Integrating the complex regulation of leaf growth by water and trophic dynamics in a functional-structural plant model of grass

Romain Barillot, Marion Gauthier, Bruno Andrieu, Jean-Louis Durand, Isabel Roldan-Ruiz, Tom de Swaef

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PLANT BIOLOGY ABSTRACTS

P1 REDOX REGULATION IN CHLOROPLASTS

ORGANISED BY: ANGEL MERIDA (CSIC SPAIN), MARIAM SAHRAWY (CSIC SPAIN) AND ANTONIO SERRATO (CSIC SPAIN)

P1.1 MECHANISMS OF PROTEIN DITHIOL-BASED REDOX REGULATION. A STRUCTURAL BIOLOGY APPROACH

TUESDAY 2 JULY, 2019 **09:00**

MÓNICA BALSERA (INSTITUTO DE RECURSOS NATURALES Y AGROBIOLOGÍA DE SALAMANCA)

@ MONICA.BALSERA@CSIC.ES

During evolution, oxyphotosynthetic organisms have developed sophisticated networks of redox signaling and modulation to regulate cell processes in response to both light and oxygen. Because of their unique physico-chemical properties, reversible chemical modification of thiols in cysteine (Cys) amino acids have acquired a prominent role as redox-sensitive thiols can act as redox switches for the control and modulation of the function of proteins. Proteins with regulatory Cys are targets of thiol-oxidoreductases, such as the thioredoxin system, which is capable of reducing disulfides in proteins connecting the redox status of enzymes to changing cellular and environmental conditions. We plan to provide structural insights into diverse mechanisms of the regulatory network based on dithiol/disulfide exchange reactions in oxygenic photosynthesis.

P1.2 SYSTEMS AND SYNTHETIC BIOLOGY OF REDOX REGULATION AND CARBON FIXATION

TUESDAY 2 JULY, 2019 **09:30**

STÉPHANE LEMAIRE (CNRS, SORBONNE UNIVERSITÉ, FRANCE)

@ STEPHANE.LEMAIRE@IBPC.FR

Redox regulation and signaling play a major role in numerous fundamental cell processes and participate in the mechanisms allowing cells to sense environmental changes and trigger adaptive responses. These regulations and signaling pathways are mainly operated by redox post-translational modifications, such as disulfide bond formation, glutathionylation or nitrosylation, which play a major role at the interface between the environment and the functional proteome. Using qualitative and quantitative large scale proteomic approaches in Chlamydomonas reinhardtii, we have unraveled an intricate redox network of more than 1000 proteins regulated by redox post-translational modifications. The Calvin-Benson cycle, responsible for photosynthetic carbon fixation, integrates multiple redox signals. Targeted biochemical and structural studies allowed to confirm the regulation of several proteins and to analyze the underlying molecular mechanisms. Synthetic biology approaches developed to study carbon fixation in Chlamydomonas will also be presented.

P1.3 NEWS ON CP12: USING CYANOBACTERIA TO HELP US UNDERSTAND ITS ROLE IN PHOTOSYNTHESIS

TUESDAY 2 JULY, 2019 **10:00**

PATRICIA E LOPEZ-CALCAGNO (UNIVERSITY OF ESSEX, UNITED KINGDOM), CHRISTINE A RAINES (UNIVERSITY OF ESSEX, UNITED KINGDOM)

@ PELOPE@ESSEX.AC.UK

Improving rates of photosynthetic carbon acquisition is an important target for increasing the potential yield of major crop species and promote food security. Recent research has demonstrated plants with greater biomass accumulation through more efficient conversion of solar energy to sugars. While these studies have focussed on a number of processes including NPQ dynamics, Calvin cycle performance and photorespiration, the manipulation of the redox regulation of photosynthesis for yield improvement remains a relatively unexploited field. We will discuss some advances in this subject, focusing on the chloroplast protein family CP12. These proteins are best known for modulating the activity of the Calvin cycle enzymes glyceraldehyde 3-phosphate dehydrogenase (GAPDH) and phosphoribulokinase (PRK), and we recently demonstrated in *Arabidopsis*, that CP12 is essential in maintaining PRK protein levels, and by doing so, maintaining photosynthesis. While higher plants have a limited variety of CP12 proteins and CP12-like proteins, homologues found in cyanobacteria have revealed a much wider a diversity. We will discuss the importance of CP12 to these organisms, and whether some of CP12's importance in maintaining PRK protein levels is conserved in the cyanobacteria *Synechocystis* sp. PCC 6803. Additionally, we will discuss the potential of exploiting these mechanisms for improving photosynthesis.

P1.4 PROTEIN ACETYLATION BY CHLOROPLAST ACETYLTRANSFERASE NSI IS NEEDED FOR STATE TRANSITIONS IN *ARABIDOPSIS THALIANA*

TUESDAY 2 JULY, 2019 **10:15**

AISTE IVANAUSKAITE (UNIVERSITY OF TURKU, FINLAND), MINNA M KOSKELA (UNIVERSITY OF TURKU, FINLAND), ANNIKA BRÜNJE (UNIVERSITY OF MÜNSTER, GERMANY), MAGDA GRABSZTUNOWICZ (UNIVERSITY OF TURKU, FINLAND), INES LASSOWSKAT (UNIVERSITY OF MÜNSTER, GERMANY), TRINH V DINH (HEIDELBERG UNIVERSITY, GERMANY), JULIA SINDLINGER (UNIVERSITY OF TÜBINGEN, GERMANY), DIRK SCHWARZER (UNIVERSITY OF TÜBINGEN, GERMANY), MARKUS WIRTZ (HEIDELBERG UNIVERSITY, GERMANY), ESA TYYSTJÄRVI (UNIVERSITY OF TURKU, FINLAND), IRIS FINKEMEIER (UNIVERSITY OF MÜNSTER, GERMANY), PAULA MULO (UNIVERSITY OF TURKU, FINLAND)

@ AISIVA@UTU.FI

Plants balance the excitation energy distribution between the photosystems II and I (PSII and PSI) in response to constantly changing light. One of the best-studied mechanisms of fine-tuning the amount of excitation energy directed to the photosystems are the state transitions. During state transitions, the mobile light-harvesting trimers (L-LHCII) change their association with the photosystems according to phosphorylation status. Phosphorylated L-LHCII is associated with PSI, thus directing more excitation energy to PSI, while the dephosphorylated form of L-LHCII is associated with PSII consequently directing more excitation energy to PSII. To date, protein phosphorylation is the only post-translational modification linked to the regulation of state transitions. In the present study we show that the NUCLEAR SHUTTLE INTERACTING (NSI) protein is an active lysine acetyltransferase and is required for state transitions in *Arabidopsis thaliana*. Intriguingly, the *nsi* knock-out plants were unable to perform state transitions, although although LHCII phosphorylation remained unaffected. Blue native gel electrophoresis revealed that despite wild type accumulation of photosynthetic protein complexes, the *nsi* plants fail to accumulate the phosphorylation dependent PSI-LHCII complex. Accordingly, chlorophyll fluorescence measurements showed a decrease in the amount of excitation energy directed to PSI. Additionally, proteomic analysis revealed several acetylation targets of NSI that could be involved in state transitions. Our results strongly suggest that NSI is a novel player required for the dynamic adaptation of plants to changing light conditions.

P1.5 REDOX CONTROL OF CHLOROPHYLL BIOSYNTHESIS

TUESDAY 2 JULY, 2019 **10:30**

BERNHARD GRIMM (HUMBOLDT-UNIVERSITÄT ZU BERLIN, GERMANY), DANIEL WITTMANN WITTMANN (HUMBOLDT-UNIVERSITÄT ZU BERLIN, GERMANY), NEHA SINHA (HUMBOLDT-UNIVERSITÄT ZU BERLIN, GERMANY), ZHIWEI HOU (HUMBOLDT-UNIVERSITÄT ZU BERLIN, GERMANY)

@ BERNHARD.GRIMM@RZ.HU-BERLIN.DE

Plants effectively coordinate the photosynthesis dependent production of energy and reducing equivalents with the activity of metabolic pathways. As the redox state of chloroplasts changes in dependency to photosynthesis activities, it is proposed that the light-dependent activation of chlorophyll biosynthesis as well as the dark suppression of 5-aminolevulinic acid (ALA) synthesis is coupled with redox control via modification of thiol groups of contributing enzymes. Thus, this posttranslational control mechanism balances chlorophyll biosynthesis in response to environmental cues and prevents accumulation of photoreactive tetrapyrrole metabolites. We previously identified several enzymes of this pathway to be targets of the reversible thiol-disulfide redox regulation by the cooperative action of the redox regulators NADPH-dependent thioredoxin reductase C (NTRC) and thioredoxin (TRX) and explored the coordinated roles of TRX m-type and f-type isoforms as well as of NTRC in the redox control of some enzymes of chlorophyll biosynthesis in triple and quadruple mutants for these redox regulators. In continuation, current results are presented about the thiol-based redox switches of the glutamyl-tRNA reductase (GluTR), ALA dehydratase (ALAD) and protoporphyrinogen oxidase (PPOX) in the pathway. Moreover, we addressed the question to which extent the dark-dependent inactivation of GluTR by the negative regulator FLU (FLOURESCENT) is based on thiol-disulfide exchange reactions.

P1.6 THE DYNAMIC REGULATION OF GRANA SIZE PLAYS A KEY ROLE IN THE OPTIMISATION OF PHOTOSYNTHESIS

TUESDAY 2 JULY, 2019 **10:45**

CHRISTOPHER DAVID HEPWORTH (THE UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), WILLIAM J WOOD (THE UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), MATTHEW P JOHNSON (THE UNIVERSITY OF SHEFFIELD, UNITED KINGDOM)

@ C.HEPWORTH@SHEFFIELD.AC.UK

Photosynthesis can be broken down into two distinct but intimately coupled sets of reactions; photosynthetic electron and proton transfer produces NAPDH and ATP, which is then consumed by the carbon fixation reactions (Calvin cycle). Due to their small pool sizes, turnover of NADPH and ATP in the chloroplast is rapid and it is therefore critical that plants balance supply with demand to avoid energy losses and photoinhibition. The linear electron transfer pathway (LET) produces ATP and NADPH in a fixed ratio of 1.28:1, while operation of the Calvin cycle requires these metabolites in a ratio of 1.5:1. One potential way of making up the shortfall is cyclic electron transfer (CET), which allows formation of ATP without net synthesis of NADPH. A critical determinant of CET is the redox poise of plastoquinone pool, which we recently found to be modulated by the size of the thylakoid grana stacks. Grana size is regulated by LHCII phosphorylation, which is controlled by the kinase/phosphatase pair STN7/TAP38. In line with this we find the *stn7* and *tap38* mutants lack the ability to modulate their grana size in response to changing light intensity. Here we compared the photosynthetic parameters of these mutants to the wild-type to understand how constitutively large (*stn7*) or small (*tap38*) grana impacts on photosynthesis under low and high light regimes. Plants with smaller grana show higher rates of CO_2 assimilation in low-light, whilst plants with larger grana perform better under high-light. Here we explore the mechanisms behind these differences.

P1.7 THE ROLE AND FUNCTION OF PLASTID TERMINAL OXIDASE AS A SINK FOR ELECTRON TRANSPORT

TUESDAY 2 JULY, 2019 **10:47**

GILES N JOHNSON (UNIVERSITY OF MANCHESTER, UNITED KINGDOM), PIOTR STEPIEN (WROCLAW UNIVERSITY OF ENVIRONMENTAL AND LIFE SCIENCES, POLAND)

@ GILES.JOHNSON@MANCHESTER.AC.UK

Plastid terminal oxidase (PTOX) was identified in mutants (*ghost, immutans*) and shown to be involved in carotenoid biosynthesis during leaf development. It has been discussed that PTOX could play a photoprotective role as a sink for electrons from Photosystem II, reducing ROS. In a number of species there is evidence that this occurs, however attempts to induce activity by overexpressing PTOX have failed. Rather, oePTOX plants have reduced fitness and increased ROS production. Our work provide insights as to where things have gone wrong and provide a way forward in using PTOX to breed stress tolerance. We have examined PTOX activity in the salt tolerant brassica *Eutrema salsigenium*. We showed that, in response to salt, PTOX is highly expressed and acts as a PSII electron sink. However, when we over-expressed the PTOX in either *Eutrema* or *Arabidopsis*, it was inactive. When *Eutrema*, but not *Arabidopsis*, oePTOX plants were salt stressed PTOX activity was induced rapidly and to a greater level than in wild type, implying that a co-factor is needed for activity. One paradox in PTOX being a PSII electron sink is that localisation studies showed these being located in different thylakoid membrane compartments – PSII in the grana stacks, PTOX on the stromal face of the stromal lamellae. This separation is expected to be a barrier to significant activity. We have now shown that, under salt stress conditions, PTOX is relocalised, migrating from the stromal lamellae to the grana, bringing it into the same fraction as PSII.

P1.8 A DEFECTIVE REDOX SIGNALLING COMING FROM TYPE-M THIOREDOXINS PROVOKES PLEIOTROPIC CHANGES IN ARABIDOPSIS THALIANA MUTANTS

TUESDAY 2 JULY, 2019 **10:49**

ANTONIO J SERRATO (SPANISH NATIONAL RESEARCH COUNCIL (CSIC), SPAIN), JOSÉ A ROJAS-GONZÁLEZ (SPANISH NATIONAL RESEARCH COUNCIL (CSIC), SPAIN), TAMARA MOLINA (SPANISH NATIONAL RESEARCH COUNCIL (CSIC), SPAIN), SABRINA BRASI (SPANISH NATIONAL RESEARCH COUNCIL (CSIC), SPAIN), DIEGO TORRES (SPANISH NATIONAL RESEARCH COUNCIL (CSIC), SPAIN), ÁNGEL MÉRIDA (SPANISH NATIONAL RESEARCH COUNCIL (CSIC), SPAIN), MARIAM SAHRAWY (SPANISH NATIONAL RESEARCH COUNCIL (CSIC), SPAIN)

@ ASERRATO@EEZ.CSIC.ES

Thioredoxins (TRXs) are small redox proteins with an active site containing two Cys and a conserved tertiary structure. TRXs catalyse the reduction of disulphide bridges in the oxidized target proteins. In plants, these reductases take part of a multigenic family, which members are classified depending on their subcellular localization and target specificities. Chloroplasts are complex organelles where key physiological processes, as photosynthesis, take place. It is maybe because this complexity that chloroplast TRXs are highly diversified, finding several types: TRX *f* (2), *m* (4), *x* (1), *y* (2) and *z* (1), with several isoforms in *Arabidopsis thaliana* (numbers in parentheses). This diversity gives an idea of the complexity of the redox-signalling network occurring in chloroplasts. As most of the chloroplast proteins are nuclear encoded, retrograde signalling (with an important redox component) is crucial to reach homeostasis. Three out of the four TRXs *m* isoforms, namely TRX *m1*, *m2* and *m4*, are the most abundant TRXs in photosynthetic tissues and have similar co-expression patterns. Our results working with *Arabidopis* single, double, and triple mutants expressing sub-optimal levels of TRXs *m* have evidenced pleiotropic changes. Mutant lines are affected negatively in (i) the biomass yield, (ii) the activation degree of enzymes of the Calvin-Benson cycle and in (iii) protective photosynthetic parameters as the non-photochemical quenching (NPQ). Additionally, some of these mutant lines seem to activate mechanisms, probably via retrograde signalling, leading to a re-modelling of the mesophyll structure as a consequence of a defective redox signalling coming from TRXs *m*.

P1.9 CHLOROPLAST SIGNALS REGULATE STOMATAL DEVELOPMENT

TUESDAY 2 JULY, 2019 **10:51**

STUART A CASSON (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), NICHOLAS ZOULIAS (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), JAMES ROWE (SAINSBURY'S LAB CAMBRIDGE, UNITED KINGDOM)

@ S.CASSON@SHEFFIELD.AC.UK

The development of stomata, the pores in the leaf epidermis, is known to be positively regulated by light and it has been demosntrated that photoreceptors regulate this process. Our data show that light can also regulate stomatal development independent of photoreceptors and operates via a chloroplast signalling pathway. Treatment with inhibitors of photosynthetic electron transport demonstrate that the redox status of the plastoquinoe pool has a critical role in regulating stomatal development. Oxidation of the PQ pool negatively regulates stomatal development, whilst reduction results in positive regulation. Oxidation of the PQ pool acts via MAP kinase signalling to negatively regulate key factors required for stomatal development, whilst reduction of the the PQ pool acts via an alternative pathway. Light is not the only signal to regulate the redox status of the PQ pool and hence this work identifies a potential mechanism through which mutliple environmental signals can regulate stomatal development.

P1.10 CHLOROPLAST DEVELOPMENT IN BARLEY LEAVES IS CONTROLLED BY WHIRLY1

THURSDAY 4 JULY, 2019 **POSTER SESSION**

NURHAYATI RAZAK (UNIVERSITY OF LEEDS, UNITED KINGDOM), CHRISTINE FOYER (UNIVERSITY OF LEEDS, UNITED KINGDOM), BARBARA KARPINSKA (UNIVERSITY OF LEEDS, UNITED KINGDOM)

@ BS13NR@LEEDS.AC.UK

The regulation of chloroplast biogenesis requires coordinated expression of genes localised in the plastome and nuclear genomes. The single-stranded DNA binding protein, WHIRLY1, which is localized in the chloroplasts and nucleus of the same cell has important but poorly characterised roles in this process. We therefore investigated the functions of WHIRLY1 in the leaves of wild type barley and two transgenic lines (W1-1 and W1-7) that have less than 5% of the wild type WHIRLY1 protein. The greening of the developing leaves was delayed in the WHIRLY1-deficient seedlings relative to the wild type. At earlier stages, the WHIRLY1-deficient seedlings had significantly lower levels of chlorophyll than the wild type. Chlorophyll a fluorescence quenching analysis revealed that the establishment of photosynthesis was delayed in the WHIRLY1-deficient leaves. The levels of nuclear-encoded chloroplast transcripts and proteins were significantly higher in the WHIRLY1-deficient leaves than the wild type. In contrast, the levels of transcripts and proteins encoded by the plastome were significantly lower in the wild type than the WHIRLY1-deficient seedlings, despite the fact that the WHIRLY1-deficient leaves. The W1-1 and W1-7 leaves had double the amount of plastid DNA (ptDNA) than the wild type, both at the early stages of development (7 days) and in green (3-week-old) leaves. The WHIRLY1-deficient seedlings showed aberrant splicing of plastid rRNAs (23S rRNA and 4.5S rRNA) and were deficient in plastid ribosomal proteins. These results demonstrate that WHIRLY1 is required for the development of fully functional chloroplasts but only at the early stages of leaf development.

P1.11 FIBRILIN-ASSISTED INTERACTION OF THIOREDOXINS M WITH THYLAKOID MEMBRANES

WEDNESDAY 3 JULY, 2019 **POSTER SESSION**

ANGEL MERIDA (INSTITUTO DE BIOQUIMICA VEGETAL Y FOTOSINTESIS, CSIC-US, SPAIN), DIEGO TORRES (INSTITUTO DE BIOQUIMICA VEGETAL Y FOTOSINTESIS, CSIC-US, SPAIN), ANTONIO J SERRATO (ESTACIÓN EXPERIMENTAL DEL ZAIDÍN, CSIC, SPAIN), ALFONSO LAZARO (ESTACIÓN EXPERIMENTAL DEL ZAIDÍN, CSIC, SPAIN), MARIAM SAHRAWY (ESTACIÓN EXPERIMENTAL DEL ZAIDÍN, CSIC, SPAIN)

@ ANGEL.MERIDA@CSIC.ES

Photosynthesis uses light as an energy source to take out electrons from water to reduce ferredoxin (Fd), which delivers electrons to the ferredoxin-thioredoxin reductase (FTR), providing reducing power to the thioredoxin (TRX) system. TRXs are redox proteins with the canonical active site WC(G/P)PC. There are several types of chloroplast TRXs: f, m, x, y and z. Each TRX type can have several isoforms, the more complex being the m-type, with four isoforms in the plant model *Arabidopsis thaliana*: TRX m1, m2, m3 and m4. Some authors have reported that TRXs m are able to deliver reducing equivalents into the thylakoid lumen through the thylakoid-membrane protein CCDA. Nevertheless, as far as we know, no direct interaction with the internal membrane system has been shown. Besides, proteomic analyses have reported the presence of stromal proteins in thylakoid-associated lipoprotein bodies called plastoglobules. The boundary layer of plastoglobules is coated by structural proteins called fibrilins (FBNs). Our working hypothesis is based on the idea that FBNs, in addition to their structural role, might function as anchor points for stromal proteins as TRXs m. By using the technique of Bimolecular Fluorescence Complementation (BiFC) we have demonstrated that TRXs m1, m2 and m4 can interact in vivo with FBN2 and FBN4, two FBNs co-expressed with redox proteins. Moreover, by immuno-blotting experiments, TRXs m have been detected in thylakoid membranes fractions. These results suggest that FBNs might be regulating or assisting the interaction of the TRX system with their non-stromal targets.

P1.12 CHLOROPLAST SIGNALS REGULATE STOMATAL DEVELOPMENT

THURSDAY 4 JULY, 2019 **POSTER SESSION**

NICHOLAS ZOULIAS (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), JAMES ROWE (SAINSBURY LABORATORY, CAMBRIDGE UNIVERSITY, UNITED KINGDOM), STUART CASSON (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM)

@ N.ZOULIAS@SHEFFIELD.AC.UK

As sessile organisms, plants need to adapt and coordinate their intrinsic developmental programmes with environmental signals such as light, CO_2 and temperature. Light has a critical role in regulating plant growth and development and photoreceptors play a key role in perceiving the light environment and initiating signalling events that control multiple developmental pathways. Using genetic and molecular techniques we have investigated the mechanisms by which light is able to modulate stomatal development. Through our research we have uncovered evidence of a photoreceptor independent light signalling mechanism originating from the chloroplast, regulating stomatal development. Disruption of electron transport from photosystem II to the plastoquinone, with the photosynthetic inhibitor DCMU resulted in a suppression of the stomatal development pathway. Our results indicate that the redox status of the plastoquinone pool is able to regulate stomatal development.

P1.13 OXYGEN PHOTOREDUCTION WHICH IS INVOLVED IN REDOX REGULATION IN CHLOROPLASTS IS STILL POORLY UNDERSTOOD

WEDNESDAY 3 JULY, 2019 **POSTER SESSION**

IRINA STRIZH (M.V. LOMONOSOV MOSCOW STATE UNIVERSITY, RUSSIA)

@ IRINA.STRIZH@MAIL.RU

Chloroplast is a very important organelle of a plant cell, which lives particularly autonomously but also gets and sends numerous signals from and to the cell of the host plant, and also donates metabolites necessary for the development of the plant. Oxygen photoreduction or the so-called Mehler reaction is the well-known phenomenon: it occurs during the high flow rate of electrons, especially under stress, when most reactions related to biochemistry proceed slowly, and electron transfer to oxygen has a much higher reaction rate constant. It is very difficult to detect the amount and path of the photoreduced oxygen due to the unstable form of superoxide anion or hydrogen peroxide, which react quickly with biomolecules. Even modern nanosensors for the reactive oxygen species cannot help to sufficiently clarify the processes that occur in the following chain: stress–slowing down biochemical reactions–photosynthetic electron flow still works–alternative acceptors, especially oxygen, accept electrons–active oxygen forms oxidize biomolecules, which can transmit a signal to the nucleus to trigger the stress response mechanism. Mathematical modeling based on the experimental biophysical and biochemical data of this process seems to be the one of the promising ways.

P2 AN EXTENDED PLANT PHENOTYPE: CHARACTERISING PLANT–SOIL MICROBIOME INTERACTIONS

ORGANISED BY: GABRIEL CASTRILLO (UNIVERSITY OF NOTTINGHAM), MALCOLM BENNETT (UNIVERSITY OF NOTTINGHAM), KARL RITZ (UNIVERSITY OF NOTTINGHAM) AND LAURENT LAPLAZE (IRD)

P2.1 DISSECTING THE ROLE OF MULTI-KINGDOM MICROBIAL CONSORTIA ON PLANT HEALTH

THURSDAY 4 JULY, 2019 **14:10**

STÉPHANE HACQUARD (MAX PLANCK INSTITUTE FOR PLANT BREEDING RESEARCH, GERMANY), PALOMA DURAN (MAX PLANCK INSTITUTE FOR PLANT BREEDING RESEARCH, GERMANY), THORSTEN THIERGART (MAX PLANCK INSTITUTE FOR PLANT BREEDING RESEARCH, GERMANY), THOMAS ELLIS (DEPARTMENT OF PLANT ECOLOGY AND EVOLUTION, EVOLUTIONARY BIOLOGY CENTRE, UPPSALA UNIVERSITY, SWEDEN), RUBEN GARRIDO-OTER (MAX PLANCK INSTITUTE FOR PLANT BREEDING RESEARCH, GERMANY), CARLOS ALONSO-BLANCO (CENTRO NACIONAL DE BIOTECNOLOGÍA, DEPARTAMENTO DE GENÉTICA MOLECULAR DE PLANTAS, SPAIN), ERIC KEMEN (DEPARTMENT OF MICROBIAL INTERACTIONS, IMITZMBP UNIVERSITY OF TÜBINGEN, GERMANY), FABRICE ROUX (LIPM INRA CNRS UNIVERSITÉ DE TOULOUSE, FRANCE), JON ÅGREN (DEPARTMENT OF PLANT ECOLOGY AND EVOLUTION, EVOLUTIONARY BIOLOGY CENTRE, UPPSALA UNIVERSITY, SWEDEN), PAUL SCHULZE-LEFERT (MAX PLANCK INSTITUTE FOR PLANT BREEDING RESEARCH, GERMANY)

@ HACQUARD@MPIPZ.MPG.DE

Roots of healthy plants are inhabited by soil-derived bacteria, fungi, and oomycetes that have evolved independently in distinct kingdoms of life. How these microorganisms interact and to what extent those interactions affect plant health are poorly understood. We monitored microbial communities at the soil-root interface in 17 European *Arabidopsis thaliana* populations across three successive years. Analysis of 5,625 microbial community profiles demonstrated that the root endosphere drives convergence in microbial community structure across sites, with few habitat-generalist taxa disproportionately colonizing plant roots across Europe. With a field reciprocal transplant between two native *A. thaliana* populations in northern and southern Europe in which soil conditions were manipulated in two different climates, we demonstrate that continental-scale variation of the root microbiota is affected by soil type and climate, but not by host genotype. Signatures of mutual exclusion were observed between bacteria and filamentous eukaryotes in plant roots across European sites, suggesting microbial inter-kingdom competition for the root niche. To test this hypothesis, we established bacterial, fungal, and oomycetal culture collections for reconstitution experiments using germ-free *A. thaliana*. In plants inoculated with mono- or multi-kingdom synthetic microbial consortia, we observed a profound impact of the bacterial root microbiota on fungal and oomycetal community structure and diversity. We demonstrated that the bacterial microbiota is essential for plant survival and protection against root-derived filamentous eukaryotes and showed that biocontrol activity of bacterial root commensals is a redundant trait that maintains microbial inter-kingdom balance for plant health.

P2.2 NON-TARGET EFFECTS ON THE SOIL MICROBIOME OF A BIOLOGICAL CONTROL FOR *FUSARIUM OXYSPORUM* F.SP. *CUBENSE*

THURSDAY 4 JULY, 2019 **14:40**

DANIEL P BEBBER (UNIVERSITY OF EXETER, UNITED KINGDOM), DAVID J STUDHOLME (UNIVERSITY OF EXETER, UNITED KINGDOM), RACHEL WARMINGTON (EDEN PROJECT, UNITED KINGDOM), BEN TEMPERTON (UNIVERSITY OF EXETER, UNITED KINGDOM), HELEN FONES (UNIVERSITY OF EXETER, UNITED KINGDOM)

@ D.BEBBER@EXETER.AC.UK

Fusarium oxysporum f.sp. *cubense* (Foc), or Fusarium Wilt, is the most feared disease for commercial banana producers globally. Control of the disease is hampered by ineffective fungicides (thought to be due to the soilborne nature of the infection), and the laborious process of banana breeding which can take decades. Much recent research has focussed on the potential for biological control of TR4 using microbes and plants. Chinese leek (*Allium tuberosum*) has root exudates effective against Foc in vitro. However, little is known of the wider soil microbiome impacts of this biocontrol in particular, nor of biological controls in general. We tested the hypothesis that *Allium tuberosum* root exudates reduce the species-richness and diversity of the soil fungal microbiome, using pot trials conducted at the Eden Project, Cornwall. Pots were grown with soil only, with Allium only, with bananas only, and with both Alliums and bananas. After 3 months, soils were sampled (both bulk soil and rhizosphere

soil), DNA extracted, and fungal ITS12 and ITS34 regions amplified and sequenced. We found that, while there were no clear differences in fungal diversity among treatments, there were strong effects of Allium alone and banana alone on soil fungal community composition. Importantly, fungal community composition did not differ between banana alone, and banana with allium, indicating that the banana rhizosphere community is maintained in the presence of the biocontrol agent. This suggests that Allium could be used to control Foc without significant non-target impacts on the soil microbiome.

P2.3 EFFECTIVENESS IN THE RHIZOBIA PLANT SYMBIOSIS AND MODULATION BY SOIL ENVIRONMENT

THURSDAY 4 JULY, 2019 **14:55**

BEATRIZ LAGUNAS (UNIVERSITY OF WARWICK, UNITED KINGDOM), CHRYSI SERGAKI (UNIVERSITY OF WARWICK, UNITED KINGDOM), RANA M F HUSSAIN (UNIVERSITY OF WARWICK, UNITED KINGDOM), PATRICK SCHÄFER (UNIVERSITY OF WARWICK, UNITED KINGDOM), MIRIAM L GIFFORD (UNIVERSITY OF WARWICK, UNITED KINGDOM)

@ B.LAGUNAS-CASTAN@WARWICK.AC.UK

Increasing plant productivity whilst minimising environmental impact is essential to achieve food security to sustain an increasing human population. Nitrogen is the main limiting nutrient for plant production. Although very abundant, it is often unavailable to plants. Legumes have developed the ability to interact with symbiotic bacteria (rhizobia), overcoming the lack of nitrogen availability in soil. In this mutualistic partnership, the rhizobia fix nitrogen from the air and supply it to the plant in exchange for carbon and amino-acid compounds. There are variations on the process efficiency outcomes depending on the plant but also the bacterial strain and the environment chosen for study. As a first approach to investigate this plant-microbe-soil complex system we are characterising the colonisation of the legume *Medicago truncatula* by three different rhizobial strains and in three different soils that vary in texture and nutrient availability. We found that inoculation with two strains led to enhanced plant yield in all environments studied but that this yield increase varied by soil type. We then analysed the influence of rhizobial inoculation on endosphere, rhizosphere and bulk soil microbiome compartments. To evaluate the impact of the microbial communities in the phenotypes observed we also performed phenotyping in our soils after gamma-irradiation. Our results shed light on the complexity of the system we are studying and the current limitations to evaluate the plant-soil-microbe continuum.

P2.4 BACTERIAL COMMUNITY MAINTENANCE OF PLANT ROOT DEVELOPMENT

THURSDAY 4 JULY, 2019 **15:10**

ISAI SALAS-GONZALEZ (THE UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL, UNITED STATES), OMRI FINKEL (THE UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL, UNITED STATES), GABRIEL CASTRILLO (THE UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), JEFF DANGL (THE UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL, UNITED STATES)

@ ISAI.SALAS.GONZALEZ@GMAIL.COM

Plants intimately associate with microbial communities collectively known as the plant microbiome. The microbiome contributes to plant processes such as development, nutrient acquisition and pathogen protection. The establishment of community assembly rules and community-host feedback patterns has been limited due to the complexity of natural microbial communities. Here, we applied a synthetic ecology approach to an amenable plant-microbiome microcosm to unravel novel community-host and microbe-microbe interactions. *Arabidopsis thaliana* plants were inoculated across a gradient of phosphate, salinity, pH and temperature conditions with a genome-sequenced bacterial inoculum composed of 185 phylogenetically diverse isolates (SynCom). Colonization patterns across the fractions and conditions sampled were quantified using 16s amplicon sequencing. We used the correlation of these abundance profiles among all members of the community to split the SynCom into four modules which exhibited a characteristic colonization pattern and high phylogenetic coherence. Subsequently, we measured plant molecular and morphological phenotypes when inoculated with each of these modules independently and in combination. Plant phenotypes induced by some modules were attenuated when co-inoculating with other modules exhibiting ecological epistasis between guilds in the community. Following our top-down approach, we identified a single genus that was responsible for dampening the effects that all other members of the community exerted over the root morphology of the plant. This demonstrates that in the context of a complex community there are multiple interactions that strongly influence plant development and that a balanced microbiome is required to equilibrate these interactions and prevent host dysbiosis.

P2.5 CHARACTERISATION OF THE REGULATORY INTERPLAY BETWEEN THE PLANT MICROBIOME AND ROOT ENDODERMAL CELL WALL DIFFUSION BARRIERS

THURSDAY 4 JULY, 2019 **15:40**

GUILHEM REYT (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), ISAI SALAS GONZALEZ (UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL, UNITED STATES), PAULINA FLIS (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM)

@ GUILHEM.REYT@NOTTINGHAM.AC.UK

Plant-associated bacteria are crucial in host adaptation to diverse environmental stresses. Beneficial microbes increase nutrient uptake and use in the host, improving plant growth and health. The capacity to colonise roots is the main factor that determines beneficial microbe's effectiveness for plant growth enhancement. Roots have evolved bi-directional diffusion barriers at the endodermis to control the flow of water and nutrients between the soil and xylem. These barriers are comprised of Casparian strips (CS) and suberin in endodermal cell walls. Mutations that disrupt these barriers cause significant alterations in normal mineral nutrient homeostasis. It is unknown how the plant root diffusion barriers and plant microbiota coordinate to control the ions balance in the plant. Here we demonstrate that the root diffusion barriers genetic control influences the plant microbiome. We identified bacterial strains that impact the function of the root barriers modulating the ion homeostasis in the plant. We further demonstrate that plant microbiota modulates the synthesis of CS and suberin under stress conditions. Our work will provide a better understanding of the role of bacteria in root function and will provide vital information for the development of effective field bio-inocula to promote useful agronomic gains.

P2.6 FUNCTIONAL SIGNATURES OF SOIL MICROBIAL COMMUNITIES IN RESPONSE TO TREE PHENOLOGY AND FOREST RESIDUE HARVESTING REVEALED BY META-OMICS ANALYSIS

THURSDAY 4 JULY, 2019 **16:40**

MARC BUÉE (INRA NANCY GRAND EST - UNIVERSITÉ DE LORRAINE, FRANCE), LUCAS AUER (INRA NANCY GRAND EST, FRANCE), FRANÇOIS MAILLARD (INRA NANCY GRAND EST, FRANCE), VINCENT LOMBARD (CNRS - AIX-MARSEILLE UNIVERSITÉ, FRANCE), BERNARD HENRISSAT (CNRS - AIX-MARSEILLE UNIVERSITÉ, FRANCE), BRIAN FOSTER (JOINT GENOME INSTITUTE, US DEPARTMENT OF ENERGY, UNITED STATES), KERRIE BARRY (JOINT GENOME INSTITUTE, US DEPARTMENT OF ENERGY, UNITED STATES), IGOR GRIGORIEV (JOINT GENOME INSTITUTE, US DEPARTMENT OF ENERGY, UNITED STATES), ANNEGRET KOHLER (INRA NANCY GRAND EST, FRANCE), FRANCIS MARTIN (INRA NANCY GRAND EST, FRANCE)

@ MARC.BUEE@INRA.FR

In forest ecosystems, soil microbes play key roles in carbon (C) sequestration and biogeochemical cycles. For example, fungi can act as decomposers of organic matter (OM) or also as driving forces in plant productivity through mycorrhizal symbiosis, providing soil-derived nutrients to their host. However, some environmental levers could strongly affect the soil microbiome functioning, related to C cycling. Therefore, we studied the impacts of tree phenology (seasonality of tree photosynthesis) and harvesting of forest residues (e.g. branches and litter layer) on microbial diversity and functions, in particular on micro-eukaryotic functional diversity. We performed two metatranscriptome studies from French forest soils sampled during two contrasted seasons or in an experimental site subjected to OM removal effects. For the first approach, we focused on fungal communities, coupling analyses of poly-A mRNA regulation with metabarcoding approaches targeting fungal DNA, and we sequenced all soil "meta-transcripts". Thanks to a ribo-depletion protocol, the second approach allowed studying simultaneously fungal and prokaryotic communities, supplemented by microbial metabarcoding also. In addition to the NCBI database, large-scale genome sequencing projects of fungi (https://genome.jgi.doe.gov/mycocosm/home) provided the references for the fungal metatranscriptomics data annotations. Moreover, the regulation of specific Carbohydrate-Active Enzyme families was investigated within bacteria community and between the ectomycorrhizal fungi and the other fungal guilds. These results reveal the relative contributions of microbial functional groups to carbon cycling and tree nutrition. Finally, these innovative projects reveal that metatranscriptomics is a promising tool for prediction of quantitative capabilities of microbiome functions in plant–soil microbe interactions.

P2.7 SYMBIOTIC *PAENIBACILLUS* SP. BACTERIUM FROM HYBRID ASPEN SHOOT CULTURE PROMOTES ROOT DEVELOPMENT IN OTHER PLANT SPECIES

THURSDAY 4 JULY, 2019 **17:10**

JONAS ZIAUKA (LITHUANIAN RESEARCH CENTRE FOR AGRICULTURE AND FORESTRY, INSTITUTE OF FORESTRY, LITHUANIA), MINDAUGAS VITKEVICIUS (VYTAUTAS MAGNUS UNIVERSITY, LITHUANIA), GABRIELE SURBLYTE (KAUNAS UNIVERSITY OF TECHNOLOGY, LITHUANIA), SIGUTE KUUSIENE (LITHUANIAN RESEARCH CENTRE FOR AGRICULTURE AND FORESTRY INSTITUTE OF FORESTRY, LITHUANIA)

@ ZIAUKA@GMAIL.COM

The studied bacterium was isolated from the in vitro culture of hybrid aspen (*Populus tremuloides* × *P. tremula*) shoot segments and identified as *Paenibacillus* sp. The ability of this bacterium to regulate plant development was tested by purposely inoculating the in vitro cultures of normally bacterium-free aspen (*P. tremula*) genotypes and apple (*Malus domestica*) seedlings. The influence of *Paenibacillus* sp. on the number of roots and shoots of aspen explants was noticed during the tests: after 6 weeks from the inoculation, the explants in inoculated cultures had 2.7-times more adventitious roots and 1.6-times more shoots than in the control group. A similarly designed experiment with the in vitro culture of isolated apple embryos revealed a positive effect of this *Paenibacillus* sp. bacterium on lateral root development: the seedlings developed from inoculated cultures had 1.8-times the number of lateral roots and their lateral roots were 1.8-times longer than in the control group. In conclusion, the obtained results point to the *Paenibacillus* sp. bacterium from hybrid aspen shoot culture as a potential positive root development regulator in different plant species.

P2.8 M-TROPHS FOR SUSTAINABLE AGRICULTURE

THURSDAY 4 JULY, 2019 **17:25**

NATALIE W BREAKFIELD (NEWLEAF SYMBIOTICS, UNITED STATES)

@ NBREAKFIELD@NEWLEAFSYM.COM

Pink-pigmented facultative methylotrophs in the genus *Methylobacterium* (M-trophs) are highly abundant members of the plant microbiome. NewLeaf Symbiotics is harnessing the power of these beneficial, native bacteria to improve yield and strengthen plants under field conditions. Every M-troph in our collection is sequenced, annotated, and stored in our computational bioinformatics platform, the Prescriptive Biologics® Knowledgebase (PBK). The beneficial nature of M-trophs allows NewLeaf to nominate strains for field trials based on maximizing genomic diversity, identifying characteristics common in successful fermentations and formulations, and determining compatibility with commonly used Ag chemistries. The PBK is used to correlate genotypes with phenotypes, and subsequent testing allows us to further refine the correlations and make predictions. By focusing on this one genus with many beneficial characteristics, we have developed this powerful comparative genomics approach to deliver products that are well adapted to sustainable agriculture.

P2.9 RHIZOSHEATH FORMATION IN PEARL MILLET: PHYSIOLOGICAL BASES AND GENETIC CONTROL

FRIDAY 5 JULY, 2019 **09:00**

LAURENT LAPLAZE (LAURENT LAPLAZE, FRANCE), MAMADOU S NDOUR (INSTITUT DE RECHERCHE POUR LE DÉVELOPPEMENT, FRANCE), MARILYNE DEBIEU (INSTITUT DE RECHERCHE POUR LE DÉVELOPPEMENT, FRANCE), MARCEL N DIOUF (INSTITUT DE RECHERCHE POUR LE DÉVELOPPEMENT, FRANCE), ALEXANDRE GRONDIN (INSTITUT DE RECHERCHE POUR LE DÉVELOPPEMENT, FRANCE), CARLA DE LA FUENTE CANTO (INSTITUT DE RECHERCHE POUR LE DÉVELOPPEMENT, FRANCE), MOHAMED BARAKAT (CEA, FRANCE), PHILIPPE ORTET (CEA, FRANCE), HANG NGAN DINH (INSTITUT DE RECHERCHE POUR LE DÉVELOPPEMENT, FRANCE), MARIAMA NGOM (INSTITUT DE RECHERCHE POUR LE DÉVELOPPEMENT, FRANCE), MAXIME STEFFEN (INSTITUT DE RECHERCHE POUR LE DÉVELOPPEMENT, FRANCE), SIXTINE PASSOT (INSTITUT DE RECHERCHE POUR LE DÉVELOPPEMENT, FRANCE), ANTONY CHAMPION (INSTITUT DE RECHERCHE POUR LE DÉVELOPPEMENT, FRANCE), CÉLIA BARRACHINA (CNRS, FRANCE), MARINE PRATLONG (CNRS, FRANCE), PASCAL GANTET (UNIVERSITÉ DE MONTPELLIER, FRANCE), PRAKASH GANGASHETTY (ICRISAT, NIGER), NDJIDO A KANE (ISRA, SENEGAL), ABDALA G DIEDHIOU (UNIVERSITÉ CHEIKH ANTA DIOP, SENEGAL), THIERRY HEULIN (CNRS, FRANCE), WAFA ACHOUAK (CNRS, FRANCE), YVES VIGOUROUX (INSTITUT DE RECHERCHE POUR LE DÉVELOPPEMENT, FRANCE), LAURENT COURNAC (INSTITUT DE RECHERCHE POUR LE DÉVELOPPEMENT, FRANCE)

@ LAURENT.LAPLAZE@IRD.FR

Pearl millet is a cereal crop that plays a major role for food security in arid regions of sub Saharan Africa and India. It is mainly grown in areas characterized by low-rainfall and poor soils. We are exploring root traits that might be used to breed pearl millet with better water and nutrient acquisition. Plants are able to modify the biophysical characteristics of the surrounding soil. In some species including pearl millet, a rhizosheath, i.e. a layer of soil that adheres strongly to roots on excavation (root-adhering soil), is produced and influences water and phosphate acquisition. However, the genetic bases of rhizosheath formation are still largely unknown. We previously showed that root-adhering soil mass is a highly heritable trait in pearl millet with a large diversity and correlated with changes in soil microbial communities. Here, we analysed how rhizosheath formation is related to root architecture, root hairs and mycorhizal traits. Moreover, we performed genetic association analysis using a panel of 181 inbred lines with 392,493 SNPs identified using Genotyping-by-Sequencing (GBS). Correcting for genetic relatedness, GWAS identified five QTLs for rhizosheath formation that were mapped to the pearl millet genome. Variations of allele frequency at the targeted regions in bulked pools of lines with extreme phenotypes are currently studied to validate these QTLs. In parallel, comparison of global gene expression in the root tip of contrasted inbred lines using RNAseq revealed 1270 differentially expressed genes. Candidate genes were identified by combining GWAS and RNAseq results and are further analyzed.

P2.10 MICROBIAL DIVERSITY AND ACTIVITY IN RHIZOSPHERE OF DIFFERENT PEARL MILLET LINES UNDER GREENHOUSE AND FIELD CONDITIONS

FRIDAY 5 JULY, 2019 **09:30**

PAPA MAMADOU SITOR NDOUR (IRD, FRANCE), CHEIKH M BARRY (UCAD, SENEGAL), MOHAMED BARAKAT (CEA, FRANCE), PHILIPPE ORTET (CEA, FRANCE), WAFA ACHOUACK (CNRS, FRANCE), LAURENT LAPLAZE (IRD, FRANCE), THIERRY HEULIN (CNRS, FRANCE), LAURENT COURNAC (IRD, FRANCE)

@ SITNDOUR@YAHOO.FR

Pearl-millet is a drought tolerant cereal crop of arid and semi-arid region with high genetic diversity that could be exploited for breeding for its intensification. In particular, the influence of the plant genome on rhizosphere microbiota might be an interesting new target to improve plant-soil interactions and plant nutrition. Indeed, these relationships can influence the soil physico-chemical and biological characteristics, which affect the availability of nutrients and water. Our study aimed to determine the interactions between different pearl-millet inbred lines showing contrasting patterns of rhizosphere soil aggregation and the characteristic of the associated microbiota. Pearl-millet lines selected for their contrasting aggregation pattern were grown in greenhouse and field conditions and their root-adhering soil (RAS) fraction was sampled. The analysis of microbial diversity and their activities was performed respectively by metabarcoding of 16S rDNA and ITS region and extracellular enzyme activities. Under semi-controlled conditions, the bacterial community diversity was higher in high-aggregation lines (lines with high RAS/root biomass ratio) compared to low-aggregation lines (lines with low RAS/root biomass ratio). In field conditions, we noticed a reduction of fungal alpha diversity in the rhizosphere of high-aggregation lines and an increase of some enzyme activities (chitinase acid phosphatase and beta-glucosidase). If we consider all pearl-millet lines, the correlations between indicators of microbiota structure, activity and soil aggregation are not significant. This suggested that other processes are likely involved in soil aggregation variability. Our observations confirm the interest of studying the plant genetic impact on microbiota assembly and its potential integration in breeding programs.

