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UNIVERSITY OF  
**ABERDEEN**



School of Biological Sciences

**POSTGRADUATE  
RESEARCH  
CONFERENCE**

Symposium  
Abstracts

*Tuesday  
16th April  
2024*

*Nature on our doorstep*

# *Welcome...*

The annual Postgraduate Research Conference is one of the highlights of the School of Biological Sciences. The impressive programme reflects the breadth, depth and quality of research ongoing within the School by the next generation of scientists. Please join in to engage with your colleagues and support their presentations. The opportunity to present your research and to discuss research with others is an important component of the training of our PhD students.

**Professor Paul Hallett**

School Postgraduate Research Co-ordinator  
Chair in Soil Physics

## *Asma Abushweka*

### NUTRITION AND IMMUNE FUNCTION IN FARMED FISH REGULATION OF INFLAMMATORY AND ANTI-INFLAMMATORY RESPONSES

Supervisors: Prof. Sam Martin, Dr Jason Holland, Dr Marlene Lorgen-Ritchie



#### ABSTRACT

Infectious diseases cause economic losses in the aquaculture sector. Nutritional intervention has the potential to control inflammation and improve resistance to pathogens. Farmed salmon were traditionally fed a diet with high levels of fish oil and fish meal but supply of these nutritional components is unable to meet the global demand. Alternatives to fish oils are vegetable oils which are increasingly used in salmon feeds, but the impact of these diets on inflammation is not fully understood. Vegetable oils do not contain omega-3 LC-PUFA but are rich in omega-6 PUFA, hence fish fed vegetable oils have limited DHA and EPA, which are precursors for many immune regulatory molecules.

The project will enhance our understanding of the effects of dietary omega-3 on inflammation in farmed Atlantic salmon (*Salmo salar*), with a focus on the mRNAs encoding enzymes involved in pro- and anti-inflammatory eicosanoid lipid mediators. Our initial steps have been to characterise several of the key genes involved in these pathways and examine the expression of different paralogues following immune response. For this RNA was extracted from head kidney tissue of Atlantic salmon stimulated with either heat killed *Vibrio* or poly I:C to induce an antibacterial or antiviral response respectively. Eicosanoid pathway involvement in inflammatory responses was indicated by elevated COX2a2 transcription stimulated by vibrio alongside a decline in ALOX5a1 transcription.

Future work in this project will analyse the transcriptomic effects of alternative dietary oils in vivo and in cell cultures using paralogue specific primers.

***Fatimah Alhawiti***

**GENETIC MAPPING OF COLD TOLERANCE  
AT GERMINATION AND SEEDLING STAGES  
IN RICE (*ORYZA SATIVA* L.)**

**Supervisors: Dr Gareth Norton, Prof. Adam Price**



**ABSTRACT**

Rice (*Oryza sativa* L.) is considered a staple food for over 50% of the global population, however, cold stress is a major limiting factor in rice development and productivity. The influence of cold on rice growth is well known, however, there are limited studies on the genetic basis of cold tolerance in rice, especially rice from the aus subgroup.

This work aimed to identify quantitative trait loci (QTLs) and, subsequently, candidate genes involved in cold tolerance at the germination stage. A total of 194 rice cultivars from the Bengal and Assam Aus Panel (BAAP) were screened under cold treatment (13°C) and control (30°C) conditions with three replicates for each treatment. The number of germinated seeds was recorded every day from the fourth day to the seventh day for the control and the fourteenth day for the cold treatment. Germination rates (GR) were calculated, also, a logistic analysis for the GRs was performed. The cold treatment significantly impacted the GRs, with significant differences in GRs between genotypes ( $P < 0.05$ ) at all days (4-14). Similarly, the values of the logistic curve parameters (asymptote,  $x_{mid}$ , and scale) were significantly different between genotypes.

Genome wide association (GWA) mapping was conducted on cold indices traits with 2 million SNPs using an efficient mixed model (EMMA), and a significance threshold of  $p < 0.0001$  was used to identify SNPs associated with the traits. It was concluded that the GR on days 6-9, and  $x_{mid}$  were potentially the best parameters to analyse QTL where they showed a wider range of genotypic variation between genotypes. A total of 42 QTLs associated with traits were identified. The Rice Genome Annotation Project database was used to obtain the annotation of all genes in the regions. Some examples of potential candidate genes for cold tolerance include OsWRKY74, BMY10, and OsPHD37.

Cold tolerance rice cultivars and QTLs/genes identified here will provide useful information for future studies on genetics and breeding cold tolerance rice.

## *Vivek Kumar Awon*

### HOW DO PLANTS, MYCORRHIZAL FUNGI AND SOIL MICROBES INTERACT TO PROMOTE CARBON AND NUTRIENT CYCLING?

Supervisors: Dr Ashish Malik, Dr Gareth Norton, Dr Peter Orrell, Prof. Katie Field



#### ABSTRACT

Phosphorus is vital for plant growth and Arbuscular Mycorrhizal Fungi (AMF) offers an alternative pathway for phosphate uptake. The hyphosphere, a unique realm influenced by AMF hyphal exudates function as a hotspot for organic phosphate mobilization. It is essential to understand the ecological functions of the hyphosphere microbiome to unravel how these interactions ultimately influence plant nutrition and performance.

To measure the carbon-phosphorous exchange between plants, AMF and hyphosphere microbiome we used an autotrophic in vitro culture system with bi-compartmental Petri plates. Host plants were positioned to allow roots to grow in one compartment and extraradical hyphae of AMF in the second compartment. This setup was utilized to investigate the effect of variable inorganic phosphate (Pi) concentrations on hyphal exudates and hyphosphere microbiome assembly. Further in vivo characterizations of the hyphosphere microbiome will be performed with isotope labeled experiments in greenhouse using compartmentalized microcosms.

We will present first results from the in vitro and in vivo experiments on how specific microbial species in hyphosphere microbiome respond to changes in carbon and phosphate availability. This study aims to elucidate the vital role of the hyphosphere microbiome in phosphate mobilization, shedding new light on its influence on plant nutrition and performance.

*Sara Bataw*

**GENOME-WIDE ASSOCIATION AND VALIDATION OF CANDIDATE GENES ASSOCIATED WITH PHOSPHATE ACCUMULATION IN RICE UNDER TWO IRRIGATION MANAGEMENT SYSTEMS**

Supervisors: Dr Gareth Norton, Prof. Adam Price



**ABSTRACT**

On a global scale, rice (*Oryza sativa* L.) is one of the most important cereal crops. Phosphorous (P) is considered a major limiting factor for rice growth and development. Phosphate (Pi) uptake is limited due to its uneven distribution and relative immobility in soils. It is predicted that global P availability is likely to decrease in the future. Therefore, finding alternatives to the continuous and costly application of P is essential. One potential is to breed rice with enhanced Pi uptake.

In this study, a genome-wide association mapping approach was used to identify QTLs and candidate genes associated with Pi concentration in rice shoots and grains of the Bengal and Assam Aus Panel (BAAP) population under two irrigation systems, alternative wetting and drying (AWD) and continuous flooded (CF) irrigation. Overall, CF conditions increased shoots Pi by 4.9% and grains Pi by 2.62% - 5.7%. Genome-wide association mapping revealed 54 QTLs associated with Pi concentration in rice.

