Understanding the protein-DNA interactions of *HiCRP* may shed light on *HiCRP*'s importance during *H. influenzae* infections. My PhD project focuses on how *HiCRP* interacts with its effector cAMP and its DNA operator site to discover the mechanisms used to regulate both operons. Using structural biology and biophysical techniques, I have found *HiCRP* is a homodimer, binds to cAMP and cGMP, and has a different structural conformation in the absence of cAMP, compared to other CRP structures. Future research will investigate how *HiCRP* might work with *HiNanR* to regulate the *nan-siaPQM* operon in the *H. influenzae* present in low glucose environments.

Madeleine Jorgensen

BSc(Hons), Hetem

Keeping it cool: A comparative analysis of pitfall trap design (covers, size, and materials) on internal trap temperature

Conservation of unique lizard taxa of Aotearoa relies on monitoring using pitfall traps. Yet, pitfall traps have the potential to expose lizards to thermal stress as the lizards are unable to behaviourally thermoregulate while inside the trap. Pitfall traps designs vary in terms of lid and container materials and size throughout Aotearoa and globally, and this variation may lead to the traps displaying differing thermal properties. My project aimed to determine the most suitable pitfall trap designs to reduce the thermal stress threat to lizards. To achieve this aim, 36 pitfall traps, each with a different combination of container material, size, and lid material and colour, were deployed in a grid on Kaitorete Spit, Canterbury, NZ, for a period of 3 months between January and March 2026. Internal temperatures of the traps were measured through operative temperature models placed inside the traps. Weather data was also collected using an on-site weather station. Internal trap temperatures were on average warmer than ambient weather station temperatures. Results showed that while container size had no effect on internal temperature, metal traps reached internal temperatures 0.85 °C higher than plastic traps. Additionally, there was a statistically significant interaction between lid material and colour, with black plastic lids resulting in the highest internal temperatures. These results suggest that the use of plastic containers, lids and light colours may reduce the risk of thermal stress for trapped lizards. As global temperatures rise, designing traps to reduce thermal stress becomes increasingly important for the welfare of lizards during monitoring.

Charlotte Kemp-Dale

MSc - BSA, Morris

Caspase 6 aggregation and activity loss in response to HOSCN oxidation

Caspase 6 is an essential executioner protein in cell death, as well as being involved in several other functions, including regulating several neurodegeneration-associated proteins and immune-associated pathways. Amongst executioner caspases, it has unique flexibility leading to partial self-activation capability and self-inhibition. Hypothiocyanous acid (HOSCN) is a compound created when neutrophils release myeloperoxidase and hydrogen peroxide, which can react with thiocyanate in the environment to make HOSCN and destroy bacteria, but the consequences of HOSCN on the surrounding human cells remain poorly understood. Previous work in our group has shown that HOSCN can switch cell death pathways to necroptosis, an inflammatory form of cell death, instead of the normal apoptosis pathway, but it is not fully understood how this process occurs. Previous work has further shown that HOSCN oxidation of the initiator caspase, caspase 8, leads to disulfide bond formation and amyloid like aggregation. This research aims to understand if executioner caspases are also sensitive to inactivation by HOSCN, focussing on caspase 6. Using recombinant protein, we have found that application of HOSCN leads to a significant decrease in protease activity, and activity is recoverable when reducing agents are added after short HOSCN-treatment timepoints. Circular dichroism and gel electrophoresis data shows oxidation and rapid aggregation of caspase 6 within an hour of HOSCN treatment. Further studies are required to determine the type of aggregation and to compare to other caspases. This research will contribute to a full understanding of oxidation-driven caspase aggregation, as the executioner caspases have not been researched to date.

Isabel Lee-Park

PhD - SDC, Tylianakis

Understanding the consequences of environmental heterogeneity on the eco-evolutionary arms race between fruit flies and their parasitoid wasps

Biological control involves the purposeful release, augmentation, or conservation of natural enemies for the control of target pests. It's a major component of Integrated Pest Management (IPM), a holistic and interdisciplinary approach for managing pests using complementary strategies that are considered economically and ecologically sustainable. Despite numerous examples of how biological control introductions have successfully suppressed agricultural pest populations and reduced reliance on chemical insecticides, recent studies suggest that pests can evolve host resistance (the ability for a host to prevent and survive parasitoid attack) to their parasitoids. Over multiple generations, variation in environmental conditions, species interactions, and genetic diversity can alter selection pressures, such that host resistance becomes more prevalent in pest populations. Thus, parasitoid virulence can decline over time, even if initial virulence is high. As environmental conditions continue to change and pests evolve faster due to shortened lifespans under climate change, understanding how host resistance rapidly evolves is critical for developing more secure biological control strategies.