P2.11 VARIETAL ADAPTATION FOR BENEFICIAL RICE MICROBE INTERACTIONS UNDER AEROBIC AND CONTINUOUSLY FLOODED CONDITIONS

FRIDAY 5 JULY, 2019 **09:45**

DAOUDA MBODJ (AFRICA RICE CENTER, SENEGAL), BABOUCARR MANNEH (AFRICA RICE CENTER, SENEGAL), ABOUBACRY KANE (UNIVERSITY CHEIKH ANTA DIOP OF DAKAR, SENEGAL), LAURENT LAPLAZE (IRD, FRANCE), ABDALA GAMBY DIEDHIOU (UNIVERSITY CHEIKH ANTA DIOP OF DAKAR, SENEGAL)

@ D.MBODJ@CGIAR.ORG

Crop inoculation with beneficial soil microbes has been proposed by several crop scientists as an alternative to agro-chemicals which often impact the environment negatively. Use of microbes in crop production, however, requires selecting optimal combinations of crop varieties with associated microbiome which increase efficiency of production systems. In this study, we investigated the response of eight rice varieties to inoculation with arbuscular mycorrhizal fungi at five fertilizer levels in two parallel trials, one under continuous flooding and another under aerobic conditions, at Fanaye, Senegal. A split-split plot design was used in each irrigation condition. With regards to grain yield under aerobic conditions (63% water-saving over continuous flooding), there was significant interaction between use of inoculation, fertilizer level and varieties implying that response of rice varieties to inoculation depended on the fertilizer level. Furthermore, under aerobic conditions at low fertilizer levels, the best response to inoculation was shown by Sahel 202 at the half-recommended fertilizer level, giving 7.4 tons/ha with inoculation and 5.6 tons/ha without inoculation. Under continuous flooding conditions, however, there was a significant increase in yield due to inoculation but this effect was similar at all fertilizer levels. Sahel 108 had the highest grain yield in continuous flooding conditions giving on average 8.2 tons/ha with inoculation and 6.8 tons/ha without inoculation. These results show the potential of using AMF to improve rice production with less fertilizers and water and presents new opportunities for the genetic improvement of rice for the ability to form beneficial rice-microbe associations to increase yield.

P2.12 ROOTING AROUND THE WHEAT MICROBIOME

FRIDAY 5 JULY, 2019 **10:00**

TIM MAUCHLINE (ROTHAMSTEAD RESEARCH, UNITED KINGDOM)

@ TIM.MAUCHLINE@ROTHAMSTED.AC.UK

The root microbiome is recruited by plants and influences plant growth, health and resource use efficiency. These microorganisms can benefit crop plants in several ways including improved plant nutritional status as well as protection against biotic and abiotic stresses. There are various factors which determine the crop microbiome community structure and understanding how agricultural practices influence the microbiome structure is imperative for the development of sustainable agricultural systems. This talk explores our work into the relative importance of several factors that shape the wheat root microbiome namely: land use conversion at the Rothamsted Highfield experiment, wheat genotype in reference to contrasting plant height, fertilisation regime at the Rothamsted Broadbalk experiment as well as the interaction of seed microbial load and land use in determining microbiome structure.

P2.13 INFLUENCE OF WHEAT GENOTYPE AND SOIL ON THE ROOT-ASSOCIATED MICROBIOME: IDENTIFICATION OF A WHEAT CORE MICROBIOME ACROSS AFRICAN AND EUROPEAN SOILS

FRIDAY 5 JULY, 2019 **10:30**

MARIE SIMONIN (IRD CIRAD UNIV MONTPELLIER IPME, FRANCE), CINDY DASILVA (IRD CIRAD UNIV MONTPELLIER IPME, FRANCE), VALERIA TERZI (CREA-GB RESEARCH CENTRE FOR GENOMICS AND BIOINFORMATICS, ITALY), EDDY NGONKEU (DEPARTMENT OF PLANT BIOLOGY, FACULTY OF SCIENCE, UNIVERSITY OF YAOUNDÉ, CAMEROON), DIÉGANE DIOUF (DÉPARTEMENT DE BIOLOGIE VÉGÉTALE, UNIVERSITÉ CHEIKH ANTA DIOP (UCAD), SENEGAL), LIONEL MOULIN (IRD CIRAD UNIV MONTPELLIER IPME, FRANCE)

@ SIMONIN.MARIE@GMAIL.COM

Here, we propose to move away from broad community or phylum patterns to fully embrace the prokaryotic and eukaryotic diversity of the plant microbiome. We used new bioinformatic tools to characterise the wheat root microbiome at the finest taxonomic scale using metabarcoding data: the exact sequence variant (ESV). In an experiment under controlled conditions, we characterised the root-associated microbiome (here rhizoplane) of eight different genotypes of winter bread wheat (*Triticum aestivum* L.) grown in eight soils collected in four different countries in Africa (Cameroon and Senegal) and Europe (France and Italy). The microbiome was characterised using amplicon sequencing of the marker genes 16S rRNA (prokaryotic diversity) and 18S rRNA (eukaryotic diversity). We found a limited effect of the wheat genotype on the root microbiome (2% of the variability) and observed that the majority of the microbial taxa were associated to multiple wheat genotypes grown in the same soil. Cultivation of wheat in different soils led to large differences in taxa richness (100 to 350 total ESVs) and community structure of the root-associated microbiome. However, despite these global differences in microbiome diversity and composition across soils, we identified a list of core taxa of only 179 ESVs (2 Archaea, 104 Bacteria, 73 Eukaryotes) that collectively represented half of the relative abundance of the root-associated microbiome in both African and European soils. We provide evidence of a wheat core microbiome and propose a “most wanted” taxa list that will be targets for future cultivation-based and genomic studies.

P2.14 STUDYING ANCESTRAL PLANT-MICROBIOTA INTERACTIONS USING SYNTHETIC PHOTOTROPHIC MICROBIAL ECOSYSTEMS

FRIDAY 5 JULY, 2019 **11:30**

RUBEN GARRIDO-OTER (MAX PLANCK INSTITUTE FOR PLANT BREEDING RESEARCH, GERMANY)

@ GARRIDOO@MPIPZ.MPG.DE

Land plants associate and interact with microbial communities derived from soil. However, the underlying fundamental principles governing these plant-microbe interactions remain elusive. Several studies have reported mutualistic interactions between unicellular plants such as green algae and bacterial members of the plant root microbiota (e.g. rhizobia), suggesting a conserved and presumably ancestral ability to associate with soil-borne bacteria common to unicellular and multicellular plants. However, it is unknown whether microscopic algae are also capable to assemble and interact with stable and complex microbial consortia. Here, we use the eukaryotic, photosynthetic, soil-borne green alga *Chlamydomonas reinhardtii* to elucidate fundamental principles governing the assembly and dynamics of microbial ecosystems formed by interactions between a photosynthetic organism and its microbiota. Co-inoculation experiments with *Chlamydomonas* and soil extracts demonstrate how this unicellular plant is able to form stable microbial consortia with bacteria recruited from the environment that tightly overlap with the core root microbiota of land plants. An extensive culture collection comprising more than 3,200 bacterial isolates found to associate with *Chlamydomonas* is used to explore ancestral plant-microbe interactions in a high throughput manner and to design synthetic, photoautotrophic microbial ecosystems that are amenable to genetic transformation and can be manipulated in the laboratory under controlled conditions.

P2.15 THE RHIZOSPHERE IN A CHIP

FRIDAY 5 JULY, 2019 **12:00**

DANIEL PATKO (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), YANGMINGHAO LIU (SCHOOL OF SCIENCE AND ENGINEERING, UNIVERSITY OF DUNDEE, UNITED KINGDOM), ILONKA ENGELHARDT (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), FELICITY O'CALLAGHAN (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), VINCENT LADMIRAL (INSTITUT CHARLES GERHARDT CNRS 5253, FRANCE), BRUNO AMEDURI (INSTITUT CHARLES GERHARDT CNRS 5253, FRANCE), MIKE P MACDONALD (SCHOOL OF SCIENCE AND ENGINEERING, UNIVERSITY OF DUNDEE, UNITED KINGDOM), LIONEL DUPUY (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM)

@ DANIEL.PATKO@HUTTON.AC.UK

The growing world population is causing unprecedented pressure on land use. Knowledge of where and how crop yield can be enhanced has become of greater importance, and this requires understanding of how plants interact with the soil environment and how biotic and abiotic stresses can be overcome. Currently, reproducing soil-plant-atmosphere systems is challenging, and this limits our ability to accelerate the discovery of processes that affect our environment. Here, we present a comprehensive approach for screening processes in the soil-plant-atmosphere, which consists of a soil like physical matrix, environmental control, biochemical probes and live quantitative imaging. The soil has been developed to allow index matching and clear optical access for imaging of plant roots and micro-organisms under a controlled environment in large transparent growth chamber. It makes possible observation of biological activity in soil macrocosms using a combination of soft polymer fluidics, material chemistry and light sheet microscopy for live imaging in vivo using both fluorescence and scattering. Finally, we show how the soil itself can be functionalised to follow the changing macrocosm of plants and microbes and demonstrate application of the system to understand colonisation of the rhizoplane, limitation to deep rooting, and for the development of a new generation of models with much enhanced resolution.

P2.16 USING WILD PEANUT SPECIES FOR IMPROVING NATIVE BIOLOGICAL NITROGEN FIXATION IN RHIZOBIA SYMBIOSIS

THURSDAY 4 JULY, 2019 **POSTER SESSION**

ARLETTE ZAZOU ZAIYA (JOINT LABORATORY OF MICROBIOLOGY, SENEGAL), DANIEL FONCEKA (CERAAS THIÈS SENEGAL, SENEGAL), SALIOU FALL (LCM (IRDISRAUCAD) DAKAR, SENEGAL), ADAM DIOUF (LCM (IRDISRAUCAD) DAKAR, SENEGAL), OUMAR TOURE (LCM (IRDISRAUCAD) DAKAR, SENEGAL), MATHIEU FAYE NDIGUE (LCM (IRDISRAUCAD) DAKAR, SENEGAL), SARAH PIGNOLY (UMR LSTM (IRD, CIRAD, INRA, UNIVERSIT. MONTPELLIER SUPAGRO) MONTPELLIER, SENEGAL), ADRIANA FABRA (DEPARTAMENTO DE CIENCIAS NATURALES, FACULTAD DE CIENCIAS EXACTAS FÍSICO-QUIMICAS Y NATURALES, UNIVE, ARGENTINA), FERNANDO IBANEZ (DEPARTAMENTO DE CIENCIAS NATURALES, FACULTAD DE CIENCIAS EXACTAS FÍSICO-QUIMICAS Y NATURALES UNIVE, ARGENTINA), VALERIE HOCHER (UMR LSTM (IRD, CIRAD, INRA, UNIVERSIT. MONTPELLIER SUPAGRO) MONTPELLIER, SENEGAL), DIEGANE DIOUF (DÉPARTEMENT DE BIOLOGIE VÉGÉTALE, UCAD DAKAR, SENEGAL), SERGIO SVISTOONOFF (UMR LSTM (IRD, CIRAD, INRA, UNIVERSIT. MONTPELLIER SUPAGRO) MONTPELLIER, FRANCE)

@ ZAIYAARLETTE@YAHOO.FR

Arachis hypogaea originated from South America and was introduced and adapted in Africa and Asia centuries ago. Peanut is now one of the most widely cultivated grain legumes and the questions of its adaptation in environments that are different to its native ecosystems, regarding associated-microorganisms, remain unanswered. We are investigating how the adaptation of peanut to West Africa impacted the nitrogen-fixing symbiosis with rhizobia. On the bacterial side we characterized a collection of 35 native strains isolated from various regions in Senegal. These strains were also used to inoculate Fleur 11, widely grown in Senegal. Our results showed that strains are distributed in three main clusters, affiliated to the genus *Bradyrhizobium*. We found that in Senegal peanut is able to recruit both effective and ineffective *Bradyrhizobium* strains suggesting that peanut nitrogen fixation could be optimized by increasing the competitiveness of the effective strains. On the plant side we have explored the variability of nitrogen fixation among Fleur11, wild relatives of peanut and synthetic allotetraploids. We used efficient strains isolated in Senegal or in Argentina and found significant differences for some species. We failed to detect any major difference between *A. hypogaea*, its wild progenitors, but in some allotetraploids nitrogen fixation started earlier. In addition to that, analysis of bacterial communities obtained from nodules of wild *Arachi* ssp. and cultivated peanut, indicate that recruitment of specific communities is strongly influenced by the plant genotype, suggesting that it is possible to improve biological nitrogen fixation of cultivated peanut by selecting varieties that recruit efficient symbionts.

P2.17 UNDERSTANDING THE CHANGES IN COMPARTMENT SPECIFIC TOMATO MICROBIOME DURING VASCULAR WILT INTERACTION BY *FUSARIUM OXYSPORUM*

WEDNESDAY 3 JULY, 2019 **POSTER SESSION**

MUGDHA SABALE (DEPARTMENT OF GENETICS UNIVERSITY OF CORDOBA, SPAIN), AMEY REDKAR (DEPARTMENT OF GENETICS, UNIVERSITY OF CORDOBA, SPAIN), STÉPHANE HACQUARD (MAX PLANCK INSTITUTE FOR PLANT BREEDING RESEARCH, GERMANY), ANTONIO DI PIETRO (DEPARTMENT OF GENETICS, UNIVERSITY OF CORDOBA, SPAIN)

@ GE2SASAM@UCO.ES

Plant roots are colonized by diverse microbes that affect plant health either in beneficial or harmful ways. These include benign rhizosphere inhabitants, as well as endophytes, some of which contribute to plant health. Alternatively, the root infecting pathogens have evolved to outcompete their microbial competitors and cause disease. *Fusarium oxysporum* is a soil-borne fungal pathogen, that causes vascular wilt disease in a broad range of crops including both monocots and dicots. The fungus grows asymptomatically in the root cortex and then colonizes the vasculature. The chemical control methods are difficult to apply, because of the low visibility of fungus in early stages. Biological control of disease by bacteria is emerging as a promising method, however the functional relevance of the root microbiome during the pathogen host interaction is largely unknown.The present work aims to understand the host compartment-specific native tomato microbiome and its role during *Fusarium* infection. Soils with diverse characteristics collected across tomato fields in Southern Spain, were used in culture dependent and independent approaches to monitor the changing microbiome under *Fusarium* infection by Amplicon Sequencing. Moreover, the isolated bacterial communities are classified based on compartments such as soil, rhizosphere, root, endophytic root and xylem. The final goal of the study is to understand the interplay and the modulation of microbiome assembly during pathogen-plant interaction.

P2.18 STUDY OF THE DIVERSITY OF ARBUSCULAR MYCORRHIZAL FUNGI (AMF) ASSOCIATED WITH MILLET IN VARIOUS AGROECOSYSTEMS IN SENEGAL

THURSDAY 4 JULY, 2019 **POSTER SESSION**

MARIE-THÉRÈSE MOFINI (INSTITUT DE RECHERCHE POUR LE DÉVELOPPEMENT (IRD), SENEGAL), ABDALA G DIEDHIOU (CHEIKH ANTA DIOP UNIVERSITY, SENEGAL), SARAH PIGNOLY (INSTITUT DE RECHERCHE POUR LE DÉVELOPPEMENT (IRD), SENEGAL), CHEIKH NDIAYE (LABORATOIRE COMMUN DE MICROBIOLOGIE (LCM), SENEGAL), MIN DOOHONG (KANSAS STATE UNIVERSITY, UNITED STATES), LAURENT LAPLAZE (INSTITUT DE RECHERCHE POUR LE DÉVELOPPEMENT (IRD), SENEGAL), ABOUBACRY KANE (CHEIKH ANTA DIOP UNIVERSITY, SENEGAL)

@ MOFINI.MARIETHERESE@YAHOO.FR

Pearl millet is a cereal domesticated in central Sahel in Africa. It is adapted to dry and hot climates and plays a major role for food security in arid and semi-arid areas of Africa and India, where it is the staple crop of more than million people. However, it lags behind other cereal crops in terms of genetic development and its average yields are low. Drought and low phosphorus availability are among the most important factors limiting millet production in West Africa. Arbuscular Mycorrhizal Fungi can enter symbiosis with most angiosperms and contribute to the plant's hydromineral nutrition. AMF are therefore important for abiotic stress tolerance in many plants. The aim of this study is to characterize the diversity of AMF in cultivated and wild pearl millet in various agroecosystems in Senegal. Soil and root samples from wild and cultivated pearl millet were collected from farmers' fields in three different locations in Senegal located along a rainfall gradient. The farmers received Souna seeds in order to limit the effect of the plant genotype. Analysis of root colonization revealed different models of mycorrhization patterns between cultivated and wild plants and among the sampled fields. DNA was extracted from the roots followed by massive sequencing using metabarcoding techniques (amplification of the ITS region followed by deep sequencing). Our analysis revealed that wild and cultivated pearl millet share similar endophytic and AM fungal populations. This suggests that wild pearl millet serve as reservoirs for both beneficial but also pathogenic fungi for cultivated pearl millet.

P2.19 EFFECT OF ARBUSCULAR MYCORRHIZAL FUNGUS ON DROUGHT TOLERANCE OF AFRICAN BAOBAB (*ADANSONIA DIGITATA* L., MALVACEAE)

WEDNESDAY 3 JULY, 2019 **POSTER SESSION**

MARÈME NIANG (ISRACERAAS, SENEGAL), PATRICK NIANG (GHENT UNIVERSITY, BELGIUM), FATIMA NDIAYE (UCAD, SENEGAL), MACOUMBA DIOUF (ISRACERAAS, SENEGAL), TAHIR DIOP (UCAD, SENEGAL), AMADOU BA (IRDLCM, SENEGAL), NDIAGA CISSE (ISRACERAAS, SENEGAL)

@ AGROMAREME@GMAIL.COM

Mycorrhizae improve root and leaf growth and are also involved in water uptake and drought-tolerance resistance. A greenhouse experiment was conducted in order to investigate the influence of arbuscular mycorrhizal fungus (AMF) inoculation (*Glomus mosseae*, *G. aggregatum* and *G. fasciculatum*) on drought tolerance in baobab (*Adansonia digitata* L., Malvaceae). We used seeds collected in different agro-climatic zones in Senegal following a defined rainfall gradient (250-1100 mm). Baobab seedlings that had grown for 1 month were subjected to progressive drought stress for 1 month with weekly records of morphological and physiological parameters. Water deficit was imposed by stopping irrigation until the end of the experiment. Inoculated plants had greater plant height, leaf number and biomass under well-watered than under drought conditions. Results show that for all provenances, inoculated plants has higher mycorrhizal intensity under well-watered (50-90% of mycorrhizal spores) than under water deficit conditions (<50%). Mycorrhizal baobab seedlings from humid areas (Sudano-Sahel and Sudan zone) had higher leaf water potential and lower biomass throughout the experiment in drought conditions. Baobab seedlings responded best to inoculation with *G. fasciculatum* and *G.aggregatum* in both dry and wet conditions. Mycorrhizae significantly improve drought tolerance of baobab seedlings, especially those from the Sahelian region.

P3 IMPACT AND FUNCTIONS OF ALTERNATIVE SPLICING IN PLANTS

ORGANISED BY: MARIA KALYNA (UNIVERSITY OF NATURAL RESOURCES AND LIFE SCIENCES), PAULA DUQUE (INSTITUTO GULBENKIAN DE CIÊNCIA) AND JOHN BROWN (UNIVERSITY OF DUNDEE)

P3.1 ADVANCES IN STUDYING ALTERNATIVE SPLICING IN PLANTS

TUESDAY 2 JULY, 2019 **14:05**

ANDREA BARTA (MAX PERUTZ LABORATORIES MEDICAL UNIVERSITY VIENNA, AUSTRIA)

@ ANDREA.BARTA@MEDUNIWIEN.AC.AT

Advanced transcriptome sequencing has uncovered extensive alternative splicing (more than 60%) in plants, and genome-wide as well as focused gene analyses have shown the regulatory power of alternative splicing on plant development and in responses to stress and environment. Alternative splicing can create new protein isoforms or change gene expression by leading to transcript isoforms that are either targeted to the nonsense-mediated decay pathway or are retained in the nucleus. Alternative splicing as a co-transcriptional process is also greatly influenced by epigenetic changes at the chromatin level. Proteins regulating splicing or alternative splicing and transcript isoforms with different fates have significant impact in gene regulatory circuits. Specifically, beside developmental programs, environmental cues like temperature and light impact significantly alternative splicing events in plants establishing alternative splicing as a fast and essential part in accommodating external signals.

P3.2 CRISPR-DIRECTED EVOLUTION OF THE SPLICEOSOME FOR RESISTANCE TO SPLICING INHIBITORS

TUESDAY 2 JULY, 2019 **14:50**

HAROON BUTT (KING ABDULLAH UNIVERSITY OF SCIENCE AND TECHNOLOGY, SAUDI ARABIA), AYMAN EID (KING ABDULLAH UNIVERSITY OF SCIENCE AND TECHNOLOGY, SAUDI ARABIA), AFAQUE A MOMIN (KING ABDULLAH UNIVERSITY OF SCIENCE AND TECHNOLOGY, SAUDI ARABIA), JEREMIE BAZIN (UNIVERSITE PARIS-SACLAY ORSAY, FRANCE), MARTIN CRESPI (UNIVERSITE PARIS-SACLAY ORSAY, FRANCE), STEFAN T AROLD (KING ABDULLAH UNIVERSITY OF SCIENCE AND TECHNOLOGY, SAUDI ARABIA), MAGDY M MAHFOUZ (KING ABDULLAH UNIVERSITY OF SCIENCE AND TECHNOLOGY, SAUDI ARABIA)

@ HAROON.BUTT.1@KAUST.EDU.SA

Increasing genetic diversity via directed evolution holds great promise to accelerate trait development and crop improvement. We developed a CRISPR/Cas-based directed evolution platform in plants to evolve the rice (*Oryza sativa*) SF3B1 spliceosomal protein for resistance to splicing inhibitors. SF3B1 mutant variants, termed SF3B1-GEX1A-Resistant (SGR), conferred variable levels of resistance to splicing inhibitors. Studies of the structural basis of the splicing inhibitor binding to SGRs corroborated the resistance phenotype. The SGR4 variant conferred strong resistance to higher concentrations of splicing inhibitors and exhibited efficient splicing compared to wild-type plants, which showed drug sensitivity and splicing repression. This directed-evolution platform can be used to interrogate and evolve the molecular functions of key biomolecules and to engineer crop traits for improved performance and adaptation under climate change conditions.

P3.3 A CRITICAL ROLE FOR ALTERNATIVE SPLICING IN MAINTAINING MINERAL HOMEOSTASIS IN RICE

TUESDAY 2 JULY, 2019 **15:10**

LUQING ZHENG (NANJING AGRICULTURAL UNIVERSITY, CHINA)

@ ZHENGLQ@NJAU.EDU.CN

Alternative splicing (AS) promotes transcriptome and proteome diversity and plays important roles in a wide range of biological processes. The roles of AS in maintaining mineral nutrient homeostasis in plants are largely unknown. Here, we obtained whole transcriptome RNA sequencing data of rice (*Oryza sativa*) roots grown in the presence or absence of various mineral nutrients (iron (Fe), zinc (Zn]), copper (Cu), manganese (Mn), and phosphorus (P)). Systematic analysis revealed 13,291 alternatively spliced genes (representing ~53.3% of multi-exon genes in the rice genome). As the overlap between differentially expressed genes (DEGs) and differentially alternatively spliced genes (DASGs) is small, a molecular understanding of the plant's response to mineral deficiency is limited by analyzing DEGs alone. The targets of AS are highly specific to each nutrient. To verify the function of AS in mineral nutrition, we characterized mutants for genes encoding Ser/Arg (SR) proteins that function in AS. We identified several SR proteins as novel regulators of Zn, Mn, and P nutrition and showed that three SR protein-encoding genes (*SR40*, *SCL57*, and *SCL25*) play a role in regulating P uptake and remobilization between the leaves and shoots of rice. Thus, AS has an important role in regulating mineral nutrient homeostasis in rice.

P3.4 GENOME-SCALE ANALYSES OF ALTERNATIVE SPLICING AND ITS REGULATION USING HIGH-THROUGHPUT NEXT GENERATION SEQUENCING TECHNOLOGIES

TUESDAY 2 JULY, 2019 **16:00**

ANIREDDY REDDY (COLORADO STATE UNIVERSITY, UNITED STATES)

@ ANIREDDY.REDDY@COLOSTATE.EDU

Alternative splicing, a key step in gene expression in eukaryotes, contributes significantly to transcriptome complexity and gene regulation. My talk will focus on how short and long read high-throughput sequencing technologies are being used to analyse alternative splicing, splice isoforms, and other post-transcriptional events and in studying the relationship between chromatin architecture and alternative splicing in plants.

P3.5 RAPID COLD-INDUCED EXPRESSION AND ALTERNATIVE SPLICING IN *ARABIDOPSIS* INVOLVES COMPLEX NETWORKS OF REGULATORS

TUESDAY 2 JULY, 2019 **16:35**

JOHN W S BROWN (UNIVERSITY OF DUNDEE, UNITED KINGDOM), NIKOLETA A TZIOUTZIOU (UNIVERSITY OF DUNDEE, UNITED KINGDOM), CRISTIANE P G CALIXTO (UNIVERSITY OF DUNDEE, UNITED KINGDOM), RUNXUAN ZHANG (JAMES HUTTON INSTITUTE, UNITED KINGDOM), WENBIN GUO (UNIVERSITY OF DUNDEE, UNITED KINGDOM), ALLAN B JAMES (UNIVERSITY OF GLASGOW, UNITED KINGDOM), HUGH G NIMMO (UNIVERSITY OF GLASGOW, UNITED KINGDOM)

@ J.W.S.BROWN@DUNDEE.AC.UK

Gene expression patterns in plants change dramatically in response to environmental stimuli. Alternative splicing (AS) is critical in the regulation of such changes at the post-transcriptional level but little is known of the dynamics of AS in the cold response. We performed an RNA-seq time-series of *Arabidopsis thaliana* plants exposed to cold in order to characterize the cold transcriptome (Calixto *et al.*, 2018). Differential expression and differential alternative splicing were identified throughout the time-course with thousands of genes changing in the first few hours of cold. Novel cold-responsive transcription factors and splicing factors/RNA-binding proteins regulated only by AS were identified among the early response genes. A higher resolution RNA-seq time-course across the first 3 h of temperature reduction (plants harvested at 20', 40', 60', 90', 120' and 180'). This identified the earliest transcription/AS changes with important regulatory transcription factors and RNA-binding proteins responding within 40-60 min of cold and were very sensitive to even small changes in temperature. These are likely to drive cascades of transcriptional and AS changes of downstream genes and together determine transcriptome reprogramming that governs the physiological and survival responses of plants to low temperature. In order to unravel the complexity of these cascades, co-transcriptional and co-splicing networks were constructed using the time-course RNA-seq. We are examining both networks to look closely at regulatory genes and their potential targets.

P3.6 THE ROLE OF CLOCK ISOFORM SWITCHES IN PLANTS PLASTIC RESPONSES TO TEMPERATURE

TUESDAY 2 JULY, 2019 **16:55**

ALLAN B JAMES (UNIVERSITY OF GLASGOW, UNITED KINGDOM), HUGH G NIMMO (UNIVERSITY OF GLASGOW, UNITED KINGDOM)

@ ALLAN.JAMES@GLASGOW.AC.UK

Plants respond to a broad dynamic range of temperature across multiple timescales, from very short (minute-to-minute), to medium term (diel), and to long-term (seasonal) changes. One way in which plants perceive, buffer and integrate this wide range of 'noisy' temperature information is via the circadian clock, similar to the established role for the clock in temperature sensation in other organisms. A significant role for alternative splicing (AS) in cooling associated transcriptome reprograming in plants has been established. Notably some of these AS changes involve transcript isoform switches, where the ratios of specific transcript isoforms flip rapidly and reversibly with temperature change. For some clock genes, isoform switches result in changes in the time-of-day phasing and amplitude of the functional, protein-coding transcripts. Clock gene expression/AS plasticity is therefore important for our understanding of how plants align their phenology to local and seasonal environmental conditions. We present data demonstrating the thermo-sensing qualities of specific clock AS events, and show that temperature signalling is likely routed via changes in the relative abundances of trans-acting splicing factors that are themselves subject to temperature associated AS. Clock function has predominantly been studied at constant acclimated temperatures. We therefore discuss our data in the context of our current understanding of the response of the clock to steady state temperatures. We propose that clock transcript isoform switching is integral to the plastic response of plants to natural fluctuating temperatures, and reveal exemplar clock temperature switches as a novel dimension to the thermo-plastic clock.

P3.7 QUANTITATIVE CHANGES IN ALTERNATIVE SPLICING UNDER COLD STRESS IN BARLEY DETERMINED USING A NEWLY ESTABLISHED BARLEY REFERENCE TRANSCRIPT DATASET CALLED BARTV1.0

TUESDAY 2 JULY, 2019 **17:15**

CRAIG G SIMPSON (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), PAULO RAPAZOTE-FLORES (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), WENBIN GUO (UNIVERSITY OF DUNDEE, UNITED KINGDOM), MICHA BAYER (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), LINDA MILNE (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), CLAUS-DIETER MAYER (BIOMATHEMATICS AND STATISTICS SCOTLAND, UNITED KINGDOM), JOHN FULLER (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), PETE E HEDLEY (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), JENNY MORRIS (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), GORDON STEPHEN (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), JOHN WS BROWN (UNIVERSITY OF DUNDEE, UNITED KINGDOM), ROBBIE WAUGH (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), RUNXUAN ZHANG (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM)

@ CRAIG.SIMPSON@HUTTON.AC.UK

A high-quality, non-redundant barley reference gene transcript dataset (Barley Reference Transcripts – BaRTv1.0) was established using 808 RNA-seq samples from 11 different RNA-seq experimental datasets from a range of tissues, cultivars, mutants and abiotic stresses. Transcripts were assembled and aligned to the Morex reference genome. Full-length cDNAs from the variety Haruna Nijo (Matsumoto *et al.*, 2011) were used to determine gene transcript coverage and high-resolution RT-PCR was used to validate alternatively spliced transcripts of 86 genes in five barley development stages. BaRTv1.0 consists of 60,444 genes and 177,240 transcripts. Overall, transcripts in this dataset are longer with less fragmentation; have improved annotations; consist of high-quality transcripts with well supported splice junctions; and provide improved quantification accuracy for RNA-seq data. Like the *Arabidopsis*, we further optimised this dataset for quantification of alternative spliced isoforms (BaRTv1.0-QUASI) by developing a transcript dataset sequence padded to the longest 5' and 3' ends to reduce quantification errors caused by mis-annotation at the UTR regions. BaRTv1.0-QUASI was used to quantify differential changes in gene expression and alternative splicing (AS) in 4-day-old dark grown germinating seedlings (20°C). Samples were transferred to a 4°C cold room and harvested at 2 and 24 h in cold. Over 60 barley genes show differential AS within 2 h of exposure to the cold, rising to over 380 by 24 h exposure. Within this group about 40 genes show an AS isoform switch.

P3.8 STRTD: A HIGH-QUALITY TRANSCRIPTOME ANNOTATION FOR DOUBLE-MONOPLOID *SOLANUM TUBEROSUM*

TUESDAY 2 JULY, 2019 **17:35**

JUAN C ENTIZNE (THE JAMES HUTTON INSTITUTE AND UNIVERSITY OF DUNDEE, UNITED KINGDOM), JOHN WS BROWN (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), RUNXUAN ZHANG (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), ESTELA DOMINGO TORRES (THE JAMES HUTTON INSTITUTE AND UNIVERSITY OF DUNDEE, UNITED KINGDOM), CRISTIANE CALIXTO (UNIVERSITY OF DUNDEE, UNITED KINGDOM), WENBIN GUO (UNIVERSITY OF DUNDEE, UNITED KINGDOM)

@ E.ENTIZNE@DUNDEE.AC.UK

Changes in the transcriptome are the basis of phenotypic responses of eukaryotic organisms to environmental or developmental cues. Re-programming of the transcriptome occurs at the transcriptional and post-transcriptional levels and includes, in particular, alternative splicing (AS). RNA-sequencing (RNA-seq) is used to quantify genome-wide transcriptional and AS changes. The accuracy of differential expression (DE) and differential alternative splicing (DAS) analysis depends on the accuracy of quantification of transcripts by alignment-free programs (Salmon, Kallisto). These require a complete, diverse and high-quality Reference Transcript Dataset (RTD). Based on the work done for the development of a high-quality annotation for *Arabidopsis* (AtRTD2) (Zhang *et al.*, 2017), we are developing a general computational pipeline to generate high-quality transcriptome annotations from existing annotations and available RNA-seq data. We applied our pipeline to generate a novel high-quality transcriptome annotation for the double-monoploid (DM) potato line *Solanum tuberosum* (StRTD). StRTD has increased diversity of non-redundant, non-chimeric and non-fragmentary, transcripts compared to the current potato transcriptome (Potato Genome Sequencing Consortium). It has been used to analyse a time-course of infection of DM by late blight and investigate NMD. Given the importance of the assembly of high-quality reference annotations for the accurate expression/AS analysis of RNA-seq datasets, this pipeline will represent a valuable tool for plant scientists. For many plants, genome sequences are limited and transcriptomes are incomplete or non-existent. The pipeline allows RTDs to be generated for plant/crop species with genome sequences using RNA-seq data and to enhance expression/AS analysis.

P3.9 RNA-BINDING PROTEINS INVOLVED IN GENE EXPRESSION AND ALTERNATIVE SPLICING IN *ARABIDOPSIS* UNDER COLD STRESS

TUESDAY 2 JULY, 2019 **17:37**

NIKOLETA A TZIOUTZIOU (UNIVERSITY OF DUNDEE, UNITED KINGDOM), CRISTIANE PG CALIXTO (UNIVERSITY OF DUNDEE, UNITED KINGDOM), RUNXUAN ZHANG (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), WENBIN GUO (UNIVERSITY OF DUNDEE, UNITED KINGDOM), ALLAN B JAMES (UNIVERSITY OF GLASGOW, UNITED KINGDOM), HUGH G NIMMO (UNIVERSITY OF GLASGOW, UNITED KINGDOM), JOHN WS BROWN (UNIVERSITY OF DUNDEE, UNITED KINGDOM)

@ N.Z.TZIOUTZIOU@DUNDEE.AC.UK

We studied the cold transcriptome of *Arabidopsis* by conducting a time-course RNA-seq experiment of plants grown to 20°C for 5 weeks and then exposed to 4°C for 4 days. Sampling every 3 h on the last day at 20°C and on the first and the fourth days at 4°C allowed us to identify changes in expression and alternative splicing in thousands of genes as well as changes in the rhythmic expression (amplitude and phase) of core clock and clock associated genes and hundreds of other downstream genes. The time-course dataset allowed us to map the timing of when each gene first becomes differentially expressed (DE) and/or differentially alternatively spliced (DAS). Around 50 splicing factors (SFs) and RNA-binding proteins (RBPs) belong to the list of genes which are most rapidly DE and/or DAS in the first 3 h of cold treatment, which may regulate downstream cascades of alternatve splicing important for cold response and acclimation. A new RNA-seq time-course across the first 3 h of temperature reduction where plants were harvested at 20', 40', 60', 90', 120' and 180' gives us a better resolution of the earliest changes in SFs/RBPs and defines those with the highest expression levels and the largest changes in alternative splicing (high ΔPS values). We are currently using mutants of these rapidly altered SFs/RBPs to characterize their physiological response to cold/freezing. Molecular phenotyping of the mutants shows a number of changes in the alternative splicing of potential regulated target genes including core clock genes.

P3.10 THE *PHYSCOMITRELLA PATENS* FAMILY OF SR PROTEIN SPLICING FACTORS

TUESDAY 2 JULY, 2019 **17:39**

JOSÉ P MELO (INSTITUTO GULBENKIAN DE CIÊNCIA, PORTUGAL), MARIA KALYNA (UNIVERSITY OF NATURAL RESOURCES AND LIFE SCIENCES, AUSTRIA), PAULA DUQUE (INSTITUTO GULBENKIAN DE CIÊNCIA, PORTUGAL)

@ JPBMELO@IGC.GULBENKIAN.PT

When plants colonised land they had to overcome many challenges. To cope with their harsh new environment, many traits gradually evolved giving rise to the plants we know today. One molecular mechanism likely to have allowed plants to cope with adverse environments is alternative splicing, a key posttranscriptional process largely modulated by SR proteins. This conserved family of splicing factors has received significant attention in higher plants, where it can be divided into six subfamilies, three of which are direct orthologs of animal SR proteins and three are plant specific. The model species *Arabidopsis thaliana* expresses 18 SR protein genes, distributed among all subfamilies, plus two SR-like proteins with a non-canonical domain structure. Several arabidopsis SR proteins have in recent years been ascribed roles in the response to abiotic stress. Comparatively, little is known of these RNA-binding proteins in early land plants. Mosses such as *Physcomitrella patens* present a valuable opportunity to study the evolutionary pathway of genes due to their close similarity with early land plants. Our preliminary in silico analyses indicate that the *P. patens* genome encodes a similar number of SR protein genes as higher plants, with all subfamilies being present though comprising a variable number of members. Future functional studies will shed light on the significance of this key family of splicing factors in early land plants and on the conservation of their role in plant stress tolerance.

P3.11 ALTERNATIVE SPLICING REGULATION OF STRESS RESPONSES IN *ARABIDOPSIS* – A LINK TO CHROMATIN?

TUESDAY 2 JULY, 2019 **17:41**

ALBA R DÍEZ (INSTITUTO GULBENKIAN DE CIÊNCIA, PORTUGAL), PAULA DUQUE (INSTITUTO GULBENKIAN DE CIÊNCIA, PORTUGAL)

@ ADIEZ@IGC.GULBENKIAN.PT

Alternative splicing has emerged as a major contributor to plant stress tolerance, but the specific genes and events involved remain mostly unknown. We are making use of natural variance in the model plant *Arabidopsis thaliana* to substantiate a role for alternative splicing in stress responses mediated by the phytohormone abscisic acid (ABA) and uncover functionally significant splicing targets. Our extensive phenotypic screen of 24 *A. thaliana* accessions, using the Col-0 ecotype as a reference, has identified variants with reduced and increased sensitivity to ABA at different developmental stages. In fact, Kn-0 and C24 are consistently respectively hypo- and hypersensitive to ABA during early seedling growth, mirrored by an under- and over-induction of ABA marker genes. We will conduct RNA-seq analysis of the Col-0, Kn-0 and C24 variants grown under control and ABA conditions to identify the gene expression and alternative splicing changes correlating with opposing ABA sensitivity. Moreover, we are addressing the hypothesis that alternative splicing in plants is regulated by stress-induced chromatin changes. Environmental stress markedly impacts both alternative splicing and chromatin remodelling in plants systems, while a functional connection between these two processes has been provided by the discovery of animal adaptor proteins that read specific chromatin marks and recruit splicing factors to the pre-mRNA. Our recent results show that loss-of-function of arabidopsis orthologues of an animal adaptor protein causes striking impairment of ABA responses at both the physiological and molecular levels. We will use these mutants to search for chromatin-regulated alternative splicing events governing plant stress tolerance.

P3.12 COMPARATIVE ANALYSIS OF THE IMPACT OF ALTERNATIVE SPLICING IN PLANT RESPONSES TO DIFFERENT TYPES OF STIMULI

TUESDAY 2 JULY, 2019 **17:43**

GUIOMAR MARTIN (INSTITUTO GULBENKIAN DE CIÊNCIA (IGC), PORTUGAL), PAULA DUQUE (INSTITUTO GULBENKIAN DE CIÊNCIA (IGC), PORTUGAL), MANUEL IRIMIA (CENTRE FOR GENOMIC REGULATION (CRG), SPAIN)

@ GUIOMARM@IGC.GULBENKIAN.PT

Plants adapt their development to different environmental and developmental cues by rearranging their transcriptome and proteome. During the last decades, much effort has been put into understanding how signalling cascades initiated by multiple stimuli adjust transcriptome diversity. These research efforts have focused mainly on the role of transcription factors in controlling gene expression. However, recent studies are beginning to uncover a key contribution of alternative splicing, a posttranscriptional mechanism that generates multiple transcripts from the same gene, to the diversification of plant transcriptomes. Despite functional evidence pointing to alternative splicing as a major player in the adaptation of plant development to different external and internal stimuli, little is known about the underlying mechanisms. Is alternative splicing controlling gene expression and protein diversity similarly in response to different stimuli? Do total gene expression and alternative splicing impact distinct or complementary molecular pathways in response to different types of stress? To assess the similarities and differences between the molecular processes controlled by transcription and alternative splicing in response to a wide range of stimuli, we have implemented Vast-tools, a computational pipeline to detect and quantify all types of alternative splicing events from RNA-seq data (https://github.com/vastgroup/vast-tools), for the model plant *Arabidopsis thaliana*. We are also generating a database of arabidopsis profiles by gathering RNA-seq samples available in the Short Read Archive (SRA) for various developmental and environmental conditions. Our comparative analysis of these profiles is shedding light on the mode of action and biological functions of alternative splicing in response to different stimuli.

P3.13 RIBONOMICS TO UNRAVEL POSTTRANSCRIPTIONAL NETWORKS IN *ARABIDOPSIS*

WEDNESDAY 3 JULY, 2019 **10:00**

DOROTHEE STAIGER (BIELEFELD UNIVERSITY, GERMANY), TINO KÖSTER (RNA BIOLOGY ANS MOLECULAR PHYSIOLOGY, BIELEFELD UNIVERSITY, GERMANY), MARTIN LEWINSKI (RNA BIOLOGY AND MOLECULAR PHYSIOLOGY, BIELEFELD UNIVERSITY, GERMANY), KATJA MEYER (RNA BIOLOGY AND MOLECULAR PHYSIOLOGY, BIELEFELD UNIVERSITY, GERMANY), MARLENE REICHEL (RNA BIOLOGY AND MOLECULAR PHYSIOLOGY, BIELEFELD UNIVERSITY, GERMANY), OLGA SCHMIDT (RNA BIOLOGY AND MOLECULAR PHYSIOLOGY, BIELEFELD UNIVERSITY, GERMANY)

@ DOROTHEE.STAIGER@UNI-BIELEFELD.DE

A key function for RNA-binding proteins in orchestrating plant development and environmental responses is well established. However, the lack of a genome-wide view on their in vivo binding targets and binding landscapes has for a long time represented a major gap in understanding the mode of action of plant RNA-binding proteins. We have for the first time adapted individual nucleotide resolution crosslinking immunoprecipitation (iCLIP) for genome-wide determining the binding repertoire of the circadian clock-regulated *Arabidopsis thaliana* glycine-rich RNA-binding protein AtGRP7. iCLIP identified around 800 transcripts with significantly enriched crosslink sites in plants expressing AtGRP7-GFP and absent in plants expressing an RNA-binding-dead AtGRP7 variant or GFP alone. To independently validate the targets, we performed RNA immunoprecipitation (RIP)-sequencing of AtGRP7-GFP plants subjected to formaldehyde fixation. Half of the iCLIP targets were also identified by RIP-seq, thus representing a set of high-confidence binders. To determine the fate of the bound targets in the cell, we cross-referenced the targets against transcriptome changes in AtGRP7 loss-of-function mutants or overexpressing plants. This revealed a predominantly negative effect of AtGRP7 on its direct targets. Additionally, we observed changes in circadian expression patterns of numerous target genes, in line with a proposed function of the protein as a molecular slave oscillator in the circadian timing system. Furthermore, several targets show changes in alternative splicing in response to altered AtGRP7 levels that frequently lead to PTC-containing transcript isoforms. In particular, AtGRP7 mediates splicing changes in response to abiotic stresses. Establishing iCLIP for plants represents a major advancement in plant RNA biology and paves the way to investigate the dynamics of posttranscriptional networks.

P3.14 SPECIFICITY OF ALTERNATIVE SPLICING REGULATION BY PLANT POLYPYRIMIDINE TRACT-BINDING PROTEINS

WEDNESDAY 3 JULY, 2019 **10:35**

RICA BURGARDT (INSTITUTE FOR MOLECULAR PHYSIOLOGY, UNIVERSITY OF MAINZ, GERMANY), GABRIELE WAGNER (CENTER FOR PLANT MOLECULAR BIOLOGY (ZMBP), UNIVERSITY OF TÜBINGEN, GERMANY), ANDREAS WACHTER (INSTITUTE FOR MOLECULAR PHYSIOLOGY, UNIVERSITY OF MAINZ, GERMANY)

@ RBURGARD@UNI-MAINZ.DE

Alternative splicing (AS) is a way of gene regulation widely used in eukaryotes. It is based on the variable definition of exons and introns on the precursor mRNA and greatly enhances transcript diversity. In the model plant *Arabidopsis thaliana*, at least 61% of all intron-containing genes are subject to AS, but how this process is regulated is still poorly understood. Our group previously identified the polypyrimidine tract-binding proteins AtPTB1 and AtPTB2 as plant AS regulators, controlling more than 450 events with implications in many physiological and developmental processes. In our current research, we investigate the mechanistic level of PTB-mediated AS in *A. thaliana*. We identified binding motifs for AtPTB1/2 in selected targets and demonstrated their importance for correct AS in vitro and in vivo. We further revealed that AtPTB1/2 exhibit tissue-specific control of individual mRNAs, including the PTB2 transcript itself. This regulation depends on PTB binding motifs and is tightly patterned, with low activity in exterior tissues like the seed coat and high activity in reproductive organs. The tissue-specific activity patterns also led to the identification of a new target, a receptor-like kinase that undergoes a PTB-dependent splicing switch and might be involved in reproduction. In total, our work provides evidence that AtPTB1/2-controlled AS in plants is a more complex and closely regulated process than previously known. Future studies will attempt to identify co-regulatory factors and uncover further biological functions to understand how tissue-specificity is conveyed in plant AS and how it shapes developmental processes.

P3.15 ALTERNATIVE SPLICING OF A HEAT STRESS TRANSCRIPTION FACTOR SHAPED THERMOTOLERANCE DURING TOMATO DOMESTICATION

WEDNESDAY 3 JULY, 2019 **10:55**

SOTIRIOS AKIS FRAGKOSTEFANAKIS (GOETHE UNIVERSITY FRANKFURT, GERMANY), REMUS ROZENKRANZ (GOETHE UNIVERSITY FRANKFURT, GERMANY), YANGJIE HU (GOETHE UNIVERSITY FRANKFURT, GERMANY), JOSÉ M JIMÉNEZ-GÓMEZ (INSTITUT JEAN-PIERRE BOURGIN, INRA AGROPARISTECH, CNRS, FRANCE), ENRICO SCHLEIFF (GOETHE UNIVERSITY FRANKFURT, GERMANY)

@ FRAGKOST@BIO.UNI-FRANKFURT.DE

Exposure to high temperatures leads to a massive molecular reprogramming to enforce protection of molecules and cellular structures which are essential for survival and recovery from stress. Heat stress has a major impact on pre-mRNA splicing landscape and consequently proteome abundance and diversity. We show that the capacity of tomato germplasm to adapt to abrupt temperature changes that cause heat stress was reduced during domestication. Differences in thermotolerance are associated with variation in temperature-sensitive pre-mRNA splicing of the heat stress transcription factor HsfA2. We identified nucleotide polymorphisms involved in splicing efficiency of the second intron of HsfA2. Temperature-sensitive alternative splicing leads to two HsfA2 protein isoforms. HsfA2-I is involved in long-term thermotolerance and gradual adaptation to heat stress, while HsfA2-II functions in immediate response and therefore stimulates the rapid adaptation capacity of plants to high temperatures. HsfA2AAA and HsfA2GAG alleles characterized by efficient intron splicing and synthesis of HsfA2-II are prominently present in wild accessions and are therefore more thermotolerant than modern cultivars. The selection for HsfA2GGG haplotype during tomato domestication moderated thermotolerance due to reduced HsfA2-II levels. Two Serine/Arginine-rich protein family members mediate intron retention in HsfA2 during heat stress, thereby ensuring the accumulation of HsfA2-I to increase plant fitness and acclimation under long-term and repeated cycles of stress. Our results give insights into a central heat stress response mechanism that contributes to plant plasticity to respond to different stress regimes.