Among the candidate genes located within the QTLs was the uncharacterised LOC\_Os\_01g02000, annotated as a phosphate transporter. To understand the function of this gene, it was knocked out using CRISPR-Cas9 in the cultivar Nipponbare. Evaluation of the CRISPR knockout was done (using wild type Nipponbare as a control). Plants were exposed to high and low P conditions. The Pi concentration in shoots was examined, there was significant genotype, treatment effects, and genotype by treatment interaction for grain yield (no. of grains and grain biomass traits) with a reduction rate of 60.5% - 42.6% in number of grains and 68% - 44.5% in grain biomass for the CRISPR plants compared to Nipponbare plants under high and low P treatments respectively. This indicates that the knockout of LOC\_Os\_01g02000 had a strong negative effect on the grain yield.

## *Dylan Bodington*

### NICHE SPECIALISATION AND PHYLOSymbIOSIS IN THE SPONGE MICROBIOME

Supervisors: Prof. Cécile Gubry-Rangin,  
Prof. Lesley Lancaster



#### ABSTRACT

The comparative diversity and biogeography of free-living marine and sponge-associated microorganisms has been studied, but the mechanisms of niche specialisation of sponge endosymbionts is still unclear. Phylosymbiosis, the relationship between microbial community similarity and host phylogeny, has been demonstrated in some marine organisms, including sponges, but the ecological and evolutionary drivers of this relationship in sponges are not well known. Among crucial sponge-associated microbes, ammonia-oxidising archaea (AOA) likely play a key role in nitrogen metabolism in the host.

Here, we analysed the diversity, host-specificity and phylosymbiosis of AOA in light of the total microbial diversity using a dataset of globally distributed sponge species, covering most orders of the class Demospongiae. The diversity of AOA did not reflect the diversity of the whole microbiome, suggesting their host-specialisation.

Using comparative phylogenetic analysis of both host phylogeny and microbiome diversity, we defined specialist and generalist AOA on the basis of their host niche distribution. A strong host-specificity was observed in the microbiome of some host species, as well as in some higher taxonomic clades. These specialist AOA are restricted to a few phylogenetic clusters, suggesting a strong metabolic specialisation and selection, and some specialists show patterns of co-phylogeny, suggesting both diversification and selection processes.

The phylosymbiotic signal varied across the sponge phylogeny, and further comparison of host clades with variation in microbial niche specialization, microbiome stability and microbial transmission could help to identify the ecological and host drivers of sponge microbiome diversity.

## *Jessica Brook*

### **BROAD SCALE MULTIPLE YEAR TEMPORAL CHANGES IN THE PHYSICAL STRUCTURE OF AGRICULTURAL SOILS ACROSS THREE CATCHMENTS IN SCOTLAND**

Supervisors: Dr Josie Geris, Dr Paul Gaffney, Peter Gilbert, Prof. Paul Hallett



#### **ABSTRACT**

Healthy soil structure is vital for successful agricultural productivity and for maintenance of ecosystem services, with structural deterioration leading to susceptibility to compaction, erosion and nutrient loss. As a result, soil structure degradation is a serious threat to agriculture and the environment in Scotland.

Through a resampling strategy using the Visual Evaluation of Soil Structure (V ESS), together with collection of quantitative soil physical data, temporal changes in soil physical structure were investigated. This research builds on a 2015/16 study of 120 fields across four river catchments in Scotland which found widespread soil physical degradation over winter, with severe degradation in 18% of topsoils and 9% of subsoils. While this previous study demonstrates short-term negative impacts caused by weather, longer-term impacts are unknown.

Resampling was conducted on a subset of 42 fields from three river catchments: the Rivers Ugie, South Esk, and East Pow, in winter 2022/23. The previous sampling strategy was repeated, sampling in-field locations, heavy traffic areas with visible soil surface damage, and field margins. In addition to V ESS, penetration resistance was measured and undisturbed soil cores collected from 2-7cm depth to examine soil physical properties.

Preliminary analysis found most soils to have V ESS scores 2 and 3 at in-field locations, and an average of 4 in degraded areas, indicating changes in land management may be required to improve overall soil physical health. Research such as this is important for providing understanding of active environmental management of soils to farmers and landowners and informing governmental policies on land management.



## *Antonio Castellano Albors*

### NEGATIVE EMISSIONS: DEVELOPING THE POTENTIAL OF PERENNIAL CROPS FOR THE BIOECONOMY

Supervisors: Prof. Astley Hastings, Dr Anita Shepherd



#### ABSTRACT

The UK Biomass Strategy 2023 states the potential benefits and contribution of negative emissions from bioenergy with carbon capture and storage (BECCS) towards achieving net-zero by 2050. According to the Climate Change Committee, up to 23,000 ha of bioenergy crops would have to be grown annually in the UK until this date for the mitigation of 2 Mt CO<sub>2</sub>e (11 Mt with CCS).

My research project lies under the interdisciplinarity Demonstrator '*Perennial Bioenergy Crops for Greenhouse Gas Removal*' (PBC4GGR) and aims to bring scientific support and best knowledge to inform and help the UK Government in the delivery of a mass-scale deployment of bioenergy crops in a sustainable and economically viable way. We will use the life cycle assessment (LCA) as a tool to study the total GHG emissions derived from the production and supply chain of commercial short rotation coppice willow from the nursery to the combustion stage, with and without CCS, along different scenarios.

A unique and comprehensive dataset from literature review and personal communications with key players in the industry and research has been created, where further analysis will help to gain knowledge about the interactions between genotype and the environment. The well-established crop growth model MiscanFor will be adapted to the phenology and physiology of *Salix spp.* The results provided by the model will serve as input to a soil carbon model to be included in the LCA. Measurements of willow growth at commercial plantations will help to fill the existing gap between research and industry.

## *Max Charles Vallarino*<sup>1</sup>

### FUNCTIONALITY OF DUPLICATED CD9 PARALOGOUS GENES IN SALMONIDS

Supervisors: Clark T.C<sup>1</sup>, Sleight V.A<sup>1</sup>, Collet B<sup>2</sup>, Boudinot P<sup>2</sup>, Martin S.A.M<sup>1</sup>



#### ABSTRACT

The sustainable expansion of aquaculture is constrained by pathogens, especially viruses. Our work focuses on the interferon-stimulated gene *cd9*, which is dramatically upregulated following viral infection in salmonids. Human CD9 codes for a cell-surface tetraspanin protein with putative roles in viral entry and inflammatory response. While CD9 presents only a single human gene copy, we find six paralogues in salmonids, resulting from whole genome and local duplications. However, only two of these paralogues (*cd9c1* and *cd9c2*), which were derived from the recent salmonid genome duplication, are highly stimulated by type I interferon (IFN).

We aim to elucidate the antiviral functionality in fish of the interferon-stimulated *cd9c1* and *cd9c2* paralogues through cell culture experiments.

We generated plasmids to overexpress two interferon-responsive *cd9c* paralogues, as well as a control non-IFN responding paralogue (*cd9b1*), by inserting the full open reading frame behind a strong promoter in an expression vector. Co-transfections of *cd9* overexpression plasmids and a GFP expression vector were performed using the CHSE (Chinook salmon embryo) cell line, and expression levels of the transfected genes were measured by qPCR. Transfected cells were assessed for visual appearance and passage time.

Viral infections will be carried out next, following which whole-transcriptome sequencing by RNA-Seq will be performed to help understand the role of *cd9* genes in antiviral activity. We expect findings to be directly relevant for fish viral diagnostic research and better viral production for vaccines.

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## *Rachael Kelday Clark*

### ENVIRONMENTALLY TRANSMITTED PATHOGENS IN WILD RED (*CERVUS ELAPHUS*) AND ROE DEER (*CAPREOLUS CAPREOLUS*): THE ROLE OF LAND USE AND BIOCLIMATE

Supervisors: Dr Mark Moseley, Dr Kath Allan, Prof. Eric Morgan, Dr Sandra Telfer



#### ABSTRACT

Wildlife can play an important role in the epidemiology of important pathogens of livestock and humans by acting as reservoirs or vectors for infection. Nontuberculous Mycobacteria (NTM) are environmentally transmitted opportunistic pathogens that can cause disease in both humans and animals. The presence of wildlife can complicate disease management as control measures, such as vaccination, are challenging in wildlife species.

