ABSTRACT BOOK

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CROSS DISCIPLINARY BIOLOGY ABSTRACTS

APC1 CONSERVATION PHYSIOLOGY: A CHANGING WORLD – PROBLEMS AND SOLUTIONS

ORGANISED BY: DR STEVEN COOKE (CARLETON UNIVERSITY, CANADA), DR CRAIG FRANKLIN (UNIVERSITY OF QUEENSLAND, AUSTRALIA), DR JODIE RUMMER (JAMES COOK UNIVERSITY, AUSTRALIA) AND DR CONNIE O'CONNOR (WILDLIFE CONSERVATION SOCIETY, CANADA)

SESSION SUPPORTED BY: CONSERVATION PHYSIOLOGY

APC1.1 PHYSIOLOGY MEETS ECOLOGY: CORAL REEF FISHES, PERFORMANCE, DISTRIBUTION, AND GLOBAL CHANGE

MONDAY 4 JULY, 2016 **11:00**

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Globally, coral reefs are more at risk to human-induced stressors - such as climate change, including ocean warming, acidification, and hypoxia events, and altered water quality due to coastal development - now, than at any other time in recorded history. Dramatic effects on fish performance, distribution, and overall ecosystem health are predicted. While the success of the fishes over their long evolutionary history is thought to have hinged on key adaptations for maintaining oxygen transport and physiological performance under challenging conditions, whether they possess the necessary plasticity and/or adaptations to keep pace with the large-scale, rapid changes plaguing their habitats today is not known. Moreover, the coral reef fishes - in particular - diversified more recently on the geological time scale, with most species radiating within the last 23 million years, a period characterised by relatively stable environmental conditions. Evolving and existing under stable environmental conditions may heighten the vulnerability of coral reef fishes to the rapidly changing conditions coral reefs are facing today. By harnessing geographic gradients, such as the latitudinal thermal profile along the Great Barrier Reef, and local extreme environments, such as the volcanic CO_2 seeps in the reefs of Papua New Guinea, as analogues for future change and integrating physiological, biochemical, and molecular techniques, the mechanisms that fish use to acclimate and adapt to these stressors can be identified. Such responses may become potential targets of natural selection and will determine which species and populations may be most at risk from climate change and other human-induced stressors.

APC1.2 THERMAL PERFORMANCE OF SIX EQUATORIAL INLAND FISHES FROM THREE CONTINENTS IN THE FACE OF CLIMATE CHANGE

MONDAY 4 JULY, 2016 **11:40**

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Global climate change interacts with and adds to a myriad of stressors exerting pressure on inland aquatic environments, and thus may impede the ability of these systems to support diverse and sustainable fish stocks. Inland fisheries are often critical to food security and poverty alleviation strategies of developing nations of the tropics. However, climate warming is predicted to have a greater impact on equatorial fishes than temperate species because they live in less seasonally fluctuating thermal environments and may live close to their upper thermal limits. However, this prediction has little empirical support. Therefore, we studied the thermal performance of six species of indigenous fishes, two species from each of three continents. We measured their capacity to supply oxygen to tissues at the prevailing temperatures as well as up to 4°C higher. We used established physiological endpoints to address a time sensitive conservation problem: how environmental change, specifically increases in water temperature, influence culturally and socio-economically important tropical freshwater fish species.

APC1.3 CONSERVATION AT A SLOW PACE: TERRESTRIAL GASTROPODS FACING FAST CHANGING CLIMATE

MONDAY 4 JULY, 2016 **11:55**

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The climate is changing rapidly, and terrestrial ectotherms are expected to be particularly vulnerable to changes in temperature, but also to an increase in extreme weather events. In conservation, physiological responses of terrestrial gastropods to such events are poorly studied. This is surprising, because terrestrial gastropods are the third-most successful group of terrestrial animals, and they are of biodiversity significance among litter dwelling species, as both invaders and native species, playing important roles in ecosystem function. When assessing threats of climate change, four different categories are used by the IUCN and can be applied to terrestrial gastropods: (i) Extreme temperature, (ii) droughts, (iii) storms and flooding, and (iv) habitat alteration. (i) In winter, terrestrial gastropods use different strategies to survive sub-zero temperatures in buffered refuges, like the litter or the soil. Absence of the insulating snow cover exposes species to high variability in temperature. The extent of cold tolerance might influence the potential of local extinction, but also of invasion. (ii) Physiological responses to droughts involve high-cost processes that protect against heat and dehydration. Some species decrease activity periods thereby reducing foraging and reproduction time. Costs and physiological limits increase mortality. (iii and iv) Although terrestrial gastropods are able to survive hypoxic conditions for several hours, storms and flooding as well as habitat erosion represent threats. Low capacity to migrate towards zones of favourable conditions might be the most limiting factor in the response to such climate change effects; specialist species are more vulnerable to habitat alteration than generalists.

APC1.4 DIVING IN A WARMING WORLD: THERMAL CONSTRAINTS ON THE DIVING CAPABILITIES OF THE ESTUARINE CROCODILE (*CROCODYLUS POROSUS*)

MONDAY 4 JULY, 2016 **12:25**

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Ectotherms face an ever-increasing risk of losing functional performance as ongoing climate change drives environmental temperatures beyond physiological limits. The threat of overheating may be particularly salient for ectothermic divers (e.g. crocodilians, marine/freshwater turtles and iguanas), with increased temperatures reducing their potential to perform obligate underwater activities. We explored the efficacy of physiological compensation in buffering the negative impacts of elevated temperatures on dive capacity in juvenile estuarine crocodiles (Crocodylus porosus). Crocodiles were exposed to one of three long-term thermal treatments, designed to emulate water temperatures under differing climate change scenarios (i.e. current summer, 28°C; 'moderate'; climate warming, 31.5°C; 'high' climate warming, 35°C), and dive capacity was subsequently tested. We show how metabolism, blood-oxygen carrying capacity and thermal acclimation treatments interact to determine the thermal sensitivity and plasticity of dive capacity. These findings are compared to body temperature and dive durations of free-ranging C. porosus.

APC1.5 AEROBIC SCOPE MEASURES REVEAL EXCEPTIONALLY HIGH TEMPERATURE PERFORMANCE IN JUVENILE CHINOOK SALMON, *ONCORHYNCHUS TSHAWYTSCHA*

MONDAY 4 JULY, 2016 **12:40**

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Understanding how temperature affects fish populations is crucial for effective conservation and management of fishes, yet the mechanisms of how changes in environmental temperature drive population declines is poorly understood. Furthermore, defining suitable thermal habitat for fishes is of fundamental importance to ensure population persistence, yet translating measures of thermal performance into regulatory numeric criteria remains difficult. Here, we tested the thermal performance of juvenile Chinook salmon across a range of environmentally relevant temperatures. Fish (initial size ca. 8.8 cm FL, 9 g) were acclimated to 14 or 20°C, and swim tunnel respirometers were used to measure basic oxygen requirements (routine metabolic rate; RMR) and oxygen demand when swimming maximally (maximum metabolic rate; MMR) at test temperatures ranging from 12 to 26°C. We calculated absolute aerobic scope (AAS=MMR-RMR), which is the capacity of each fish to supply oxygen to tissues above and beyond a basic routine need, as well as factorial aerobic scope (FAS=MMR/RMR). MMR, AAS, and FAS did not significantly differ between the two acclimation groups, while RMR was lower in fish acclimated to 20°C. Overall, RMR, MMR, and AAS increased as test temperatures increased, and AAS was maintained until mortality rates abruptly increased at 25°C. These results will be compared to those for other salmonids and the implications of our findings for informing management actions will be discussed.

APC1.6 MEASURING HOW A CHANGING PHYSICAL WORLD WILL IMPACT THE PERFORMANCE OF LARGE TERRESTRIAL MAMMALS

MONDAY 4 JULY, 2016 **13:55**

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Habitat fragmentation will preclude many large terrestrial mammals from shifting their range in the face of climate change. Predicting how trapped large mammals will respond to environmental change requires measurement of their sensitivity and exposure to changes in the environment, as well as the extent to which phenotypic plasticity can buffer them against the changes. Methods used to assess the responses of laboratory mammals to changing physical environments do not adequately predict how mammals living in their natural habitats, and subject to a complex array of stressors, will respond. In free-living mammals, behavioural modifications, such as a shift to nocturnal foraging or selection of a cool microclimate, may buffer the mammals against thermal and water stress, but may carry a cost, for example by reducing foraging time or increasing predation risk. Large mammals also use autonomic responses to buffer themselves against changing environments, but those buffers may be compromised by a changing physical environment. Restriction of food energy or water, likely to become more prevalent, especially in arid areas, with climate change, leads to a trade-off in which the precision of thermoregulation is relaxed, resulting in large daily fluctuations in body temperature. We propose use of the amplitude of the 24 h body temperature rhythm as an index of the performance status of mammals. Long-term biologging of body core temperature in large free-living mammals provides a tool to investigate which species will cope physiologically, or not cope, when confronting a changing physical world.

APC1.7 THERMAL BIOLOGY, BEHAVIOUR AND HEALTH OF URBAN HEDGEHOGS

MONDAY 4 JULY, 2016 **14:35**

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We have little understanding as to why some species thrive and others perish in urban habitat. Small mammals that tolerate urbanisation likely take advantage of biological traits that allow a quick response to environmental disturbance. The European hedgehog *Erinaceus europaeus* is a species that shows higher population densities in cities than in rural areas. The physiological mechanisms responsible for its ecological success in urban environments remain unknown, yet these data are crucial for informing conservation strategies. We aimed to address this knowledge gap by studying several physiological and behavioural variables of free-ranging individuals in a large city in northern Germany. Specifically, we monitored skin temperature, activity patterns, metabolic rates and nest microclimate throughout the year. Additionally, we assessed health risks using a long-term dataset collected at a hedgehog care station. Our results show that hedgehogs were flexible in some thermoregulatory and behavioural traits (e.g. individual differences in torpor patterns, temporal organisation of activity in gardens vs. parks, smaller home ranges and more simply constructed nests than rural conspecifics), while other variables remained more conservative (e.g. hibernation duration, rates of metabolism and rewarming from torpor). The primary health concerns were abscesses developed from physical injuries caused by anthropogenic hazards (e.g. fences, nets, pits) or gardeners disturbing nests. Our study provides important baseline data highlighting the importance of ecophysiological flexibility in the successful persistence of hedgehogs in disturbed environments, which will be useful for advising conservation strategies for small mammals in general.

APC1.8 OCEAN ACIDIFICATION AFFECTS LOCOMOTOR BEHAVIOUR AND LATERALIZATION OF A KEYSTONE MARINE MOLLUSC

MONDAY 4 JULY, 2016 **14:50**

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We investigated the effect of elevated levels of pCO_2 and temperature on locomotor behaviour during prey searching in the marine gastropod *Concholepas concholepas*, a rocky-shore keystone predator from the south-eastern Pacific coast of South America. Several locomotor and behavioural traits such as movement duration, decision time, obstacle avoidance and lateralization were measured using a T-Maze tank with a prey item positioned behind a barrier at the end of a runway. Two contrasting pCO_2 levels and temperatures representing present day (control conditions: pCO_2 500 µatm temperature 15°C) and near-future scenarios (pCO_2 1400 µatm and temperature 19°C) were used to rear the experimental individuals for 6 months. Regardless of the experimental conditions, no significant differences were found in the relative and absolute lateralization before and after 6 months of treatment. However, regardless of temperature, relative lateralization was significantly repeatable for animals tested after 6 months at control pCO_2, while elevated pCO_2 appears to affect the individual ability to retain relative lateralization at both experimental temperatures. We suggest that these effects may be related to malfunctioning at the neurotransmitter level caused by elevated pCO_2. Other measures of locomotor behaviour were not repeatable. However, movement duration and decision time were significantly increased and obstacle avoidance was decreased at elevated pCO_2, suggesting that elevated pCO_2 may have a negative effect on the locomotory behaviour and sensory ability of *C. concholepas* and similar species in the presence of a prey odour and thus decrease their ability to forage efficiently.

APC1.9 DIGESTION PHYSIOLOGY PREDICTS SENSITIVITY TO OCEAN ACIDIFICATION IN NON-CALCIFYING MARINE LARVAE

MONDAY 4 JULY, 2016 **15:05**

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Marine larval stages are often the weakest link when a species is confronted with acidified seawater as predicted for near future ocean acidification scenarios. Special attention has been dedicated to marine calcifiers which were predicted to be particularly sensitive to changes in seawater carbonate chemistry. However, recent studies demonstrated that some non-calcifying species also respond sensitively to acidified seawater but the underlying physiological processes remain unexplored.

We used larvae of the hemichordate (Ptychodera flava) and the sea star (Archaster typicus) to assess the effects of near future acidification levels on these non-calcifying marine organisms. Larval stages of the hemichordate respond highly sensitively (100% mortality after 8 days) to simulated near-future acidification levels. Microelectrode measurements demonstrated that this species has highly regulated alkaline (pH 10.13±0.04) digestive systems and metabolic rates increase 4-fold in response to acidified sea water. In contrast, the sea star larvae are less sensitive, showing only a slight developmental delay. Larval stages of A. typicus do not regulate gastric pH, but conform to the surrounding seawater.

Our results demonstrate that non-calcifying marine larvae may respond very differently to simulated near-future ocean acidification. Interspecific comparisons within the Ambulacraria indicate that the alkaline gastric pH and the rigidity to maintain gastric pH, and thus functionality, represents a unifying physiological feature for the sensitivity to ocean acidification. These findings highlight the importance of understanding fundamental physiological processes in marine species to generate hypothesis driven approaches to unravel potential adaptation mechanisms in times of rapid climate change.

APC1.10 THE EFFECTS OF SIMULATED OCEAN ACIDIFICATION ON GLOBAL TRANSCRIPTOMIC PROFILING IN A MARINE TELEOST

MONDAY 4 JULY, 2016 **15:20**

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Marine fishes exposed to end-of-the-century levels of ocean acidification (OA) show altered sensory behaviour that is likely to affect survival of both individuals and populations. Recently we have found that elevated CO_2 seawater can have a direct negative effect on the olfactory sensitivity of European sea bass (*Dicentrarchus labrax*), an economically important species. The main objective of the current research was to elucidate the molecular mechanisms underpinning the negative effects of OA on sea bass sense of smell using high-throughput sequencing. Sea bass were exposed for 2 and 7 days to either control (~400 µatm) or OA (~1000 µatm) seawater and 4-6 tissues replicate samples for each treatment were sampled from the olfactory epithelium (OE) and the olfactory bulb (OB-brain). Samples were sequenced using an Illumina HighSeq 2500 platform and a high quality de novo transcriptome was built using the Trinity pipeline. After 2 days of exposure, differentially expressed genes in the OE predominantly included those involved in sodium bicarbonate transport. After 7 days of exposure many more genes were differentially expressed including those involved in ion transport, peptidase activity, olfactory receptors, and alternative splicing. Overall fewer genes were differentially expressed in the OB. These data highlight the temporal dynamics of the response to OA at the molecular level underpinning the decrease in olfactory sensitivity. This study provides a better understanding of which genes are involved in coping with elevated CO_2, helping us predict which species are more likely to be affected by OA in the future.

APC1.11 STEPPING INTO THE WILD: TUNING OXIDATIVE BALANCE TO CHANGING ENVIRONMENTS

MONDAY 4 JULY, 2016 **16:10**

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The world is changing dramatically. This current pace of change is such that many organisms face rapid, severe and, often, unpredictable fluctuations in their physical and biotic environments. The emerging field of conservation physiology explores the physiological responses of organisms to human-induced environmental changes and attempts to develop physiological markers that can help to predict how these changes will impact on the viability of natural populations in the short- to, possibly, the long-term. Recent research in evolutionary ecology and conservation physiology has shown that the assessment of oxidative status metrics, such as oxidative damage and antioxidant molecules, may provide conservation practitioners additional physiological tools to predict individual perspectives of reproduction and survival and to assess a posteriori the effect of environmental stressors on fitness-related traits of a given species of conservation concern. To foster awareness of conservation practitioners, recent studies on the link between life-history traits and oxidative stress and on the impact of environmental perturbations on oxidative status metrics will be presented.

APC1.12 ANTI- AND PRO-OXIDANT GENE EXPRESSION AND OXIDATIVE DAMAGE IN THE BLUBBER TISSUE OF GREY SEAL (*HALICHOERUS GRYPUS*) PUPS DURING SUCKLING AND THE POST WEANING FAST

MONDAY 4 JULY, 2016 **16:40**

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The ability to respond adequately to stress is crucial to fitness and survival. Cellular defences play key roles in protecting against natural and anthropogenic stressors. Grey seal pups experience rapid physiological changes during development. They feed on 40-60% fat milk, triple in body mass during their first 18-21 days of life, and undergo a post weaning fast of up to four weeks. High fat intake, rapid fat deposition and prolonged food deprivation can stimulate reactive oxygen species production in other species. We used qPCR to investigate changes in gene expression of pro- and antioxidant enzymes in blubber tissue during suckling and fasting in pups on the Isle of May, Scotland, during October to December 2013 (n=15). Glutathione peroxidase (GPx), superoxide dismutase (SOD) and NADPH oxidase 4 (NOX4) were significantly upregulated during the post weaning fast, whereas catalase (CAT) and glutathione-S-transferase (GST) were down regulated during this period (LME; p>0.05). There was no difference in malondialdehyde (MDA) concentration, an index of oxidative damage, during suckling or fasting. MDA was not related to gene expression changes. This suggests antioxidant defences are important and effective in avoiding oxidative stress in blubber during fasting. These mechanisms mirror those in muscle tissue of fasting Northern elephant seal pups. Our data highlight that suckling is not associated with higher antioxidant gene expression, despite high fat intake and rapid fat tissue expansion. The ability of pups to avoid ROS production and oxidative damage in blubber under these conditions warrants further attention.

APC1.13 HYPERCAPNIA, BRAIN IONS AND FISH BEHAVIOUR: GABAERGIC NEUROTRANSMISSION IN FISHES APPEARS FINE TUNED TO THE PREVAILING CO_2 LEVELS IN THEIR HABITAT

MONDAY 4 JULY, 2016 **16:55**

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Projected rises in aquatic CO_2 levels appear to trigger acid–base regulatory responses in fishes that lead to altered GABAergic neurotransmission and disrupted behaviour. It is thought that changes in Cl- and HCO_3- gradients across neural membranes interfere with the function of GABA-gated anion channels (GABAA receptors). So far, such alterations have been revealed experimentally by exposing species living in low-pCO_2 environments (around 400 µatm), like many oceanic habitats, to elevated pCO_2 (usually around 1000 µatm). We have now explored the opposite situation, hypothesizing that fishes living in typically hypercapnic environments also display behavioural alterations if exposed to low CO_2 levels. This would indicate that ion regulation in the fish brain is fine-tuned to the prevailing CO_2 conditions. We quantified pH regulatory variables and behavioural responses of *Pangasianodon hypophthalmus*, a fish native to the hypercapnic Mekong River, acclimated to high-pCO_2 (30 000 µatm) or low-pCO_2 (400 µatm) water. The brain and blood pH were found to be actively regulated and the low-pCO_2 fish displayed significantly higher activity levels, which were reduced after treatment with gabazine, a GABAA receptor blocker. This indicates an involvement of the GABAA receptor and altered Cl- and HCO_3- ion gradients. Goldman calculations suggested that low levels of environmental CO_2 can cause significant changes in neural ion gradients in *P. hypophthalmus*. We conclude that brain ion regulation in fishes is fine-tuned to the prevailing ambient CO_2 conditions and is prone to disruption if these conditions change.

