UNIVERSITY OF
ABERDEEN

School of Biological Sciences

POSTGRADUATE RESEARCH CONFERENCE

Presentation Abstracts

12th & 13th April 2018

Nature on our doorstep

Welcome…

to the School of Biological Sciences Postgraduate Research Conference 2018.

This is an important component of the training of our PhD students, and gives an opportunity to see the breadth and depth of research on-going within the School. We are sure you will enjoy the experience and encourage you to engage with your colleagues and support their presentations.

Professor Chris Secombes
School Postgraduate Co-ordinator
Regius Professor of Natural History

Presentation abstracts can be found in this section.
The full programme can be found in the centre pages.

Session 1

Chair:
Barry Nourice

Abstracts

Thursday 12th April 2018

Yeh-Fang Hu

UNDERSTANDING THE ROLE OF INTERFERON-Y IN RAINBOW TROUT (*ONCORHYNCHUS MYKISS*) IMMUNE RESPONSES

Supervisors: Prof. Chris Secombes & Dr Tiehui Wang

ABSTRACT

Interferon (IFN)-γ is a major effector cytokine in host-defence, and is produced mainly by T cells and NK cells in mammals. It drives the Th1 immune response and promotes protection against intracellular infections. IFN-γ orthologues have been discovered in several fish species and are functionally conserved suggesting that the Th1 type immune response is present in early vertebrates. To investigate these responses in fish, we have validated monoclonal antibodies (mAbs) which were raised to four different peptide immunogens, V27, N2, VAB3 and V91 against salmonid IFN-γ. Results show all of these mAbs react specifically to their peptide immunogens in ELISA and by Western blotting. They can also detect recombinant and indigenous IFN-γ in different assays. Among them, VAB3 shows the strongest ability to recognise immunogens followed by N2 and V91. Further methods, such as intracellular staining for flow cytometry and immunohistochemistry, are being established to monitor IFN-γ expression in vitro and in vivo following vaccination, antigen re-stimulation and cytokine stimulation.

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Panthita Ruang-Areerate

GENOME-WIDE ASSOCIATION MAPPING FOR GRAIN MANGANESE IN RICE (*ORYZA SATIVA* L.) USING DIFFERENT MARKER DENSITIES

Supervisors: Prof. Adam Price, Dr Alex Douglas & Dr Gareth Norton

ABSTRACT

Rice (*Oryza sativa* L.) is an important crop, in terms of contribution of calories to the global human diet. In this study, we present genome-wide association (GWA) mapping using 44,100 and 700,000 single nucleotide polymorphism (44K and 700K SNP) datasets across 385 diverse rice cultivars of the Rice Diversity Panel 1 to assess the impact of marker density on GWA mapping. Analysis was performed for manganese (Mn) concentration in rice grain where the cultivars were grown under either flooded or unflooded cultivation over multiple years. Genetic variation associated with the trait was analysed in all cultivars as well as specific four major subpopulations. A total of 94 significant SNPs were associated with the elemental phenotype when using the 44K SNP dataset, while 578 significant SNPs were associated with the phenotype when using the 700K SNP dataset. Interestingly, two strong quantitative trait loci (QTLs) for grain Mn were detected on chromosome 3 and 7 using the 700K SNP dataset, which were not detected using the 44K SNP dataset. In addition, eight candidate genes were identified for grain Mn in rice. This work demonstrated the detection of additional novel QTLs and candidate genes for the trait when using high marker density.

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Jessica Jones

AGE AND GROWTH IN DISTINCT MALE MORPHOTYPES OF A LOLIGINID SQUID (*DORYTEUTHIS GAHI*) IN FALKLAND ISLANDS WATERS

Supervisors: Prof. Ursula Witte, Dr Alexander Arkhipkin, Prof. Graham Pierce, Prof. Frithjof Kuepper, Dr Paul Brickle

ABSTRACT

Understanding patterns in migration and the degree of connectivity within a population is necessary for stock assessment and management. The Patagonian long-finned squid *Doryteuthis gahi* is a commercially important species within Falkland Islands waters. The population structure consists of two temporally distinct spawning cohorts. Mixing between cohorts maintains genetic homogeneity within Falkland Islands waters, yet the mechanisms connecting these cohorts are yet to be fully resolved. A recent study has suggested that two distinct morphotypes of male squid occur in this species. The elongated mantles and large fins of the rare 'super large' males were suggested to be a morphological adaption to facilitate extended migrations and connect geographically distinct subpopulations. Very few age data are available on these larger individuals. Thus, to test the hypothesis that this 'super large' morphotype provides temporal connectivity between cohorts in addition to geographical connectivity, statoliths were used to estimate the age of mature males belonging to both morphotypes and to determine the age structure of the population. To investigate when these 'super bulls' occur and how temperature affects size, hatching dates were back calculated and monthly temperature histories were reconstructed using CTD data collected within the designated fishing zone. Results indicate that 'super large' morphotypes are a similar age to their smaller counterparts and are not responsible for providing temporal connectivity, but hatching occurs year-round for the rest of the population, resulting in overlap between cohorts.

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Jonathan Cope

INTROGRESSING RESILIENCE AND RESOURCE USE EFFICIENCY TRAITS FROM SCOTS BERE TO ELITE BARLEY LINES (REBEL)

Supervisors: Dr Gareth Norton, Dr Timothy George & Dr Adrian Newton

ABSTRACT

With the increasing population it is important to increase the total yield of most crops, importantly the staple cereal crops. Whilst modern elite barley varieties are high yielding and responsive to high levels of agronomic inputs they have plateau in ‘on farm yield’, with little evidence of an overall increase in abiotic and biotic stress tolerance due to the low priority in breeding for increased stress, low input or marginal environments.

A potential source of viable resilience and resource use efficiency traits are landraces local to areas of marginal land, such as the Scots Bere from the Highlands and Islands of Scotland. The Bere are a deeply historically rooted landrace of barley which has been grown on predominately marginal land for the last half millennia; allowing them to yield well under marginal conditions with impoverished soils. By introgressing them into elite cultivar backgrounds they may contribute biotic and abiotic stress-tolerance genes and nutritional genes that enable them to efficiently and resiliently yield under low input and stress-prone environments.

The overall aim of the proposed project is to assess and genetically characterise these traits thereby improving low-input performance and yield stability in elite barley. Screening for biotic stress resistance to pathogens such as *Rhynchosporium commune* & *Puccinia hordei*, abiotic stress resistance to stresses such as Mn deficiency & salt toxicity, and a combination of one abiotic and one biotic stress to asses the interaction within the genotype.

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Session 2

Chair:
Jessica Jones

Abstracts

Thursday 12th April 2018

Barry Nourice

BIOCHAR AS A POTENTIAL REMEDY FOR SALINE IRRIGATION ON CROP AND COASTAL CALCAREOUS SOIL IN SEYCHELLES

Supervisors: Prof. Graeme Paton & Dr Gareth Norton

ABSTRACT

Salinisation of irrigation water due to marine intrusion in aquifers is a challenge to low lying coastal farms in the Seychelles. The increased sodium content can cause a loss in crop yield. A pot experiment to assess the mitigation potential of biochar (BC) on saline irrigation impacted soils was conducted. Chinese cabbage (*Brassica rapa* L. subsp. *pekinensis*), an important cash crop for coastal farms in the Seychelles, was selected. The studied soil was a calcareous sand (Shioya series) from a coastal farm in the Seychelles. The seeds were sown in seedling media and then 14 days old seedlings were transplanted to treatment pots with BC (at 0%, 5% and 10% w/w, < 1 mm) and three levels of saline irrigation water (0, 2 and 5 dS m^{-1}). The day and night temperature were maintained at 28 ± 2 and 25 ± 2 °C respectively. With 30 replicates were BC saline treatment combination. Humidity was maintained between 75 to 80%. Each pot received 30 ml irrigation water on a daily basis using a modified drip system. Application of BC significantly reduced the uptake of sodium by the Chinese cabbage plants under the 2 and 5 dS m^{-1} irrigation treatment, compared to the 0 % biochar control. Exchangeable sodium percentage (ESP) in the soil decreased significantly with in the BC treated soils compared to the control soils, a similar impact was observed with regards to the sodium absorption ratio (SAR), in the pore water. Overall the application of biochar reduced the impact of saline irrigation water on the soil, pore water and the plant. This proves, that in this scenario a BC application (at least to single crop cycle) can be used as a salinity mitigation option in soil based agricultural production. There is a need to extend the range of soils, crops and salinity in these trials to better understand the role of BC in sustainably mitigating against encroaching saline irrigation.

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Ahmed Attaya Mohamed

STUDIES ON THE SALMONID GUT IMMUNE RESPONSE TO A NOVEL ORAL VACCINE DELIVERY SYSTEM

Supervisors: Prof. Chris Secombes, Dr Jun Zou & Dr Sohye Yoon

ABSTRACT

Vaccines are mainly administered by IP injection in fish aquaculture systems. This route does not suit mass vaccination and can cause flesh melanisation due to the vaccine adjuvant component. If optimised, oral vaccination would be a preferred delivery route, but is problematic, primarily because the gut immune response is still not well-understood and there is a lack of a commercially valid vaccine vehicle to protect the antigen against gastric degradation. This research project aims to advance the potential of oral vaccine delivery in fish (rainbow trout) in terms of identifying the main leucocyte types in the gut and markers for effective oral vaccination and antigen uptake. In addition, it will evaluate a novel silicon nanoparticle based vehicle (ProSilic) for use with a bacterial (*Aeromonas salmonicida*) vaccine. Initially the vehicle + antigens will be assessed for their stimulatory impact on different cell types and stability in acidic media, and subsequently the induction of immune parameters and level of protection achieved *in vivo* will be determined. To date the results have shown the gut is an immunologically competent tissue and that effective oral vaccination results in the modulation of key immune molecules at the transcript and protein levels in the gut. ProSilic conjugated antigens have shown superior stimulatory activity over unconjugated antigens and greater stability against acid treatment. The ability of the ProSilic vehicle to induce protective responses *in vivo* will be studied next.