Using wild deer as sentinels, we aim to use serological and molecular approaches to explore the environmental variables that facilitate survival and transmission of environmentally transmitted pathogens. Serum samples were sent for serological testing to explore if deer have been exposed to livestock pathogens. DNA was extracted from faecal samples and PCRs were used to detect the presence of mycobacterial species using several biomarkers for non-tuberculosis mycobacteria.

Preliminary phylogenetic results have revealed a diversity of novel mycobacteria in wild deer, with some species closely related to important known pathogenic strains that can cause disease in both animals and immunocompromised humans and can interfere with TB testing in livestock resulting in false positives.

Future work will include expanding sampling across different habitats including areas of higher elevation and sampling additional tissues to widen pathogen screening. We will also use next generation sequencing to compare the mycobacterial diversity found in deer with livestock samples from the same area to explore the 'mycobacteriome' and understand if transmission or a common source of exposure exists between livestock and deer.

## *Jane Devlin*

### **TO DROP OR NOT TO DROP: INVESTIGATING THE LINK BETWEEN INSECT-POLLINATOR ACTIVITY AND JUNE DROP IN SWEET CHERRY (*PRUNUS AVIUM*)**

**Supervisors: Dr Dominic Williams, Dr Alison Karley, Dr Fabio Manfredini**



#### **ABSTRACT**

Sweet cherry in the UK undergoes a natural process generally referred to as ‘Cherry run-off’ or ‘June drop’, during which immature fruit are abscised from the plant. The quantity of fruit lost annually to June drop is highly variable. These fluctuations in yields makes cherry an unpredictable crop for farmers, driving the need to further investigate the causes of June drop to understand how this process can be mitigated.

This study aimed to use high-definition time-lapse cameras to investigate plant-pollinator interactions on cherry trees and reveal what role pollinators have on fruit retention during June drop. Twelve cameras were used to record pollinator activity on flowering cherry trees for 17 days between 11am and 5pm, when pollinator activity is at its peak. The cameras were deployed within two distinct pollinator density treatments, high and low. The different densities were accomplished using commercial bumblebee colonies in netted areas to simulate possible scenarios that can be found in cherry orchards. The recordings were compared to in-person observations to validate time-lapse cameras for pollinator studies.

Preliminary analysis reveals that cameras in high-density areas captured more floral visits than those in low density areas, which is consistent with in-person observations. Preliminary results also indicate that trees in high density areas retained a higher proportion of fruit during the June drop than those in low density areas. This study will greatly contribute to the understanding of how remote monitoring can help identify fluctuations in pollinator activity levels and their subsequent role in fruit loss.

## *Jonathan Ellis*

### INVESTIGATING COD STOCK STRUCTURE IN THE IRISH AND CELTIC SEA USING OTOLITH MICROCHEMISTRY

Supervisors: Dr C. Tara Marshall, Dr Pia Schuchert,  
Dr D. Michael Scantlebury, Prof. Paul G. Fernandes



#### ABSTRACT

Cod in the Irish Sea and Celtic Sea are managed as separate stocks, but recent movement of Irish Sea cod into the Celtic Sea suggests that their stock structure has changed. Updating understanding of stock structure will help improve the accuracy of stock assessments to better manage and protect the stocks.

Here we investigated stock structure of cod in the Irish Sea and Celtic Sea using otolith microchemistry. Otoliths from the Irish Sea (113) and Celtic Sea (37) were analysed using LA-ICPMS with trace elements measured on core-edge transects across cross-sections. Edge chemistry was tested for differences between capture locations, and classification was performed using a random forest model. Stock origin was predicted from outer core chemistry using the model and K-means clustering was performed on inner and outer core chemistry.

Ba and Mn concentrations in edge sections differed significantly between the seas. Classification success was higher for Irish Sea otoliths ( $F1 = 0.82$ ) than Celtic Sea otoliths ( $F1 = 0.54$ ), and most fish were predicted to have a Celtic Sea origin. Core chemistry did not cluster according to capture location or predicted stock origin. Similarities in edge chemistry are likely due to tidal mixing between the seas, with Mn and Ba differences due to coastal influences. Stock origins in the Celtic Sea suggests stock mixing, but this may reflect overlap in environmental conditions.

These findings present no strong evidence to separate Irish Sea and Celtic Sea cod using otolith microchemistry. Stock management may improve from their merging which is supported by previous tagging and genetic evidence.

## *Faraj Elsakloul*

### **SALINE-SODICITY AND SOIL PHYSICAL IMPACTS ON ROOT GROWTH AND NUTRIENT CAPTURE**

Supervisors: Dr Maria Marin, Dr Gareth Norton,  
Prof. Paul Hallett



#### **ABSTRACT**

Salt affects approximately 840 million hectares globally, comprising roughly 683 million hectares are saline and 157 million hectares are saline-sodic. Saline-sodic soil causes direct impact which is an osmotic stress, and this creates a hydraulic stress on roots that decreases the capacity for root water uptake, morphological changes, and ionic imbalance which interference with nutrient uptake. Additionally, indirect impacts can arise due to the increase in penetration resistance and decrease soil aeration that reduce root growth. However, despite a large body of work on the impact of salinity-sodicity on soil physical behaviour and plant growth, few studies have explored the interactions between these processes.

The present study investigates the combined effects of 0, 0.5 g of sodium chloride, compaction (50, 200 kPa), and water potentials (-5, -20, and -50 kPa) on sandy loam and clay loam soils. The investigation entails the collection and analysis of data pertaining to compression characteristics, bulk density, water content, air-filled porosity, and penetration resistance. Additionally, the lengths of barley and wheat seedling roots were measured 48 hours after sowing.

We observed that the combined influence of increased salinity, compaction, and reduced water potential increased penetration resistance to 2.38MPa reduced aeration <10% in clay loam soil. This reduced barley root to 32.12% while wheat had a greater reduction 20% due to physical and chemical impacts. However, in sandy loam soil, barley exhibited greater root growth (54.2%) compared to control (100%), attributable to the presence of macropores facilitating downward root growth into the soil whereas wheat had more reduction 28.4%.

Macropores in sodicity-salinity soil could also be explored further by quantifying soil structure changes and the location of roots using non-invasive imaging. This study was limited to a rapid seedling assay. Whether the impacts observed continue through to a mature plant needs exploration with larger controlled soil samples containing plants grown for a longer period.

## *Farzana Mustafa Era*

### GENOME WIDE ASSOCIATION GENETICS OF RICE FOR SALINITY TOLERANCE AT MATURITY STAGE UNDER FIELD CONDITION

Supervisors: Dr Gareth Norton, Prof. Adam H. Price,  
Dr Akm Aminul Islam



#### ABSTRACT

Rice (*Oryza sativa* L.) is one of the ancient, cultivated crops which is consumed by over half of the world's population. Globally the percentage of soil affected by salinity is increasing, with irrigated areas of particular concern. Rice is highly salt sensitive crop that may lose 50% of its yield at a soil electrical conductivity (EC) value of only ~6 dsm<sup>-1</sup>.

About 150 genotypes from Bengal and Assam Aus Population (BAAP) was used for this experiment having four replications with three different salt treatments i.e. control (0 dsm<sup>-1</sup>), 2 dsm<sup>-1</sup> and 4 dsm<sup>-1</sup>. The seeds were sown in a long tube were placed in a box. Sea water collected from Cox's Bazar was diluted up to the desired level by adding ground water.