APC1.14 EXPRESSION OF GENES INVOLVED IN BRAIN GABAERGIC TRANSMISSION IN THREE-SPINED STICKLEBACK (GASTEROSTEUS ACULEATUS) EXPOSED TO NEAR-FUTURE pCO_2

MONDAY 4 JULY, 2016 **17:10**

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Changes in the function of the main inhibitory neuroreceptor GABAA has been suggested as general mechanism behind the sensory and behaviour alterations seen in ocean acidification studies on fish. When exposed to elevated pCO_2, fish regulate their acid-base balance by accumulating HCO_3- in the blood and tissues, accompanied by a release of H+ and Cl- to the water. These ion-regulatory changes might affect the ions gradient across the neural membranes and interfering with the GABAA receptor function, possibly making it excitatory rather than inhibitory. We here present the first comprehensive analysis of expression of genes involved in the GABAergic transmission and of genes involved in transmembrane ions transport in fish brain. mRNA transcripts were quantified in brains of three-spined stickleback (Gasterosteus aculeatus) kept under control (333 ± 30 µatm CO_2) or high CO_2 tensions (991 ± 57 µatm CO_2) for 43 days. In the high-CO_2 group there was an increased mRNA expression of some GABAA receptor subunit isoforms. Moreover, exposure to elevated CO_2 altered the expression of NKCC1 and NDAE, two transporters involved in regulating intracellular Cl- and in HCO_3-neurons.

APC1.15 SPECIES INTRODUCTIONS IN DESERT RIPARIAN ECOSYSTEMS: THE CASCADING IMPACTS OF LOCAL ADAPTATION AND RESOURCE ALLOCATION STRATEGIES ON BIOTIC INTERACTIONS

TUESDAY 5 JULY, 2016 **10:30**

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Riparian ecosystems in desert regions of North America are recognized as hot spots of biodiversity that support many threatened species, and are located in a region that is suffering among the highest rates of climate change. *Populus fremontii* is a foundation species of this critical habitat, but is threatened both by climate change and the non-native tree / shrub *Tamarix* spp. in large part because both are known to disrupt the symbiotic relationship between *P. fremontii* and mycorrhizal communities. The recent introduction of a specialist herbivore (D*iorhabda* spp.) as a biocontrol of *Tamarix* is significantly altering the relationship between this non-native shrub and its habitat. *Diorhabda* feeds exclusively on *Tamarix* foliage resulting in varying rates of dieback and mortality depending on genetic variation in resource allocation strategies and landscape-scale growing conditions. We anticipate that 1) defoliation by *Diorhabda* will significantly reduce the negative impact of *Tamarix* on *P. fremontii* / mycorrhizal associations, 2) certain *P. fremontii* genotypes will be more positively impacted by *Tamarix* dieback and mortality than others due to various selection pressures to cope with competition, stress and *Tamarix* presence, and 3) Spatial variability in climate and climate change will modify the capacity for *Tamarix* to survive episodic defoliation by *Diorhabda* that will also modify the complex interaction between *Tamarix* and *P. fremontii* and its associated soil communities.

APC1.16 UNDERSTANDING THE CAUSES OF GLOBAL AMPHIBIAN DECLINES: HOW IMPORTANT IS ENVIRONMENTAL CONTEXT?

TUESDAY 5 JULY, 2016 **11:10**

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Around the world, hundreds of amphibian populations are disappearing despite the availability of pristine habitat. These mysterious population declines exemplify the severity of the current biodiversity crisis and present one of the greatest challenges for conservation: they demonstrate that the influence of humans on the environment is so pervasive that even species in protected habitats are not safe from extinction. One possible explanation for these declines is exposure to increased ultraviolet-B radiation (UVBR) caused by human-induced ozone depletion. Studies on the impact of increased UVBR have predominantly considered UVBR in isolation of other environmental factors. Such studies have shown that exposure to UVBR is detrimental to the health of amphibians, causing mortality, malformations and reduced growth. In nature, however, amphibians often contend with numerous abiotic and biotic factors simultaneously. For instance, amphibians must cope with variations in temperature and aquatic oxygen while also competing with others for resources and avoiding predation, all of which can be detrimental to their health and survival. Importantly, such natural challenges are present in the pristine habitats where amphibians are declining. I will present examples of our research showing how these natural challenges alter the impact of UVBR on amphibians. I will also discuss how the effect of UVBR combined with other factors varies across response variables and across levels of UVBR. Our research demonstrates that consideration of additional environmental factors together with anthropogenic factors is vital for understanding the contribution of human-induced environmental change to biodiversity loss.

APC1.17 EVIDENCE FOR CHRONIC STRESS IN MARGINAL POPULATIONS: A CASE STUDY OF THE CAPE MOUNTAIN ZEBRA

TUESDAY 5 JULY, 2016 **11:25**

JESSICA LEA (UNIVERSITY OF MANCHESTER, UNITED KINGDOM), SUSANNE SHULTZ (UNIVERSITY OF MANCHESTER, UNITED KINGDOM), GRAHAM KERLEY (NELSON MANDELA METROPOLITAN UNIVERSITY, SOUTH AFRICA), SUE WALKER (CHESTER ZOO, UNITED KINGDOM), JOHN JACKSON (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), SHELBY MATEVICH (UNIVERSITY OF MANCHESTER, UNITED KINGDOM)

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Many species have undergone long-term range contraction caused by anthropogenic activities, resulting in their conservation in areas of low ecological suitability. A core issue lies in the active management of a species in suboptimal habitat due to an inaccurate perception of its historical distribution and ecology. The Cape mountain zebra has been identified as one such species, with several populations classified as 'ecological refugees'. These populations are characterized by low habitat and diet quality and poor performance. Establishing the links between habitat marginality, population performance and individual physiology is crucial for managing vulnerable populations. We use faecal hormone sampling techniques to assess the physiological status of Cape mountain zebra individuals in populations with both high and low quality habitat. Faecal glucocorticoid levels were significantly elevated in populations with poor habitat quality and performance. In addition, we found a significant interaction between habitat quality and rainfall season, where during the dry season faecal glucocorticoids remain high across all populations. Our results indicate that populations of Cape mountain zebra in ecologically unsuitable conditions are chronically stressed, and that this may be negatively impacting reproductive rates. This highlights the potential cost of confining a species to marginal habitat, whether knowingly or not, and is particularly alarming when considering critically endangered species that have only one or a few populations left. We emphasize the importance of taking into account historical distribution and ecology when undertaking conservation planning on any scale.

APC1.18 ENVIRONMENTAL DRIVERS OF IMMUNE FUNCTION IN ECTOTHERMS

TUESDAY 5 JULY, 2016 **11:40**

REBECCA L CRAMP (UNIVERSITY OF QUEENSLAND, AUSTRALIA), LESLEY A ALTON (MONASH UNIVERSITY, AUSTRALIA), CRAIG E FRANKLIN (UNIVERSITY OF QUEENSLAND, AUSTRALIA)

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As a consequence of rapid environmental change, the world is facing its sixth major biological extinction event. A recent surge in the rate of emergence of infectious diseases of wildlife has contributed significantly to this biodiversity crisis. In addition to the cost to biodiversity, there is a significant risk to human health from emerging infectious diseases with a wildlife origin (zoonoses), with more than 60% of recent human emerging infectious diseases being zoonotic. Consequently, understanding the drivers underpinning the emergence of novel diseases in animals is important as a ‘first line of defence’ for managing the emergence of potential zoonotic diseases of humans. How organisms respond immunologically to pathogens and how their environment shapes this response is one consideration likely to determine the impact of emerging diseases, not only at the level of the organism, but at the community and species levels as well. Recent work in our laboratory has examined two key environmental drivers of physiological function, temperature and solar UV-B radiation, and their influence on various aspects of immune function and disease susceptibility in frogs and fish. In this presentation, we will present several examples of how these two key environmental factors affect or influence aspects of immune function and how the effect of one can be modulated by the presence of the other.

APC1.19 MALE MONKEYS GET KICKED WHEN THEY’RE DOWN: INCREASED INJURY RATES DURING FEVERS

TUESDAY 5 JULY, 2016 **12:10**

ROBYN S HETEM (UNIVERSITY OF THE WITWATERSRAND, SOUTH AFRICA), RICHARD MCFARLAND (UNIVERSITY OF WISCONSIN–MADISO, UNITED STATES), DUNCAN MITCHELL (UNIVERSITY OF THE WITWATERSRAND, SOUTH AFRICA), SHANE K MALONEY (UNIVERSITY OF WESTERN AUSTRALIA, AUSTRALIA), PETER S HENZI (UNIVERSITY OF LETHBRIDGE, CANADA), LOUISE BARRETT (UNIVERSITY OF LETHBRIDGE, CANADA), CHRISTOPHER YOUNG (UNIVERSITY OF SOUTH AFRICA, SOUTH AFRICA), ANDREA FULLER (UNIVERSITY OF THE WITWATERSRAND, SOUTH AFRICA)

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Fevers during infection, and the associated sickness behaviours, often are considered an adaptive response by the host. Yet, within a social context it may be advantageous to suppress sickness behaviours, such as lethargy and anorexia, to improve reproductive success or social status. We implanted data loggers to obtain continuous, remote measures of core body temperature of free-living vervet monkeys (Chlorocebus pygerythrus) and conducted concurrent behavioural observations. We detected 63 spontaneous febrile episodes (defined as a 0.5°C elevation in mean 24h body temperature) in 30 individuals (16 males) over a five-year period. Fevers lasted between 2 and 14 days and were characterized by an upward displacement of the nychthemeral rhythm of body temperature. Mean 24h body temperature increased significantly from 37.9±0.3°C when monkeys were afebrile to 38.9±0.3°C when they were febrile (t_{29}=18.6, $P<0.0001$). Mean 24h minimum body temperature increased by 0.9±0.4°C and 24h maximum body temperature increased by 0.8±0.3°C during the fever. Average maximum body temperature reached during the fevers was 40.6±0.5°C. Injury rate was an order of magnitude higher when the monkeys were febrile than when they were afebrile, and occurred when the monkeys had established fevers. Male monkeys during the breeding period sustained an injury every 12 febrile days. Male monkeys appear to be able to detect when other males are sick and act to reduce the competitiveness of those males. Knowledge of how social factors modulate the welfare of infected animals is an important aspect to consider in understanding ecological implications of disease.

APC1.40 LIFE ON A MISMATCHED DIET: LESSONS FROM FARMED ATLANTIC SALMON

THURSDAY 7 JULY, 2016 **12:25**

ELZBIETA KROL (UNIVERSITY OF ABERDEEN, UNITED KINGDOM), ALEX DOUGLAS (UNIVERSITY OF ABERDEEN, UNITED KINGDOM), CHRISTOPHER J SECOMBES (UNIVERSITY OF ABERDEEN, UNITED KINGDOM), SAMUEL AM MARTIN (UNIVERSITY OF ABERDEEN, UNITED KINGDOM)

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Increasing numbers of animals are exposed to diets they did not evolve to digest, absorb and utilise. These evolutionary mismatched diets typically come with novel sets of toxins, antigens and microbial challenges, which have been implicated in the predisposition to gut inflammation (enteritis) and other gastrointestinal diseases in humans, zoo animals and pets, domesticated livestock and poultry. Evidence is also growing that many wild animals are facing dietary shifts and nutritional challenges resulting from global climate change. Understanding the impacts of mismatched diets on animal health and performance has been limited by the lack of rodent models for diet-induced enteritis. Here, we argue that important insights can be gained by studying carnivorous fish that are typically fed plant protein diets in aquaculture settings. We examined the gut transcriptome responses to different plant proteins in Atlantic salmon and demonstrated that these responses were plant-specific, with relatively few transcriptomic alterations common for all plant proteins used. When different plant proteins were simultaneously included in the diet, they induced less extensive alterations of the gut transcriptome than single plant protein diets. The mixed plant protein diets were also associated with improved body composition of fish relative to the single plant protein diets, providing evidence for a link between the magnitude of changes in the gut transcriptome and whole-animal performance. Our results indicate that farmed fish provide an attractive animal model for investigating the complex interactions between the digestive system and evolutionary mismatched diets in vertebrates, at both whole-animal and molecular levels.

APC1.20 PATHOGENS OF PLENTY: INTEGRATION OF MOLECULAR, PROTEOMIC, CELLULAR, AND ORGANISMAL-LEVEL ASSESSMENTS OF WILD MIGRATING SALMON TO DISCERN THE PATHOGENIC POTENTIAL OF DOZENS OF MICROBES

TUESDAY 5 JULY, 2016 **13:40**

KRISTI M MILLER (PACIFIC BIOLOGICAL STATION FISHERIES AND OCEANS CANADA, CANADA), ANGELA D SCHULZE (PACIFIC BIOLOGICAL STATION, CANADA), AMY TABATA (PACIFIC BIOLOGICAL STATION, CANADA), SHAORONG LI (PACIFIC BIOLOGICAL STATION, CANADA), KARIA K KAUKINEN (PACIFIC BIOLOGICAL STATION, CANADA), EMILIANO DI CICCO (PACIFIC BIOLOGICAL STATION, CANADA), SCOTT G HINCH (UNIVERSITY OF BRITISH COLUMBIA, CANADA), KEN M JEFFRIES (UC DAVIS, UNITED STATES), NATHAN FUREY (UNIVERSITY OF BRITISH COLUMBIA, CANADA), ARTHUR BASS (UNIVERSITY OF BRITISH COLUMBIA, CANADA), AMY TEFFER (UNIVERSITY OF VICTORIA, CANADA), BRIAN RIDDELL (PACIFIC SALMON FOUNDATION, CANADA)

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Wild salmon populations have been declining across multiple species in many countries around the world. Cumulative and/or synergistic stressors affecting salmon in their vulnerable smolt out-migration stage are suspected to be important determinants of year-class strength, but which factors are most important is still not known. A role for infectious disease in salmon declines is suspected, but insufficient data exists on disease impacts on wild salmon to determine which, if any, diseases may cause substantial losses in the ocean. We devised a multidisciplinary program integrating broad-scale microbe monitoring with physiological impact assessments at the molecular, cellular and organismal levels to tackle these questions. Central to the research was the development of a high throughput pathogen monitoring tool based on microfluidic quantitative PCR to simultaneously detect dozens of salmon pathogens. This platform is being applied to determine which pathogens causing diseases in salmon worldwide are carried by BC salmon, to assess their distributional shifts over time and space in wild, enhancement hatchery, and farmed salmon, and to identify pathogens associated with salmon survival in tracking, predation, and stress-challenge studies. Disease phenotypes are being identified by merging pathogen monitoring with host gene expression profiling and histopathology. Ultimately, this research will identify pathogens of greatest biosecurity risk to wild salmon.

APC1.21 LATE-PROGRESSION AMOEBIC GILL DISEASE IMPAIRS TEMPERATURE TOLERANCE IN INFECTED ATLANTIC SALMON *(SALMO SALAR)*

TUESDAY 5 JULY, 2016 **14:20**

ALYSSA BOWDEN (IMAS UNIVERSITY OF TASMANIA, AUSTRALIA), T D CLARK (IMAS UNIVERSITY OF TASMANIA, AUSTRALIA), S J ANDREWARTHA (CSIRO AGRICULTURE, AUSTRALIA), N ELLIOTT (CSIRO AGRICULTURE, AUSTRALIA), P FRAPPELL (IMAS UNIVERSITY OF TASMANIA, AUSTRALIA)

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Amoebic gill disease (AGD) is the most prevalent health issue affecting Atlantic salmon industries in southeast Tasmania and is a major cause of mortalities in farmed populations. The amoeba attach solely to the gills and cause hyperplastic lesions which generally lead to lamellar fusion. AGD-associated mortality is presumed to be related to respiratory failure due to the loss of functional gill area, but this has yet to be conclusively confirmed. Tasmanian outbreaks proliferate in the summer months in parallel with increasing temperature. Infected fish suffer higher mortality rates at high temperatures, so this study took the first step to investigating the host response to AGD under elevated temperatures through a critical thermal maxima (CT_{max}) test. It was hypothesised that infected individuals would be less tolerant to elevated temperatures than naive fish. Water temperature was increased at a rate of 2°C/hr and CT_{max} was recorded at loss of equilibrium. Subsequently, fish were gill scored using the standard farm criteria to determine level of infection and blood samples were taken to measure blood parameters and stress hormones. Preliminary results support our hypothesis of lowered thermal tolerance in diseased individuals, but this was only manifested once the disease had progressed substantially such that gill scores reached high values of 4–5.

APC1.22 LONG-TERM ENVIRONMENTAL INFLUENCE UPON HYPOXIA TOLERANCE IN FISH: DOES THE CARDIORESPIRATORY SYSTEM PLAY A ROLE?

TUESDAY 5 JULY, 2016 **14:35**

GUY CLAIREAUX (UNIVERSITÉ DE BRETAGNE OCCIDENTALE, FRANCE), FLORIAN MAUDUIT (UNIVERSITÉ DE BRETAGNE OCCIDENTALE, FRANCE), HÉLÈNE OLLIVIER (UNIVERSITÉ DE BRETAGNE OCCIDENTALE, FRANCE), NICOLAS LE BAYON (IFREMER, FRANCE), OLIVIER MOUCHEL (IFREMER, FRANCE), JOSÉ L ZAMBONINO (IFREMER, FRANCE)

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Using a population of 400 individually tagged European seabass we designed an experiment with the objective of travelling down the levels of biological complexity to highlight some entry points of the environmental influence upon fish tolerance to hypoxia. This experiment spanned over 2 years and targeted the cardiorespiratory system. Young-of-the-year seabass were submitted to a hypoxia challenge test which allowed the determination of individuals' incipient lethal oxygen saturation. Our experimental population was then divided in two subgroups. One subgroup was kept in the laboratory (LAB), while the second was transferred to semi natural tidal ponds (POND) for a period of six months. Fish were then recovered from the ponds, brought back to the laboratory and regrouped with those that remained in the laboratory. After 4 months under common garden conditions, we observed that fish from the POND group displayed higher tolerance to hypoxia than fish from the LAB group, and that this difference persisted after 1 year. Respirometry showed no difference between LAB and POND with regards to maximal and standard metabolic rates as well as critical oxygen level. ECG of anaesthetised individuals submitted to a standardized hypoxia revealed that fish from POND and LAB groups responded differently. However, maximal heart rates measured following atropine injection were similar. Ventricular strip preparations tested under hypoxic conditions showed no difference between POND and LAB. We conclude that the cardiorespiratory system poorly explains the improved hypoxia tolerance observed in the POND. Capacity for metabolic depression and anaerobic metabolism will have to be examined.

