LA1 - LATE ANIMAL ABSTRACTS

LA1.1 REGION-SPECIFIC RESPONSE OF TIGHT JUNCTION PROTEINS IN ADULT RAINBOW TROUT SKIN TO ACUTE AND CHRONIC ION-POOR WATER TREATMENT

TUESDAY 5 JULY 2016 **POSTER SESSION**

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Freshwater (FW) fishes exist in aquatic habitats that are more dilute than their internal fluids. This leads to constant passive ion loss across all tissues exposed to the surrounding FW. Ion barrier properties of adult teleost skin in FW are well documented. Despite its complex structure and extensive contact with the external environment, the skin of adult fishes is classically regarded as a static, passive barrier to diffusional ion loss. However, there are studies demonstrating changes in passive permeability of the skin with changing environmental salinity. Previous studies have shown that several tight junction (TJ) proteins alter in transcript abundance during salinity acclimation. Despite this, almost nothing is known about how the molecular components of the TJ complex in this boundary tissue are regulated. This study examined regional TJ protein response to environmental change (acclimation to ion-poor water, IPW) in FW rainbow trout (*Oncorhynchus mykiss*) skin. Changes in spatial TJ protein abundance of the trout skin were examined during a time-course IPW acclimation. Differences in Claudin (*cldn*) mRNA abundance were detected along the dorsoventral axis of rainbow trout skin. Additionally, acute and chronic treatment with IPW resulted in an alteration of *cldn* mRNA abundance in a region-specific and time-dependent manner. Following 14 days of IPW acclimation, regional protein abundance of Cldn-8d and -10c was altered. Osmoregulatory hormones, cortisol and prolactin, and their receptors were implicated in the regulation of Cldn transcript abundance. These data provide a unique look at the region-specific regulation of TJ complex components in adult fish skin.

LA1.2 WING PETIOLATION EFFECTS ON THE STRUCTURE OF LEADING-EDGE VORTICES OVER INSECT-LIKE FLAPPING WINGS

TUESDAY 5 JULY 2016 **POSTER SESSION**

NATHAN PHILLIPS (ROYAL VETERINARY COLLEGE, UNITED KINGDOM), KEVIN KNOWLES (CRANFIELD UNIVERSITY, UNITED KINGDOM), RICHARD J BOMPHREY (ROYAL VETERINARY COLLEGE, UNITED KINGDOM)

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Insect wing shapes in the natural world are very diverse but the aerodynamic implications of wing shape changes are not well understood. We investigated the effect of one aspect of wing design known as 'petiolation' which quantifies the distance from the thorax to the wing planform. A more petiolate wing confers predictable aerobatic benefits but will require more power to flap for a given frequency and stroke amplitude. Thus, the implications for evolved wing designs are of fundamental importance. We investigated the effect of petiolation on the lift-augmenting leading edge vortex, a key flow structure exploited by many insects, using a custom-designed, mechanical flapping apparatus (the 'Flapperatus'). Five identical rectangular wings (with constant wing area and aspect ratio) with varying degrees of petiolation were fitted to the device. The wings were flapped with insect-like kinematics at an insect-relevant Reynolds number of 1400 (based on the mean wingtip speed). For each wing design, spatially-dense three-dimensional velocity measurements were taken across the entire wing span at numerous instances using Stereoscopic Particle Image Velocimetry (stereo-PIV). The resulting data were analysed to reconstruct a volumetric representation of the flow field, revealing the impacts of petiolation on the structure, size and strength of the leading-edge vortex.