Using multi-generational laboratory experiments, I explore how three levels of the same host-parasitoid system shape eco-evolutionary dynamics. At the local patch level, I manipulate the host's resource environment by varying protein, carbohydrate, and ethanol availability. At the interaction level, I test how differences in the timing of parasitoid colonization (priority effects) and interspecific competition influence the evolution and prevalence of host resistance evolution. At the landscape level, I subject both hosts and parasitoids to heat-shock events and limited nectar availability to simulate sudden periods of intense heat associated with climate change.

Hamish Lindsay

MSc - BSA, Stott

Turning waste kiwifruit into blue pigment with *Galdieria sulphuraria*

~50,000 tonnes of New Zealand's kiwifruit goes to waste each year, much of which becomes low-value stock feed. This fruit still contains sugars that could support microalgal growth. Phycocyanin is a high-value natural blue pigment currently produced mainly from *Spirulina*, which requires light for growth. The hot-spring red alga *Galdieria sulphuraria* offers a different approach because it can grow on sugar in the dark while still producing phycocyanin. I am investigating whether New Zealand isolates of *G. sulphuraria* could use waste kiwifruit as a substrate for pigment production.

I first screened candidate isolates from the Taupō Volcanic Zone under heterotrophic conditions at 45 °C and pH 2.5 using a sugar mixture designed to mimic gold kiwifruit. Of the three isolates tested so far, the fastest-growing isolate, from Kuirau Park, doubled in as little as 5.7 hours but produced almost no phycocyanin. In contrast, CM1.3Y, isolated from a Craters of the Moon steam vent, reached a similar culture density while producing a phycocyanin-associated fluorescence signal about 24 times higher. A third isolate did not grow on the sugar mixture.

CM1.3Y is therefore the leading isolate from this initial screen. I will next test the remaining isolates, compare growth on kiwifruit juice and glucose, and determine how oxygen availability affects growth and pigment production. This work will test whether rejected kiwifruit can be converted from a low-value waste stream into a substrate for producing natural blue pigment in the dark.

Jiawang Ma

PhD - BSA, Gieseeg

Oxidized LDL induces macrophage death through ERK signalling in U937-derived macrophages

In the progression of atherosclerosis, oxidized low-density lipoprotein (oxLDL) can trigger macrophage death which destabilises artery plaque leading to heart attacks. Previous studies on the macrophage-like U937 cells showed that this death is caspase-independent and dependent on NADPH oxidase activation which produces superoxide. How oxLDL induces NADPH oxidase activation and macrophage death remains unclear. We investigated whether extracellular signal-regulated kinase (ERK) forms part of that signal.

We exposed U937 cells to copper-oxidized human low-density lipoprotein at the LD70 concentration. ERK phosphorylation was measured by western blotting analysis and superoxide generation by flow cytometry. The effect of inhibition of ERK phosphorylation was examined using the inhibitor PD98059.

After treatment, oxLDL induced ERK phosphorylation between 2 and 6 hours. Superoxide generation, assessed by DHE staining, increased significantly between 4 and 6 hours. The inhibitor PD98059 blocked ERK phosphorylation and inhibited the superoxide generation.

These observations suggest that ERK signalling helps connect oxLDL exposure to oxidant production, providing a possible signalling pathway to macrophage death. Our working hypothesis is that receptor-mediated signalling activates NADPH oxidase through ERK and p47 phosphorylation. Identifying the initiating receptors and directly testing the phosphorylation of p47 will help determine how oxLDL activates the cells' own oxidant-generating system.

Chiara Mercer

PhD - BSA, Meisrimler

When effectors collide: Interaction BLR05 and BLR09 *in planta*

Phytopathogenic oomycetes cause devastating plant diseases that threaten food security. During infection oomycetes secrete effector proteins to manipulate host immunity and promote infection. BLR05 and BLR09 are two RxLR effector proteins produced by obligate biotroph *Bremia lactucae* (downy mildew of lettuce). These two effectors localise to the hosts endoplasmic reticulum and interact with tail-anchored NAC [no apical meristem (NAM), *Arabidopsis thaliana* transcription activation factor (ATAF1/2) and cup-shaped cotyledon (CUC2)] transcription factors: ANAC013, ANAC017, and LsNAC069. BLR05 and BLR09 suppress the stress-induced nuclear relocation of LsNAC069, with stronger effect in the presence of both effectors. It is unknown how these two effectors work together during infection. The aim of this study is to investigate whether BLR05 and BLR09 interact with one another to enhance NAC suppression.