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Session 3

Chair:
Johanna
Van Paassen

Abstracts

Friday 13th April 2018

Rita Razauskaite

SOIL CARBON SEQUESTRATION IN LONG TERM MANAGED GRASSLAND AND BROADLEAF FOREST

Supervisors: Prof. Jo Smith & Dr Elena Vanguelova

ABSTRACT

It is increasingly important to adequately understand and quantify the change in terrestrial carbon sinks under native woodland compared to common agricultural land uses. This study has employed deep soil sampling (1.1m) by depth and horizon in a long term *Quercus robur* forest, where a 27 site chronosequence was divided into young (<36 year), mid rotation (50> >75), mature (76> >110 year) and ancient forest (>220 year) stands, and a paired grassland site in Southern England, together with physical fractionation of soil carbon. It aims to quantify differences in soil carbon accumulation by depth and soil horizon, and quantify the distribution of carbon in fractions of different recalcitrance. The known forest and agricultural land use history allows us to hypothesize that land has reached steady state with respect to carbon and nitrogen. The results therefore provide insights into the potential benefits of future forest management and grassland afforestation on a seasonally waterlogged clay soils in a maritime temperate climate.

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Ewan Oleghe

RESIDUES WITH VARYING RECALCITRANCE INTERACT DIFFERENTLY WITH SEED OR ROOT EXUDATE COMPOUNDS TO AFFECT THE BIOPHYSICAL BEHAVIOUR OF SOIL

Supervisors: Prof. Paul Hallett, Prof. Liz Baggs & Dr Muhammad Naveed

ABSTRACT

Plants have a massive impact on the physical behaviour of soil due to seed and root exudates altering mineral: organic matter associations. In this study we explored how the recalcitrance of residues in soil interacts with seed or root exudate compounds to influence microbial respiration, mechanical behaviour and hydrological properties. Sandy loam and clay loam soils were amended with one of ground green barley powder, barley straw or poultry manure at 40 t ha^{-1}, and either chia seed exudate at 1.84 mg C g^{-1} soil or root exudate compounds at 14.4 mg C g^{-1} soil. On disks packed to 1.3 g cm^{-3}, uniaxial compression, penetration resistance, water sorptivity, water retention and porosity were measured at time 0, after 14 days incubation and then after three cycles of wetting and drying to simulate weathering. Application of seed and root exudate increased carbon dioxide (CO2) emissions from 0.309 ± 0.006 to 15.107 ± 0.711 µg C-CO2 g soil^{-1} hour^{-1} for the sandy loam soil and 0.171 ± 0.005 to 10.558 ± 0.780 C-CO_2 g soil^{-1} hour^{-1} for the clay loam soil. There were large changes in physical parameters caused by seed or root exudate amendment coupled with residues, their decomposition and weathering. After incubation and weathering, soils with added seed or root exudates were more mechanically stable, as measured by penetration resistance (22-58% increase) or compression index (25 to 43% decrease), with less impact from residues. Future studies should account for the magnitude and nature of microbial carbon mineralization on soil properties, considering its impact in flocculation of organic carbon and clay fractions at the microscale in soils amended with residues.

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Aoife Leonard

MALADAPTIVE PLASTICITY FACILITATES ADAPTATION TO NOVEL TEMPERATURES DURING AN EXPERIMENTAL RANGE SHIFT

Supervisors: Dr Lesley Lancaster, Dr Mike Ritchie &
Dr Jorgen Ripa

ABSTRACT

Many organisms are responding to climate change with dramatic range shifts, involving plastic and genetic changes to cope with novel climate regimes found at higher latitudes. Using experimental lineages of the seed beetle *Callosobruchus maculatus*, we simulated initial phase of colonisation to progressively cooler and/or more variable conditions, to investigate how adaptation and phenotypic plasticity contribute to changes in thermal tolerance during colonisation of novel climates. We show that replicate lineages exhibit maladaptive plasticity in thermal tolerance during the initial stages of adaptation to novel, progressively cooler and more variable climates. Maladaptive plasticity is associated with rapid evolutionary gain of improved heat and cold tolerances. However, the net result is a pattern of countergradient variation in which maladaptive plasticity prevents the expression of the evolved benefit in the novel environment. In contrast, when range-shifting lineages encounter climates which are progressively cooler, but not more variable, than ancestral temperatures, individuals respond with beneficial, ancestral acclimation abilities, and no evolved changes in thermal tolerances are observed under any rearing conditions. We propose that the ordering of thermal adaptation during a range expansion to novel, more variable climates found at high latitudes and elevations may typically involve genetic compensation arising from maladaptive plasticity in the initial stages of adaptation, preceding the potential later evolution of adaptive thermal plasticity as environments become more predictable. This may have important implications for a time limit, during the maladaptive phase, on our ability to control populations establishing in a novel thermal environment.

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Emem Udoh

BEHAVIOURAL RESPONSES TO SHORT-TERM CALORIE RESTRICTION

Supervisors: Dr Sharon Mitchell, Dr Catherine Hambly & Prof. John Speakman

ABSTRACT

Calorie restriction (CR) provides numerous health and life span benefits. CR also presents an energy deficit that elicits compensatory behavioural responses as the body endeavours to return to energy balance. One such behaviour in mice on CR is food anticipatory activity (FAA) measured 3 hrs prior to provision of their restricted rations. This study examined the behavioural changes of FAA in detail.

Adult male C57BL/6 mice on graded levels of CR (0-40%, with 10% increments) for 12 weeks were recorded by video in the 9th or 10th week of CR for 5hrs before feeding. The HomeCageScan® software permitted automated analysis of mouse behaviour. Behaviours were categorised into resting (remain low, stationary, pause, sleep), low (groom, sniff and stretch body) and high (walking, rearing and hanging on the cage bars) intensity activities.

Compared to the controls, the 40CR group increased light phase activity. The distance travelled was 12-fold higher in 40CR relative to the controls. Highly active (FAA) behaviours comprised only 2% of the time for controls but 22% for the 40CR group The remaining time was spent on resting (71% and 64% for the controls and 40CR respectively) and low intensity behaviours (26% and 13% for the controls and 40CR respectively). This study showed a clear difference in the types and levels of activities shown by mice on CR. Further analysis will compare these specific behaviours across all the levels of CR and integrate them to circulating hormone levels.

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Session 4

Chair:
Marc Faber

Abstracts

Friday 13th April 2018

Mohammed Nuru Yakubu

PHYSIOLOGICAL AND GENETIC STUDY OF THE THREE-WAY INTERACTIONS BETWEEN RICE, ARBUSCULAR MYCORRHIZAL FUNGI, AND THE PARASITIC WEED *STRIGA*

Supervisors: Prof. Adam Price

ABSTRACT

Striga constitutes a major limitation to cereal crop production and control methods are scant. Identifying cultivars that avoid or reduce the impact of the parasites on the host plant is crucial. This study evaluates a diverse collection of rice cultivars for *Striga* resistance, the influence of AMF (*Rhizophagus intraradices*) on the *Striga*-rice host interaction and examines evidence that variation in the presence or absence *Max1* gene on chromosome 1, involved in strigolactone synthesis, is implicated in resistance.

Using pot experiment, 31 rice cultivars mostly from Nigeria but including some checks were screened for *Striga* resistance. Resistant genotypes were characterized by the ability of the cultivar to support no or few emerged *Striga.* Multiplexed PCR analysis was used to determine the presence or absence of the *Max1* gene among the tested cultivars.

Six of the cultivars showed good resistance to *Striga* while six were clearly susceptible. The product of the PCR analysis suggested 27 out of the 31 cultivars lack the *Max1* ortholog. The insertion/deletion was not associated with resistance.

In all the cultivars AMF increased the distance from the host plant to emerged *Striga*. AMF protected three genotypes against *Striga* but did not protect the cultivar Azucena. These variations imply a role for signalling between rice and Striga which may be related to strigolactones despite the lack of association between resistance and the *Max1* polymorphism.

The outcome of this research will be useful providing strategies for *Striga* control, be it breeding or mycorrhizal applicaiton.

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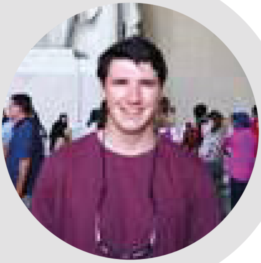
Thomas Clark

THE ROLE OF FUNCTIONAL AMINO ACIDS AS REGULATORS OF METABOLIC PATHWAYS IN ATLANTIC SALMON (*SALMO SALAR*) AND RAINBOW TROUT (*ONCORHYNCHUS MYKISS*)

Supervisors: Dr Daniel Macqueen, Prof. Sam Martin
& Dr John Tinsley (Biomar Uk Ltd.)



ABSTRACT

Functional amino acids are of major current interest in aquaculture, with recent evidence of beneficial effects on fish growth and health, however their effects are still poorly understood. A functional amino acid can be defined as an amino acid that participates in and regulates key metabolic pathways to improve the health, survival, growth or development of an organism. This project has investigated the role of functional amino acids on key gene pathways and their potential benefits as dietary supplements. Work has focused around supplementation of the urea cycle amino acids (arginine, ornithine and citrulline) over the course of two feeding trials. Both growth parameters and immune function were investigated through the response of key genes in metabolic and immune pathways both in-vitro and in-vivo. This work will help define the impacts and mechanisms of functional amino acid supplementation in salmonid diets with the ultimate aim of improving health and performance in aquaculture.