LA1.3 VIDEOGRAMMETRY AS A TECHNIQUE FOR MORPHING-WINGED VERTEBRATE FLIGHT

TUESDAY 5 JULY 2016 **POSTER SESSION**

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Videogrammetry is the reconstruction of 3D surfaces through time using video data. The term is typically reserved for approaches relying upon automated feature matching and/or disparity maps using stereo camera pairs. The resulting dense cloud of points is useful in describing soft structures with continuous deformation; where shape, or change in shape, may be the measure of interest. Vertebrates change the shape of their wings during gliding and flapping flight and this capacity to morph greatly increases their aerial performance. The wings are very amenable to videogrammetry but, despite this, relatively few studies have been performed to date. For example, bats are excellent subjects because the extreme thinness (a few tens of microns) of their compliant and flexible wing membranes means that reconstruction of a single surface provides a good estimate of the complete 3-dimensional wing shape. When that shape is monitored through time, it can provide useful insights into aeroelastic phenomena. In contrast, bird wing thickness is far from negligible and requires reconstruction of both upper and lower surfaces. Fortunately, many birds frequently glide which facilitates imaging. We are using videogrammetry to explore wing and tail morphing under static and dynamic loading regimes for which shape will be the primary factor that dictates flight performance.

LA1.4 HOW ALBATROSSES AND FULMARS PREVENT A CRASH LANDING

TUESDAY 5 JULY 2016 **POSTER SESSION**

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Albatrosses and Fulmars are seabirds that have wing spans of over 3 m, which are amongst the largest of extant birds. Such a large wing span is better suitable for gliding flight than for flapping, and real flapping flight is therefore hardly observed in these birds. However, especially during slow speed flight such as take-off and landing, the static lift production of gliding flight does not suffice to provide enough lift to get or keep the bird airborne. Many smaller birds that use gliding flight as their main flight mode, e.g. gulls, switch to a short period of flapping during high lift demand. Since the long and slender wings of Albatrosses and Fulmars hardly allow for flapping due to the high inertia of the long wings, these birds show a different behaviour during take-off and landing instead, which may be associated with a different lift production mechanism. In this study we show that the oscillatory wing-tilting behaviour of Albatrosses and Fulmars during take-off and landing causes periodic lift enhancement by invoking periodic unsteady flow over the wing, providing a significant increase in average lift.

LA2 - LATE PLANT ABSTRACTS

LA2.1 MOLECULAR CYTOGENETIC CHARACTERIZATION OF RYE CHROMATIN INTROGRESSED MULTIPLE BREAD WHEAT LINES GENERATED THROUGH CHROMOSOME ELIMINATION MEDIATED DOUBLED HAPLOIDY AND SELECTION

TUESDAY 5 JULY 2016 **POSTER SESSION**

NAVDEEP SINGH JAMWAL (CSK HIMACHAL PRADESH AGRICULTURAL UNIVERSITY, INDIA), HARINDER KUMAR CHAUDHARY (CSK HIMACHAL PRADESH AGRICULTURAL UNIVERSITY, INDIA), JS (PAT) HESLOP-HARRISON (UNIVERSITY OF LEICESTER, UNITED KINGDOM), TRUDE SCHWARZACHER (UNIVERSITY OF LEICESTER, UNITED KINGDOM)

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Wheat (*Triticum aestivum*) is the major staple food crops of North-West Himalayan regions of India and always under constant pressure of abiotic and biotic stresses. The resistance to these stresses can be incorporated into cultivable wheat from certain potential sources like rye (*Secale cereale*). Besides resistance to stresses, rye can also contribute high protein and lysine content and enhanced phosphorus uptake efficiency into wheat via triticale (*x Triticosecale*) as a bridging species. In the present investigation, indigenous Himalayan rye and five elite triticale lines have been used for genetic upgradation by using doubled haploidy breeding, a non-conventional breeding technique at Molecular Cytogenetics & Tissue Culture Lab, CSKHPAU, India. Doubled haploidy breeding following *Imperata cylindrical*-mediated chromosome elimination approach is used to generate various homozygous lines from backcrosses and advanced generations of triticale × wheat and wheat x rye hybrids. Fluorescence and Genomic in *situ* hybridization (FISH & GISH) approaches are used for the screening of doubled haploids and other stable lines for identification of alien chromatin in wheat with new recombinants. Using these molecular cytogenetic tools, new substitution/addition and translocation lines have been identified in the Triticale n wheat derived recombinant, TW-6-1-4 and the Indigenous wheat × Himalayan rye derived doubled haploid, Tyari-2n rye. The doubled haploids and other stable lines have also been screened for identification of yellow rust resistant lines in mid and trans-Himalayan regions in India. The study exhibited the importance of using the diverse germplasm resources of North-West Himalayas for the targeted genetic upgradation of bread wheat.