To investigate the interaction between BLR05 and BLR09 fluorescent and epitope-tagged constructs were used. Constructs were transiently expressed using *Agrobacterium*-mediated expression in *Nicotiana benthamiana*. Förster resonance energy transfer with fluorescence lifetime imaging microscopy, and co-immunoprecipitation were used to assess effector-effector colocalisation, association, and proximity *in planta*. Results indicate that BLR05 and BLR09 interact at the endoplasmic reticulum, with an estimated fluorophore proximity of 6 nm. This interaction may contribute to the observed enhanced NAC suppression.

This research explores a previously unexplored mechanism in which oomycete effectors interact with each other to enhance suppression of host immunity. Uncovering how BLR05 and BLR09 work together will expand our understanding of how oomycete effectors manipulate host responses and may provide insights towards downy mildew disease management.

Aaron Millar

PhD - BEL, Chapman

Using artificial polyploids to unlock how polyploidy affects plant environmental responses

Polyploidy, where cells have additional sets of chromosomes, is a widespread and pivotal force in plant evolution. However, the precise effects and role of polyploidy is complex and highly debated. One key question is whether polyploidy improves the ability to respond to environmental variation. A major barrier to answering this question is that natural polyploids have experienced many other genetic changes that make discerning the effect of polyploidy events themselves challenging. To resolve this issue, we created new, artificial tetraploids of the evolutionary model species *Erythranthe guttata*, which we compared to their diploid siblings in shade and drought, competition, and temperature trials. Tetraploids and diploids had distinct phenotypes, with tetraploids having greater biomass, larger leaves, and higher photosynthetic rates, but producing fewer flowers and vegetatively reproductive shoots. Phenotypic plasticity differences, though limited, allowed some ploidies to better exploit favourable environmental conditions. Diploids were more plastic than tetraploids to water in shoot length, and to competition in shoot and flower number. Tetraploids were more plastic than diploids to light in leaf sizes. Unlike in nature, artificial *E. guttata* tetraploids in our experiment were notably less fit than diploids. These results suggest that selection and later evolution may play a greater role in the success of polyploid lineages than polyploid events themselves. The size advantages tetraploids exhibit could form the basis of future adaptations. Individual lineages also varied in fitness, with a minority of polyploid lineages potentially being more fit than diploids, highlighting the role of selective filtering in polyploid success.

Prakriti Mishra

MSc - SDC, Dickie

Resolving the identities and ectomycorrhizal status of fungi associated with Canterbury pines

Ectomycorrhizal (EcM) fungi form important symbiotic relationships with pine roots, supporting nutrient uptake and tree health, yet the fungal communities associated with introduced pines in New Zealand are not well characterised. Understanding these fungal associations may help explain how introduced pines establish and spread in New Zealand.

My research aims to determine both the identities and the ecological status of these fungi by combining root-tip morphology, ITS sequencing, and multi-gene phylogenetic analysis. Three groups are of particular interest because their identities or trophic roles remain unresolved: an abundant root coloniser tentatively placed in *Sistotrema* but lacking a recognised sporocarp, the Atheliaceae (*Amphinema*/*Tylospora*) complex, and *Chalciporus piperatus*.

EcM root tips from sites around Canterbury were described morphologically and the ITS region was sequenced from the first 32 tips in both directions, then compared against reference databases using BLAST. Of the three groups of interest, only the Atheliaceae have been recovered so far. Other taxa included *Boletus edulis*, *Amanita muscaria*, Thelephoraceae (*Tomentellopsis*), Sebacinaceae, and *Phialocephala*, a genus commonly associated with dark septate endophytes. Where morphology could be matched to sequence, tips with BLAST matches to Atheliaceae differed in mantle surface and emanating hyphae, suggesting more than one fungus within this group.

BLAST alone cannot establish either identity or ecological role. Multi-gene phylogenetics will help resolve phylogenetic placement, while morphology will provide evidence for ecological status: a distinct mantle-forming morphotype associated with *Phialocephala* or *Chalciporus* could provide evidence for an ectomycorrhizal association.