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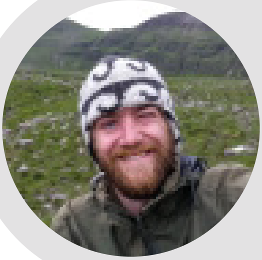

Richard Hassall

UNDERSTANDING MICROPARASITE DIVERSITY AND CO-OCCURRENCE IN SPATIALLY STRUCTURED HOST POPULATIONS

Supervisors: Dr Sandra Telfer, Prof. Stuart Piertney & Prof. Xavier Lambin

ABSTRACT

The ability of pathogens to adapt to changing conditions and compete is dependent on genetic diversity. In the case of bacteria, horizontal gene transfer allows gene flow between genetically distinct individuals and can introduce beneficial traits that aid persistence in the face of difference selection pressures. The probability of genetic exchanges generating new diversity will depend on the likelihood of different genotypes or species co-occurring within the same host and the existing diversity of the pathogen community in which they exist. Both may be influenced by the spatial structure of a host population, where host dispersal may act to introduce new genotypes or species to a pathogen community.

Here we use microparasites from the genus *Bartonella* as a model system for understanding how the spatial structure of host populations may influence both existing diversity and co-occurrence. We focus on *Bartonella* species infecting two contrasting water vole populations. A metapopulation, where subpopulations are linked by frequent dispersal events, and an isolated island population. We first determine how the spatial structure of a host population influences the co-occurrence of different species within hosts, after which, we investigate how spatial structure influences the diversity of *Bartonella* genotypes in each system.

We find different species are less likely to co-occur when host population are spatially structured and a greater likelihood of species co-occurring in more continuous populations, however the diversity of genotypes in these populations does not appear to be influenced by limitations on host dispersal. These links between host population structure and microparasite diversity/co-occurrence allow to us to tease apart the ecological processes that may increase the generation of diversity in pathogen communities.

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Loic Cecilio

EVALUATING ECOSYSTEM RESILIENCE IN A MOSAIC OF AGRICULTURAL LAND AND FOREST FRAGMENTS OF THE WESTERN AMAZON

Supervisors: Prof. David Burslem

ABSTRACT

Natural regeneration of tropical forests following clearance for agriculture contributes to the recovery of biodiversity and ecosystem function. It is particularly important to examine these components of resilience in species-rich tropical forest environments at the frontier of land-use change. The objectives of this study were to determine the recovery forest biomass and plant species richness after agricultural abandonment. Plots of 8 by 25 meters were established in 15 primary and 50 secondary forests stand of known previous land use and abandonment age ranging from 0.5 to 70 years. On these plots, all woody plant stems > 2.5 cm diameter at breast height (dbh) were inventoried and counts of 4079 plants of 430 different species of woody plants were made. Soil was sampled at 10 cm depth from 5 locations evenly distributed across each plot. These data were fitted to models of stand age to estimate the rate of recovery of above-ground biomass among other metrics of stand recovery.

Biomass (accounting only for trees > 5cm dbh) ranged from 0 to 330 tons of Carbon per Ha increasing with age, but rate of carbon accumulation averaged 110 tonnes of Carbon/Ha after 20 years, less than predicted by recent tropical Americas' model based on 3 climatic variables. This lower recovery rate shows unexplained variation, maybe due to forest erosion and intensive agriculture development in the landscape. Soil geochemical variables appeared to be highly inter-correlated and influenced by land use intensity, suggesting that human management intensity should be accounted to predict biomass accumulation.

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Session 5

Chair:
Alicia Bertolotti

Abstracts

Friday 13th April 2018

Johanna Van Paassen

A WEE BIT OF P - PHOSPHORUS ADDITION INCREASES CARBON ASSIMILATION IN SCOTTISH UPLAND ECOSYSTEMS

**Supervisors: Dr Sarah Woodin, Dr Andrea Britton,
Dr Lorna Street, Prof. David Johnson & Dr Andrew Coupar**

ABSTRACT

In Scottish upland ecosystems plant growth and decomposition are limited by nutrients, temperature and moisture, resulting in a deep organic layer. Under elevated atmospheric nitrogen (N) deposition, plant growth can be enhanced, but plants can also shift towards phosphorus (P) limitation. Combined with increased decomposition, this can result in a thinner organic layer and a net loss of carbon (C). Addition of P to ecosystems receiving elevated N deposition has the potential to relieve P limitation and thus promote plant productivity over decomposition. This study asks how P addition affects short term C cycling in N-enriched upland ecosystems, investigating the fate of the added P, and the effect of this P on moss growth, C assimilation and C loss.

In a field experiment, small amounts of P have been added to three of the most common vegetation types in the Scottish uplands: a dry heath, a wet heath and an acid grassland - all of which are receiving relatively high atmospheric N inputs (16-22 kg N ha^{-1} y^{-1}). Results after one year show increased foliar P in mosses and grasses, stimulation of moss growth in the dry heath, and a trend of decreased moss growth in the wet heath. Moreover we found increased gross primary production in response to P addition in both the dry and wet heath. However, there is little influence of P addition on ecosystem respiration. This confirms the potential of P addition to increase C assimilation in these ecosystems in the short term.

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Oihane Fernandez-Betelu

COMPARING TEMPORAL PATTERNS OF DOLPHINS AND THEIR PREY IN THE INNER MORAY FIRTH (NE SCOTLAND)

Supervisors: Dr Isla Graham & Prof. Paul Thompson

ABSTRACT

Previous studies found that diel, tidal and seasonal cycles had site-specific effects on the presence of bottlenose dolphins (*Tursiops truncatus*) in the inner Moray Firth. In Sutors, a constricted channel, dolphins were present most of the year, and were diurnal during summer and nocturnal in autumn, with no apparent tidal preference. By contrast, in Chanonry, another channel less than 15 km away, dolphins were detected mainly in summer and mostly during the flood stage of the tide. Since marine mammals' patterns of presence are often linked to their prey, we hypothesised that the observed cyclical occurrence of dolphins was linked to the cyclicity of fish in the area. In this study we will test this hypothesis, collecting fish data at both sites, focusing on the main contrasts in these dolphin patterns. A scientific echo sounder (WBT mini) coupled with a 38/200 kHz transducer is used to carry out monthly transects in both channels. Preliminary data observations have suggested there are important tidal effects on the presence of fish, which are more abundant during the flood than ebb stage of the tide at both sites. Further surveys are planned to compare fish abundance at different stages of the tide and different times of day at both sites. In addition, we plan to use camera and video/baited traps to identify fish species seen on the echo sounder.

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Manu Kumar Gundappa

THE DANUBE SALMON GENOME – TESTING THE IMPORTANCE OF WHOLE GENOME DUPLICATION IN SALMONID LIFE-HISTORY EVOLUTION

Supervisors: Prof. Sam Martin, Dr Dan Macqueen,
Prof. David Hazlerigg, Dr Simen Sandve & Dr Jurgen Geist

ABSTRACT

Anadromy represents a complex set of physiological adaptations present in many salmonid species, which allows for dual exploitation of fresh and marine habitats during life. The genomic-evolutionary basis for this fascinating life-history strategy remains poorly characterized, but is widely linked to an ancestral whole genome duplication (WGD) event that defines all salmonid fish. Salmonids likely evolved from a freshwater ancestor, a life-history retained in several lineages, including the Danube salmon (*Hucho hucho*), which is part of a sister group to a clade of ancestrally anadromous species including Atlantic and Pacific salmon. Due to its key phylogenetic position, we sequenced and annotated a high-quality draft Danube salmon genome. A haploid individual was Illumina sequenced to improve assembly contiguity by removing heterozygosity. Paired-end and mate-pair libraries were sequenced at ~80/40x respective coverage (2x250bp reads). Nanopore sequencing data has been generated at 5x coverage and we are now generating 30x PACBIO coverage, which will be used to increase genome contiguity. Genome annotation was performed combining multiple approaches and exploiting novel transcriptome data. We also plan to generate a genetic map to anchor the genome assembly to chromosomes later this year. The Danube salmon genome will be used for comparative analysis of salmonid genomes to characterize the evolution of duplicated genes retained from WGD and their role in the evolution of anadromy.

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Anna Harte

CHARACTERISATION OF ATLANTIC SALMON (*SALMO SALAR*) BETA-DEFENSINS AND THEIR CONSTITUTIVE AND STIMULATED EXPRESSION

Supervisors: Prof. Chris Secombes & Dr Tiehui Wang
(Fish Immunology Research Centre, Aberdeen)

ABSTRACT

Beta defensins are cationic antimicrobial peptides that are found in almost all studied vertebrate species, and play an important role in the innate immune system. Although they are well described in mammals and some species of fish, they have not yet been characterised in Atlantic salmon (*Salmo salar*). Atlantic salmon is an economically important species to aquaculture industries around the world, and improving knowledge of the immune system can aid in the development of disease mitigation measures.

In this study, 7 beta defensins transcripts were found in the Atlantic salmon genome using BLAST, and the constitutive and stimulated expression in a range of tissues was determined using qPCR. Tissues stimulated with parasites, whole bacteria and viral PAMPs showed that beta defensins 4 and 5b were significantly modulated during infection/stimulation, suggesting an important role for these defensins in immunological responses. A phylogenetic analysis was also performed to determine the evolutionary relationship between each transcript and in comparison to other species. This showed that each of the first 4 defensins found were closely related to equivalent rainbow trout (*Oncorhynchus mykiss*) molecules with a high level of sequence similarity, but that beta defensins 5a and 5b were novel and had relatively low sequence homology to any other trout beta defensin genes.

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Image: Jean-Paul Schmit

Session 6

Chair:
Loic Cecilio

Abstracts

Friday 13th April 2018

Nabilah Mohamad Ali

THE EFFECTS OF DIFFERENT LEVELS OF BEAN PROTEIN ON THE IMMUNE RESPONSES AND INTESTINAL WALL INTEGRITY OF ATLANTIC SALMON (*SALMO SALAR*)

Supervisors: Prof. Sam Martin, Dr Alex Douglas &
Dr Ela Krol

ABSTRACT

Development of new diets is important for the continued expansion of the salmon aquaculture industry. The current study focusses on new protein sources for salmon feeds, in this case bean protein concentrate was used to replace fish meal. A ten week feeding trial, was carried out with fish fed with either 10% or 20% bean protein concentrate, replacing fish meal, or a control diet rich in fish meal. At the end of the trial, the salmon were challenged by intra peritoneal injection with the bacterial pathogen with *Aeromonas salmonicida* or PBS as control. Total RNA was collected from liver and distal intestines (n=6). The expression of immune related genes was determined using RNA from liver and distal intestines. In addition, expression of several structural genes were also investigated in the intestine to assess the integrity of the intestinal wall following diet change and also how the fish on different diets responded to the pathogen. The finding of the study will give insights on how the salmon immune system responds under different diet regimes. Additionally, the impact of bacterial pathogens on the intestinal function will be investigated for the first time. This study was financially supported by Innovate UK and also Ministry of Higher Education Malaysia for the PhD studentship.