LA2.2 THE SCHENGEN MUTANTS – HOW TO SEAL A CELL LAYER

TUESDAY 5 JULY 2016 **POSTER SESSION**

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In a forward genetic screen aimed at identifying factors involved in the formation of the endodermal diffusion barrier, three mutants were found that display a similar, specific phenotype, consisting of a fragmented, but normally localised Casparian strip. While *SGN3* and *SGN1* were found to encode an LRR receptor-like kinase and a receptor-like cytoplasmi kinase, respectively, *SGN2* turned out to be identical to TPST, an enzyme reponsible for sulfating peptide ligands. We therefore speculated that the SGN3-ligand might be a sulfated peptide, but could exclude involvement of previously known ones. Here I report on the identification of a stele expressed peptide that complements the *sgn2/tpst* CS phenotype at nanomolar concentrations and leads to strong delocalisation of Casparian Strip domain proteins (CASPs), as well as to massive overlignifiation, specifically of the endodermis - effects that are dependent of the presence of SGN3. I will propose a tentative model as to the role of this putative SGN3-ligand in ensuring the formation of a tightly sealed Casparian strip network.

LA2.3 VISUALISING PHLOEM CELL SURFACES AND TRACKING DEVELOPMENT OF THE VASCULATURE OF THE SUGAR BEET (BETA VULGARIS) STORAGE ROOT

TUESDAY 5 JULY 2016 **POSTER SESSION**

BELINDA J TOWNSEND (DEP. OF PLANT BIOLOGY CROP SCIENCE ROTHAMSTED RESEARCH, UNITED KINGDOM), RACHEL O'NEILL (DEP. OF PLANT BIOLOGY CROP SCIENCE ROTHAMSTED RESEARCH, UNITED KINGDOM), THOMAS A TORODE (CENTRE FOR PLANT SCIENCES UNIVERSITY OF LEEDS, UNITED KINGDOM), WILLIAM GT WILLATS (DEP. OF PLANT ENVIRONMENTAL SCIENCES UNIVERSITY OF COPENHAGEN, DENMARK), MADS CLAUSEN (DEP. OF PLANT ENVIRONMENTAL SCIENCES UNIVERSITY OF COPENHAGEN, DENMARK), J. PAUL KNOX (CENTRE FOR PLANT SCIENCES UNIVERSITY OF LEEDS, UNITED KINGDOM)

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Sugar beet (*Beta vulgaris subsp. vulgaris*) is grown as a commercial root crop for the extraction of sugar in temperate regions of the world. The vasculature of the sugar beet storage root is unusual, with successive supernumerary cambium that are thought to influence the amount of sucrose that can be stored in the parenchyma cells. The distance between cambial rings is important for the diffusion of sucrose and water via the apoplastic space. This work descibes a new monoclonal antibody (LM26) that has been found to bind specifically to phloem sieve elements in sugar beet roots. It binds to a galactan domain with a single galactose substitution, originally identified in garlic but not phloem specific. LM26 was used as a visual marker to track the appearance and positions of phloem cells in the sugar beet storage root. A transcriptomics study of a sugar beet storage root developmental time course overlaps the developmental stages observed using the LM26 antibody. Correlating this visual marker of development with gene expression information will identify pre-breeding targets for sugar beet with higher sucrose yields and tailored cell wall properties for industrial applications.