APC1.23 PHENANTHRENE IS THE CARDIOTOXIC POLYCYCLIC AROMATIC HYDROCARBON

TUESDAY 5 JULY, 2016 **14:50**

HOLLY SHIELS (UNIVERSITY OF MANCHESTER, UNITED KINGDOM), FABIEN BRETTE (UNIVERSITY OF BORDEAUX, FRANCE), GINA GALLI (UNIVERSITY OF MANCHESTER, UNITED KINGDOM), CAROLINE CROS (UNIVERSITY OF BORDEAUX, FRANCE), JOHN INCARDONA (NOAA, UNITED STATES), NATHANIEL SCHOLZ (NOAA, UNITED STATES), BARBARA BLOCK (STANFORD UNIVERSITY, UNITED STATES)

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The Deepwater Horizon disaster drew global attention to the toxicity of crude oil and the potential for adverse health effects among spill responders and the numerous animals in the northern Gulf of Mexico. Crude oil from the spill released complex mixtures of polycyclic aromatic hydrocarbons (PAHs) into marine areas including pelagic spawning habitats for tunas, billfish, and other ecologically important top predators. PAH exposure of whole fishes during development and exposure to heart cells from adults, reveal the heart is vulnerable to oil-toxicity. However, the precise PAHs that cause cardiotoxicity, as well as the mechanisms underlying contractile dysfunction, are not known. Here we used electrophysiological and confocal microscopy techniques in tunas (Pacific bluefin tuna, Thunnus Orientalis, yellowfin tuna, Thunnus albacares) and Pacific mackerel (Scomber japonicus) to demonstrate that phenanthrene, a PAH with a benzene 3-ring structure, is the key compound disrupting cardiac function. Phenanthrene prolongs the action potential due to potassium channel blockade and decreases the amplitude of the cellular Ca2+ transients that drive force generation. Because there are many important environmental sources of phenanthrene in addition to petroleum based oil spills, including urban air pollution, our findings suggest that phenanthrene may be a major worldwide cause of vertebrate cardiac dysfunction.

APC1.30 THE ENERGETIC TRIANGLE: A PHYSIOLOGY-BASED LIFE-HISTORY CLASSIFICATION SCHEME FOR REEF CORALS

TUESDAY 5 JULY, 2016 **16:00**

MIA HOOGENBOOM (JAMES COOK UNIVERSITY, AUSTRALIA)

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Conserving and restoring ecosystems requires understanding of how environmental change affects populations and communities. Many of the environmental changes associated with global warming impact on organisms at the physiological level and, therefore, predicting changes in population dynamics and community structure requires the effects of environmental change on the physiology and demographic rates of individuals to be quantified. Here I describe a novel functional classification of stony corals, the ecosystem engineers of coral reefs, that is based explicitly on physiological energetics and that helps to bridge between effects on individual organisms and on communities. All of the myriad functional classification schemes described in the literature are founded on the underlying concept that organisms apportion resources between reproduction, survival and growth. However, few of these schemes explicitly link organismal traits to energy allocation. In this study I present new data, and review several decades of literature data, to identify patterns of energy acquisition and allocation among stony corals, and to ordinate species based on their energy allocation to structural tissue biomass, reproductive tissues and skeleton growth (a metric for space acquisition by these organisms). I then explore how the position of species in this ordination changes as individuals grow over time and, using general relationships between temperature and metabolic rates, I demonstrate how patterns of energy allocation might change to maintain e.g. growth at the expense of reproduction in a changed environment.

APC1.31 METABOLIC AND GROWTH EFFECTS OF DAILY ACUTE HEAT CHALLENGE ON A COLD WATER PISCIVORE

TUESDAY 5 JULY, 2016 **16:30**

MATTHEW GUZZO (UNIVERSITY OF MANITOBA, CANADA), NEIL MOCHNACZ (FISHERIES AND OCEANS CANADA, CANADA), TRAVIS DURHACK (FISHERIES AND OCEANS CANADA, CANADA), BENJAMIN KISSINGER (UNIVERSITY OF MANITOBA, CANADA), JASON TREBERG (UNIVERSITY OF MANITOBA, CANADA)

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Temperature is an important environmental factor influencing fish physiology. In small north-temperate lakes, nearshore prey makes up the majority of cold water piscivore diets; however, because these lakes thermally-stratify during summer, nearshore regions often exceed the optimal temperature limits for most cold water piscivores, but not for the prey. To cope, piscivores make short excursions into the nearshore to feed and quickly return to cold water to digest. With air temperatures predicted to increase, many historically-isothermal northern lakes may begin to stratify and lakes that already stratify may achieve longer, warmer stratified periods. To understand the impact of these limnological changes on cold water fish, we performed a lab experiment to test: (1) if daily short excursions into supra-optimal temperatures impact growth and metabolic rate; and, (2) if increasing supra-optimal temperatures would strengthen impacts. Juvenile lake charr (Salvelinus namaycush) were held at ~10 °C (optimum temperature) with treatments exposed to 17 or 22 °C for ~5 min daily over 64 days. All groups were offered a ration of ~1.5% body mass daily. Heat exposures were mild but recurrent, with treatment fish subjected to supra-optimal temperatures for only ~1% of the experimental duration. Control fish consumed more food than the daily heat challenged fish but growth was similar across treatments suggesting the daily acute heat challenge may increase food conversion efficiency. Standard metabolic rate was similar among treatments; however, control fish had lower maximum metabolic rates and lower metabolic scope than fish that were exposed to warm water.

APC1.32 ARE RESPIRATORY EFFECTS OF GLOBAL WARMING AND OCEAN ACIDIFICATION EXPLAINED BY A UNIFYING OCLTT CONCEPT?

TUESDAY 5 JULY, 2016 **16:45**

SJANNIE LEFEVRE (UNIVERSITY OF OSLO, NORWAY)

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The changing climate prompts a desire to understand and thereby a need to study and ultimately predict the outcome for marine ectothermic animals. The concept of "Oxygen and Capacity Limited Thermal Tolerance" (OCLTT), which is inspired by the Fry paradigm of a bell-shaped "increase-optimum-decrease"-type response of absolute aerobic scope (AAS) to increasing temperature, while also including proposed negative and synergistic effects of elevated CO_2 levels, has been suggested as a unifying framework. In my talk, I will present a meta-analysis of available data examining the following questions: does AAS in general follow a bell-shaped curve i.e. is there always an optimum temperature? Does CO_2 in general cause an increase in resting oxygen demand ($\dot{M}O2_{rest}$), and thereby reduce AAS? And is the combined effect of CO_2 and temperature on $\dot{M}O2_{rest}$ and AAS generally larger than expected from their sum i.e. is the interaction synergistic? I calculated log response ratios to be able to compare results from a wide range of studies, including both fish and invertebrates. When examining the data as a whole, from the perspective of the above predictions, it becomes evident that there is a heterogeneity that is difficult to reconcile with the idea of a single unifying principle. While it is clear that climate change can have severe physiological effects, and that AAS might be a useful variable for predicting the outcomes in some cases, malfunction of other physiological mechanisms must be considered and generalizations such as the OCLTT concept should be used with caution.nservation interventions. This presentation will explore the role of experimental biology in evidence-based conservation.

APC1.45 WHY IS THE HATCHING SUCCESS OF GREEN TURTLES ON RAINE ISLAND SO LOW?

TUESDAY 5 JULY, 2016 **17:00**

DAVID T BOOTH (UNIVERSITY OF QUEENSLAND, AUSTRALIA), ANDY DUNSTAN (QUEENSLAND GOVERNMENT, AUSTRALIA)

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Raine Island is the biggest green turtle rookery in the world. However, in recent years the hatching success of nests has been exceeding low < 30%, with considerable death occurring very early in incubation. Initially increased frequency of nests being inundated with sea water at high tides due to sand loss from the beach was hypothesised to be responsible for this high within nest mortality. However, a beach manipulation that increased the level of nests well above the water inundation level also resulted in a high level of within nest mortality. We hypothesis that either low oxygen gas tensions and/or high microbial load may be responsible for high within nest mortality and have begun measurements to investigate if low oxygen tensions are associated with high mortality. Interestingly, hatching success increased remarkably in a low nest density year, suggesting that a nest density dependent process is involved in determining the within nest mortality of developing embryos.

APC1.34 SENTINEL OYSTERS: MONITORING REAL-TIME PHYSIOLOGY TO INFORM AQUACULTURE PRODUCTION

THURSDAY 7 JULY, 2016 **09:40**

SARAH ANDREWARTHA (CSIRO AGRICULTURE, AUSTRALIA), JOHN W MCCULLOCH (CSIRO MARINE LABORATORIES, AUSTRALIA), ANDREW HELLICAR (CSIRO MARINE LABORATORIES, AUSTRALIA), PETER B FRAPPELL (CSIRO AGRICULTURE, AUSTRALIA), NICK G ELLIOTT (UNIVERSITY OF TASMANIA, AUSTRALIA)

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Monitoring stock welfare and productivity remains a key challenge for most aquaculture sectors. Integrating sentinel animals fitted with biosensors that monitor heart rate and other relevant variables with environmental sensing can address this challenge. Timely estimates of daily energy expenditure and indicators of stress/pathology resulting from multi-parameter environmental changes can be provided and enable management actions. A thorough understanding of how physiology and behaviour respond to the variety of environmental and production stressors experienced is required to enable on-farm data to be interpreted. Here we present the effects of temperature, salinity and dissolved oxygen on the relationship between heart rate and metabolic rate in summer acclimated Pacific oysters (*Crassostrea gigas*). The laboratory calibration data are used to predict daily energy expenditure in sentinel oysters in two locations: on a commercial lease and in a more estuarine environment. Integrating these into production and wellbeing models drive decision support systems that predict animal condition and wellbeing in the context of current and projected environmental conditions.

APC1.35 IMPACT OF TEMPERATURE AND ACIDIFICATION ON HYPOXIA TOLERANCE OF NORTHERN SHRIMP, *PANDALUS BOREALIS*

THURSDAY 7 JULY, 2016 **09:55**

DENIS CHABOT (FISHERIES AND OCEANS CANADA, CANADA), TANYA HANSEN (FISHERIES AND OCEANS CANADA, CANADA), LAÉLIEN BASSI (UNIVERSITÉ DE LILLE, FRANCE), LUC BEAUDIN (FISHERIES AND OCEANS CANADA, CANADA), PIERO CALOSI (UNIVERSITÉ DU QUÉBEC À RIMOUSKI, CANADA)

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The Northern shrimp, *Pandalus borealis*, is an important commercial species in the estuary and gulf of St. Lawrence (EGSL), eastern Canada. Deep trenches that are chronically acidic and hypoxic characterize the EGSL. *P. borealis* is hypoxia-tolerant at 5 °C and current surface pH (~8), but hypoxia tolerance at current deep-water pH (~7.75) is unknown. Deep-water is expected to become warmer, more acidic and hypoxic due to climate change, with unknown effects on distribution and productivity of *P. borealis*. Shrimp were acclimated for a minimum of 4 weeks at one of 5 temperatures (3, 6, 9, 12 and 15 °C) and 3 pH (8.0, 7.75, 7.55). Because of high mortality at 15 °C, shrimp were acclimated to 12 °C and brought to 15 °C for 48 h prior to the experiment. Standard and maximum metabolic rates (SMR and MMR) and critical oxygen level (O_2crit) of female *P. borealis* were measured. pH had no detectable effect on SMR, MMR or O_2crit. MMR was stable from 3 to 15 °C, but SMR increased rapidly with temperature. Aerobic scope (AS = MMR - SMR) decreased as temperature increased above 6 °C. AS was still positive at 15 °C, despite the very high mortality rate. Hypoxia tolerance diminished as temperature increased. As *P. borealis* already has a much reduced AS at current temperature and oxygen levels in the most hypoxic regions of the EGSL, projected warmer temperatures and lower oxygen levels are likely to cause habitat loss for this species.

APC1.36 ASSESSING FISH HEALTH: DEVELOPMENT OF A NEW METHODOLOGY THAT IMPROVE THE CONSERVATION PHYSIOLOGY TOOL BOX

THURSDAY 7 JULY, 2016 **10:10**

FLORIAN MAUDUIT (UNIVERSITÉ DE BRETAGNE OCCIDENTALE, FRANCE)

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The recent rejuvenation of ecological physiology into conservation physiology aimed at applying physiological concepts, tools, and knowledge to understanding how organisms, populations, and ecosystems respond to environmental change and stressors. In that context, one challenge is to assess species and populations' coping ability and resilience. In Human medicine, the notion of health is defined as the ability of one patient to do what it has to do. Health is the integrative outcome of earlier-life environment, exposures and experience and it informs about the patient's vulnerability and resilience to challenges and changes. Unfortunately, current definition of animal health lags behind how health is defined and assessed in human. To bridge this gap, our study aimed at validating a methodology to evaluate health in fish populations. We first applied high-throughput, non-lethal challenge tests on a population of 700 juveniles of sea bass to assess hypoxia tolerance, temperature susceptibility and critical swimming speed as proxies of individuals' functional integrity. Experimental population was then transferred into semi-natural tidal ponds and correlates of Darwinian fitness (growth and survival) were monitored over a period of 4 months. We found that hypoxia tolerance and swimming capacity, but not temperature susceptibility, were predictive of fish ecological performance in the field. However, we have identified several pitfalls that must be taken to consideration. Interpretation of fish responses to health assessment tests must take into consideration such as inter-population variability, the environmental shaping of phenotypic diversity and the modulating effect of behaviour and learning.

APC1.37 KNOW YOUR ENEMY: USING PHYSIOLOGICAL KNOWLEDGE TO CONTROL INVASIVE SEA LAMPREY

THURSDAY 7 JULY, 2016 **10:55**

MICHAEL SIEFKES (GREAT LAKES FISHERY COMMISSION, UNITED STATES)

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The parasitic sea lamprey (*Petromyzon marinus*) caused the devastating collapse of native fish communities after invading the Laurentian Great Lakes during the early 1900s. Economic tragedy across the Great Lakes basin ensued with the loss of the fishing industry and severe impacts to property values and tourism resulting from sea lamprey-induced ecological changes. To control the sea lamprey and restore the once vibrant Great Lakes ecosystem and economy, the Great Lakes Fishery Commission (Commission) was formed by treaty between Canada and the United States in 1955. The Commission developed a sea lamprey control program based on the application of 3-trifluoromethyl-4-nitrophenol (TFM), which successfully kills sedentary sea lamprey larvae in their natal streams while having little effect on most non-target organisms; sea lamprey cannot metabolize TFM through glucuronidation as well as other fishes. Since 1958, regular application of TFM to sea lamprey-producing Great Lakes tributaries has suppressed sea lamprey populations by >90% from their peak abundance. Great Lakes fish communities have rebounded and the economy is now thriving. To compliment the application of TFM, the Commission is also exploring use of sea lamprey pheromones and alarm cues to manipulate behaviours for control purposes such as improving trapping of adult sea lampreys during spawning migrations and influencing sea lamprey distribution to more effectively target TFM applications. Overall, the Commission capitalizes on the unique physiology of the sea lamprey to successfully control a once devastating invasive species.

APC1.38 MODELLING THE SPREAD OF PARASITOID WASPS FROM POINT RELEASE

THURSDAY 7 JULY, 2016 **11:25**

CHRISTOPHER STRICKLAND (SAMSI AND THE UNIVERSITY OF NORTH CAROLINA CHAPEL HILL, UNITED STATES), NADIAH P KRISTENSEN (NATIONAL UNIVERSITY OF SINGAPORE, SINGAPORE), LAURA MILLER (UNIVERSITY OF NORTH CAROLINA CHAPEL HILL, UNITED STATES)

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Parasitic hymenoptera are a group of insects which are critical for biological pest control and increasingly being used in agriculture to protect crops via direct release. However, due to their small size (often less than 1 mm), movement and long-distance dispersal of these wasps have long been poorly understood and likely underestimated. Recent data collected by Kristensen et al. (2013) on the wind-borne dispersal pattern of Eretmocerus hayati (0.7 mm long) provides a new and significant opportunity to finally develop a detailed, validated, multi-scale model for the initial spread of invasive insects and biological control introductions. In this talk I will present a new mathematical model for parasitoid wasp dispersal from point release, as in the case of biocontrol. The model is derived from underlying stochastic processes and, as a special case of the Fokker-Planck equation, is fully deterministic. The Python implementation of this model is capable of running month long simulations on the scale of 15 km^2 while maintaining a resolution of 10 m^2, all within two minutes on a common workstation. Speed is an essential component to our model because it allows flexibility in fitting parameters to data. Validation of the model includes comparison with two multi-scale, first-release data sets described in Kristensen et et al. (2013).

APC1.39 CONSERVING IMPERILED FISHES: FINDING SOLUTIONS THROUGH PHYSIOLOGICAL AND BEHAVIORAL STUDIES

THURSDAY 7 JULY, 2016 **13:50**

NANN A FANGUE (UNIVERSITY OF CALIFORNIA DAVIS, UNITED STATES), DENNIS E COCHERELL (UNIVERSITY OF CALIFORNIA DAVIS, UNITED STATES), JAMILYNN B POLETTO (UNIVERSITY OF CALIFORNIA DAVIS, UNITED STATES)

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Approximately 80% of freshwater fishes are facing extinction over the next 100 years, and in California, native freshwater and anadromous fishes reflect this trend. Anthropogenic threats to species viability can alter habitats beyond native species'; environmental tolerances and may result in extirpation. California has a long history of habitat fragmentation and degradation (i.e., the presence of dams, and water withdrawals associated with agricultural and urban use), and in combination with climate change, suitable habitat for fishes has been greatly reduced. In this talk, I will highlight results from two main areas of research. The first addresses the impact of water diversions on the susceptibility of several California native fishes to entrainment (i.e. becoming sucked into diversion pumps and structures), as well as the evaluation of the efficacy of behavioral deterrents designed to minimize entrainment. In the second example, I will discuss a variety of approaches that we use to define suitable thermal habitat for native fishes, as well as the challenges associated with then translating these measures of thermal performance into regulatory numeric criteria. In both examples, I will emphasize how we transform our physiological and behavioral results into actionable outcomes for fishes in order to promote conservation and achieve biodiversity goals.

APC1.41 EFFECTS OF TEMPERATURE AND FEEDING RATE ON THE GROWTH OF LARVAL GREEN STURGEON: IMPLICATIONS FOR SURVIVAL OF EARLY LIFE STAGES

THURSDAY 7 JULY, 2016 **14:30**

JAMILYNN B. POLETTO (UNIVERSITY OF CALIFORNIA DAVIS, UNITED STATES), BENJAMIN MARTIN (NOAA SOUTHWEST FISHERIES SCIENCE CENTER, UNITED STATES), ERIC DANNER (NOAA SOUTHWEST FISHERIES SCIENCE CENTER, UNITED STATES), DENNIS E. COCHERELL (UNIVERSITY OF CALIFORNIA DAVIS, UNITED STATES), JOSEPH J. CECH JR. (UNIVERSITY OF CALIFORNIA DAVIS, UNITED STATES), NANN A. FANGUE (UNIVERSITY OF CALIFORNIA DAVIS, UNITED STATES)

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Both temperature and food availability have significant effects on the growth and survival of native fishes, particularly during early developmental stages. Therefore, we reared larval green sturgeon (initial age ca. 27 days post hatch) at four different temperatures (11, 14, 17, and 20°C) and two different food rates (100% and 25% of optimal) to assess the effects of these stressors and their interactions on larval growth. We compared the overall size (fork length, total length, and mass), specific growth rate (cm/day), and condition factor of larval fish after being held in rearing conditions for 3 and 6 weeks. Our results can be used to develop models of the early life history requirements of green sturgeon and to inform management actions seeking to increase larval and juvenile recruitment success.