Leila Nolan

PhD - BSA, Dobson

Assessing allergenic risk in a changing food system

Science is advancing faster than regulation can keep up. Cultivated meat is a clear example: by growing animal cells rather than raising and slaughtering whole animals, this emerging technology could transform how we produce meat and potentially reduce some of the environmental pressures associated with conventional production. However, as new technologies change how food is produced, we also need to ask a fundamental question: how do we know these new foods are safe?

Allergenicity provides a useful case study. Current food safety frameworks use a range of approaches to identify potential allergens, but some of the techniques currently used do not capture the complexity of how allergic responses occur. For example, simulated digestion can be used to investigate protein stability, yet commonly used pepsin-based tests do not fully represent human digestion, and protein survival alone does not determine whether a protein will cause an allergic response. As cultivated meat develops, there is an opportunity to apply more comprehensive approaches before these technologies become established in regulation.

My research investigates current and emerging approaches for assessing allergenicity in cultivated bovine, porcine and fish meats, bringing together evidence from proteomics, bioinformatics, digestion, and immunological testing. By evaluating what these approaches can, and cannot, tell us about allergenic risk, this work identifies gaps in the current evidence base and explores methods that could strengthen future safety assessments.

The goal is not simply to determine whether cultivated meat is safe, but to generate the scientific evidence needed to determine what we should be testing, how we should test it, and what evidence regulators may need as food technology continues to change

Hunters among the leaves: Predatory behaviour of two endemic meshweaving spiders in the field

Spiders (pūngāwere) are carnivorous arthropods which play an essential role in nutrient cycling and regulating insect populations in diverse ecosystems around the world. Despite their importance, spiders are under-researched, both globally and here in Aotearoa New Zealand. My thesis aims to explore the morphology and natural history of two poorly studied endemic spiders: *Paradictyna ilamia* and *Viridictyna* sp. I will discuss the natural history of these species. I conducted weekly monitoring of tagged leaves on which spiders were found through spring and summer (2025–2026). Each week, I recorded the number of individual prey items on each tagged leaf, identified prey order, and kept tallies of observed prey items by taxon. Initial observations suggest that the diets of *P. ilamia* and *Viridictyna* sp. primarily consist of insects of orders Diptera (flies), Hemiptera (true bugs), Psocodea (lice), and Hymenoptera (specifically wasps). These results will contribute to knowledge of ecosystem functioning, with potential implications for conservation and management. Additionally, comparing the dietary niches of similar taxa can help with understanding biodiversity and evolution.

Anisiia Prokshina

PhD - BSA, Nelson

No smoke but mirrors: The ability of kea (*Nestor notabilis*) to use mirror reflections

Mirror use in animals has attracted the attention of researchers for over 50 years. The most well-known experiment is the mirror self-recognition test. To pass it, the subject is required to show self-directed behaviour in front of the mirror. Although some species pass the test, kea, alongside numerous other species, fail. We investigated whether kea would be able to use the mirror in a context that does not require self-recognition. In our first experiment, we introduced kea to a four-box apparatus and gave them a mirror-mediated spatial location task. Using the mirror reflection, kea had to find a rewarding token hidden in one of the two boxes during the two-box test, or in one of the four boxes during the four-box test. While only two out of seven kea spontaneously located the token during the two-box test, five out five kea successfully found a token hidden in a novel location in the four-box test. Our second experiment aimed to check whether kea can distinguish physical reality from the mirror reflection. In this task, kea had to pick a side where they could see two physical rewarding tokens and ignore the side where one of the rewarding tokens was actually reflected by the mirror. Preliminary results suggest that kea fail to distinguish between the real token and the reflected one. Our experiments demonstrate that despite the ability to use the mirror to locate an object hidden in the real world, kea do not distinguish between real objects and reflected ones.

Megan Rawlins

MSc - BSA, Morris

Amyloid fibril formation by ankyrin-repeat proteins following cysteine thiolate oxidation

Protein aggregation occurs when proteins change from their normal native fold and group together into larger structures. Formation of these aggregates is commonly associated with diseases like Alzheimer's and Parkinson's.

However, amyloid fibrils, a highly ordered form of aggregate, can also form reversibly and serve functional roles. The ankyrin-repeat protein, p16, undergoes reversible amyloid formation when a specific cysteine amino acid in its structure is chemically modified by oxidation. This discovery revealed a previously unrecognised way for amyloids to form and raised the question of whether other proteins with similar structures undergo similar transitions. I aimed to determine whether other cysteine-containing ankyrin-repeat proteins form amyloids following oxidation.