All the traits showed significant treatments effect. Salt injury score (SIS), stomatal conductivity, grain biomass had significant genotype and treatment effects whereas SIS had highly significant ( $p < 0.001$ ) negative correlation with grain biomass (-0.55). Plant height, shoot biomass, stomatal conductivity and SIS showed normal frequency distribution in three of the treatments. Salt tolerant accessions have been identified.

Genome Wide Association Genetics will be studied to identify QTLs and candidate genes responsible for salt tolerance from those genotypes of BAAP.

## *Tegan Gaetano*

### IMPORTANCE AND SUSTAINABILITY OF ENDANGERED COMMUNITIES OF BEE POLLINATORS IN THE MACHAIR, A CHANGING COASTAL ECOSYSTEM

Supervisors: Prof. Robin Pakeman, Prof. Lesley Lancaster,  
Dr Paul Williams, Dr Fabio Manfredini



#### ABSTRACT

Unique to the north- and west-facing soft coasts of Scotland and Ireland, machair is a **biodiverse ecosystem mosaic** of dune networks protecting wildflower-rich grasslands, rotationally cultivated croftland and inland lochs. Totalling only 25-30,000 ha, machair is home to **over 70 species of insect pollinators** including nationally endangered species such as the **Great Yellow Bumblebee** (*Bombus distinguendus*). Since 1970, over 80% of this species' range has diminished and it is now confined to island patches of machair.

Previous investigations into what makes machair habitats suitable for pollinating insects have emphasized food plant abundance and diversity. However, few have explored the underlying **nutritional landscape** of machair flowering plants, including the role of **sodium and other micronutrients**. Given the high environmental availability of sodium and other marine nutrients in coastal habitats, machair plants dependent on insects for pollination may selectively incorporate these elements into their rewards.

**Land use intensification and climate change** pose significant threats to coastal ecosystems such as machair. Historically and in the future, these forces are expected to influence the **distribution of machair wildflowers and their nutrients**, further endangering rare bee pollinators.



## *Devonne Gardiner*

### TEMPORAL TRENDS AND ENVIRONMENTAL DRIVERS OF PREGNANCY IN THE GULF OF ST LAWRENCE'S MINKE WHALES (*BALAENOPTERA ACUTOROSTRATA*)

Supervisors: Dr Davina Derous, Dr Joanna Kershaw



#### ABSTRACT

Evaluating the health of baleen whale populations is crucial for understanding effects of environmental change on these top predators but has been difficult historically. Methodological advances, particularly in endocrine profiling, have enabled reproductive rates of populations to be measured as a proxy for population health.

In this study, endocrine profiling, sightings data, and environmental data are combined to investigate reproductive rates of minke whales (*Balaenoptera acutorostrata*) in the Gulf of St Lawrence, Canada from 2006-2015. This is an important summer feeding ground for several baleen whale species in the North Atlantic but has undergone major ecosystem change. Minke whales have been observed to behave differently to other mysticetes in the GSL, for example, sexing analyses revealed a strong female sex bias and very few calves sighted throughout the study period.

The present work examines the health of the GSL minke population and investigates impacts of fluctuations in prey availability on pregnancy rates. Blubber biopsy samples ( $n = 129$ ) were used to assign pregnancy status at the time of sampling through quantification of progesterone. Annual pregnancy rates were significantly higher than other mysticetes in the GSL, with >50% of minke biopsies identified as pregnant each year, and no significant decline in pregnancy rates observed over the study period. Pregnancy rates in female minke whales is partially explained by differences in prey availability in the previous year.

These data support the theory that minke whales in the GSL are predominantly pregnant females using the area as a feeding ground prior to giving birth elsewhere. Being generalist feeders, it is likely minke whales have enough plasticity to cope with fluctuating food availability.

## *Stephen Gillanders*

### INVASIVE EARWIGS IN THE FALKLANDS: HOW BIG IS THE THREAT?

Supervisors: Dr John Baird, Dr Juliano Morimoto,  
Dr Colin McClure, Dr Paul Brickle, Dr Archie Murchie



#### ABSTRACT

First detected in the Falkland Islands (FI) in the 1990s, the European earwig *F. auricularia* can now be found in large numbers in both the urban and wild environment. Earwigs are considered pests causing damage to horticulture and regarded as a public nuisance; however the ecological impacts of this invasion have not been investigated. I am looking at the invasion history of this species and its current population dynamics.

Considering its generalist feeding strategy and ability to occupy multiple ecological niches, which can particularly impact rare or sensitive native species, *F. auricularia* has the potential to significantly impact recipient communities and affect ecosystem functioning. I am trying to understand whether native invertebrate communities are disrupted by the expansion of *F. auricularia*. Understanding the diet composition of earwigs in FI is key to ecological risk assessment. Estimating any predation pressure on earwigs can predict consequences of any future eradication or reduction in earwig populations.

The prevailing ecological theory states that the success of earwigs in Falklands is due to competitive advantages or absence of natural predation pressure. I want to acknowledge and suggest that earwigs can change their environments considerably when they invade a new area, but also take advantage of disturbed environments, poor biosecurity controls and low functional diversity.

Current control measures use extensive applications of chemical pesticides which are both costly and harmful to non-target species and aquatic environment and carry risk of resistance development. I want to form a conclusion whether this problem is more social than ecological.

## *Kleopatra Grammatiki*

### IMPACT OF BRINE DISCHARGE FROM TWO SEAWATER DESALINATION PLANT OUTFALLS ON THE MARINE ENVIRONMENT IN CYPRUS

Supervisors: Prof. Frithjof C. Kuepper,  
Prof. Pieter Van West, Prof. Jeppe L. Nielsen



#### ABSTRACT

Population growth, as well as our growing needs due to increasing living standards, together with events of droughts and climate change have rendered seawater desalination a crucial technology in terms of water security. More than 80% of the desalinated water in the EU is produced in the Mediterranean region, via reverse osmosis. This technology produces a hypersaline brine, which is being discharged into mostly shallow coastal waters, exposing marine communities to high salinity and possibly also various chemicals.

Previous studies have highlighted the negative impacts on ecologically valuable key benthic ecosystems, such as seagrass meadows, as well as invertebrate communities, but this impact has not been studied in significant depth across the entire breadth of eukaryotic diversity, and there is a lack of long-term studies. This work provides a seasonal monitoring survey around the brine outfalls of two large-scale desalination plants located in Larnaca and Dhekelia, Cyprus, in order to assess the impact of brine discharge on marine communities.

We used metabarcoding of benthic and pelagic environmental DNA to assess the diversity of benthic and pelagic invertebrate and microalgal communities at and around the desalination brine discharge points, along the axis of the brine plume. The results suggest that, interestingly, diversity is higher around the outfalls. Furthermore, the impact of water column stratification is being investigated.

## *Amy Guest*

### **SIGNIFICANCE OF PEAT DUST AND TERRESTRIAL EROSION ON MARINE COMMUNITIES AROUND HUMMOCK ISLAND, FALKLAND ISLANDS**

Supervisors: Prof. Stuart Piertney, Prof. Alex Douglas, Dr Paul Brickle



#### **ABSTRACT**

The Falkland Islands are experiencing coastal erosion caused by overgrazing and natural fires. This can lead to an influx of peat particles into inshore coastal waters via both rain runoff and wind, that can blanket rocks, sand and kelp forests. The effects of this peat on marine invertebrate community structure is unknown.