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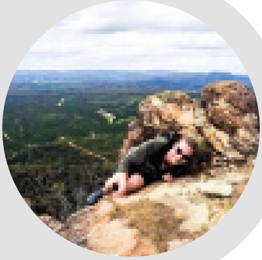
Craig Christie

ESTABLISHMENT OF A NOVEL IN VITRO FEEDING SYSTEM FOR THE HONEYBEE MITE, *VARROA DESTRUCTOR*

Supervisors: Dr Alan Bowman, Dr Ewan Campbell & Dr Giles E. Budge



ABSTRACT

Varroa destructor is an ectoparasitic mite of Apis mellifera, the western honeybee. *Varroa's* role as a vector of pathogens, most notably Deformed Wing Virus (DWV), is viewed as a leading cause of declining honeybee health globally. A better understanding of *Varroa* biology and the process by which they transmit pathogens would permit the development and implementation of new control methods. Here, a novel in vitro feeding platform is presented, a tool by which *Varroa* can be maintained off-host allowing research into their physiology, the testing of novel treatments and their role as a vector of honeybee pathogens. Through this platform *Varroa* survival was extended to >50% after 10 days through incorporation of honeybee haemolymph at 25% (v / v) in an artificial diet designed to be iso-osmotic with honeybee haemolymph. Additionally, this protocol was employed to evaluate the efficacy of a broad-spectrum systemic pesticide, ivermectin, demonstrating the assay's role as a screening platform for potential varroacides acting over prolonged periods. By substituting honeybee haemolymph in the diet with virus-free *Schistocerca gregaria haemolymph*, DWV transmission was examined. Following 4 days of in vitro feeding by *Varroa*, diet packets contained detectable DWV. Overall, this platform presents an artificial system in which *Varroa* can be maintained *in vitro* for similar periods as on their natural host, providing a useful tool for studies requiring long-term survival and delivers a tightly controlled, standardised method for varroacide testing and vector-pathogen transmission studies.

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Marc Faber

PROLIFERATIVE KIDNEY DISEASE IN RAINBOW TROUT: CHARACTERISATION

Supervisors: Prof. Chris Secombes & Dr Jason Holland

ABSTRACT

Proliferative kidney disease (PKD) is one of the most serious diseases affecting trout aquaculture in the UK. Caused by the myxozoan parasite, *Tetracapsuloides bryosalmonae*, PKD is elicited by the temperature-dependent development of parasite spore sacs in colonial bryozoans. Released spores gain entry into fish and proliferate in kidney tissues causing a chronic lymphoid hyperplasia that results in clinical disease. This PhD is part of and funded by the EU project PARAFISHCONTROL. The objectives are to assess early host immune responses shortly after infection, characterise biomarkers of infection and test the protective efficacy of novel parasite antigens and other immune therapeutic approaches. A successful treatment, based on the reduction of disease pathology and parasite burden, could markedly reduce fish mortalities leading to improved productivity and fish welfare. In addition to prophylaxis, a better understanding of the modes of infection and the utility of novel disease biomarkers will allow for better disease monitoring in farmed and wild fish populations.

The development and utility of host-specific parasite transcriptome assemblies have been highly effective as *in silico* filtering tools to uncover novel parasite antigens for vaccine studies.

Fully sequenced and characterized vaccine candidates have been cloned into a eukaryotic secretory expression vector for DNA immunization. The efficacy of DNA vaccination has been determined in two field trials at a rainbow trout farm (Hampshire, UK) known to be enzootic for PKD. Parasite genes, encoding proteins known to be involved in nutrition, cell-cell interactions, or currently of unknown function, exhibited reduced, albeit variable, kidney pathology.

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Alicia Bertolotti

COPY NUMBER VARIATION IN THE ATLANTIC SALMON (*SALMO SALAR*) GENOME

Supervisors: Prof. Sam Martin, Dr Daniel Macqueen, Dr Ryan Layer, Dr Torfinn Nome, Dr Simen Sandve & Dr Sigbjorn Lien

ABSTRACT

A high-quality reference genome was recently published for the Atlantic salmon (*Salmo salar*), a species of considerable economic, cultural and scientific importance. This resource has opened up new opportunities to understand the role of the genome in population-level variation and evolutionary processes. There is a heavy current focus on single nucleotide polymorphisms, and larger structural genomic variation has not yet been characterized. Copy number variations (CNVs) represent duplicated or deleted regions of chromosomal DNA (>1Kb) that vary in copy number among individuals. CNVs frequently overlap genes and have been widely implicated in phenotypic variation of agricultural, evolutionary and clinical relevance. We have been developing bioinformatic pipelines with 10x coverage whole-genome re-sequencing data of 454 individuals from across the species-range to robustly characterise the CNV landscape of Atlantic salmon. Analysis of this encompassing dataset is ongoing, but we already know that at least 2% of the genome is CNV, with demonstrable regional variation in CNV occurrence linked to a salmonid-specific whole genome duplication (WGD) event that occurred 88-103 Ma. Ongoing work is investigating population variation in CNVs, both for wild and farmed fish, and testing whether functional redundancy and duplicate gene retention post-WGD has influenced CNV retention and evolution.

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PROGRAMME

Thursday
12th April 2018

All Welcome

School of Biological Sciences

POSTGRADUATE RESEARCH CONFERENCE

ZOOLOGY BUILDING FOYER & LECTURE THEATRE

13:45	Arrival
14:00	Welcome: Professor Graeme Paton, Head of School
Session 1	Chair: Barry Nourice
14:15	Yeh-Fang Hu
14:30	Panthita Ruangareerate
14:45	Jessica Jones
15:00	Jonathan Cope
15:15 - 16:00	Coffee and poster session viewing A
Session 2	Chair: Jessica Jones
16:00	Barry Nourice
16:15	Ahmed Mohamed
17:00	Close

PROGRAMME

Friday
13th April 2018

All Welcome

09:30	**Arrival**
Session 3	**Chair: Johanna van Paassen**
10:00	Rita Razauskaite
10:15	Ewan Oleghe
10:30	Aoife Leonard
10:45	Emem Udoh
11:00 - 11:45	**Coffee and poster session viewing B**
Session 4	**Chair: Marc Faber**
11:45	Mohammed Yakubu
12:00	Thomas Clark
12:15	Richard Hassall
12:30	Loic Cecilio
12:45 - 14:00	**Lunch Break**
Session 5	**Chair: Alicia Bertolotti**
14:00	Johanna van Paassen
14:15	Oihane Fernandez
14:30	Manu Kumar Gundappa
14:45	Anna Harte
15:00 - 15:30	**Coffee**
Session 6	**Chair: Loic Cecilio**
15:30	Nabilah Mohamad Ali
15:45	Craig Christie
16:00	Marc Faber
16:15	Alicia Bertolotti
16:30	**Presentation of prizes and closing comments** **Professor Graeme Paton**
16:45	**Zoo and Roots Society Social Event**