I investigated two ankyrin-repeat proteins, OSTF1 and RFXANK, by expressing and purifying protein constructs from *Escherichia coli*, then characterising their aggregation following cysteine oxidation. Non-reducing SDS-PAGE assessed the formation of cysteine cross-links, and fluorescence assays using amyloid-binding dyes tracked amyloid formation under different conditions. Changes in protein structure were assessed using circular dichroism, and fibrils were visualised with electron microscopy. Both OSTF1 and RFXANK showed amyloid formation similar to p16, but their aggregation behaviour differed in the presence of salt, physiological oxidants and reducing agents.

These findings indicate that oxidation-associated aggregation is not restricted to the p16 family and suggest that cysteine-containing ankyrin-repeat proteins may share a common oxidation-regulated aggregation mechanism.

Kiara Reddy

MSc - BSA, Osborne

Does prenatal cannabis exposure affect neurodevelopmental gene expression and behaviour in rats?

Prenatal cannabis exposure (PCE) occurs when a fetus is exposed *in-utero* to cannabinoids, such as tetrahydrocannabinol (THC) and cannabidiol (CBD), through cannabis consumption during pregnancy. PCE has been associated with neonatal and developmental outcomes, including reduced birth weight, preterm birth and fetal growth restriction. Reduced public stigma around cannabis use, conflicting global regulation, and heightened stressors, such as the COVID-19 pandemic, have resulted in increased substance use in adult populations, including pregnant women. However, controlled modelled evidence for the effects of PCE on neurodevelopment remains limited, particularly at the level of the transcriptome and methylome, and whether these effects persist into adulthood. This study aims to determine whether behavioural changes and differential gene expression are correlated in rats exposed to CBD during prenatal development. Anxiety-like and risk-assessment behaviours were assessed using the light/dark box test to determine whether developmental CBD-exposure alters these behaviours. Whole transcriptome analysis of the prefrontal cortex, hippocampus and striatum was used to identify differential gene expression in traits relative to human neurodevelopmental conditions. Because most human PCE involves THC-containing cannabis, this CBD-only model isolates the contribution of CBD exposure during pregnancy. These analyses will determine whether developmental CBD exposure alters gene expression in brain regions relevant to human neurodevelopmental conditions, and whether these changes are observable in behaviour. Further work may investigate whether DNA methylation mediates these gene expression changes, helping clarify the role of PCE on neurodevelopment into adulthood.

Jeslin Sabatini

PhD - BSA, Osborne

Repeated eccentric contractions reveal an intermediate injury phenotype in muscle expressing microdystrophin

Dystrophin protein stabilises skeletal muscle fibres as they transmit force during eccentric contractions (ECCs), such as walking downstairs. Absence of dystrophin causes Duchenne muscular dystrophy (DMD), resulting in increased susceptibility to ECC-induced strength loss. Microdystrophin (μ Dys), a gene therapy designed to restore muscle function in DMD, is typically evaluated by protection against ECC-induced strength loss following a single bout of ECC, despite skeletal muscle being repeatedly exposed to ECCs during day-to-day activities. Thus, my research examined how repeated bouts of ECCs impact skeletal muscle strength in mice expressing μ Dys.

Anterior hindlimb muscles of healthy wildtype (WT), mdx (a mouse model of DMD), and transgenic mice expressing a clinically relevant μ Dys from birth were exposed to five bouts of 50 *in vivo* ECCs, separated by 1 hour, with recovery of strength assessed at 1, 7, and 28 days.

I found that muscle expressing μ Dys exhibited 49% total strength loss, greater than WT muscle (40%) but less than mdx muscle (68%; $p < 0.0001$). Yet, in all genotypes, 84–90% of total strength loss occurred in bout 1. No differences in the rate of strength recovery were observed across recovery days, with all genotypes returning to baseline strength by day 7.

My findings suggest that overall strength loss following repeated ECCs reveals an intermediate phenotype in muscle endogenously expressing μ Dys. However, skeletal muscle retains the capacity to produce and recover strength following repeated ECCs, independent of dystrophin expression.

Daniya Shahid

PhD - BSA, Herbold

Sex-specific miRNA and mRNA regulation in *Pinus radiata* cones

The molecular mechanism controlling reproductive phase transition in gymnosperms remains poorly understood. While the microRNA (miRNA)-transcription factor (TF) pathways governing the floral transition are well characterised in angiosperms, the equivalent regulatory systems in the economically vital conifer, *Pinus radiata*, remain unknown. To address this, we constructed tissue-resolved gene regulatory networks (GRNs) for the first time by integrating miRNA, mRNA, and TF expression data across the tree's entire reproductive landscape.