APC1.42 IMPROVING FISH PASSAGE THROUGH CULVERTS: INTEGRATION OF HYDRODYNAMICS AND SWIMMING PERFORMANCE

THURSDAY 7 JULY, 2016 **14:45**

CRAIG E FRANKLIN (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), HUBERT CHANSON (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), REBECCA L CRAMP (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), MATTHEW GORDOS (NSW DPI FISHERIES, AUSTRALIA), PIPPA KERN (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), ESSIE M RODGERS (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), CAROLINE THOMPSON (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA)

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A key component of river and stream management is to ensure that native migratory fish have unimpeded access to required habitat to complete necessary life cycle stages. Regrettably, over the past two centuries, man-made instream structures (e.g. dams, weirs, and road crossings) have significantly impeded habitat connectivity and have created barriers to fish movement. While the impacts of large dams and weirs on fish populations are well acknowledged, smaller-scale instream structures like waterway crossing culverts have until recently been overlooked despite having as great or greater impact on fish populations. To address these concerns, many agencies responsible for healthy waterways have created guidelines for the design and construction of fish-friendly culverts. However, problematically these guidelines are often based on limited empirical data from a few select large bodied fish species, or come from anecdotal information from field observations. A critical factor in considering the design and effectiveness of waterways crossings in passing native fish is quantifying the swimming performance of fish, and in particular their ability to swim against the artificial flows created by instream structures. In this study biologists and engineers have been integrating data on the swimming ability of Australian fish species with culvert hydrodynamic modelling to better understand fish requirements in and around road crossings. Results will also be presented on the effects of culvert roughening on swimming performance. These data are being used to strengthen national design guidelines and provide the tools engineers and planners need to balance fish migration with effective water management.

APC1.43 FOG, FORAGING AND THE FUTURE OF TWO SYMPATRIC LIZARD SPECIES IN THE NAMIB DESERT

THURSDAY 7 JULY, 2016 **15:45**

DUNCAN MITCHELL (UNIVERSITY OF THE WITWATERSRAND, SOUTH AFRICA), IAN W MURRAY (UNIVERSITY OF THE WITWATERSRAND, SOUTH AFRICA), STEPHAN WOODBORNE (ITHEMBA LABORATORIES AND UNIVERSITY OF PRETORIA, SOUTH AFRICA), ANDREA FULLER (UNIVERSITY OF THE WITWATERSRAND, SOUTH AFRICA), HILARY M LEASE (WHITMAN COLLEGE, UNITED STATES), ROBYN S HETEM (UNIVERSITY OF THE WITWATERSRAND, SOUTH AFRICA)

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Rhoptropus bradfieldi and *Pedioplanis husabensis* are endemic lizards of similar size (snout-vent length ~50mm) that live in the same rocky Namib habitat. Both are threatened by climate change and by uranium mining. We studied their activity, body temperature, body water turnover using $^2H^{18}O$, and diet using $\delta^{13}C$ and $\delta^{15}N$ analysis of body tissues and items in their trophic cascade. We noosed stationary lizards (31–62 in a cohort) in summer and autumn. At lower ambient temperatures, *R. bradfieldi* was significantly cooler than was *P. husabensis*, the difference resulting mainly from their foraging behaviour and consequently their microclimate. *R. bradfieldi* is a sit-and-wait forager on rocks, while *P. husabensis* is an active forager, venturing off rocks onto nearby hot sand. Stable isotope analysis showed that the summer diet of *P. husabensis* was 63% termites, and that of *R. bradfieldi* 38% ants and 35% wasps. The high water content of termites allowed metabolic and pre-formed water to exceed the water needs of *P. husabensis*, but metabolic and pre-formed water contributed only 30% of the daily water influx rate ($0.07\ ml\ d^{-1}$) of *R. bradfieldi*. Consequently *R. bradfieldi* must have been consuming free water, with advective fog the most-likely source. The prey of both species was deriving energy almost entirely from C_4/CAM plants, presumably mainly grasses. If, under climate change, fogs become less frequent and regular, the future for *R. bradfieldi* is bleak. Also, climate change will lead to loss of C_4/CAM plant biomass, potentially compromising the future of both species.

APC1.44 THE EFFECT OF COPPER EXPOSURE ON SEXUAL BEHAVIOR IN BANK VOLE (*MYODES GLAREOLUS*)

THURSDAY 7 JULY, 2016 **16:00**

AGATA E MISKA-SCHRAMM (JAGIELLONIAN UNIVERSITY, POLAND)

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The influence of copper pollution on the natural environment constantly increases. This trace element accumulates in plants and water what may be especially dangerous for herbivores.

In contaminated areas, lower density of small rodents is observed. This decline of rodent number may be caused by decline in reproductive abilities or dysfunctional sexual behavior. My previous research proven, that copper mainly debilitates males' reproductive system and prolongs sexual maturation.

The aim of the presented study was to assess the effect of copper influence on small rodents' sexual behavior using bank vole (*Myodes glareolus*, Schreber 1780) as a model species.

In the presented research, copper was administered at concentrations similar to those recorded in industrial districts (Cu I-150mg/kg, Cu II-600mg/kg, C-control). After 12 weeks of copper exposure, the preference test was performed; female behavior was recorded in the following combinations: ♀C vs ♂C & ♂Cu I and ♀C vs ♂C & ♂Cu II. The assessed parameters were: total activity, number of approaches and sniffs and the time of sniffing. Additionally, the behavior and vocalization of male-female pairs were recorded during open-field tests in the following combinations: ♂C vs & ♀C; ♂Cu I vs ♀C; ♂Cu II vs ♀C. Assessed parameters were: latency to first approach, attack, number of aggressive and nonaggressive approaches, sniffs and ultrasonic calls.

Results have shown that copper did not affect intersexual behaviors. However, the preference tests proven that copper, especially in higher concentration, decreased males' sexual attractiveness depicted by the decline of total activity, number of female approaches and sniffs.

APC1.46 NOVEL INSIGHT INTO THE DEVELOPMENTAL PHYSIOLOGY OF TURTLE EGGS PROVIDES A NEW TOOL FOR CONSERVATION

THURSDAY 7 JULY, 2016 **16:15**

SEAN A WILLIAMSON (MONASH UNIVERSITY, AUSTRALIA), ROGER D EVANS (MONASH UNIVERSITY, AUSTRALIA), RICHARD D REINA (MONASH UNIVERSITY, AUSTRALIA)

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An increase in the partial pressure of oxygen, at the time of oviposition, is the trigger that breaks turtle eggs from pre-ovipositional embryonic arrest. Significant levels of mortality occur when eggs are moved within 12 hours to 14 days after oviposition in some species. This movement-induced mortality is likely to be linked to the recommencement of embryonic development. We aimed to identify the amount of time an embryo takes to recommence development following oviposition and whether embryos can re-enter embryonic arrest. Green sea turtle (Chelonia mydas) eggs were randomly placed into hypoxia at one of ten time intervals between 30 mins to 72 hrs post oviposition. Each treatment group remained in hypoxia for three days. An 11th group of eggs remained in normoxia throughout incubation, serving as a control for the experiment. Development and survival rate of embryos was then compared to determine both the time taken to break arrest and ability to re-enter arrest. Our experiment identified that, after oviposition, between 12 to 16 hours of exposure to normoxic conditions is required to recommence embryonic development in green sea turtles. The information gained from this experiment enables turtle conservation groups to better understand the ideal time to relocate eggs. In addition, the experiment also revealed that green sea turtle embryos are unable to re-enter a state of arrest following recommencement of development. The findings of this research have the potential to improve conservation outcomes, through reducing rates of embryonic death or reproductive failure during translocation.

APC1.24 CIRCULATING POLYCHLORINATED BIPHENYLS ARE ASSOCIATED WITH ALTERED ADIPONECTIN LEVELS AND WEANING MASS IN GREY SEAL PUPS

TUESDAY 5 JULY, 2016 **POSTER SESSION**

KIMBERLEY A BENNETT (ABERTAY UNIVERSITY, UNITED KINGDOM), MAXIM FABRY (UNIVERSITÉ DE LIÈGE, BELGIUM), JACK HUGHES (PLYMOUTH UNIVERSITY, UNITED KINGDOM), AILSA J HALL (SMRU UNIVERSITY OF ST ANDREWS, UNITED KINGDOM), JEAN-PIERRE THOME (UNIVERSITÉ DE LIÈGE, BELGIUM), PADDY POMEROY (SMRU UNIVERSITY OF ST ANDREWS, UNITED KINGDOM), CATHY DEBIER (UNIVERSITÉ CATHOLIQUE DE LOUVAIN, BELGIUM)

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Appropriate regulation of energy balance is crucial for health, fitness and survival. Evidence in humans and other mammals suggests persistent organic pollutants (POPs) can disrupt energy balance, and alter adiponectin levels, contributing to obesity related disorders. Seals experience high POP burdens as a result of their position as top predators and the bioaccumulation and magnification of POPs up the food chain. We investigated whether a suite of 11 circulating POPs, including the pesticides lindane, DDT and its metabolites, PCBs and PBDEs were associated with plasma adiponectin levels, blubber adiponectin mRNA abundance or mass changes in suckling and fasting grey seal pups (n=9). After accounting for differences between feeding and fasting, adiponectin levels were positively related to circulating CB101 levels (LME: p=0.0323). Adiponectin mRNA abundance was not related to circulating POP concentrations. Mass increase rate during suckling was positively related to maternal postpartum mass (LM: T=0.328; $F_{(1,7)}=10.76$; $R^2=0.5495$; p=0.0135) and none of the POPs improved the model fit. CB52 was negatively related to weaning mass (LM: T=3.063; $F_{(1,7)}=9.38$; $R^2=0.52$; p=0.0183). Our data suggest POPs disrupt normal energy balance in grey seal pups. Altered adiponectin levels may influence inflammatory responses and insulin sensitivity, and lower weaning mass may impact on survival. Causal relationships between POPs and energy balance effects and their consequences require investigation in a larger sample, and mechanisms through which POPs alter energy balance in seals need to be identified.

APC1.25 CRUDE OIL EXPOSURE DOES NOT AFFECT THE CONTRACTILE PROPERTIES OF MAHI MAHI *(CORYPHAENA HIPPURUS)* CARDIAC MUSCLE

TUESDAY 5 JULY, 2016 **POSTER SESSION**

TERENCE S GARNER (UNIVERSITY OF MANCHESTER, UNITED KINGDOM), HOLLY A SHIELS (UNIVERSITY OF MANCHESTER, UNITED KINGDOM), JOHN STIEGLITZ (UNIVERSITY OF MIAMI, UNITED STATES), DANIEL D BENETTI (UNIVERSITY OF MIAMI, UNITED STATES), GINA LJ GALLI (UNIVERSITY OF MANCHESTER, UNITED KINGDOM), DANE A CROSSLEY II (UNIVERSITY OF NORTH TEXAS, UNITED STATES), MARTIN GROSELL (UNIVERSITY OF MIAMI, UNITED STATES)

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In 2010, the Deepwater Horizon oil spill released 210 million gallons of crude oil into the Gulf of Mexico. Crude oil has been shown to have cardiotoxic effects on fish and prior work on mahi mahi has highlighted a reduced cardiac output in response to short-term oil exposure. We investigated the effects of acute and chronic crude oil exposure on the contractility of isolated cardiac tissue from adult mahi mahi and used chemical inhibitors to identify any effect on calcium cycling targeting the sarcoplasmic reticulum and adrenergic signalling pathways. Direct exposure of cardiac muscle to high energy water accommodated fractions (HEWAF) of crude oil at 10% concentration had no effect on muscle contractility. Further, cardiac tissue collected from fish exposed to 10% HEWAF solution for 24h did not display reduced contractility, compared with controls. Concurrent with this, there was no difference in the contribution of the sarcoplasmic reticulum to contractility between fish exposed to HEWAF for 24h and unexposed fish. Our data is consistent with the effects of oil on cellular calcium cycling in mahi mahi but contrary to data previously obtained for bluefin tuna and suggests that the reduced cardiac output previously observed in juvenile mahi mahi after oil exposure may result from some factor other than contractility.

APC1.26 INTERACTIVE EFFECT OF OCEAN ACIDIFICATION AND SALINITY REDUCTION ON ECOPHYSIOLOGICAL PERFORMANCE OF EUROPEAN SEABASS *(DICENTRARCHUS LABRAX)*

TUESDAY 5 JULY, 2016 **POSTER SESSION**

NITIN PIPRALIA (UNIVERSITY OF ANTWERP, BELGIUM), AMIT KUMAR SINHA (UNIVERSITY OF ANTWERP, BELGIUM), RONNY BLUST (UNIVERSITY OF ANTWERP, BELGIUM), GUDRUN DE BOECK (UNIVERSITY OF ANTWERP, BELGIUM)

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A rise in $p\text{CO}_2$ results in higher dissolution in ocean surface water. This leads to a decrease in ocean pH, referred as ocean acidification. This is a potential threat to marine fish, and effects may get worse for estuarine fish which deal with the additional stress of salinity changes due to the migration into low salinity water. To understand the interactive impact of these two environmental stresses on the ecophysiologal performance of fish, we investigated various physiological, biochemical and ion-regulatory adaptive response in European sea bass at $p\text{CO}_2$ levels of 380 µatm, 900 µatm and 1900 µatm, along with salinity gradients of 32ppt, 10ppt and 2.5ppt. Overall, we hypothesize that effect of ocean acidification would be exacerbated with a shift to decreased ambient salinity. Plasma acid-base balance, iono-osmoregulation, oxygen consumption, ammonia metabolism, energy budget and ion-regulatory enzymes were assayed as the potential indices of compensatory responses. Results show that ammonia excretion rate was facilitated under the combined effect of ocean acidification and salinity reduction while oxygen consumption and hepatic energy budget of fish were well regulated. Acid-base balance in terms of plasma pH and HCO_3- were adversely affected following ocean acidification and salinity stress as single and combined factor. Na^+ and Cl^- levels in plasma remained stable, suggesting an excellent ion-regulatory capacity of the fish which was also reflected by the kinetic profile of Na^+/K^+-ATPase activity. In brief, the combined effect of ocean acidification and salinity reduction significantly affect the fish acid-base balance, but not iono-osmoregulation or energy metabolism.

APC1.27 THE PHYSIOLOGY OF GROWTH IN THE BLOOM-FORMING GREEN ALGA *ULVA SPP*

TUESDAY 5 JULY, 2016 **POSTER SESSION**

KEVIN J YUN (DURHAM UNIVERSITY, UNITED KINGDOM), CHRISTOPHER D SAUNTER (DURHAM UNIVERSITY, UNITED KINGDOM), JOHN H BOTHWELL (DURHAM UNIVERSITY, UNITED KINGDOM), GEORGIA E CAMPBELL (DURHAM UNIVERSITY, UNITED KINGDOM), TIM J HAWKINS (DURHAM UNIVERSITY, UNITED KINGDOM)

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Macroalgal blooms ('green tides') are a growing problem on many coastlines worldwide, including here in the UK. These blooms can suffocate marine life and decimate local populations, but their environmental and anthropogenic drivers remain poorly understood. Accordingly, we are using the bloom-forming green seaweed species, *Ulva spp.* (a.k.a. 'sea lettuce') to understand how the physiology of their growth and reproduction can both lead to blooms and be exploited for conservation. Using a combination of mathematical modelling, high-resolution imaging, and molecular approaches, we ask two main questions: a) how do physiological responses at the cellular scale drive seaweed thallus growth and b) how can patterns of thallus growth inform marine conservation efforts? Currently, the main method of tracking the growth of macroalgal biomass is its physical removal and measurement on weighing scales. This method is limited by its poor temporal resolution and intrusiveness. We have therefore developed an optical imaging system linked to automated image analysis software to allow real-time measurement of circadian growth rhythms in response to the environmental factors that determine *Ulva spp.* proliferation. These macroscopic growth results are supplemented by Light Sheet Microscopy data of stained samples, which correlates overall growth rates with patterns of cellular size and distributions. This combination of methods provides much greater resolution of the growth responses of *Ulva* in various conditions; this is now being linked to global bloom formation using hydrodynamic models.

APC1.28 THE PHYSIOLOGY OF GROWTH IN THE BLLATITUDINAL VARIATION IN GROWTH AND METABOLIC RATE IN INVASIVE SLUG SPECIES, *ARION VULGARIS*

TUESDAY 5 JULY, 2016 **POSTER SESSION**

PAULINA KRAMARZ (JAGIELLONIAN UNIVERSITY, POLAND),
KAROLINA NAUMIEC (JAGIELLONIAN UNIVERSITY, POLAND),
ULF BAUCHINGER (JAGIELLONIAN UNIVERSITY, POLAND)

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One of the hypotheses explaining species invasiveness states that invasive species demonstrate rapid response to natural selection. Thus, we can expect differences in fitness related traits between populations of invasive species from latitudes (different climatic regions). We measured growth rate and metabolic rate, both traits that influence other traits such us development time and body size, and thus fitness of an individual.

Arion vulgaris is regarded as one of the 100 most invasive species in Europe. We collected adult specimens of *A. vulgaris* in 12 sites across Europe (from Northern Norway to Southern France) transferred them to identical conditions of 15°C (optimal temperature for this species), 80% RH and standard food and let them reproduce. Similar aged juveniles were kept individually and weighed regularly to estimate growth rate and respiration rate was measured at rearing conditions.

In our common garden experiment we observed significant population differences in standard metabolic rate (SMR) statistically corrected for body mass. Individuals derived from the most Northern population had the lowest SMR, but growth rate was intermediate and did not differ from other populations. In general, we did not observe clear patterns in SMR and growth rate between populations that origin from different latitude. Although, we don't observe clear latitudinal patterns in our common garden experiment our result of progeny growth and SMR of the most extreme Northern population suggest physiological adaptations to new environments, which may support invasive potential of *Arion vulgaris*.

APC1.29 COMBINED INFLUENCES OF WATER pH AND TEMPERATURE UPON THE SWIMMING CAPACITY OF EUROPEAN SEA BASS LARVAE

TUESDAY 5 JULY, 2016 **POSTER SESSION**

LOUISE COMINASSI (UNIVERSITY OF HAMBURG, GERMANY),
MARTA MOYANO (UNIVERSITY OF HAMBURG, GERMANY),
GUY CLAIREAUX (UBO, FRANCE), SARAH HOWALD (AWI, GERMANY), PATRICK QUAZUGUEL (IFREMER, FRANCE),
MYRON PECK (UNIVERSITY OF HAMBURG, GERMANY)

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Swimming capacity is a determining factor of Darwinian fitness as it influences a multiplicity of fundamental performances, including the ability to acquire food, to find mate, to avoid predators and hostile environment. Swimming ability is also an integrated maker of the functioning of a cluster of physiological functions that contribute to locomotion and which include, for instance, oxygen extraction and transport, osmoregulation, muscle contraction. For that reason, swimming capacity is generally considered as a proper indicator of fish health. Carbon dioxide emissions accumulating in the atmosphere and being absorbed by the world's oceans are resulting in decreased marine pH. This is occurring together with global warming, representing a new challenge for marine life. In this study we examined the effect of predicted ocean acidification and warming (OAW) on the swimming capacity of fish larvae. Since 2 days post hatch (dph), European sea bass (Dicentrarchus labrax) larvae were exposed to a combination of three levels of $p\mathrm{CO}_2$ (400, 800, 1200 µatm; pH 8.1, 7.8, 7.6) and two temperatures (15, 20°C). Larvae maximal swimming speed was measured between 15 and 60 dph. We found that larvae swimming capacity increased rapidly with size and that, at the same age, fast growing, 20°C-reared larvae reached higher swimming speed than their 15°C-reared counterpart. However, water pH did not affect larvae swimming capacity.