LA2.4 CONTROL OF LEAF CELLULAR PROLIFERATION, DIFFERENTIATION AND GROWTH BY LIGHT: ESTABLISHING AND DISTINGUISHING THE ROLES OF HORMONAL - AND SUGAR-SIGNALLING

TUESDAY 5 JULY 2016 **11:00**

SARA FARAHI BILOOEI (ROYAL HOLLOWAY UNIVERSITY, UNITED KINGDOM), BINISH MOHAMMAD (ROYAL HOLLOWAY UNIVERSITY, UNITED KINGDOM), ENRIQUE LOPEZ-JUEZ (ROYAL HOLLOWAY UNIVERSITY, UNITED KINGDOM), LACI BOGRE (ROYAL HOLLOWAY UNIVERSITY, UNITED KINGDOM)

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Light induces the shoot apical meristem to initiate the production of leaf primordia and eventually leaves, but this process is arrested in the dark. We have in the past observed that, as judged by gene expression signatures, the arrested meristem and primordia in the dark show a strong response to auxin. We now report that they also show a strong 'starvation' gene expression. These signatures are rapidly turned by light into strong cytokinin and 'feast' gene expression. The leaf primordia transfer to dark leads to disappearance of mitotic reporter activity but this will reappear in the light. Our data suggest that the seedling meristem and young leaf primordia may specifically experience carbon starvation in the dark, this being quickly repressed when transferred to the light. Plants' transfer from low light (LL) to high light (HL) results in extra proliferation and growth. A leaf grown in HL is composed of several layers of larger cells. From those observations, we propose that energy signalling processes are also central to leaf growth under natural, varying light conditions. The present study aims to identify the exact location of the observed gene expression responses of Arabidopsis meristems and leaf primordia in dark and light, investigate the signalling pathway of the starvation/feast response of meristematic activity, understand what are the different roles of both control mechanisms, and test their involvement in different light quantities. Ultimately we hope to be able to control the extent and type of leaf growth.

LA2.5 DOF DOMAIN TRANSCRIPTION FACTORS CONTROL RADIAL PATTERNING OF THE VASCULAR TISSUE IN ARABIDOPSIS

TUESDAY 5 JULY 2016 **POSTER SESSION**

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The radial pattern of a root vascular tissue develops under the influence of two plant hormones: auxin and cytokinin. Their mutually inhibitory interaction is reflected by spatially non-overlapping signalling domains. While auxin response maximum occupies the xylem axis, characterized by a fixed number of cell files, cytokinin controls radial expansion of the adjacent zones developing into procambium and phloem. Periclinal cell divisions in the root meristem gradually separate phloem sieve element (SE) from the central xylem axis. This process, however, can be interrupted by symplastic separation of the SE precursor cells from their immediate surroundings. We have identified a group of DOF domain transcription factors which are transcribed in the SE precursor cells but their protein products travel to adjacent cells to coordinate orientation of cell division and hence procambial/phloem patterning. We are currently analysing how cytokinin signalling regulates expression of the DOF genes. We are also addressing the question of how the mobility of the DOF proteins is controlled and how this influences formation of tissue borders in the vascular cylinder. We have preliminary evidence indicating that the xylem associated class III HD-ZIP transcription factors restrict mobility of DOFs.

LA3 - LATE CELL ABSTRACTS

LA3.1 ACINETOBACTER BAUMANNII PHENYLACETIC ACID METABOLISM INFLUENCES INFECTION OUTCOME THROUGH A DIRECT EFFECT ON NEUTROPHIL CHEMOTAXIS

