

**P1 REDOX REGULATION IN CHLOROPLASTS**

**ORGANISED BY: ANGEL MERIDA (CSIC SPAIN), MARTAM SAWHRY (CSIC SPAIN) AND ANTONIO SERRATO (CSIC SPAIN)**

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

**MÓNICA BALSERA (INSTITUTO DE RECURSOS NATURALES Y AGRIBIOLOGÍA DE SALAMANCA)**

During evolution, oxido-photosynthetic organisms have developed sophisticated networks of redox signals and we propose that regulatory cell processes in response to both light and oxygen. Because of their unique physico-chemical properties, reversible chemical modification of cysteines (CySH) would 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 functions in chloroplasts, such as those involved in photoprotection (e.g., CPR) and photosynthetic electron transport (e.g., TRX), have acquired roles as redox sensors. Recent advances in understanding these processes and the redox regulation of chloroplasts have allowed cells to sense environmental changes and trigger adaptive response. These redox sensors are mainly operated by redox post-translational modifications, such as dithiol and disulfide formation, glutathionylation or nitrosylation, which play a major role at the interface between the environment and the functional proteins. Using qualitative and quantitative 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.

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

**STÉPHANE LEMAIRE (CNRS, SORBONNE UNIVERSITÉ, FRANCE)**

Stephane.Lemaire@ibpc.fr

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

**MÓNICA BALSERA (CSIC, SPAIN)**

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 redox sensors are mainly operated by redox post-translational modifications, such as dithiol and disulfide formation, glutathionylation or nitrosylation, which play a major role at the interface between the environment and the functional proteins. Using qualitative and quantitative 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.

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

**MONICA.BALSERASCIC.ES**

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

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

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

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

**AISTE IVANUSAUSKAITĖ (UNIVERSITY OF TURKU, FINLAND), MENNA M KOSKA (UNIVERSITY OF TURKU, FINLAND), ANNAKA BRÖLJE (UNIVERSITY OF MÜNSTER, GERMANY), MAGDA GRABZITNIIWICZ (UNIVERSITY OF TURKU, FINLAND), INES LASOSKAT (UNIVERSITY OF MÜNSTER, GERMANY), TRINE V DENN (HEIDELBERG UNIVERSITY, GERMANY), JULIA SINDLING (UNIVERSITY OF TÖRINGEN, GERMANY), DITK SCHWARZER (UNIVERSITY OF TÖRINGEN, GERMANY), MARKUS KURZ (HEIDELBERG UNIVERSITY, GERMANY), ESA TYYSTÄRKI (UNIVERSITY OF TURKU, FINLAND), IRIS FINKEIMSEE (UNIVERSITY OF MÜNSTER, GERMANY), PAULA MULO (UNIVERSITY OF TURKU, FINLAND)**

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 associates with PSI, thus directing more excitation energy to PSI, while the dephosphorylated form of L-LHCII is associated with PSI and LHCII. Finally, we showed that NSI is a novel player required for the dynamic adaptation of plants to changing light conditions.

**AISTIVANTU@FI**

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**P1.5 REDOX CONTROL OF CHLOROPHYLL BIOSYNTHESIS**

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

**BÉRARDIN GRÖMP (HUMBOLDT-UNIVERSITÄT ZU BERLIN, GERMANY), DANIEL WITTMANN WITTMANN (HUMBOLDT-UNIVERSITÄT ZU BERLIN, GERMANY), MEHA SINHA (HUMBOLDT-UNIVERSITÄT ZU BERLIN, GERMANY), ZHONG HOU (HUMBOLDT-UNIVERSITÄT ZU BERLIN, GERMANY)**

Plants effectively coordinate the photosynthesis dependent production of energy and reducing equivalents with the activity of metabolic pathways. At 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 modifications of thiols groups of contributing enzymes. Thus, this posttranslational control mechanism balances chlorophyll biosynthesis in response to environmental cues and prevents accumulation of photosynthetic tetrapyrole 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 regulatory NAPDH-dependent thiolredoxin reductase C (NTRC) and thiolredoxin (TRX) and explored the coordinated roles of TRX as a type II and type I 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 (FLUORESCENT) is based on thiol-disulfide exchange reactions.