Our GRN analysis identified a miR156/miR529-SQUAMOSA promoter binding protein-like (SPL-like) module in female cones. This is consistent with the module controlling the angiosperm juvenile-to-adult transition, suggesting an evolutionarily conserved fundamental role in conifer cone initiation.

We also report the first evidence of an AP2(APETALA2)-miR319-TCP (TEOSINTE BRANCHED1/CYCLOIDEA/PCF) regulatory module specific to male cones in a gymnosperm. This network mirrors the SEP3(SEPATA3)-miR319-TCP4 feed-forward loop controlling *Arabidopsis* floral organ development, revealing that an analogous regulatory architecture operates in gymnosperms. Finally, we also identified a novel *P. radiata* male-cone-specific miRNA that operates independently of miR156/miR529 and targets SPL genes, which are well-known drivers of floral meristem identity in angiosperms. This discovery demonstrates that, alongside conserved pathways, unique conifer-specific pathways also regulate core reproductive genes, thereby reshaping our understanding of the evolution of plant reproductive control in gymnosperms.

Our findings will provide critical insights into the molecular framework of conifer cone initiation and identity, with implications for optimising reproductive development in plantation forestry.

Jessie Sims-Johns

MSc – SDC, Kross

Testing a novel sausage bait in alpine areas in Aotearoa

The introduction of more than 30 mammal species to New Zealand has contributed to widespread declines and extinctions among native fauna. Carnivorous pests such as weasels, feral cats, ferrets and stoats have an enormous effect on many native birds. Current methods do not directly target carnivorous pests, introducing a gap in conservation management. The Department of Conservation (DOC) have developed a novel rabbit-based sausage bait to target carnivores, designed for aerial deployment in Aotearoa. My project utilises camera traps and sausage-bait stations to evaluate the effectiveness of a non-toxic version of the rabbit-based sausage bait for predator control in alpine environments. I aim to determine which target and non-target species interact with the new bait, with a particular focus on non-target alpine specialists such as kea (*Nestor notabilis*). Kea are highly curious and readily investigate novel food sources, which puts them at risk to unintended exposure during poison operations targeting introduced pest species in New Zealand. In addition, I will examine species' behavioural interactions with the bait and assess how these interactions vary seasonally. Preliminary results indicate that over half of the baits were taken by target species, while native non-target species generally showed low interest. This research aims to provide valuable insights into the efficacy and risks of this novel bait in alpine ecosystems, informing evidence-based invasive species management and helping safeguard unique species and biodiversity in Aotearoa.

Brooke Smith

MSc - BEL, Chapman

Assessing polyploid performance when grown in competition with diploid counterparts under nutrient limitation in young yellow monkeyflower (*Erythranthe guttata*) seedlings

Invasive plants transform landscapes by impacting both biotic communities and abiotic factors, causing major ecological damage and economic costs. One property linked to the success of invasive plants is polyploidy, the presence of more than two full sets of chromosomes. These additional chromosomes result in a range of effects, some species-specific and others more broadly observed. Common traits include reproductive isolation and increased cell size. Cell enlargement is associated with larger leaves, larger flowers, greater biomass, reduced growth rate, and increased nutrient requirements. New polyploid individuals often germinate surrounded by and competing with diploids.

My research asked how do the traits of young yellow monkeyflower (*Erythranthe guttata*) polyploids compare to their diploid counterparts, and how does soil nutrient content influence their performance when grown in competition with diploids?

To answer this question, I conducted a 10-week glasshouse experiment where I planted 192 pots containing one central seedling (either polyploid or diploid) surrounded by three diploids. This arrangement mimics natural emergence under field conditions. To test the effect of nutrient availability, the pots contained either nutrient-poor or nutrient-rich potting mix. I recorded a suite of both vegetative and sexually competitive traits, including leaf area, growth rate, biomass, branch number, floral timing and floral abundance. Together these results will clarify whether polyploidy confers a competitive advantage early in their establishment and under resource scarcity.

S. Philip Stewart

MSc - BSA, Yewdall

An extreme enzyme from an extremophile: Characterising SybCA, a novel β -carbonic anhydrase from *Sulfurihydrogenibium* *yellowstonense*.