P3.16 THE SR45 SPLICING FACTOR PLAYS OPPOSING ROLES IN THE REGULATION OF STRESS RESPONSES DURING EARLY PLANT DEVELOPMENT

WEDNESDAY 3 JULY, 2019 **11:15**

DORA SZAKONYI (INSTITUTO GULBENKIAN DE CIÊNCIA, PORTUGAL), RAQUEL F CARVALHO (INSTITUTO GULBENKIAN DE CIÊNCIA, PORTUGAL), PAULA DUQUE (INSTITUTO GULBENKIAN DE CIÊNCIA, PORTUGAL)

@ DSZAKONYI@IGC.GULBENKIAN.PT

The capacity to cope with adverse environmental conditions is critical for plant survival and reproduction. Abiotic stress signals trigger abscisic acid (ABA) dependent molecular pathways leading to key adaptive changes in growth and development. We previously reported that the *Arabidopsis thaliana* SR45 splicing factor negatively regulates ABA and sugar signalling during cotyledon development. We demonstrated that under high glucose conditions, an SR45 loss-of-function mutant contains higher amounts of the SnRK1 protein – an energy-sensing kinase coordinating sugar and stress responses – which are suppressed by a proteasome inhibitor indicating that SR45 promotes targeting of SnRK1 for degradation. Our results also showed that SR45 controls alternative splicing of multiple genes, including 5PTase13 phosphatase, a known regulator of SnRK1 stability in vitro. However, gel-shift assays indicate that SR45 is unable to bind directly the 5PTase13 RNA, and transient expression of the two 5PTase13 splice variants in isolated arabidopsis leaf protoplasts does not differentially affect SnRK1 levels, refuting a role for 5PTase13 in SR45-mediated control of sugar responses. Remarkably, our latest results reveal that loss of SR45 function causes hyposensitivity to ABA and sugars during seed germination, with molecular markers corroborating the notion that the SR45 splicing factor shifts from positively to negatively regulating ABA-mediated stress responses during the first steps of plant growth. We are currently searching for splicing targets underlying these opposing SR45 stress functions during early plant development.

P3.17 ALTERNATIVE SPLICING CONTROL OF ABIOTIC STRESS RESPONSES

WEDNESDAY 3 JULY, 2019 **11:35**

PAULA DUQUE (INSTITUTO GULBENKIAN DE CIÊNCIA, PORTUGAL)

@ DUQUEP@IGC.GULBENKIAN.PT

Alternative mRNA splicing is a highly prevalent posttranscriptional gene expression regulation mechanism in eukaryotic genomes, whose functional significance remains poorly understood in plant systems. As a potent enhancer of the genome's coding and regulatory capacities that is markedly affected by external cues in plants, alternative splicing is likely to play a determinant role in the ability of these organisms to cope with environmental stress. Arginine/serine-rich (SR) proteins are highly conserved RNA-binding proteins playing key roles in alternative splicing. Ongoing work in our lab with the SR protein family of the model organism *Arabidopsis thaliana* is providing functional links between alternative splicing and plant responses to abiotic stress, particularly those mediated by the abscisic acid (ABA) hormone. Interestingly, these splicing factors appear to display different modes of ABA signaling regulation and act specifically during the initial stages of plant growth and development.

P3.18 THE *ARABIDOPSIS* SR PROTEIN SR34A NEGATIVELY REGULATES ABA-MEDIATED STRESS RESPONSES DURING SEED GERMINATION AND EARLY SEEDLING DEVELOPMENT

WEDNESDAY 3 JULY, 2019 **12:10**

TOM LALOUM (INSTITUTO GULBENKIAN DE CIENCIA, PORTUGAL), PAULA DUQUE (INSTITUTO GULBENKIAN DE CIENCIA, PORTUGAL)

@ TLALOUM@IGC.GULBENKIAN.PT

Plant osmotic stresses promote the synthesis of the hormone abscisic acid (ABA), which triggers major gene expression changes and physiological responses to adapt to environmental stress. While the transcriptional and posttranslational control of ABA-mediated plant stress responses has been well established, emerging evidence points also to a central role for posttranscriptional regulation in this process. In agreement, plant mutants defective in different RNA-binding proteins have been found to be severely impaired in their response to stresses mediated by the ABA hormone. We recently identified the *Arabidopsis thaliana SR34a* gene — encoding a serine/arginine-rich (SR) protein belonging to a conserved family of splicing factors with key roles in alternative splicing — as a negative regulator of ABA-mediated stress responses. In fact, a true loss-of-function mutant for this SR protein, *sr34a-1*, displays marked hypersensitivity to exogenous ABA application, as well as to high salinity and drought stress during seed germination and the transition from heterotrophic to autotrophic growth (cotyledon greening). Accordingly, the expression of several ABA marker genes is clearly upregulated in *sr34a-1*. To gain mechanistic insight into the mode of action of SR34a, the RNAs targeted by this splicing factor will be identified using complemented mutant lines expressing a green fluorescent protein (GFP)-tagged version of SR34a under the control of its endogenous promoter and a combination of iCLIP and RNA-seq analyses. Results stemming from this work are expected to contribute to elucidate how SR proteins and alternative splicing control plant physiological responses under environmental stress.

P3.19 A NOVEL RNA-BINDING PROTEIN INVOLVED IN ABA SIGNALLING AND METABOLISM

WEDNESDAY 3 JULY, 2019 **12:12**

RUI ALBUQUERQUE MARTINS (INSTITUTO GULBENKIAN DE CIÊNCIA, PORTUGAL), JAMES ROWE (SAINSBURY LABORATORY, CAMBRIDGE UNIVERSITY, UNITED KINGDOM), ALEXANDER M JONES (SAINSBURY LABORATORY, CAMBRIDGE UNIVERSITY, UNITED KINGDOM), PAULA DUQUE (INSTITUTO GULBENKIAN DE CIÊNCIA, PORTUGAL)

@ RFMARTINS@IGC.GULBENKIAN.PT

Alternative splicing is a key posttranscriptional gene regulatory mechanism that greatly expands the coding capacity of eukaryotic genomes. Although the functional relevance of alternative splicing in plant systems remains poorly understood, recent evidence points to functional roles for serine/arginine-rich (SR) proteins, which are major modulators of alternative splicing. Indeed, several loss-of-function mutants for several *Arabidopsis thaliana* SR proteins have been found to exhibit altered stress responses as well as sensitivity and/or metabolism of the phytohormone abscisic acid (ABA). Here we show that knocking out the *A. thaliana RSZ21* gene leads to ABA hyposensitivity at different stages of early seedling development. These physiological phenotypes are corroborated at the molecular level by a reduced ABA-mediated induction of established ABA marker genes such as RAB18, confirming that the RSZ21 protein acts as a positive regulator of ABA responses. Moreover, reduced induction of the key ABA biosynthesis gene *NCED3* in response to salt stress in the *rsz21-1* mutant suggests a role in ABA biosynthesis. The regulation and molecular mode of action of this SR protein in ABA-mediated stress responses will be investigated combining transcriptomic, biochemical and cell biology approaches to assess whether ABA levels and dynamics are affected by RSZ21 function and identify the mRNAs targeted to modulate the response to stress. Elucidating the mechanisms governing posttranscriptional control of ABA signalling and metabolism may open the way to development of novel strategies to improve plant tolerance to adverse environmental conditions.

P3.20 ALTERNATIVE TRANSCRIPTS OF *ARABIDOPSIS* MAJOR FACILITATOR SUPERFAMILY TRANSPORTER GENE DETERMINE FUNCTIONAL ROLES IN THE RESPONSE TO ENVIRONMENTAL AND HORMONAL CUES

WEDNESDAY 3 JULY, 2019 **12:14**

MARÍA NIÑO-GONZÁLEZ (INSTITUTO GULBENKIAN DE CIÊNCIA, PORTUGAL), PAULA DUQUE (INSTITUTO GULBENKIAN DE CIÊNCIA, PORTUGAL)

@ MFGONZALEZ@IGC.GULBENKIAN.PT

The Major Facilitator Superfamily (MFS) represents the second largest family of transporters on earth and is one of only two groups of transporters common to all forms of life. As with many other gene families, the MFS is largely expanded in plants; in fact, the genome of the model plant *Arabidopsis thaliana* appears to encode over 200 MFS genes, the vast majority of which remain uncharacterised. Several arabidopsis MFS transporters have been studied in our laboratory, revealing not only key roles in the response to environmental stress, but also striking examples of the biological relevance of alternative splicing – a key posttranscriptional mechanism to generate proteome diversity and regulate gene expression – in plant systems. Here, we describe ongoing work aimed at the functional characterisation of an *A. thaliana* gene encoding a novel MFS transporter, which we have temporarily named MFS18. Our results show that, apart from the canonical transcript encoding the full-length protein, two alternative variants are generated through alternative splicing or polyadenylation. Both these variant mRNAs code for the same truncated protein due to the use of the same intronic stop codon. Loss of the canonical transcript causes hypocotyl hypersensitivity to the hormone gibberellin (GA), whereas hypersensitivity to chilling has been observed in mutant seedlings lacking the alternative transcripts. Together, these results corroborate a functional role for the MFS18 transporter in the control of plant cell expansion in response to cold stress and GA, mediated by the different transcripts generated from this arabidopsis gene.

P3.21 ROLES FOR SNRNP BIOGENESIS IN PLANT DEVELOPMENT AND ENVIRONMENTAL RESPONSES

WEDNESDAY 3 JULY, 2019 **14:30**

MISATO OHTANI (NAIST-BS, JAPAN)

@ MISATO@BS.NAIST.JP

Small nuclear ribonucleoproteins (snRNPs), which contain small nuclear RNAs (snRNAs) and their specific interacting proteins, are core components of the spliceosome, the molecular machinery for pre-mRNA splicing. snRNPs are built up through the complicated stepwise processes; first, snRNAs, essential components of snRNPs, should be transcribed, processed, and modified by the specific regulators, and then the matured snRNAs will interact with specific proteins in a step-by-step manner, to become snRNPs. Interestingly, the *Arabidopsis* mutants of snRNP biogenesis factors have been shown to be defective not only for plant development but also for the responses to environmental factors, such as temperature and salinity. In this talk, based on our recent findings of the snRNA transcription-deficient mutant *srd2* and the snRNA cap hypermethylation-deficient mutant *attgs*, I would like to discuss roles for active regulation of snRNP biogenesis in plant development and environmental response.

P3.22 MERISTEM-DEFECTIVE, A NOVEL SPLICING FACTOR WHICH IS ESSENTIAL FOR ROOT MERISTEM DEVELOPMENT IN *ARABIDOPSIS*

WEDNESDAY 3 JULY, 2019 **15:05**

HELEN L THOMPSON (DURHAM UNIVERSITY, UNITED KINGDOM), WEIRAN SHEN (DURHAM UNIVERSITY, UNITED KINGDOM), DAVID DOLAN (DURHAM UNIVERSITY, UNITED KINGDOM), CRISTIANE CALIXTO (DUNDEE UNIVERSITY, UNITED KINGDOM), MEDHAVI KAKKAR (DURHAM UNIVERSITY, UNITED KINGDOM), SINA MOZAFFARI-JOVIN (MAX PLANCK INSTITUTE OF BIOPHYSICAL CHEMISTRY, GERMANY), CARL JONES (DURHAM UNIVERSITY, UNITED KINGDOM), JENNIFER TOPPING (DURHAM UNIVERSITY, UNITED KINGDOM), SUSHMA N GRELLSCHEID (DURHAM UNIVERSITY, UNITED KINGDOM), KEITH LINDSEY (DURHAM UNIVERSITY, UNITED KINGDOM)

@ HELEN.L.THOMPSON@DURHAM.AC.UK

Around 61% of *Arabidopsis* intron-containing genes undergo alternative splicing and splice isoform variants have been reported in different cell types, organs and developmental stages. Examples have been shown of involvement in abiotic stress response, circadian clock gene regulation and development. We are investigating the role of a novel splicing factor MDF in the development of the *Arabidopsis* root meristem. The MDF gene is predominantly expressed in localised areas of increased mitotic activity such as the root and apical meristems and functions independently of auxin regulation. The null T-DNA mutant *mdf-1* displays aberrant root meristem development and key meristem regulatory genes are down regulated. MDF is homologous to human SART1 and our modelling predicts it has a similar tertiary structure. SART1 interacts with Prp6 and Prp8 in the human U4/U6 snRNP during B complex formation and we are investigating whether MDF interacts similarly with the *Arabidopsis* spliceosome. Our RNA sequencing and HR-RTPCR analysis show that in *mdf-1* key components of the splicing cycle are alternatively spliced along with a subset of SR genes reported to be associated with root development. MDF also appears to have a role in the abiotic stress response through the isoform switching of two splice variants. We will present our model of how MDF regulates the balance between stem cell identity, meristem activity and differentiation through alternative splicing of other splicing factors and meristem-specific genes.

P3.23 A LONG NON-CODING RNA REGULATES ALTERNATIVE SPLICING

WEDNESDAY 3 JULY, 2019 **15:25**

MARTIN CRESPI (INSTITUTE OF PLANT SCIENCES PARIS-SACLAY, FRANCE), J BAZIN (INSTITUTE OF PLANT SCIENCES PARIS-SACLAY, FRANCE), T ROULÉ (INSTITUTE OF PLANT SCIENCES PARIS-SACLAY, FRANCE), C HARTMANN (INSTITUTE OF PLANT SCIENCES PARIS-SACLAY, FRANCE), T BLEIN (INSTITUTE OF PLANT SCIENCES PARIS-SACLAY, FRANCE), C CHARON (INSTITUTE OF PLANT SCIENCES PARIS-SACLAY, FRANCE), L LUCERO (UNIVERSIDAD NACIONAL DEL LITORAL, ARGENTINA), F ARIEL (UNIVERSIDAD NACIONAL DEL LITORAL, ARGENTINA)

@ MARTIN.CRESPI@IPS2.UNIVERSITE-PARIS-SACLAY.FR

Non-coding RNAs have emerged as major components of the eukaryotic transcriptome. Long non-coding RNAs (lncRNAs) act either directly or are processed to shorter miRNA and siRNAs and act through specific ribonucleoprotein complexes to modulate the expression of mRNA targets. Genome-wide RNA sequencing in roots identified many *Arabidopsis* lncRNAs, such as si/miRNA precursors, antisense or intergenic lncRNAs. In addition, ribosome profiling has allowed us to more precisely define the coding potential of lncRNA and to pinpoint a role of small ORF translation in ta-siRNA biogenesis. Targeted analysis of lncRNA identified that the ALTERNATIVE SPLICING COMPETITOR (ASCO) lncRNA interacts with Nuclear Speckle RNA Binding Proteins (NSRs) to regulate alternative splicing (AS) patterns of several mRNAs linking ASCO action to alternative splicing. The effect of the knockdown of ASCO (RNAi) at genome-wide level showed that only a minor subset of genes overlapped with the AS defects of the *nsra/b* double mutant. In particular, a high number of deregulated and alternatively spliced genes in ASCO RNAi plants were related to flagellin response and biotic stress. In agreement, ASCO-deregulated plants are more sensitive to flagellin. Furthermore, we demonstrated that ASCO also interacts with PRP8a, a key component of the spliceosome. Our results hint the existence of a dynamic network between lncRNAs and splicing factors to modulate transcriptome diversity during development, conditioning the response to environmental cues.

P3.24 EXPLORING FUNCTIONS OF NONSENSE-MEDIATED RNA DECAY IN PLANTS: RNA QUALITY CONTROL AND BEYOND

WEDNESDAY 3 JULY, 2019 **16:30**

KAREL RIHA (CEITEC MASARYK UNIVERSITY, CZECH REPUBLIC), VIVEK K RAXWAL (CEITEC MASARYK UNIVERSITY, CZECH REPUBLIC), JUAN C ENTIZNE (UNIVERSITY OF DUNDEE, UNITED KINGDOM), JIRADET GLOGGNITZER (INSTITUTE OF BIOCHEMISTRY ETH, SWITZERLAND), WENBIN GUO (UNIVERSITY OF DUNDEE, UNITED KINGDOM), CRAIG SIMPSON (UNIVERSITY OF DUNDEE, UNITED KINGDOM), JOHN BROWN (UNIVERSITY OF DUNDEE, UNITED KINGDOM)

@ KAREL.RIHA@CEITEC.MUNI.CZ

Nonsense-mediated RNA decay (NMD) is an evolutionary conserved RNA control mechanism that targets aberrant transcripts for degradation. NMD was also implicated in broader regulation of gene expression. We discovered that NMD suppresses defense response through regulating stability of TNL immune receptors. NMD is downregulated upon bacterial infection and this mechanism contributes to bolstering plant defense. We performed in depth comparative analysis of plants lacking the key proteins involved in different steps of NMD. Although SMG7 and UPF1 act non-redundantly on the consecutive steps of NMD, we observed different impact of *smg7* and *upf1* null mutations on plant growth and transcriptome. *UPF1* inactivation had much greater effect on accumulation of aberrantly spliced mRNA and transcriptome homeostasis than *SMG7*, indicating existence of yet unknown branch of NMD in plants that is parallel to SMG7/5/6 pathway. Transcriptome assembly in *upf1* plants revealed novel alternatively spliced isoforms never detected before underlying impact of NMD on transcriptome maintenance. To examine the impact of UPF1 on translation, we analyzed RNA in monosomal and polysomal fractions of ribosomes in *upf1* mutants. We observed a global shift of mRNAs from polysomes to monosomes. Interestingly, NMD targets as well as low expressing mRNA with short half-life were shifted from monsomes to polysomes in *upf1* indicating role of UPF1 in suppressing translation of aberrant RNAs. Particularly striking was increase in translation of TNL immune receptors. Regulation of TNLs via UPF1/NMD-mediated mRNA stability and translational de-repression offers a dynamic mechanism for rapid activation of TNLs in response to pathogen attack.

P3.25 TWO UPSTREAM ORFS OF AN *ARABIDOPSIS* ZINC TRANSPORTER ACT AS A FAIL-SAFE MECHANISM TO REPRESS TRANSLATION

WEDNESDAY 3 JULY, 2019 **17:05**

ESTHER NOVO-UZAL (INSTITUTO GULBENKIAN DE CIÊNCIA, PORTUGAL), DÓRA SZAKONYI (INSTITUTO GULBENKIAN DE CIÊNCIA, PORTUGAL), PAULA DUQUE (INSTITUTO GULBENKIAN DE CIÊNCIA, PORTUGAL)

@ ENOVO@IGC.GULBENKIAN.PT

Upstream open reading frames (uORFs) are protein-coding regions in the 5' untranslated region (UTR) of mRNAs. They are known to be able to affect translation of the main ORF (mORF), usually reducing the levels of protein production due to a decrease in translation efficiency. Around 20-50% of eukaryotic genes contain uORFs, and in the model plant *Arabidopsis thaliana* these genes have been estimated to be 35%, with about half harbouring multiple uORFs. Nevertheless, very few uORFs in plant genes have been examined for their functional significance. We identified three uORFs, named uORF1, uORF2 and uORF3, in the arabidopsis ZIF2 (Zinc-Induced Facilitator 2) gene. ZIF2 is a membrane transporter that mediates vacuolar compartmentalization of zinc in root cortical cells, thereby conferring plant tolerance to the heavy metal. We have found that simultaneous disruption of all uORFs results in a marked increase in the activity of the luciferase reporter gene, demonstrating the ability of at least one ZIF2 uORF to inhibit mORF translation. Disruption of each individual uORF revealed that uORF2 is the main player in the observed translational repression, whereas uORF1 does not affect translation and uORF3 is translated and inhibits mORF translation only in the absence of uORF2. We thus postulate that the ZIF2 uORF3 acts as a fail-safe mechanism to inhibit translation, to our knowledge the first observation of such a mode of regulation in plant systems.

P4 STOMATAL AND PHOTOSYNTHETIC REGULATION OF WATER USE EFFICIENCY

ORGANISED BY: ANDREW LEAKEY (UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN) AND TRACY LAWSON (UNIVERSITY OF ESSEX)

P4.1 WHERE AND WHEN IS HIGH VS LOW STOMATAL CONDUCTANCE FAVORABLE TO BIOMASS ACCUMULATION: A PROBABILISTIC APPROACH

THURSDAY 4 JULY, 2019 **09:00**

FRANCOIS TARDIEU (INRA MONTPELLIER, FRANCE), BORIS PARENT (INRA MONTPELLIER, FRANCE), LLORENÇ C BOSQUET (INRA MONTPELLIER, FRANCE), SANTIAGO A PRADO (INRA MONTPELLIER, FRANCE), CLAUDE WELCKER (INRA MONTPELLIER, FRANCE)

@ TARDIEU@SUPAGRO.INRA.FR

The control of stomatal conductance involves numerous processes, with a genetic variability each, including hydraulics and the synthesis of different hormones by different organs. This complexity of mechanisms is overridden by evolutionary constraints, summarised by simple rules operating over weeks, vs minutes for stomatal control. (i) Stomatal closure, or intrinsically low stomatal conductance, is favourable whenever saving water is useful to complete the plant cycle with sufficient available soil water resource. (ii) It is unfavourable whenever this risk is low, because of photosynthesis reduction, and/or in case of heat stress because transpiration prevents leaf heating. The relevance of these rules was demonstrated, firstly, via the analysis/modelling of the behaviour of plants with contrasting abilities to synthesize abscisic acid and, secondly, via the genetic analysis of a multi-site field experiment that revealed that a locus controlling ABA synthesis has positive or negative effects on yield depending on environmental scenarios. Hence, designing plants with optimum stomatal conductance is a probabilistic exercise that involves the most likely environmental scenarios in a given site, with current or future climates. Because it is not feasible to analyse gas exchanges of hundreds of genotypes for genetic analyses, we propose an indirect method for deriving the parameters of stomatal behaviour based on phenomic analyses of transpiration and leaf area. This method, applied to a large dataset, provided genomic regions affecting stomatal conductance with conditional effects. Resulting genotypic parameters can be inserted in a model that predicts where and when a given stomatal behaviour favours biomass and yield.

P4.2 NOVEL ASPECTS OF CARBON DIOXIDE SIGNALLING IN STOMATA

THURSDAY 4 JULY, 2019 **09:30**

DEIRDRE H MCLACHLAN (UNIVERSITY OF BRISTOL, UNITED KINGDOM), PENG SUN (UNIVERSITY OF BRISTOL, UNITED KINGDOM), ALISTAIR M HETHERINGTON (UNIVERSITY OF BRISTOL, UNITED KINGDOM)

@ BZDML@BRISTOL.AC.UK

Stomata are pores on the surface of leaves that allow CO_2 entry for photosynthesis and also contribute to the regulation of the transpiration stream. As water loss from evapotranspiration could potentially lead to dehydration stress, the pore aperture is tightly controlled. Stomatal aperture is modified to suit the prevailing environmental conditions and this process involves sensing and responding to multiple individual stimuli. In this study, we have investigated the mechanism of CO_2-induced stomatal closure and compared it with two other well-studied closure pathways - to the stress hormone ABA and to the microbial stress peptide flg22. We have used gas exchange, direct aperture measurements and intracellular imaging to examine the signalling pathways for CO_2, and their integration with the flg22 and ABA pathways. This has allowed us to identify new components of the signalling pathways that lead to CO_2-induced stomatal closure. More surprisingly, we have discovered that alternate CO_2 signalling pathways are used depending on the plant growth conditions. This has revealed an extra layer of complexity to the mechanisms behind the integration of signals and the interplay with metabolic state.

P4.3 STOMATAL BLUE LIGHT RESPONSE AND THE IMPACT ON ASSIMILATION AND WATER USE EFFICIENCY

THURSDAY 4 JULY, 2019 **09:45**

TRACY LAWSON (UNIVERSITY OF ESSEX, UNITED KINGDOM), JACK SA MATTHEWS (UNIVERSITY OF ESSEX, UNITED KINGDOM), SILVERE VIALET-CHABRAND (UNIVERSITY OF ESSEX, UNITED KINGDOM)

@ TLAWSON@ESSEX.AC.UK

Stomata control the uptake of CO_2 for photosynthesis and at the same time water loss through transpiration, which aids in nutrient uptake and evaporative cooling of the leaf. Stomata open in response to increasing light, however this response depends on the wavelengths of light, and generally two different responses have been identified. The first is named the "red" light or mesophyll response, and occurs at high light intensities and is linked directly to the rate of photosynthesis. The second is the "specific blue" light response, which occurs and is saturated at light levels too low to drive photosynthesis. This means that under red blue combinations stomata are often more open than they need to be to achieve maximum CO_2 uptake for photosynthesis, and therefore the ratio of carbon gain to water loss through stomatal conductance (g_s), known as intrinsic water use efficiency (W_i), is reduced. We have quantified the impact of blue light on g_s, assimilation rate (A) and W_i in a range of different species and have compared these responses to the effect of red light alone. We discuss these findings in the light of manipulating the blue light response for improving W_i in crop plants.

P4.4 IMAGING WATER USE EFFICIENCY UNDER DYNAMIC ENVIRONMENTAL CONDITIONS

THURSDAY 4 JULY, 2019 **10:00**

SILVERE VIALET-CHABRAND (UNIVERSITY OF ESSEX, UNITED KINGDOM), MARTIN BATTLE (UNIVERSITY OF ESSEX, UNITED KINGDOM), TRACY LAWSON (UNIVERSITY OF ESSEX, UNITED KINGDOM)

@ SRMVIA@ESSEX.AC.UK

Plant phenotyping, the quantitative description of plants' anatomical, ontogenetical, physiological and biochemical properties, is key to assess genetic diversity and identify targets for genetic manipulation to improve plant performance and yield. Intrinsic water use efficiency (W_i), net CO_2 assimilation rate (A) divided by stomatal conductance to water vapor (g_{sw}) is an important physiological trait displaying complex diurnal kinetics that are difficult to measure with high throughput. Under dynamic environmental conditions, differences in A between plants can be due to differences in photosynthetic capacities, enzymatic activation (e.g. PSII, RuBisCO) and stomatal limitation of CO_2 diffusion to the sites of carboxylation, all of which influence W_i. Temporal responses of g_{sw} are generally an order of magnitude slower than A and not only limit A but also have an impact on leaf transpiration and temperature, influencing plant yield and water budget. Although very precise, the scalability of leaf gas exchange methods to estimate A and g_{sw} is limited and is becoming a major technical bottleneck for large scale genetic studies. In contrast, chlorophyll fluorescence imaging and thermography allow rapid, non-contact measurement of a large number of plants, however their biological interpretation is more challenging. Deriving g_{sw} from thermograms using energy balance equations is still extremely difficult and is not widely used. Recent advances in imaging methods and interpretation of chlorophyll fluorescence imaging and thermography are presented with insights on how stomatal behaviour impact the spatial and temporal response of W_i under a dynamic environment.

P4.5 IONIC EFFECTS MAY ALTER THE CONSERVED STOMATAL DYNAMICS WITHIN CUCURBITACEAE

THURSDAY 4 JULY, 2019 **10:15**

TSU-WEI CHEN (INSTITUT FÜR GARTENBAULICHE PRODUKTIONSSYSTEME, GERMANY), JENNIFER MEIER (INSTITUT FÜR GARTENBAULICHE PRODUKTIONSSYSTEME, GERMANY)

@ CHEN@GEM.UNI-HANNOVER.DE

Recent data showed significant variabilities in dynamics of stomatal conductance (g_s) between and within plant genus and showed the correlations between the morphological traits, stomatal dynamics (SD) and whole-plant water use. Here we examined the diversity in SD and morphology in 10 cucurbits lines or F1-cultivars representing the major phylogenetic clades in Cucurbitaceae (five cultivars in *Cucumis sativus*, two cultivars in *Curcubita maxima* and one cultivar in *Lagenaria siceraria*, *Luffa cylindrical* and *Momordica charantia*). SD in response to light-on and light-off (from 100 to 1,000 µmol photon/m^2/s and *vice versa*) was characterized by the time constant (k) for g_s to achieve steady-state, the initial lag in response to the changing light environment (λ) and the maximum rate of stomatal opening (S_{max}). Despite significant differences in their stomatal morphology, the studies species and cultivars are not different in their k and S_{max}, indicating conserved SD in high water-consuming cucurbit crops. Interestingly, positive correlation was found between λ and stomatal length. Using the cultivar "Aramon" of *Cucumis sativus*, we further tested the ionic effects on the SD by applying seven different mixtures of 30 mM NaCl, $NaNO_3$, KCl and KNO_3 after the developmental acclimation of the measured leaves. These treatments allowed obtaining healthy leaves without differences in their stomatal morphology but significantly diverse cation and anion concentrations. High K^+ concentrations in leaves retarded k ($p < 0.001$) without affecting the maximal g_s, S_{max} and λ while the effects of Na^+ were opposite, highlighting the effects of cations on stomatal dynamics.

P4.6 CUTTING EDGE SCIENCE: INVESTIGATING CELL WALL STRUCTURE IN GRASS STOMATA USING LASER MICRODISSECTION

THURSDAY 4 JULY, 2019 10:17

SHAUNI MCGREGOR (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), JULIE GRAY (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), ANDREW FLEMING (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM)

SRMCGREGOR1@SHEFFIELD.AC.UK

Plants control their rate of gas exchange and water loss to best suit the current environment by changing the size of their stomatal pores. This is achieved by the guard cells, which reversibly change shape in order to modulate the aperture of the stomatal pore. To facilitate this shape change, the guard cell wall is repeatedly deformed and must undergo recurrent stress and strain, which is reflected in the specialised structure of the guard cell wall. Grass species, which provide approximately half of the calories consumed by humans worldwide, have a characteristic stomatal structure and cell wall composition. However, how the characteristic cell wall composition of the grasses affects stomatal function is currently unknown. My research shows that walls of grass stomata are high in the polysaccharide xylan, and that different types of xylans are differentially distributed across grass stomatal complexes. I will report on experiments aimed at identifying which xylan synthesis genes are involved in generating these cell wall epitope patterns in grass stomata and progress towards generating mutants in these genes to test their functional significance. This approach exploits laser microdissection, a technique that enables specific cell types to be isolated for downstream analysis, offering an innovative approach to screen for gene expression in grass stomata at a single cell level.

P4.7 EXPLAINING VARIATION IN STOMATAL APERTURES AT A WHOLE LEAF SCALE

THURSDAY 4 JULY, 2019 10:19

GLYNDWR S JONES (UNIVERSITY OF BRISTOL, UNITED KINGDOM), DEIRDRE M MCLACHLAN (UNIVERSITY OF BRISTOL, UNITED KINGDOM), COLIN BROWNLEE (MARINE BIOLOGICAL ASSOCIATION, UNITED KINGDOM), ALISTAIR M HETHERINGTON (UNIVERSITY OF BRISTOL, UNITED KINGDOM)

GJ14238@BRISTOL.AC.UK

Stomata are pores on the surface of leaves which open and close in response to environmental stimuli. Stomatal apertures vary across the surface of the plant leaf and this heterogeneity is described as stomatal patchiness. This phenomenon has been difficult to study as it is hard to measure the changes in apertures of stomata in different regions concurrently. However, a novel development in optical imaging (www.strathclydemesolab.com) has now made this possible. The Mesolens allows very wide field images to be captured at low magnification, but with exceptionally high resolution. Post-capture it is then possible to “zoom in” on different areas of the leaf and measure the apertures of stomata. As the Mesolens also has fluorescence capabilities it is possible to monitor intracellular signalling dynamics during aperture changes by using fluorescent indicators. We have shown that in response to fundamental stimuli, there are quantifiable differences in stomatal apertures in different leaf regions. In addition to this we have used the *arabidopsis* calcium reporter line R-Geco mTurquoise to show differences in calcium dynamics of individual stomata on a whole leaf scale as well as stimulus specific differences in patterns of calcium signal propagation across a leaf. By using a combination of fluorescence imaging and stomatal aperture measurements it is possible to further our understanding of how stomata vary in their responses to stimuli and how these signals are propagated throughout a leaf.

P4.8 PHYSIOLOGICAL PERFORMANCE UNDER SUPRA-OPTIMAL TEMPERATURES OF HYPOMORPHIC *ARABIDOPSIS* MUTANTS ALTERED IN STOMATAL ABUNDANCE

THURSDAY 4 JULY, 2019 10:21

MONTAÑA MENA (FACULTAD DE CIENCIAS AMBIENTALES Y BIOQUÍMICA, UNIVERSIDAD DE CASTILLA-LA MANCHA, SPAIN), MARÍA LUISA PÉREZ-BUENO (DEPARTMENT OF BIOCHEMISTRY AND MOLECULAR AND CELL BIOLOGY OF PLANTS, EEZ-CSIC, SPAIN), JONATAN ILLESCAS (FACULTAD DE CIENCIAS AMBIENTALES Y BIOQUÍMICA, UNIVERSIDAD DE CASTILLA-LA MANCHA, SPAIN), AMANDA MARTÍN-FORERO (FACULTAD DE CIENCIAS AMBIENTALES Y BIOQUÍMICA, UNIVERSIDAD DE CASTILLA-LA MANCHA, SPAIN), ALBERTO DE MARCOS (FACULTAD DE CIENCIAS AMBIENTALES Y BIOQUÍMIC, UNIVERSIDAD DE CASTILLA-LA MANCHA, SPAIN), CARMEN FENOLL (FACULTAD DE CIENCIAS AMBIENTALES Y BIOQUÍMICA, UNIVERSIDAD DE CASTILLA-LA MANCHA, SPAIN), MATILDE BARÓN (DEPARTMENT OF BIOCHEMISTRY AND MOLECULAR AND CELL BIOLOGY OF PLANTS, EEZ-CSIC, SPAIN)

MONTANA.MENA@UCLM.ES

Plants regulate gas exchange with the atmosphere through stomata, dynamic microscopic valves that develop in the otherwise gas-impermeable aerial epidermis. Stomata number, size and distribution determine the maximum potential for gas exchange, influencing transpiration and photosynthesis – and thence plant survival and performance – under different environments. In *Arabidopsis*, stomatal abundance (SA) is a complex character established during leaf growth by a network of key regulatory genes of this developmental process, the outcome of these networks influenced by gene activity and environmental growth conditions. In this work, we examine the behaviour, under different growth temperatures, of a set of viable mutants carrying hypomorphic alleles for some of these genes, which display distinct SA phenotypes. We assessed their physiological performance through non-invasive imaging techniques at optimal (22°C) and supra-optimal (30°C) growth temperatures, as well as their capacity for adaptation when shifted from 22°C to 30°C. We evaluated the photosynthetic activity in terms of PSII functionality, and the stress severity by the capacity for photoprotection (non-photochemical quenching). We also measured the surface temperature to estimate differences in transpiration. In parallel, we recorded morphological traits such as stomatal density, stomatal size and leaf thickness, and examined the impact of temperature regimes on plant growth by measuring leaf numbers, projected rosette area, dry weight and Feret’s diameter of the rosette in the various genotypes grown under the different conditions. We will present the results of comparisons among genotypes and growth conditions, aimed at establishing possible correlations between genetically determined SA and physiological performance under supraoptimal temperatures.

P4.9 STOMATAL DEVELOPMENT IS TIGHTLY CONNECTED WITH SYNTHESIS OF THE EPICUTICULAR WAXES IN MODEL PLANT *ARABIDOPSIS THALIANA*

THURSDAY 4 JULY, 2019 10:23

MARIE HRONKOVÁ (BIOLOGY CENTRE CAS, INSTITUTE OF PLANT MOLECULAR BIOLOGY, CZECH REPUBLIC), JITKA NEUWIRTHOVÁ (UNIVERSITY OF SOUTH BOHEMIA IN CESKE BUDEJOVICE FACULTY OF SIENCE, CZECH REPUBLIC), DANA WIESNEROVÁ (BIOLOGY CENTRE CAS, INSTITUTE OF PLANT MOLECULAR BIOLOGY, CZECH REPUBLIC), MARIE ŠIMKOVÁ (BIOLOGY CENTRE CAS, INSTITUTE OF PLANT MOLECULAR BIOLOGY, CZECH REPUBLIC), CHARLOTTE PETRUSCHKE (DEPARTMENT OF ECOPHYSIOLOGY, IZMB UNIVERSITY OF BONN, GERMANY), VIKTORIA ZEISLER- DIEHL (DEPARTMENT OF ECOPHYSIOLOGY, IZMB UNIVERSITY OF BONN, GERMANY), LUKAS SCHREIBER (UNIVERSITY OF SOUTH BOHEMIA IN CESKE BUDEJOVICE FACULTY OF SIENCE, GERMANY), JIŘÍ ŠANTRŮČEK (UNIVERSITY OF SOUTH BOHEMIA IN CESKE BUDEJOVICE FACULTY OF SIENCE, CZECH REPUBLIC)

HRONKOVA@UMBR.CAS.CZ

Stomata, as epidermal pores, play a pivotal role in developmental plasticity under different environmental conditions because they markedly balance gas exchange, mainly transpiration. Moreover, the aerial parts of plants are covered by a layer of cuticle. This affects water use efficiency (WUE), which is crucial for plants especially under drought conditions. Stomatal development in the epidermis is strongly promoted by high light intensity. In parallel, the amount and compound structure of cuticular waxes seem to be tightly integrated with stomatal development by a complex of signalling and communication links among the leaf tissue layers. Light also represents an important external factor promoting the formation of epicuticular waxes. Based on our experiments with both stomatal (*StRNAi*, *epf1,2* and *tmm*: changes in stomatal density) and cuticular (*cut1/cer6* and *att1:* modified waxes and cutin amounts) mutants of *Arabidopsis thaliana*, we can conclude that changes in stomatal density relate to the amount and compound structure of epicuticular waxes by a so far unknown mechanism that is likely side specific. The development of stomatal density is, however, more likely influenced by the amount and compound structure of epicuticular waxes than by the amount of cutin. This may represent a way by which plants optimise their WUE.

P4.10 MANIPULATION OF STOMATAL DENSITY IN CEREALS: CURRENT UNDERSTANDING AND FUTURE OPPORTUNITIES

THURSDAY 4 JULY, 2019 10:25

EMILY L HARRISON (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), ROBERT CAINE (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), CHRISTOPHER HEPWORTH (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), JULIE GRAY (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM)

E.L.HARRISON@SHEFFIELD.AC.UK

As we enter a time of unprecedented climate change, there is an urgent need to develop water-use-efficient crops that are able to withstand multiple abiotic stresses, including dwindling water availability, increasingly extreme droughts and rising temperatures. Plants primarily regulate their water loss and temperature via adjustments to specialised epidermal pores called stomata, through changes in stomatal aperture or by altering how stomata develop on young leaves. The EPIDERMAL PATTERNING FACTOR (EPF) family of secreted peptides are involved in regulating stomatal development; through manipulation of these genes, we have already engineered several important crop species, including rice and barley, to have significantly fewer stomata. In this poster, we explore how this reduction in stomatal density has optimised transpiration and led to improved water-use-efficiency and drought tolerance in these key C$_3$ staple crops, without deleterious effects on yield. We are now beginning to investigate the manipulation of EPF gene expression in the world’s most abundantly produced crop; C$_4$ maize. Currently, it is unclear how altering stomatal density, and thus stomatal conductance, will impact on the carbon concentrating mechanism present in the C$_4$ photosynthetic pathway. Here, the potential physiological consequences of this are discussed.

P4.11 WATER USE EFFICIENCY SORGHUM TECHNOLOGIES: INCREASING STOMATAL RESISTANCE TO WATER LOSS IN SORGHUM

THURSDAY 4 JULY, 2019 **11:00**

JOHN FERGUSON (UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN, UNITED STATES), NATHAN MILLER (UNIVERSITY OF WISCONSIN-MADISON, UNITED STATES), SHIRLEY SATO (UNIVERSITY OF NEBRASKA-LINCOLN, UNITED STATES), PETER SCHMUCKER (UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN, UNITED STATES), ANNA DMITIEVA (UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN, UNITED STATES), CHARLES PIGNON (UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN, UNITED STATES), TIM WERTIN (UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN, UNITED STATES), KEVIN XIE (UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN, UNITED STATES), DUSTIN MAYFIELD-JONES (UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN, UNITED STATES), DYLAN ALLEN (UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN, UNITED STATES), MICHAEL GORE (CORNELL UNIVERSITY, UNITED STATES), EDWARD BUCKLER (CORNELL UNIVERSITY, UNITED STATES), PATRICK J BROWN (UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN, UNITED STATES), TOM CLEMENTE (UNIVERSITY OF WISCONSIN-MADISON, UNITED STATES), EDGAR SPALDING (UNIVERSITY OF WISCONSIN-MADISON, UNITED STATES), ANDREW D.B. LEAKEY (UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN, UNITED STATES)

@ FERGUSON@ILLINOIS.EDU

Water use efficiency (WUE) is a key target trait for crop improvement since water availability is the primary limitation to crop yield globally. WUE is defined as the ratio of carbon fixed through photosynthesis to water lost via transpiration. This exchange is modulated by the morphology and patterning of stomatal complexes. Modelling suggests that reducing stomatal density in C4 crops such as Sorghum could in turn reduce stomatal conductance, thereby improving WUE. To this end, we are employing two approaches to improve the WUE of Sorghum. Firstly, we are transgenically manipulating stomatal density by altering the expression of key genes involved in stomatal development. Secondly, we are screening the natural diversity of tropical accessions for WUE and stomatal-related traits. Through our transgenic approach, we have substantially increased the drought resistance of Sorghum and increased WUE by >20%. These transgenic lines have been further tested in field conditions under a novel rainout shelter in 2018. Our assessment of the natural diversity has facilitated the identification of candidate genes through association mapping and illuminated the significance of stomatal density for regulating WUE.

P4.12 ENGINEERING STOMATA TO REDUCE CROP WATER USE

THURSDAY 4 JULY, 2019 **11:30**

JULIE GRAY (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), PAUL QUICK (INTERNATIONAL RICE RESEARCH INSTITUTE, PHILIPPINES), ROBERT CAINE (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), JIA XIN (INTERNATIONAL RICE RESEARCH INSTITUTE, PHILIPPINES), LEE HUNT (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), EMILY HARRISON (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), JENNIFER SLOAN (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM)

@ J.E.GRAY@SHEFFIELD.AC.UK

Stomata are pores that open to allow carbon dioxide to enter and close to reduce water loss. Understanding the signalling components controlling stomatal development has allowed us to study the physiological effects of altering stomatal conductance. By manipulating the level of peptide signals we have produced model and crop species with a wide range of stomatal densities. We have created cereal plants overexpressing epidermal patterning factors which suppress stomatal development, and gene edited plants to knockout an antagonising peptide factor which normally promotes stomatal development. Under controlled environment conditions, our crops with reduced stomatal density have lower levels of transpiration, require less water to grow and yet maintain seed yields. They also have enhanced drought tolerance and improved water use efficiency. For example, rice seedlings with approximately half the usual number of stomata use only 60% of the normal amount of water and are better able to survive drought, even at high temperature (40°C).

P4.13 DEVELOPMENTAL INNOVATIONS OF STOMATAL FORM AND FUNCTION IN GRASSES

THURSDAY 4 JULY, 2019 **14:10**

MICHAEL T RAISSIG (HEIDELBERG UNIVERSITY, GERMANY), TIAGO DG NUNES (HEIDELBERG UNIVERSITY, GERMANY), DAN ZHANG (HEIDELBERG UNIVERSITY, GERMANY), HEIKE LINDNER (HEIDELBERG UNIVERSITY, GERMANY)

@ MICHAEL.RAISSIG@COS.UNI-HEIDELBERG.DE

Plants optimize carbon assimilation while limiting water loss by adjusting stomatal aperture. In grasses, a developmental innovation – the addition of subsidiary cells (SCs) flanking two dumbbell-shaped guard cells (GCs) – is supposedly linked to the grass family's improved stomatal gas exchange efficiency. A mutant screen in the wheat relative and model grass *Brachypodium distachyon* identified a transcription factor necessary and sufficient for SC formation. Unexpectedly, the transcription factor is an ortholog of the stomatal regulator *AtMUTE*, which defines GC precursor fate in *Arabidopsis*. The novel role of *BdMUTE* in specifying lateral SCs appears linked to its acquisition of cell-to-cell mobility in *Brachypodium*. Physiological analyses on *bdmute* mutant plants lacking SCs experimentally support classic hypotheses that SCs permit greater stomatal responsiveness to enhance water use efficiency and larger range of pore apertures to increase photosynthetic capacity. Recently, we profiled the transcriptome of developing and mature leaf regions of both wild-type and SC-less *bdmute* plants to identify novel factors regulating SC development and SC function, respectively. Discovering genes required for SC function will help understand how SCs actually improve stomatal gas exchange dynamics in grasses. Understanding how SCs are formed and enable grasses to breathe more efficiently might allow engineering of stomatal properties in many different crops to improve water use efficiency and plant performance.

P4.14 IDENTIFICATION AND FUNCTIONAL CHARACTERIZATION OF GENES IN THE GUARD CELL CO_2 SIGNALING PATHWAY IN MAIZE

THURSDAY 4 JULY, 2019 **14:40**

ANTHONY J STUDER (UNIVERSITY OF ILLINOIS, UNITED STATES), ROBERT J TWOHEY III (UNIVERSITY OF ILLINOIS, UNITED STATES)

@ ASTUDER@ILLINOIS.EDU

The balance of CO_2 uptake for photosynthesis and transpirational water loss is a dynamic process that is controlled by guard cells. Guard cell aperture changes in response to a variety of environmental factors such as atmospheric CO_2 levels, humidity, light, and temperature. The CO_2 signaling pathway has been previously described in *Arabidopsis*, although there is evidence that the monocot pathway is not functionally identical to the pathway found in dicot species. Our work uses physiological analysis of genetic mutants to dissect the pathway in maize. Due to a relatively recent whole-genome duplication, many paralogous gene copies exist, which complicates the functional characterization and requires double and triple mutants. Leaf level gas exchange measurements were used to look at the physiological response of the mutants to environmental stimuli, and leaf imaging was employed to assay possible changes in stomatal patterning. Unlike in *Arabidopsis*, none of the signaling mutants showed a change in stomatal patterning. Also, our data suggest that the signaling pathway may be non-linear. Finally, some of the mutants affected not only guard cell signaling but also net photosynthesis, indicating a possible dual function. Understanding the guard cell CO_2 signaling pathway is one avenue to explore the relationship between photosynthesis and transpiration. Other lines of research that relate to the optimization of transpiration for increase water-use efficiency will also be discussed.