Here we examine how surface erosion and peat influx influences marine communities at Hummock Island, West Falkland. The study employed SCUBA to carry out 20 m belt transect surveys in the shallow (0-20 m) depths across 18 stations. Quadrats of 0.25 m<sup>2</sup> were placed on the seabed every one metre along the transect, on alternating sides, with 10 photographs per transect collected totalling 180 photos. Invertebrates in the photo-quadrats were identified to the lowest possible taxonomic level and counted. Peat dust was found at 11 of the 18 stations and peat levels per quadrat were calculated as percent area cover. Stations with no peat cover were used as the control.

Multivariate data analyses of the transects and quadrat data showed that only highly mobile species are associated with high-percentage peat cover. Less mobile species and sessile filter feeders are generally absent and or at much lower densities. The data are discussed with recourse with implications to Falkland Islands marine coastal management. This study is especially relevant given evidence of increasingly drier and warmer climates in the Falkland Islands which are likely to cause further coastal erosion and increased levels of peat dust transfer to inshore marine environments.

*Jack Henderson*

**CROP PRODUCTION SUSTAINABILITY  
THROUGH THE MICROBIAL LENS**

Supervisors: Prof. Cecile Gubry-Rangin,  
Prof. Marcel Jaspars



**ABSTRACT**

Nitrification is the microbial metabolism of reduced forms of nitrogen (e.g. Ammonium) into Nitrate, which leaches out of soil, leaving it nitrogen poor, and causes eutrophication of water sources. Nitrification also results in production of copious amounts of Nitrous Oxide, a powerful greenhouse gas, and is responsible for excessive nitrogen loss in agricultural systems. Excessive nitrogen loss necessitates high fertilisation, which in turn encourages nitrification.

Biological nitrification inhibition (BNI) is the plant mediated inhibition of nitrification via exudation of bioactive metabolites. BNI enabled agriculture could increase sustainability while helping deliver global food security by decreasing synthetic nitrogen requirements. BNI has been demonstrated in several crops – including wheat, rice and maize – and there is the suggestion for strong BNI potential in barley.

Barley is the most cultivated cereal crop in Scotland and is of great importance to the economy. Demonstration of BNI activity in barley is an important first step in the development of high NUE barley cultivars. In addition, gaining understanding of conditions in which BNI activity is optimal in barley will provide a basis for further studies of the underpinning mechanisms of BNI in barley.

## *Danielle C Jordan*

### DECIPHERING CALCIUM TRANSPORT MECHANISMS IN MOLLUSCAN BIOMINERALIZATION USING GENOME-EDITING

Supervisors: Dr Victoria A Sleight, Prof. Sam Martin, Dr Tim Bean, Dr Iveta Matejusova



#### ABSTRACT

Biom mineralization is the process that forms minerals on the interior of the organism (endoskeleton) or exterior of the organism (exoskeleton). Molluscs owe part of their evolutionary success to their ability to biomineralize, but little is known about the mechanisms for calcium transport to the shell secretion site in the mantle. There are two possible mechanisms for calcium transport that are supported in literature: paracellular (between cells) and transcellular (through cells). Prior research indicates that molluscs likely use a combination of both paracellular and transcellular pathways to transport calcium for shell deposition.

This project seeks to understand the genes regulating calcium transport in molluscs using the slipper limpet, *Crepidula fornicata*, as a model organism. *C. fornicata* was chosen as a model organism for this study due to its long history as a molluscan model for developmental studies.

We have used RNA-sequencing data gathered from all developmental stages of *C. fornicata* to identify preliminary candidate genes, and hybridization chain reaction (HCR) will serve as a spatial analysis to confirm the precise cellular location of these candidates. Once expression of the candidate genes has been confirmed to the shell gland or developing mantle tissue, CRISPR-cas9 will be used to knock-out the candidate genes via microinjection and study the resulting phenotype in relation to calcium transport.

## *Alexander Nti Kani (DSc)*

### CRITICAL METALS, THE GAME CHANGER!

Supervisors: Prof. Graeme I. Paton,  
Dr Lenka Mbadugha



### ABSTRACT

The global transition to a carbon-free energy system is increasing the demand for critical metals (CMs), such as cobalt (Co), manganese (Mn), and nickel (Ni). These metals are crucial for the development of various green technologies, including Li-ion batteries, fuel cells, wind generators, photovoltaic systems and more.

This surge necessitates an urgent identification of sustainable sources.

Unfortunately, the UK lags behind European, American, and Asian counterparts in securing local supplies, threatening its net-zero emission goals. The rising demand for critical metals is further driven by the growing use of electronic gadgets and electric vehicles.

In this work, we explored mine waste as a potential source for CMs. The efficiency and effectiveness of seven (7) different single extraction systems in targeting labile fractions of Co, Mn, and Ni from mine waste was evaluated. In addition, the resupply of water-extractable metal pools was tested, resulting in a complete depletion. The cumulative water-extractable Co, Mn, Ni concentrations were  $2.24 \pm 0.58$ ,  $12.86 \pm 1.20$  and  $5.61 \pm 0.79$  mg/kg. The pseudo-total concentrations were  $58.07 \pm 2.6$ ,  $3398.08 \pm 20.80$  and  $351.57 \pm 15.00$  mg/kg for Co, Mn, and Ni, respectively.

Chemical leaching was shown to be an effective extraction method with a potential to mitigate environmental impacts of CMs leaching from the mine waste. However, to prove the economic viability and to justify the use of mine waste as a potential resource for CMs, resins will be used in the final phase of this work to enhance the recovery.

## *Khadija Majid*

### GENETIC DIVERSITY AND ZONOTIC IMPORTANCE OF UNCULTURED PATHOGENIC LEPTOSPIRA SPECIES IN AFRICA: INSIGHTS FROM TANZANIA AND SOUTH AFRICA

Supervisors: Dr Mark Moseley, Dr Sandra Telfer, Dr Chris Sutherland, Dr Derek Sloan



#### ABSTRACT

This study investigates the distribution, genetic diversity, and zoonotic importance of pathogenic *Leptospira* species in various water systems across Africa, specifically focusing on Tanzania (Kilombero) and South Africa (Cape Town and Johannesburg). Leptospirosis, a neglected environmental zoonotic disease affecting both humans and animals, poses a considerable global health threat. The genus *Leptospira* comprises over sixty species, grouped into four main clades based on pathogenicity: Saprophytic (S1 and S2) and Pathogenic (P1 and P2), each representing distinct lineages with varying levels of virulence. Annually, about 1 million people contract the disease resulting in 300,000 to 500,000 severe cases and 60,000 reported deaths. Higher morbidity rates are predicted in regions with poor disease surveillance like Africa. Despite its prevalence in Sub-Saharan Africa, the distribution and diversity of *Leptospira* spp. are poorly understood due to limited research. The study aims to address this gap by using environmental surveillance and genetic typing to characterise the distribution and diversity of pathogenic *Leptospira* in Tanzania, Cape Town, and Johannesburg, and compare it to other global regions.

Samples from both wet and dry seasons were collected in triplicate from the environment from 25 sites in Johannesburg (n=8) and Cape Town (n=17) river systems, and 7 sites in Kilombero, including 6 water taps (n=6) and a rice puddle (n=1). Soil samples were processed for DNA extraction and screened for *Leptospira* DNA using a semi-nested PCR assay. Positive samples were sequenced to assess the genetic diversity. *Leptospira* DNA was detected at 24/25 sites in South Africa and all 7 sites in Tanzania, but not in every sample within sites. Higher probability of *Leptospira* DNA detection was observed in specific locations such as the middle channel of water taps and outside the ridge at the rice puddle. Preliminary sequencing results demonstrated the presence of pathogenic species associated with human and animal disease and novel, potentially pathogenic *Leptospira* spp., highlighting the wide diversity of potentially pathogenic *Leptospira* spp. in the African environment. This study emphasizes the need for enhanced surveillance and control measures to mitigate public health risks associated with leptospirosis in Africa and beyond.