Carbonic anhydrases (CAs) are metalloenzymes that catalyse the hydration of carbon dioxide (CO_2) to bicarbonate (HCO_3^-) with potential applications in enzymatic removal of CO_2 . β -CAs are found in bacteria, yeast, plants, and archaea, but are not as well characterized as mammalian α -CAs. β -CAs are unique in that some are affected by pH, switching between active (pH >8) and inactive (pH <8) states, and some are allosterically regulated by HCO_3^- . No other class of CA described so far carries these characteristics.

Sulfurihydrogenibium yellowstonense is a thermophilic bacterium that expresses SspCA, the most thermostable α -CA described in the literature, as well as a previously uncharacterized β -CA, SybCA.

My thesis aims to characterize this enzyme, including testing for stability in extreme physical and chemical environments. I have found that SybCA is primarily a dimer in solution, remains stable at temperatures of up to 95 °C, and is incredibly resistant to salt (NaCl, >1.5M) and chemical denaturation (urea, 4M). My recent screens have yielded promising protein crystals.

The remainder of my thesis will investigate SybCA protein structure using crystallography and adapting a colorimetric assay to study SybCA's CO_2 hydration activity. If time allows, I will test how SybCA structure and function is affected between pH 4-10, and whether HCO_3^- has an allosteric effect.

These findings outline SybCA as an extreme enzyme with the capacity to do work in harsh physical and chemical contexts. Understanding the basis of structural stability in SybCA could inform development and design of more robust proteins for biotechnologies like carbon sequestration.

William Taylor

PhD - BSA, Herbold

Applied metagenomics for drinking water quality

Microbes in New Zealand drinking water are assessed primarily by culturing methods to detect coliforms and *Escherichia coli*. Across the country there were 220 reported *E. coli* detections in 2024 alone, impacting more than 1.8 million people. Drinking water contamination is often due to infrastructure degradation or faecal contamination of source waters. My research uses amplicon and metagenomic sequencing to investigate microbial contamination of drinking water and the threats posed to human health.

Working with councils and local iwi, I sampled drinking water from across the country. So far, I have collected and analysed more than 600 samples. These include source waters such as rivers, streams, groundwater, and rainwater catchment systems, as well as from households and testing kits during contamination events. The systems range from small supplies of less than 20 people to municipal supplies that provide water for whole cities.

I found that drinking water systems differ from one another, containing both unique and dynamic bacterial communities that can change even hour to hour. Using enrichments, isolates, and metagenomics, I have been able to identify novel species and show that contamination detections from geographically close sites were unrelated and identify real risks to human health.

My research demonstrates the real beneficial health outcomes using applied molecular methods and from working in conjunction with water suppliers including iwi, rūnanga, and councils. Moving forward, my project will expand this approach to other sites to assist in source water evaluations and inform policy changes for safer drinking water.

Mary Buford Turnage

PhD - SDC, Kross

Shared ground: Winter field selection by birds on Canterbury farmland and implications for conservation and disease risk

There is little known on the value of farm fields for wild birds in Aotearoa New Zealand, nor of the contexts contributing to bird use of individual fields. The central Canterbury region is one of the most intensively farmed livestock landscapes in the country. Understanding the conditions under which birds use particular fields and their spatial relationship to livestock in those fields could aid conservation and zoonotic disease spillover prevention strategies. I assessed wild bird proximity to livestock and the role of field and landscape composition in that spatial overlap. I observed 10,754 birds from 32 species including 10 water-associated species, 15 species native to Aotearoa, and several of conservation concern. Fields without bird observations were uncommon; 71% contained three or more species and 60% contained 10 or more individuals. Wild bird field use in winter appears to be influenced more by field management decisions than by landscape composition and follows species-specific ecological traits. Species richness and the abundances of many birds increased in pastures with bare ground coverage. We have identified possible transmission pathways for zoonotic disease between the coast, farms, and forests in Canterbury. Seven birds were regularly observed within 2m of cattle, all insectivorous and likely attracted to enhanced food opportunity in mud around cows. We recommend further research on pathogen transmissibility in these environments and developing strategies with farmers to minimize the creation of extreme muddy conditions in the event of an outbreak (i.e., alternate grazing patterns or utilizing bird deterrents).

Claire Wang

MSc - BSA, Thomsen

The legacies of shell-formers drive overlooked estuarine biodiversity.