P4.15 LEAF STRUCTURAL, ANATOMICAL AND BIOCHEMICAL DETERMINANTS OF MESOPHYLL CO_2 CONDUCTANCE IN C_4 GRASSES

THURSDAY 4 JULY, 2019 **14:55**

ASAPH COUSINS (WASHINGTON STATE UNIVERSITY, UNITED STATES), VARSHA S PATHARE (WASHINGTON STATE UNIVERSITY, UNITED STATES), NURIA KOTEYEVA (KOMAROV BOTANICAL INSTITUTE OF THE RUSSIAN ACADEMY OF SCIENCES, RUSSIA)

@ ACOUSINS@WSU.EDU

Mesophyll conductance (g_m) describes the movement of CO_2 from substomatal cavities to the site of carboxylation in mesophyll cell. This is an important trait that could be modified to enhance photosynthetic rates (A_{net}) and intrinsic transpiration efficiency (TE_i). However, little is known about what leaf traits influence g_m in C_4 species. Therefore, we evaluated the structural, anatomical and biochemical traits that could explain g_m-variability in 18 C_4 grasses. There was a four-fold variation in g_m among the C_4 grasses that positively related to A_{net} and TE_i but not stomatal conductance (g_s). The lack of correlation between g_m and g_s suggests that enhancing g_m can improve A_{net} and TE_i without an increase in g_s and water loss. Leaf traits such as leaf thickness ($Thick_{leaf}$), stomatal ratio (SR), adaxial stomatal densities (SD_{ada}) and mesophyll surface area exposed to intercellular air spaces (S_{mes}) all had positive relationships between g_m. This suggests that greater SR and SD_{ada} reduced the effective CO_2 diffusion pathlength and increases in S_{mes} provided more parallel pathways for CO_2 diffusion into the mesophyll cells thereby increasing g_m. There was also a positive relationship of g_m with carbonic anhydrase activities (k_{CA}) and leaf N content (N_{area}), suggesting some biochemical influence on g_m. Taken together, our results suggest that SR, SD_{ada}, S_{mes} and k_{CA} are the potential traits that could be modified for enhancing g_m and TE_i in C_4 grasses. (Supported by U.S. Department of Energy, Grant #DE-SC0001685.)

P4.16 DISSECTING THE COORDINATION OF LEGUME STOMATAL AND ROOT DEVELOPMENT TO ENHANCE CROP WATER USE EFFICIENCY

THURSDAY 4 JULY, 2019 **15:25**

CASPAR CC CHATER (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), OSWALDO VALDÉS-LÓPEZ (FES IZTACALA UNAM, MEXICO), ROSA BRIANDA DE LA SANCHA PÉREZ (IBT UNAM, MEXICO), CORAL MARTINEZ MARTINEZ (IBT UNAM, MEXICO), ALEJANDRA COVARRUBIAS ROBLES (IBT UNAM, MEXICO), JULIE GRAY (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM)

@ C.CHATER@SHEFFIELD.AC.UK

Legume crops are generally sensitive to water deficit and drought stress. Water use efficiency (WUE), the ratio of carbon uptake to water loss through stomata, is a useful breeding target to improve crop drought responses and yield. Lowering stomatal conductance (g_s), through reducing stomatal density (*SD*) improves WUE, and legume crops may benefit from this without a corresponding photosynthetic penalty. Rhizobial nitrogen (N) fixation enhances legume leaf N content, enabling photosynthesis at lower g_s, and thus mitigating leaf water loss. By reducing *SD* in legume crops we may therefore enhance WUE, N use efficiency (NUE), and yields under water deficit and replete conditions. High WUE legumes could therefore play a central role in the sustainable intensification of global agriculture under climate change, requiring fewer water and fertiliser inputs. Low *SD* can be obtained by inhibiting stomatal development, but this can also change rhizosphere development and root water dynamics. As rhizobial symbiosis is central to legume NUE and WUE, an understanding of the coordination between *SD*, g_s, and root traits including nodulation, is essential if we are to develop novel legume crops for sustainable agriculture. Here we explore these relationships and their implications for breeding high WUE 'Climate-Ready' legumes for future food security.

P4.17 DYNAMIC CHANGES IN ABA CONTENT IN WATER-STRESSED *POPULUS NIGRA*: EFFECTS ON CARBON FIXATION, SOLUBLE CARBOHYDRATES AND HYDRAULIC RECOVERY

THURSDAY 4 JULY, 2019 **15:40**

CECILIA BRUNETTI (NATIONAL RESEARCH COUNCIL TREES AND TIMBER INSTITUTE, ITALY), ANTONELLA GORI (UNIVERSITY OF FLORENCE DAGRI, ITALY), TADEJA SAVI (UNIVERSITY OF NATURAL RESOURCES AND LIFE SCIENCES, DIVISION OF VITICULTURE AND POMOLOGY DEPARTMENT, AUSTRIA), ANDREA NARDINI (UNIVERSITY OF TRIESTE DEPARTMENT OF LIFE SCIENCE, ITALY), FRANCESCO LORETO (NATIONAL RESEARCH COUNCIL DISBA, ITALY), MAURO CENTRITTO (NATIONAL RESEARCH COUNCIL, TREES AND TIMBER INSTITUTE, ITALY)

@ CBRUNETTI@IVALSA.CNR.IT

Drought compromises plants ability to replace transpired water vapour with water absorbed from the soil. Hydraulic and chemical signals operate in tandem to regulate systemic plant responses to drought to avoid extensive xylem dysfunction. The hormone abscisic acid (ABA) plays a major role in regulating stomatal closure and acts as a root-to-shoot signal under water deficit. *Populus nigra* seedlings were used as model systems to investigate how hormonal and hydraulic signals contribute to optimize stomatal (g_s), mesophyll (g_m) and leaf hydraulic (K_{leaf}) conductance under well-watered (WW) and water-stressed conditions (WS); a possible role for ABA in mobilizing non-structural carbohydrates (NSC) within the leaf and stem; and a possible relationship between NSC and xylem hydraulic function upon drought and re-watering. Our results demonstrate that ABA regulates the photosynthetic machinery on a daily basis in both WW and WS conditions to optimize water use efficiency (WUE). In addition, a possible relationship between ABA and NSC in the leaves and stem are reported, suggesting potential roles of this hormone in carbohydrate metabolism. We also hypothesize that the mobilization of stem carbohydrates might promote the restoration of xylem transport capacity.

P4.18 THE EFFECT OF ELEVATED CARBON DIOXIDE ON PHOTOSYNTHESIS IN MATURE OAK WOODLANDS

THURSDAY 4 JULY, 2019 **15:55**

ANNA M GARDNER (UNIVERSITY OF BIRMINGHAM, UNITED KINGDOM)

@ AXG042@STUDENT.BHAM.AC.UK

Anthropogenic carbon dioxide (CO_2) is the main greenhouse gas driving change in the Earth's climate. Rising CO_2 is expected to stimulate photosynthesis, but limited studies have been conducted on mature forests. It is uncertain how mature temperate forest ecosystems may respond to the future CO_2 emissions and what interacting environmental factors may influence this. This experiment has been conducted at the Birmingham Institute of Forest Research Free Air Carbon Enrichment Experiment (BIFoR-FACE). BIFoR-FACE is set in a mature oak (*Quercus robur* L.) woodland and provides additional CO_2 to 30m diameter experimental plots. This simulates the future atmospheric conditions in 50 years' time (+150ppm). Gas exchange measurements have been conducted in the second year of CO_2 fumigation (2018) in the upper canopy of oak trees from bud burst (June) to leaf fall (October). This study used a paired plot design (n=3) using elevated CO_2 plots (eCO_2) (550ppm) and ambient control plots (aCO_2) (400ppm). Measurements of carbon assimilation and water exchange between the oak leaves and the atmosphere have been used to calculate photosynthesis, stomatal conductance and water use efficiency. The first season results have seen an increase in carbon assimilation, in the eCO_2 plots, in addition to a decrease of stomatal conductance and overall increase in water use efficiency. The effect of eCO_2 has been influenced by season and diurnal fluctuations in environmental variables. These data will help understand the physiological responses, at the leaf level, and resilience of mature temperate forest ecosystems to climate change.

P4.19 ORGANIC ELECTRONIC ION PUMP FOR ANIONIC HORMONE DELIVERY IN INTACT PLANTS

THURSDAY 4 JULY, 2019 **15:57**

MIRIAM HUERTA (LINKÖPING UNIVERSITY, SWEDEN), IWONA BERNACKA-WOJCIK (LINKÖPING UNIVERSITY, SWEDEN), TOBIAS ABRAHAMSSON (LINKÖPING UNIVERSITY, SWEDEN), ROGER GABRIELSSON (LINKÖPING UNIVERSITY, SWEDEN), MAGNUS BERGGREN (LINKÖPING UNIVERSITY, SWEDEN), DANIEL SIMON (LINKÖPING UNIVERSITY, SWEDEN), ELENI STAVRINIDOU (LINKÖPING UNIVERSITY, SWEDEN)

@ MIRIAM.HUERTA@LIU.SE

Plants are the main source of food, oxygen, renewable energy, materials, and regulators of the ecosystem. Stomata consist of a pair of guard cells that form microscopic pores in the leaves, which main role is the active gasses exchange and water evaporation enabling photosynthesis and transpiration. Abscisic acid, ABA, plays an essential role in the signaling mechanism that triggers the stomata closure. The organic electronic ion pump (OEIP) is an electrophoretic device that allows precise delivery of ions and charged biomolecules with high spatiotemporal resolution. This device has been applied in mammalian systems for therapy, mainly. Here, we report for the first time the use of OEIP for electronic control of ABA delivery in order to regulate the stomata closure in intact plants. For the delivery of the phyto-hormone ABA, we used a new generation of the ion pump that is based on glass capillary tubes and has an overall diameter of 60µm. The small diameter of the pump allows easy insertion in leaves of intact plants through the epidermis into the internal area of the leaf. We demonstrated that the stomata close after ABA delivery with the organic electronic ion pump and the stomata near to the ion pump close faster than the ones further away. In addition, we did not observe any significant wound effect nearby the insertion of the pump suggesting that our method is noninvasive. Our technology offers a new tool for studying ABA signaling in plants with implications in plant responses to environmental changes.

P4.20 A LACK OF ABA BIOSYNTHETIC OR SIGNALLING MACHINERY LEADS TO SLOWED STOMATAL MOVEMENTS

THURSDAY 4 JULY, 2019 **15:59**

ASHLEY J PRIDGEON (UNIVERSITY OF BRISTOL, UNITED KINGDOM), ALISTAIR M HETHERINGTON (UNIVERSITY OF BRISTOL, UNITED KINGDOM)

@ ASHLEY.PRIDGEON@BRISTOL.AC.UK

Abscisic acid (ABA) is a hormone that has been extensively studied especially in the context of the plant drought response. It is known to affect various aspects of plant physiology, including the promotion of stomatal closure and the inhibition of stomatal opening. However, the function of ABA and its associated biosynthesis and signalling machinery isn't strictly limited to the drought response. Research is pointing towards ABA playing a more general role in modulating plant responses to a variety of signals. One of the fundamental signals that stomata respond to is light (quality and quantity). When exposed to white light stomata open, and when the light is reduced or taken away stomata close. Here we investigate ABA's role in modulating stomatal responses to light. Using ABA biosynthesis and signalling mutants we show a lack of ABA production or perception leads to a deceleration of stomatal movement in response to changing levels of light.

P4.21 THE ROLE OF GUARD CELL CHLOROPLASTS IN STOMATAL BEHAVIOUR AND CO-ORDINATION WITH MESOPHYLL PHOTOSYNTHESIS

THURSDAY 4 JULY, 2019 **16:01**

AMNAH M ALAMRI (UNIVERSITY OF ESSEX, UNITED KINGDOM), ULI BECHTOLD (UNIVERSITY OF ESSEX, UNITED KINGDOM), TRACY LAWSON (UNIVERSITY OF ESSEX, UNITED KINGDOM)

@ AA16381@ESSEX.AC.U

An expanding global population and a changing climate are major factors influencing crop yields, increasing pressure to find solutions to ensure sufficient food and fuel production for future generations. The biomass of a crop depends on the cumulative rate of photosynthesis and the rate of carbon fixation can be limited by the internal concentration of CO_2. Stomata regulate gaseous exchange between the leaf interior and the external air surrounding the leaf, thereby, controlling CO_2 uptake for photosynthesis, and simultaneously water loss and evaporative cooling through transpiration. Both stomatal conductance (g_s) and photosynthesis (*A*) respond to changes in environmental conditions and a close correlation between *A* and g_s is often reported. However, the mechanism(s) that co-ordinate stomatal behaviour with *A* are not clear. Guard cells contain functional chloroplasts and we have examined the role of these guard cell chloroplasts in stomatal function and in particular its role in the coordination between stomatal behaviour and mesophyll photosynthesis. In order to do this, we have produced transgenic tobacco (*Nicotianatabacum*) plants with altered expression levels of the Calvin cycle enzyme Sedoheptulose-1,7, bis-phosphatase (SBPase) and the electron transport protein, Rieske FeS specifically in guard cells. The impact of these manipulations on photosynthesis and stomatal behaviour is discussed.

P4.22 IS CARBON ISOTOPE DISCRIMINATION A RELIABLE TRAIT TO SUPPORT CHICKPEA CROP IMPROVEMENT PROGRAMS?

THURSDAY 4 JULY, 2019 **16:03**

MILLICENT R SMITH (ICRISAT, INDIA), RUTWIK BARMUKH (ICRISAT, INDIA), MANISH ROORKIWAL (ICRISAT, INDIA), JANA KHOLOVA (ICRISAT, INDIA), ALICE KUJUR (ICRISAT, INDIA), ERIN L LOCKHART (UNIVERSITY OF SYDNEY, AUSTRALIA), JAMES MALONEY (UNIVERSITY OF SYDNEY, AUSTRALIA), MARGARET M BARBOUR (UNIVERSITY OF SYDNEY, AUSTRALIA), RAJEEV K VARSHNEY (ICRISAT, INDIA)

@ MILLICENT.R.SMITH@GMAIL.COM

A key goal for chickpea improvement at ICRISAT is to increase water use efficiency (WUE). The use of carbon isotope discrimination ($\delta^{13}C$) as a proxy for transpiration efficiency (TE) has been tested widely in attempts to investigate plant water use. However, $\delta^{13}C$ estimated from chickpea has not related well to TE in previous studies. We explore the influence of leaf acids and extraction techniques on $\delta^{13}C$ and apply this new method for $\delta^{13}C$ collection to a fine mapping population, varying for traits related to TE. Methods testing demonstrated that the removal of leaf acids prior to analysis of the leaf soluble carbohydrate pool led to a closer correlation with intrinsic WUE (A/g_s). To test this method on a larger scale, we used the robust gravimetric method to estimate TE (dry matter produced per unit of water transpired) using a fine mapping population phenotyped in lysimeters and the LeasyScan platform while simultaneously sampling $\delta^{13}C$ to assess TE at the leaf level. Alongside $\delta^{13}C$ and TE, water use over the season, canopy traits, root traits and agronomic traits were measured. We found that a significant proportion of variation for agronomic performance was explained by crop vigour and TE related parameters. Analysis is continuing to investigate QTLs underlying measured traits and narrow down the candidate genes functionally associated with WUE. This research will assist the crop improvement program to design chickpea well-suited to target environments prone to water stress eventually translating to food security and better incomes for chickpea farming communities.

P4.23 IMAGING THE MESOPHYLL IN 3D TO ELUCIDATE THE STRUCTURE/ FUNCTION RELATIONSHIPS IN LEAVES OF WHEAT AND ITS WILD RELATIVES

THURSDAY 4 JULY, 2019 **16:05**

MATTHEW WILSON (THE UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), MARJORIE LUNDGREN (THE UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), ANDREW MATHERS (THE UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), CRAIG STURROCK (THE UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), SACHA MOONEY (THE UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), COLIN OSBORNE (THE UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), ANDREW FLEMING (THE UNIVERSITY OF SHEFFIELD, UNITED KINGDOM)

@ MJWILSON2@SHEFFIELD.AC.UK

Stomatal characteristics and the internal arrangement of mesophyll cells within leaves have a direct impact upon photosynthesis and water use efficiency (WUE). My research has revealed that there is a relationship between stomatal patterning, stomatal size and stomatal conductance in *Triticum* species. Hexaploid wheat (*Triticum aestivum*) has fewer, larger stomata than those found on the leaves of its wild relatives (*T. baeoticum*, *T. urartu* = 2n; *T. araraticum*, *T. dicoccoides* = 4n). Diploid lines have the highest frequency of small stomata, whilst tetraploid lines have intermediate stomatal size and density. These differences in stomatal size and density are mirrored by stomatal conductance. Diploid lines have a higher stomatal conductance than their hexaploid counterparts, with tetraploid lines having middling conductance rates. Furthermore, using X-ray µCT to investigate internal leaf structure suggests that there is a positive correlation between the level of intercellular airspace in the leaf (mesophyll porosity - % airspace/volume) and stomatal conductance. Additionally, I have successfully developed a method via which the wheat mesophyll can be reconstructed in 3D to cellular resolution using confocal imaging and processing using LithographX software. Using this technique I have been able to investigate whether stomatal size/density changes observed during domestication are paralleled by alterations in mesophyll cell size and shape.

P4.24 3D IMAGING OF GUARD CELLS

THURSDAY 4 JULY, 2019 **16:07**

ELLIE HEALICON (THE UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), JULIE GRAY (THE UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), ANDREW FLEMING (THE UNIVERSITY OF SHEFFIELD, UNITED KINGDOM)

@ EGHEALICON1@SHEFFIELD.AC.UK

Stomata are critical for plant survival by regulating plant response to internal and environmental changes, such as drought, temperature and presence of pathogens. For stomata to function, the guard cells undergo extreme and repeated shrinking and stretching and must withstand internal pressure changes more than that of which a deep-sea diver would experience. Modelling indicates that cell shape is crucial for understanding how guard cells mechanically respond to such shifts in pressure, yet there has been limited characterisation of 3D guard cell shape change during opening/closure of stomata. I present a method of imaging stomata using confocal microscopy, creating 3D reconstructions of the guard cells using open-source LithographX software. These reconstructions provide quantitative data on the guard cell volume and surface area changes that occur during stomatal opening/closure, as well as information on the shape changes that underpin these data. I will report on on-going experiments from both wild-type and mutant plants which display altered stomatal function, with the aim of discovering the extent to which cell shape (rather than cell wall material properties) modulates stomatal function. These data will feed into stomatal mechanical models, providing a deeper insight into the interaction of cell shape and function.

P4.25 WATER USE EFFICIENCY ACROSS SCALES

THURSDAY 4 JULY, 2019 **16:40**

BELINDA E MEDLYN (HAWKESBURY INSTITUTE FOR THE ENVIRONMENT, WESTERN SYDNEY UNIVERSITY, AUSTRALIA)

@ B.MEDLYN@WESTERNSYDNEY.EDU.AU

Water use efficiency (WUE), plant uptake of carbon per unit water lost, can be expressed on a wide range of temporal and spatial scales – from the leaf to the ecosystem, from seconds to years. A wide range of techniques can be used to measure WUE, including leaf gas exchange, stable isotopes, eddy covariance, and whole-plant measurements, all of which yield results on different scales. How comparable should we expect these results to be – and how comparable are they? In this talk I will discuss several recent studies in which we have attempted to compare water use efficiency, and its responses to environmental change, across different scales. I will highlight areas of disagreement among the different measures and discuss research directions needed to resolve these discrepancies.

P4.26 QUANTIFYING IMPACTS OF MANIPULATING PHOTOSYNTHESIS AND STOMATAL CONDUCTANCE ON CROP YIELD IN VARIABLE RAINFALL ENVIRONMENTS

THURSDAY 4 JULY, 2019 **17:10**

ALEX WU (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), GRAEME L HAMMER (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), AL DOHERTY (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), SUSANNE VON CAEMMERER (AUSTRALIAN NATIONAL UNIVERSITY, AUSTRALIA), GRAHAM D FARQUHAR (AUSTRALIAN NATIONAL UNIVERSITY, AUSTRALIA)

@ C.WU1@UQ.EDU.AU

Advances in crop productivity are likely to come from enhancing photosynthetic efficiency. However, yield consequences of photosynthetic manipulation are confounded by complex feedback effects arising from interactions with crop growth and development processes, and the prevailing environment. In dryland cropping situations, water availability is particularly important as it impacts whole-plant growth through limiting stomatal conductance and photosynthesis. Here we present a novel cross-scale modelling capability that connects the interplay of leaf level photosynthesis–stomatal conductance with crop growth and development dynamics in a manner that addresses the feedforward-feedback effects across the scales of biological organisation. The model links photosynthesis and stomatal conductance via an equilibrium C_i/C_a ratio, a property consistent with stomatal optimisation theory. Under water non-limiting conditions, photosynthesis is the driver of leaf gas exchange, while conductance dominates under water-limited conditions. The state of water limitation is determined by the crop system water supply-demand balance, which interacts with the prevailing environment. The cross-scale model was validated using data on crop biomass and yield for wheat and sorghum from diverse field experiments. Consequences for yield were simulated for major photosynthetic enhancement targets related to leaf CO_2 and light energy capture efficiencies and their combinations. Predicted impacts ranged markedly and were dependent on the photosynthetic enhancement, crop type, and environment, especially the degree of water limitation. The importance of interdependencies operating across scales of biological organisation was highlighted as was the need to enhance understanding and modelling of the photosynthesis-stomatal conductance link to better quantify impacts of enhancing photosynthesis.

P4.27 PREDICTIVE MODELLING OF STOMATA ACROSS SCALES FROM MOLECULE TO THE FIELD

THURSDAY 4 JULY, 2019 **17:25**

MICHAEL BLATT (UNIVERSITY OF GLASGOW, UNITED KINGDOM), MAREIKE JEZEK (UNIVERSITY OF GLASGOW, UNITED KINGDOM)

@ MICHAEL.BLATT@GLASGOW.AC.UK

Stomatal movements depend on the transport and metabolism of osmotic solutes that drive water flux, reversible changes in guard cell volume and turgor. Much detail is known of the molecular mechanics of these processes, sufficient to model guard cells with true predictive power. By contrast, models at the whole-plant and canopy levels define stomata with a simple set of linear empirical relations, disconnected from their underlying mechanics. These models cannot inform on the underlying molecular characteristics of the guard cells that give rise to stomatal conductance (g_s) and therefore cannot guide efforts to 'reverse engineer' stomatal traits in the field. To address this challenge, we recently introduced the OnGuard2 modelling platform. This platform utilizes the molecular mechanics of ion transport, metabolism and signalling of the guard cell to define transpiration in the whole plant. OnGuard2 faithfully reproduces g_s kinetics in *Arabidopsis*, its dependence on VPD and on water feed to the leaf and has yielded predictions, several of which we have since verified experimentally. Further developments are underway to introduce CO_2 and photosynthetic carbon fixation within this framework will bridge the gap between microscale models of the guard cell and macroscale models of whole-plant transpiration and carbon assimilation.

P4.28 ACCLIMATION TO DYNAMIC LIGHT INFLUENCES THE RAPIDITY AND DIURNAL RESPONSE OF STOMATAL CONDUCTANCE IN *POPULUS NIGRA*

THURSDAY 4 JULY, 2019 **POSTER SESSION**

JACK SA MATTHEWS (UNIVERSITY OF ESSEX, UNITED KINGDOM), SILVERE RM VIALET-CHABRAND (UNIVERSITY OF ESSEX, UNITED KINGDOM), TRACY LAWSON (UNIVERSITY OF ESSEX, UNITED KINGDOM)

@ JSAMAT@ESSEX.AC.UK

Plant acclimation to growth light has been studied extensively, yet little is known about the effect of dynamic fluctuations in light on stomatal behaviour and acclimatory responses. To assess the impact of growth light regime on stomatal acclimation, we grew *Populus nigra* (black poplar) under different intensities of dynamic light at the University of Essex. As part of the work we characterized changes in stomatal development and responses under a 'real' light environment, and investigated the impact on photosynthesis and water use efficiency. We demonstrate that acclimation of stomatal conductance (g_s) is influenced by growth light intensity, modifying stomatal kinetics at different times of the day; resulting in alterations in the rapidity and magnitude of the g_s response over the diurnal period. Further quantified is the response of g_s to different step changes in light intensity; with plants grown under low light exhibiting faster g_s responses when subjected to a step change at low light levels, whilst the reverse is true at high light steps. This represents an interesting strategy, where plants acclimate by increasing g_s faster to light levels that they experience more often during growth and development, either as a way of maximizing carbon uptake or for the conservation of energy by limiting unnecessary stomatal movement. From these findings, we conclude that acclimation of g_s to growth light could be an important strategy for maintaining carbon fixation, overall plant water status, and water use efficiency under dynamic light conditions.

P4.29 NITROGEN ASSIMILATION AND ABIOTIC STRESS TOLERANCE

WEDNESDAY 3 JULY, 2019 **POSTER SESSION**

JOANNA LANDYMORE (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), JULIE E GRAY (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), ANGELA HODGE (UNIVERSITY OF YORK, UNITED KINGDOM)

@ JLANDYMORE1@SHEFFIELD.AC.UK

The need to restrict crop irrigation and the use of nitrogenous fertilisers, coupled with global population growth and climate change, is increasing the strain on the food supply. We are studying the abiotic stress responses of *Arabidopsis* mutants to investigate the links between plant nitrogen status and stress signalling. Nitrogen is an essential plant nutrient taken up from the soil by the roots in the form of nitrate and/or ammonium. Plant nitrogen status and abiotic stress responses are intrinsically linked; when a plant experiences salt or drought stress, a signalling pathway is initiated which results in stomatal closure, reduced stomatal water loss and decreased nitrate uptake through the roots. This drop in nitrate uptake will affect plant growth as well as the ability of the plant to respond to stress signals. The most important enzyme in the process of plant nitrogen assimilation is nitrate reductase which is encoded by two *Arabidopsis* genes; *NIA1* and *NIA2*. The nitrate reductase enzyme reduces nitrate to nitrite, and is also responsible for the reduction of nitrite to nitric oxide. Nitric oxide is a signalling molecule that has been shown to trigger many plant stress responses. We are using mutant plants which lack NIA1 and NIA2 are therefore unable to produce nitrate reductase, to study the role of nitrogen status and nitric oxide in salt and drought stress responses. Understanding such control mechanisms could help us to produce more stress tolerant or water use efficient plants.

P4.30 IMAGING WATER USE EFFICIENCY UNDER DYNAMIC ENVIRONMENTAL CONDITIONS

THURSDAY 4 JULY, 2019 **POSTER SESSION**

SILVERE VIALET-CHABRAND (UNIVERSITY OF ESSEX, UNITED KINGDOM), MARTIN BATTLE (UNIVERSITY OF ESSEX, UNITED KINGDOM), TRACY LAWSON (UNIVERSITY OF ESSEX, UNITED KINGDOM)

@ SRMVIA@ESSEX.AC.UK

Plant phenotyping, the quantitative description of plants' anatomical, ontogenetical, physiological and biochemical properties, is key to assess genetic diversity and identify targets for genetic manipulation to improve plant performance and yield. Intrinsic water use efficiency (W_i), net CO_2 assimilation rate (A) divided by stomatal conductance to water vapor (g_{sw}) is an important physiological trait displaying complex diurnal kinetics that are difficult to measure with high throughput. Under dynamic environmental conditions, differences in A between plants can be due to differences in photosynthetic capacities, enzymatic activation (e.g. PSII, RuBisCO) and stomatal limitation of CO_2 diffusion to the sites of carboxylation, all of which influence W_i. Temporal responses of g_{sw} are generally an order of magnitude slower than A and not only limit A but also have an impact on leaf transpiration and temperature, influencing plant yield and water budget. Although very precise, the scalability of leaf gas exchange methods to estimate A and g_{sw} is limited and is becoming a major technical bottleneck for large scale genetic studies. In contrast, chlorophyll fluorescence imaging and thermography allow rapid, non-contact measurement of a large number of plants, however their biological interpretation is more challenging. Deriving g_{sw} from thermograms using energy balance equations is still extremely difficult and is not widely used. Recent advances in imaging methods and interpretation of chlorophyll fluorescence imaging and thermography are presented with insights on how stomatal behaviour impact the spatial and temporal response of W_i under a dynamic environment.

P5 MECHANISMS AND MITIGATION OF PLANT WATER DEFICIT: FROM THE BOTTOM UP

ORGANISED BY: IAN DODD (UNIVERSITY OF LANCASTER) AND ANTONIO DIAZ-ESPEJO (CSIC SPAIN)

P5.1 ROOT HYDRAULICS: ARCHITECTURE & ANATOMY INTERACTIONS

WEDNESDAY 3 JULY, 2019 **10:00**

VALENTIN COUVREUR (UNIVERSITÉ CATHOLIQUE DE LOUVAIN, EARTH AND LIFE INSTITUTE, LOUVAIN-LA-NEUVE, BELGIUM), GUILLAUME LOBET (FZ JUELICH, JUELICH, GERMANY; UNIVERSITÉ CATHOLIQUE DE LOUVAIN, EARTH AND LIFE INSTITUTE, LOUVAIN-LA-NEUVE, BELGIUM), MATHIEU JAVAUX (UNIVERSITÉ CATHOLIQUE DE LOUVAIN, EARTH AND LIFE INSTITUTE, LOUVAIN-LA-NEUVE, BELGIUM; FZ JUELICH, JUELICH, GERMANY), BERTRAND MULLER3, FRANÇOIS CHAUMONT (UNIVERSITÉ CATHOLIQUE DE LOUVAIN, EARTH AND LIFE INSTITUTE, LOUVAIN-LA-NEUVE, BELGIUM), FRANÇOIS TARDIEU (INRA, LEPSE, MONTPELLIER, FRANCE), XAVIER DRAYE (UNIVERSITÉ CATHOLIQUE DE LOUVAIN, EARTH AND LIFE INSTITUTE, LOUVAIN-LA-NEUVE, BELGIUM)

@ XAVIER.DRAYE@UCLOUVAIN.BE

Advanced transcriptome sequencing has uncovered extensive alternative splicing (more than 60%) in plants, and genome-wide as well as focused gene analyses have shown the regulatory power of alternative splicing on plant development and in responses to stress and environment. Alternative splicing can create new protein isoforms or change gene expression by leading to transcript isoforms that are either targeted to the NMD pathway or are retained in the nucleus. Alternative splicing as a co-transcriptional process is also greatly influenced by epigenetic changes at the chromatin level. Proteins regulating splicing or alternative splicing and transcript isoforms with different fates have significant impact in gene regulatory circuits. Specifically, beside deve

P5.2 PRIMARY ROOT GROWTH IN PEARL MILLET: GENETICS AND PHYSIOLOGICAL BASE OF A PIVOTAL ADAPTIVE TRAIT FOR DRY ENVIRONMENTS

WEDNESDAY 3 JULY, 2019 **10:30**

CARLA DE LA FUENTE CANTÓ (INSTITUT DE RECHERCHE POUR LE DÉVELOPPEMENT (IRD), FRANCE), MARILYNE DEBIEU (DIADE UNIVERSITY OF MONTPELLIER IRD, FRANCE), SIXTINE PASSOT (DIADE UNIVERSITY OF MONTPELLIER IRD, FRANCE), ALEXANDRE GRONDIN (DIADE UNIVERSITY OF MONTPELLIER IRD, FRANCE), MAXIME STEFFEN (DIADE UNIVERSITY OF MONTPELLIER IRD, FRANCE), HN DINH (DIADE UNIVERSITY OF MONTPELLIER IRD, FRANCE), JONATHAN ATKINSON (UNIVERSITY OF NOTTINGHAM SUTTON BONINGTON, UNITED KINGDOM), ANTONY CHAMPION (DIADE UNIVERSITY OF MONTPELLIER IRD, FRANCE), CELIA BARRACHINA (MONTPELLIER GENOMIX MONTPELLIER, FRANCE), MARINE PRATLONG (MONTPELLIER GENOMIX MONTPELLIER, FRANCE), PASCAL GANTET (DIADE UNIVERSITY OF MONTPELLIER IRD, FRANCE), MALCOLM BENNETT (UNIVERSITY OF NOTTINGHAM SUTTON BONINGTON, UNITED KINGDOM), PRAKASH GANGASHETTY (ICRISAT, NIGER), NDJIDO KANE (LMI LAPSE DAKAR, SENEGAL), DARREN WELLS (UNIVERSITY OF NOTTINGHAM SUTTON BONINGTON, UNITED KINGDOM), YVES VIGOUROUX (DIADE UNIVERSITY OF MONTPELLIER IRD, FRANCE), LAURENT LAPLAZE (LMI LAPSE DAKAR (SENEGAL) DIADE UNIVERSITY OF MONTPELLIER IRD, FRANCE)

@ CARLA.DE-LA-FUENTE-CANTO@IRD.FR

Pearl millet is a staple crop growing in the semi-arid tropical regions of Asia and Africa. The crop is adapted and cultivated in soils lacking water and nutrients where other cereals would fail. We investigated belowground traits associated with these adaptations with an aim for breeding more climate-resilient varieties. We targeted primary root growth as an important trait for early seedling establishment. Preliminary results in West-African field trials suggest a positive impact of primary root growth on crop yield in dry low-P conditions. We characterised the phenotypic variation of the trait in a genetically diverse panel of 120 inbred lines using high-throughput phenotyping platforms. A Genome Wide Association Study (GWAS) revealed nine significant marker-trait associations for the trait. Inbred lines with contrasted phenotype were used to assess differences in root tips transcriptome (RNAseq) and develop two large F2 QTL populations. QTLs in F2 populations were analysed using bulked pools of lines with extreme phenotype. The combination of GWAS, gene expression analysis and bulk segregant analysis revealed interesting QTLs and candidate genes in the regulation of pearl millet root growth. Backcrossed lines will be used to further test our results in field trials.

P5.3 DYNAMIC RESPONSE OF LOCAL ROOT WATER UPTAKE TO LIGHT INTENSITY CHANGES

WEDNESDAY 3 JULY, 2019 **10:45**

DAGMAR VAN DUSSCHOTEN (IBG-2 FORSCHUNGSZENTRUM JUELICH, GERMANY), YANNIK MUELLERS (IBG-2 FORSCHUNGSZENTRUM JUELICH, GERMANY), JOHANNES KOCHS (IBG-2 FORSCHUNGSZENTRUM JUELICH, GERMANY), DANIEL PFLUGFELDER (IBG-2 FORSCHUNGSZENTRUM JUELICH, GERMANY), HENDRIK POORTER (IBG-2 FORSCHUNGSZENTRUM JUELICH, GERMANY), JOHANNES A POSTMA (IBG-2 FORSCHUNGSZENTRUM JUELICH, GERMANY)

@ D.VAN.DUSSCHOTEN@FZ-JUELICH.DE

Local root water uptake (RWU) is dependent on shoot transpiration rates as well as several root characteristics and the surrounding soil water content (θ). Quantification of RWU is quite hard due to the relatively fast redistribution of water within the soil. Poor sensitivity and low spatial resolution of currently available soil water sensors pose additional challenges. We present a new, affordable soil water sensor, the Soil Water Profiler (SWaP) with much higher sensitivity and better spatial resolution. It partially envelopes, and thereby can be shifted along, a cylindrical plant container. We can scan single cylinders in a few minutes to determine total change of water in the column (mL plant water uptake) as well as the local changes in θ with a precision of 2e^{-5} cm^3/cm^3 at a 1D resolution in the order of 1cm. Due to the sensors' high precision and fast dynamics we can derive local RWU values utilizing light intensity changes. Using four sensors, we continuously scanned four plants while they were subjected to different light intensities provided by a home-built, water-cooled, programmable LED panel (up to 1400 µE/(m^2.s)). Before and after scanning, the root length distribution was determined using magnetic resonance imaging (MRI). We used the SWaP to monitor RWU of a variety of plants in response to step-wise changes in the light intensity. We show that not only the amplitude of the RWU profiles changes rapidly, but also the shape of the RWU profiles changes with time after a light intensity jump.

P5.4 ORGAN-SPECIFIC DYNAMICS AND ROLES OF STRIGOLACTONES UNDER DROUGHT

WEDNESDAY 3 JULY, 2019 **11:00**

FRANCESCA CARDINALE (UNIVERSITY OF TURIN, ITALY), IVAN VISENTIN (UNIVERSITY OF TURIN, ITALY), CLAUDIO LOVISOLO (UNIVERSITY OF TURIN, ITALY), ANDREA SCHUBERT (UNIVERSITY OF TURIN, ITALY)

@ FRANCESCA.CARDINALE@UNITO.IT

The phytohormones strigolactones (SL) are mostly produced in roots to be exuded in soil and transported to the shoot, where they modulate development. SL biosynthesis in shoots is necessary also for acclimatisation to drought in several plant species, mostly because it promotes stomata closure in abscisic acid (ABA)-dependent and independent ways. In tomato (*Solanum lycopersicum* L.) and other dicots under drought, their synthesis partly shifts from roots to shoots, indicating organ specificity in their metabolism and role. Such drop in root-synthesised SL acts as a systemic indication of stress unlinked from shootward ABA translocation and sufficient to prime the plant for better stress avoidance. Downstream effectors linking SL action under stress to ABA-dependent or independent responses, however, are less characterised. We found that endogenous SL are absolutely required for miR156 induction by drought and that exogenous SL are sufficient for miR156 accumulation in tomato leaves. The effects of SL are exerted on *MIR156* genes at the transcriptional and pri-miRNA processing level. mir156 is a highly conserved microRNA with roles in development and stress responses; its effects on target mRNA stability, tomato ecophysiology and stomatal behaviour suggest it as a good candidate mediator of the ABA-dependent subset of drought responses triggered by SL. The systemic mobility of miR156 defines it also as a SL-related signal feeding back from the shoot to the root in response to drought.

This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement n. 727929-TOMRES

P5.5 PHYSIOLOGICAL, PHYTOHORMONAL AND MOLECULAR RESPONSES OF ROOT-SHOOT COMMUNICATION IN SOYBEAN UNDER DROUGHT CONDITIONS

WEDNESDAY 3 JULY, 2019 **11:30**

PEDRO CASTRO (LANCASTER UNIVERSITY, UNITED KINGDOM), JAIME PUÉRTOLAS (LANCASTER UNIVERSITY, UNITED KINGDOM), IAN C DODD (LANCASTER UNIVERSITY, UNITED KINGDOM), HON-MING LAM (CHINESE UNIVERSITY OF HONG KONG, HONG KONG), JIANHUA ZHANG (HONG KONG BAPTIST UNIVERSITY, HONG KONG)

@ P.CASTROVALDECANTOS@LANCASTER.AC.UK

Soybean is an important global crop for human and animal nutrition, but its production is affected by environmental stresses such as drought. Crops adapt to these stresses by producing multiple internal signals between roots and shoots. Understanding the relationships between physiological (water potential and stomatal conductance), biochemical (phytohormones) and gene expression changes can inform management approaches and offers opportunities to enhance water-limited yields. Soil and atmospheric water deficits can decrease tissue water status stimulating hormone (ABA, JA) accumulation in roots and leaves, thereby promoting stomatal closure to limit water loses. Several genes control each step of the biosynthesis and catabolism of these hormones, but the site of stress perception has attracted considerable debate. One paradigm is that roots are the primary organ to perceive soil drying, generating root-to-shoot signalling to the leaves to initiate stomatal closure. Alternatively, recent studies demonstrate the importance of leaves in generating rapid responses to increased atmospheric VPD. The surgical technique of girdling (removal of stem phloem tissue) suppresses shoot-to-root signalling, allowing the interdependence of root-to-shoot and shoot-to-root signalling to be evaluated at gene expression, biochemical and physiological levels.

P5.6 IMPROVED EARLY ADAPTIVE SIGNALLING IN ROOTS ACCOUNTS FOR DIFFERENTIAL SALT TOLERANCE IN *QUINOA ACCESSIONS*

WEDNESDAY 3 JULY, 2019 **11:45**

NADIA BAZIHIZINA (UNIVERSITÀ DEGLI STUDI DI FIRENZE, ITALY), STEFANO MANCUSO (UNIVERSITÀ DEGLI STUDI DI FIRENZE, ITALY), SERGEY SHABALA (UNIVERSITY OF TASMANIA, AUSTRALIA)

@ NADIA.BAZIHIZINA@UNIFI.IT

Epidermal bladder cells (EBCs) play a key role in the salt tolerance of salt-secreting halophytes by acting as an external salt dump under conditions of excess Na$^+$. Nevertheless, after testing the ST of more than 100 quinoa accessions, we observed dramatic differences in EBC density not always correlated with greater salt tolerance. To elucidate possible mechanism(s) underlying this enhanced tolerance in accessions with low EBC density, two accessions with contrasting salt tolerance and EBC density were selected. At the shoot level, mesophyll K$^+$ retention and gas exchange data indicate that reductions in photosynthetic rates were due to stomatal limitations rather than biochemical ones. This suggests that, in the tolerant accession, improved responses at the root level reduced the inhibition of water flux across cell membranes thereby explaining their improved gas exchanges. Confirming the greater sensitivity at the root level of accession 30, compared with the tolerant accession 68, we found a decline in cell viability and an increase in H_2O_2 production in both the apical and mature root zones following salinity stress. As signalling processes are fundamental in root responses to salinity stress, we also monitored ion fluxes following the addition of NaCl and reactive oxygen species. Our results suggests that, independently of shoot based tolerance mechanisms (including EBC density), improved signalling in the tolerant accession, based on OH$^-$-activation of K$^+$ channels, elicited specific detoxification mechanisms in roots. This in turn improved root membrane functionality, stomatal regulation and gas exchanges in the shoots following the addition of NaCl.

P5.7 IN SILICO AND FUNCTIONAL ANALYSES OF GENES ASSOCIATED WITH DESICCATION AND SALINITY TOLERANCE IN MONOCOT RESURRECTION PLANTS *XEROPHYTA SCHLECHTERI* AND *ERAGROSTIS NINDENSIS*

WEDNESDAY 3 JULY, 2019 **12:00**

MARIAM AWLIA (UNIVERSITY OF CAPE TOWN, SOUTH AFRICA), JILL FARRANT (UNIVERSITY OF CAPE TOWN, SOUTH AFRICA), HENK WM HILHORST (WAGENINGEN UNIVERSITY RESEARCH, NETHERLANDS)

@ MARIAM.AWLIA@KAUST.EDU.SA

Drought and salinity severely affect plant production, causing a global crisis in the wake of climate change. Resurrection plants, relative to crops, are unique in their ability to survive severe desiccation (to less than 10% of cellular water) and recover fully on rehydration, but no study has comprehensively investigated the combined effect with salt stress. Identifying the endogenous regulation of this genetic toolkit in monocot resurrection plants under drought and salinity, both individually and in combination, would shed light on their involvement with desiccation and salinity tolerance. By assessing the physiological responses to salinity and drought tolerance in the slow-growing resurrection plant *Xerophyta schlechteri* and the fast-growing *Eragrostis nindensis* and integrating existing transcriptomic data, the responses and crosstalk between drought and salt stress would be determined. The co-expression networks inferred from *X. schlechteri* and *E. nindensis* in terms of transcriptome, metabolome or epigenome data will establish the connections between salt and drought tolerant clusters, thereby identifying the genes relevant to these two tolerance strategies. Understanding and harnessing the tolerance strategies and genetic toolkit that resurrection plants have could allow the identification of the appropriate genes in crops for improved tolerance to stress.

P5.8 ADVANCES IN PROCESS-BASED MODELING OF STOMATAL RESPONSES TO WATER STATUS

WEDNESDAY 3 JULY, 2019 **14:30**

TOM BUCKLEY (UNIVERSITY OF CALIFORNIA DAVIS, UNITED STATES)

@ TNBUCKLEY@UCDAVIS.EDU

Recent work has clarified the role of hydroactive mechanisms driving stomatal responses to changes in VPD, hydraulic conductance and soil moisture, but has also raised new hypotheses and additional mechanisms that had previously been overlooked, such as the role of vapor and heat transport within the leaf. In this talk, I will discuss these topics and describe a new process-based model that improves upon, and generalizes, previously published models.

P5.9 A MODELLING APPROACH TO QUANTIFY THE INFLUENCE OF STOMATAL BEHAVIOUR AND SALINITY STRESS ON WATER USE EFFICIENCY OF CUCUMBER PLANTS

WEDNESDAY 3 JULY, 2019 **15:00**

DANY MOUALEU-NGANGUE (LEIBNIZ UNIVERSITÄT HANNOVER, GERMANY)

MOUALEU@GEM.UNI-HANNOVER.DE

Water use efficiency (WUE) is driven mainly by leaf traits that reduce transpiration and important processes for leaf productivity. Stomatal behaviour plays a key role on both transpiration rate and net assimilation, and is therefore crucial for improving WUE. On the other hand, salinity was reported to lead to stomatal closure leading to a decrease of the dry matter production. Salinity also affects physiological and morphological plant and leaf traits. The role of dynamic properties of stomata in regulating WUE of a cucumber plant under salinity stress will be examined using a dynamical model. The model combines the dynamics of the canopy stomatal conductance with the models of solute accumulation in the mesophyll and water flow to the mesophyll as driven by atmospheric conditions, and the effect of salinity on the photosynthetic capacity. The potential canopy photosynthesis rate will be computed at each time point, and using the current value of stomatal conductance, the effective value of the net assimilation will be derived together with the transpiration rate which will be estimated using the Penman-Monteith equation. Comparison of WUE under different light conditions will reveal the dynamics of WUE on cloudy compared to a sunny day. Variation of the daily WUE with respect to stomatal parameters and salinity stress will be presented for different scenarios of sunny and cloudy days.

P5.10 DOES ROOT-SOURCED ABA AFFECT STOMATAL RESPONSES TO CHANGES IN EVAPORATIVE DEMAND?

WEDNESDAY 3 JULY, 2019 **15:15**

ANTONIO DIAZ-ESPEJO (IRNAS CSIC, SPAIN), IAN C DODD (LANCASTER UNIVERSITY, UNITED KINGDOM), JAIME PUERTOLAS (LANCASTER UNIVERSITY, UNITED KINGDOM)

A.DIAZ@CSIC.ES

Recent years have seen a change in the paradigm for the main source of ABA involved in regulating stomatal responses. Most evidence now considers the leaves as the main “factories” of this phytohormone, which has motivated scientists to reconsider how stomatal conductance is regulated in response to water deficits. Independently of its origin, it is doubtless that some ABA is recirculated from the roots, via the xylem, to leaves, and these xylem ABA concentrations can be sufficient to elicit stomatal closure when fed to detached leaves in a transpiration assay. This study aimed to assess to what extent this leaf-exogenous ABA plays a major role in regulating stomatal conductance. Since it is very difficult empirically to separate ABA according to its origin, reciprocal- and self-grafts of wild-type (WT) and ABA-deficient (flacca) tomatoes were exposed to step-changes in vapour pressure deficit. The resultant stomatal changes were analysed according to a hydromechanical model of stomatal conductance, which was built on robust assumptions of stomatal response to environmental stimuli. Although plants with flacca rootstocks had much lower xylem ABA concentrations than those with WT rootstocks, the hydromechanical model did not show substantial differences in stomatal response between the different graft combinations. Thus leaf-exogenous ABA seems to play a limited role in the down-regulation of stomatal conductance to increased evaporative demand.