## *Claire McNamee*

### UNDERSTANDING MICROBIAL PROCESSES IN PEATLANDS TO ASSESS THE SUCCESS OF RESTORATION EFFORTS IN ENHANCING CARBON STORAGE UNDER FUTURE CLIMATE

Supervisors: Dr Ashish Malik, Dr Peter Gilbert



#### ABSTRACT

Peatland ecosystems, found on only 3% of the Earth's surface, are a hotspot for carbon sequestration, holding approximately 400-500 Gt of carbon. It is estimated that the drainage of peatlands within the UK results in significant emissions of greenhouse gas emissions. As a result of this, peatland restoration has become increasingly popular, to mitigate the change from carbon source to carbon sink.

Peatlands are a net carbon sink because the rates of photosynthesis far exceed the rates of microbial decomposition. However, with a lack of understanding of microbial process in peatlands and their sensitivity to climate extremes, there is an urgent need to understand the ecology and physiology of soil decomposer communities in response to changes in land use and climate together.

Here, using a range of different techniques over a range of different peatland health conditions (near natural, restored, and damaged peatlands under different water table depth), we aim to assess the change in microbial processes and carbon sequestration in peatlands within the Flow Country of Scotland. We highlight the change in diversity of specific taxa and genes, with the aim of linking these differences with the soil organic matter chemistry.

The goal is to link functional genes and chemical reactions to understand the consequences of microbial physiology on decomposition of organic matter that impacts the ecosystem C balance. This knowledge will provide the basis for better prediction and management of microbial processes in peatlands and to assess the success of restoration efforts to enhance carbon storage under future climate.

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## *Onome Felicia Omovie-Stephen*

### MEASUREMENT AND MANAGEMENT OF SOIL ORGANIC CARBON FORMS IN ITS DYNAMIC PATHWAY TO MITIGATE THE IMPACT OF CLIMATE CRISIS

Supervisors: Prof. Graeme I. Paton, Dr Lenka Mbadugha



#### ABSTRACT

The Earth's temperature is on the rise due to global warming, primarily caused by greenhouse gases, with atmospheric carbon dioxide (CO<sub>2</sub>) being the leading contributor. Soil serves as the largest carbon sink in the terrestrial carbon cycle, storing approximately three-times more carbon than the atmosphere.

Soil organic matter (SOM) constitutes a significant portion of soil, containing 50-58% of soil organic carbon (SOC). SOC plays a vital role in promoting soil biological activities. Additionally, it contributes to reducing greenhouse gas emissions while enhancing soil aggregation and water retention. The most reliable method for assessing SOC changes is through its measurement. However, changes in SOC stability resulting from soil activities and land use practices are not easily detected through total SOC measurement alone.

Thus, this study adopted carbon fractionation, measuring various SOC fractions, including dissolved organic carbon (DOC), hot water extractable carbon (HWEC), particulate organic matter carbon (POMC), microbial biomass carbon (MBC), hydrophilic dissolved organic carbon (Hy-DOC), hydrophobic dissolved organic carbon (Hb-DOC), permanganate oxidizable carbon (POXC), and mineralized carbon (basal respiration). Furthermore, SOC dynamics across different land uses (grassland, cultivated soils, and forest soils) and the impact of long-term soil storage on SOC concentrations were evaluated. Soil depths were examined to understand SOC movement within the soil profile.

Results indicated that HWEC exhibited the highest SOC concentration, followed by POXC, while DOC had the lowest concentration. Long-term soil storage did not significantly alter SOC concentrations over 1 year.

## *John Agyeman Prempeh*

### THE EFFECT OF SELECTIVE LOGGING ON BIOMASS AND CARBON STOCK IN BOBIRI FOREST RESERVE IN GHANA

Supervisors: Prof. David F.R.P. Burslem,  
Dr Christopher Kettle



#### ABSTRACT

Carbon emissions from deforestation and forest degradation through selective logging poses a major challenge for global climate change mitigation. The quantification of biomass and carbon stock distribution in local forest ecosystems constitute a major part of the global forest carbon budget and a bulwark for predicting future climate change.

Bobiri Forest Reserve in Ghana has experienced unsustainable timber exploitation lately. The effects of selective logging on biomass and carbon stock accumulation using three different allometric equations were evaluated. Inventory data of about 3,775 trees was retrieved from unpublished database in 1990 and 1,615 in 2020/21 on eight permanent sampling plots (PSPs). The species were measured at  $\geq 10$  cm diameter at breast height (DBH) with each plot subdivided into 20m X 100m to enhance enumeration.

There was higher biomass estimation in 1990 (3086902.84kg) with a reduction of 36.56 percent in 2021 (1958197.40kg) after a thirty-year period. Similarly, the carbon stock was higher in the 1990 (1450.84 t C) with a reduction of 36.56 percent in the 2021 (920.35 t C) estimation. The reduction in biomass and carbon stock occurred on six plots except plots (2) and (8) which increased in both biomass of (9729.45kg, 22394.44kg) and carbon stock of (4.57 t C, 10.53 t C) from 1990 to 2020/21.

The comparative analysis using three different allometric equations indicated that equation (1) computed highest biomass and carbon stock estimates followed by equations (2) and (3). The total reduction in biomass and carbon in 2021 is attributable to selective logging on the PSPs though these plots are earmarked for research activities hence the need to protect the plots from unsustainable logging which has caused a reduction in biomass and carbon stock in the thirty-year period.

## *Camila Rocabado-Penanco*

### UNRAVELLING THE EFFECTS OF ENVIRONMENTAL CHANGES ON GENETIC VARIATION OF BENEFICIAL ARTHROPODS IN AGROECOSYSTEM

Supervisors: Dr Greta Bocedi, Dr Roslyn Henry



#### ABSTRACT

The study aims to investigate the effect of past land use and climate change on Danish butterflies' distribution changes.

The method used was nested species distribution models, incorporating annual climate variables for the "global" model (encompassing Europe) and land use data for the "regional" model (covering Denmark). This way, the global model is capable of quantifying the species' response to bioclimatic conditions across their entire range, while informing the regional model of the species' climatic suitability limits to create a better-informed regional model.

The use of annual climate variables makes it possible to take into account climate change and the fact that short-lived species such as butterflies, the subject of this study, are affected by short-term climatic fluctuations. The resulting SDMs provide insights into the extent of range changes due to climate and land use change.

## *Stewart Rosell*

### eDNA SURVEILLANCE FOR INVASIVE NEW ZEALAND FLATWORM, *ARTHURDENDYUS TRIANGULATUS*

Supervisors: Dr John Baird



#### ABSTRACT

Environmental DNA (eDNA) is being developed as a surveillance method for many terrestrial invertebrate species. This can be more efficient than using visual inspection and avoid destructive sampling during inspections of horticultural products.

New Zealand flatworm is a widespread invasive species which predated on earthworms and presents challenges for traditional biosecurity inspection methods. It is cryptic and difficult to detect using visual inspections. Other non-native flatworm species are important invasive species in Europe, for example *Obama nungara*. Alternatives to visual inspections such as eDNA could improve detection and control of these species.

In this study we are developing eDNA based methods for detecting non-native flatworms, using *A. triangulatus* for proof-of-concept research. These methods could be applied in horticulture as surveillance for any of the 22 non-native land flatworm species in Europe.