PC1 SYNTHETIC BIOLOGY: SYSTEMS DESIGN AND RE-WIRING

ORGANISED BY: DR KATHERINE DENBY (UNIVERSITY OF WARWICK, UNITED KINGDOM),
DR VARDIS NTOUKAKIS (UNIVERSITY OF WARWICK, UNITED KINGDOM),
DR KAREN POLLIZZI (IMPERIAL COLLEGE LONDON, UNITED KINGDOM) AND
DR MATIAS ZURBRIGGEN (HEINRICH HEINE UNIVERSITY, GERMANY)

PC1.1 ENGINEERING NITROGEN FIXING SYMBIOTIC ASSOCIATIONS IN CEREALS

TUESDAY 5 JULY, 2016 **13:40**

GILES OLDROYD (JOHN INNES CENTRE, UNITED KINGDOM)

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Sustained crop yields are dependent on inorganic fertiliser application, but it comes at a high price, both in the cost of the fertiliser and the environmental damage that results from its use. A number of plant species have evolved beneficial interactions with micro-organisms that facilitate the uptake of nutrients. Legumes form symbiotic interactions with mycorrhizal fungi that facilitate phosphate uptake and with rhizobial bacteria that provide the plant with a source of nitrogen. The establishment of these symbioses involves a molecular communication between the plant and the symbiotic micro-organisms in the soil. Mycorrhizal fungi and rhizobial bacteria release signals that are recognised by the host plant and lead to developmental changes associated with the accommodation of the symbionts. Genetic dissection in the legumeMedicago truncatula has defined the signalling pathways involved in these symbioses. A number of the genes required for the mycorrhizal interaction are also necessary for the rhizobial interaction, indicating a conserved symbiosis signalling pathway. This implies that the evolution of nodulation involved the recruitment of a signalling pathway already functioning in mycorrhizal signalling. This signalling pathway is present in most plant species, including cereals suggesting that engineering the perception of rhizobial bacteria in cereals is simplified and requires an understanding of the legume specific components that activate and are activated by the common symbiosis signalling pathway. We are in the process of engineering this signalling pathway in cereals to promote the recognition of rhizobial bacteria as the first step in engineering biological nitrogen fixation into cereal crops.

PC1.2 THE PROPAGATION OF PERTURBATIONS IN REWIRED BACTERIAL GENE NETWORKS

TUESDAY 5 JULY, 2016 **14:20**

MARK ISALAN (IMPERIAL COLLEGE LONDON, UNITED KINGDOM)

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What happens to gene expression when you add new links to a gene regulatory network? To answer this question, we profiled 85 network rewirings in E. coli and found that concerted patterns of differential expression propagate from reconnected hub genes. Perturbations from related rewirings have more similar transcription profiles and a statistical analysis revealed around ~20 underlying states of the system, associating particular gene groups with rewiring constructs. Interestingly, both transcription factor connectivity and promoter activity associate with perturbation size. This dataset of systematically-related perturbations enables reverse engineering and discovery of underlying network interactions, as well as providing guidelines for construct design in synthetic biology.

PC1.3 ENGINEERING MICROBIAL EFFECTOR SYSTEMS IN PLANTS

TUESDAY 5 JULY, 2016 **14:45**

VARDIS NTOUKAKIS (UNIVERSITY OF WARWICK, UNITED KINGDOM)

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Plants' highly versatile metabolic capabilities and ability to capture energy from sunlight makes them ideal platforms for energy-efficient generation of diverse products. A key for achieving increased productivity in plants will be the development of a synthetic control system that can allow temporal control of bespoke plant pathways in an orthogonal fashion, i.e. without causing trade-offs in other natural responses. In nature, microbes have evolved a myriad of signalling molecules and proteins (i.e. effectors) that can manipulate specific signalling and gene regulatory networks in an effort to reprogram plant behaviour. We systematically screen for effectors that inhibit or activate specific plant pathways involved in plant development, immunity and metabolism. These effectors may work on protein kinase cascades, at the receptor level or at the downstream transcriptional level and we use combinations of such effectors to reduce network interference and optimise plant productivity.

PC1.4 RE-WIRING SIGNALING PATHWAYS TO ENHANCE STRESS TOLERANCE

TUESDAY 5 JULY, 2016 **15:05**

IULIA GHERMAN (UNIVERSITY OF WARWICK, UNITED KINGDOM), CHRISTOPHER PENFOLD (UNIVERSITY OF OXFORD, UNITED KINGDOM), MATHIAS FOO (UNIVERSITY OF WARWICK, UNITED KINGDOM), DAVID WILD (UNIVERSITY OF WARWICK, UNITED KINGDOM), DECLAN BATES (UNIVERSITY OF WARWICK, UNITED KINGDOM), KATHERINE DENBY (UNIVERSITY OF WARWICK, UNITED KINGDOM)

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Abiotic and biotic stress conditions result in large-scale transcriptional reprogramming in plants. We are elucidating these complex regulatory networks from experimentally derived time series data of Arabidopsis leaves after infection with bacterial and fungal pathogens, as well as during senescence. Using a combination of network inference algorithms together with biological knockout and yeast one-hybrid data, we have constructed a high confidence transcription factor network for each stress individually. This allows us to identify key regulators of the Arabidopsis stress response, as well as genes that are co-regulated across multiple stresses. Knockouts and overexpression of individual transcription factors can be simulated to determine the impact these perturbations have on the rest of the network. Algorithms such as Approximate Bayesian Computation allow us to test different combinations of re-wiring the network to achieve the desired gene expression in our key regulators. This is done with the goal of establishing the re-wirings that enhance the plant defence response to pathogens. In order to validate the conclusions of our networks and re-wiring simulations, the target transcription factors will be expressed in a protoplast system under different spatial and temporal promoters. After a few rounds of the design-build-test cycle, the experiments will be performed in Arabidopsis plants and phenotypes with enhanced resistance will be selected for.

PC1.5 SYNTHETIC APPROACHES TO EXPLORING EVOLUTION AND DEVELOPMENT

TUESDAY 5 JULY, 2016 **16:00**

JAMIE A DAVIES (UNIVERSITY OF EDINBURGH, UNITED KINGDOM)

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Most biology is analytical and aims to understand life as it evolved on Earth. Researchers study organisms, make hypotheses, and test them experimentally usually by perturbing a component with mutation or drugs. The results of many such experiments are brought together in text books to formulate general principles, much simpler than the complicated mechanisms by which they are realized in specific instances. A robust way to test correctness of these ideas is to build something that uses them in their simple form, and test whether it works. Recently, a small number of synthetic biologists have started to apply this idea to embryology. They have constructed modules, based on developmental principles, to programme naive cells to make patterns in response to gradients or completely de-novo, and to perform simple morphogenetic tasks: there are even primitive working examples of patterning-followed-by-morphogenesis, driven entirely by designed genetic modules. As well as having applications in tissue engineering, this approach provides a powerful test-bed for basic ideas about developmental mechanisms. Furthermore, interesting evo-devo insights may come from exploration of 'roads not taken', through constructing invented mechanisms that work but seem not to have arisen in evolved life. This presentation will illustrate these approaches, drawing from our own work and that of others.

PC1.6 SYNTHETIC CELL-BASED SENSORS WITH PROGRAMMED SENSITIVITY, SELECTIVITY AND DYNAMIC RANGE

TUESDAY 5 JULY, 2016 **16:40**

BAOJUN WANG (UNIVERSITY OF EDINBURGH, UNITED KINGDOM)

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We use single bacterial cells, programmed with engineered modular genetic sensors and digital logic or analogue amplifying gene circuits, to sense, integrate and amplify multiple customized environment and health realted signals. We have shown these engineered gene circuits can predictably and significantly increase the selectivity, sensitivity and output dynamic range of cellular sensors for toxic heavy metal ions including arsenic and mercury in an aqueous environment. By example, we engineered a selective double-input AND gated sensor for zinc in E. coli in which the AND gate functions as a filter by filtering out the nonspecific signals from the two promiscuous zinc input sensors. We next engineered a set of orthogonal activator-based high-gain transcriptional amplifiers, and cascaded them in multiple layers to in tandem amplify transduced sensor signal to increase sensitivity and output dynamic range. With the amplifier-cascade, we increased the sensitivity >4000 fold with detection limit <0.01 ppb, and the output dynamic range 500 fold for a mercury sensor (WHO safe limit 2 ppb). Our approach is modular and can be readily applied to improving the sensing limit and performance of a range of cellular sensors to meet their real world detection requirement in environment and healthcare.

PC1.8 REFINEMENT OF THE PHYTOBRICKS STANDARDS FOR PLANT SYNTHETIC BIOLOGY

WEDNESDAY 6 JULY, 2016 **09:40**

DIEGO ORZAEZ (IBMCP-UPV-CSIC, SPAIN), MARTA VAZQUEZ-VILAR (IBMCP-CSIC, SPAIN), ASUN FERNÁNDEZ-DEL-CARMEN (IBMCP-CSIC, SPAIN), JOAN BERNABÉ (IBMCP-CSIC, SPAIN), ALFREDO QUIJANO (IBMCP-CSIC, SPAIN), ALEJANDRO SARRIÓN-PERDIGONES (IBMCP-CSIC, SPAIN), ROCIO OCHOA (IBMCP-CSIC, SPAIN), PEIO ZIARSOLO (UPV, SPAIN), JOSÉ BLANCA (UPV, SPAIN), ANTONIO GRANELL (IBMCP-CSIC, SPAIN)

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Modular DNA cloning has been quickly embraced by the Plant Biotechnology community due to its efficiency in resolving multigene engineering goals. The adoption of common rules for describing synthetic DNA parts (phytobricks) and for the composition of multigene modules has been proposed as an optimal strategy for speeding up advancements in the field. Recent efforts in this direction include the adoption of a Plant Standard Syntax for Modular Cloning and the development of collections of synthetic parts. Here we propose further refinements in the characterization of phytobricks with the definition of standard experimental conditions and the registering of the information obtained under such conditions as metadata for the description of synthetic DNA elements. To incorporate these new features, we developed a new version (v3.0) of the GoldenBraid assembly system and database, now incorporating experimental data. Consequently, Phytobricks in GB3.0 display associated datasheets that inform of their assembly genealogy and also about their functionality under predefined experimental conditions. Thus, we used the dual luciferase/renilla reporter system in Nicotiana benthamiana transient agroinfiltration experiments to estimate the relative transcriptional activities (RTA) conferred by regulatory elements, and showed the reproducibility of this method to characterize synthetic phytobricks. Following this scheme, we constructed a number of small genetic circuits, e.g. (i) a reversible switch based on site-specific recombinases, (ii) a glucocorticoid-regulated myb/bHLH transcriptional activation module, and (iii) several CRISPR/Cas9-based programmable transcriptional factors. All in all, these designs confirm that GB3.0 phytobrick documentation can serve to anticipate the qualitative behaviour of new circuit configurations.

PC1.9 SYNTHETIC EXTRACELLULAR MATRICES FROM EXTRUDED NANOFIBROUS SCAFFOLDS

WEDNESDAY 6 JULY, 2016 **10:10**

DOROTHEA BRÜGGEMANN (UNIVERSITY OF BREMEN, GERMANY)

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Cells are embedded into the extracellular matrix (ECM), which forms a complex network of different protein nanofibres and polysaccharides. This natural composite material plays a major role in many biological functions like the mechanical support of large tissues or cell adhesion and proliferation. Here, we present a novel synthetic extracellular matrix system based on extruded biopolymer nanofibres, which will help us to understand and control cellular functions on the nanoscale.Using a novel extrusion method we were able to prepare scaffolds from various biopolymer nanofibres, which resemble the nano-architecture of the native ECM. Nanoporous aluminium oxide was employed as template material to extrude different ECM proteins in physiological buffers. Thus, we obtained either randomly oriented meshes or highly aligned bundles of biopolymer nanofibres. Our extrusion approach also facilitated the first-time preparation of nanofibrous composites, which contain different proteins and polysaccharides within single nanofibres. Adjusting the nanopore diameter and protein concentration enabled us to control the diameter of single nanofibres, which we analysed with scanning electron microscopy. Most interestingly, by adjusting the pore diameter and protein concentration we were able to induce varying degrees of structural changes in extruded fibronectin fibres, which we analysed with Förster resonance energy transfer measurements in a confocal laser scanning microscope. Next, we will study the biological functionality of synthetic extracellular matrices from composite nanofibres on a cellular level to promote the design of novel tissue engineering scaffolds.

PC1.10 GENOMIC ENGINEERING BY TRANSPOSABLE ELEMENTS IN VERTEBRATES

WEDNESDAY 6 JULY, 2016 **11:00**

ZSUZSANNA IZSVÁK (MAX DELBRÜCK CENTER FOR MOLECULAR MEDICINE, GERMANY)

DNA-based transposons are natural, non-viral DNA delivery vehicles. Similarly to retroviruses, transposons integrate into the chromosomes of host cells, but their life-cycle does not involve reverse transcription, and they are not infectious. Transposon-based, integrating vectors open up new possibilities in genome engineering. Molecular reconstruction of the Sleeping Beauty (SB) transposon represents a milestone in applying transposition-mediated gene delivery in various vertebrate species. During the last decade, the SB system has been developed into a technology platform for vertebrate genetics with application areas including gene therapy, transgenesis, somatic and germline mutagenesis. These efforts revolutionized genomic manipulations in vertebrates, including tissue culture, animal biotechnology, gene function annotation to connect genetics and physiology in vertebrate models, cancer research to identify gene networks protecting against cancer, and gene therapeutic applications. The hyperactive Sleeping Beauty

(SB100X, Molecule of the Year in 2009) transposon system represents the first non-viral vector capable of stable gene transfer coupled with long-term therapeutic gene expression at a comparable efficiency to viral strategies. The SB system has advantageous attributes for stable, long-term expression both in vitro and in vivo. Regarding therapeutic application, the SB system has favourable safety profile as it has inert transcriptional activities, it does not target transcriptionally active regions for integration and has reduced immune complications. Importantly, the SB vector does not have no strict limitation of the size of expression cassettes, can tolerate larger and more complex therapeutic genes and exert relative resistance to gene silencing. The SB system has been recently translated for clinical applications.

PC1.11 SEEING GREEN: ENGINEERING GREEN LIGHT SENSITIVITY FOR PLANTS

WEDNESDAY 6 JULY, 2016 **11:30**

MARTIN W BATTLE (UNIVERSITY OF ESSEX, UNITED KINGDOM),
MATTHEW A JONES (UNIVERSITY OF ESSEX, UNITED KINGDOM)

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Light is a remarkably versatile and precise tool, the prevalent nature of which has caused it to become a common stimulus in biological processes, ranging from the incredibly complex to the beautifully simple. By engineering photoreceptor pathways into cells which are naturally unresponsive to light we are able to manipulate gene expression directly without introducing intrusive stimuli such as chemicals. The application of optogenetics to plant systems has been limited by the wide range of endogenous photoreceptors present, although plants are typically far less responsive to green light than to other parts of the visible spectrum. We have designed a green light-sensitive optogenetic construct which will allow for light controlled manipulation of gene expression in planta without influencing wild type photoreceptors. Using Golden Gate cloning, we have designed this construct with modularity in mind, allowing for the replacement of target genes in the system. Currently the system is being characterised using luciferase and YFP reporter genes as outputs but we see broad potential for future research.

PC1.12 WE DO IT OUR (PATH)WAY: BRINGING INORGANIC CARBON INTO LIFE WITH SYNTHETIC CO_2-FIXATION

WEDNESDAY 6 JULY, 2016 **13:50**

TOBIAS J ERB (MAX PLANCK INSTITUTE FOR TERRESTRIAL MICROBIOLOGY, GERMANY)

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Carbon dioxide (CO_2) is a potent greenhouse gas that is a critical factor in global warming. At the same time atmospheric CO_2 is a cheap and readily carbon source. Yet, synthetic chemistry lacks suitable catalysts to functionalize the CO_2-molecule, emphasizing the need to understand and exploit the CO_2-mechanisms offered by Nature. Here, I will (1) discuss the evolution and limitation of naturally existing CO_2-fixing enzymes and pathways. I will (2) present strategies for the *de novo*-design of CO_2-fixing reactions and pathways, and (3) outline how such artificial pathways can be realized in vitro and in vivo to create minimal CO_2-fixation modules and novel CO_2-fixing microorganisms.

PC1.13 UNTANGLING THE GLYCOSYLATION NETWORK WITH A SYNTHETIC GOLGI REACTOR

WEDNESDAY 6 JULY, 2016 **14:30**

KATE E ROYLE (IMPERIAL COLLEGE, UNITED KINGDOM),
OLEKSIY KLYMENKO (IMPERIAL COLLEGE, UNITED KINGDOM),
CLEO KONTORAVDI (IMPERIAL COLLEGE, UNITED KINGDOM),
KAREN POLIZZI (IMPERIAL COLLEGE, UNITED KINGDOM)

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Glycosylation is the co- and post-translational addition of oligosaccharides to peptide backbones. As it has important roles in structure and function, it can direct protein folding and degradation, effecting wide ranging processes including the immune response and disease. During N-linked glycosylation, enzymes of the endoplasmic reticulum and Golgi sequentially act to build and trim the oligosaccharide. Due to the numerous enzymes, their overlapping distributions, and substrate promiscuity this complex process can generate hundreds of different glycans, each with ramifications on protein function. To gain insight into the kinetic principles governing this process, we are designing and evaluating a synthetic Golgi reactor. By disengaging the glycoenzymes from the cell, we can linearize the network into individual, sequential modules and characterise them as parts, building on our fundamental understanding of the process. From an industrial viewpoint, such a reactor would allow the design and engineering of protein therapeutics. To date, our research has focused on computationally modelling the process to implement various scenarios. Results have provided guidelines for the design including structural decisions (reactor structure, enzyme immobilisation, column length), process conditions (flow rate, pressure drop and enzyme concentration) in addition to the identification and quantification of co-product inhibition. Concurrently, we are expressing and characterising human glycoenzymes and substrate regeneration pathways with a view to generating a functional prototype. Finally, we are developing a streamlined cloning method to connect with upstream protein expression and, crucially, provide a range of therapeutically relevant proteins with which to challenge and evaluate the system.

PC1.14 TRITERPENE METABOLISM ENGINEERING IN PLANTS

WEDNESDAY 6 JULY, 2016 **14:50**

AYMERIC LEVEAU (JOHN INNES CENTRE, UNITED KINGDOM),
ANNE OSBOURN (JOHN INNES CENTRE, UNITED KINGDOM)

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The research within our group focuses heavily on plant metabolic engineering. On one hand, we are interested in unravelling the biosynthetic gene networks involved in the production of high-value chemicals in plants. On the other hand, we are investigating how these may be applied to produce new-to-nature compounds with biological activities of interest. Most of our work is dedicated to the study and the production of triterpenoids, one of the most numerous and diverse groups of plant natural products with a wide range of applications in the food, cosmetics, pharmaceutical, and industrial biotechnology sectors. We are currently applying a synthetic biology approach to assemble triterpene biosynthetic pathways in various plant hosts in order to achieve crop bio-protection or production of pharmaceutical compounds. To accelerate gene discovery, functional characterisation and facilitate the building of large multigene constructs, we have developed a triterpene engineering toolkit relying on the use of the Modular Golden Gate cloning method and the Hypertrans system. Together, these enable rapid assembly and high-level expression of candidate genes and pathways in the model plant Nicotiana benthamiana. In parallel, these tools are being applied for stable transformation of major economically important crop species. Through the incorporation of gene regulatory elements from our library, the capacity to produce simple and complex triterpenes in a coordinated, tissue-specific manner is being investigated.