P5.11 LINKING ANATOMY-MEDIATED PHOTOSYNTHESIS CAPACITY WITH WATER: LEAF HYDRAULICS, DESICCATION TOLERANCE AND THE BULK MODULUS OF ELASTICITY

WEDNESDAY 3 JULY, 2019 **16:30**

JAUME FLEXAS (INAGEA, SPAIN), ALICIA PERERA-CASTRO (INAGEA, SPAIN), MARC CARRIQUI (INAGEA, SPAIN), JAVIER GULIAS (INAGEA, SPAIN), MIQUEL NADAL (INAGEA, SPAIN)

JAUME.FLEXAS@UIB.ES

Mesophyll conductance to CO_2 (g_m) is as much limiting for photosynthesis as stomatal conductance is and, in some organisms, even more. The maximum gm of a given species is determined by the specific anatomical arrangements of the mesophyll, with a dominant role of cell wall thickness (CWT) and the fraction of mesophyll cells covered by chloroplasts (S_c/S). Significant and important differences in g_m exist between phylogenetically distant plant groups. Specifically, a decreasing trend for CWT and an increasing trend for S_c/S is observed from bryophytes to vascular plants and, among these, from ferns to angiosperms. Such trends correspond well with scaling maximum photosynthesis rates in each group. We hypothesize that this trend reflects a trade-off between photosynthetic capacity and desiccation tolerance, the latter being generalized in bryophytes, common in ferns and rare in higher plants. To test this hypothesis, we have conducted field campaigns in extreme environments of the world, including hot and cold deserts, like Atacama, salty planes in Los Andes, the Arctic and Antarctica, among others. Preliminary results confirm the hypothesized trade-off; a few outliers to this trade-off were found in particular environments, which are promising candidates for ‘high fitness species’ in a climate change situation. In addition, g_m was found to be related to leaf hydraulic characteristics and to the bulk modulus of elasticity. The findings are discussed in terms of evolution and adaptation, highlighting their potential effects in plant fitness.

P5.12 INTEGRATING METABOLOMIC ANALYSIS INTO THE PHYSIOLOGICAL FRAMEWORK: POSSIBLE INFORMATION ON THE DEPLETION OF C AND N STORAGE COMPOUNDS IN DROUGHTED LEAVES

WEDNESDAY 3 JULY, 2019 **17:00**

ANTONELLA GORI (DAGRI - DEPARTMENT OF AGRI-FOOD PRODUCTION AND ENVIRONMENTAL SCIENCES, ITALY), ANATOLY P SOBOLEV (CNR - ISTITUTO DI METODOLOGIE CHIMICHE LABORATORIO DI RISONANZA MAGNETICA “ANNALAURA SEGRE, ITALY), DONATELLA CAPITANI (CNR - ISTITUTO DI METODOLOGIE CHIMICHE LABORATORIO DI RISONANZA MAGNETICA “ANNALAURA SEGRE, ITALY), FRANCESCO LORETO (DISBA-CNR, ITALY), MAURO CENTRITTO (CNR-IVALSA, ITALY), CECILIA BRUNETTI (CNR-IVALSA, ITALY)

ANTONELLA.GORI@UNIFI.IT

Plant responses to drought involve a complex interaction of physiological and biochemical processes. The elucidation of these processes as well as their integrative networks is critical to enhance drought tolerance in woody species. In the present study, black poplar (*Populus nigra*) plants subjected to water deficit were used as the model system to elucidate the effect of drought on leaf metabolic profile, and to investigate how the regulation of multiple biochemical pathways are involved in the control of leaf physiological homeostasis. Water stress was imposed by withholding water in order to obtain moderate- and severe-water-stressed plants, whereas well-watered plants were irrigated to pot capacity. Physiological parameters were monitored and water soluble metabolites were extracted from leaves and analyzed with NMR spectroscopy.

Metabolomic analysis highlighted pools of metabolites that affected the physiological adjustments of poplar under drought. In particular, stress triggered changes in primary metabolism, especially increases in amino acids, tricarboxylic acids and non-structural carbohydrates, suggesting changes in resources allocation and possible mobilization of storage compounds.

These results provide a framework for better understanding multiple mechanisms in plant responses to drought. The use of metabolomics as a tool to monitor stress-responsive markers of C and N utilization is also discussed.

P5.13 IDENTIFYING VARIATION IN WHEAT FOR THE PHYSIOLOGICAL MECHANISMS REGULATING WATER USE EFFICIENCY

WEDNESDAY 3 JULY, 2019 **17:15**

BAILEY M KRETZLER (LANCASTER UNIVERSITY - LANCASTER ENVIRONMENT CENTRE, UNITED KINGDOM), IAN C DODD (LANCASTER UNIVERSITY - LANCASTER ENVIRONMENT CENTRE, UNITED KINGDOM), ELIZABETE CARMO-SILVA (LANCASTER UNIVERSITY - LANCASTER ENVIRONMENT CENTRE, UNITED KINGDOM)

KRETZLERBAILEY@GMAIL.COM

Wheat is an important grain crop in many regions around the world. With some of these areas facing drought induced yield decline, it is imperative to investigate genetic variation in mechanisms of wheat response to water deficit. In assessing variability among spring wheat genotypes, a mixture of domesticated cultivars and ancestral varieties (Landraces) were exposed to cycles of soil drying while measuring water use efficiency at both the whole plant (WUEwp) and leaf level (WUEi). These measures are defined as biomass gain per water consumed (WUEwp) and carbon assimilation per rate of transpiration (WUEi). Genotypic differences were observed for WUEwp and rate of decline in stomatal conductance under soil drying. In contrast, no variation existed for WUEi between genotypes, as indicated by consistent stomatal limitation to leaf photosynthetic rate. Further studies will investigate if the disconnect is due to variation in stomatal sensitivity between genotypes, leaf developmental stage, or both. Since phytohormones such as ABA and Ethylene may play a role in regulating stomatal conductance, it is important to quantify expression and sensitivity across soil moisture and leaf age. Doing so could identify the mechanisms regulating water use and biomass gain across wheat development, establishing criteria for screening germplasm within drought focused breeding endeavours.

P5.14 FIELD-GROWN POTATO SUSTAINS LEAF PHOTOSYNTHESIS RATES AND LEAF WATER STATUS UNDER SOIL COMPACTION AND DROUGHT STRESSES

WEDNESDAY 3 JULY, 2019 **17:30**

KATHARINA HUNTENBURG (LANCASTER UNIVERSITY, UNITED KINGDOM), MARK A STALHAM (NIAB CUF, UNITED KINGDOM), IAN C DODD (LANCASTER UNIVERSITY, UNITED KINGDOM)

K.HUNTENBURG@LANCASTER.AC.UK

The UK summer of 2018 was particularly hot with the months from June to August being on average 2°C warmer than the 30-year average, with only 3 days of considerable rainfall (> 5 mm) in this period. Such summer conditions may be a template for climate change scenarios, since summer mean air temperatures and precipitation are predicted to increase by 3°C and decrease by 20–30% respectively. During this summer, a factorial field experiment (soil compaction x irrigation treatment) showed that potatoes grown in compacted soil and maintained well watered (< 25mm soil moisture deficit) produced smaller shoots and lower yields than in uncompacted soil, but the effect of compaction on aboveground biomass and yield in dry soil (allowed to attain a deficit of < 60 mm) was not significant. As an overall effect, deficit irrigation reduced yield and biomass compared with more frequent irrigation. However, leaf water status and photosynthesis rates did not differ between treatments. Thus, potatoes under either long-term soil water deficit and/or compaction stress adjust their growth according to soil water availability, rather than altering leaf gas exchange. Since leaf water status was conserved across treatments, changes in root-to-shoot signalling likely limit growth. This will be investigated by analysing leaf xylem sap samples collected during the season. Similar factorial controlled environment experiments with plants grown in specialised pots that fit in a pressure chamber will allow more detailed investigation of this signalling, by collecting root xylem sap at flow rates comparable to whole transpiration.

P5.15 LONG-DISTANCE PHYTOHORMONAL SIGNALLING OF SOIL DRYING AND COMPACTION IN THE SOLANACEAE?

WEDNESDAY 3 JULY, 2019 **17:45**

IAN C DODD (LANCASTER UNIVERSITY, UNITED KINGDOM), SARAH M DONALDSON (LANCASTER UNIVERSITY, UNITED KINGDOM), KATHARINA HUNTENBURG (LANCASTER UNIVERSITY, UNITED KINGDOM), ALFONSO ALBACETE (CEBAS-CSIC MURCIA, SPAIN)

@ I.DODD@LANCASTER.AC.UK

Plants can respond sensitively to drying soil, with leaf growth inhibition and stomatal closure preceding any quantitative difference in leaf water potential, or visual difference in leaf turgor, by several days. Attention has focused on soil drying induced synthesis and metabolism of phytohormones, which can change tissue hormone concentrations and xylem sap composition. The advent of multi-analyte phytohormone analyses, with xylem sap sampling at sap flow rates approximating transpiration, allows their role as sensors of soil drying to be investigated. When water was withheld from tomato (*Solanum lycopersicum*) plants grown in a mineral substrate at two different bulk densities (1.4 vs 1.74 g/cm^3), soil-drying-induced changes in root xylem sap composition were accentuated in plants grown at low bulk density, likely due to greater soil drying. At the same soil water content, high bulk density decreased xylem abscisic acid (ABA) concentration, likely due to low oxygen availability to the root system. Moreover, high bulk density increased xylem jasmonic acid (JA) concentration, while xylem cytokinin (*trans*-zeatin, tZ, and isopentenyladenine, iP) concentrations did not change. Soil drying also increased xylem salicylic acid (SA) concentrations. Preliminary analyses in similar experiments suggest these responses are conserved in potato (*Solanum tuberosum*). Whether these changes in xylem sap affect tissue phytohormone concentrations, and are due to local or long-distance processes, will be investigated by self- and reciprocal-grafting of mutants that are deficient in or overexpress selected phytohormone groups.

P5.16 CHARACTERISTICS OF DEEP ROOT SYSTEM IN DROUGHT TOLERANT CULTIVAR OF COWPEA

THURSDAY 4 JULY, 2019 **POSTER SESSION**

YUKA TATSUMI (KYUSHU UNIVERSITY, JAPAN), SHINYA MURAKAMI (KYUSHU UNIVERSITY, JAPAN), NORIMITSU HAMAOKA (KYUSHU UNIVERSITY, JAPAN), MARI IWAYA-INOUE (KYUSHU UNIVERSITY, JAPAN), YUSHI ISHIBASHI (KYUSHU UNIVERSITY, JAPAN)

@ TATSUMI.YUKA.635@S.KYUSHU-U.AC.JP

Cowpea (*Vigna unguiculata* (L.) Walp) is one of the legume crops cultivated in semiarid area, and have the characteristics of highly drought tolerant. In general, deep root system enables plants absorb water from deep soil layer. It is known that typical upland rice cultivars have deeper rooting system than lowland ones, suggesting that the deep rooting characteristics may be one of ways to improve their drought resistance. We, therefore, focused on deep rooting system in cowpea. Characteristics of deep root system were evaluated by using 'basket' method and gene expression analysis. The ratio of the deep root number and dry weight per total lateral roots in drought tolerant cultivar '205' was significantly higher than those of drought sensitive '555'. These results suggested that drought tolerant cultivar has deeper rooting traits than the sensitive one. The drought tolerant traits were mainly regulated by BR-related gene, *BZR1*, which relates to lateral root development. The expression of *BZR1* in deep roots was significantly higher compared to shallow roots in the drought-tolerant cultivar. Similarly, the expression of MSBP1 and Hy5 were also higher in deep roots. Taken together, the deep root system in cowpea may contribute to its drought tolerance through enhanced water uptake from deeper soil layer.

P6 HEAT AND DROUGHT TOLERANCE – FROM THE LAB TO IMPACT IN THE FIELD

ORGANISED BY: MATTHEW GILLIHAM (UNIVERSITY OF ADELAIDE), ZOE WILSON (UNIVERSITY OF NOTTINGHAM), MALCOLM HAWKESFORD (ROTHAMSTED RESEACH) AND OWEN ATKIN (AUSTRALIAN NATIONAL UNIVERSITY)

P6.1 GLOBAL VARIABILITY IN PHOTOSYNTHETIC HEAT TOLERANCE QUANTIFIED USING CHLOROPHYLL-A FLUORESCENCE

FRIDAY 5 JULY, 2019 **09:00**

OWEN K ATKIN (AUSTRALIAN NATIONAL UNIVERSITY, AUSTRALIA), LINGLING ZHU (AUSTRALIAN NATIONAL UNIVERSITY, AUSTRALIA), ODHRAN S O'SULLIVAN (AUSTRALIAN NATIONAL UNIVERSITY, AUSTRALIA), MARY A HESKEL (MACALESTER COLLEGE, UNITED STATES), KEITH J BLOOMFIELD (IMPERIAL COLLEGE LONDON, UNITED KINGDOM), LASANTHA K WEERASINGHE (UNIVERSITY OF PERADENIYA, SRI LANKA), MARK G TJOELKER (WESTERN SYDNEY UNIVERSITY, AUSTRALIA), PETER B REICH (UNIVERSITY OF MINNESOTA, UNITED STATES), KEVIN L GRIFFIN (COLUMBIA UNIVERSITY, UNITED STATES), VAUGHAN HURRY (SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES, SWEDEN), PATRICK MEIR (AUSTRALIAN NATIONAL UNIVERSITY, AUSTRALIA), MATTHEW H TURNBULL (UNIVERSITY OF CANTERBURY, NEW ZEALAND)

@ OWEN.ATKIN@ANU.EDU.AU

High-temperature tolerance in plants is important in a warming world, with extreme heat waves potentially leading to lethal heating of leaves. To assess whether there are global patterns in high-temperature tolerance of photosynthesis, we quantified T_{crit} (high temperature where minimal chlorophyll-a fluorescence rises rapidly and thus photosystem II is disrupted) in upper canopy leaves of >260 plant species spanning seven biomes. At six thermally contrasting sites across Australia, we also quantified seasonal adjustments in T_{crit}, with glasshouse studies used to assess inherent differences in T_{crit} among species. In summer, mean site-based T_{crit} values ranged from 41.5°C in the Alaskan arctic to 50.8°C in lowland tropical rainforests of Peruvian Amazon; the ~8°C increase in T_{crit} values from polar to equatorial regions is much less than expected based on the 20°C span in high-temperature extremes across the globe. Thus, with only modest high-temperature tolerance at sites that experience summer heat waves, species in mid-latitude (~20–50°C) regions have the narrowest thermal safety margins in upper canopy leaves. T_{crit} was also found to acclimate to seasonal changes in temperature (summer > winter, increasing on average 0.34°C per °C increase in growth temperature). The glasshouse studies revealed that T_{crit} was inherently higher in species from warmer habitats (increasing 0.16°C per °C increase in origin annual mean maximum temperature). The significance of these findings for how future, hotter climates may influence plant species in thermally contrasting biomes will be discussed.

P6.2 OPTIMISING THE REGULATION OF CO_2 ASSIMILATION TO ENHANCE THE STABILITY OF WHEAT GRAIN YIELDS IN THE CHANGING CLIMATE

FRIDAY 5 JULY, 2019 **09:30**

ELIZABETE CARMO-SILVA (LANCASTER UNIVERSITY, UNITED KINGDOM)

@ E.CARMOSILVA@LANCASTER.AC.UK

Wheat yields are threatened by changes in the environment that affect both grain weight and grain number. During booting and through post-anthesis, the flag leaf is a major contributor of carbohydrates to fill the grain. The enzyme Rubisco (ribulose-1,5-bisphosphate carboxylase/oxygenase) is responsible for the initial step in CO_2 assimilation. It is not a very efficient enzyme and, therefore, large amounts are present in the leaves to support adequate photosynthetic rates. In wheat, Rubisco can represent more than 50% of the total soluble protein in the leaves. Due to its central role in carbon metabolism, the activity of Rubisco is heavily regulated. Sugar-phosphate derivatives with a structure resembling the substrate bind the active sites of Rubisco tightly and lock the enzyme in a closed inactive conformation. It is hypothesised that: (1) under optimal conditions, maintaining Rubisco highly active contributes to greater rates of CO_2 assimilation leading to higher grain yields; conversely, (2) under conditions of stress, particularly at elevated temperatures, Rubisco inhibitors may protect the enzyme from proteolytic breakdown and enable fast recovery of CO_2 assimilation rates upon relief from stress. Progress in testing these hypotheses will be discussed in light of the opportunities and challenges for improving wheat grain yields in the changing climate.

P6.3 POLLEN DEVELOPMENT THE WEAKEST LINK – DEVELOPING RESILIENCE TO TEMPERATURE STRESS DURING REPRODUCTION

FRIDAY 5 JULY, 2019 **10:00**

ZOE WILSON (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), B TALLE (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), J FERNANDEZ GOMES (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), A TIDY (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), P BARRETO (UNIVERSITY OF CAMPINAS, BRAZIL), P ARRUDA (UNIVERSITY OF CAMPINAS, BRAZIL)

@ ZOE.WILSON@NOTTINGHAM.AC.UK

Pollen formation is highly sensitive to temperature stress; high temperatures during flowering therefore pose a serious threat to current and long-term crop yields. This is particularly the case since flowering and seed set typically occur during a single, transient stage of plant development, which unlike vegetative associated-stress, cannot be rescued if conditions subsequently improve. High temperatures reduce the number of flowering branches and therefore the number of flowers per plant, however abnormalities in pollen formation result in male sterility and thus failure of seed set. There is thus the potential for devastating yield losses if resilience to reproductive temperature stress is not developed. We have been using various approaches to identify the changes associated with heat stress during pollen development in arabidopsis, rice, wheat and barley. We have been capitalising upon genetic variability in tolerance to high temperature to conduct GWAS and RNASeq to identify tolerance and expression changes associated with reproductive heat stress. These data will be discussed. In addition we have used transgenic approaches to modify Uncoupling Protein1 (UCP1) expression to reconfigure cellular metabolism as an alternative approach to develop abiotic resilience. It is thought that control of Uncoupling Protein expression is one of the mechanisms eukaryotic cells use to regulate ROS production. We observed that flowers from UCP1 overexpression lines act as stronger photoassimilate sinks during abiotic stress, resulting in enhanced drought resilience and increased yield.

P6.4 RESILIENT BEANS FOR CLIMATE CHANGE: TEMPERATURE THRESHOLDS, CRITICALLY SENSITIVE STAGES AND UNDERLYING ADAPTATIONS TO HEAT AND CLIMATE CHANGE

FRIDAY 5 JULY, 2019 **10:30**

JAVIER A MIRET (UNIVERSITY OF READING, SCHOOL OF AGRICULTURE POLICY AND DEVELOPMENT, UNITED KINGDOM), TESS DILKS (ROTHAMSTED RESEARCH, PLANT SCIENCES DEPARTMENT, UNITED KINGDOM), CHETAN DEVA (UNIVERSITY OF LEEDS, SCHOOL OF EARTH AND ENVIRONMENT, UNITED KINGDOM), HERNAN DEGIOVANNI (SCOTLAND'S RURAL COLLEGE, DEPARTMENT OF LAND ECONOMY, ENVIRONMENT AND SOCIETY, UNITED KINGDOM), SANDRA SAKALAUSKIENE (LANCASTER UNIVERSITY, LANCASTER ENVIRONMENT CENTRE, UNITED KINGDOM), BENJAMIN E SCHIEK (INTERNATIONAL CENTER FOR TROPICAL AGRICULTURE (CIAT), DECISION AND POLICY ANALYSIS, COLOMBIA), STEVEN D PRAGER (INTERNATIONAL CENTER FOR TROPICAL AGRICULTURE (CIAT), DECISION AND POLICY ANALYSIS, COLOMBIA), BODO RAATZ (INTERNATIONAL CENTER FOR TROPICAL AGRICULTURE (CIAT), AGROBIODIVERSITY (BEAN PROGRAM), COLOMBIA), MILAN O URBAN (INTERNATIONAL CENTER FOR TROPICAL AGRICULTURE (CIAT), AGROBIODIVERSITY (BEAN PROGRAM), COLOMBIA), JULIAN RAMIREZ-VILLEGAS (INTERNATIONAL CENTER FOR TROPICAL AGRICULTURE (CIAT), DECISION AND POLICY ANALYSIS, COLOMBIA), STEPHEN BEEBE (INTERNATIONAL CENTER FOR TROPICAL AGRICULTURE (CIAT), AGROBIODIVERSITY (BEAN PROGRAM), COLOMBIA), IAN C DODD (LANCASTER UNIVERSITY, LANCASTER ENVIRONMENT CENTRE, UNITED KINGDOM), ANDREW BARNES (SCOTLAND'S RURAL COLLEGE, DEPTARTMEN OF LAND ECONOMY, ENVIRONMENT AND SOCIETY, UNITED KINGDOM), SIGRID HEUER (ROTHAMSTED RESEARCH, PLANT SCIENCES DEPARTMENT, UNITED KINGDOM), ANDREW JUAN CHALLINOR (UNIVERSITY OF LEEDS, SCHOOL OF EARTH AND ENVIRONMENT, UNITED KINGDOM), DONAL O'SULLIVAN (UNIVERSITY OF READING, SCHOOL OF AGRICULTURE POLICY AND DEVELOPMENT, UNITED KINGDOM)

@ J.MIRRETBARRIO@READING.AC.UK

Common beans (*Phaseolus vulgaris* L.) are widely proposed as a highly nutritious and marketable crop for ex-combatants in Colombia, but high temperatures may constrain productivity. Two major knowledge gaps undermine the efficiency of current breeding for heat tolerance. First, the physiological mechanisms underpinning existing genetic variation in heat tolerance are poorly understood; second, current breeding programs and crop-climate models may not reflect the predicted future overall seasonal stress patterns or diurnal temperature excursions. We address these gaps by characterising the impacts of precisely timed heat/drought stresses in development, photosynthesis and reproduction through the precise phenotyping of critically sensitive stages and temperature thresholds through the growing season. Genotypes previously identified as heat tolerant present a diversity of responses through the range of future temperatures and climate change scenarios, as well as thorough the crop cycle. With these key tolerance traits, we are developing novel methods for the breeding, screening and adoption of heat-tolerant beans; with validation in field sites across Colombia. Within the project, we work to incorporate the new physiological knowledge in improved crop-climate models, site selection, breeding traits and markers, and adoption pathways with the ultimate aim of developing nutritive and climate-resilient beans for improved livelihoods.

P6.5 NOVEL CYTOKININ ANTAGONISTS AS A METHOD FOR CROP ENHANCEMENT UNDER ABIOTIC STRESS CONDITIONS

FRIDAY 5 JULY, 2019 **10:45**

BRITTANY HEAP (LANCASTER UNIVERSITY, UNITED KINGDOM), GABRIELA TOLEDO-ORTIZ (LANCASTER UNIVERSITY, UNITED KINGDOM), MARTIN MCAINSH (LANCASTER UNIVERSITY, UNITED KINGDOM)

B.HEAP2@LANCASTER.AC.UK

Abiotic stresses account for over 50% crop yield losses globally, however, strategies for abiotic stress mitigation are largely under-developed and applications to reduce the impact of abiotic stress on crops are currently lacking. Therefore, new approaches are urgently required to increase crop yields under abiotic stress in order to feed a growing population in increasingly stressful environmental conditions. Novel compounds have been synthesised and screened for root growth promotion activity with the objective of eliminating the effects of abiotic stress on crop yields. The novel compounds under test are analogues of a known cytokinin antagonist, which is a non-competitive inhibitor of the cytokinin receptor 1 (CRE1) in two model crop species: *Arabidopsis thaliana* and *Oryza sativa*. Cytokinins are a class of plant hormones that regulate cell division and differentiation in plants, they play an opposing role in the roots and shoots. Working antagonistically with auxin, cytokinins promote cell differentiation and proliferation in the zone of elongation and inhibit lateral root formation and root elongation. Upon application of the active compounds, the decreased cytokinin function in the root zone leads to longer roots and an increased number of lateral roots with no cost to shoot growth. Research suggests that inhibition of CRE1 may act as a bio-fortification tool, along with increasing the plants resilience to abiotic stress. The role of the novel cytokinin antagonist in promoting root growth and parameters relating to nutritional quality of the crop will be analysed.

P6.6 GENE ACTION OF DROUGHT TOLERANCE AND ACHENE YIELD RELATED TRAITS IN SUNFLOWER (*HELINANTHUS ANNUUS* L.)

FRIDAY 5 JULY, 2019 **10:47**

HUMERA RAZZAQ (UNIVERSITY OF AGRICULTURE FAISALABAD, PAKISTAN)

HUMERARAZZAQ@GMAIL.COM

SSixty sunflower accessions were evaluated under polyethylene glycol (PEG-6000)-mediated drought stress. Selected tolerant and sensitive accessions were crossed in line × tester fashion and the resultant F1 along with their parents were evaluated for drought tolerance in the field and PEG-mediated drought in the lab. Data were recorded on morphological and physiological parameters. Genetic variation among the entries under normal and drought stress treatments indicated that this breeding material may be used for the development of drought-tolerant types. Combining ability analysis exhibited variable direction and magnitude of general combining ability (GCA) effects among line and testers and specific combining ability effects (SCA) among crosses. The lines A-23, G-33 and 017583 and testers HA-133 and 017577 were the best general combiners under normal and drought-stress treatments. Results of SCA indicated that crosses G G-61×017577, A-79×CM-621, A-48×CM-621, 017592×CM-621, 017592×017577 and A-75×017577 were the best specific combiners. Crosses G-61×HA-124 and A-48×HA-341 had mid parent, better parent and commercial heterosis for various traits under treatments. An additive type of gene action was observed for germination percentage, days to 50% flowering, days to 50% maturity, stem diameter and oil content while other traits showed non-additive gene action. The association of traits based on correlation and path analyses suggested that seedling fresh weight, dry weight and hundred achene weight might be used as criteria for selecting sunflower for drought tolerance and high achene yield.

P6.7 TASTING THE SPOTLIGHT: THE PATH OF THE SUN TRIGGERS DIURNAL AND SPATIAL FLUCTUATIONS IN THE COMPOSITION OF WINE GRAPES

FRIDAY 5 JULY, 2019 **10:49**

NOAM RESHEF (CORNELL UNIVERSITY, UNITED STATES), NURIT AGAM (THE JACOB BLAUSTEIN INSTITUTES FOR DESERT RESEARCH BEN-GURION UNIVERSITY OF THE NEGEV, ISRAEL), AARON FAIT (THE JACOB BLAUSTEIN INSTITUTES FOR DESERT RESEARCH BEN-GURION UNIVERSITY OF THE NEGEV, ISRAEL)

NR444@CORNELL.EDU

Micrometeorological conditions such as solar irradiance and temperature are important factors affecting fruit composition. In recent years, their effect on the composition of wine grapes received considerable attention, owing to the paramount influence of abiotic defense-related compounds on fruit and wine quality. Nevertheless, to this day we are unable to anticipate compositional consequences of a given set of conditions, and are uncertain as to whether they represent acclimatization, or are imposed by the environment. In addition, the fundamental question of how fruits respond to the substantial spatiotemporal variations accompanying the diurnal path of the sun, remains largely unexplored. To address these questions, we created an extensive gradient of irradiance levels in the fruit-zone by harnessing the strong and stable solar irradiance in the Negev desert. The role of sunlight in the spatial variability of grape composition was analyzed by using the three-dimensional structure of the grape cluster and integrating berry-level metabolomics and micrometeorology. In addition, the impact of sun path on the diurnal metabolic processes in the grape were analyzed for the first time. We found that grapes successfully adapt to strong solar irradiance by repartitioning within primary metabolites and the major flavonoid groups. However, this leads to inferior sensorial characteristics commonly associated with warm/arid climate. We show that the spatiotemporal solar regime in a vineyard generates spatial variability and diurnal fluctuations in fruit composition. Taken together, precise solar irradiance management is essential to improving fruit quality and homogeneity and mitigating the detrimental consequences of warm and arid conditions.

P6.8 GENE ACTION OF YIELD AND ITS RELATED ATTRIBUTES IN *BRASSICA NAPUS* L. UNDER NORMAL AND DROUGHT STRESS

FRIDAY 5 JULY, 2019 **10:51**

HINA SALEEM (UNIVERSITY OF AGRICULTURE FAISALABAD, PAKISTAN), HUMERA RAZZAQ (UNIVERSITY OF AGRICULTURE, PAKISTAN)

HINAH3099@GMAIL.COM

Climate change is a major issue worldwide due to global warming. Abiotic stresses, particularly drought stress, has crucial effects on plants. Drought stress decreases crop production and yield in *Brassica napus*. The present study was conducted to determine the gene action of various yield and its related attributes in *B. napus* under drought stress. For this purpose eight drought-tolerant and three drought-sensitive accessions were collected from oilseed research group and were hybridised using the line × tester mating design. Developed breeding material along with their parents were evaluated at the seedling stage in the lab and at the maturity stage in the field. A completely randomised design was implemented using factorial structured treatment levels of T0=0 (normal), T1=8% and T2=16% PEG-6000. For maturity traits, the experiment was conducted in the field using a randomised complete block design. Three treatments were applied to create drought stress (T0=normal irrigation, T1=alternate irrigation and T2=no irrigation). Data were recorded for qualitative and quantitative traits and were analysed by using ANOVA, mean comparison test, line × tester analysis, correlation and path analysis. The results indicated that the variance in specific combining ability was greater than that of general combining ability in all drought stress treatments, and that there was no additive gene action. Line × tester analysis had more proportional contribution under T0=63.69, T1=61.45, T2=51.92 followed by lines T0=28.62, T1=21.45, T2=47.66, testers T0=7.69, T1=17.09 and T2=6.41. Cross Zmm-5×Rainbow performed best in normal and drought conditions.

P6.9 CONCRETE CONVERSATIONS: EXPERIMENTS WITH MOSS AND MICROTOPOGRAPHY ON AN URBAN GRADIENT

FRIDAY 5 JULY, 2019 **10:53**

ALISON M HAYNES (UNIVERSITY OF WOLLONGONG, AUSTRALIA), SHARON ROBINSON (UNIVERSITY OF WOLLONGONG, AUSTRALIA), KRISTINE FRENCH (UNIVERSITY OF WOLLONGONG, AUSTRALIA)

ALISON.HAYNES@INTERNODE.ON.NET

As organisms experience the environment at their own suite of scales, a multiscale approach is useful when determining the drivers of biodiversity. For small organisms such as moss, microtopography such as small scale undulations and cavities is relevant because it is linked to the availability of resources including insolation and water. At a larger scale, urbanisation often involves increased light intensity, heat, pollution and drought, creating a multiple stress environment. Between these two extremes, site characteristics, particularly shade, are also expected to influence physiological processes such as respiration and photosynthesis and hence growth. To test the response of moss establishment at different scales I created four concrete tile designs with differing microtopography (niche v relief; smooth v textured). I cast 240 tiles and fixed them to 15 pavers which I placed in private gardens on an urban gradient in Wollongong, NSW, Australia. Each panel was inoculated with a mixture of moss and associated soil from 40 sites within the study region. Measurements of light and temperature were taken seasonally. Overall, tiles with more rugosity and a niche (concave) design are expected to promote moss establishment; so too shady sites that are cooler in summer months; with urbanisation, pollution, and larger scale processes such as population fragmentation detering establishment. Initial results show decreased moss establishment with increasing urbanisation and higher establishment in 'niche' (concave) tiles. This experiment will enhance our understanding of the effects of urbanisation on plant microclimate and contribute to research in urban greening.

P6.10 RESPONSE OF *BRASSICA NAPUS* L. ACCESSIONS UNDER DROUGHT STRESS CONDITIONS AT BOTH SEEDLING AND MATURITY STAGES

FRIDAY 5 JULY, 2019 **10:55**

BAREERA NASIR (UNIVERSITY OF AGRICULTURE FAISALABAD, PAKISTAN), ZAINAB BALOCH (UNIVERSITY OF AGRICULTURE FAISALABAD, PAKISTAN), HUMERA RAZZAQ (UNIVERSITY OF AGRICULTURE FAISALABAD, PAKISTAN)

BAREERANASIR64@GMAIL.COM

Fluctuations in climate can increase or decrease the production of many crops. Any change in climate could pose a challenge for researchers and farmers. *Brassica napus* is an important oilseed crop and is prone to several abiotic stresses, especially drought stress. In the present study, growth and tolerance responses of 10 accessions of *B. napus* were evaluated under laboratory and field conditions. For hydroponics, seeds of each accession were sown in polythene bags in a triplicate, completely randomised design using factorial structured treatments. Fifteen days after sowing, seedlings were transplanted to the hydroponics at three drought stress levels: T0=0 (control), T1=9% and T2=18% of polyethylene glycol. Data were recorded on various seedling parameters after 15 days of transplantation. For in vitro culture, seeds were grown in MS zero media and explants were used for callus culture, using the same treatment design as for hydroponics. Various drought-tolerant characteristics were measured after 21 days of callus formation. Field experiments were conducted in a randomised complete block design with split plot arrangement having three replications and three treatments: T0=6 irrigations (control), T1=3 irrigations and T2=no irrigation. Data on yield and its related traits were recorded. Recorded data of these three experiments were subjected to ANOVA, multiple comparison test correlation and path analyses. Drought-tolerant accessions may be used for the development of drought-tolerant types.

P6.11 MUTATION INDUCTION IN SUNFLOWER (*HELIANTHUS ANNUUS* L.) TO MITIGATE THE CLIMATE CHANGE

FRIDAY 5 JULY, 2019 **10:57**

SANIA ASHRAF (UNIVERSITY OF AGRICULTURE FAISALABAD, PAKISTAN)

@ SANIAMALIK3502@GMAIL.COM

Climate change is a global challenge that has no borders and to combat, it requires coordinated work by all countries. Average global temperatures have risen every decade since the 1970s, and the 10 warmest years on record have all occurred since 1997. Agricultural production is susceptible to weather and climate. The impacts of climate change are already responsible for killing an estimated 315,000 people every year and damaging ecosystems. And this is just the beginning – the science predicts that anything more than a 2°C rise in global temperatures puts us on the road to potentially catastrophic problems. There will be more flooding, more droughts, more disease, more famine and more war, creating hundreds of millions of refugees and causing the destruction of entire ecosystems and species. More work on abiotic stresses is needed to develop a diverse germplasm. There is a need to focus on diverse food and miracle crops like sunflower. Its oil consists of polyunsaturated fatty acids, vitamins A, D, E and K, and phosphorus. In the present studies, sunflower accessions were collected, and two different mutagens (UV and Colchicine) were used to induce the mutation. Mutated seeds were sown in the field for the evaluation and a comparison with non-mutated seeds. Complete character profiling was done, and a mutated library was developed. Selection of promising accessions was done on the basis of biometrical approaches and they are recommended for the development to feed the population.

P6.12 THE ROLE OF CHLORIDE HOMEOSTASIS ON PLANT DROUGHT RESISTANCE

FRIDAY 5 JULY, 2019 **11:30**

JOSE M COLMENERO-FLORES (INSTITUTO DE RECURSOS NATURALES Y AGROBIOLOGÍA (CSIC), SPAIN), JUAN D FRANCO-NAVARRO (INSTITUTO DE RECURSOS NATURALES Y AGROBIOLOGÍA (CSIC), SPAIN), PALOMA CUBERO-FONT (INSTITUTO DE RECURSOS NATURALES Y AGROBIOLOGÍA (CSIC), SPAIN), MIGUEL A ROSALES (INSTITUTO DE RECURSOS NATURALES Y AGROBIOLOGÍA (CSIC), SPAIN), TOBIAS MAIERHOFER (INSTITUTE FOR MOLECULAR PLANT PHYSIOLOGY AND BIOPHYSICS (UNIVERSITY OF WÜRZBURG), GERMANY), DIETMAR GEIGER (INSTITUTE FOR MOLECULAR PLANT PHYSIOLOGY AND BIOPHYSICS (UNIVERSITY OF WÜRZBURG), GERMANY), RAINER HEDRICH (INSTITUTE FOR MOLECULAR PLANT PHYSIOLOGY AND BIOPHYSICS (UNIVERSITY OF WÜRZBURG), GERMANY), ANTONIO DÍAZ-ESPEJO (INSTITUTO DE RECURSOS NATURALES Y AGROBIOLOGÍA (CSIC), SPAIN)

@ CHEMACF@IRNASE.CSIC.ES

At the cellular level, osmoregulatory mechanisms have been described by which inorganic ion fluxes, particularly K^+, NO_3^-, Cl^- and Na^+, play key roles in drought acclimatization responses like the rapid turgor recovery of leaf and root cells, and the stomatal closure. However, there is little information on the regulation of inorganic ion homeostasis at the whole-plant level. In this regard, more attention has been paid to the ionic macronutrients K^+ and NO_3^-, while Na^+ and Cl^- have traditionally been considered as toxic ions for crops. But unlike Na^+, plants make an important use of metabolic energy to accumulate Cl^-. Apart from being an essential micronutrient, we have described Cl^- as a beneficial macronutrient, playing specific roles in promoting plant growth and water balance. Macronutrient Cl^- levels reduce stomatal conductance without a concomitant decrease of the net photosynthesis rate. Since stomata-mediated water loss through transpiration is inherent in the need of C_3 plants to capture CO_2, simultaneous increase of photosynthesis and water-use efficiency is of great relevance to achieve a sustainable increase of C_3 crop productivity. We will describe how chloride regulates water relations in plants and its impact on drought resistance. As described for K^+, Cl^- plays also an important role in the ABA-dependent root osmotic regulation, which is required to stimulate root growth under water deficit conditions. Anion channels involved in net Cl^- uptake and root-to-shoot anion translocation have been identified. We will discuss also how environmental conditions regulate Cl^- uptake, long-distance transport and Cl^- vs NO_3^- discrimination.

P6.13 γ-AMINOBUTYRIC ACID (GABA) IS A PLANT SIGNALLING MOLECULE

FRIDAY 5 JULY, 2019 **12:00**

MATTHEW GILLIHAM (UNIVERSITY OF ADELAIDE, AUSTRALIA), BO XU (UNIVERSITY OF ADELAIDE, AUSTRALIA), YU LONG (UNIVERSITY OF ADELAIDE, AUSTRALIA)

@ MATTHEW.GILLIHAM@ADELAIDE.EDU.AU

The non-protein amino acid γ-aminobutyric acid (GABA) has been proposed to be an ancient messenger for cellular communication conserved across kingdoms. GABA has well-defined signalling roles in animals; however, whilst GABA accumulates in plant tissues under stress, and can regulate plant tissue growth, it has not been determined if, how and when GABA acts as an endogenous plant signalling molecule. Here, we establish that endogenous GABA is a bona fide plant signal by demonstrating it antagonises stomatal movements in response to opening and closing stimuli, and modulates plant gas exchange through the direct inhibition of plasma membrane and tonoplast-localised anion transporters within stomatal guard cells. Furthermore, we show that GABA production within guard cells is necessary and sufficient to influence stomatal aperture by restoring drought tolerance to mutant plants with reduced GABA synthesis through stomatal specific genetic complementation, but not through mesophyll-specific complementation. We show that GABA control of stomatal movement is widely conserved across plant families including valuable dicot and monocot crops. Our findings demonstrate that GABA is a novel plant stress signalling molecule that acts via a mechanism not found in animals to fine tune plant gas exchange. This discovery opens novel avenues for manipulating crop water use and tolerance to biotic and abiotic stress.

P6.14 SLAC1 ANION CHANNEL OF GRASSES ALLOWS FOR THE CONTROL OF STOMATAL APERTURE BY NITRATE

FRIDAY 5 JULY, 2019 **15:00**

RAINER HEDRICH (MOLECULAR PLANT BIOLOGY AND BIOPHYSICS, UNIVERITY WUERZBURG, GERMANY), DIETMAR GEIGER (MOLECULAR PLANT BIOLOGY AND BIOPHYSICS, UNIVERITY WUERZBURG, GERMANY)

@ HEDRICH@BOTANIK.UNI-WUERZBURG.DE

The latest major group of plants to evolve were the grasses. These became important in the mid-Paleogene about 40 million years ago. During evolution leaf CO_2 uptake and transpirational water loss were optimized by the acquisition of grass specific stomatal complexes. In contrast to the kidney-shaped guard cells typical of the dicots such as *Arabidopsis*, in the grasses and agronomically important cereals, the guard cells are dumbbell-shaped and are associated with morphologically distinct subsidiary cells. We studied the molecular basis of guard cell action in the major cereal crop barley. Upon feeding ABA to xylem sap of an intact barley leaf, stomata closed in a nitrate dependent manner. This process was initiated by activation of guard cell SLAC-type anion channel currents. HvSLAC1 expressed in *Xenopus* oocytes gave rise to S-type anion currents that increased severalfold upon stimulation with nitrate. We identified a tandem amino acid residue motif that within the SLAC1 channels differs fundamentally between monocots and dicots. Our work reveals a marked difference between monocot and dicot guard cells and prompts questions into the selective pressures during evolution that resulted in fundamental changes in the regulation of SLAC1 function.

P6.15 THE ROLE OF BARLEY ABI5 TRANSCRIPTION FACTOR IN DROUGHT RESPONSE

FRIDAY 5 JULY, 2019 **15:30**

ANNA COLLIN (DEPARTMENT OF GENETICS, UNIVERSITY OF SILESIA IN KATOWICE, POLAND), AGATA DASZKOWSKA-GOLEC (DEPARTMENT OF GENETICS, UNIVERSITY OF SILESIA IN KATOWICE, POLAND), IWONA SZAREJKO (DEPARTMENT OF GENETICS, UNIVERSITY OF SILESIA IN KATOWICE, POLAND)

@ ANNA.SKUBACZ@GMAIL.COM

ABA INSENSITIVE 5 (ABI5) is a basic leucine zipper (bZIP) transcription factor which regulates expression of stress-responsive genes in ABA-dependent way. We identified a new missense mutation in the barley *ABI5* gene using TILLING strategy. The *hvabi5* mutant showed a higher relative water content (RWC), decreased photosynthesis efficiency, reduced stomatal conductance, higher flavonoid content and diminished endogenous ABA content compared to WT under drought stress. We performed the global expression analysis (Barley Agilent Microarrays) of *hvabi5* and WT under drought and we identified 2,306 differentially expressed genes (DEGs) between both genotypes. With the aim of hunting the potential HvABI5 targets within the list of DEGs, we performed the analysis of the DEG promoter sequences and we identified 179 putative HvABI5 targets. We further analyzed the expression of 52 putative HvABI5 targets under drought and eight of them under ABA treatment in both *hvabi5* and its WT. Four genes associated with chlorophyll biosynthesis (*Geranylgeranyl Diphosphate Reductase*), gibberellin biosynthesis (*Ent-Kaurene Synthase Like 5*) and abiotic stress response (*Phospholipase A2* and *Carotenoid Cleavage Dioxygenase 1*) showed expression patterns highly correlated with *HvABI5* expression level under drought and ABA treatment. Physical interaction between their promoters and HvABI5 protein is further tested using Yeast One-Hybrid System. Our results may reveal the part of the mechanism of barley response to drought which is dependent on HvABI5 action.

This work was supported by National Science Center Poland, project 2017/25/N/NZ9/01941 "The role of HvABI5 transcription factor in spring barley (*Hordeum vulgare* L.) response to drought stress", 2018-2020.

P6.16 UNDERSTANDING PHYSIOLOGICAL AND MORPHOLOGICAL TRAITS CONTRIBUTING TO DROUGHT TOLERANCE IN BARLEY AND ASSESSMENT OF METHODS FOR DROUGHT TOLERANCE EVALUATION

FRIDAY 5 JULY, 2019 **15:45**

LANA SHABALA (UNIVERSITY OF TASMANIA, AUSTRALIA), MD HASANUZZAMAN (UNIVERSITY OF TASMANIA, AUSTRALIA), MEIXUE ZHOU (UNIVERSITY OF TASMANIA, AUSTRALIA), SERGEY SHABALA (UNIVERSITY OF TASMANIA, AUSTRALIA)

@ L.SHABALA@UTAS.EDU.AU

Drought stress is a major limiting factor for crop production in the arid and semi-arid regions and plant breeders are in the need for a convenient, reproducible and rapid screening methods to be used as a proxy for drought tolerance for a large number of genotypes. Eighty barley (*Hordeum vulgare* L.) genotypes from different geographical locations contrasting in drought stress tolerance have been screened for a range of physiological and agronomical indices in glasshouse trails. Barley seedlings were gradually brought to severe drought by withholding irrigation for 30 days under glasshouse conditions and the drought tolerance scored based on the degree of the leaf wilting, fresh and dry biomass and relative water content. These characteristics were related to stomatal conductance, stomatal density, residual transpiration and leaf sap Na, K, Cl contents measured in control (irrigated) plants. Our results suggest that drought tolerant genotypes have lower stomatal conductance, and lower water content, Na^+, K^+, and Cl^- contents in their tissue under control conditions than the drought sensitive ones. In a follow-up work, we assessed various screening methods for their suitability to breeders for rapid and reliable evaluation of drought tolerance in different barley varieties. Six barley genotypes subjected to different drought treatments were evaluated by measuring transpiration rate, quantum yield of PSII (chlorophyll fluorescence Fv/Fm ratio), SPAD chlorophyll meter reading, dry biomass and shoot water content. The results suggest that transpiration measurements at the recovery stage could be the most sensitive method for separating contrasting genotypes.

P6.17 COMPARATIVE PHYSIOLOGICAL, BIOCHEMICAL AND PROTEOMIC ANALYSIS OF TWO SORGHUM VARIETIES IN RESPONSE TO DROUGHT STRESS

FRIDAY 5 JULY, 2019 **16:00**

RUDO NGARA (UNIVERSITY OF THE FREE STATE, SOUTH AFRICA), TATENDA GOCHE (UNIVERSITY OF THE FREE STATE, SOUTH AFRICA), STEPHEN CHIVASA (DURHAM UNIVERSITY, UNITED KINGDOM)

@ NGARAR@UFS.AC.ZA

Drought stress limits crop productivity in sub-Saharan Africa. With the global climatic change, increasingly more severe drought episodes are predicted to occur. As such, there is need to develop drought-tolerant crops for the changing environments. Sorghum, a naturally drought-tolerant cereal, with a wide genetic diversity and a fully sequenced genome is a good model system for use in understanding plant responses to water deficits. In this study, two sorghum varieties with contrasting phenotypic traits to drought were used to investigate the physiological, biochemical and molecular changes in response to water deficits. Physiological and growth measurements of the plants subjected to drought stress and during recovery revealed striking differences between the two sorghum varieties. The leaf relative water content, leaf and root biomass/length and chlorophyll content were protected in the drought-tolerant variety, while the susceptible variety was adversely affected during stress and failed to recover after re-watering. Furthermore, the drought-tolerant variety accumulated much higher levels of proline and glycine betaine for use as osmoprotectants in both leaves and roots compared to the susceptible variety. Subsequent analysis of the root proteome using isobaric tags for relative and absolute quantitation also revealed distinct profiles of stress responsive proteins in the two sorghum varieties. Quantitative real time-polymerase chain reaction of a few target drought-responsive genes also revealed both tissue and varietal specific expressional differences. Overall, the current study has generated a knowledge base on mechanisms that are utilized by sorghum plants in drought stress adaptation.