Photo by Julian Zwengel on Unsplash:

<https://unsplash.com/photos/a-close-up-of-a-worm-crawling-on-the-ground-EVRvIM-Nzf4>

*Ethan Ross*

**ADVANCES IN DNA BARCODING USING OXFORD  
NANOPORE SEQUENCING FOR MONITORING  
SCOTTISH SEAGRASS BIODIVERSITY**

Supervisors: Dr Kara Layton, Dr J Sigwart,  
Prof. Stuart Piertney



**ABSTRACT**

Seagrasses and their species-rich communities provide vital ecosystem services including blue carbon storage, coastal protection and supporting fisheries but have recently faced global declines. Species richness is a critical factor in the ecosystem functions which underpin these services but remains difficult to estimate using traditional survey methods. Given this, seagrass beds are ideal candidate habitats to monitor with environmental DNA (eDNA) metabarcoding methods which use traces of DNA released by resident organisms to identify the species present on a habitat. However, detection using these methods relies on a pre-existing reference library of DNA sequences from known species.

This talk will focus on the first chapter of the project which focusses on generating reference sequences for the macroinvertebrates which inhabit the subtidal seagrass beds off the west coast of Scotland. Over 500 macroinvertebrates have been collected over the past two years, representing 120+ species. Specifically, I will focus on a recent methodological comparison between two different sequencing technologies, Sanger, and Oxford Nanopore for generating reference sequences at scale.

This work contributes to ongoing efforts to advance DNA barcode reference libraries for UK marine invertebrates. Additionally, it will improve identification of resident species using eDNA metabarcoding in latter stages of this project with the goal of establishing biodiversity baselines for these vital habitats.

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## *Tilly Scott*

### TRANSPOSABLE ELEMENT PROLIFERATION HAS IMPACTED THE EVOLUTION OF DEEP-SEA AMPHIPODS

Supervisors: Prof. Stuart Piertney, Dr Marius Wenzel



#### ABSTRACT

The evolutionary mechanisms that underpin invertebrate adaptation to the deep sea are poorly understood. The deep sea is an underexplored extreme environment, with immense hydrostatic pressure, near-freezing temperatures, and limited food resources. Despite the extreme environmental conditions, amphipods colonised the Abyssal and Hadal zones after the last deep-sea mass extinction and became the dominant macrofauna. Here, I provide evidence that transposable elements (TE) played a critical role in the evolution of amphipods.

TE were predicted from existing reduced representation DNA sequencing of three deep-sea amphipods, *Bathycallisoma schellenbergi*, *Hirondellea gigas*, and *Paralicella* sp.. TE account for over 70% of the assembled sequences, a very high proportion and far more than shallow-water amphipods. TE in the 'Long Interspersed Nuclear Element' order were the most abundant, occupying 28-42% of the assembled sequences, particularly the TE family *I*, which occupied 32.8% in *B. schellenbergi*. This supports the hypothesis that TE proliferation increased the genome size of deep-sea amphipods.

To provide insights into TE suppression by cytosine methylation, I have conducted the first analysis of the global percentage of 5-methyl-cytosines in deep-sea amphipods, revealing that deep-sea amphipods show extreme hypomethylation. This, in combination with strongly skewed Repeat Landscapes, reveals that TE are likely not currently suppressed by methylated cytosines and are young and active in deep-sea amphipods. This work emphasises the important role of TE in adaptive evolution. With whole genome sequencing of deep-sea amphipods, we will better understand the evolutionary impact of TE activity.

## *Tonwong Sudto*

### INTENTION OF RICE FARMERS TOWARDS SUSTAINABLE AGRICULTURE PRACTICES IN THAILAND

Supervisors: Dr Sylvia Vetter, Dr David McBey, Prof. Pete Smith



#### ABSTRACT

As in other Asian countries, rice is incredibly important in Thailand, serving as a staple in daily meals and as a crucial export commodity. Paddy land covers nearly 50% of Thailand's agricultural landscape, using management practices that have long relied on continuously flooded conditions. These methods contribute significantly to greenhouse gas (GHG) emissions, mainly methane, and are a major contributor to Thailand's agrifood systems. To address this challenge, the Thai Government promotes Sustainable Agriculture Practices (SAPs) among rice farmers, such as Alternate Wetting and Drying (AWD) and straw management to reduce GHG emissions and increase soil organic carbon. However, despite these efforts, only a minority of farmers adopt SAPs, and overall uptake remains low.

To understand the intentions of Thai rice farmers towards adopting SAPs, we explore factors influencing their decisions, utilizing the COM-B model (Capability, Opportunity, Motivation - Behaviour) to identify key barriers and facilitators. Through qualitative interviews and quantitative surveys, we explore factors influencing their decisions.

Initial results from our interviews suggest that farmers possess an understanding of, and skills for, AWD but adapting to SAPs requires more time and machinery for straw management. Land ownership poses barriers to AWD adoption due to reluctance to invest in land levelling. Interpersonal influences, like joining farmer communities, facilitate support from the government and knowledge sharing within communities. Economic motivations drive farmers' decisions towards adopting sustainable practices, alongside social status considerations. Further interviews and analysis are planned to expand the dataset and inform policies for effective sustainable agriculture behavioural changes.

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***Rhian Taylor***

**SEASONAL VARIATIONS IN THE ZOOPLANKTON AND ICHTHYOPLANKTON COMMUNITY COMPOSITION FOR THE NEAR-SHORE ENVIRONMENT OF THE FALKLAND ISLANDS**

Supervisors: Prof. Stuart Piertney, Prof. Alex Douglas, Dr Paul Brickle, Dr Jessie Van Der Grient



**ABSTRACT**

Zooplankton play a fundamental role in energy transfer across marine food webs. In so called wasp-waist ecosystems, species at the mid-trophic level (small-bodied fish and squid) control energy flow in the food web. In the Falkland Islands zooplankton may also have this role, with species such as *Grimothea gregaria* and *Themisto gaudichaudii* identified as an important food source for commercial fish species, penguins, whales, and other higher-trophic species.

This project aims to (i) identify a comprehensive list of Falklands coastal zooplankton species and (ii) understand how this community varies seasonally, including identifying changes in biomass and diversity. To these ends, zooplankton surveys were conducted every 1-2 months from September 2022 to March 2024 at three sites in East Falklands, consisting of three replicate 500µm and 300µm mesh net samples. Samples from seven collections (October 2022 to August 2023) were sorted and weighed with species identified to the highest taxonomic level either morphologically or using DNA barcoding.

These results will enable the visualisation of changes in biomass and structure within the zooplankton community, including any change in species dominance, between seasons. The important *Grimothea gregaria* larvae shows clear variation between collections, with larvae found in high abundance in spring and autumn samples, but very occasionally in summer and winter.

This study will provide insight into this important community and further our understanding of how the Falklands marine ecosystem functions. Differences observed in zooplankton seasonality are considered in relation to informing fisheries management strategies and provide baseline data for future zooplankton studies.

Photo by Cristian Palmer on Unsplash:  
<https://unsplash.com/photos/body-of-water-3leBubkp5hk>

## *Chris James Leven Tembo*

### GENETIC VARIATION IN RICE ROOT COLONIZATION BY ARBUSCULAR MYCORRHIZAL FUNGI DEPENDS ON FUNGAL IDENTITY

Supervisors: Prof. Adam H. Price



#### ABSTRACT

As water-saving technologies are increasingly considered in rice cultivation worldwide, the interactions between rice and arbuscular mycorrhizal fungi (AMF) will become important. A wide genetic variation in rice root colonization with model AMF species, *Rhizophagus irregularis*, has been established. However, fewer studies have tested this against different AMF species.