PC1.15 IMPROVEMENT OF RESOURCE USE EFFICIENCY AND PRODUCTIVITY IN CROP PLANTS

WEDNESDAY 6 JULY, 2016 **15:45**

GRETA NÖLKE (FRAUNHOFER IME, GERMANY), MARCEL HOUDELET (FRAUNHOFER IME, GERMANY), CHRISTOPH PETERHÄNSEL (LEIBNIZ-UNIVERSITY, GERMANY), STEFAN SCHILLBERG (FRAUNHOFER IME, GERMANY)

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The combination of global population growth, an emerging bioenergy economy and the loss of agricultural land to urbanization means that greater agricultural productivity is required per hectare of land to meet demands for food. Although boosting productivity is a significant challenge in agricultural research, one straightforward approach is to enhance the efficiency of photosynthesis and thus the amount of fixed carbon. In C3 plants, photorespiration reduces the efficiency of photosynthesis by removing carbon from the Calvin-Benson cycle, nitrogen and reducing power. Reducing the metabolic flux through the photorespiration pathway could increase resource-use efficiency, promote growth and increase yield. Here we discuss our efforts to increase the yield of potato by developing a method to enhance photosynthetic carbon fixation based on expression of a polyprotein (DEFp) comprising all three subunits (D, E and F) of *Escherichia coli* glycolate dehydrogenase (GlcDH). The recombinant DEFp was active in-planta, leading to reduction of photorespiration and strong improvement of tuber yield under greenhouse and controlled field experiment. This approach has the potential to increase the biomass and yield of diverse crops.

PC1.16 FUNCTIONAL METAGENOMIC MINING AND COMPREHENSIVE PATHWAY OPTIMIZATION USING SYNTHETIC SELECTIONS

WEDNESDAY 6 JULY, 2016 **16:15**

HANS GENEE (BIOSYNTIA APS, DENMARK), ANNE P BALI (TECHNICAL UNIVERSITY OF DENMARK, DENMARK), SØREN PETERSEN (TECHNICAL UNIVERSITY OF DENMARK, DENMARK), LUISA GRONENBERG (BIOSYNTIA APS, DENMARK), BRIAN OLSON (JOINT GENOME INSTITUTE, DENMARK), SANGEETA NATH (JOINT GENOME INSTITUTE, UNITED STATES), LEANNE CHAN (JOINT BIO-ENERGY INSTITUTE, UNITED STATES), METTE KRISTENSEN (TECHNICAL UNIVERSITY OF DENMARK, DENMARK), SCOTT HARRISON (TECHNICAL UNIVERSITY OF DENMARK, DENMARK), NATHAN HILLSON (JOINT BIO-ENERGY INSTITUTE, UNITED STATES), BO SALOMONSEN (BIOSYNTIA APS, DENMARK), MADS BONDE (TECHNICAL UNIVERSITY OF DENMARK, DENMARK), SOLVEJ SIEDLER (TECHNICAL UNIVERSITY OF DENMARK, DENMARK), EDWARD BAIDOO (JOINT BIO-ENERGY INSTITUTE, UNITED STATES), JAY KEASLING (JOINT BIO-ENERGY INSTITUTE, UNITED STATES), CHRISTOPHER PETZHOLD (JOINT BIO-ENERGY INSTITUTE, UNITED STATES), SAMUEL DEUTSCH (JOINT GENOME INSTITUTE, UNITED STATES), MORTEN SOMMER (TECHNICAL UNIVERSITY OF DENMARK, DENMARK)

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Efficient optimization of biosynthetic pathways and discovery of novel genes are key to a future of sustainable production of valuable natural products. However, the complex genotypic-phenotypic relations that govern pathway productivity render the engineering of optimized strains a slow and ad hoc process. In this talk, I present a method that deploys biosensor-based synthetic selection systems to enable high-throughput mining and functional validation of biological functions. We developed a synthetic selection system for thiamine pyrophosphate, a key co-factor of crucial interest for industrial biotechnology and human health. Using this system we mined soil and gut metagenomes for thiamine transporters and identified several members of a novel transporter class (PnuT). Using the synthetic selection approach, we further probed the substrate specificity of PnuT and identified key residues that modulate substrate specificity. Additionally, to probe the sequence-function landscape of the complex and tightly regulated thiamine biosynthesis pathway of *Escherichia coli*, and to speed up the engineering of optimized strains, we applied the synthetic selection to interrogate 16,384 refactored pathway variants that sample the synthetic design space. This approach enabled rapid identification of new and non-intuitive pathway configurations leading to high thiamine production levels. Combined, our results demonstrate how synthetic biology approaches can effectively be deployed to functionally mine metagenomes and elucidate sequence-function relationships of complex transport and biosynthesis systems in bacteria.

PC1.17 CELL-FREE METABOLIC ENGINEERING OF FINE CHEMICAL ENZYME PATHWAYS

WEDNESDAY 6 JULY, 2016 **16:35**

SIMON J MOORE (IMPERIAL COLLEGE LONDON, UNITED KINGDOM), KAREN M POLIZZI (IMPERIAL COLLEGE LONDON, UNITED KINGDOM), PAUL S FREEMONT (IMPERIAL COLLEGE LONDON, UNITED KINGDOM)

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Pathway engineering studies often neglect a key requirement to balance the supply and demand of enzyme loading at the biochemical level. Furthermore, toxic intermediates can also hinder growth and promote genetic instability, so fine tuning of gene expression is a key requirement to hit the 'metabolic sweet spot' of pathway design. Our main aim is to draw a link in how cell-free prototyping can aid pathway design *in vivo*. Using raspberry ketone as a model pathway, we have designed a synthetic cell-free enzyme competition system to quantify steady state in vitro kinetics of ketone synthesis and cofactor regeneration. This has been designed and tested to study the effects of enzyme loading and cofactor availability on metabolic flux, using LC-MS to monitor time-course reactions. We have also discovered a substrate-binding protein that fluoresces and serves as a real-time indicator of pathway activity in vitro. We are attempting to engineer this fluorescence protein as a potential small molecule biosensor to aid *in vivo* gene expression optimisation. In summary, the benzalacetone synthase represents a rate-limiting step in the pathway, whilst substrate inhibition occurs by increasing the enzyme levels of the early stage enzymes. Using this cell-free insight, we have implemented an *in vivo* pathway using combinatorial pathway refactoring and natural riboswitch insulators to improve genetic stability. To fine tune enzyme levels in synchrony with pathway flux, we are currently quantifying enzyme-GFP fusions and ^{15}N peptide LC-MS to correlate enzyme levels to pathway performance in parallel with our cell-free design.

PC1.7 OPTICALLY CONTROLLED SIGNALLING PROCESSES IN MAMMALIAN CELLS

THURSDAY 7 JULY, 2016 **09:00**

WILFRIED WEBER (UNIVERSITY OF FRIEBURG, GERMANY), KONRAD MÜLLER (UNIVERSITY OF FRIEBURG, GERMANY), MAXIMILIAN HÖRNER (UNIVERSITY OF FRIEBURG, GERMANY)

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Optical control of biological signalling processes in mammalian cells allows dissecting physiological and pathological processes with unmatched spatiotemporal resolution. By functionally rewiring plant and bacterial photoreceptors to growth factors, synthetic polymers, kinases or transcription factors, we achieve optical control along the whole signal transduction cascade. We demonstrate optically controlled reversible administration of extracellular biological and mechanical cues, the reversible activation of kinase cascades as well as the multichromatic induction of different promoters. We apply these optogenetic tools to control cell migration, mechano-signalling as well as cell differentiation.

PC1.18 LIGHT-DRIVEN PRODUCTION OF STRUCTURALLY COMPLEX DITERPENOIDS

THURSDAY 7 JULY, 2016 **10:55**

BIRGER LINDBERG MØLLER (UNIVERSITY OF COPENHAGEN, DENMARK), IRINI PATERAKI (UNIVERSITY OF COPENHAGEN, DENMARK), ALLISON MAREE HESKES (UNIVERSITY OF COPENHAGEN, DENMARK), JOHAN ANDERSEN-RANBERG (UNIVERSITY OF COPENHAGEN, DENMARK), AGNIESZKA ZYGADLO NIELSEN (UNIVERSITY OF COPENHAGEN, DENMARK), POUL ERIK JENSEN (UNIVERSITY OF COPENHAGEN, DENMARK)

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With 12,000+ known structures, diterpenoids are a prime example of bio-active natural products produced by plants. Many are used as highly valuable pharmaceuticals, fragrances, natural plant growth promoters, food ingredients such as flavors or as colorants and spices. Unfortunately, they are typically produced in minute amounts in plants and their structural complexity render them difficult to prepare from fossil resources using organic chemical synthesis. Terpenoid synthases, cytochrome P450s and acyl transferases are key multienzyme families involved in diterpenoid synthesis. Using mass spec based imaging of the target plant tissue, tracer studies, single cell-type based metabolomics and transcriptomics, functional characterization of gene candidates using transient expression in tobacco and LC-MS-NMR based structural identification, elucidation of even highly complex biosynthetic pathways is now possible within a reasonably short time frame. Terpenoid metabolism is modular right from assembly of the C5 building blocks to the final structurally complex diterpenoid. Using the approaches of synthetic biology for combinatorial biosynthesis, the functional modules may be assembled in new combinations to expand the landscape of diterpenoid structural diversity into new-to-nature structures. The entire pathway for forskolin was elucidated. Forskolin is a cyclic AMP booster approved for treatment of glaucoma but also used as a weight loss aid. The forskolin pathway is being used as test model system for large scale light driven production of high value diterpenoids following targeting of the pathway to the thylaloid membrane and using cyanobacteria or moss as photosynthetic production hosts grown in contained photo-bioreactors.

PC1.19 SYNTHETIC BIOLOGY FOR THE DESIGN OF MOLECULAR BIOORIGAMI: NEW MODULAR PROTEIN STRUCTURES AND FOLDING PATHWAYS

THURSDAY 7 JULY, 2016 **13:50**

ROMAN JERALA (NATIONAL INSTITUTE OF CHEMISTRY, SLOVENIA)

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Proteins are the most advanced nanostructures, defined by the sequence of amino acids. Nature provides a limited number of protein folds, which have been optimized during evolution. New protein folds are very challenging to design due to the delicate balance of numerous weak long range noncovalent interactions stabilizing proteins structure. Design of polypeptide-based modular polyhedra was inspired by the DNA-based nanostructures. The folding problem of proteins was bypassed by designing topological protein folds by relying on the well-understood specificity of coiled-coil dimers and used them as modules to guide the polypeptide chain between vertices of the selected polyhedral cage. The principle was demonstrated by the construction of a nanoscale protein tetrahedral cage from a single polypeptide chain composed of 12 coiled-coil forming segments. In this assembly 6 edges of the polyhedron are defined by orthogonal coiled-coil dimers. This principle represents a new platform of structural scaffold formation that could be extended to other polyhedra and for different applications. Modularity of designed structures could also allow the design of the folding pathway, which is required particularly for the design of knotted structures as the chain needs to be steered through the previously formed loops in a predefined order. Folding of knots is encoded by the arrangement of modules of different stability based on derived topological and kinetic rules. We anticipate that this strategy could be used to design the folding of other knotted programmable molecules.

PC1.20 INTERFACING GREEN AND RED SYNTHETIC BIOLOGY FOR THE UNDERSTANDING OF SIGNALING PROCESSES

THURSDAY 7 JULY, 2016 **14:30**

MATIAS ZURBRIGGEN (HEINRICH HEINE UNIVERSITY, GERMANY)

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We integrate plant and mammalian cell systems to develop synthetic chemically and light-regulated switches and biosensors for the targeted control and monitoring of cellular processes at high spatiotemporal and quantitative resolution. The synthetic tools and methods are also implemented in orthogonal cellular platforms for studying biological signaling networks, including the reconstruction of light and plant hormone responses. Central to this strategy is the development of mathematical model-descriptions of the systems. Finally we apply the knowledge obtained into biotechnological applications.

PC1.21 IN VIVO BIOSENSORS FOR MAMMALIAN BIOPROCESSING

THURSDAY 7 JULY, 2016 **14:50**

KAREN POLIZZI (IMPERIAL COLLEGE LONDON, UNITED KINGDOM), LISA GOERS (IMPERIAL COLLEGE LONDON, UNITED KINGDOM), SIMON J MOORE (IMPERIAL COLLEGE LONDON, UNITED KINGDOM), LINDA DEKKER (IMPERIAL COLLEGE LONDON, UNITED KINGDOM), PAUL S FREEMONT (IMPERIAL COLLEGE LONDON, UNITED KINGDOM)

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The ability to tailor organisms for the synthesis of useful products also allows us to input genetic circuits that can be used to report the internal state of the cell. Genetically encoded biosensors are potentially a very powerful strategy for bioprocess development where sample sizes can be very limited and non-invasive monitoring techniques can vastly improve high throughput screening strategies. We are interested in using biosensors of a variety of types to gain information on cells during bioprocessing.

This talk will focus on the example of therapeutic glycoprotein production using mammalian cell cultures. The process of glycosylation is not templated, meaning the cells produce a heterogeneous mixture of proteins bearing different glycoforms, many of which have different activities in patients. Beyond genetic modification of cells, we can manipulate the environment of cells to try and target specific glycoforms using bioprocess engineering. In my lab, we use a combination of different types of biosensors to get information the metabolism of cells during glycoprotein production to try and develop strategies for manipulating glycoform. By monitoring key metabolite concentrations and applying predictive mathematical modelling of the, we can 'tune' the glycoform to have the desired effect. In this context, my talk will focus on different types of biosensors for monitoring key metabolites in mammalian bioprocessing.

PC1.22 ENGINEERING AN EXPANDED CHEMICAL PALETTE IN CELLS

THURSDAY 7 JULY, 2016 **15:45**

HAL S ALPER (THE UNIVERSITY OF TEXAS AT AUSTIN, UNITED STATES)

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An industrial biotechnology revolution is approaching. Recent technical advances are leading to a rapid transformation of the chemical palette available in cells making it conceivable to produce nearly any organic molecule of interest-from biofuels to biopolymers to pharmaceuticals. However, these feats require the ability to 'hijack' native cellular machinery and metabolism and navigate the complexity inherent in cellular regulation. In this vain, this talk will describe recent advances in engineering various yeasts for the production of important products, such as organic acids and oleochemicals, with a focus on the synthetic biology tools and paradigms required along the way. Collectively, these case studies demonstrate the power and utility of using yeasts as a production host for chemicals.

PC2 GENERAL PLANT AND CELL BIOLOGY

ORGANISED BY: PROF VICKY BUCHANAN- WOLLASTON (UNIVERSITY OF WARWICK, UNITED KINGDOM) AND PROF JOHN LOVE (UNIVERSITY OF EXETER, UNITED KINGDOM)

PC2.1 ENVIRONMENTAL REGULATION OF STOMATAL DEVELOPMENT

📅 **MONDAY 4 JULY, 2016** 🕒 **11:00**

👤 STUART A CASSON (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), NICHOLAS ZOULIAS (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), JAMES ROWE (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), JORDAN BROWN (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), EMMA BAILEY (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM)

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Plant development is plastic and is determined by both genotype and the environment. Stomata, the microscopic pores on the leaf surface, are an excellent model for examining how environmental signals modulate plant development. Factors such as light quantity and quality as well as atmospheric carbon dioxide have a major impact on stomatal development. Our work has demonstrated that plant photoreceptors play a critical role in regulating stomatal development in response to environmental signals and consequently, significantly impact on plant performance. We will present data that examines the mechanism by which light regulates stomatal development, as well as how signals such as light and CO_2 interact to regulate this process.

PC2.2 IN THE ZONE, QUANTIFYING LEAF DEVELOPMENT AT THE CELLULAR LEVEL

📅 **MONDAY 4 JULY, 2016** 🕒 **11:15**

👤 ROSS CARTER (JOHN INNES CENTRE, UNITED KINGDOM), RACHEL PRIOR (JOHN INNES CENTRE, UNITED KINGDOM), MICHAEL BEVAN (JOHN INNES CENTRE, UNITED KINGDOM), STAN MAREE (JOHN INNES CENTRE, UNITED KINGDOM), VERONICA GRIENEISEN (JOHN INNES CENTRE, UNITED KINGDOM)

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Morphogenesis in plants occurs through a combination of cell growth and cell division. These processes are highly regulated in both time and space throughout development. In leaves and other organs with determinate growth, cell division mainly occurs in the so called ‘proliferation zone’ located towards the base of the leaf. As cells proliferate and the organ grows, it has been proposed that cells are propelled out of this putative ‘proliferation zone’ and consequently stop mitotic divisions and initiate endoreduplication, differentiation and expansion. However, very little evidence, either cell biological or mechanist, exist to support this growth model.

We have carried out a quantitative characterisation of leaf growth in Arabidopsis using a set of mutants that appear to prolong the duration of cell proliferation. Leaf growth was analysed using a combination of techniques. Whole organ confocal imaging and advanced image analysis, including custom image segmentation methods, were employed to extract quantitative data. A recently published mathematical tensor approach was used to quantify the different processes contributing to morphogenesis and our data allows us to infer cell divisions and directly measure cell shape and cell size during growth.

These measurements quantify development at the cellular level, and have generated exciting new insights into leaf growth and the mechanisms influencing cell proliferation during organ formation.

PC2.3 ADAPTING A COMMERCIAL LIGHTSHEET MICROSCOPE FOR LONG-TERM STUDIES OF ARABIDOPSIS ROOT DEVELOPMENT

📅 **MONDAY 4 JULY, 2016** 🕒 **11:30**

👤 BRITTA MC KUEMPERS (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), DARREN WELLS (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), ANTHONY BISHOPP (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM)

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Lightsheet microscopes avoid several problems of confocal microscopy such as photobleaching but they come with their own challenges especially regarding sample preparation. Several labs have built their own lightsheet microscopes but a few commercial options are available now. We have been working to adapt one of the commercial set-ups to cater to our needs using readily available Fluorinated Ethylene Propylene (FEP) tubes which are customised in our lab without the need of specialist equipment. A simple lighting system is used for different day length settings and a perfusion system allows different treatments and supplements. This enables us to grow the plant inside the microscope chamber over several days and we can follow its development throughout. The possibility to rotate the sample allows imaging from different perspectives. Using various fluorescent markers, we can follow in vivo the development and specification of the vasculature in the root tip and emerging lateral roots.

PC2.4 PHENOTYPIC CLUSTERING CHARACTERIZES THE *ARABIDOPSIS THALIANA* CELL WALL INTEGRITY MAINTENANCE NETWORK

MONDAY 4 JULY, 2016 **11:45**

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Plant cell walls fulfil essential functions during plant development and stress responses. Cell wall integrity (CWI) has to be maintained during these different processes. Although a number of possible CWI maintenance sensors and mediators have been identified, neither their specific functions nor their relationships with each other have been well resolved.

We impaired CWI by inhibiting cellulose biosynthesis using isoxaben (ISX) and analyzed the responses in mutant alleles for 22 Arabidopsis candidate genes. Quantitative data for phytohormone (jasmonic acid and salicylic acid) accumulation, ectopic lignification and root growth was integrated through phenotypic clustering to determine candidate gene functions in CWI maintenance. The results show that receptor-like kinases (RLKs) mediating plant immunity apparently only modulate the responses to CWI impairment. In parallel, treatment with cell wall-degrading enzymes only partially mimicked ISX-treatment, suggesting that responses to CWI-impairment are not dependent on intact immune signaling. The putative stretch-activated calcium channel MCA1 and the plastid-localized mechanosensitive channels MSL2/3 are required only for phytohormone accumulation, whereas the RLKs THE1 and FEI2 are required for both phytohormone and ectopic lignin accumulation. The nitrate reductases NIA1 and NIA2 are required for all ISX-induced responses, suggesting an essential function of either nitrate reduction to nitrite or nitrite reduction to nitric oxide during CWI maintenance. Our results provide a global overview of CWI maintenance signalling processes, insights into the mode of action of the mechanism and assign functions to particular candidate genes.