P6.18 LED LIGHTING, BUT NOT SEED PRIMING, ENHANCES GROWTH AND DROUGHT SENSITIVITY IN LETTUCE (*LACTUCA SATIVA*) AND ROCKET (*ERUCA SATIVA*) SEEDLINGS

FRIDAY 5 JULY, 2019 **16:45**

JOSHUA D KLEIN (VOLCANI CENTER, ISRAEL), DANNY GINZBURG (VOLCANI CENTER, ISRAEL)

@ VCJOSH2000@YAHOO.COM

Seed priming and LED lighting increase concentrations of nutritionally-valuable metabolites in plants. Morphological and physiological bases of drought tolerance were explored in rocket and lettuce seedlings resulting from priming with homobrassinolide, prohydrojasmon, or carvacrol and subsequent exposure of seedlings to different ratios of red and blue light. Seedlings were grown under white (control), 100R:0B%, 75R:25B%, 50R:50B%, 25R:75B%, or 0R:100B% LEDs before being moved under white fluorescent lights. Plants were droughted for 7 days and then irrigated for 7 days or were irrigated throughout. Priming did not affect rocket or lettuce morphology, physiology, or drought tolerance. Combined exposure to red and blue wavelengths enhanced leaf area and specific weight along with pigment and flavonoid biosynthesis. Rocket droughted under R:B lighting, and lettuce droughted under monochromatic light had lower RWC and increased membrane leakage, despite increased ABA concentrations and antioxidant activity. Rocket and lettuce exposed to combined R:B lighting before drought had greater plant fresh weight. Increased concentrations of antioxidant metabolites did not consistently correlate with tolerance to drought. Combined R:B light treatments increased stomatal density in both plants. All LED regimes which increased stomatal aperture area per unit leaf area (AALA) resulted in decreased RWC at the end of drought. AALA was negatively correlated with end-drought RWC ($R2=-0.80$) in rocket, but not in lettuce. The relationship between stomatal development and antioxidant activity on drought tolerance was species-specific. Despite the benefits of growing leafy greens under LED lights, growers must consider vulnerability to drought under such conditions.

P6.19 PHENOTYPING WHEAT TRIALS FOR CANOPY TEMPERATURE USING DRONES AND THERMAL IMAGERY

FRIDAY 5 JULY, 2019 **17:00**

MALCOLM J HAWKESFORD (ROTHAMSTED RESEARCH, UNITED KINGDOM), ANDREW RICHE (ROTHAMSTED RESEARCH, UNITED KINGDOM), MARCH CASTLE (ROTHAMSTED RESEARCH, UNITED KINGDOM), ADAM MICHALSKI (WROCŁAW UNIVERSITY OF ENVIRONMENTAL AND LIFE SCIENCES, POLAND), SIMON GRIFFITHS (JOHN INNES CENTRE, UNITED KINGDOM), CLARE LISTER (JOHN INNES CENTRE, UNITED KINGDOM)

@ MALCOLM.HAWKESFORD@ROTHAMSTED.AC.UK

Canopy temperature is depressed by high transpiration rates which in turn is dependent on the water availability to the crop. Water availability is directly dependent on the soil water profile but access by the crop influenced by rooting depth and activity. Ground-based measurement of canopy temperature using IR sensors is feasible, but the time taken to cover a large number of plots in a trial is problematic as ambient temperatures can very rapidly during the day. A solution is to use an image-based approach, capturing detail of an entire field trial from an aerial perspective. Thermal video was captured using a radiometrically calibrated camera mounted on a multirotor drone, flying at 50m altitude, and over 200 images extracted per flight. The images were corrected for vignetting and then ortho-mosaiced. Ground control points suitable for recognition in thermal images were placed in the experiment to enable precise geolocation of the orthophoto. The approach has been validated using a wheat *Paragon* x *Garcia* mapping population segregating for drought resistance. The population was grown with and without irrigation at Church Farm, Norfolk, UK, in successive years. Substantial differences in canopy temperature were identified dependent on irrigation status, time of day and genotype and QTL were mapped.

P6.20 ENABLING REMOTE SENSING OF DROUGHT STRESS IN CROPS

FRIDAY 5 JULY, 2019 **17:30**

ANGELA C BURNETT (BROOKHAVEN NATIONAL LABORATORY, UNITED STATES), SHAWN P SERBIN (BROOKHAVEN NATIONAL LABORATORY, UNITED STATES), KENNETH DAVIDSON (BROOKHAVEN NATIONAL LABORATORY, UNITED STATES), KIM ELY (BROOKHAVEN NATIONAL LABORATORY, UNITED STATES), ALISTAIR ROGERS (BROOKHAVEN NATIONAL LABORATORY, UNITED STATES)

@ AVENETIANMORNING@GMAIL.COM

Drought is a major environmental challenge faced by people and plants, and is predicted to increase throughout this century. One aspect of fighting for food security in the face of drought involves physiological breeding – the use of measurements of photosynthesis and water use efficiency to evaluate traits for drought resilience. However, such measurements are traditionally time-consuming and low-throughput. Remote sensing of vegetation, in contrast, is rapid and high-throughput, thereby facilitating screening for plant breeding amongst other applications. Our research investigates the relationship between physiological and biochemical indicators of drought stress, and spectral signatures collected using remote sensing, in order to establish correlations so that remote sensing may be used to monitor drought stress and water use efficiency. In this drought experiment, plants of *Helianthus annuus* (sunflower), *Sorghum bicolor* (sorghum), *Raphanus sativus* (radish), *Populus canadensis* (poplar), *Cucurbita pepo* (zucchini) and *Capsicum annuum* (bell pepper) were grown in a glasshouse and exposed to a complete dry-down. Gas exchange measurements, leaf-level spectroscopy, and harvesting for biochemical analysis were performed regularly throughout soil dry-down and plant senescence. Initial results suggest a promising correlation between remote sensing and traditional measurements, and show an earlier detection of drought stress by spectroscopy compared to gas exchange. Improvement of remote sensing for physiological traits linked to drought stress will be instrumental in developing physiological breeding for resilient crops in a thirsty world.

P6.21 DESIGNER ROOTS FOR FUTURE WHEATS

FRIDAY 5 JULY, 2019 **17:45**

LEE HICKEY (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), KAI VOSS-FELS (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), CECILE RICHARD (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), JACK CHRISTOPHER (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), ANGÉLA JUHÁSZ (MURDOCH UNIVERSITY, AUSTRALIA), INDEEWARI DISSANAYAKE (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), MILOS TANURDZIC (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), GABRIEL KEEBLE-GAGNERE (DEPARTMENT OF ECONOMIC DEVELOPMENT JOBS TRANSPORT AND RESOURCES, AUSTRALIA), RUDI APPELS (DEPARTMENT OF ECONOMIC DEVELOPMENT JOBS TRANSPORT AND RESOURCES, AUSTRALIA), JOSQUIN TIBBITS (DEPARTMENT OF ECONOMIC DEVELOPMENT JOBS TRANSPORT AND RESOURCES, AUSTRALIA)

@ L.HICKEY@UQ.EDU.AU

In 2018, wheat farmers in Australia and Europe experienced major yield losses due to severe and widespread drought and heat stress. Improving the root systems of future wheat cultivars could enhance the ability of crops to capture water from deep soil layers, thereby minimizing or avoiding stress. Furthermore, with increasing pressure to reduce inputs such as chemical fertilizers, mechanisms for improved nutrient-use efficiency are required. Thus, to enable targeted genetic manipulation of modern wheat varieties, the discovery of key loci underpinning root development and response to nutrients is a high priority for research and pre-breeding programs worldwide. In this seminar, we highlight how the wheat reference sequence and the application of new genomic visualization tools (e.g. Pretzel) are accelerating our efforts to identify key genes involved in nutrient and root development pathways. We hope this work will soon empower wheat breeders to deploy future wheat varieties with improved nutrient-use efficiency and designer root systems.

P6.22 THE EFFECT OF CLIMATE CHANGE ON ANIMALS

THURSDAY 4 JULY, 2019 **POSTER SESSION**

SEGUN B MICHAEL (GLOBAL NETWORK FOR SUSTAINABLE DEVELOPMENT, UNITED STATES)

@ SEGUNCONCEPT@YAHOO.COM

The challenge of climate change in continents of the world in the 21st century cannot be wished away. In Northern Nigeria and the Sahel Region of Africa, desertification and drought have resulted in the shrinkage of animals in terms of losing wealth which mostly lead to death. In Northern Nigeria, herders are forced to migrate in search of pasture and water to feed their cows due to drought mainly as a result of the shrinkage of the Lake Chad Basin which serves as a means of irrigation and source of water to farmers during the planting season. A major contributing factor to desertification and drought from climate change in Nigeria is the indiscriminate felling of trees used for cooking which release immense carbon monoxide into the atmosphere that further deplete the ozone layer. The loss of weight in animals which most times lead to death is huge economic loss to people in the rural areas of Nigeria whose major source of income is agriculture. The effect of climate change is devastating due to increase in temperature combined with a decrease in rainfall which lead to increase water stress for vegetation and severity of droughts. A warmer climate (global warming) affect productivity of animals and also lead to natural disasters such as wildfire experienced in some continents of the world. The actualization of the United Nations Sustainable Development Goal (SDG) 13: Climate Action is very important to overcome the challenge of climate change.

P6.23 EXPLORING THE POSSIBILITY OF WATER-STRESS AS RESOURCE: THE CASE OF DIFFERENT TOMATO GENOTYPES

WEDNESDAY 3 JULY, 2019 **POSTER SESSION**

ERMENEGILDA VITALE (DEPARTMENT OF BIOLOGY, UNIVERSITY FEDERICO II OF NAPLES, ITALY), CARMEN ARENA (DEPARTMENT OF BIOLOGY, UNIVERSITY FEDERICO II OF NAPLES, ITALY), MARIA MANUELA RIGANO (DEPARTMENT OF AGRICULTURAL SCIENCES, UNIVERSITY FEDERICO II OF NAPLES, ITALY), AMALIA BARONE (DEPARTMENT OF AGRICULTURAL SCIENCES, UNIVERSITY FEDERICO II OF NAPLES, ITALY), ANTONIO DI MATTEO (DEPARTMENT OF AGRICULTURAL SCIENCES, UNIVERSITY FEDERICO II OF NAPLES, ITALY), CARMEN ARENA (DEPARTMENT OF BIOLOGY, UNIVERSITY FEDERICO II OF NAPLES, ITALY)

@ C.ARENA@UNINA.IT

Water stress is an increasing environmental constraint, especially in Mediterranean ecosystems, affecting tomato growth and yield in Mediterranean areas. The selection of new tomato genotypes more resistant to water deficit and enriched in antioxidants compounds could represent a valuable solution to overcome the drought constraint in these areas. This study investigated the physiological response and adaptation mechanisms of two tomato genotypes: sensitive M82 (*Solanum lycopersicum* L.) and tolerant IL925, to prolonged water stress. Plants of both genotypes were subjected to three different water regimes: irrigation with 100% (R3), 50% (R2) and 25% (R1) field capacity and compared for photosynthesis, leaf functional traits and pigment content. Moreover, fruits were analysed for antioxidant compounds. Our results showed that compared to M82, IL925 was more tolerant of prolonged water deficit, especially under the most limited water regime R1. More specifically, IL925 showed higher leaf specific mass and leaf dry matter content compared to M82, traits favouring a reduced water loss by tissues as well as higher levels of polyphenols and carotenoids active against PSII oxidative damages when photosynthetic capacity is reduced. Besides under severe water stress IL925 also exhibited a higher PSII photochemical efficiency associated with a lower non-photochemical quenching. In this genotype prolonged severe water stress induces the formation of fruits richer in antioxidants (phenols, ascorbic acid, carotenoids) compared to M82, indicating how a stress factor can act as a resource in specific tomato varieties.

P6.24 EFFECTS OF PHYSIOLOGY ON THREE EDAMAME CULTIVARS UNDER DROUGHT STRESS

THURSDAY 4 JULY, 2019 **POSTER SESSION**

CHUNG-TSE CHEN (GRADUATE INSTITUTE OF BIOTECHNOLOGY, NATIONAL CHUNG HSING UNIVERSITY, TAIWAN), YU-SIAN WU (DEPARTMENT OF AGRONOMY, NATIONAL CHUNG HSING UNIVERSITY, TAIWAN), CHUN-TANG LU (CROP SCIENCE DIVISION, TAIWAN AGRICULTURAL RESEARCH INSTITUTE, TAIWAN), CHIN-YING YANG (DEPARTMENT OF AGRONOMY, NATIONAL CHUNG HSING UNIVERSITY, TAIWAN)

@ EMIYANG@DRAGON.NCHU.EDU.TW

Edamame (*Glycine max* L.) is a crop of economic importance with high nutritious value. Edamame beans are a good source of protein and nutritious elements. Kaohsiung No. 9 (KH9), Kaohsiung No. 11 (KH11) and Xiang-Ji (XJ) are three major edamame cultivars in Taiwan. KH9 is the most popular cultivar in Taiwan and has the longest growth duration and highest yield among these three cultivars. In contrast to the other two cultivars, XJ is a cultivar of Japanese origin and has a smaller phenotype, shorter growth duration and unique aromatic taro flavor to its beans. Recent studies have shown that edamame has indispensable water requirements in all developmental stages, especially from blooming through pod filling stages. Insufficient irrigation causes aborted blossoms, small pods and shriveled beans and thus greatly reduces the production of edamame. We examined the aforementioned three cultivars under drought conditions during the blooming period. The soil water content was as low as 10% after no irrigation for 10 days; a control sample was included for comparison. The pod numbers decreased in all three cultivars after the drought treatment; however, the percentages of pod reduction differed between the cultivars, with 57%, 4.1%, and 37.5% of pods lost from XJ, KH9 and KH11, respectively, after 10 days of the drought treatment. XJ was the most sensitive cultivar to drought stress and KH9 was the most tolerant cultivar. Our results revealed that drought tolerance differed between these cultivars.

P6.25 EFFECT OF ENVIRONMENTAL STRESS ON OILSEED RAPE REPRODUCTION

WEDNESDAY 3 JULY, 2019 **POSTER SESSION**

ALISON C TIDY (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM)

@ ALISON.TIDY@NOTTINGHAM.AC.UK

Agriculture is facing the crucial challenge of adapting crop productivity to changes in the climate; environmental stress during flowering has a direct and negative impact on yield. This is due to pollen and ovule development being highly sensitive to environmental stress, with reduced male and female fertility, and therefore ultimate seed set. Over 70 million tons of oilseed rape are being produced worldwide yearly and therefore understanding environmental sensitivity within *Brassica* is pivotal for optimising crop performance under changing climates. The BnaDFFS panel of approximately 100 diverse *Brassica* lines grown world-wide was used to compare the effects of both cold and heat stress on different genotypes – with a focus on pollen viability, pollen germination, ovule development and final seed yield. The knowledge gained will help to address the delivery of more robust oilseed rape lines to combat environmental stress losses by targeting robust fertility under changing environments. GWAS analysis will be used to provide candidate genes for future breeding programs to genetically mitigate the potentially deleterious effects of future climate scenarios.

P6.26 CHLORIDE AT MACRONUTRIENT LEVELS INCREASES DROUGHT RESISTANCE BY IMPROVING WATER BALANCE AND WATER-USE EFFICIENCY

THURSDAY 4 JULY, 2019 **POSTER SESSION**

MIGUEL A ROSALES (CSIC, SPAIN), JUAN D FRANCO-NAVARRO (CSIC, SPAIN), PABLO DÍAZ-RUEDA (CSIC, SPAIN), CARLOS RIVERO (CSIC, SPAIN), JAVIER BRUMÓS (IVIA, SPAIN), ALFREDO RUBIO-CASAL (UNIVERSITY OF SEVILLE, SPAIN), ALFONSO DE CIRES (UNIVERSITY OF SEVILLE, SPAIN), JOSÉ M COLMENERO-FLORES (CSIC, SPAIN)

@ MIGUELROSALES8@GMAIL.COM

Chloride (Cl^-) has been recently described as a beneficial macronutrient in well-irrigated plants, playing specific roles in promoting plant growth, photosynthetic performance and water-use efficiency (WUE). Therefore, a new research framework is opened in the search for adaptive mechanisms that regulate water homeostasis and, in particular, the plant ability to withstand water deficit. Drought is now recognized as the abiotic stress that most importantly affects global crop productivity. Understanding how plants use water for optimal biomass production has become a fundamental issue worldwide. In this work, we aim to elucidate whether Cl^- nutrition at macronutrient levels stimulates drought resistance and which physiological mechanisms are involved. To that end, tobacco plants were treated for 30 days with three nutritional treatments added to the basal solution: CL (5 mM Cl^-), N (5 mM nitrate), and SP (1.25 mM sulphate and 1.875 mM phosphate), containing all of them the same cationic balance. Then, plants were subjected to two irrigation regimes for 20 days: control (100% field capacity) and moderate drought (60% field capacity). Results showed that, in comparison to SP and N treatments, Cl^- application (CL treatment) improved plant growth, leaf development, water balance parameters and WUE under drought conditions. Interestingly, N-treated plants exhibited the strongest growth reduction during drought, showing higher stress symptoms caused by an inefficient water use. Therefore, we propose that the abundant uptake and accumulation of Cl^- responds to an adaptive function that improves water relations and drought resistance in higher plants.

P6.27 A MAJOR ROOT ARCHITECTURE QTL AFFECTING RESPONSE TO WATER LIMITATION IN DURUM WHEAT

WEDNESDAY 3 JULY, 2019 **POSTER SESSION**

LEE HICKEY (LEE HICKEY, AUSTRALIA), K HASSOUNI (INTERNATIONAL CENTRE FOR THE AGRICULTURAL RESEARCH IN THE DRY AREAS, MOROCCO), F BASSI (INTERNATIONAL CENTRE FOR THE AGRICULTURAL RESEARCH IN THE DRY AREAS, MOROCCO), E DINGLASAN (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), C YOUSSEF (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), G QUARRY (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), A AKSOY (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), E MAZZUCOTELLI (GENOMIC RESEARCH CENTRE, ITALY), A JUHÁSZ (MURDOCH UNIVERSITY, AUSTRALIA), J ABLE (THE UNIVERSITY OF ADELAIDE, AUSTRALIA), J CHRISTOPHER (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), K VOSS-FELS (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), S ALAHMAD (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA)

@ L.HICKEY@UQ.EDU.AU

The optimal root system architecture (RSA) of a crop is context dependent and critical for efficient resource capture in the soil. Narrow root growth angle promoting deeper root growth is often associated with improved access to water and nutrients in deep soils during terminal drought. RSA, therefore is a drought-adaptive trait that could minimise yield losses in regions with limited rainfall. Here, GWAS for seminal root angle (SRA) identified seven marker-trait associations clustered on chromosome 6A, representing a major quantitative trait locus (*qSRA-6A*) which also displayed high levels of pairwise LD ($r^2 = 0.67$). Subsequent haplotype analysis revealed significant differences between major groups. Candidate gene analysis revealed loci related to gravitropism, polar growth and hormonal signalling. No differences were observed for root biomass between lines carrying hap1 and hap2 for *qSRA-6A*, highlighting the opportunity to perform marker-assisted selection for the *qSRA-6A* locus and directly select for wide or narrow RSA, without influencing root biomass. Our study revealed that the genetic predisposition for deep rooting was best expressed under water-limitation yet the root system displayed plasticity producing root growth in response to water availability in upper soil layers. We discuss the potential to deploy root architectural traits in cultivars to enhance yield stability in environments that experience limited rainfall.

P6.28 THE RESURRECTION PLANT *CRATEROSTIGMA PUMILUM* REVEALS IMPORTANCE OF CHLOROPLAST REGULATION DURING DESICCATION

THURSDAY 4 JULY, 2019 **POSTER SESSION**

S FRANCOIS DU TOIT (UNIVERSITY OF CAPE TOWN, SOUTH AFRICA), JILL M FARRANT (UNIVERSITY OF CAPE TOWN, SOUTH AFRICA), ZIV REICH (WEIZMANN INSTITUTE OF SCIENCE, ISRAEL)

@ DTTSTE011@MYUCT.AC.ZA

With the progression of climate change, water for agricultural purposes is becoming increasingly limited, posing a threat to global food security. Resurrection plants provide a genetic and physiological case study for developing improved agriculture in water-limited conditions. They can survive on less than 10% of their cellular water for prolonged periods and still fully recover upon rehydration. Since photosynthesis is vital for plant survival, making use of homoiochlorophyllous resurrection plants, which maintain their photosynthetic apparatus during desiccation, can reveal insights into chloroplast gene regulation during desiccation, rehydration and associated senescence. Identifying potential sites of host nuclear regulation on the chloroplast genome of *Craterostigma pumilum* will allow the comparison of transcription patterns of senescent and non-senescent tissues in *C. pumilum*. Possible break downs in this regulation during desiccation would suggest reasons behind desiccation-associated senescence. These insights have the potential to educate the development of plants with an increased tolerance to drought, and therefore, create more sustainable global agriculture.

P6.29 METABOLOMIC ANALYSIS OF *ZYGNEMA* SP. VEGETATIVE AND PRE-AKINETE FIELD SAMPLES FROM SVALBARD

WEDNESDAY 3 JULY, 2019 **POSTER SESSION**

ANDREAS HOLZINGER (UNIVERSITY OF INNSBRUCK, AUSTRIA), ERWANN ARC (UNIVERSITY OF INNSBRUCK, AUSTRIA), ILSE KRANNER (UNIVERSITY OF INNSBRUCK, AUSTRIA), MARTINA PICHRTOVÁ (CHARLES UNIVERSITY PRAGUE, CZECH REPUBLIC)

@ ANDREAS.HOLZINGER@UIBK.AC.AT

Zygnema sp. is a genus of common streptophyte green algae that form conspicuous mats in the high Arctic. We collected field samples near Longyearbyen, Svalbard with a vegetative (large vacuoles, bright green chloroplasts), and a pre-akinete appearance (many storage compounds, thick cell walls) and screened for their metabolite composition by GC-MS. The samples were also characterized by light- and transmission electron microscopy. We were able to detect 171 compounds out of which 116 metabolites were successfully identified. 83 compounds showed significant differences between the investigated groups. Most of the amino-acids detected like hydroxyproline, cysteine or glutamine were down-accumulated in the pre-akinete samples. Among the detected free fatty acids, oleic acid (C18:1), linoleic acid (C18:2) and paullinic acid (C20:1) were significantly up-accumulated in pre-akinetes. Most low-molecular-weight organic acids were down-accumulated in pre-akinetes. In contrast, sugars and sugar alcohols were found to be up-accumulated in pre-akinetes, particularly galactinol, gentiobiose, raffinose and trehalose. Monosaccharides like mannose and ribose were down-accumulated in pre-akinetes. In summary, substantial differences in low-molecular-weight metabolites exist between vegetative cells and pre-akinetes. Whereas vegetative cells are metabolically more active, considering the abundance of amino acids and low-molecular-weight organic acids, pre-akinetes contain more osmotically active sugars and sugar alcohols, as well as storage compounds. This is helpful to surviving unfavorable environmental conditions like desiccation in summer and freezing in winter.

P7 GENE NETWORKS FOR CROP IMPROVEMENT

ORGANISED BY: PHILIPPA BORRILL (UNIVERSITY OF BIRMINGHAM) AND ANDREA BRÄUTIGAM (UNIVERSITY OF BIELEFELD)

P7.1 THE TRANSCRIPTIONAL REGULATION OF SENESCENCE IN WHEAT

WEDNESDAY 3 JULY, 2019 **14:30**

PHILIPPA BORRILL (UNIVERSITY OF BIRMINGHAM, UNITED KINGDOM)

@ P.BORRILL@BHAM.AC.UK

Monocarpic senescence in crops is essential to enable nutrient remobilisation from photosynthetic tissues to the grain. This process must be tightly regulated to prevent premature senescence adversely affecting yields, however few genes controlling senescence have been identified in wheat. We are using a gene network modelling approach to identify novel regulatory genes controlling the early processes in senescence. We have generated an RNA-Seq time-course of ten time-points from anthesis until the first visible signs of flag leaf senescence. To understand the key genes driving transcriptional changes, we used gene regulatory network modelling to identify hub genes regulating the transcriptional processes across this time-course. Using the sequenced mutant populations now available for wheat, we have generated null mutants in hub genes identified in the network. Preliminary results show that two of these hub genes have roles in monocarpic senescence. Further studies are in progress to characterise the effects of these novel senescence regulators on nutrient remobilisation. The availability of new genomic resources for wheat, such as a high-quality genome sequence and sequenced mutant populations, has enabled the study of genes regulating senescence at an unprecedented resolution. These genes may represent new breeding targets to adapt senescence to the environment and to modulate grain nutrient content which is influenced by the rate of senescence.

P7.2 CONTEXT-SPECIFIC GENE-REGULATORY NETWORKS IN MAIZE

WEDNESDAY 3 JULY, 2019 **15:00**

ZORAN NIKOLOSKI (MAX PLANCK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY)

@ NIKOLOSKI@MPIMP-GOLM.MPG.DE

Gene regulation, like metabolism, is dependent on the context in which it takes place--the cell type, tissue, environmental conditions, or a combination thereof. There is a plethora of computational approaches which have been employed, on their own or in combination, to reconstruct gene regulatory networks in model plants and crops. However, these approaches do not allow to separate regulatory interactions which occur in multiple context from those which are specific to a context. Here, we present regularized regression approaches which take such constraints into consideration to extract context-specific gene-regulatory networks from a recently gathered time-series transcriptomics data from maize. We discuss extensions of the approach to include genomics data for improved performance.

P7.3 TRANSLATING BIOLOGICAL NETWORKS FROM MODEL SPECIES TO CROPS THROUGH THE APPLICATION OF CROSS-SPECIES SEQUENCE AND EXPRESSION ANALYSIS

WEDNESDAY 3 JULY, 2019 **15:30**

KLAAS VANDEPOELE (GHENT UNIVERSITY - VIB, BELGIUM), DRIES VANEECHOUTTE (GHENT UNIVERSITY - VIB, BELGIUM)

@ KLAAS.VANDEPOELE@PSB.VIB-UGENT.BE

Accelerated by technological innovations, genome-wide data describing functional properties including gene expression, protein–protein interactions and protein–DNA interactions are becoming available for an increasing number of model organisms. Comparative sequence analysis is a successful tool to study homologous gene families (genes sharing common ancestry), define gene functions between orthologs (homologs separated by a speciation event) and identify lineage- and species-specific genes. Most annotations of newly sequenced genomes are based on similarity with sequences for which functional information is available. However, the rampant nature of small gene and whole-genome duplication events (polyploidy) in different plant lineages poses a major challenge on identifying the subset of orthologs, out of all possible combination, which are functionally conserved. Here, we present how expression context conservation (ECC), a metric combining gene orthology and co-expression information, can be used to identify biological sub-networks conserved in different plants. Starting from a comparison between Arabidopsis and rice orthologs, we report highly variable levels of ECC for different biological processes, indicating potential network re-wiring. Extending this analysis towards other crops like maize and wheat, we show how comparative network analysis can be used to translate biological networks, to model expression divergence in polyploidy crops, and to identify the importance of lineage-specific genes in different signaling pathways.

P7.4 GENETIC MANIPULATION OF ROOT ARCHITECTURAL TRAITS IN BARLEY (HORDEUM VULGAREL.) USING DART MARKER SYSTEM

WEDNESDAY 3 JULY, 2019 **15:50**

MUHAMMAD Q FAROOQI (THE UNIVERSITY OF WESTERN AUSTRALIA, AUSTRALIA)

@ MUHAMMADQUDRATULLAH.FAROOQI@UWA.EDU.AU

A collection of 191 barley (Hordeum vulgareL.) were grown to assess variability in number of root traits under an established semi-hydroponic system. A total of 26 traits were analysed, out of which 16 had significantly varied traits (coefficient of variation CV ≥0.25). Furthermore, the barley lines used in this study were genotyped using Diversity Array Technology (DArT) protocol for the genetic dissection of understudied root traits. Therefore, the objective of this study was to investigate efficient computing options to generate relationship matrix based on markers and root traits information as well as their inverses. Population structure and genetic association studied were undertaken based on 15988 SilicoDArT markers with missing of <10%. The study revealed that these SilicoDArTs were highly efficient in classifying the barley lines in groups based on population structure and clustering analysis. The genetic diversification among lines was evaluated with routine statistics, principal component, linkage disequilibrium and neighbor joining tree. The pattern of linkage disequilibrium showed significant LD with r^2 =0.24. In population structure analysis, the barley lines were distributed into two main groups based on threshold level of 0.8 on membrane probability. Principal component analysis (PCA), kinship and phylogenetic relationship were performed to understand interrelationship among measured root traits, and to find an overview of similarities and differences among barley lines. The genetic characterization of barley lines based on various root traits would provide the basis for improved adaptation of new germplasm under specific environment.

P7.5 SEGREGATION DISTORTION: FACT OR FICTION?

WEDNESDAY 3 JULY, 2019 **15:52**

ALEX COULTON (THE UNIVERSITY OF BRISTOL, UNITED KINGDOM)

@ ALEX.COULTON@BRISTOL.AC.UK

Segregation distortion is the phenomenon in which progreny derived from a biparental cross deviate from Mendelian ratios of inheritance. This phenomenon is reported in a wide variety of crop species, including wheat, cotton, rice, chickpea and barley. In the current literature there is inconsistency in the type of statistical test used to detect segregation distortion, with some authors settling for a simple chi-square test with a p-value threshold of 0.05, others stricter thresholds, whilst others use corrections for multiple testing, including FDR (False discovery rate) and Bonferroni corrections. This is problematic, as it means that studies are not comparable, which hinders our knowledge of segregation distortion as a whole. Here we use an in silico simulation of a biparental mapping population in which we can apply selection pressure at an arbitrary locus to assess segregation distortion and evaluate which test is optimal for its detection whilst avoiding false-positives. In addition to this simulation work, we also use an empirical biparental mapping population of a cross between wheat varieties Avalon and Cadenza with multiple replicates to assess how reproducible a particular pattern of segregation distortion is.

P7.6 INFLUENCE OF HEADING DATE DIFFERENCE ON GENE FLOW FROM GM TO NON-GM RICES

WEDNESDAY 3 JULY, 2019 **15:54**

DOHWON YUN (NATIONAL INSTITUTE OF AGRICULTURAL SCIENCES, KOREA (SOUTH)), SUNGDUG OH (NATIONAL INSTITUTE OF AGRICULTURAL SCIENCES, KOREA (SOUTH)), ANCHEOL CHANG (NATIONAL INSTITUTE OF AGRICULTURAL SCIENCES, KOREA (SOUTH)), GANGSUB LEE (NATIONAL INSTITUTE OF AGRICULTURAL SCIENCES, KOREA (SOUTH))

@ DWYUN@KOREA.KR

Genetically modified (GM) crops have been increased continuously over the world and concerns about the potential risks of GM crops have also been increasing. Even though GM crops have not been cultivated commercially in Korea, it is necessary to develop technology for safety assesment of GM crops. In this study, we investigated the influence of heading date difference on gene flow from GM to non-GM rice. In the experimental design, The PAC gene GM rice was placed in the center as a pollen donor and non-GM rice were placed in eight directions as pollen receivers. Five pollen receiver rice cultivars were Unkawng, Daebo, Saegyejinmi, Nakdong, and Ilmi which had different flowering times. A total of 266,436, 300,237, 305,223, 273,373, and 290,759 seeds were collected from Unkawng, Daebo, Saegyejinmi, Nakdong, and Ilmi, respectively, which were planted around PAC GM rice. The GM×non-GM hybrids were detected by repeated spraying of herbicide and PAT immunostrip assay. Finally, the hybrids were confirmed by PCR analysis using PAC gene specific primer. The hybrids were found in Nakdong which had the same heading date with PAC GM rice. The hybridization rate was 0.0007% at Nakdong. All of GM×non-GM hybrids were located within 2 m distance from the PAC rice zone.

P7.7 THE REAL SOUR GRAPES – INTEGRATED QTL MAPPING WITH OMICS APPROACHES TO ELUCIDATE MALIC ACID REGULATION ACROSS GRAPEVINE SPECIES

WEDNESDAY 3 JULY, 2019 **15:56**

NOAM RESHEF (CORNELL UNIVERSITY, UNITED STATES), ELIZABETH A. BURZYNSKI-CHANG (DEPARTMENT OF FOOD SCIENCE CORNELL UNIVERSITY, UNITED STATES), AVINASH KARN (HORTICULTURE SECTION SCHOOL OF INTEGRATIVE PLANT SCIENCE CORNELL UNIVERSITY, UNITED STATES), JASON LONDO (USDA-ARS GRAPE GENETICS RESEARCH UNIT, UNITED STATES), BRUCE REISCH (HORTICULTURE SECTION SCHOOL OF INTEGRATIVE PLANT SCIENCE CORNELL UNIVERSITY, UNITED STATES), GAVIN L. SACKS (DEPARTMENT OF FOOD SCIENCE CORNELL UNIVERSITY, UNITED STATES)

@ NR444@CORNELL.EDU

Malate is a major organic acid in the world's leading fruit crops and a key determinant of fruit sourness. In domesticated grapes (V. vinifera), malate demonstrates biphasic behavior on a per-berry basis, reaching a maximum at the onset of ripening (veraison) before being degraded during maturation. Wild grapevine species endemic to North America (e.g. V. cinerea, V. riparia) possess valuable disease and cold tolerance traits. However, many wild species are known to have high malate even at sugar maturity. As a result, hybrid grape cultivars with wild Vitis background can have excessive malate content and sourness due to background genetics, decreasing suitability for winemaking and other applications. Thus, there is motivation to identify genetic markers and regulatory elements responsible for high malate in wild Vitis. We studied malate behavior during fruit development in wild Vitis cinerea and riparia, and vinifera, and used an F1 interspecific mapping population with cinerea and vinifera background to identify new QTLs associated with variation in malate levels. We observed that, compared to vinifera, wild Vitis accessions show limited malate dissimilation, and in some cases accumulation, during ripening. Preliminary metabolomic analyses revealed that this modified malate behavior was accompanied by the accumulation of several amino acids. Identified QTLs explain 31 and 16% of the variance in malate accumulation and dissimilation, respectively. These data will be integrated with developmental transcriptomic analyses of wild genotypes and segregating progenies to detect candidate genes regulating grape malate content, and develop genus-wide transferable markers for breeding environmentally and economically-sustainable grapevine cultivars.

P7.8 ATTRACTOR, A CIRCADIAN CLOCK TRANSCRIPTIONAL NETWORK BASED ON CHIP-SEQ DATA UNVEILS POTENTIAL GENE MODULES FOR CROP IMPROVEMENT

WEDNESDAY 3 JULY, 2019 **16:30**

FRANCISCO J ROMERO-CAMPERO (UNIVERSITY OF SEVILLE, SPAIN), PEDRO DE LOS REYES (CONSEJO SUPERIOR DE INVESTIGACIONES CIENTÍFICAS, SPAIN), ANA B ROMERO-LOSADA (UNIVERSIDAD DE SEVILLA, SPAIN), FEDERICO VALVERDE (UNIVERSIDAD DE SEVILLA, SPAIN)

@ FRAN@US.ES

The circadian clock, the molecular mechanism that provides plants with the ability to sense, adapt and anticipate to 24 h day-night cycles, constitute a central system in plant physiology and development. Relevant biological processes for crop improvement such as the biosynthesis of compounds of biotechnological interest (i.e. carotenoids, fatty acids and starch) are directly regulated by the circadian clock. Accordingly, the circadian clock has been intensively studied applying omics technologies, targeting the analysis of individual genes without taking into account the complex interactions among them. This makes imperative the application of integrative molecular systems biology techniques to produce global and systemic views of the circadian clock from the rapidly accumulating omic data freely available from databases. Network science has emerged as the central paradigm to achieve this goal. In this study, we have constructed a transcriptional network integrating ChIP-seq data produced under the same light/dark regime for 16 key regulators of the circadian clock in Arabidopsis, including CCA1, LHY, TOC1, PRR5/7/9, LUX and ELF3. The nodes in our network are annotated with the GO terms and promoter sequence of the corresponding genes. Topological analysis and network motifs identification together with GO and DNA motifs enrichments analysis identified network subgraphs or modules that capture the coordinated regulation exerted by several key regulators over common gene sets. These were significantly enriched in processes of biotechnological interest and could potentially be interesting in agro food industry. Finally, an interactive web-based software tool has been developed to allow independent researchers to explore our network.

P7.9 GROWTH-DEFENCE TRADE-OFF IN WHEAT IS CONTROLLED BY A TRANSCRIPTIONAL MEMORY CIRCUIT

WEDNESDAY 3 JULY, 2019 **16:50**

CORINA VLOT (HELMHOLTZ ZENTRUM MUENCHEN INSTITUTE OF BIOCHEMICAL PLANT PATHOLOGY, GERMANY), DANIEL LANG (HELMHOLTZ ZENTRUM MUENCHEN RESEARCH UNIT PLANT GENOMES AND SYSTEMS BIOLOGY, GERMANY), SANJUKTA DEY (HELMHOLTZ ZENTRUM MUENCHEN INSTITUTE OF BIOCHEMICAL PLANT PATHOLOGY, GERMANY), KLAUS FX MAYER (HELMHOLTZ ZENTRUM MUENCHEN RESEARCH UNIT PLANT GENOMES AND SYSTEMS BIOLOGY, GERMANY)

@ CORINA.VLOT@HELMHOLTZ-MUENCHEN.DE

Innate immune memory provides systemic broad-spectrum disease resistance in animals and plants. In this process, fitness costs are reduced by as yet poorly understood priming mechanisms. Here, we address the question how wheat (Triticum aestivum) balances growth and defence. Employing a multi-scale modeling approach, we reconstructed gene regulatory networks and discovered five stimulus-specific response meta-modules that act in concert to balance the growth-defence trade-off in wheat systemic immunity. These co-expression modules displayed specific response profiles and harbored a recurring, functional dichotomy balancing between primary metabolism and defence processes. The balancing action was achieved by a transition between two alternate regulatory patterns occurring after two consecutive physiological events. First, innate immune memory was induced by infecting leaves of 3-week-old plants with Pseudomonas syringae. This led to transient, broad-scale on/off switches in the response of defined meta-modules to this primary stimulus. In stage 2 of the experiments systemic uninfected leaves were infected with Xanthomonas translucens. The primary stimulus reduced the susceptibility of the plants to X. translucens. The implementation of this primed immunity correlated with bi-stable toggle switches within the defence-associated meta-module, which via inter-modular interactions affected at least two other meta-modules associated with primary metabolism and growth. Reciprocal negative regulatory interactions between these meta-modules provided strong bifurcation between two metabolic states that allow wheat to balance growth and defence-associated processes. The gene regulatory network within the defence meta-module provided insights into defined transcription factors that might act as central switches to secure both growth and defence and will be discussed.

P7.10 RECONSTRUCTING A HORMONE SIGNALLING PATHWAY FROM TRANSCRIPTION FACTOR ACTIVITY TO PHENOTYPIC OUTPUTS

WEDNESDAY 3 JULY, 2019 **17:10**

MATHEW G LEWSEY (LA TROBE UNIVERSITY, AUSTRALIA), MARK ZANDER (SALK INSTITUTE FOR BIOLOGICAL STUDIES, UNITED STATES), JOSEPH R ECKER (SALK INSTITUTE FOR BIOLOGICAL STUDIES HOWARD HUGHES MEDICAL INSTITUTE, UNITED STATES), SHAO-SHAN CAROL HUANG (NEW YORK UNIVERSITY, UNITED STATES), RONAN O'MALLEY (DOE JOINT GENOME INSTITUTE, UNITED STATES), MINGTANG XIE (CIBUS, UNITED STATES), SHELLY TRIGG (UNIVERSITY OF WASHINGTON, UNITED STATES), SIDDHARTHA JAIN (CARNEGIE MELLON UNIVERSITY, UNITED STATES), ROBERTO SOLANO (CENTRO NACIONAL DE BIOTECNOLOGÍA-CSIC, SPAIN), ZIV BAR-JOSEPH (CARNEGIE MELLON UNIVERSITY, UNITED STATES)

@ M.LEWSEY@LATROBE.EDU.AU

We have investigated the genome regulatory program that controls responses to the hormone jasmonate in etiolated seedlings. There is much interest currently in understanding the systems-level actions of transcription factors. However, such studies can provide greater biological insight if set in the context of the signal transduction pathway that initiates gene expression changes and the downstream organismal phenotypes they control. We have conducted an integrated analysis of the response to jasmonate, spanning from signal perception and transduction, through activity of master and secondary-regulatory transcription factors, to chromatin remodelling and gene expression outputs. We make use of genome-wide target maps for hundreds of transcription factors, dynamic histone modification analysis, massively multiplexed protein-protein interactome data and time series transcriptome analysis. This enables us to predict previously unknown components of the jasmonate regulatory mechanism and validate them through targeted mutant studies. The result is a comprehensive understanding of how a plant hormone remodels cellular function and plant behaviour.

P7.11 PLANT CBP20 (CAP-BINDING PROTEIN 20) INVOLVEMENT IN DROUGHT STRESS –THE PART OF A COMPLEX JIGSAW HAS BEEN SOLVED

WEDNESDAY 3 JULY, 2019 **17:30**

AGATA DASZKOWSKA-GOLEC (UNIVERSITY OF SILESIA IN KATOWICE, POLAND), ANNA COLLIN (UNIVERSITY OF SILESIA IN KATOWICE, POLAND), IWONA SZAREJKO (UNIVERSITY OF SILESIA IN KATOWICE, POLAND)

@ AGATA.DASZKOWSKA@US.EDU.PL

CBC (Cap Binding Complex) consisting of two subunits – CBP20 (Cap Binding Protein 20) and CBP80 was identified over 20 years ago in HeLa cells on the basis of its affinity to ^{7}mG cap structure at the 5' end of mRNA. Thereafter, CBPs were identified in different species including yeast, animals, and plants. *CBP20* encodes a small subunit of CBC that directly binds the cap, however, actual binding requires the presence of the CBP80 responsible for the

conformational changes of CBP20. Studies with the use of plant *cbp20* and *cbp80* mutants revealed the involvement of both genes in the RNA metabolism and ABA-related response to drought. However, the molecular basis of their drought-tolerant phenotype was uncharted till now. Here, we present the detailed investigation of *cbp20* mutants in Arabidopsis and barley that revealed a possible mechanism of CBP20-dependent gene expression tuning under drought. A deep examination of miRNAome and transcriptome (RNA-seq) combined with the analyses of publicly available transcriptomic data allowed us to (i) pinpoint the subset of genes responding to drought in CBP20-dependent manner and (ii) determine evolutionarily conserved part of that pathway in plants. Moreover, we were able to define the interactions between the processes controlled by CBP20 (such as splicing, miRNA biogenesis) and expression regulation of several loci involved in stress response. Furthermore, their changed expression was linked to drought tolerance of the mutants studied. Summarizing, here we provide the first attempt of understanding the role of CBC under drought stress at the molecular level in plants.

P7.12 ANALYSIS OF GENETIC VARIABILITY USING SALT TOLERANT MUTANTS SELECTED IN MUTAGENIZED MAIZE

WEDNESDAY 3 JULY, 2019 **17:50**

DOOL YI KIM (NATIONAL INSTITUTE OF CROP SCIENCE, KOREA (SOUTH)), KYUNG HWA KIM (NATIONAL INSTITUTE OF CROP SCIENCE, KOREA (SOUTH)), CHUL OH CHO (NATIONAL INSTITUTE OF CROP SCIENCE, KOREA (SOUTH)), MAN SOO CHOI (NATIONAL INSTITUTE OF CROP SCIENCE, KOREA (SOUTH)), JAE BUHM CHUN (NATIONAL INSTITUTE OF CROP SCIENCE, KOREA (SOUTH)), MI SUK SEO (NATIONAL INSTITUTE OF CROP SCIENCE, KOREA (SOUTH)), NAM HEE JEONG (NATIONAL INSTITUTE OF CROP SCIENCE, KOREA (SOUTH)), MI NA JIN (NATIONAL INSTITUTE OF CROP SCIENCE, KOREA (SOUTH))

@ DYKIM22@KOREA.KR

The maize was mutagenized with ethyl methane sulfate (EMS) to enhance its genetic variability including disease resistance, abiotic stress, and yielding ability. The two maize inbred lines were treated with 0.3%, 0.5%, 0.7%, and 0.9% EMS respectively for 8 hours. The results of phenotyping analysis of mutagenized maize population under each treatment condition that had not obtained the M2 generation seeds from condition treated with 0.7% and 0.9% EMS(v/v) for 8 hours. Otherwise, over the course of eight hours, 0.5 % EMS(v/v)- treated conditions showed a variation in phenotype, but we were able to obtained the M_2 generation seed that was mutated to analyze the concentration of salt. A total of 1041 independent M_2 familiar of EMS-induced maize inbred mutants have been investigated for salt tolerance. We selected salt-tolerant maize inbred lines from mutants populations treated with 0.7% NaCl in a greenhouse for three weeks. The salt-tolerant mutation was identified in the M_2 mutant populations. Furthermore, our RT-PCR result demonstrated that increased in the expression levels of genes related to salt stress. We generated whole-genome sequencing data to the two maize inbred mutants for gene variations in the enhanced salt-tolerant population. We expect the results to have a significant effect on the genetic modification of mutant maize inbred lines and comparative genetics.

P7.13 RICE GROWING IN HIGH DENSITY: HOW TO DEAL WITH UNWANTED NEIGHBOURS?