TUESDAY 5 JULY 2016 **POSTER SESSION**

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Innate cellular immune responses are a critical first-line defense against invading bacterial pathogens. Leukocyte migration from the bloodstream to a site of infection is mediated by chemotactic factors that are often host-derived. More recently, there has been a greater appreciation of the importance of bacterial factors driving neutrophil movement during infection. Here, we describe the development of a zebrafish infection model to study A*cinetobacter baumannii* pathogenesis. Using isogenic *A. baumannii* mutants lacking expression of virulence effector proteins, we demonstrated that bacterial drivers of disease severity are conserved between zebrafish and mammals. Utilizing transgenic zebrafish with fluorescent phagocytes, we showed that a mutation of an established *A. baumannii* global virulence regulator led to marked changes in neutrophil behavior involving rapid neutrophil influx to a localized site of infection, followed by prolonged neutrophil dwelling. This neutrophilic response augmented bacterial clearance and was secondary to an impaired *A. baumannii phenylacetic* acid catabolism pathway, which led to accumulation of phenylacetate. Purified phenylacetate was confirmed to be a neutrophil chemoattractant. These data identify a previously unknown mechanism of bacterial-guided neutrophil chemotaxis in vivo, providing novel insights into the role of bacterial metabolism in host innate immune evasion. Furthermore, the work provides a potentially new therapeutic paradigm of targeting a bacterial metabolic.

LA3.2 A SIMPLE WAY TO ARREST THE METAPHASE CHROMOSOME FROM ROOT TIP CELLS OF SUNFLOWER (HELIANTHUS ANNUUS L.)

TUESDAY 5 JULY 2016 **POSTER SESSION**

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In this study, an easy and efficient metaphase chromosome preparation method from sunflower was described which can also be applied to most of the other plants. Squeezing out the meristematic cells from the root tip region onto the surface of the slide is the main step of this method, leading to monolayer and clean preparations. In order to arrest cells in metaphase, colchicine (0.05% (w/v)) for 3 hours, ice-cold water for 24 hours and colchicine (0.05% (w/v)) for 3 hours followed by ice-cold water for 24 hours were compared to each other. Metaphase index was measured by following the formula (Metaphase cells/Total cells) × 100. Ice-cold water pretreated resulted on the highest metaphase index (up to 35% in some accession of sunflower). Some preparations were used for karyotyping and some for in situ hybridization. The described method can be reliably applied the laboratory with any basic types of equipment.

LA3.3 RICE MATRIX METALLOPROTEINASE 1 GENE, A KEY REGULATOR OF CELL SHAPE AND TISSUE DEVELOPMENT

TUESDAY 5 JULY 2016 **POSTER SESSION**

PRABIR KUMAR DAS (INDIAN INSTITUTE OF TECHNOLOGY KHARAGPUR, INDIA), DR. MRINAL KUMAR MAITI (INDIAN INSTITUTE OF TECHNOLOGY KHARAGPUR, INDIA)

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Matrix metalloproteinases (MMPs) are a group of proteins present normally in the extracellular matrix (ECM) of both animal and plant systems. These proteins belong to the metzincin superfamily, and have diverse and critical functional roles in growth, development and defence. We have identified a MMP homologue gene in rice (Oryza sativa) genome through bioinformatics, and designated as OsMMP1. The cloned OsMMP1 CDS was used for preparation of different genetic constructs. One genetic construct (OsMMP1 expression driven by T7 promoter) was introduced into Escherichia coli in order to check the recombinant protein production, and another construct (OsMMP1 expression driven by 2X35S CaMV promoter) was used for stable transgenic expression in tobacco plant to develop 'gain-of-function' phenotype. The recombinant OsMMP1 protein generated in bacterium was used for various biochemical assays and raising polyclonal antibody that is required for different immunological experiments. To investigate the spatio-temporal regulation of OsMMP1 gene, transgenic tobacco plants were developed through OsMMP1 promoter-reporter gene fusion construct. Transgenic tobacco lines expressing OsMMP1 has developed different morphological and cellular alterations in reproductive stage and as well as in vegetative stage. Delayed anther dehiscence was observed in transgenic tobacco. The transgenic tobacco lines were much resistence to cell wall biosynthesis inhibitor, where control pat failed to develop normal growth. The expression of green fluorescence protein in anther, stigma, ovule, root, and leaf strogly evident that the gene plays a pivotal role in development. Results obtained from immunodetection and infiltration-centrifugation indicates that this protein is highly expressed in extracellular matrix.