PC2.19 INVESTIGATING CONSERVATION OF FUNCTION FOR GRAS/SCARECROW-LIKE TRANSCRIPTION FACTORS IN ROOT ARCHITECTURE AND NODULATION

MONDAY 4 JULY, 2016 **13:55**

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Nodulation is host initiated symbiotic process between a plant and the soil rhizobia in response to specific lipochitooligosaccharides (Nod factors) produced by the bacteria in the rhizosphere. This process forms a mutually beneficial relationship whereby the plant can access nitrogen fixed in the soil in exchange for carbohydrates, via the rhizobia housed within these nodules.

Two key SCARECROW-LIKE/GRAS transcription factors have been identified within this pathway in Medicago truncatula, MtNSP1 and MtNSP2. These transcription factors are highly conserved and are present in the non-nodulating plant Arabidopsis thaliana (AtSCL29/26). Previous research in the Gifford lab has revealed a global repressive behaviour on lateral root initiation in AtSCL26 mutants, which is governed through the cell-type specific control of nitrogen and gibberellic acid regulators.

My research will investigate conservation of function of the MtSNP1/2 and AtSCL29/26 transcription factors when trans-complimented between the species under their own, and the 35s promoter. Recent research has shown a conservation function with trans-complementation of these genes between Medicago truncatula and their orthologs in Orzya sativa with nodules forming on a non-nodulating species.

PC2.20 COMPARATIVE ANALYSIS OF RNA BINDING DOMAIN CONTAINING PROTEINS IN ARABIDOPSIS AND RICE

MONDAY 4 JULY, 2016 **14:10**

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RNA Binding Domain (RBD)-containing proteins (RBPs) represent a large family of proteins comprising about 600 hypothetical members in rice. RBPs are recognized as key regulatory factors in the post-transcriptional regulation of gene expression in eukaryotes. Despite the fact that the role of RBPs in plant responses to diverse environmental stresses has been studied, only few proteins have been functionally characterized till date. Our previous studies however, showed that OsRBD1, a member of the multi-gene RBP family, interacts with an important stress regulator, OsSRO1a in rice. To get insights into the role of this multi-membered family in plants, we performed a comparative analysis of RBPs in Arabidopsis and rice. Our analysis revealed the presence of 241 RBPs in Arabidopsis and 453 RBPs in rice and these were found to be distributed on all chromosomes in both the genomes. Further, phylogenetic analysis showed that RBPs could be essentially categorized into different groups as they possessed high sequence divergence. Furthermore, in silico interactions studies in both Arabidopsis and rice revealed that RBPs interact with proteins involved in various essential functions, specifically transport and translation. Besides, we also found that in rice, RBPs often co-exist with other domains involved in diverse functions, as compared to Arabidopsis. Notably, analysis of publicly available microarray data showed these RBPs were differentially regulated in response to various abiotic stresses in both Arabidopsis and rice. Taken together, through this study we report a genome-wide analysis of RBPs in rice and Arabidopsis, highlighting their role in abiotic stress response.

PC2.21 HOOKLESS1 IS A PUTATIVE LYS-ACETYLTRANSFERASE THAT INTERACTS WITH AN ABC TRANSPORTER

MONDAY 4 JULY, 2016 **14:25**

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Lysine acetylation of non-histone proteins is an emergent post-translational modification. The number of identified Lys-acetylated proteins has been increasing steadily over the past years, and this reversible modification is now considered crucial in the regulation of important metabolic pathways. Despite advances in the characterization of mammalian and yeast Lys-acetyltransferases, the identity of their plant counterparts remains elusive. The Arabidopsis thaliana protein HOOKLESS1 (HLS1) contains an acetyltranferase domain and is localized in the nucleus and the cytoplasm of cells. This protein has previously been described as an integrator of multiple hormonal signals during plant development. When expressed in yeast, HLS1 can complement the phenotype of mutants impaired in acetylation. We show that HLS1 interacts with the A. thaliana inositol-hexakisphosphate (IP_6) transporter ABCC5 (ABC subfamily C transporter 5) using a Yeast Two-Hybrid system and Co-Immunoprecipitation. Moreover, A. thaliana plants defective in HLS1 and ABCC5 proteins share similar defects in guard cell function, which suggests that both proteins act together in guard cell signal transduction. We are currently testing the hypothesis that HLS1 can acetylate ABCC5 and thus modulate its transport activity. To our knowledge, this would be the first description of a Lys-acetyltransferase that can regulate the function of a non-histone protein in plants. It would also provide an example of how a transporter can be regulated by Lys-acetylation, and contribute to clarify the role of Lys-acetylation in the hormonal control of cellular functions.

PC2.22 REDEFINING THE ECO-PHYSIOLOGICAL DYNAMICS OF BUD DORMANCY IN GRAPEVINE

MONDAY 4 JULY, 2016 **14:35**

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Grapevine bud dormancy is a complex phenomenon orchestrated through interactions between inherent biological and ecological processes within the auxillary buds in response to environmental cues. The seasonal dynamics and intricate cellular signalling propelling dormancy are yet to be clearly understood. We followed regulation of bud dormancy from mid-summer through to spring in vines growing in the mediterranean southwest of Western Australia with prime emphasis on resolving the spatio-temporal dynamics of oxygen metabolism and signalling. The buds were deeply dormant immediately post-summer and manifested considerable dormancy release prior to winter onset which was seen reflected in the higher proportion of G1 cells (dormancy) during summer and a relatively greater proportion of G2 and S phase cells (growth), parallelled by bud hydration and increase in overall respiration late-autumn. The meristematic core of dormant buds were maintained in a hypoxic state (low pO_2 value ~5kPa) in summer and relieved to normoxia in autumn before returning to hypoxia, prior to budburst in spring when normoxia ensues. The respiratory quotients ($[CO_2]/[O_2]$) of intact buds revealed values from 0.3 to 1.5. This when viewed together with the dynamic changes in internal oxygen environment within the bud, suggests that the unusually low respiratory quotient is the product of spatial variability within the bud rather than that of swapping of respiratory substrates. Overall, there was tight regulation of cell cycle, moisture content, respiration and internal tissue oxygen environment throughout dormancy onset, maintenance and release and is speculated to influence metabolism and bud response to environmental cues.

PC2.24 METABOLOMIC ANALYSES REVEAL A ROLE FOR SALICYLIC ACID AND ALTERNATIVE OXIDASE IN CONTROL OF STRESS-INDUCED PROTEOLYSIS IN GRAZED FORAGES

MONDAY 4 JULY, 2016 **14:55**

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Inefficient capture of forage N in the rumen leads to a requirement for protein supplementation and release of nitrogenous pollutants to the environment. During grazing, endogenous plant proteases contribute to ruminal proteolysis. If this stress-induced proteolysis could be slowed, rumen nitrogen use efficiency would be improved, benefiting farmers and the environment. We tested whether the stress hormone salicylic acid (SA) would influence plant-mediated proteolysis in the rumen using the Arabidopsis thaliana SA deficient lines nahG and sid2. These lines and the wild type Col-0 (control) were subjected to anaerobic in vitro incubation at 39 o C to mimic the rumen environment with plant tissue harvested at time points between 0 h and 24 h. All leaf samples exhibited a decrease in foliar protein content in the different lines but this was significantly delayed in samples from nahG and sid2. Metabolomic analyses identified TCA cycle intermediates as sources of differences between Col-0 and SA-deficient lines. SA is known to contribute to the maintenance of electron transport and the TCA cycle during stress by inducing alternative oxidase (AOX) expression. To test the role of AOX, we examined foliar proteolytic rates in Arabidopsis lines with reduced AOX (AOX-KO) or over-expressing AOX (AOX-OE) exposed to rumen-like conditions. The AOX-OE line exhibited delayed proteolysis. We suggest that SA-mediated modulation of AOX in the rumen maintains ATP production via the TCA cycle to influence the rates of proteolysis.

PC2.25 THE METABOLISM OF POTATO DORMANCY BREAK

MONDAY 4 JULY, 2016 **15:10**

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Dormancy break during storage is a major issue for the potato production chain, with effective sprouting control being challenged by increasingly strict regulation of widely-used chemical inhibitors. A deeper understanding of the process of dormancy release is required to facilitate novel approaches to this problem. Sprouting involves the activation of meristems in which cells with the potential to divide remain in a quiescent state until triggered to proliferate. Although we have a good understanding of the transcriptional and signalling networks operating in active meristems, the link to the metabolic processes which are the ultimate cause of growth is unclear. This project addresses the fundamental question: what is the pattern of metabolism in and around the meristem as dormancy release occurs? This will give insight into both the potential mechanism of dormancy release and generate metabolic profiles for use as markers for the different stages of dormancy release. Metabolic changes associated with quiescent meristem reactivation are being studied using a metabolomics analysis (using an ESI-TOF-MS system) of a staged developmental series of dissected axillary buds. Initial metabolite markers for early dormancy response have been identified using MS/MS and are being quantified using Ultra Performance Liquid Chromatography (UPLC). Key metabolites will be imaged using MALDI to provide a high resolution spatial analysis of the patterns of metabolism that occur in and around the meristem during dormancy break, generating leads for new approaches to sprouting control.

PC2.26 QUANTIFICATION AND QTL ANALYSIS OF FOLATE CONTENT IN *SOLANUM LYCOPERSICUM × SOLANUM PIMPINELLIFOLIUM* RECOMBINANT INBRED LINES (RILs)

MONDAY 4 JULY, 2016 **15:25**

ROXANNA SEDA (UNIVERSITY OF PUERTO RICO, PUERTO RICO), BETSY AMPOFO (BOYCE THOMPSON INSTITUTE CORNELL UNIVERSITY CAMPUS ITHACA NY, UNITED STATES), ITAY GONDA (BOYCE THOMPSON INSTITUTE CORNELL UNIVERSITY CAMPUS ITHACA NY, UNITED STATES), JAMES GIOVANNONI (USDA-ARS BOYCE THOMPSON INSTITUTE CORNELL UNIVERSITY CAMPUS ITHACA NY, UNITED STATES)

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Deficiency of folate and its derivatives (vitamin B9) is a worldwide problem that can impact human health. Fruits constitute important components of the human diet, fueling the interest for the enhancement of folate content in crops. According to the USDA, tomato is the second most consumed vegetable in the U.S., but provides roughly 4% of the recommended dietary allowance of folate. The focus of this project was to identify loci affecting folate production using mapping data of a recombinant inbred lines (RILs) population by the means of quantitative trait loci (QTLs) analysis. Total folate content was determined in 103 lines of a *Solanum lycopersicum* (NCEBR1) × *Solanum pimpinellifolium* (LA2093) RIL population using a *Lactobacillus rhamnosus* microbiological assay whose growth is folate-dependent. The parents of the population showed differences in their folate content: NCEBR1 contains 9.2 µg folates/100 g FW, while the wild LA2093 contains 26.4 µg folates/100 g FW. Furthermore, significant QTLs were detected after multiple QTL mapping (MQM) analysis on chromosomes 6 and 7. Interaction plots reveal that high folate content may result from the combination of LA2093 alleles on chromosome 7 and 6 as well as from a combination of an NCEBR1 allele on chromosome 4 and an LA2093 allele on chromosome 6. These findings parallel previous S. pennellii introgression lines data where a QTL for high folate was observed on chromosome 6. These QTLs, in conjunction with RNA-seq data, will be used to facilitate the identification of candidate genes governing folate content in tomatoes.

PC2.27 A ROLE FOR THE CELL WALL IN MEDIATING PLANT FREEZING TOLERANCE

MONDAY 4 JULY, 2016 **16:10**

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Plant species vary enormously in their ability to survive freezing conditions. Many species from the cooler parts of the world can increase their tolerance of sub-zero temperatures through the process known as cold acclimation. During cold acclimation, exposure to low, non-freezing temperatures elicits a program of transcriptional, metabolic and morphological changes necessary for survival of subsequent freezing. Although studies have shown that cold acclimation results in compositional changes to the cell wall, there has been little evidence to date that these changes have any functional significance with respect to freezing tolerance. We demonstrate that a mutation known to alter cell wall structure and composition also decreases plant freezing tolerance. Arabidopsis *mur1* mutants lack the enzyme that catalyses the synthesis of L-fucose and consequently exhibit reduced fucosylation of the cell wall pectin polysaccharide rhamnogalacturonan-II (RG-II). This results in the failure of RGII monomers to dimerise via-borate ester cross-links between adjacent fucosylated side chains and leads to reduced growth and tensile strength of plants. We have demonstrated that a chemical inhibitor of fucose synthesis renders wild type plants freezing-sensitive, mimicking the *mur1* mutation. Restoring RGII cross-linking by the application of supplemental boric acid reverses the freezing-sensitive phenotype of *mur1* mutants, suggesting that freezing-tolerance is dependent upon RGII cross-linking specifically, rather than due to other consequences of of L-fucose depletion. We discuss the results of further experiments to determine whether pectin cross-linking is necessary for basal freezing tolerance or plays a role in the gain of freezing tolerance through cold acclimation.

PC2.28 PLANTS CHANGE COLD PERCEPTION SYSTEM DEPENDING ON THE ENVIRONMENT

MONDAY 4 JULY, 2016 **16:25**

HAYATO HIRAKI (THE UNITED GRADUATE SCHOOL OF AGRICULTURAL SCIENCE, IWATE UNIVERSITY, JAPAN), MATSUO UEMURA (CRYOBIOFRONTIER RESEARCH CENTER, IWATE UNIVERSITY, JAPAN), YUKIO KAWAMURA (CRYOBIOFRONTIER RESEARCH CENTER IWATE, UNIVERSITY JAPAN, JAPAN)

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Cold perception is important function for environmental adaptation of plants. Ca^{2+} signal acts as a second messenger in cold perception. Some studies, including our own, showed that several cooling conditions caused quite different shape of Ca^{2+} signals, indicating that Ca^{2+} signals may be a clue how plants sense cold. However, the detailed mechanism of cold perception is still unknown. Here, we focused on the Ca^{2+} signal to estimate the plant cold perception system through the Ca^{2+} signal. We developed the experimental system to observe Ca^{2+} signals by combining confocal cryomicroscope and transgenic Arabidopsis plants expressing FRET-based Ca^{2+} sensor Yellow Cameleon 3.60. To know the temperature range which plants can increase Ca^{2+} concentration, both non-acclimated and 2°C 7-day-acclimated plants were cooled from 2°C. In these results, non-acclimated plant showed the delay of beginning of increase in Ca^{2+} concentration, but cold-acclimated plant showed a rapid Ca^{2+} elevation when cooled from 2°C. By contrast, cold-acclimated plants could not increase Ca^{2+} concentration when they were cooled from 20°C. These results suggest that plants cannot sense wide temperature range, but can change the range. In addition, to know the difference between leaf and root, both were cooled from 20°C to 0°C. In this result, leaf cells have much longer lag time for beginning of increase in Ca^{2+} concentration compared with root cells, indicating that each cell senses low-temperature independently. In conclusion, each plant cell may sense low-temperature with regulating its sensitivity to low-temperature and temperature range for inducing Ca^{2+} signals depending on the environment.

PC2.29 A PRELIMINARY STUDY OF THE POTENTIAL OF HIGH RESOLUTION THERMAL IMAGING FOR DROUGHT TOLERANCE ASSESSMENT OF MAIZE (Z. MAIZE)

MONDAY 4 JULY, 2016 **16:40**

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Stomatal conductance and transpiration are critical variables for the assessment of crop behavior under drought, but are hardly used by breeders for practical and throughput-related reasons. Our project evaluates the potential of high resolution thermal imaging systems which provide accurate measurements of leaf temperature, which correlates theoretically, though not necessarily linearly, with stomatal conductance, transpiration and some roots characteristics. In this study, we have specifically investigated two main directions. Firstly, we have studied the potential of these systems to evaluate crop response to soil water deficit in the field. Some indices gave good performances like those that are based on the temperature of leaf below cob which was correlated to the yield. Secondly, we have tried to develop methods using thermal imaging systems to evaluate characteristics involved in drought tolerance such as roots characteristics. In the latter case, we used an inclined field where groundwater was kept artificially at constant level. The results of this experiment were partly consistent with expected root-derived responses to water deficit.

PC2.30 STOMATA UNDER STRESS: HOW GUARD CELLS RESPOND TO PATHOGEN INFECTION

MONDAY 4 JULY, 2016 **16:55**

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Stomatal closure is a mechanism by which pathogen infection is prevented. The guard cells forming the stomatal pore are highly specialized cells that translate intracellular signalling cues into a dynamic, reversible biomechanical output. This places constraints on the plasma membrane, where the pathogen-sensing receptors must be present and regulated, resulting in adaptive changes in the trafficking machineries that transport the receptors. To investigate the role of membrane trafficking in guard cells, we performed a large-scale, image-based screen and identified a Rab7 GTPase that is specific to stomatal closure induced by bacterial flagellin (flg22), uncoupled from closure triggered by abiotic stress. Time course experiments revealed thatrab7mutants fail to sustain stomatal closure in response to flg22. A possible role for this Rab7 GTPase in transport from multivesicular bodies (MVBs) to the tonoplast has previously been reported. However,rab7mutants are not generally defective in FM4-64 uptake to the vacuole as well as vacuole morphology, suggesting a potentially receptor-specific role in trafficking. The plasma membrane-localized FLAGELLIN SENSING2 (FLS2) receptor is known to internalize upon activation by its ligand flg22. Preliminary experiments suggest that flg22-induced FLS2 degradation could be altered inrab7mutants. To corroborate these initial findings, work is underway to characterise FLS2-GFP subcellular dynamics and various endomembrane compartments and selected cargoes inrab7mutant backgrounds, with stable Arabidopsis transgenic lines expressing fluorescent markers. Overall, our results reveal a specific role of membrane trafficking in the regulation of stomatal aperture in response to pathogen infection.

PC2.7 INTEGRATION MECHANISM OF COLD AND PHOTOPERIOD SIGNALS IN PLANT COLD ACCLIMATION

TUESDAY 5 JULY, 2016 **POSTER SESSION**

MAKI KANAYA (GRADUATE SCHOOL OF AGRICULTURE, IWATE UNIVERSITY, JAPAN), YOKO TOMINAGA (CRYOBIOFRONTIER RESEARCH CENTER, IWATE UNIVERSITY, JAPAN), MATSUO UEMURA (CRYOBIOFRONTIER RESEARCH CENTER, IWATE UNIVERSITY, JAPAN), YUKIO KAWAMURA (CRYOBIOFRONTIER RESEARCH CENTER, IWATE UNIVERSITY, JAPAN)

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Before winter, plants enhance their freezing tolerance to survive. This phenomenon is known as cold acclimation (CA). Signs of winter coming such as decreasing photoperiod and temperature may be triggered to start CA. Previous studies have reported that the photoperiod signal via the red/far-red photoreceptor phytochrome B (phyB) is involved in the CA pathway. However, it is still unclear how both cold and photoperiod signals are integrated in CA process. Here, we studied the effect of daily changes in photoperiod and temperature during CA, especially focusing on the role of phyB. First, two weeks-old wild-type (WT) *Arabidopsis thaliana* and *phyB* mutant seedlings were cold-acclimated at 2°C for one week under three day-length conditions: short-day, mid-day and long-day. After freezing tolerance tests (FTs), the survival rates were evaluated by chlorophyll fluorescence imaging. The results showed that longer dark period tended to result in higher survival rates at -6aC. Additionally, the survival rate of WT under the mid-day condition was significantly higher than that of phyB at -6°C. Second, to test the effect of daily temperature change, plants were acclimated at 2°C/2°C (day/night), 11°C/2°C and 11°C/11°C under the mid-day condition, and FTs were performed. The results showed that the survival rate treated at 11°C/2°C is highest in FTs at -6°C. Furthermore, the rates of WT are higher than those of phyB in all conditions. In conclusion, long dark period and daily temperature change may be playing an important role in natural CA, and *phyB* may help these processes especially before midwinter.