WEDNESDAY 3 JULY, 2019 **17:52**

MARTINA HUBER (UTRECHT UNIVERSITY, NETHERLANDS), ABDELBAGI ISMAIL (INTERNATIONAL RICE RESEARCH INSTITUTE, PHILIPPINES), RASHMI SASIDHARAN (UTRECHT UNIVERSITY, NETHERLANDS), KAISA KAJALA (UTRECHT UNIVERSITY, NETHERLANDS), RONALD PIERIK (UTRECHT UNIVERSITY, NETHERLANDS)

@ M.HUBER@UU.NL

How do you cope with competition against neighbours if you cannot run away? How does a rice plant in the field fight against the weeds growing next to it? In modern rice farming the major constraint is the weeds. Since rice feeds more than half of the worlds population as a staple food, tackling this issue is of great relevance. The main goals of this project are: First, to explore the plethora of existing different rice varieties, to find relevant aspects of the plant architecture that make rice more competitive against weeds. For this, we phenotyped a rice diversity panel of 344 varieties for traits associated with shading. Second, connect the phenotype to its underlying genes. The genomes of the screened population of rice varieties are already known, which enables us to perform a genome-wide association study. The next step is the transcriptome analysis of contrasting varieties upon RNA sequencing. The identification of the genetic basis will provide a better understanding of the interplay of gene regulation and gene expression, leading to a plasticity in plant architecture due to neighbour competition for light. To get a holistic picture, a functional validation of the selected varieties carrying the candidate genes will be tested in the field. Ultimately, these findings will provide insights about genetic loci and how they regulate specific aspects of plant architecture due to competition with weed for light. It will help to reduce the amount of herbicide usage and enable us to make rice-farming more sustainable.

P7.14 EXAMINING THE PLASTICITY OF GENE REGULATORY NETWORKS TO IMPROVE CROP TOLERANCE TO TEMPERATURE STRESS

THURSDAY 4 JULY, 2019 **09:00**

COLLEEN DOHERTY (NORTH CAROLINA STATE UNIVERSITY)

@ COLLEEN_DOHERTY@NCSU.EDU

The construction of a descriptive stress-response regulatory network can enable both the prediction of activity in novel conditions and the identification of candidate targets to improve stress responses. Yet the responses to abiotic stresses such as heat are both dynamic and plastic; the network wiring between regulators and targets is sensitive to both intrinsic factors and environmental conditions. We take advantage of both the temporal dynamics and plasticity of the transcriptional networks to investigate the mechanisms of how warmer nighttime temperatures impact growth and yield in rice. The molecular responses to warmer nighttime temperatures are identified by separating the temporal regulatory networks that persist and those that are altered under this stress. We identify the candidate regulators that mediate this plasticity.

Identifying regulatory relationships that are plastic can guide breeding efforts and provide robust targets for improving stress tolerance. Our perturbation-based analysis identifies candidates for breeding and provides insights into the mechanisms of warm nighttime temperature sensitivity in rice.

P7.15 SYSTEMATIC DISCOVERY OF GENE REGULATORY ELEMENTS USING CHROMATIN STRUCTURE IN PLANT GENOMES

THURSDAY 4 JULY, 2019 **09:30**

BOB SCHMITZ (UNIVERSITY OF GEORGIA, UNITED STATES)

@ SCHMITZ@UGA.EDU

Significant progress has been made in recent years in plant genome assembly and gene annotation. However, the systematic identification of plant cis-regulatory DNA elements remains a challenge, as methods that are highly effective in animals do not translate to plants. A comprehensive and well-curated data set of plant cis-regulatory DNA elements is instrumental to understanding transcriptional regulation during development and/or in response to external stimuli. In addition, cis-regulatory DNA elements are also hotspots for genetic variations underlying key agronomical traits. We have discovered a plant-specific chromatin signature that is indicative of cis-regulatory DNA elements. We are using this newly identified signature in combination with high-throughput validation assays to systematically identify, analyze and functionally validate cis-regulatory elements in important crop species.

P7.16 ELUCIDATING AND RE-DESIGNING REGULATORY NETWORKS UNDERLYING PLANT-PATHOGEN INTERACTION

THURSDAY 4 JULY, 2019 **10:00**

KATHERINE DENBY (UNIVERSITY OF YORK, UNITED KINGDOM), ELSPETH RANSOM (UNIVERSITY OF YORK, UNITED KINGDOM), IULIA GHERMAN (UNIVERSITY OF YORK, UNITED KINGDOM), GILL HIGGINS (UNIVERSITY OF YORK, UNITED KINGDOM), FABIAN VAISTIJ (UNIVERSITY OF YORK, UNITED KINGDOM), RYAN CARTER (UNIVERSITY OF YORK, UNITED KINGDOM)

@ KATHERINE.DENBY@YORK.AC.UK

Plant responses to biotic stress involve large-scale transcriptional reprogramming. We are elucidating the gene regulatory networks underlying these transcriptional responses to pathogen infection using a combination of experimental and computational/mathematical tools. We generated high-resolution time series expression data from Arabidopsis leaves following infection with bacterial and fungal pathogens. These time series data sets have enabled us to identify transient changes in gene expression and resolve the chronology of plant defence responses. We have generated transcriptional network models predicting regulatory relationships between differentially expressed transcription factors and identified key regulators of the Arabidopsis defence response from our networks. Crucially many of these key regulators were not previously known to affect susceptibility to plant pathogens. We have applied this time series-based network analysis gene discovery strategy to lettuce to predict genes conferring disease resistance against two fungal pathogens, Botrytis cinerea and Sclerotinia sclerotiorum, and speed up the breeding of these traits. Dual RNAseq time series enabled us to capture temporal transcriptome changes in both host and pathogen to investigate the how the lettuce defence response against these two pathogens is regulated, probe the molecular basis of plant-pathogen interaction and predict key regulators of virulence in the pathogens and resistance in the crop plant.

P7.17 INTEGRATIVE MODELING AND VISUALIZATION FOR THE DEVELOPMENT OF IN SILICO CROPS

THURSDAY 4 JULY, 2019 **11:00**

AMY MARSHALL-COLON (UNIVERSITY OF ILLINOIS URBANA-CHAMPAIGN DEPARTMENT OF PLANT BIOLOGY, UNITED STATES), KAVYA KANNAN (UNIVERSITY OF ILLINOIS URBANA-CHAMPAIGN DEPARTMENT OF PLANT BIOLOGY, UNITED STATES), YU WANG (UNIVERSITY OF ILLINOIS URBANA-CHAMPAIGN INSTITUTE FOR GENOMIC BIOLOGY, UNITED STATES), MEAGAN LANG (UNIVERSITY OF ILLINOIS URBANA-CHAMPAIGN NATIONAL CENTER FOR SUPERCOMPUTING APPLICATIONS, UNITED STATES), GHANA CHALLA (UNIVERSITY OF ILLINOIS URBANA-CHAMPAIGN INSTITUTE FOR SUSTAINABILITY ENERGY AND ENVIRONMENT, UNITED STATES), STEPHEN LONG (UNIVERSITY OF ILLINOIS URBANA-CHAMPAIGN DEPARTMENT OF PLANT BIOLOGY, UNITED STATES)

@ AMYMC@ILLINOIS.EDU

Current crop models predict an increasing gap between food supply and demand over the next 50 years. Technology is needed to predict the fitness of existing germplasm in response to global change, and also to design of crop ideotypes. I will highlight our efforts to generate virtual plant models that capture whole system dynamics in response to in silico environmental and genetic perturbations, using the Crops in silico (Cis) computational framework. We used the Cis multi-scale modeling platform to: i) integrate models of gene expression, photosynthetic metabolism, and leaf physiology to evaluate the effect of photosynthesis and transpiration under various environmental conditions; and ii) combine modeling and advanced visualization approaches to make direct observations about changes in plant structure, light capture, biomass, and yield in response to environmental perturbations. Outcomes of these efforts include i) accurate prediction of soybean photosynthesis under high atmospheric [CO2]; ii) identification of transcription factors that potentially regulate photosynthesis; and iii) simulated light capture in a 3D soybean canopy. The improved accuracy of model predictions and the realistic rendering of model simulated plants is a step toward the in silico “testing” of ideotype designs under different environmental conditions. This enables researchers to perform dozens of in silico perturbations to evaluate ideotype performance under varying scenarios. In silico exploration has the potential to help researchers target components of the underlying crop genetics for engineering, to ultimately enhance crop yield and nutritional quality.

P7.18 THE WHEAT NAC TRANSCRIPTION FACTOR NAC-3 IS A POSITIVE REGULATOR OF SENESCENCE

THURSDAY 4 JULY, 2019 **11:30**

SOPHIE A HARRINGTON (JOHN INNES CENTRE, UNITED KINGDOM), ANNA E BACKHAUS (JOHN INNES CENTRE, UNITED KINGDOM), PHILIPPA BORRILL (UNIVERSITY OF BIRMINGHAM, UNITED KINGDOM), CRISTOBAL UAUY (JOHN INNES CENTRE, UNITED KINGDOM)

@ SOPHIE.HARRINGTON@JIC.AC.UK

Protein and nutrient content in wheat grains is highly influenced by the timing of senescence, yet we understand relatively little about the regulation of this complex trait. NAC transcription factors (TF) (e.g. *NAM-1*, Uauy *et al.* 2006) have been shown to regulate monocarpic senescence in wheat and provide a useful entry point for understanding these processes. We have identified a NAC TF, *NAC-3*, which is upregulated in senescing flag leaves (Ramírez-González *et al.* 2018; Borrill *et al.* 2018). *NAC-3* double mutants from the tetraploid TILLING population exhibit delayed senescence with respect to wild-type plants. Intriguingly, we have shown that the NAM-1 and NAC-3 proteins interact, suggesting they may work together to regulate senescence. To investigate whether they work on the same pathway, we used Genie3 transcriptional networks to identify putative shared downstream targets (Ramírez-González *et al.* 2018). The utility of the Genie3 predictions was first validated using publicly-available, independent RNA-Seq data from TILLING knock-out lines of the *NAM* genes (Pearce *et al.* 2014). The Genie3-predicted downstream targets of the *NAM* genes overlapped with differentially expressed genes identified from the RNA-Seq data significantly more than expected by chance, indicating that the Genie3 network can provide biologically-informative predictions of downstream genes. We then found that *NAC-3* and *NAM-1* shared significantly more predicted targets than would be expected by chance, suggesting that they may act on similar biological pathways. These results suggest that the NAC TF *NAC-3* is a positive regulator of monocarpic senescence in wheat and may act in tandem with *NAM-1*.

P7.19 IDENTIFICATION OF QTLS FOR RESISTANCE TO BACTERIAL WILT CAUSED BY RALSTONIA SOLANACEARUM IN CHILI PEPPER

THURSDAY 4 JULY, 2019 **11:50**

JUNDAE LEE (CHONBUK NATIONAL UNIVERSITY, KOREA (SOUTH))

@ AJFALL@JBNU.AC.KR

Bacterial wilt caused by *Ralstonia* solanacearum is one of the most serious diseases in chili pepper (*Capsicum annuum* L.). In this study, we aimed to identify QTLs resistant to bacterial wilt in the F_2 population derived from a resistant pepper cultivar ‘Konesian hot’ using genotyping-by-sequencing (GBS) analysis. A total of 96 F2 individuals were evaluated for the resistance with disease index scores 0 (resistant) to 3 (susceptible) at every 7 days after inoculation for 6 weeks. A total of 12,228 SNP genotypes were obtained using GBS analysis. Using the SNP data, a pepper genetic linkage map consisting of 1,168 SNP markers was constructed. The map contained 12 linkage groups with a total linkage distance of 2,320.2 cM. QTL analysis using a composite interval mapping (CIM) method revealed six QTLs including *Bwr6w-12.1*, *Bwr6w-9.1*, Bwr6w-8.1, *Bwr5w-9.2*, *Bwr5w-7.1*, and *Bwr5w-10.2*, which showed R^2 values of 2.98, 11.57, 8.39, 17.51, 4.69, and 13.10%, respectively. This information will be helpful to develop molecular markers linked to the QTLs and to improve bacterial wilt resistance in pepper.

P7.20 TRANSCRIPTION FACTORS REGULATING ANTHOCYANIN BIOSYNTHESIS IN CHRYSANTHEMUM

THURSDAY 4 JULY, 2019 **POSTER SESSION**

SUN-HYUNG LIM (NATIONAL INSTITUTE OF AGRICULTURAL SCIENCE, KOREA (SOUTH)), BO-RA PARK (NATIONAL INSTITUTE OF AGRICULTURAL SCIENCE, KOREA (SOUTH)), DA-HYE KIM (NATIONAL INSTITUTE OF AGRICULTURAL SCIENCE, KOREA (SOUTH)), SANGKYU PARK (NATIONAL INSTITUTE OF AGRICULTURAL SCIENCE, KOREA (SOUTH)), JONG-YEOL LEE (NATIONAL INSTITUTE OF AGRICULTURAL SCIENCE, KOREA (SOUTH))

@ LIMSH2@KOREA.KR

Chrysanthemum plants are one of popular ornamental plants with various ranging from yellow to purple flower due to the accumulation of anthocyanins. The MYB-bHLH-WDR (MBW) complex activates anthocyanin biosynthesis through the transcriptional regulation. To understand the mechanism of anthocyanin biosynthesis, we investigated the role of bHLH and MYB genes from different ray floret colored Chrysanthemum cultivars cultivars including OB, GP and RM, which showed white, pink and red ray floret colors, respectively. We evaluated the transcript level of structural and regulatory genes at the different stages of ray florets. Through the analysis with structure and subcellular localization, it confirmed that bHLH gene in OB was mutated and was abnormally localized in Arabidopsis protoplasts. Yeast one hybrid (Y1H) and yeast two hybrid (Y2H) analysis showed that MYB from OB has the same function with that from RM, but MYB and bHLH from OB cannot interact with each other. To confirm the function of MYB and bHLH in planta, we performed a transient assay with tobacco leaves. It revealed that simultaneous expression of MYB and bHLH from RM accumulate anthocyanins, but that from OB did not show any pigment, indicating that the white colored OB was caused by bHLH mutation. These results strongly suggested that of MYB and bHLH are involved in the regulation of anthocyanin biosynthesis in chrysanthemum flowers.

P7.21 STEPWISE PATHWAY ENGINEERING TO THE BIOSYNTHESIS OF ZEAXANTHIN, ASTAXANTHIN AND CAPSANTHIN IN RICE ENDOSPERM

WEDNESDAY 3 JULY, 2019 **POSTER SESSION**

SUN-HWA HA (KYUNG HEE UNIVERSITY, KOREA (SOUTH)), JAE KWANG KIM (INCHEON NATIONAL UNIVERSITY, KOREA (SOUTH)), SUN-HYUNG LIM (NATIONAL INSTITUTE OF AGRICULTURAL SCIENCE, KOREA (SOUTH))

@ SUNHWA@KHU.AC.KR

Carotenoid pigments are valuable components of the human diet. A notable example is β-carotene, or provitamin A, which is converted into the derivatives astaxanthin and capsanthin, via the common intermediate zeaxanthin. To generate rice varieties producing diverse carotenoids beyond β-carotene, we specifically used a Capsicumβ-carotene hydroxylase gene, B(CaBch) and a codon optimized version of the same gene, stB(stBch) to increase zeaxanthin synthesis. We also used a recombinant BAK gene (CaBch-2A-HpBkt), consisting of the CaBch sequence and a Haematococcus β-carotene ketolase gene (HpBkt) linked by a bicistronic 2A sequence, as well as a codon optimized recombinant stBAK gene (stBch-2A-stBkt) to create astaxanthin synthesis. The four cassettes to seed-specifically express the B, stB, BAK and stBAK genes were individually combined with a PAC gene (CaPsy-2A-PaCrtI) cassette to previously impart β-carotene-enriched trait in rice endosperm. The single T-DNA vectors of B-PAC, stB-PAC, BAK-PAC and stBAK-PAC resulted in the accumulation of zeaxanthin and astaxanthin in the endosperm of the transgenic rice seeds. In addition, an extended version on the carotenoid pathway was introduced into rice to allow the production of capsanthin, by intercrossing a B-PAC rice line with a Ccs rice line, which harbors a Capsicum capsanthin-capsorubin synthase gene. Ultimately, we developed three functional rice varieties: B-PAC (0.8μg/g zeaxanthin, deep yellow), stBAK-PAC(1.4 μg/g ketocarotenoids, including astaxanthin, pinkish red) and B-PACxCcs (0.4 μg/g of ketoxanthophylls, including capsanthin, orange-red). Collectively, a combination of genetic engineering and conventional breeding is effective for multi-step metabolic engineering and biochemical pathway extension.

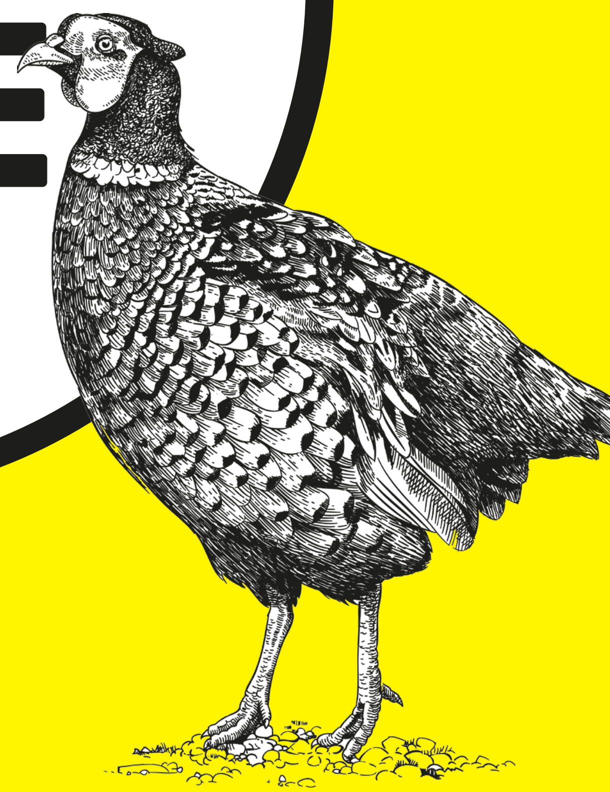
P7.22 IDENTIFICATION OF SALT-RESPONSIVE PHOSPHOPROTEINS IN ROOTS OF TRANSGENIC RICE OVER-EXPRESSING SUCROSE NONFERMENTING 1-RELATED PROTEIN KINASE2

THURSDAY 4 JULY, 2019 **POSTER SESSION**

IN SUN YOON (NATIONAL INSTITUTE OF AGRICULTURAL SCIENCES, KOREA (SOUTH)), SUYEON KIM (NATIONAL INSTITUTE OF AGRICULTURAL SCIENCES, KOREA (SOUTH)), MI HYUN CHO (NATIONAL INSTITUTE OF AGRICULTURAL SCIENCES, KOREA (SOUTH)), BEOM GI KIM (NATIONAL INSTITUTE OF AGRICULTURAL SCIENCES, KOREA (SOUTH)), KYUNG HWAN KIM (NATIONAL INSTITUTE OF AGRICULTURAL SCIENCES, KOREA (SOUTH))

@ ISYOON@KOREA.KR

Soil salinity is one of the major environmental stress limit productivity of rice worldwide. Sucrose nonfermenting 1-related protein kinase2 (SnRK2) family is known as a key regulator of ABA and hyper-osmotic stress signaling, but little is known about its targets under the salt stress. In the present study, salt-responsive phosphoproteins were analyzed in roots of transgenic rice over-expressing rice SnRK2 kinase. Phosphoproteins were visualized and quantified by fluorescence staining of two-dimensional (2-D) gel using Pro-Q Diamond. Phosphopeptides were identified by MALDI-TOF/TOF analysis. Compared to wild type rice, 21 differentially phosphorylated proteins (DP) were identified in roots of the SnRK2 transgenic rice under the salt stress. DP1405, a lipid binding START domain protein of unknown function, contains multiple potential SnRK2 phosphorylation sites. Transgenic rice overexpressing DP1405 showed enhanced salt tolerance. Our results suggest that DP1405 is a novel protein related to SnRK2 signaling conferring salt tolerant trait in rice. Supported by grant (PJ01318203) from RDA.



P8 IN SILICO PLANTS

ORGANISED BY: STEPHEN LONG (UNIVERSITY OF ILLINOIS)
AND LEE SWEETLOVE (OXFORD UNIVERSITY)

P8.1 FROM MATHS TO FIELD – MODELING TO GUIDE CROP PHOTOSYNTHETIC EFFICIENCY FOR HIGHER PRODUCTIVITY

FRIDAY 5 JULY, 2019 **09:00**

STEPHEN LONG (UNIVERSITY OF ILLINOIS, UNITED STATES AND LANCASTER UNIVERSITY, UNITED KINGDOM), YU WANG (UNIVERSITY OF ILLINOIS, UNITED STATES)

@ SLONG@ILLINOIS.EDU

Demand for our major crops may rise 60% by 2050. The major yield increases of the Green Revolution were driven by genetic increases in yield potential. But the approaches used are now reaching their biological limits. Photosynthetic efficiency falls far below its biological potential and was almost untouched by the Green Revolution, representing an apparently untapped means to achieving further gains in yield potential. As the best known, and one of the most highly conserved, plant processes it photosynthesis become amenable to dynamic modeling in which each discrete step of the process may be represented and in turn integrated into biophysical models of developing crop canopies. Application of optimization routines via high-performance computing, has predicted changes that could substantially improve photosynthetic efficiency in both C^3 and C^4 crops (Long *et al.*, 2015). Some of these have now been realized through bioengineering in field trials. This paper will review this modeling and its development, giving particular emphasis to the re-emerging area of non steady-state photosynthesis, as a route to improving efficiency (Kromdijk *et al.*, 2016; Glowacka *et al.*, 2018).

P8.2 LIKELIHOOD-FREE INFERENCE REVEALS PHYSICAL MECHANISMS AND PARAMETERS GOVERNING ROOT ARCHITECTURE

FRIDAY 5 JULY, 2019 **09:30**

CLARE ZIEGLER (UNIVERSITY OF BIRMINGHAM, UNITED KINGDOM), ROSEMARY J DYSON (UNIVERSITY OF BIRMINGHAM, UNITED KINGDOM), IAIN G JOHNSTON (UNIVERSITY OF BIRMINGHAM, UNITED KINGDOM)

@ CXZ551@STUDENT.BHAM.AC.UK

Plant root systems play vital roles in the biosphere, environment, and agriculture, but the quantitative principles governing their growth and architecture remain poorly understood. The `forward problem’ of what root forms can arise from given models and parameters has been well studied through modelling and simulation, but comparatively little attention has been given to the `inverse problem’: what models and parameters are responsible for producing an experimentally observed root system? This talk will detail the use of approximate Bayesian computation (ABC) to infer mechanistic parameters governing root growth and architecture, along with its application to synthetic and experimental root data to identify growth mechanisms and characterise growth parameters in different mutants. Our highly adaptable framework can be used to gain mechanistic insight into the generation of observed root system architectures.

P8.3 A NEW 3D SHOOT-ROOT MODEL FOR SIMULATING RHIZODEPOSITION PROCESSES IN THE CONTEXT OF WHOLE PLANT GROWTH

FRIDAY 5 JULY, 2019 **09:45**

FRÉDÉRIC REES (UMR ECOSYS INRA AGROPARISTECH, UNIVERSITÉ PARIS-SACLAY, FRANCE), CHRISTOPHE PRADAL (AGAP CIRAD INRA MONTPELLIER SUP AGRO, UNIV MONTPELLIER, FRANCE), LOÏC PAGÈS (UR 1115 PSH INRA, FRANCE), CÉLINE RICHARD-MOLARD (UMR ECOSYS INRA AGROPARISTECH, UNIVERSITÉ PARIS-SACLAY, FRANCE), CLAIRE CHENU (UMR ECOSYS INRA AGROPARISTECH, UNIVERSITÉ PARIS-SACLAY, FRANCE), BRUNO ANDRIEU (UMR ECOSYS INRA AGROPARISTECH, UNIVERSITÉ PARIS-SACLAY, FRANCE)

@ FREDERIC.REES@INRA.FR

Rhizodeposition, i.e. the release of any organic material by roots, has been suggested to represent a major input of carbon in soils and to shape biological activity in the rhizosphere. Various rhizodeposits can be emitted by roots, e.g. soluble exudates, secreted mucilage, sloughed cells, or volatile organic compounds. Despite their short lifetime, some of these products have been shown to favor plant growth by increasing water or nutrient uptake, by promoting plant resistance, or by acting as signals. Rhizodeposition also represents a significant share of plant’s carbon budget and may affect plant growth in this way. So far, no computational model has integrated the variety of rhizodeposition processes into plant functioning. Our goal is to develop such a model in order to investigate in a more mechanistic way the effects of contrasted plant traits, crop management or climate change on plant growth and soil carbon sequestration. As an important step in this direction, we focus here on the integration of the carbon fluxes related to rhizodeposition processes into a functional-structural plant model. After summarizing the current knowledge on the mechanisms and carbon-costs associated to rhizodeposition, we will present a 3D shoot-root model implemented in the OpenAlea platform, which integrates a new rhizodeposition model, a root architecture model (ArchiSimple) and a model of C and N metabolism in the whole plant

(CN-Wheat). The possibilities opened up by this integrative model will be illustrated by simulations of net sugar exudation fluxes distributed across a dynamic, 3D wheat root system interacting with soil.

P8.4 AVERTING ROBO-BEES: IN-SILICO ANALYSIS OF THE PERCEPTION OF FLOWERING PLANTS BY INSECT POLLINATORS

FRIDAY 5 JULY, 2019 **10:00**

ROS GLEADOW (MONASH UNIVERSITY MELBOURNE, AUSTRALIA), ALAN DORIN (FACULTY OF IT, MONASH UNIVERSITY, AUSTRALIA), JIM HANAN (HORTICULTURAL SCIENCE QAFFI, UNIVERSITY OF QUEENSLAND, AUSTRALIA)

@ ROS.GLEADOW@MONASH.EDU

Food security and the sustainability of native ecosystems depends on plant-insect interactions in countless ways. Recently reported rapid and immense declines in insect numbers due to climate change, the use of pesticides and herbicides, the introduction of agricultural monocultures, and the destruction of insect native habitat, are of grave concern. Some researchers are working towards a future where natural insect pollinators might be replaced with free-flying robotic bees, an ecologically problematic proposal. We argue instead that computer simulation of insect-plant interactions is a far more measured and ecologically sound application of technology that could assist us in managing the coming “Insect Armageddon”. Specifically, we identify insect-plant interactions within current agricultural systems as being weighted too heavily in favour of the plants. We propose, using computer simulations, to balance attention more evenly over the insect–plant system. One important aspect of plant-insect relationships we simulate is how pollinating insects detect flowers against different background colours, and in different planting arrangements. This provides insight into how flowers are detected and pollinated, allowing us to demonstrate that the cropping environments in greenhouses and on broadacre farms can interfere with insects’ ability to carry out important ecological services that benefit human food production. Our in-silico models should help us to understand the likely impacts of Anthropocene activity on the relationships between flowering plants and insects, and to mitigate against futures where insect populations have crashed or been irrecoverably altered.

P8.5 MODELING AND VISUALIZATION OF PHYLLOTACTIC AND VASCULAR PATTERNING IN FLOWER HEADS

FRIDAY 5 JULY, 2019 **10:30**

PRZEMYSLAW PRUSINKIEWICZ (UNIVERSITY OF CALGARY, CANADA), TENG ZHANG (UNIVERSITY OF HELSINKI, FINLAND), MIKOLAJ CIESLAK (UNIVERSITY OF CALGARY, CANADA), PHILMO GU (UNIVERSITY OF CALGARY, CANADA), JEREMY HART (UNIVERSITY OF CALGARY, CANADA), ANDREW OWENS (UNIVERSITY OF CALGARY, CANADA), FONG WANG (UNIVERSITY OF HELSINKI, FINLAND), TEEMU TEERI (UNIVERSITY OF HELSINKI, FINLAND), PAULA ELOMAAA (UNIVERSITY OF HELSINKI, FINLAND)

@ PWP@UCALGARY.CA

Phyllotaxis – the distribution of plant organs such as leaves and flowers on their supporting axes – is a key attribute of plant architecture. The geometric regularity of phyllotactic patterns has attracted multidisciplinary interest since the early 1800s, yet the most iconic example of phyllotaxis, the patterning of flowers in the heads of the sunflower family of plants, has remained unexplained. Based on experimental data integrating confocal microscopy, scanning electron microscopy, and X-ray micro-computed tomography of developing gerbera and sunflower heads, we have constructed computational models that plausibly explain phyllotactic patterning in heads. Our data have also revealed, and computational models allowed to explain, the development and structure of the vascular systems in heads. These results were obtained through a tight interplay between laboratory experiments, 2D and 3D imaging, computational model construction, and mathematical reasoning. In addition to revealing previously unobserved mechanisms and structures, our data and models point to common mechanisms in the development of heads, branched inflorescences, and leaves.

P8.6 DESIGNING SORGHUM CROPS FOR ADAPTATION TO THE DROUGHT AND HEAT RISKS ANTICIPATED IN FUTURE CLIMATES

FRIDAY 5 JULY, 2019 **11:30**

GRAEME HAMMER (UNIVERSITY OF QUEENSLAND, AUSTRALIA), GREG MCLEAN (QUEENSLAND DEPARTMENT OF AGRICULTURE AND FISHERIES, AUSTRALIA), ERIK VAN OOSTEROM (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), SCOTT CHAPMAN (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), BANGYOU ZHENG (CSIRO AGRICULTURE, AUSTRALIA), ALEX WU (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), AL DOHERTY (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), DAVID JORDAN (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA)

@ G.HAMMER@UQ.EDU.AU

Climate risks pervade agriculture. They generate major consequences on crop production. We do not know what the next season will be like, let alone the season 30 years hence. Yet farmers need to decide on genotype and management combinations in advance of the season and in the face of this production environment risk. Further, breeders must consider target adaptive traits for future genotypes up to 10 years ahead of their commercial release. Here we present the case for next generation thinking on design of G*M*E for advancing crop adaptation in future climates. We focus on adaptation to drought and heat in sorghum, but the concepts are generic. There exists considerable knowledge of climate, both past and future, from climate records and climate models. This gives us insight into climate variability and trends. We know that CO_2 and temperature are increasing, and this alone influences drought and heat risks for crops. We also have considerable knowledge of crop growth and development responses to CO_2, drought and heat, along with the physiology and genetics of underpinning mechanisms. This knowledge has been integrated into advanced crop simulation models that are now sufficiently credible to explore G*M*E scenarios via simulation of comprehensive “adaptation landscapes”. Here we combine this existing knowledge and modelling capability to explore the design of crops best suited to current and future environments. The contrasting time points of the G*M*E analyses elucidate the consequences of climate trends and trajectories likely needed in design of future crops adapted to climate risks.

P8.7 USING METABOLIC MODELLING TO UNDERSTAND THE LIMITATIONS TO PHOTOSYNTHESIS UNDER CHANGING ENVIRONMENTAL CONDITIONS

FRIDAY 5 JULY, 2019 **12:00**

HELENA A HERRMANN (THE UNIVERSITY OF MANCHESTER, UNITED KINGDOM), JEAN-MARC SCHWARTZ (THE UNIVERSITY OF MANCHESTER, UNITED KINGDOM), GILES N JOHNSON (THE UNIVERSITY OF MANCHESTER, UNITED KINGDOM)

@ HELENA.HERRMANN@MANCHESTER.AC.UK

As the global climate changes through this century, there will be a need to shift plant growth to times of the year when temperatures are suboptimal and more variable. In order to breed plants for a shifted growth season, we need to understand the limits on photosynthesis across different environmental conditions. We use both kinetic and constraint-based modelling techniques in order to understand the metabolic changes required for photosynthetic acclimation to changing environmental conditions. Using modelling and experimental data from six different temperature conditions, we identify metabolic changes required for photosynthetic acclimation of *Arabidopsis thaliana* across its physiological temperature range. Pioneering the use of flux sampling for studying network robustness in wild-type and mutant plants we identify necessary metabolic changes required for cold acclimation. Using dynamic modelling we predict which of the reactions linking photosynthetic uptake to leaf carbon storage and export are most temperature sensitive and are searching for a metabolic temperature sensor.

P8.8 COMPUTATIONAL MODEL FOR PREDICTING MONOLIGNOL TRANSCRIPT AND PROTEIN ABUNDANCES IN *POPULUS TRICHOCARPA* UNDER SINGLE AND COMBINATORIAL MONOLIGNOL GENE KNOCKDOWNS

FRIDAY 5 JULY, 2019 **12:15**

MEGAN L MATTHEWS (NORTH CAROLINA STATE UNIVERSITY, UNITED STATES), JACK P WANG (NORTH CAROLINA STATE UNIVERSITY, UNITED STATES), DAVID C MUDDIMAN (NORTH CAROLINA STATE UNIVERSITY, UNITED STATES), RONALD R SEDEROFF (NORTH CAROLINA STATE UNIVERSITY, UNITED STATES), VINCENT L CHIANG (NORTH CAROLINA STATE UNIVERSITY, UNITED STATES), CRANOS M WILLIAMS (NORTH CAROLINA STATE UNIVERSITY, UNITED STATES)

@ MLMATTH2@NCSU.EDU

Accurate manipulation of metabolites in the monolignol biosynthesis pathway is a key step for controlling lignin content, structure, and other wood properties that are important to the bioenergy and biomaterial industries. A crucial component of this is predicting how single and combinatorial knockdowns of monolignol specific genes at the transcript level influence monolignol proteins, which are the driving mechanisms of the monolignol biosynthesis pathway. Computational models have been developed to estimate protein abundances from transcript perturbations of monolignol specific genes. The accuracy of these models, however, are hindered by their inability to capture indirect influences that arise when one or more genes are perturbed. We created a computational model based on a sparse maximum likelihood approach to estimate the resulting monolignol transcript and protein abundances in *Populus trichocarpa* based on desired single or combinatorial knockdowns of specific monolignol genes. Using *in-silico* simulations of this model and root mean square error, we show that our model more accurately estimates transcript and protein abundances from xylem tissue when individual and families of monolignol genes were perturbed. Our model captures relationships such as those between the *Ptr4CL* and *PtrCAld5H* gene families, potentially explaining the observed decrease in S/G ratio reported in the literature when *4CL* is knocked down. This approach provides a useful computational tool for further exploring the cascaded impact of single and combinatorial modifications on lignin and other wood properties. Additionally, it can be used to guide future experiments for elucidating the mechanisms responsible for the estimated indirect influences.

P8.9 DESIGNING RICE IDEOTYPE FOR DIFFERENT ENVIRONMENTS USING WACNI – A MODEL OF WHOLE PLANT C-N INTERACTION

FRIDAY 5 JULY, 2019 **15:00**

XINGUANG ZHU (INSTITUTE OF PLANT PHYSIOLOGY AND ECOLOGY CHINESE ACADEMY OF SCIENCES, CHINA), TIANGEN CHANG (INSTITUTE OF PLANT PHYSIOLOGY AND ECOLOGY CHINESE ACADEMY OF SCIENCES, CHINA)

@ ZHUXG@SIPPE.AC.CN

On the face of the rapid advances in genome editing technology and greatly expanded knowledge on plant genome and genes, there is a strong demand to develop an effective tool to guide designing crops for higher yields. Here we developed a highly mechanistic model of WholeplAnt Carbon Nitrogen Interaction (WACNI), which predicts crop yield based on major metabolic and biophysical processes in source, sink and transport tissues. WACNI accurately predicted the yield responses of so far reported source, sink and transport related genetic manipulations on rice grain yields. Systematic sensitivity analysis with WACNI was used to classify the source, sink and transport related molecular processes into four categories, i.e. universal yield enhancers, universal yield inhibitors, conditional yield enhancers and weak yield regulators. Simulations using WACNI further show that even without a major change in leaf photosynthetic properties, 54.6% to 73% grain yield increase can be potentially achieved by optimizing these molecular processes during the rice grain filling period while simply combining all the 'superior' molecular modules together cannot achieve the optimal yield level. A common macroscopic feature in all these designed high-yield lines is that they all show 'a sustained and steady growth of grain sink', which might be used as a generic selection criteria in high-yield rice breeding. Overall, WACNI can serve as a tool to facilitate plant source sink interaction research and guide future crops breeding by design.

P8.10 LEAF AND AXES MOVEMENTS ALONG GRASS ONTOGENY

FRIDAY 5 JULY, 2019 **15:30**

BRUNO ANDRIEU (INRA, UMR ECOSYS, FRANCE), MARIEM ABICHOU (INRA, UMR ECOSYS, FRANCE), CHRISTIAN FOURNIER (INRA, UMR LEPSE, FRANCE), CORINNE ROBERT (INRA, UMR ECOSYS, FRANCE)

@ BRUNO.ANDRIEU@INRA.FR

Plant 3D geometry changes during ontogeny, which originates partly from the production of new leaves and axes with characteristics differing from the older ones, and from progressive changes in the display of organs after they have completed their growth. Crop plants show such important changes, that significantly impact light capture and more generally environment perception, yet relatively little effort has been dedicated to characterizing the movements of mature organs and represent them in models. We investigated the ontogenetic movement of leaves and axes in wheat plants varieties with contrasted statures and will compare with those reported in the literature for other grasses. At leaf level, ample movements occur all along leaf live with differences between the basal leaves and the leaves attached to long internodes. At shoot level, large movements also exist for the inclination of axes, including the main stem, so that axes become nearly vertical only late in their development. The combined movements of leaves relatively to their axe and of axes relatively the vertical result in a complex pattern of leaf orientation at crop level, while each type of movement considered separately follows relatively patterns that can be described with a small number of parameters. Differences exist in the amplitudes of movement between species, cultivars and depending on plant density. We illustrate the importance of representing these movements in plant models for the calculation of plant-environment interaction and for exploring the adaptation of genotypes to crop management.

P8.11 STUDYING THE EFFECTS OF ROOT SENESCENCE ON CROP FITNESS AND SOIL NUTRIENT CAPTURE IN SILICO

FRIDAY 5 JULY, 2019 **15:35**

ERNST D SCHÄFER (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), MARKUS R OWEN (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), MALCOLM J BENNETT (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), ETIENNE FARCOT (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), JONATHAN P LYNCH (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM)

@ ERNST.SCHAFER@NOTTINGHAM.AC.UK

The global human population is predicted to be between 9 and 10 billion by 2050, with most of this population growth taking place in developing countries. At the same time, climate change is expected to have a negative impact on crop yields in these countries and put further pressure on vulnerable ecosystems around the world. Because of this it is important to develop alternative agricultural practices that do not rely on the extensive use of pesticides or fertilizers, which requires us to improve crop yields in low-nutrient conditions where root loss due to pests is significant. A root loss module was developed for OpenSimRoot, a functional-structural root system simulation. Using this, the shoot dry weights, our measure of performance, of 54 phenotypes of barley, bean and maize were assessed in a variety of conditions and subject to different amounts of root loss to yield insight into the effects of nutrient and root loss stress on crop development. Our simulations indicate that root loss is generally detrimental in low-phosphorus environments for most phenotypes. However, some phenotypes show resilience to root loss or even an increase in shoot dry weight in both low-phosphorus and low-nitrate conditions. Our result indicate that not only do different crops show qualitatively different responses to nutrient and root loss stress, but the optimal phenotypes for high-nutrient, root loss free environments are not generally the best performers in high stress scenarios. This shows the importance of developing new varieties that are suitable to meet future challenges.

P8.12 HOW SUGARS INTERPLAY WITH HORMONES IN THE REGULATION OF AXILLARY BUD OUTGROWTH

FRIDAY 5 JULY, 2019 **15:40**

JESSICA BERTHELOOT (IRHS, INRA, AGROCAMPUS-OUEST UNIVERSITÉ D'ANGERS, SFR 4207 QUASAV, FRANCE), FRANÇOIS BARBIER (SCHOOL OF BIOLOGICAL SCIENCES, THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), FRÉDÉRIC BOUDON (CIRAD, UMR AGAP UNIV. MONTPELLIER, FRANCE), MARIA DOLORES PEREZ-GARCIA (IRHS, INRA, AGROCAMPUS-OUEST, UNIVERSITÉ D'ANGERS, SFR 4207 QUASAV, FRANCE), SYLVIE CITERNE (INSTITUT JEAN-PIERRE BOURGIN CENTRE DE VERSAILLES-GRIGNON (IJPB), INRA, AGRO-PARISTECH CNRS, FRANCE), ELISABETH DUN (SCHOOL OF BIOLOGICAL SCIENCES, THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), CHRISTINE BEVERIDGE (SCHOOL OF BIOLOGICAL SCIENCES, THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), CHRISTOPHE GODIN (LABORATOIRE REPRODUCTION ET DÉVELOPPEMENT DES PLANTES, UNIV LYON ENS DE LYON, FRANCE), SOULAIMAN SAKR (IRHS, INRA, AGROCAMPUS-OUEST UNIVERSITÉ D'ANGERS, SFR 4207 QUASAV, FRANCE)

@ JESSICA.BERTHELOOT@INRA.FR

The outgrowth of axillary buds is a main trait of plant adaptation to environment. The regulation of bud outgrowth involves an intricate network of several endogenous regulators including hormones and sugars. In the process of apical dominance, apically-derived auxin in the stem indirectly inhibits bud outgrowth through cytokinins and strigolactones. Sugar diversion to the growing shoot tip away from the bud also contributes to this phenomenon. The present study aims at understanding and modelling how sugars interact with the hormonal network in the shoot. Using rose and pea, experiments were made both on decapitated plants and nodal stem segments in vitro, and consisted in varying stem hormone and sugar levels. We show that sugars antagonized, dose-dependently, the auxin inhibition of bud outgrowth. Sugars reduced the bud inhibition by strigolactones but sugars did not antagonize the auxin repressing effect on cytokinin levels in the stem. These observations were assembled in a computer model, where sugars act mainly by suppressing bud response to strigolactones, independently of cytokinins. This model quantitatively captured all of the observed crosstalk among sugar and hormones for bud outgrowth responses. Since sugars and hormones are both altered by plant environment, this study paves the way for modelling the response of bud outgrowth to environmental factors.

P8.13 CROP2ML: A CROP MODELING METALANGUAGE SHARED BETWEEN DIFFERENT CROP SIMULATION PLATFORMS

FRIDAY 5 JULY, 2019 **15:45**

CYRILLE AHMED MIDINGOYI (INRA, FRANCE), CHRISTOPHE PRADAL (CIRAD, FRANCE), ANDREAS ENDERS (UNIVERSITY OF BONN, GERMANY), DAVIDE FUMAGALLI (JRC, ITALY), HÉLÈNE RAYNAL (INRA, FRANCE), IOANNIS ATHANASIADIS (WAGENINGEN UNIVERSITY, NETHERLANDS), CHERYL PORTER (UNIVERSITY OF FLORIDA, UNITED STATES), GERRIT HOOGENBOOM (UNIVERSITY OF FLORIDA, UNITED STATES), DEAN HOLZWORTH (CSIRO, AUSTRALIA), FRÉDÉRICK GARCIA (INRA, FRANCE), PETER THORBURN (CSIRO, AUSTRALIA), MARCELLO DONATELLI (CREA, ITALY), PIERRE MARTRE (INRA, FRANCE)

@ CYRILLE.MIDINGOYI@INRA.FR

Process-based crop simulation models are popular tools to analyze and predict the response of agricultural systems to climatic, agronomic and, more recently genetic, factors. They are often developed in crop simulation platforms to ensure their future extension and to couple different crop models with a soil model and a crop management event scheduler. The comparison and improvement of these models are difficult due to the lack of efficient method for exchanging biophysical processes between platforms. Models are often implemented in different programming languages, in different platforms using different formalisms. Even when modular approaches and reuse techniques are proposed by these platforms, there is little exchange of crop model components between them despite theoretical and application interests. To this end, the aim of the Agricultural Model Exchange Initiative (AMEI), initiated by several leading groups in this field, is to facilitate model intercomparison and model component exchange. Crop2ML, a high-level metalanguage, has been designed to enable (1) the description and the composition of crop model components independently of the formalism of simulation platforms; and (2) the exchange of components between them. Crop2ML language is based on a declarative architecture of modular model representation with an intermediate modeling language to describe biophysical processes and their transformation to existing platforms. We will present AMEI vision of crop model exchange and the main features of Crop2ML. This approach was applied on two complex models (crop energy balance and a wheat phenology model), which have been shared among the different simulation platforms.

P8.14 INVESTIGATING SHOOT GROWTH AND CARBON COMPETITION BETWEEN ORGANS IN MACADAMIA USING IN SILICO PLANTS

FRIDAY 5 JULY, 2019 **16:00**

INIGO AUZMENDI (QUEENSLAND ALLIANCE FOR AGRICULTURE AND FOOD INNOVATION (QAAFI), THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), JIM HANAN (QUEENSLAND ALLIANCE FOR AGRICULTURE AND FOOD INNOVATION (QAAFI), THE UNIVERSITY OF QUEENSLAND, AUSTRALIA)

@ I.AUZMENDI@UQ.EDU.AU

Understanding how individual shoots grow is a first step to improve the management of tree canopies and orchards. Field experiments have been carried out with this purpose for several species and conditions. However, aspects such as leaf incident light, growth and carbon competition interact and cannot be easily measured, making it difficult to analyse data and obtain clear conclusions. In silico plants that integrate these aspects and their interactions could be a helpful tool. We built a computational model based on L-systems that simulates light environment, carbon assimilation, competition for carbon, and growth of individual organs within the shoot (stem and leaves). This functional-structural model simulates macadamia shoot architecture and physiological mechanisms at organ level in daily time steps. Multi-factor experiments with different conditions were performed using the in silico macadamia shoots. These simulations produced two kinds of outputs: visually realistic 3D representations of daily shoot growth; and data for each organ, which were employed to produce graphs and to compare with field observations. The simple shoot growth model showed that carbon competition and availability were enough to explain some field observations such as differences in shoot elongation and dry weight accumulation. These were emergent properties of the model that reproduced patterns observed in the field. The simulations presented are not mere graphical representations of field data, but a tool to detect gaps in our knowledge and propose new hypotheses and ideas that can explain our observations, improving our understanding and suggesting possible consequences of the management in the field.

P8.15 ROOTS FOR THE 10B: MODELING PHENES AND PHENOTYPES FOR SOIL RESOURCE CAPTURE

FRIDAY 5 JULY, 2019 **16:45**

JONATHAN LYNCH (PENNSYLVANIA STATE UNIVERSITY, UNITED STATES, AND NOTTINGHAM UNIVERSITY, UNITED KINGDOM)

@ JPL4@PSU.EDU

Improved root phenotypes offer avenues for creating the more drought tolerant, nutrient efficient crops that are urgently needed in global agriculture. Functional-structural plant models (FSPM) are an important tool for this enterprise, given the complex, dynamic interplay between root phenotypes and soil resource availability in time and space, and difficulties inherent in the direct observation of key root processes. For example, the FSPMs SimRoot and OpenSimRoot have been useful in identifying root architectural, anatomical, and physiological phenotypes for improved capture of water and nutrients, in understanding tradeoffs for contrasting soil resources, phene synergism, and in guiding root phenotyping strategies. These tools are becoming increasingly capable, and are being integrated with shoot models to develop in silico plants as virtual laboratories. Integration of these tools with models simulating gene networks, the plant and soil microbiomes, and ecosystem function will create unprecedented opportunities to understand the interplay of plant genotype, phenotype, and environment, and in so doing guide the development of the crops and cropping systems of the 21st century.