Biodiversity underpins ecosystem functioning but is threatened by anthropogenic activities like climate change. Estuarine biodiversity is typically measured around bare sediments or seagrass meadows. However, buried bivalves build long-lasting shells, that, after death, can accumulate on sediment surfaces. It is largely unknown how dead shells affect biodiversity. This research gap was addressed by comparing epifauna associated with intertidal surface shells to mudflats and seagrass beds in the Avon-Heathcote estuary (Ihutai, New Zealand). First, epifauna was surveyed in 429 quadrats (25x25 cm), representing different habitats, sites, shore distances, and seasons. Second, cleaned dead shells were added to 25x25 cm plots in a 4-factorial experiment in eastern Ihutai, testing how dead shells (vs. control plots without shells) affect epifauna across 2 seasons (summer vs. winter), 2 shore distances (inshore vs. offshore), and 2 habitats (mud vs. seagrass) with 3 replicates (= 96 plots). This recolonization experiment was maintained for a month whereafter epifauna was measured as in the survey. Preliminary analysis suggest that shells increased epifaunal diversity by facilitating both sessile (e.g., barnacles) and mobile (e.g., limpets, snails) taxa that use shells for attachment, shelter, and foraging. Results were consistent across methodologies, seasons, sites, distances, and habitats, but with stronger effects on mudflats than in seagrass beds, because the latter already provide habitat for epifauna. My research suggests that epifaunal diversity may have been overlooked in past estuary studies and that future changes to accumulations of dead shells, could reshape biodiversity and ecosystem functioning.

Ethan Williams

BSc(Hons), Dobson

Characterising the structure and function of PAX2, a novel Gram-negative endolysin

The discovery of novel antimicrobial therapeutics is of key importance. Typically, bacterial infections are treated with antimicrobial drugs, also known as antibiotics. However, their use exposes bacteria to an immense selection pressure to evolve resistance mechanisms, allowing them to evade the drugs' effects and render such treatments ineffective – this is a phenomenon known as antimicrobial resistance (AMR).

A particular class of viruses known as bacteriophage show promise in this regard. These viruses exclusively target bacteria, and in the late stage of their infection cycle they produce proteins called endolysins. These cleave bonds in peptidoglycan, a vital component of cell walls in bacteria – to this end, endolysins disrupt the structural integrity of the target cell, causing lysis. My research focuses on a yet uncharacterised endolysin called PAX2, originating from a *Pseudomonas aeruginosa* bacteriophage.

In my work, I have made efforts to characterise the structure and the function of this enzyme. Computational analysis including bioinformatic investigation and molecular dynamics simulations were used to identify homologous enzymes, conserved residues, and biomolecular interactions. Functional experiments were conducted to quantify the breadth of PAX2's antibacterial spectrum and its rate of catalysis. Structural techniques such as small angle X-ray scattering (SAXS) and macromolecular crystallography have also been carried out.

Through this research, I have shown that PAX2 is catalytically active against its substrate, and that it can natively kill target bacteria without the need for outer membrane permeabilisation. A close structural homolog of PAX2 was also identified, and residues involved with catalysis and substrate binding were predicted. Finally, SAXS and *in-silico* work demonstrated PAX2's dual-domain architecture, a rare trait among endolysins that target Gram-negative bacteria.

Katelyn (Lyn) Young

BSc(Hons), Meisrimler

What sequence alone misses: Structural diversity of *Phytophthora cinnamomi* crinkler effectors

The genus *Phytophthora* comprises a destructive group of oomycetes that infect a broad range of hosts across diverse environments, including numerous endemic species within Aotearoa New Zealand. *Phytophthora* species secrete effector proteins to suppress defence responses and manipulate host processes to facilitate infection. Crinklers (CRNs) are a diverse group of cytoplasmic effectors reported in all *Phytophthora* genomes sequenced to date, yet their functions and organisation remain poorly understood.

Previous studies have shown that CRNs are a group of structurally diverse effectors, yet their current identification relies largely on conserved sequence motifs. However, the extent to which they reflect true structural organisation remains unclear. This project investigated the structural organisation of CRNs, and the relationship between conserved sequence motifs and predicted structural features. Of 49 CRNs reported in the *Phytophthora cinnamomi* GKB4 genome from South Africa, 17 were selected based on predicted effector status and presence of conserved sequence motifs. These proteins were analysed through sequence alignment, structural prediction, and structural comparison to investigate patterns of conservation and divergence.

The 17 CRNs exhibited substantial structural diversity, with sequence-based motif patterns not always corresponding to distinct structural organisation. Structural similarities were found to extend beyond conserved sequence motifs, suggesting that structural features may provide additional information for understanding CRN organisation and evolution.

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