UNIVERSITY OF ABERDEEN

School of Biological Sciences

POSTGRADUATE RESEARCH CONFERENCE

Poster Abstracts

12th & 13th April 2018

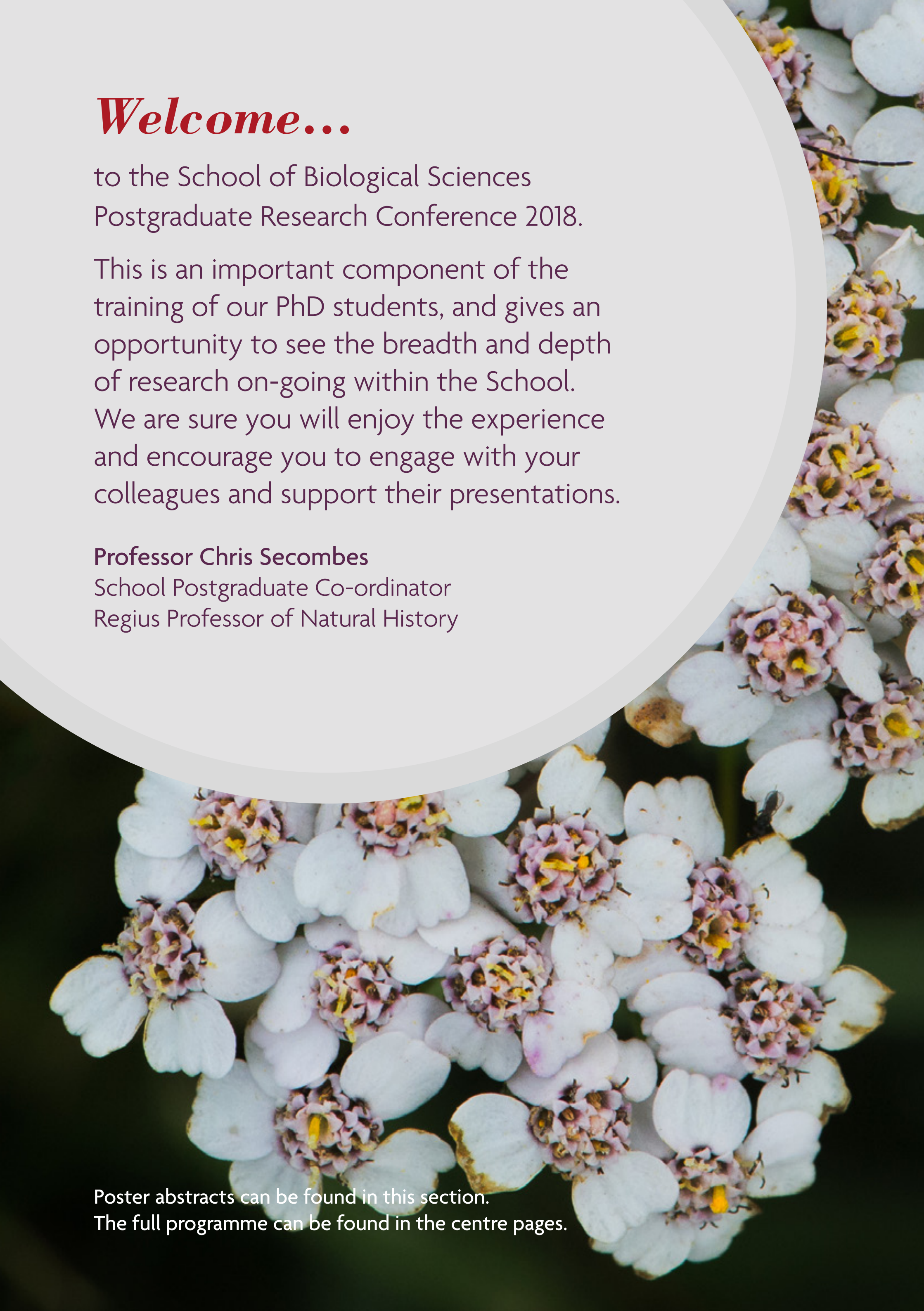
Nature on our doorstep

Welcome…

to the School of Biological Sciences Postgraduate Research Conference 2018.

This is an important component of the training of our PhD students, and gives an opportunity to see the breadth and depth of research on-going within the School. We are sure you will enjoy the experience and encourage you to engage with your colleagues and support their presentations.

Professor Chris Secombes
School Postgraduate Co-ordinator
Regius Professor of Natural History



Poster abstracts can be found in this section.
The full programme can be found in the centre pages.

Sapar Dossanov

DO FORMER METALLIFEROUS MINE SITES IN THE UK STILL POSE A HUMAN AND ENVIRONMENTAL RISK?

Supervisors: Prof. Graeme Paton & Dr Astley Hasting

ABSTRACT

Abandoned metalliferous mines have pollution sources that could pose significant environmental and public health risks. Potentially toxic elements associated with historic mining activities can be mobilised such that they enter the water environment or human/ecological food chains. This has been confirmed in numerous incidents where populations have been exposed to contaminated soil, food, and water.

Two sites in the Northern Pennines were selected for this study: Killhope a former lead and zinc mine and Langley a smelter site. Sampling of soils and waters was performed within defined processing zones. Soils were analysed using both exhaustive and non-exhaustive techniques. Site specific action concentrations that reflected risk defined trigger values were calculated using appropriate models.

In the context of environmental risk assessment the values recorded at these mine sites can be considered as exceptionally high. The value need to be compared against those values defined to protect specified receptors and in some cases these were greatly exceeded. Humans and animals can be excluded from these areas, and thus the risk mitigated.

However, the greater threat is probably to the water environment due to the elevated concentration of target elements and the expansive are over which they are located.

The lessons learned in sites can be translated internationally to active mining areas.

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Idongesit Ikpewe

THE IMPACT OF TEMPERATURE ON GROWTH RATES OF DEMERSAL FISH SPECIES IN THE WEST OF SCOTLAND

Supervisors: Alan R. Baudron, C. Tara Marshall & Paul G. Fernandes

ABSTRACT

Temperature, along with food availability, is often regarded as a major determinant of ectothermic growth. The temperature-size rule (TSR) predicts that increased temperature would result in faster growth but a smaller asymptotic length. There is empirical support for the TSR in ectotherms including several commercial fish species. Sea temperatures in the West of Scotland has risen by approximately 1°C over the past three decades. The present study investigated whether changes in the growth rates of haddock (*Melanogrammus aeglefinus*), cod (*Gadus morhua*), saithe (*Pollachius virens*), whiting (*Merlangius merlangus*) and Norway pout (*Trisopterus esmarkii*) were consistent with the TSR. Data for age-length-keys (ALKs) used in these analyses were obtained from Marine Scotland laboratory, while temperature data were obtained from ICES Report on Ocean Climate. For each species, the Von Bertalanffy growth function (VBGF) was fit on a cohort-by-cohort basis beginning in 1986, excepting Norway pout for which data began in 1990. For haddock asymptotic length ($L\infty$) was significantly, negatively correlated with temperature while the growth rate (K) was positively correlated. Over the study period a 28% decrease in the $L\infty$ of haddock was associated with a temperature increase of 1°C. The correlations between temperature and the VBGF parameters were not significant for saithe, whiting, Norway pout or cod. The significant result for haddock is consistent with the TSR which was also previously detected in North Sea haddock. Reason why haddock are unique in this regards are discussed.

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Keziah Hobson

INVESTIGATING THE RECOVERY OF A NATIVE PREDATOR

Supervisors: Prof. Xavier Lambin

ABSTRACT

The European pine marten (*Martes martes*) was once found across Britain, however was restricted to the north-west of Scotland with a few isolated populations distributed throughout the mainland by the mid-19thC. Over the past few decades the species has shown promising signs of recovery. Furthermore, pine martens have been successfully reintroduced to Wales, and other reintroductions are proposed for England. Much of the motivation to accelerate the recovery of this native predator is due to the potential impact on the invasive grey squirrel population, although little is known about the wider impacts. This project aims to identify the socio-ecological factors influencing the rate and geographical extent of pine marten recovery and the relationship with people throughout its current and potential future range. Spatially-explicit capture recapture and molecular analyses across a multi-season survey will be used to investigate the variables influencing population dynamics. Social surveys will collect information on stakeholders' attitudes towards the species and to identify key elements influencing levels of tolerance. These data will be combined to investigate the relationship between the ecological and social components of the recovery, and how these relate to time and geographical context. Pine marten recovery has the potential to bring substantial benefits to red squirrel conservation and the forestry industry. However, without a clearer understanding of the species' population dynamics and, importantly, its interaction with people it is difficult to predict or manage the outcomes. The interface between people and wildlife continues to expand, and it is therefore crucial we better understand these relationships in order to facilitate coexistence.

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Thomas Busbridge

OTOLITH MICROSTRUCTURE AND CHEMISTRY VALIDATE AGE AND SUBSEQUENTLY PROVIDE INSIGHTS INTO EARLY LIFE HISTORY AND BEHAVIOUR IN SOUTHERN BLUE WHITING (*MICROMESISTIUS AUSTRALIS AUSTRALIS,* NORMAN 1937)

Supervisors: Alexander I Arkhipkin, Simon R Chenery,
C. Tara Marshall and Paul Brickle.

ABSTRACT

Accurate age determination for commercial fishes is essential for effective fisheries management however validation of the ageing methodology is frequently overlooked. The microstructure of Patagonian southern blue whiting (*Micromesistius australis australis*) otoliths reveals check marks within the otolith microstructure that have potentially led to overestimations of age. This study aims to use otolith microstructure and trace elemental analyses to correctly interpret the otolith microstructure and produce the first validated ageing methodology for *M. a. australis* found in Falkland Islands waters. Firstly, daily increment formation was confirmed by conducting daily increment analyses on otoliths from individuals of a single cohort over the course of 1 year. Daily increment counts were used to determine the location of the first winter check and marginal increment analysis was further conducted on otoliths from 1-5 year old individuals to validate the annual formation of subsequent winter checks. Otolith microstructure was further investigated and revealed accessory growth centres and a subsequent check mark. Trace elemental analyses (LA-ICP-MS) was conducted to further investigate these structures. Results revealed significant changes in otolith chemistry, confirming a marked change in physiology and/or a change from a pelagic to a demersal habitat. This study confirms the location of the first winter check through daily increment counts and trace elemental analyses, and provides a validated ageing methodology which will benefit the accuracy of age determination and subsequent age-based stock assessments and growth models for *M. a. australis* found in Falkland Islands waters.

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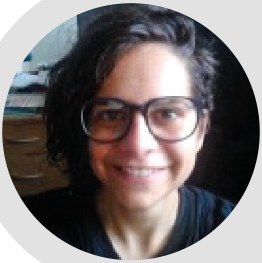

Anna Ferretto

CAN WE SET A BOUNDARY FOR LOSS OF BIODIVERSITY IN SCOTLAND?

Supervisors: Prof. Pete Smith

ABSTRACT

Planetary Boundaries (Rockstrom et al., 2009) are limits in nine environmental variables that should not be exceeded if humanity wants to avoid the risk of sudden shifts in the environment. In some countries, including Scotland (Malcolm et al., 2014), these boundaries have been downscaled and evaluated at a national level. In Scotland, some of these nine boundaries are missing, either because of a lack of data or because a lack of a meaningful way to set them. One of them is Loss of Biodiversity. Many data on biodiversity are available for Scotland: what is missing is a method to quantify the boundary. We are using Cole's solution (Cole et al., 2014): biodiversity is evaluated following the IUCN Red list of Ecosystems (Keith et al., 2013), and the boundary is set at zero ecosystems endangered. The IUCN's guidelines include five criteria which evaluate the reduction in geographic distribution, the restricted geographic distribution, the degradation of abiotic environment, the alteration of biotic interactions and a quantitative risk analysis. Initial analyses have focussed on peatland; we will then extend the procedure to as many other Scottish ecosystems as possible to have a comprehensive picture of the state of the Scottish habitats. Our first step, which will be discussed in detail, is the first criterion, specifically a comparison of future peatland distribution - derived using multiple bioclimatic models (Clark et al., 2010) - with the current and past distributions.