PC2.8 THE ROLE OF ALL SIX SIGMA FACTORS IN PHOTOSYNTHESIS, GROWTH AND DEVELOPMENT OF ARABIDOPSIS THALIANA

TUESDAY 5 JULY, 2016 **POSTER SESSION**

KELLY A ATKINS (UNIVERSITY OF BRISTOL, UNITED KINGDOM), ANTONY N DODD (UNIVERSITY OF BRISTOL, UNITED KINGDOM)

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A defining feature of higher plants is that photosynthesis in chloroplasts captures the energy within sunlight in order to fuel growth and reproduction. Following the endosymbiosis event(s) believed to underlie the origin of chloroplasts, many genes migrated to the nucleus from the ancestral chloroplast genome. Nevertheless, the chloroplast genome of higher plants encodes many essential components of the photosynthetic apparatus.

Sigma factors are bacteria-like RNA polymerase subunits that are responsible for promoter recognition and transcription initiation of chloroplast genes by plastid-encoded plastid RNA polymerase (PEP). In higher plants, sigma factors are encoded by the nuclear genome, which is thought to allow nuclear control of chloroplast gene transcription. The nuclear genome of Arabidopsis thaliana encodes six sigma factors (SIGMA FACTOR1 (SIG1)-SIG6), which are regulated by environmental cues and developmental stage. For example, SIG5 is regulated by the circadian clock and participates in the communication of circadian timing from the nucleus to the chloroplast. The relationship between all sigma factors and plant productivity is being explored in systematic comparative phenotyping studies, to elucidate their role in photosynthesis, growth and development.

PC2.9 INTERACTION OF MICRORNA160 AND *AUXIN RESPONSE FACTOR10, 16, AND 17* AFFECTS HEAT RESPONSES IN ARABIDOPSIS

TUESDAY 5 JULY, 2016 **POSTER SESSION**

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High temperature negatively affects plant growth and development, reduces crop yield, and even causes cell death. MicroRNAs (miRNAs) are one of the most important factors regulating gene expression and involved in plant growth, development, and stress defense. The roles of miRNAs in Arabidopsis under high temperature were analyzed in this study. Results indicated that *miR160* and its precursors were induced by heat; conversely, its targets, *ARF10*, *ARF16*, and *ARF17*, were significantly repressed. Transgenic plants overexpressing *miR160* precursor a (160OE) and *miR160* target mimic inhibitor (MIM160) were generated to investigate the functions of *miR160* in heat stress. The expression of *ARF10*, *ARF16*, and *ARF17* under heat stress was decreased and increased in 160OE and MIM160 plants, respectively. Under heat stress, the seed germination rates, survival rates, hypocotyl elongation lengths, and rachis lengths of 160OE were better or longer than those of WT. However, these phenotypes of MIM160 plants were reduced after heat treatment. Therefore, *miR160* regulated its target genes to regulate thermotolerance of plants. In addition, *arf10*, *arf16*, and *arf17* mutants also presented better adaption to heat than WT. These results indicated that *miR160* targets, which are *ARF10*, *ARF16*, and *ARF17*, might function as negative factors in plant under heat stress. Furthermore, the expression of *HSP70B*, *HSP21*, *HSP17.6A*, and *HSP17.6II* was affected in 160OE and MIM160 plants under heat stress. Conclusively, *miR160* and its targets altered plant development and *HSPs* expression to regulate plant responses in heat stress.

PC2.10 THE ROLE OF NODULE SPECIFIC CYSTEINE RICH (NCR) PEPTIDES IN CONTROLLING NODULATION

TUESDAY 5 JULY, 2016 **POSTER SESSION**

MINGKEE ACHOM (UNIVERSITY OF WARWICK, UNITED KINGDOM),
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Legume plants house nitrogen-fixing endosymbiotic rhizobia in specialised polyploid cells forming nodules. The plant genes involved in nodulation process and their regulatory functions have not yet been fully elucidated. Medicago truncatula,a legume with an indeterminate nodule-type has been found to express a large group of nodule-cysteine rich peptides (NCRs) (>500, Nallu et al., 2013) during the different stages of nodulation pathway.

Due to their large numbers and sequence diversity, it is possible that these genes are putatively involved as signalling molecules with multiple functions in the control of nodulation and development. Recent work has begun to shed some lights on the function of NCRs. However, these initial insights likely represent only a portion of the functional activity of this large family with diverse expression profiles. Analysis of NCR genes that are differentially expressed during nodulation and nitrogen influx discovered six motifs: motif 1 (AAGGGACAACA), motif 2 (AGAGACAT), motif 3 (TCATGAAA), motif 4 (TATAA), motif 5 (CAACACA) and motif 6 (TTTTAC) in the promoters of subsets of differentially expressed NCR genes. Since these putative promoters were strongly rhizobia and nitrogen-regulated, we suggest that NCRs may be acting as regulators of nodule numbers depending on the plant N status.

PC2.11 AGE-RELATED CHANGES IN THE EXPRESSION OF CORNIFIED ENVELOPE PROTEINS IN HUMAN SKIN

TUESDAY 5 JULY, 2016 **POSTER SESSION**

CLAUDIA NEUHOFER (DEPARTMENT OF CELL BIOLOGY AND PHYSIOLOGY, UNIVERSITY OF SALZBURG, AUSTRIA),
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The most important function of the cornified envelope (CE), the outermost layer of the epidermis, is to act as a protection barrier against different environmental factors. It consists of various lipids and proteins, for example loricrin and filaggrin, which are main components of the CE, members of the SPRR-family (Small Proline-Rich Protein) like SPRR2C, as well as SLC1A6 (Solute Carrier Family 1 Member 6). In the present work, we demonstrate that during aging dramatic changes occur in the composition of the CE. SPRR2C gene transcription is up-regulated whereas the proteins loricrin and filaggrin are down-regulated. SLC1A6 protein is expressed in the stratum corneum in aging skin while it is present in the stratum granulosum in young skin. This knowledge is of critical importance to understand chronic wound formation and ulcers in old age.

PC2.12 SUPPLEMENTAL MANGANESE REGULATES THE COORDINATED ACTIONS OF ANTIOXIDANT DEFENCE AND GLYOXALASE SYSTEM IN RICE SEEDLINGS TO MITIGATE CADMIUM TOXICITY

TUESDAY 5 JULY, 2016 **POSTER SESSION**

ANISUR RAHMAN (KAGAWA UNIVERSITY, JAPAN), KAMRUN NAHAR (KAGAWA UNIVERSITY, JAPAN), MIRZA HASANUZZAMAN (SHER-E-BANGLA AGRICULTURAL UNIVERSITY, BANGLADESH), MASAYUKI FUJITA (KAGAWA UNIVERSITY, JAPAN)

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We investigated the regulatory role of exogenous manganese (Mn) in conferring cadmium (Cd) stress tolerance in rice seedlings. Hydroponically grown 14-d-old rice (*Oryza sativa* L. cv. BRRI dhan29) seedlings were exposed to 0.3 mM $CdCl_2$ (Cd) alone and combined with 0.3 mM $MnSO_4$ (Mn) for three days. Exposure of rice seedlings to Cd caused growth inhibition, chlorosis, nutrient imbalance and higher Cd accumulation. Higher amount of Cd uptake caused oxidative stress through the overproduction of reactive oxygen species (ROS) and methylglyoxal (MG) and resulted in lipid peroxidation and loss of plasma membrane integrity. Cadmium-induced higher ROS and MG production disrupted antioxidant defence and glyoxalase system, respectively. Application of Mn in non-stressed rice seedlings did not show any significant effect, whereas, exogenous application of Mn to Cd-treated rice seedlings partly recovered Cd-induced water loss, chlorosis, growth inhibition and nutrient imbalance by reducing Cd uptake and their further translocation. Supplemental Mn increased the ascorbate (AsA) content, activities of superoxide dismutase (SOD), catalase (CAT), monodehydroascorbate reductase (MDHAR) and dehydroascorbate reductase (DHAR) in the antioxidant system, and increased the activities of glyoxalase I (Gly I) and glyoxalase II (Gly II) of glyoxalase system under Cd stress condition. The Mn-induced improved antioxidant defence and glyoxalase system reduced Cd-induced oxidative damages by reducing ROS production, MG formation, lipid peroxidation and disintegrity of plasma membrane.

PC2.13 DEVELOPING MICROBIAL EFFECTORS AS TOOLS FOR ENGINEERING PLANT PATHWAYS

TUESDAY 5 JULY, 2016 **POSTER SESSION**

WEIJIE HUANG (UNIVERSITY OF WARWICK, UNITED KINGDOM), SILKE LEHMANN (UNIVERSITY OF WARWICK, UNITED KINGDOM), ANA DOMINGUEZ FERRERAS (UNIVERSITY OF WARWICK, UNITED KINGDOM), KATHERINE DENBY (UNIVERSITY OF WARWICK, UNITED KINGDOM), PATRICK SCHAFER (UNIVERSITY OF WARWICK, UNITED KINGDOM), VARDIS NTOUKAKIS (UNIVERSITY OF WARWICK, UNITED KINGDOM)

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Most plant-interacting microbes, either pathogenic or mutualistic, are capable of delivering multiple proteins into host cells to facilitate colonization. These proteins, collectively known as effectors, have an established role in modulating the plant innate immune system. However, it has become clear that the effectors also target multiple physiological pathways and this intrinsic versatility is central for microbes to achieve a successful interaction with their hosts. Here we study the impact of microbial effectors on various plant pathways, with the aim to use them as tools for engineer bespoke pathways in planta. As a starting point, an array of effectors from the pathogenic bacterial *Pseudomonas syringae*, the oomycete *Hyaloperonospora arabidopsidis* and a mutualistic endophyte *Piriformospora indica*, are used in a protoplast-based screening to probe their functions on multiple pathways, including hormonal, abiotic stress-related, defense-related as well as other developmental pathways.

PC2.14 IDENTIFYING INFECTION-SITE-SPECIFIC TRANSCRIPTIONAL EVENTS IN THE ARABIDOPSIS RESPONSE TO DOWNY MILDEW

TUESDAY 5 JULY, 2016 **POSTER SESSION**

TIMOTHY LR COKER (UNIVERSITY OF WARWICK, UNITED KINGDOM), VOLKAN CEVIK (UNIVERSITY OF WARWICK, UNITED KINGDOM), JIM L BEYNON (UNIVERSITY OF WARWICK, UNITED KINGDOM), MIRIAM L GIFFORD (UNIVERSITY OF WARWICK, UNITED KINGDOM)

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Changes in gene expression form a crucial part of the plant response to infection, and whole-leaf expression profiling has played a valuable role in identifying genes and processes that contribute to the interactions between the model plant Arabidopsis thaliana and a diverse range of pathogens. However, with some pathogens such as downy mildew caused by the biotrophic oomycete Hyaloperonospora arabidopsidis (Hpa), whole-leaf profiling may fail to capture the complete Arabidopsis response encompassing responses of non-infected as well as infected cells within the leaf. Highly localised expression changes that occur in infected cells may be diluted by the comparative abundance of non-infected cells, or local and systemic responses of a differing nature may become conflated. To address this we applied the technique of Fluorescence Activated Cell Sorting (FACS) to the study of plant-pathogen interactions. We isolated haustoriated (Hpa-proximal) and non-haustoriated (Hpa-distal) cells from infected seedling samples using FACS, and measured global gene expression. When compared with an uninfected control, 278 transcripts were identified as differentially expressed, the vast majority of which were differentially expressed specifically in Hpa-proximal cells. By comparing our data to previous, whole organ studies, we discovered many locally responding genes that can be implicated as novel in the Hpa response, and that were uncovered for the first time using our sensitive FACS technique. We are now using transcriptional reporters to further understand expression of a subset of these genes on a spatial scale, and are exploring the effect of gene knockouts on plant susceptibility to Hpa.

PC2.15 PLANT BIOTECHNOLOGY: EXPLOITING ANTIMICROBIAL POTENTIAL OF *SPONDIAS PURPUREA*

TUESDAY 5 JULY, 2016 **POSTER SESSION**

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Plant reproductive growth is an important process, providing food and natural resources for industry. Plant extracts have served as an important source of medicine and cosmetics industries. People have been interested in obtaining active compounds from natural sources, plant extracts, could be a rich source of bioactive compounds. Secondary plant metabolites can exhibit sophisticated activities including antimicrobial activity. In this study, antimicrobial activity of hydroalcoholic extracts obtained from leafs and wood of *Spondias purpurea* were observed. These extracts were tested against bacteria and fungi by disk diffusion, MIC and MBC methods. Both extracts showed different inhibition against microorganisms in the different methods tested as also showed bactericidal or bacteriostatic capacity.

PC2.16 RESTORED PHENOTYPES BY ATG8 COMPLEMENTATION

TUESDAY 5 JULY, 2016 **POSTER SESSION**

ALANNA C. F. PEREIRA (UNIVERSIDADE ESTADUAL DE SANTA CRUZ, BRAZIL), FABIANA A. C. SILVA (UNIVERSIDADE ESTADUAL DE SANTA CRUZ, BRAZIL), CRISTINA PUNGARTNIK (UNIVERSIDADE ESTADUAL DE SANTA CRUZ, BRAZIL), MARTIM BRENDEL (UNIVERSIDADE ESTADUAL DE SANTA CRUZ, BRAZIL)

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Autophagy (ATG) is a cellular process that causes degradation of long-lived proteins and recycling of cellular components to assure survival during periods of nutritional lack or other environmental stresses. In this process *Atg8* protein is essential for formation of the system. The role of the secretory pathway in autophagy is largely by studies in yeast, the importance of the autophagy process can be verified in mutants *atg8Δ* the *S. cerevisiae* for saw present characterized phenotype already. *M. perniciosa* putative autophagy gene MpATG8 was tested by introducing it into yeast mutant *atg8Δ* and testing for heterologous expression via phenotypic sporulation complementation and TcPR-10p sensitivity, the pathogenesis-related protein PR-10 of *Theobroma cacao* has antifungal action and ribonuclease activity *in vitro*. Formation of oxygen radicals (ROS) after exposure to TcPR-10p was observed using fluorescence microscopy with dihydroethidium-stained cells. WT and mutant *atg8Δ* transformed with a single-copy vector containing Mp*ATG8* gene showed practically the same resistance to TcPR-10p and similar formation of ROS, while mutant *atg8Δ* was sensitive and exhibited increased ROS accumulation. This suggests that the protein codified by MpATG8 is functionally expressed in *S. cerevisiae* and protects against TcPR-10p whereas mutant *atg8Δ* accumulates ROS under the same conditions, also our results show the sporulation could be restored in *atg8Δ*/*atg8Δ* diploids when transformed with one copy of MpATG8.

PC2.17 IDENTIFYING AND CHARACTERISING PUTATIVE ALDOSE 6-PHOSPHATE REDUCTASES IN *ARABIDOPSIS THALIANA*

TUESDAY 5 JULY, 2016 **POSTER SESSION**

MICHAEL HANDFORD (UNIVERSIDAD DE CHILE, CHILE), KARINA OLIVOS (UNIVERSIDAD DE CHILE, CHILE), BÁRBARA ROJAS (UNIVERSIDAD DE CHILE, CHILE), PAMELA CABEDO (UNIVERSIDAD DE CHILE, CHILE), CLAUDIA STANGE (UNIVERSIDAD DE CHILE, CHILE)

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In *Rosaceae* and *Plantaginaceae* species, sugar alcohols like sorbitol are phloem-translocated and allow more efficient use of carbon, act as compatible solutes in abiotic stress and facilitate boron mobilisation. The key enzyme required for sorbitol synthesis is aldose-6-P reductase (A6PR), which reduces glucose-6-P to sorbitol-6-P, which is then converted to sorbitol. Once in sink organs, sorbitol is oxidised by sorbitol dehydrogenase (SDH) to fructose. Curiously, A6PR- and SDH-like enzyme activity is found in families that synthesise and transport sucrose, and in *Arabidopsis* (a sucrose-translocating *Brassicaceae*), we have identified two proteins with the structural features and >65% amino acid identity with known plant A6PRs; we call these AtA6PR1 and AtA6PR2. We demonstrate that *AtA6PR1* and *AtA6PR2* are differentially-expressed in different *Arabidopsis* organs. By transient transformation of tobacco, we show that GFP-fusion proteins of both reductases are localised in the cytosol. Potential mutant lines have been genotyped, and along with studies of the relative expression of both genes in wild-type plants grown under different abiotic stresses, we are determining their physiological role in this non-sorbitol translocating species. Additionally, when *AtA6PR1* is over-expressed in wild-type and sdh- mutant *Arabidopsis* lines, the starch content increases. Currently, similar experiments are underway with *AtA6PR2* with the overall aim of analysing the effects that a potential mis-balance in sorbitol metabolism has on the plant. Progress in the biochemical characterisation of these proteins will also be presented. Funding: Fondecyt 1140527 and Conicyt Master scholarship (22160896 to KO).

PC2.18 IDENTIFICATION AND CHARACTERISATION OF TWO PUTATIVE LIPOYL SYNTHASES (LIP1) IN *SOLANUM LYCOPERSICUM* (TOMATO)

TUESDAY 5 JULY, 2016 **POSTER SESSION**

MICHAEL HANDFORD (UNIVERSIDAD DE CHILE, CHILE), JORGE ARAYA (UNIVERSIDAD DE CHILE, CHILE), SIMÓN MIRANDA (UNIVERSIDAD DE CHILE, CHILE)

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Lipoic acid (LA) is a functional and structural metabolite with powerful antioxidant capacities present in eukaryotic and prokaryotic organisms. LA is both lipid- and water-soluble, and is the prosthetic group of a number of key multi-subunit enzymes complexes, including pyruvate decarboxylase and α-ketoglutarate dehydrogenase. LA synthesis and incorporation into these proteins (lipoylation) proceeds *de novo* or via a salvage pathway. During de novo synthesis, octanoyl transferase (LIP2) uses recently-synthesised octanoyl groups linked to the acyl carrier protein to transoctanylate target proteins. Subsequently, lipoyl synthase (LIP1) catalyses the final step by inserting two sulphur atoms into the prosthetic group. Whilst a number of the enzymes have been functionally-characterised in Arabidopsis thaliana, the aim of the current work is to identify and evaluate the role of this pathway in a fruit-bearing species. Towards this aim, we identified two proteins in tomato (*Solanum lycopersicum*) with the molecular characteristics of LIP1. We call these proteins SlLIP1c and SlLIP1m, which possess 78% and 84% amino acid identity with AtLIP1, respectively. Confirming bioinformatic predictions, SlLIP1c has a plastidial localisation whereas SlLIP1m is mitochondrial, as shown by confocal microscopy. Experiments to determine the molecular function of both proteins are underway, by functional complementation of a bacterial mutant, and their stable over-expression in *Arabidopsis* and tomato. Funding: Conicyt Anillo ACT-1110 (to MH), and Conicyt Doctoral (21160916 to JA) and Master (22151178 to SM) scholarships.