P8.16 OPTIMAL ACCLIMATION OF LEAF TRAITS TO HIGH TEMPERATURE IN *ARABIDOPSIS*

FRIDAY 5 JULY, 2019 **17:15**

ALEJANDRO MORALES SIERRA (WAGENINGEN UNIVERSITY AND RESEARCH, NETHERLANDS), MARTIJN VAN ZANTEN (UTRECHT UNIVERSITY, NETHERLANDS), XINYOU YIN (WAGENINGEN UNIVERSITY AND RESEARCH, NETHERLANDS), JOCHEM B EVERS (WAGENINGEN UNIVERSITY AND RESEARCH, NETHERLANDS), RASHMI SASIDHARAN (UTRECHT UNIVERSITY, NETHERLANDS), NIELS ANTEN (WAGENINGEN UNIVERSITY AND RESEARCH, NETHERLANDS)

@ ALEJANDRO.MORALESSIERRA@WUR.NL

The environment surrounding leaves (phylloenvironment) determines the rate of photosynthesis, depending on the physiological and morphological traits of the leaf. The phylloenvironment results from the exchange of energy, CO_2 and H_2O with the surrounding air, which is affected by the architecture of the plant. Leaf traits and plant architecture are known to adjust to the growth environment (i.e. acclimation), a process which is often assumed to lead to higher photosynthesis (i.e. optimal photosynthetic acclimation theory). In this study, we use *Arabidopsis thaliana* as a model organism and address the question of whether the observed acclimation to high temperature (i.e. thermomorphogenesis) leads to higher photosynthesis. A novel 3D computational model of arabidopsis was developed to simulate the phylloenvironment and leaf photosynthetic rates and was validated with experiments in climate-controlled chambers using natural accessions and mutants. The model was then used to calculate the optimal combination of leaf traits and plant architecture by maximizing photosynthesis under different environmental conditions. The simulated optimal combinations of traits under high temperature depended strongly on light intensity, wind speed and the conditions of the soil surface (i.e. whether wet or dry). The main finding was that acclimation to high temperature was particularly beneficial to photosynthesis under high light intensities and less so (or even detrimental) under low light intensities. However, thermomorphogenesis in arabidopsis only occurs at low light intensities. These results suggest that thermomorphogenesis in arabidopsis is not optimal for photosynthesis and that it may have a different ecological function, questioning the optimal photosynthetic acclimation theory.

P8.17 INTEGRATING THE COMPLEX REGULATION OF LEAF GROWTH BY WATER AND TROPHIC DYNAMICS IN A FUNCTIONAL-STRUCTURAL PLANT MODEL OF GRASS

FRIDAY 5 JULY, 2019 **17:30**

ROMAIN BARILLOT (INRA, FRANCE), MARION GAUTHIER (INRA, FRANCE), BRUNO ANDRIEU (INRA, FRANCE), JEAN-LOUIS DURAND (INRA, FRANCE), ISABEL ROLDÁN-RUIZ (ILVO, BELGIUM), TOM DE SWAEF (ILVO, BELGIUM)

@ ROMAIN.BARILLOT@INRA.FR

Climate change challenges agricultural production due to interacting effects of reduced water availability, increased atmospheric CO_2 concentration and altered temperature dynamics. Plant morphogenesis plays a crucial role in resource capture but there are no integrative models available which account for its regulation by the interplay between water, nitrogen, light, CO_2 and temperature. In the present study, we describe a comprehensive functional-structural plant model (FSPM) encompassing the regulation of leaf growth by water and trophic dynamics in grass. The model is defined at individual tiller scale, composed of interconnected laminae, sheaths and internodes. Leaf elongation kinetics are divided into two phases whose durations depend on coordination rules between successive leaves. During the early phase, which mainly consists in cell production, we assumed leaf growth to be regulated by carbon and nitrogen concentrations, while water is considered non-limiting during this meristematic process. In the second phase which includes cell elongation, leaf growth is driven by turgor pressure, which is tightly coupled to leaf water content variations and osmotic pressure, thus resulting in elastic deformation and plastic irreversible growth. The water flow throughout the hydraulic architecture of the tiller is calculated from organ transpiration and water potential differences. Carbon and nitrogen concentrations, which affect leaf growth and osmotic pressure, are simulated at organ scale using a detailed description of the metabolic processes involved in resource capture and allocation. The model ability to improve our understanding of the effects of drought on plant morphogenesis under contrasted temperatures and CO_2 levels will be discussed.

P8.18 COMPUTING A MORE EFFICIENT LEAF USING METABOLIC NETWORK MODELS

FRIDAY 5 JULY, 2019 **17:45**

LEE J SWEETLOVE (OXFORD UNIVERSITY, UNITED KINGDOM), SANU SHAMEER (UNIVERSITY OF OXFORD, UNITED KINGDOM), R GEORGE RATCLIFFE (UNIVERSITY OF OXFORD, UNITED KINGDOM)

@ LEE.SWEETLOVE@PLANTS.OX.AC.UK

Metabolism underpins the growth of plants and in many circumstances limits growth. Although primary metabolism in plants is very well characterised in terms of the enzymes present and the biochemical reactions catalysed, the complexity of the network and its regulation mean that we are still surprisingly poor at predicting metabolic behaviour in response to developmental and environmental transitions. We are even worse at predicting how to engineer metabolism to improve the efficiency of crop plants in modern high-intensity agro-ecosystems. For the last 10 years, my group have been building and analysing computational models of plant metabolic networks that have allowed us to address the complexity problem. Using these models, we are now able to make predictions about metabolic behaviour and infer the system-level trade-offs and balances that are managed in order to sustain plant growth and development. In this talk I will concentrate on what we have learnt about the metabolism of leaves in the context of efficiency of use of energy, nutrients and water.

P8.19 RAISING GENETIC YIELD POTENTIAL BY DESIGNING WHEAT IDEOTYPES UNDER CLIMATE CHANGE

WEDNESDAY 3 JULY, 2019 **POSTER SESSION**

MIKHAIL SEMENOV (ROTHAMSTED RESEARCH, UNITED KINGDOM), NIMAI SENAPATI (ROTHAMSTED RESEARCH, UNITED KINGDOM)

@ MIKHAIL.SEMENOV@ROTHAMSTED.AC.UK

Designing crop ideotypes is a key step to raise genetic yield potential in a target environment. In the present study, we designed wheat ideotypes based on the *Sirius* process-based wheat model to increase wheat yield potential for the 2050-climate in two high productive countries, viz. the United Kingdom (UK) and New Zealand (NZ). A wheat ideotype was defined as a subset of *Sirius* cultivar parameters that were optimized to maximize yield potential for both water-limited (IW_{2050}) and potential (IP_{2050}) conditions by exploring the full parameter ranges. A substantial increase in yield potential, 43–51%, over current cv. Claire, was predicted for IW_{2050}, whereas a 51–62% increase was obtained for IP_{2050}. The genetic yield potentials of wheat were 16% (2.6 tonnes/ha) and 31% (5 tonnes/ha) greater in NZ than in the UK under 2050-climate in water-limited and potential conditions, respectively. Modelling predicts the possibility of considerable increase in yield potential of winter wheat under climate change in high productive countries. Wheat ideotypes optimized for future climates could provide plant scientists and breeders with a road map for selection of the target traits for improvement and genetic adaptation to raise the genetic yield potential.

P8.20 EVALUATING PHOTOSYNTHETIC INDUCTION USING GAS EXCHANGE DATA

THURSDAY 4 JULY, 2019 **POSTER SESSION**

SAMUEL H TAYLOR (LANCASTER UNIVERSITY, UNITED KINGDOM), DOUGLAS J ORR (LANCASTER UNIVERSITY, UNITED KINGDOM), ELIZABETE CARMO-SILVA (LANCASTER UNIVERSITY, UNITED KINGDOM), STEPHEN P LONG (LANCASTER UNIVERSITY, UNITED KINGDOM)

@ S.TAYLOR19@LANCASTER.AC.UK

Photosynthetic induction is of tremendous interest for improvement of crop plant productivity. In wheat, for example, slow recovery of Rubisco activity during induction may limit diurnal CO_2 assimilation by up to 20%. Methods to evaluate photosynthetic limitation during induction were principally developed more than two decades ago. In the interim, three relevant changes have occurred: 1) approaches to modelling photosynthesis based on gas exchange and chlorophyll fluorescence data have advanced, increasing the number of parameters that can be estimated; 2) new generations of photosynthesis systems have improved the ease with which photosynthetic response curves and cuvette-level experiments can be used to measure induction responses; 3) the 'phenomics era' has arrived, placing emphasis on high throughput screening of plant performance that potentially limits the detail captured per plant when using time intensive measurements like gas exchange responses. Using example gas exchange datasets I will illustrate and compare approaches we have developed that phenotype diffusive and biochemical limitations influencing photosynthetic induction.

P8.21 LEAF SHAPE MODELS FOR VIRTUAL CUCUMBER

WEDNESDAY 3 JULY, 2019 **POSTER SESSION**

KATRIN KAHLEN (HOCHSCHULE GEISENHEIM UNIVERSITY, GERMANY), DOMINIK SCHMIDT (HOCHSCHULE GEISENHEIM UNIVERSITY, GERMANY)

@ KATRIN.KAHLEN@HS-GM.DE

Leaf shape plays a key role in the interaction of a plant with its environment and, particularly, in the plant's light harvest. Effects of the environment on the interplay of canopy architecture and physiological functioning can be estimated by using functional-structural plant models (FSPMs or virtual plant models). In order to reduce the complexity of canopy simulations, leaf shape models used in FSPMs are often simple prototypes, which are scaled in relation to the size of the leaves. The functional-structural plant model L-Cucumber is such a FSPM, whose leaf prototype mimics average real leaf shape of unstressed cucumber plants well. However, adaptation processes or stress responses may lead to non-proportional changes in leaf geometries, which, for example, may result in adapted length to width ratios or additional leaf curvatures. The current leaf model in L-Cucumber does mimic such changes in the leaf shape. Thus, the aim of this study was to improve the prototype model of leaf shape of L-Cucumber in order to account for dynamics and sensitivity to the environment. Three-dimensional leaf coordinate data from a salt stress experiment were analysed with a robust Bayesian linear mixed effects model for estimating leaf shape depending on rank, size and treatment level. First results indicate visible effects on leaf shape for all factors. In a next step, L-Cucumber simulations with an environment-sensitive dynamic leaf shape model will be compared to the original model to determine, whether detected shape changes will significantly affect simulation results.

P8.22 A SIMPLE MECHANISTIC MODEL OF CARBON ALLOCATION PERFORMS BETTER THAN THE STATISTICAL PARTITIONING MODEL IN CROP GROWTH MODELS

THURSDAY 4 JULY, 2019 **POSTER SESSION**

JUSTIN M MCGRATH (UNIVERSITY OF ILLINOIS URBANA-CHAMPAIGN, UNITED STATES), STEPHEN P LONG (UNIVERSITY OF ILLINOIS URBANA-CHAMPAIGN, UNITED STATES)

@ JMCGRATH@ILLINOIS.EDU

Crop growth models are useful tools for predicting yield in future environments and identifying traits to target for breeding. The models as a whole are combinations of statistical and mechanistic models, which each have benefits and drawbacks. A major disadvantage of statistical models is that their validity cannot be guaranteed outside of the observed range of input data. Carbon allocation among tissues is often modeled statistically by allocating fractions of photosynthetic carbon gain to tissues (e.g., 50% to leaves, 30% to stems, etc.) based on previous observations. With proper training data, these will estimate long-term averages, but the model responds only to temperature, not other environmental factors. Thus, yield in any given year could be estimated poorly. Here we replace the partitioning model in the BioCro model with a utilization model that allocates carbon using source and sink concentrations and a rate constant. This provides a simple mechanistic integration of carbon transport in the plant. The model better predicts yield when using out-of-training input compared to the partitioning model. Interestingly, it also reproduces the daily cycle of soluble carbon concentration seen in plants (although out of phase with observed data) as an emergent property. The utilization model can also easily be extended to respond to environmental factors, such as day length and water status, which is comparably difficult with the partitioning model. This model is more computationally difficult to solve than the partitioning model, but is likely more suitable for addressing a many scientific questions.

P8.23 ADD GRIT FOR TRACTION: REPRESENTATION OF SOIL STRUCTURE IMPROVES FIT OF A ROOT GROWTH MODEL

WEDNESDAY 3 JULY, 2019 **POSTER SESSION**

CHRISTOPHER K BLACK (PENNSYLVANIA STATE UNIVERSITY, UNITED STATES), ERNST D SCHÄFER (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), JONATHAN P LYNCH (PENNSYLVANIA STATE UNIVERSITY, UNITED STATES)

@ CKB23@PSU.EDU

Plant roots grow in a dynamic and heterogeneous environment that requires efficient foraging to achieve optimal resource capture. Understanding root growth strategy is necessary for agronomic and ecological studies, but unfortunately the dynamic and heterogeneous soil environment also makes roots difficult to observe or sample, so many experiments rely on observations from roots growth under uniform artificial laboratory conditions. As a result, many computational root growth models have until recently focused on representing root growth in a homogeneous medium, which facilitates comparisons against laboratory experiments but limits model predictive power about real-world growth scenarios. To improve the real-world applicability of the structural-functional root growth model OpenSimRoot, we have updated it to include calculations of soil physical structure. The model calculates soil penetration resistance from soil bulk density, porosity, water status, and profile position, and uses them to adjust root diameter and extension rate. When parameterized with measured soil moisture and bulk density, the model captures >50% of observed variation in field penetrometer measurements, and simulations of maize growth predict shallower rooting and reduced total root length in soils with plowpan layers, consistent with field observations. Both the impedance term and the growth response are calculated locally for each root tip, allowing flexible simulations of scenarios with both spatial heterogeneity (e.g. plowpans, dry layers, macropores) and developmental plasticity (e.g. growth impedance responses that differ with age or root class).

P9 TIME, TEMPERATURE, AND A TRANSFORMING WORLD

ORGANISED BY: COLLEEN DOHERTY (NORTH CAROLINA STATE UNIVERSITY)

P9.1 WHEN DO TREES GROW? ENVIRONMENTAL SIGNALS WHICH START AND STOP GROWTH IN DOUGLAS-FIR (*PSEUDOTSUGA MENZIESII*)

TUESDAY 2 JULY, 2019 **09:00**

CONSTANCE A HARRINGTON (USDA PACIFIC NORTHWEST RESEARCH STATION, UNITED STATES)

@ CHARRINGTON@FS.FED.US

Douglas-fir has several types of meristems responsible for growth of stems and roots and each tissue has its own environmental signals responsible for growth initiation and cessation. Plants become dormant in the fall and the species has an obligate chilling requirement (both chilling and forcing temperatures during the dormant season are required for bursting of the terminal bud). Non-terminal vegetative buds and stem vascular meristems will resume growth in the spring more promptly after chilling but it is not an obligate requirement. Specific soil conditions and photoperiod do not generally control the resumption of growth after dormancy. On the other hand, cessation of height and diameter growth are both triggered by declining photoperiod and temperature, and other factors such as soil moisture (plant stress) may also be involved. Premature cessation of diameter growth can be triggered by high air temperatures (> 40°C) during long photoperiods. As long as soil moisture is adequate, root growth is controlled by soil temperature. Understanding the phenology of Douglas-fir has been greatly facilitated with a combination of controlled experiments and long-term, fine-scale monitoring of plant growth under a range of environmental conditions. There is genetic variation in phenology of Douglas-fir with the greatest variation among genotypes in the timing of terminal budburst. This timing influences responses such as avoiding frost, completing substantial growth prior to summer drought, and the severity of needle cast diseases associated with availability of young foliage. Understanding the factors which control growth allows modeling of future phenology under different climate scenarios.

P9.2 INTEGRATED ANALYSIS OF WOODY ROOTS RESPONSE TO MECHANICAL CONSTRAINTS

TUESDAY 2 JULY, 2019 **09:30**

DALILA TRUPIANO (DEPARTMENT OF BIOSCIENCES AND TERRITORY - UNIVERSITY OF MOLISE, ITALY), ELENA DE ZIO (DEPARTMENT OF BIOSCIENCES AND TERRITORY - UNIVERSITY OF MOLISE, ITALY), ANTONIO MONTAGNOLI (DEPARTMENT OF BIOTECHNOLOGY AND LIFE SCIENCE - UNIVERSITY OF INSUBRIA, ITALY), GABRIELLA SFERRA (DEPARTMENT OF BIOSCIENCES AND TERRITORY - UNIVERSITY OF MOLISE, ITALY), KARIN LJUNG (SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES, SWEDEN), DONATO CHIATANTE (DEPARTMENT OF BIOTECHNOLOGY AND LIFE SCIENCE - UNIVERSITY OF INSUBRIA, ITALY), GABRIELLA S SCIPPA (DEPARTMENT OF BIOSCIENCES AND TERRITORY - UNIVERSITY OF MOLISE, ITALY)

@ DALILA.TRUPIANO@UNIMOL.IT

Progress has been made in understanding the physiological and molecular basis of root response to mechanical stress, especially in the model plant *Arabidopsis thaliana*, in which bending causes the initiation of lateral root primordia toward the convex side of the bent root (Ditengou *et al.*, 2008; Richter *et al.*, 2009). Conversely, woody roots are still poorly investigated due to intrinsic difficulties in excavation and sampling. By using a simple experimental system, we previously found that the intensity of tension and compression forces in bent woody roots (*Populus nigra* L.) elicit asymmetric responses in the two bent root sides, important to regulate processes such as cambial cell proliferation, reaction wood (RW) formation and lignin accumulation in the concave side and lateral roots formation in the convex side (De Zio *et al.*, 2016). Thus, cambial zone and its surrounding areas were isolated from convex and concave sides of bent poplar root and analyzed by UHPLC-MS/MS to profile IAA metabolites, ABA and CKs. In the concave side, IAA gradient plays a pivotal role in the control of cambial growth rate and xylem differentiation, and it could be at the basis of the strictly unidirectional RW production toward this side. Furthermore, the higher levels of ABA and all CKs metabolites in the concave side support their involvement in RW production, whereby ABA could mediate the adaptation to the deforming conditions generated by bending, while CKs could act in synergy with IAA to control cell division and differentiation (De Zio *et al.*, 2019).

P9.3 TRANSCRIPTIONAL INTEGRATION BETWEEN TEMPERATURE AND THE CIRCADIAN CLOCK

TUESDAY 2 JULY, 2019 **09:45**

DAWN NAGEL (UNIVERSITY OF CALIFORNIA RIVERSIDE, UNITED STATES)

@ DAWNN@UCR.EDU

The circadian clock enables plants to coordinate daily external signals with internal processes, conferring enhanced fitness and growth vigor. While external cues such as temperature can entrain the clock, an important feature of the clock is the ability to maintain a relatively constant period over a range of physiological temperatures. The precise mechanism of how varying degrees of temperature is perceived and integrated to balance the sensitivity and imperturbability of the clock remains poorly understood. A previous functional genomics study identified several temperature responsive transcription factors (TRTF) that interact with the morning and daytime expressed clock genes in *Arabidopsis*. Investigation of the functional role of TRTF-C on the expression of CCA1 and PRR7 suggests that at cooler temperatures, TRTF-C plays an important regulatory role at both the transcriptional and post-transcriptional level of these clock genes. As a result, changes in mRNA abundance contributes to a circadian phase defect. The findings from this study will provide new mechanistic insights into how plants perceive and integrate temperature signals to the circadian clock, and potentially aid in the improvement of crop thermo-tolerance.

P9.4 MOLECULAR SIGNATURES FOR LOW TEMPERATURE MEMORY IN *ARABIDOPSIS*

TUESDAY 2 JULY, 2019 **10:15**

ELLEN ZUTHER (MAX PLANCK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY), STEPHANIE SCHAARSCHMIDT (MAX PLANCK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY), AXEL FISCHER (MAX PLANCK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY), ALEXANDER ERBAN (MAX PLANCK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY), MAJKEN PAGTER (DEPARTMENT OF CHEMISTRY AND BIOSCIENCE, AALBORG UNIVERSITY, DENMARK), UMARAH MUBEEN (MAX PLANCK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY), DIRK WALTHER (MAX PLANCK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY), PATRICK GIAVALISCO (MAX PLANCK INSTITUTE FOR BIOLOGY OF AGING, GERMANY), JOACHIM KOPKA (MAX PLANCK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY), HEIKE SPRENGER (VIB-UGENT CENTER FOR PLANT SYSTEMS BIOLOGY, BELGIUM), DIRK K. HINCHA (MAX PLANCK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY)

@ ZUTHER@MPIMP-GOLM.MPG.DE

Plants from temperate regions increase their freezing tolerance during exposure to low, non-freezing temperatures, a process called cold acclimation or cold priming as plants become better prepared for subsequent stresses. Adaptation to alternating temperatures enables plants to survive winter and to cope with recurring cold periods. In spring loss of freezing tolerance occurs during a tightly regulated deacclimation balancing between transition to reproductive growth and the need for maintained freezing tolerance. Cold priming has been intensively investigated whereas processes underlying cold memory are unknown. We showed that the freezing tolerance of two *Arabidopsis* accessions Col-0 and N14 was higher after priming at 4°C, a lag phase at 20°C and a second cold trigger compared to only primed plants implicating cold stress memory. The triggering response differed from the priming response at the levels of gene expression (RNA-Seq), lipid (UPLC-MS), and metabolite composition (GC-MS). Unique differentially expressed genes after triggering were overrepresented in categories such as lipid and secondary metabolism, stress, redox and cell wall related functions in Col-0 and growth-related functions in N14. Furthermore arabidopsides were accumulated with proposed functions in signalling or as precursors of jasmonic acid. The more freezing tolerant N14 maintained levels of cold-induced metabolites during the lag phase whereas strong accumulation occurred in the less freezing tolerant Col-0 after triggering pointing to genetic differences of transcriptomic and metabolic patterns during cold memory. This is to our knowledge the first report on molecular and metabolic changes accompanying cold stress memory and triggering by a second cold stress.

P9.5 A GENETIC FRAMEWORK FOR TEMPERATURE DEPENDENT ROOT GROWTH REGULATION AND ITS LINK TO CLIMATE ADAPTION

TUESDAY 2 JULY, 2019 **10:30**

WOLFGANG BUSCH (SALK INSTITUTE, UNITED STATES), CHRISTOPHE GAILLOCHET (SALK INSTITUTE, UNITED STATES)

@ WBUSCH@SALK.EDU

Temperature is one of the most universal and profound environmental factors for organisms. Land plants can be exposed to dramatic changes in temperature not only throughout a growth season, but even throughout a single day. Despite the importance of adaptive responses to fluctuating temperatures, our current understanding of the molecular mechanisms controlling plant responses to changing temperatures is very incomplete. Moreover, much of what is known for land plants is centred on aboveground tissues. However, root growth also responds profoundly to temperature changes. We aim to understand how temperature is sensed and how the sensing of temperature elicits root growth responses. We have profiled root and hypocotyl growth in mutants of known shoot thermo-response-related genes and pathways. Interestingly we find pronounced differences between root and shoot growth responses for a number of these mutants. We also make use of the vast phenotypic and genetic natural variation in *Arabidopsis thaliana*, a species that has colonized regions with vastly different temperature profiles. We find starkly distinct growth responses to high temperature in different accessions of *Arabidopsis*. Using genome wide association studies for root growth at different temperatures, we have found a number of high confidence candidate genes, some of which overlap with genes associated to temperature parameters at the sites of origin of these accessions. We are currently investigating the role of selected candidate gene and the molecular pathways they are associated with in temperature responses and explore links to adaptation to different temperatures.

P9.6 UNRAVELING THE MOLECULAR MECHANISMS UNDERLYING PLANT CLOCK FUNCTION

TUESDAY 2 JULY, 2019 **14:00**

JOSE PRUNEDA-PAZ (UNIVERSITY OF CALIFORNIA, SAN DIEGO)

@ PRUNEDAPAZ@UCSD.EDU

Like most organisms that live on our planet, plants evolved an accurate mechanism to time physiological responses throughout the day. This mechanism, known as the circadian clock, integrates with most major plant signaling modules. One goal of my research program is to investigate how biotic and abiotic stress regulates the plant clock function in the *Arabidopsis* model. In particular, we are focused on uncovering the transcriptional mechanisms that modulate: 1) the clock function upon biotic and abiotic stress and 2) the circadian control of stress responses. For that, we established approaches to investigate how the *Arabidopsis* clock function is modulated by bacterial pathogens or temperature stress and to identify genome-wide transcription factor - DNA interactions. I will present recent improvements to our transcription factor screening approach and illustrate how this strategy allowed us to discover novel temperature-responsive regulators of the plant clock.

P9.7 *ARABIDOPSIS* JMJD5/JMJ30 ACTS INDEPENDENTLY OF LUX ARRHYTHMO WITHIN THE PLANT CIRCADIAN CLOCK TO ENABLE TEMPERATURE COMPENSATION

TUESDAY 2 JULY, 2019 **14:30**

MATT A JONES (UNIVERSITY OF ESSEX, UNITED KINGDOM), KENGO MOROHASHI (TOKYO UNIVERSITY OF SCIENCE NODA, JAPAN), ERICH GROTEWOLD (MICHIGAN STATE UNIVERSITY, UNITED STATES), STACEY L HARMER (UNIVERSITY OF CALIFORNIA DAVIS, UNITED STATES)

@ MATTHEW.JONES@ESSEX.AC.UK

The circadian system ensures that plants respond appropriately to environmental change by predicting regular transitions that occur during diel cycles. In order to be most useful, the circadian system needs to be compensated against daily and seasonal changes in temperature that would otherwise alter the pace of this biological oscillator. We demonstrate that an evening-phased protein, the putative histone demethylase JMJD5, contributes to temperature compensation. *JMJD5* is co-expressed with components of the Evening Complex, an agglomeration of proteins including EARLY FLOWERING3 (ELF3), ELF4, and LUX ARRHYTHYMO (LUX), which also integrates temperature changes into the molecular clockwork. One role of the Evening Complex is to regulate expression of *PSEUDORESPONSE REGULATOR9* (*PRR9*) and *PRR7*, important components of the temperature compensation mechanism. Surprisingly we find that LUX, but not other Evening Complex components, is dispensable for clock function at low temperatures. Further genetic analysis suggests JMJD5 acts in a parallel pathway to LUX within the circadian system. Although an intact JMJD5 catalytic domain is required for its function within the clock, our findings suggest JMJD5 does not directly regulate H3K36 methylation at circadian loci. Such data refine our understanding of how JMDJ5 acts within the *Arabidopsis* circadian system.

P9.8 THE “TEMPERATURE NICHE” OF PLANT PATHOGENS

TUESDAY 2 JULY, 2019 **14:45**

THOMAS CHALONER (UNIVERSITY OF EXETER, UNITED KINGDOM), SARAH GURR (UNIVERSITY OF EXETER, UNITED KINGDOM), DAN BEBBER (UNIVERSITY OF EXETER, UNITED KINGDOM)

@ T.CHALONER@EXETER.AC.UK

The ability of a plant pathogen to successfully establish in an area, as well as disperse into virgin territory, is determined by many complex and interacting processes. These include host availability, accessible migratory routes, and abiotic factors such as moisture availability and temperature. Each stage of a pathogen’s life cycle (i.e. infection, disease development, and sporulation) can only occur within a thermal limit, whereby optimum temperature is bounded by a minimum and maximum temperature. As temperature deviates from optimum, the rate of a biological process declines from maximum, towards zero. Hence, optimum, minimum, and maximum temperature – collectively referred to as cardinal temperature (CT) – define a pathogens temperature response, for a given stage of its life cycle. CT in-part shapes pathogen biogeography and resultant crop risk, both in space and time, by restricting pathogens to areas of climatic suitability. Here, published CT estimates were collated for >600 plant pathogenic fungi and oomycetes. Utilising this dataset, we first test the hypothesis that temperature has an asymmetric effect on biological processes, i.e. from optimum, temperature increases have a greater inhibitory effect than temperature decreases. Second, we test the hypothesis that temperature-specialist pathogens also specialise in other niche axes. Third, we test the hypothesis that the evolutionary capacity of pathogens to alter their CT is limited. Finally, we investigate how climatic change may alter global pathogen biogeography. Our research aims to improve our fundamental understanding of both the “temperature niche” of species and how temperature influences the plant pathogen ecology and evolution.

P9.9 NIGHT-TIME TEMPERATURE AND FLOWER-OPENING TIME DYNAMICS AFFECT CROP ADAPTATION IN A CHANGING CLIMATE

WEDNESDAY 3 JULY, 2019 **10:00**

KRISHNA JAGADISH (KANSAS STATE UNIVERSITY, UNITED STATES)

@ KJAGADISH@KSU.EDU

Heat escape mechanisms allow crops to move heat-sensitive processes, such as flowering to cooler times of the day, thus increasing their survival on exposure to heat stress. However, increase in night-time temperatures can alter this flowering strategy and other heat stress responses. In both rice and wheat, increasing night-time temperatures have a significant negative impact on yield and quality. I will present our research on flower-opening time and the impacts of night-time temperature on grain yield and quality by exploring the physiological, metabolomic and enzymatic responses and strategies developed to better adapt these sensitive staple crops to a changing warmer climate.

P9.10 CONTROL OF FLOWER INITIATION IN THE MONOECIOUS *QUERCUS SUBER* L.

WEDNESDAY 3 JULY, 2019 **10:30**

MARIA MANUELA R COSTA (UNIVERSIDADE DO MINHO, PORTUGAL), RÓMULO SOBRAL (UNIVERIDADE DO MINHO, PORTUGAL), HELENA SILVA (UNIVERSIDADE DO MINHO, PORTUGAL)

@ MANUELA.COSTA@BIO.UMINHO.PT

Several plant species display a temporal separation of the male and female flower organ development to enhance outbreeding, however, little is known regarding the genetic mechanisms controlling this temporal separation. *Quercus suber* is a monoecious oak tree with accentuated protandry: in late winter, unisexual male flowers emerge close to the dormant buds, whereas unisexual female flowers emerge in spring (4 to 8 weeks after male flowering). Here, cork oak homologs of key floral regulatory genes were identified by phylogenetic profiling and their role in flower development accessed by performing functional studies in *Arabidopsis thaliana*. The expression profile of flower regulators (inducers and repressors) throughout the year, in leaves and buds, suggests that the development of male and female flowers may be preceded by temporarily separated induction events. Female flowers are most likely induced during the vegetative flush occurring in spring, whereas male flowers may be induced in early summer and start forming inside the buds, but complete their development only in the growth season of the following year, displaying a long period of anthesis that spans the dormant period. The results portray a genetic mechanism highly dependent on environment conditions that may justify poor reproductive success in tree species with similar reproductive habits.

P9.11 SEASONAL ENVIRONMENTAL RESPONSES AND ADAPTATIONS REVEALED BY FIELD TRANSCRIPTOME IN PLANTS

WEDNESDAY 3 JULY, 2019 **11:00**

AKIKO SATAKE (KYUSHU UNIVERSITY, JAPAN)

@ AKIKO.SATAKE@KYUDAI.JP

The intermittent and synchronized production of a large amount of flowers and seeds is called masting or mast seeding. Fagaceae is a family of flowering plants that includes typical masting species such as beech, oak, and tanbark oak. Applying recent advances in molecular and genetic studies about flowering time control to masting species is increasingly useful to unravel the underlying mechanism of masting. To unravel genetic basis of masting dynamics in the Fagacea family, we performed comparative field transcriptomics of three Fagaceae species, *Fagus crenata*, *Quercus glauca*, and *Lithocarpus edulis*, at Ito campus of Kyushu University in Japan. Our transcriptome analyses unraveled the non-intuitive relationship between seasonal environment and expression profiles of genes involved in flowering-time control, nitrogen/sugar transport, and photosynthesis. Although many orthologus genes exhibited conserved expression patterns, there were groups that show distinctly different expression pattern between species. We also identified co-expression patterns that are shared among species and estimated the contribution of lineage-specific gene expression to reproductive phenotypes. Our co-expression analyses and comparison of protein coding sequences provide insights into transcriptome evolution in the context reproductive strategy in trees.

P9.12 TRANSCRIPTOMIC PROFILES ACCURATELY PREDICT THE DORMANCY STAGES IN SWEET CHERRY FLOWER BUDS

WEDNESDAY 3 JULY, 2019 **11:30**

BÉNÉDICTE WENDEN (UMR 1332 BFP, INRA, UNIV. BORDEAUX, FRANCE), NOÉMIE VIMONT (INRA, AGRO INNOVATION INTERNATIONAL - CENTRE MONDIAL D’INNOVATION - GROUPE ROULLIER, FRANCE), MATHIEU FOUCHÉ (INRA, FRANCE), JOSÉ ANTONIO CAMPOY (INRA, FRANCE), MEIXUEZI TONG (THE SAINSBURY LABORATORY, UNIVERSITY OF CAMBRIDGE, UNITED KINGDOM), MUSTAPHA ARKOUN (AGRO INNOVATION INTERNATIONAL - CENTRE MONDIAL D’INNOVATION - GROUPE ROULLIER, FRANCE), JEAN-CLAUDE YVIN (AGRO INNOVATION INTERNATIONAL - CENTRE MONDIAL D’INNOVATION - GROUPE ROULLIER, FRANCE), PHILIP A WIGGE (THE SAINSBURY LABORATORY, UNIVERSITY OF CAMBRIDGE, UNITED KINGDOM), ELISABETH DIRLEWANGER (INRA, FRANCE), SANDRA CORTIJO (THE SAINSBURY LABORATORY, UNIVERSITY OF CAMBRIDGE, UNITED KINGDOM)

@ BENEDICTE.WENDEN@INRA.FR

Bud dormancy is a crucial stage in perennial trees and allows survival over winter and optimal subsequent flowering and fruit production. Environmental conditions, and in particular temperature, have been shown to influence bud dormancy. Recent work highlighted some physiological and molecular events happening during bud dormancy in trees. However, we still lack a global understanding of transcriptional changes happening during bud dormancy. We conducted a fine tune temporal transcriptomic analysis of sweet cherry (*Prunus avium* L.) flower buds from bud organogenesis until the end of bud dormancy using next-generation sequencing. We observe that buds in organogenesis, paradormancy, endodormancy and ecodormancy are characterised by distinct transcriptional states, and associated with different pathways. We also found that transcriptional profiles of just seven genes are enough to predict the main cherry tree flower bud dormancy stages. Our results indicate that transcriptional changes happening during dormancy are robust and conserved between different sweet cherry cultivars. Our work opens up avenues for the development of future molecular phenology models.

P9.13 DYNAMIC PLASTICITY OF THE *ARABIDOPSIS* CIRCADIAN OSCILLATOR IN RESPONSE TO SUGAR SIGNALS

WEDNESDAY 3 JULY, 2019 **14:30**

ALEX AR WEBB (UNIVERSITY OF CAMBRIDGE, UNITED KINGDOM)

@ AARW2@CAM.AC.UK

The defining characteristic of circadian rhythms is that they have a period of about 24 h. However, circadian period is not fixed, it is variable. Many signals regulate the speed of the circadian clock in a reversible manner, with the effect dependent on the time of the day, a process we have called dynamic plasticity (Webb *et al.,* 2019). We have been investigating the mechanism and purpose of the dynamic plasticity of the circadian oscillator to sugar signals. We have previously demonstrated that sugars can speed up the circadian oscillator and identified three signalling pathways by which sugars act, including one dependent on the regulation of the expression of the circadian clock gene *PSEUDO-RESPONSE REGULATOR 7* (*PRR7*) by the energy sensitive transcription factor bZIP63 (Frank *et al.,* 2018). We are now investigating why the circadian oscillator responds to sugar signals. We will describe new data that demonstrates that the circadian oscillator responds to endogenous changes in sugars that affect the entrainment of the circadian oscillator to light intensity and photoperiod dependent on the correct functioning of *PRR7.* Experimentation and mathematical modelling demonstrate that responses of the circadian oscillator to responses to moderate changes in light intensity can be explained in terms of changes in sugar signalling associated with the management of transient starch reserves in the leaf. Our data suggest that response the circadian oscillator to endogenous sugar signals is required for the correct timing of internal events with respect to the environment.

P9.14 A CONNECTOR INTEGRATING CARBON PARTITIONING AND DEMAND IN PLANTS

WEDNESDAY 3 JULY, 2019 **15:00**

CAMILA CALDANA (MAX PLANCK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY), CAROLINA C MONTE BELLO (MAX PLANCK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY), MARINA CM MARTINS (UNIVERSITY OF SAO PAULO, BRAZIL), AKIKO SATAKE (KYUSHU UNIVERSITY, JAPAN), MOTORHIDE SEKI (KYUSHU UNIVERSITY, JAPAN), ALEX WEBB (UNIVERSITY OF CAMBRIDGE, UNITED KINGDOM), ANTHONY ARTINS (MAX PLANCK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY)

@ CALDANA@MPIMP-GOLM.MPG.DE

As sessile organisms, plants have a great plasticity to adapt to fluctuating environmental conditions adjusting their growth and developmental demands. The Target of Rapamycin (TOR) pathway has emerged as a central hub in this network, integrating metabolic signals, energy status and hormones to a wide range of growth-mediated processes. Our group is interested in understanding how the TOR pathway fine-tunes carbon partitioning accordingly to the diel and photoperiod changes to optimize biosynthetic growth. Although starch is an important carbon sink, it also serves as a source for overall growth and development under periods of carbon limitation, such as darkness. The efficient release of sugars from starch reserves can have profound consequences on plant growth. Not surprisingly, a common phenotype of transgenic *Arabidopsis* lines with repression of TORC components is an increase in starch content. By combining molecular and chemical genetics approaches, biochemical and physiological assays, and omics technologies, we showed that down-regulation of TORC leads to accumulation of starch in the light, which is independent of its synthesis mediated by ADP glucose pyrophosphorylase. In contrast, the levels of maltose, the main starch breakdown product, were lower in plants exposed to short-term inhibition of TORC when compared to the control, suggesting an impaired starch breakdown in the light. Our results further indicate that TOR-mediated control of starch degradation seems to be particularly photoperiod-dependent, operating at specific time-points of the diel cycle. Unravelling the key regulatory modes in this process is of great significance for elucidating how carbon availability is translated into growth.

P9.15 THE IMPACT OF ELEVATED CARBON DIOXIDE ON FINE ROOT GROWTH IN A TEMPERATE OAK FOREST

WEDNESDAY 3 JULY, 2019 **15:15**

CLARE ZIEGLER (UNIVERSITY OF BIRMINGHAM, UNITED KINGDOM), ROSEMARY J DYSON (UNIVERSITY OF BIRMINGHAM, UNITED KINGDOM), IAIN G JOHNSTON (UNIVERSITY OF BIRMINGHAM, UNITED KINGDOM)

@ CXZ551@STUDENT.BHAM.AC.UK

As an important carbon sink, investigations into the effect of elevated carbon dioxide on temperate forests are essential to understanding the future impact of climate change. The Birmingham Institute of Forest Research (BIFoR) offers a glimpse

into the future, by raising the levels of CO_2 to that predicted for 2050 allowing for direct observation of the impacts on the ecosystem of a 150 year old oak forest. Fine roots represent a key element of forest ecosystems, estimated to contribute up to 33% of global production. Roots play an important role in carbon, water, and nutrient cycling but are often under investigated due to difficulties in data collection. Nondestructive monitoring of root growth is challenging, and data is affected by heterogeneity across sampling locations. This talk will detail the results of root growth research conducted using minirhizotrons and soil cores at the BIFoR research site, and the application of stochastic modelling to investigate differences in fine root populations grown under ambient and elevated CO_2.

P9.16 WHY WE DO NEED MORE EXPERIMENTAL PHENOLOGY

WEDNESDAY 3 JULY, 2019 **16:30**

ISABELLE CHUINE (CNRS, FRANCE)

@ ISABELLE.CHUINE@CEFE.CNRS.FR

The phenology of plants is a key regulator of agro-ecosystem processes and biosphere feedbacks to the climate system. Phenology process-based models are classically used in ecology and agronomy to project future phenological changes. They are integrated into more complex plant models used to predict species distribution range shifts and agronomic yields, and into terrestrial biosphere models. Although they describe known or suspected cause-effect relationships between physiological processes and some driving factors in the plants' environment, their ability to provide accurate projections in future climatic conditions has been recently questioned. These models are still very simple compared to the actual complexity of the regulation of cell activity by environmental factors. However, their robustness could be significantly improved if data on the timing of bud endodormancy (dormancy triggered by endogenous factors) release were available. Indeed, they are, most of the time, parameterized using inverse modelling technics with data on bud break date only, which are not sufficient to estimate the parameters that determine the dynamics of endodormancy accurately. Yet, the dynamics of endodormancy release, which is mainly affected by chilling temperature during winter, currently represents the major source of uncertainty for the future. I will present an overview of the ongoing questions in forest tree phenology and an attempt to solve some of them experimentally. My take home message will be that there is an urgent need for more experimental phenology and for high throughput technics able to produce data on the endodormancy dynamics in non-model species.

P9.17 PHYLOGEOGRAPHY AND NICHE-MODELLING RELATIVE TO PAST AND FUTURE CLIMATE SCENARIOS IN *LINUM BIENNE*, THE WILD RELATIVE OF CULTIVATED FLAX

WEDNESDAY 3 JULY, 2019 **17:00**

BEATRICE LANDONI (UNIVERSITY OF PORTSMOUTH, UNITED KINGDOM), JUAN VIRUEL (RBG KEW, UNITED KINGDOM), ROCIO PEREZ-BARRALES (UNIVERSITY OF PORTSMOUTH, UNITED KINGDOM)

@ UP869307@MYPORT.AC.UK

This study aims to describe the phylogenetic relationships within the species *Linum bienne* across its whole distribution and in relation to past and future climate. *L. bienne* is an herbaceous species present in the Near East, the Mediterranean basin, and the Atlantic coasts of Europe, which makes *L. bienne* ideal for studying plant adaptation to different climates. Surprisingly it is poorly described, especially considering its contribution in *L. usitatissimum* domestication, an oil and fibre crop. Unlike *L. bienne*, genomic data are available for *L. usitatissimum,* including its whole chloroplast genome. Relatively variable and small, cp-genomes increasingly appear in barcoding, biogeography, adaptation, and agronomic studies. To reach our aim we need to: 1) assemble and annotate the *L. bienne* cp-genome; 2) describe the species variation in relation to its current distribution; 3) explore the adaptive value of cp-genomes. 89 *L. bienne* accessions from 44 populations, five ruderal *L. usitatissimum* accessions, and one accession for *L. narbonense* (outgroup) were sequenced with Illumina HiSeq X (150×150bp). Raw reads were quality checked and mapped (Bowtie2) to the available *L. usitatissimum* reference (NC_036356.1), yielding an average 200× coverage. Following variant calling (bcftools, vcfR), we ran a discriminant analysis of principal components. The first two components (~80% total variance) align accessions along the west-east axis of *L. bienne* distribution, with *L. usitatissimum* at the east-end of the spectrum. Follow-up analyses include phylogenetic reconstruction using maximum likelihood and niche modelling using the WorldClim datasets.

P9.18 THE INTERDEPENDENT REGULATION OF PHOTOSYNTHESIS AND THE CIRCADIAN CLOCK IN WHEAT

WEDNESDAY 3 JULY, 2019 **17:15**

GARETH STEED (UNIVERSITY OF CAMBRIDGE, UNITED KINGDOM), LAURA TAYLOR (UNIVERSITY OF CAMBRIDGE, UNITED KINGDOM), MATTHEW HANNAH (BASF AGRICULTURAL SOLUTIONS, BELGIUM), ALEX AR WEBB (UNIVERSITY OF CAMBRIDGE, UNITED KINGDOM)

@ GS532@CAM.AC.UK

The circadian clock is an endogenous timing mechanism that allows organisms to coordinate physical and behavioural processes with the natural light dark cycle. Synchronisation between the circadian clock and environment in *Arabidopsis thaliana* can increase carbon assimilation (Dodd *et al.*, 2005) and therefore has the potential to contribute towards yield increases which are desperately needed to fill the predicted yield gap (Hawkesford *et al.*, 2013). I am investigating the mechanism and extent to which the circadian clock and photosynthesis regulate each other in wheat. Despite the central importance of the circadian clock relatively little is known of its genetic composition within wheat. Several wheat orthologues of *Arabidopsis thaliana* clock genes have been identified which affect flowering time. The wheat orthologue of *ELF3* underlies the *Eps-A*^{m}*1* locus in *Triticum monococcum* (Alvarez *et al*., 2016) and an orthologue of *LUX ARRYTHMO/PHYTOCLOCK 1* (*LUX*) underlies the *Eps-3A*^{m} locus in *T. monococcum* which leads to a distorted circadian clock (Gawronski *et al*., 2014). We have developed lines from the *T. turgidum* "Kronos" TILLING population that carry mutations in circadian clock genes. To non-invasively measure circadian rhythms I have optimised chlorophyll *a* fluorescence imaging and developed a novel, low-cost, leaf temperature measuring tool. I have used RT-qPCR to determine the effect of mutations on gene expression and investigated the impact that the major product of photosynthesis, sucrose, has on the wheat circadian clock. I have recently phenotyped yield traits to understand whether mutations of the wheat circadian clock could be agronomically useful.

P9.19 FISH IN A BIOGEOCHEMICAL BARREL: TAKING AIM AT THE EVOLUTIONARY CONSEQUENCES OF NUTRIENT CO-LIMITATION IN FRESHWATER

WEDNESDAY 3 JULY, 2019 **POSTER SESSION**

IAIN D C HILL (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), SCOTT D YOUNG (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), ANDREW D C MACCOLL (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM)

@ IAIN.HILL@NOTTINGHAM.AC.UK

How does the chemistry of the abiotic environment affect biotic evolution? Organisms require approximately 25 elements to construct themselves, and the occurrence of these varies spatiotemporally in the environment, yet we know almost nothing about the elemental composition of animals beyond that of the commonest elements (C, N, P, K). The potential consequences of elemental variation could have great significance for organismal adaptation and interactions with the environment. The adaptive radiation of three-spined sticklebacks inhabiting lochs on the island of North Uist, Scotland provides an ideal study system to explore the effects of elemental variation due to the differences in chemical composition of the various water bodies on the island which were formed, inhabited and isolated as the last ice age receded. To examine this, we have taken samples of fish and recorded environmental variables from individual lochs and analysed these through inductively coupled plasma mass spectrometry. We use these results to relate the elemental composition of the fish to the chemical composition of the study sites, revealing site specific variations in stoichiometry that are likely the result of a combination of abiotic, dietary, plastic and evolutionary differences. We will investigate these varying causes using subsequent common garden experiments. Anthropogenic changes to the environment manifest not only in the well documented effects on global climate, but also the chemical composition of most factors associated with the modern world. Increasing our understanding about these factors, will arm us to mitigate potentially detrimental shifts in environmental conditions.