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Valeria Mazzola

ASSESSING THE GHG BALANCE FROM A SCOTTISH RAISED BOG-EDGE-WOODLAND

Supervisors: Prof. Jo Smith, Dr Georgios Xenakis &
Dr Jagadeesh Yeluripati

ABSTRACT

Lowland raised bogs are a rare and threatened habitat and, according to Forestry Commission, only 11% of the raised bogs in Scotland is in near natural condition. More specifically, bog woodlands consist of low-density forest vegetation on deep peats (usually Scots pine and Birch), whose growth is constrained by the presence of high water content in the soil. Since the rarity of this habitat has limited the amount of research effort expended on them, basic knowledge on how they function is badly needed in order to provide guidance on their management. Our project aims to fill some of the gaps in raised bog-edge woodlands knowledge, trying to understand the dynamics occurring between forest and bog at both soil-atmosphere and tree-atmosphere interface, using a variety of methods and techniques. The experiment plan provide for the use of different chamber techniques together with the use of Li-6400, Los Gatos Ultra-Portable Gas Analyser and gas chromatography analysis. The main aim is to assess the greenhouse gas balance (GHG) in the bog-edge woodland of Maud Moss (Banchory), to investigate how trees physiology may affect, directly or indirectly, CO_2 and CH_4 fluxes from the site due to their effect on the water table of the bog. Our interest is to understand if scots pine bog-edge woodland can be considered just a transient phase occurring as bog becomes fully wooded or a long-lived natural habitat in its own right.

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Fiona Bakke

PROTEOMIC ANALYSIS OF RAINBOW TROUT IMMUNE PROTEINS: IMPLICATIONS FOR AQUACULTURE VACCINE DEVELOPMENT

Supervisors: Dr Dan Macqueen & Dr David Stead
(Medical Sciences)

ABSTRACT

Infectious diseases pose a significant threat to the economic stability and expansion of finfish aquaculture. Vaccination is widely considered the best prevention strategy, but evaluation of immune protection typically relies on measuring immune gene expression at the mRNA level from terminally-acquired tissue samples. Due largely to post-translational modifications, mRNA expression may not correlate with tissue protein levels, providing an incomplete representation of the nature and kinetics of the immune response. In addition, inter-individual variation necessitates the use of large numbers of experimental animals to obtain sufficient statistical power. To overcome these limitations, we used a long-term, proteome-scale approach to identify and quantify changes in immune protein levels in rainbow trout (*Oncorhynchus mykiss*) plasma. These changes provide an indication of similar changes in other tissues, while also permitting non-lethal sampling. Although all experimental fish mounted an antigen-specific humoral response, the timing and magnitude of this, and the response trajectories of most immune-relevant proteins, differed significantly between individuals. Within this, certain immunological proteins were found to be more consistently expressed across all fish, suggesting that they could serve as useful biomarkers of an immune response. Together our data emphasise the importance both of judicious selection of immunological biomarkers, and of careful assessment of changes in the expression of these over longer-term study periods, when considering whether or not an effective antigen-specific immune response has been mounted. More generally, this approach offers a more accurate and holistic understanding of the fish immune response, while also dramatically reducing the number of experimental animals required.

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Diane Anderson-Aidoo

IN VITRO MODELS OF MACROPHAGE ACTIVATION IN TRYPANOSOME BRUCEI INFECTION

Supervisors: Dr Jeremy Sternberg & Dr Alan Bowman

ABSTRACT

Pathogenesis in African trypanosome infection is associated with a dysregulation of inflammatory regulation and an over-activation of type 1 macrophage responses. This is driven in part by components of the variant surface antigen, though other factors have been implicated. The mechanisms of this process are poorly understood. The requirement for MyD88 signalling provides circumstantial evidence of TLR signalling, but no direct evidence has been presented for this. We are developing experimental platforms to define the interaction of trypanosomes with innate immune receptors, with the aim of identifying key immunomodulatory parasite components. In an in vitro system using murine macrophage like RAW264 cells, we demonstrate that culture adapted T.brucei, conditioned medium and lysate caused upregulation of inflammatory cytokine production (specifically TNF-α and IL-6). We confirmed these findings in RAW264 reporter cells that express alkaline phosphatase after PRR signalling leading to NF-KB activation. We also have used TLR overexpressing HEK reporter cells to demonstrate that the parasites trigger signalling via TLR4 and TLR2 in vitro. We will use this system to identify the ligands involved in these responses.

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Sri Mulyati

WHY DO FOREST CONFLICTS PERSIST? A CASE STUDY FROM INDONESIA

Supervisors: Prof. Michelle Pinard & Prof. Steve Redpath

ABSTRACT

Protected areas in Indonesia are owned by the state and managed and controlled by the government. Often, however, protected forest areas are encroached illegally by the people for croplands or settlements. We investigated the history of the conflict in Kateri Wildlife Sanctuary (4.699,32 ha) in East Nusa Tenggara, one of the protected areas in Indonesia, under the management of the Natural Resource Conservation Agency East Nusa Tenggara (BBKSDA NTT), Ministry of Environment and Forestry (MoEF). The forest conflict in Kateri Wildlife Sanctuary emerged in 1999 between the refugees from Timor Leste (newcomer residents), BBKSDA NTT, and local communities (long-term residents), over the use of the forest land. The authority sees the encroachment as an illegal activity, while the newcomer residents feel they have the right to use the forest areas as sources for their livelihoods; the long-term residents feel that as the local community, they have more rights over the use of the forest than the newcomers and that the authority is not serious about enforcing the law. Since 2006, many parties have worked to resolve the conflict, however, the conflict persists. This study aims to investigate how individuals within the three main stakeholder groups (government, long term-resident, and newcomer resident) value the protected area, and how those values relates to their understanding of the conflict and motivation to engage with efforts to resolve the conflict.

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Rebecca L Smith

THE CONSERVATION OF THE HOODED CAPUCHIN (SAPAJUS CAY) AND THE UPPER PARANA ATLANTIC FOREST THROUGH SCIENTIFIC RESEARCH AND COMMUNITY ENGAGEMENT

Supervisors: Dr David Lusseau & Prof. Stuart Piertney

ABSTRACT

The Upper Paraná Atlantic Forest of Eastern Paraguay has been devastated by the encroachment of vast monocultures of soybean plantations. What little remains of the Paraguayan Atlantic Forest exists as small, isolated fragments in a matrix environment of soy fields, cattle ranches and human settlements. The hooded capuchin (*Sapajus cay*) is the only representative of its genus in Paraguay and little is known about its socioecology. This charismatic species is an excellent flagship species; appealing to the public, and the only primate that is almost completely restricted to the Atlantic Forest. Feeding and social ecological models will determine the effect of food availability on sociality. A spatial ecological model of range use, range overlap and territoriality will be developed to determine minimum forest fragment size sufficient to support multiple groups of hooded capuchins. Levels of disturbance will be categorised through detailed habitat surveys and the use of the forest strata in areas of different disturbance will indicate the monkeys' ability to adapt to degraded areas. Ethnoprimatological surveys will evaluate local knowledge of, and attitudes towards, primates in communities surrounding protected areas and to investigate the levels of anthropogenic pressures, such as hunting and logging, on primates in San Rafael National Park. Understanding the ecological needs of this species in fragmented and degraded forest, while promoting their need for conservation to the general public, will allow the development of a conservation strategy, which could be beneficial in the long term to the numerous other species of the Paraguayan Atlantic Forest.

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Deon Roos

THE BEST OF A BAD SITUATION: THE IMPACTS OF AGRICULTURAL CARBON EMISSIONS REDUCTION METHODS ON OUTBREAK RISKS OF PEST SPECIES

Supervisors: Prof. Xavier Lambin

ABSTRACT

Rodents are facultative farmland pests that can greatly reduce crop yields and impact food security during population outbreaks. Rodents are often controlled by spreading biocides, a management option that is expensive and environmentally costly because of effects on non-target species. An alternative, lower cost option could be to modify farming practices to reduce the availability of refuges for rodents and their subsequent colonisation of crops. Farming, however, must simultaneously meet multiple goals including the reduction of the carbon (C) emissions, water use, soil quality and soil erosion. Crop establishment through zero-tillage is promoted in many regions to reduce C emissions, moisture loss, and increase yields. It could, however, create favourable refuge habitats for fossorial rodent crop pests benefitting from burrow persistence and reduced disturbance between crop rotations. To what extent this farming practice has a short or enduring, local or larger scale impact on fossorial rodent crop use is as yet unknown. Using a 2 ha experimental field, we report here on an experiment that investigates how farming practices affect field use by a main European rodent pest between outbreak events. Our results show that tillage practices are much greater predictors of rodent occurrence compared to other aspects such as crop type or distance from source populations, supporting the hypothesis that tillage practices play a key role in common vole habitat distribution. The finding suggests that, when possible, switching from ZT to alternative tillage practices may reduce the risk of an outbreak.

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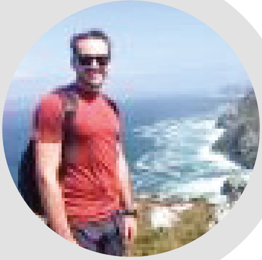
Michael Gallagher



NOVEL GENOMICS-LED APPROACHES TO CHARACTERISE VIRAL DISEASES IN ATLANTIC SALMON

Supervisors: Dr Dan Macqueen & Dr Yvetta Matejusova (Marine Scotland Science)

ABSTRACT

Global farmed production of salmonid fishes is worth >£8 billion annually, accounting for ~15% of total traded farmed fish. However, a major bottleneck limiting growth of this industry is loss caused by infectious viral diseases, which can have devastating economic impacts, with few effective therapeutics or preventative vaccines available. Genome-wide surveillance is currently lacking for salmonid viruses, despite the fact that such approaches have shown great promise for understanding pathogen dynamics and evolution, which can be applied to monitor and control disease outbreaks. This presentation reports my investigations into the usefulness of current-generation sequencing technologies to achieve accurate and economically-feasible whole genome sequencing of two distinct viruses: salmonid alphavirus and infectious salmonid anaemia virus. Long-range PCR and targeted sequence capture have been performed before sequencing using the MinION and Illumina platforms, respectively. These approaches have enabled us to recover full-length genomes for each virus, including ultra-deep coverage via the sequence capture approach. This study aims to better understand viral evolution, phylogeography and population dynamics. We hope that application of such data within the aquaculture industry will ultimately help control the spread of devastating diseases and contribute to economic and food security.