To address this, we conducted a greenhouse pot experiment using five rice cultivars and three AMF species (*R. irregularis*, *F. mosseae*, and *C. claroideum*) applied singly or as a community. We found that the root colonization rates varied depending on the host and the AMF species. Additionally, the growth responses of rice cultivars varied across the AMF species. While colonization rates with a community of AMF were consistent with previous studies, the rest of the AMF treatments were not consistent and depended on the host cultivar.

Inoculation with *C. claroideum* improved plant growth and nitrogen uptake, while *R. irregularis*, *F. mosseae*, and a community of AMF reduced plant growth parameters, and phosphorus and nitrogen uptake. The reduction in plant growth, and P and N uptake was independent of colonization rates, indicating the interplay of other factors that require elucidation. Similarly, a field study using a commercially available AMF inoculant on ten rice cultivars found significant differences in root colonization that were cultivar-dependent and changed over time. However, root colonization did not influence plant growth, yield or nutrient uptake.

These studies highlight that further research into the biological significance of differing colonization rates between rice cultivars is needed.

## *Danni Thompson*

### COLONY AND INDIVIDUAL LEVEL VARIATION IN FORAGING BEHAVIOUR

Supervisors: Dr Thomas Bodey, Prof. Beth Scott,  
Dr Ana Payo-Payo, Dr Al Baylis



#### ABSTRACT

Individual-level mechanisms are important for understanding ecological, demographic and evolutionary processes. Phenotypic differences can lead to individual specialisation, particularly regarding resource use, with both behavioural and physiological variation affecting the ability of individuals to detect, capture, handle, and digest prey. This variation between individuals, if sustained, results in individual specialisation across the dietary niche. Both competitive interactions and environmental heterogeneity drive the prevalence of individual specialisation within populations, but few studies consider these drivers together.

The Falkland Islands shag *Leucocarbo atriceps albiventer* is an understudied nearshore, colonial species. Their widespread distribution across the archipelago in colonies of varying size, and with access to either oceanic or more inshore waters, allows for a natural experiment to differentiate between the effects of environmental heterogeneity and intraspecific competition as drivers of individual specialisation.

By deploying GPS and TDR tags on breeding adults at multiple differently sized colonies, this study system provides a novel opportunity to identify the strength and extent of interactions between these key drivers. Here we present preliminary results from three colonies, revealing high levels of individual variation in foraging travel behaviours resulting in significant colony-level differences in space use.

Such information is central to informing the development of Falkland Islands Marine Managed Areas by identifying key foraging locations and, ultimately, prey species of importance for an important but poorly known nearshore predator.

## *Alexandra Tranganida*

### EVALUATING RNA QUALITY IN BLUBBER COLLECTED WITHIN 100 HOURS OF DEATH IN A MARINE MAMMAL: IMPLICATIONS FOR 'OMICS APPROACHES

Supervisors: Dr Joanna Kershaw, Dr Davina Deros



#### ABSTRACT

Omics applications (e.g., transcriptomics) are powerful tools to investigate animal physiology. Applying these techniques in marine mammal research is limited in part due to the challenges of collecting high quality samples. It is particularly important that samples are collected and preserved appropriately to minimise degradation.

Using tissues from stranded animals provides an invaluable tool to gain insight into the challenges free-ranging animals face, including human-caused disturbances. There is currently lack of information on the suitability of samples from stranded marine mammals in 'omics studies. Tissues may degrade or undergo post-mortem metabolic changes by the time a stranding is reported and samples collected, thus leading to inaccurate results. Here, I evaluated the impact of postmortem interval and sample storage condition on blubber total RNA quantity and quality.

Blubber samples (n=59) were collected over four days from a freshly stranded grey seal (*Halichoerus grypus*) stored outside (ambient temperature: 3.3-10.2°C). Samples were: 1) preserved in RNA stabilising buffer for 24 hours and then snap frozen, 2) snap frozen immediately upon collection, or 3), stored at -80°C with no prior preservation method. Total RNA was extracted using a standard phenol-chloroform protocol. RNA quantity was measured by spectrophotometry, and quality was assessed by gel electrophoresis and the RNA integrity number (RIN).

We show that high quality samples (RIN>7) sufficient for downstream applications were extracted up to 100 hours postmortem. There was a negative correlation of RIN with postmortem interval, that differed depending on storage condition.

*Haneen Wazzan*

## THE IMPACT OF FAST-FOOD CONSUMPTION ON HEALTH: A SYSTEMATIC REVIEW AND META-ANALYSIS

Supervisors: Dr Smita Dick, Dr Catherine Hambly, Prof. John Speakman



### ABSTRACT

**Background:** Obesity is a growing health concern. Associated with chronic diseases, it imposes a significant burden on healthcare costs. Food is crucial in weight management. Usually, out-of-home food has a high energy content which can contribute to excessive energy intake and obesity. Dietary factors which affect appetite and food intake regulation must therefore be found.

**Objective:** To examine the evidence from intervention studies on the relationship between fast food consumption and its effect on weight and satiety hormones in adults.

**Methods:** In this systematic evaluation of the relationship between fast-food intake and weight and satiety hormone changes, five databases were searched as well as the reference lists of the included papers.

**Results:** Fourteen trials met the inclusion criteria. Eight long-term trials showed that two fast-food meals per day for four weeks with sedentary behaviour increased body weight significantly from  $67.6 \pm 9.1$  to  $74.0 \pm 11$  kg ( $p < 0.001$ ). Two long-term trials and four short-term trials investigated the effects of fast-food meals on hormone response (ghrelin, GLP-1, PYY, CCK, GIP, adiponectin, resistin, adipokine, PAI-1, adipsin, lipocalin, and leptin). The result showed no constant differences across the studies on the level of appetite hormones after fast-food meals in short- and long-term studies.

**Conclusion:** The current results are a part of the systematic review that looked at the effect of fast food on health. The study's findings revealed that long-term fast-food consumption significantly increased body weight. Additionally, the results for the level of appetite hormones after fast-food meals in short- and long-term studies were inconsistent.

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## *Hamish Williams*

### PHYSIOLOGICAL RESPONSES OF ACTINIA EQUINA FROM OIL EXPOSURE, PRIMED AND UN-PRIMED

Supervisors: Dr David Fisher, Dr Marius Wenzel, Prof. Stuart Piertney, Dr Mark Hartl



#### ABSTRACT

Oil pollution is one of the significant anthropogenic stressors which has been recorded to have significant impacts on organisms physiologically, in many instances reducing their ability to function normally, and significantly increasing the risks of mortality. There has also been recorded evidence that when tackled quickly and efficiently, shorelines are able to recover after an exposure event. However, there still remains some unknown consequences such as how exposure to oil stress may impact future exposures to stress, in addition to some organisms having relatively limited research into how oil stress impacts their physiology, and what type of responses that may be induced as a consequence.

*Actinia equina*, a beadlet anemone is commonly found amongst rocky shorelines across the globe, and as such is positioned as a potential ideal candidate for longitudinal studies of exposure to oil pollution. In this study, anemones were exposed to diesel (a proxy for crude oil) in two separate experiments: the first, where anemones were either exposed or not exposed to diesel; and a second experiment where one group was exposed initially to diesel, then after a seven-day period, both groups were exposed to diesel.

Differential expression analyses and subsequent enrichment analyses revealed that both experiments had a significant change in physiology from diesel exposure, but that their responses were different from each other, sharing no differentially expressed genes in common, with a greater number of enriched terms being identified from the differentially expressed gene list of the first experiment, but a larger number of enriched terms on a genome scale in the second experiment.

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