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Emmanuel Awulu

CHARACTERISATION AND OPTIMISATION OF SOS-*lux* BIOSENSORS *E. coli* C600 pPSL-1 AND *E. coli* DPD1718 FOR MUTAGENIC SCREENING OF POLYCYCLIC AROMATIC HYDROCARBONS (PAHs)

Supervisors: Dr Jerry Sternberg & Prof. John Speakman

ABSTRACT

The pyrolytic processes of organic-sourced compounds for energy are major sources of environmental contamination especially in countries with oil-driven economies and poor environmental laws and regulations. Most of these products of pyrolysis especially the polycyclic aromatic hydrocarbons (PAHs), have been described by International Agency for Research on Cancer (IARC) as carcinogens. There is need for rapid and relevant screening of these pollutants both chemically and biologically. Not only should the nature and quantity be known but so too should the causal carcinogenic nature. This study investigates *in vitro* methodologies using Mitomycin C (MMC) (DNA crosslinker) to characterise and optimise microbial *SOS-LUX* based biosensors *E. coli* C600 pPSL-1 and *E. coli* DPD1718. These will be used to screen selected PAHs in the absence and presence of liver homogenates extract (S9 mix) for potential toxicity and mutagenicity. *E. coli* C600 pPSL-1 and *E. coli* DPD1718 responded in a dose-dependent manner to MMC demonstrating its potentials in the screening of PAHs for toxicity and mutagenicity in a time effective manner. Moving forward, these assays will be calibrated against other cellular systems to place in context the potential impact of such pollutants in the environment.

www.abdn.ac.uk/staffnet/profiles/e.awulu/

Naveed Bhatti

DO OCCUPANCY MODELS WORK FOR MONITORING POPULATIONS OF SESSILE SPECIES?

Supervisors: Dr Andrea Britton, Dr Thomas Cornulier, Dr David Genney, Dr Ruth Mitchell, Dr Jackie Potts & Dr Sarah Woodin

ABSTRACT

The ability to accurately monitor population trends over time is vital for the conservation of rare species. However, detecting change in population sizes is challenging unless the changes are very large, or monitoring continues over a long time period. For rare lichens, previous studies using conventional methods have shown that large sample sizes (>2000 monitoring plots) are required, but even this may be insufficient to give accurate trends for many species.

An efficient approach is required that addresses the potentially large errors in population size estimates due to low detection rates and observer variability. A potential solution uses occupancy models. These models do not measure the true number of occupied units but estimate occupancy by accounting for imperfect detection and variation in observer detection rates using repeat survey data. Sessile, slow-growing organisms, like lichens, may be particularly suitable for such studies due to their low turnover between surveys. Repeat surveys for occupancy modelling may be carried out by a single observer, but especially with sessile organisms, their detection rate may vary spatially and temporally due to memory effects. This challenges standard model assumptions that detection is independent within and between surveys. Using different observers can overcome this but it introduces inter-observer variability errors.

Here we present a study using a population of artificial lichens to test the ability of occupancy models to estimate the true population size. We also discuss optimum numbers of sampling units and observers in relation to the accuracy of the estimate.

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Kathryn Grace Logan

ENVIRONMENTAL IMPACTS OF REPLACING CONVENTIONALLY FUELLED VEHICLES WITH ELECTRIC VEHICLES IN SCOTLAND: A UNIVERSITY CASE STUDY

Supervisors: Dr Astley Hastings & Prof. John D Nelson

ABSTRACT

A biennial transport survey conducted by the University of Aberdeen (UoA) collated data on commuting habits to and from the campus between 2006 and 2016. Analysis of commuting behaviour from staff at UoA was used to predict the effects of replacing conventionally fuelled vehicle (CFVs) with electric vehicles (EVs) on ecosystem services by comparing carbon dioxide (CO_2) estimations. Implications for land use have occurred due to the construction of new renewable energy infrastructure, coinciding with a reduction in fossil fuels.

Impacts on ecosystem services from electrifying transportation will be highly varied. The extent of this demand is reliant on several factors such as daily charging time, vehicle type and manufacturing processes. Switching to EV's from CFV's will have an impact on land use, for example construction of charging points and the required infrastructure. Development of renewable energy sources also need to be accounted for when establishing the true impacts on provisioning services.

Over this ten-year period, 52% of staff used a CFV as their main mode of transportation. CO_2 emissions produced from CFVs by staff decreased, with staff driving increasing. The decrease in emissions was linked to the vehicle age under EU legalisation to improve vehicle efficacy. This would suggest that current measures to reduce CO_2 emissions are effective and should continue.

Land use changes could result in new conflicts between transport, energy demand and ecosystem services before and after construction phases. This would also allow for consideration of the implications of climate change.

www.abdn.ac.uk/staffnet/profiles/k.logan/

Petra Lackova

KNOWLEDGE AND LEARNING IN WHITE-TAILED EAGLE CONFLICT

Supervisors: Prof. Steve Redpath, Dr Justin Irvine,
Dr Antonia Eastwood, Dr Juliette Young,
Dr Nils Bunnefeld, Dr Ross Lilley & Dr Rene Van Der Wal

ABSTRACT

Today around 100 breeding pairs of the white-tailed eagle nest in Scotland. After being driven to local extinction through persecution a century ago, the eagle population has been on the rise as a result of a series of reintroductions. While a success story in wildlife conservation, the re-introduction has escalated a conflict over white-tailed eagle predation of sheep, with wider discussions on the legitimacy of re-introductions. Our PhD project follows the progress of using adaptive co-management to address the conservation conflict. This management approach requires joint development, trialling and adapting management actions in a dynamic cycle of learning-by-doing. In conservation conflicts, such processes that foster collaboration, the generation of new knowledge and learning are thought to deliver conflict mitigation. Yet, evidence on the application of adaptive co-management in conservation conflicts is limited. Here, we address this gap by exploring how knowledge co-production effects learning and the integration of competing claims. We combine participant observation, document analysis, and in-depth interviews with members of partnerships responsible for managing the conflict. Preliminary findings indicate that fairer representation of diverse knowledge improved perceptions on the legitimacy of the management approach that had been dominated by scientific evidence. However, efforts to co-produce new knowledge led to disputes over expertise and credibility, which further reinforced continuing struggles over power imbalances, trust and transparency. We discuss the potential of collaborative monitoring to capture such unintended outcomes of the co-production process, promote learning, and improve peoples' ability to respond to change and develop more appropriate and effective interventions.

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Megan Simpson

IS OXIDATIVE STRESS INCREASED AT PEAK LACTATION IN C57BL/6 FEMALES?

Supervisors: Dr Sharon Mitchell &
Prof. John Speakman

ABSTRACT

The oxidative stress theory of ageing (OSTA), postulated by Harman in 1956, remains one of the most popular theories. The OSTA postulates ageing is a consequence of the accumulation of cellular oxidative damage. Oxidative stress is defined as an imbalance in the generation of reactive oxygen species and cellular defence systems such as the endogenous antioxidant enzyme, catalase. Reproduction, in particular lactation, is energetically demanding and according to the OSTA would result in the activation of defence systems as a consequence of an increased risk of oxidative stress. Previous research in this area has been inconclusive. The disparities may stem from the differences in tissues, assays and laboratory versus wild animals used. Here I report a comprehensive analysis measuring the activity of catalase in nine tissues.

Ten reproductive C57BL/6 female mice completed two successive parturitions. Females were sacrificed at peak lactation of the second parturition along with age-matched virgin mice (n=20). Brain, liver, kidney, heart, lung, small intestine, stomach, colon and brown adipose tissue (BAT) were harvested and snap frozen. The activity of catalase was measured using a spectrophotometer based assay. The Bradford assay measured protein content. Analysis revealed that catalase activity was significantly lower in the kidneys and BAT of lactating individuals compared to their non-reproductive counterparts ($t_{(27.9)}=2.5$, $p=0.019$; $t_{(28)}=4.3$, $p<0.001$ respectively). The reduction in catalase activity may indicate lower levels of oxidative stress in the kidneys or BAT however, further analysis of antioxidants as well as oxidative damage is required to clarify these results.

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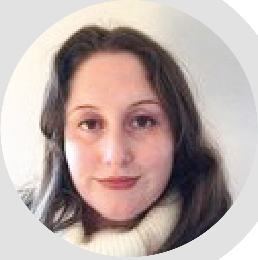
Frances Sandison

LIFE CYCLE ASSESSMENT OF THE SHETLAND PELAGIC FISHERY

**Supervisors: Dr C. Tara Marshall, Dr Astley Hastings,
Dr Beth Mouat & Dr Paul Macdonald**



ABSTRACT

With the global population estimated to rise to up to 9.7 billion people by 2050, and increasing pressure on food production systems by the changing climate, there is a growing interest in identifying and developing ‘climate smart’ food production. Because of the commonly reported low environmental impacts of small pelagic fisheries, the Scottish Pelagic fishing Industry has been identified as a potential for climate smart food development.

This project examines the climate related environmental impacts of the Scottish caught pelagic fish by means of an attributional Life Cycle Assessment. Initial stage analysis focused on the capture phase of the Shetland based section of the fleet. Primary data was obtained with suitable permissions by means of access to electronic log books, invoices and purchase ledgers, and by detailed interviews with skippers, book keepers and engineers. Secondary data was gained through the EcoInvent database where primary data could not be sourced. The Life Cycle assessment was undertaken using SimaPro 8.3 software.

Initial findings are in keeping with existing studies on the topic, showing global warming potential to be the biggest contributing category of the analysis. The burning of diesel fuel during the fishing stage was the biggest single contributor to the impact results, though prior to 2015 refrigeration leakage was also notable. Overall the findings of this study highlight Scottish pelagic fish as being a relatively low impact food source. Frances splits her time between the University of Aberdeen campus and that of the NAFC Marine Centre in Shetland.

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Jennifer Wardle

S.M.A.R.T. – A LOAD OF MANURE?

Supervisors: Prof. Jo Smith, Dr Davide Dionisi,
Dr Anke Fischer, Dr Lisa Avery & Dr David Vega-Maza

ABSTRACT

Rural communities in Ethiopia are almost 100% dependent on biomass burning to provide energy for cooking. Evidence suggests that increased demand for fuel, due to population growth, is causing an escalation in the use of ‘dirty’ fuels, such as crop residues and cow dung. This reduces the quantity of carbon and nutrients returned to the soil, posing a threat to food security.

Different initiatives to return more organic matter to the soil, while also providing access to energy were considered. A household survey (n = 112) was conducted across 4 ‘kebeles’ (community councils) in rural areas of the Halaba region. Results indicate that anaerobic digestion (AD) holds great potential, due to high levels of acceptance and its multifaceted benefits. Small-scale AD has been adopted in over 50 million households in Asia. This success has not been replicated in sub-Saharan Africa, partially due to shortage of water. Our research therefore attempts to devise technical solutions to ameliorate this problem using laboratory experiments with bench-scale reactors.

However, technical fixes alone cannot overcome the challenges of energy provision and food security, as they are embedded in a wider socio-economic structure. A second survey found that less than 19% of installed digesters were functional. Over 39% of digesters had never been functional, while others had been abandoned due to lack of support and follow-up. The findings suggest that implementers strive for success in meeting measurable, numerical targets, but fail to focus on quality, longevity or even start-up capabilities.

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Abubakar Umar Yuguda

CHROMIUM ASSIMILATION, SENSITIVITY AND RESPONSE BY MAIZE (*ZEA MAYS*) CV. F1 EARLIBIRD

Supervisors: Prof. Graeme Paton & Dr Lenka Mbadugha

ABSTRACT

Chromium is one of the most toxic metals in the environment. Effluent containing chromium salts from tannery industries are potentailly released into the environment without adequate treatment, together with other anthropogenic sources they can significantly contributed to chromium accumulation in soils. In this work a bioassay for maize (*Zea mays*) cv. F1 earlibird was used to measure germination response and root elongation sensitivity to chromium, followed by a hydroponic experiment to examine the uptake and accumulation of chromium species by maize. Seeds were exposed to chromium species (Cr (III) and Cr (VI)) at dose ranges 0 µM, 10 µM, 50 µM, 100 µM, 250 µM and 500 µM in a filter paper contact test for four days. The hydroponic consisted of testing response plant and accumulation of chromium after two weeks when treated with 0 µM, 50 µM, 100 µM, 200 µM and 300 µM Cr(III) and Cr(VI) prepared in Hoagland nutrient. Maize showed tolerance to Cr (III) in term of germination with the reduction at highest concentration of only 50%, but senstive to Cr (VI) with an 80% reduction in germination. The response of root elongation display similar pattern to germination with Cr (VI) presenting 70% inhibition at 50 µM and 80% inhibition for Cr (III) at 100 µM. Both the Cr species were accumulated by the plant and mostly retained in the root, Cr (III) was poorly translocted with 23.34 µg/plant dwt was found in the shoot compared to 104 µg/plant dwt retain in the root. Cr (VI) was transported to the shoot with 54.61 µg/plant dwt and 80.51 µg/plant dwt retain in the root. The assimilatrion of Cr (VI) by maize (*Zea mays*) *cv*. F1 earlibird is an indication of the plant potential tolerance and phytoextraction ability.

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Amira Alzadjali

TOXICITY AND BIOAVAILABILITY OF HEAVY METALS IN ENVIRONMENTAL SAMPLES

Supervisors: Prof. Graeme Paton & Dr Lenka Mbadugha

ABSTRACT

Certain heavy metals are essential for living organisms and are needed for normal growth and metabolism. However, at elevated concentration even these elements can prove harmful to biota and the environment. In recent years, genetically modified whole cell microbial biosensors have been used to determine the bioavailability of heavy metals, a technique that complements traditional analytical chemistry.

The aim of this study was to characterise selected biosensors and improve their sensitivity to heavy metals prior to their application to environmental samples. This is about understanding and refining the assay – a step often overlooked in this discipline. A Cu induced biosensor and a constitutively marked biosensor were optimized by testing them against different Cu concentrations and different washing media. Initially, two washing media, modified minimal media (MMM) and Davis minimal media (DMM) were used with zero percent of glucose and under Cu concentrations varying between 0.001 to 7 mg/L. Glucose (0.04% and 0.8%) was then added to the two media to test its impact on the bioassay sensitivity. This is a novel step as many papers suggest that glucose will bind with Cu rendering it non-bioavailable. The Cu induced biosensor washed by MMM with glucose (both 0.04% and 0.8%) had a LOEC of 0.005 mg/l Cu. The DMM without glucose washed biosensor had the lowest sensitivity with LOEC 0.05 mg/l. For the constitutively marked biosensor, the bioluminescence (RLU) values increased after washing with media that contained glucose. To better understand the process the performance respiration was measured and compared with the luminescence response. This dual reporting approach enabled the assays to be developed and devised such that it was both more sensitive and more reproducible.

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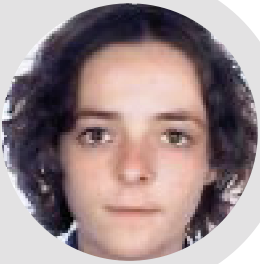
Anne-Sophie Bouchon

VERTICILLIUM WILT ON CACAO IN DR CONGO AND UGANDA

Supervisors: Prof. Steve Woodward & Prof. David Burslem



ABSTRACT

The most damaging cacao disease in the North West of the Democratic Republic of Congo and in West Uganda is Verticillium wilt, a vascular disease. Due to its important impact on production, a project in collaboration with Esco, the University of Aberdeen and Cocoa Research UK, was implemented in 2017. It is difficult to manage the causal fungus, *Verticillium dahliae*, as it can remain dormant in the soil as microsclerotia for many years (at least 14 years) and has many alternative hosts. Currently, the only way to manage it is by growing resistant varieties (as for olive, strawberry…). Little work has been done on Verticillium wilt of cacao, although it is reported in several countries: Brazil, Peru, Colombia and Uganda. Our goals are to assess and understand the distribution and diversity of the pathogen in DR Congo and Uganda. In addition, we seek to characterize the cacao germplasm currently grown in the region to assess the susceptibility of different cocoa landraces.
The characterization of *Verticillium dahliae* isolated in 2017 is also discussed.

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Ali Hroobi

A COMPARISON OF DEFORMED WING VIRUS VARIANT STRAINS IN THE INDIGENOUS AND IMPORTED HONEY BEE RACES IN SAUDI ARABIA

Supervisors: Dr Alan Bowman & Dr Ewan Campbell

ABSTRACT

Deformed wing virus (DWV) is a RNA-viral pathogen, transmitted by *Varroa destructor* to honey bees, and is one of the leading causes of honey bee colony loss worldwide. Saudi Arabia imports approximately 100000 hives annually. The presence of honey bee viruses have never been investigated in the exotic imported honey bee *Apis mellifera ligustica* or in the indigenous honey bee *Apis mellifera jementica*. The aim of this study was to assess and compare the titre of DWV variant strains under different climatic conditions, geographical locations and proximity between hives of different honey bee subspecies in Saudi Arabia. A real-time reverse transcription-polymerase chain reaction (qRT-PCR) assay was used to enable the specific detection and absolute quantification of DWV variants (DWV-A and –B). In some cases PCR products were sequenced and compared to the genetic databases. Indigenous bees, A. *jementica*, have a much lower incidence of DWV compared to the imported bee, A. *ligustica* but this was increased when A. ligustica colonies were kept in proximity to A. *jementica* colonies. DWV-B had the highest prevalence across all localities compared with DWV-A. DWV strains from A. *ligustica* had European-type sequences whereas A. *jementica* had Middle Eastern-type sequences. The information obtained from this study has important implications for enhancing our understanding of the distribution and prevalence of DWV variant strains in Saudi Arabia and viral titres and provides baseline data for future analyses to increase the awareness of long-term impacts of DWV on bee populations in the country.

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Jazmin Osorio-Mendoza

IMPACT OF ENERGY DEMANDS AND DIET ON FEEDING BEHAVIOUR

Supervisors: Prof. John Speakman, Dr Sharon Mitchell & Dr Catherine Hambly

ABSTRACT

Studies comparing the variation in protein content reported a positive relationship between the proportion of protein in diet and satiety (Stubbs 1995, Crovetti et al. 1998, Hill and Blundell 1986, Latner and Schwartz 1999). Food consumption increases metabolic rate and thermogenesis during and after meal. Consequently, a rise in resting metabolic rate (RMR), oxygen consumption and body temperature (T_b) may be involved in the process of hunger inhibition (Westerterp-plantenga et al. 1990, Westerterp-Plantenga et al. 1999, Westerterp-Plantenga et al. 2006). Meal size could be used therefore to determine when hunger will occur (Himms-Hagen 1995). In this study, the duration of hunger periods in C57BL/6 mice fed diets of different macronutrient composition was analyzed. This hypothesis was tested in three different conditions: 1. Varying levels of dietary protein at room temperature; 2. Elevated energy demands by wheel running; 3. Elevated energy demands by wheel running but simultaneously increased capacity to dissipate heat by exposure to cold (10±1°C). At room temperature, a significant difference was observed in the food consumption, food intake was high on the low protein compared to moderate and high protein (3.2 ±0.3g versus 2.7 ±0.4g or 2.5 ±0.4g respectively, $P<0.001$). Low protein mice also had significantly higher intake (2.9±0.5g) compared with moderate protein (2.5±0.1g, $p=0.002$) and high protein (2.4±0.3g, $p=0.001$) when mice were exposed to room temperature and running wheels. Contrary to this, there was no difference among the diets ($F_{2,20}=3.602$, $P=0.5$) in food intake when exposed to both low temperature and the running wheel. The prediction that mice will have longer satiety periods and/or smaller meals when fed HP can be accepted.

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