**BÉRARDIN.GROM@H-GERMANY.DE**
**P1.8 A DEFECTIVE REDOX SIGNALLING COMING FROM TYPE-M THIOREDOKINS PROVOKES PLEIOTROPIC CHANGES IN ARABIDOPSIS THALIANA MUTANTS**

**TUESDAY 2 JULY, 2019**

**ANTONIO J. SERRATO (SPANISH NATIONAL RESEARCH COUNCIL (CSIC), SPAIN), JOSÉ A. ROJAS-GONZÁLEZ (SPANISH NATIONAL RESEARCH COUNCIL (CSIC), SPAIN), TAPARA ROLINA (SPANISH NATIONAL RESEARCH COUNCIL (CSIC), SPAIN), SABANAS BRAS (SPANISH NATIONAL RESEARCH COUNCIL (CSIC), SPAIN), DIEGO TORRES (SPANISH NATIONAL RESEARCH COUNCIL (CSIC), SPAIN), ANÍBAL MÉRIDA (SPANISH NATIONAL RESEARCH COUNCIL (CSIC), SPAIN), MARILIA SAAHRAV (SPANISH NATIONAL RESEARCH COUNCIL (CSIC), SPAIN)**

Thioredoxins (TRXs) are small redox proteins with a conserved active site containing two Cys and a conserved tertiary structure. TRXs catalyse the reduction of sulphide 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 may be because of this complexity that chloroplast TRXs are highly diversified, finding several types: TRX(F)/G, m(4), x(1), y(2) and z(1), with several isoforms in Arabidopsis thaliana (numbers in brackets). The expression of the diversity of the redox-signalling network occurring in chloroplasts. As most of the chloroplast proteins are nuclear encoded, retrograde signalling only occurs in the nucleus from reductant components to any homostat. Three out of the four TRXs isoforms, namely TRXm(1), m(2) and m(4), are the most abundant TRXs in photosynthetic tissues and have similar co-expression patterns. Our work with Arabidopsis single, double, and triple mutants expressing sub-optimal levels of TRXs has evidenced pleiotropic changes (NPD). Mutant lines are affected negatively in (i) the biomass yield, (ii) the activation degree of enzymes of the Calvin-Benson cycle and (iii) protective photosynthetic parameters as the non-photochemical quenching (FNP). Additionally, some moderate mutations in the plastid seem to modulate mechanisms, probably via retrograde signalling, leading to a remodeling of the thylakoid structure as consequence of a defective redox signalling coming from TRXm.

**P1.9 CHLOROPLAST SIGNALS REGULATE STOMATAL DEVELOPMENT**

**TUESDAY 2 JULY, 2019**

**STUART A. CASSON (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), NICKOLAS ZOULAS (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), JAMES ROOME (SALINBURY’S LAB CAMBRIDGE, UNITED KINGDOM)**

The development of stomata, the pores in the leaf epidermis, is known to be positively regulated by light and has been demonstrated that photoresponsive regulators of this process. Our data show that light can also regulate stomatal development independent of photoceptors and carbon assimilates in seedlings. A plastid signalling pathway has been hypothesized to inhibit photomorphogenic electron transport demonstrated that the redox status of the plastid 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 via MAP kinases signaling to negatively regulate key factors required for stomatal development, while reduction of the PQ pool acts via an alternative pathway. Light is not only signifying to regulate the redox status of the PQ pool and the expression of a potential mechanism through which multiple environmental signals can regulate stomatal development.

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

**THURSDAY 4 JULY, 2019**

**NURHAYATI RAZAK (UNIVERSITY OF LEEDS, UNITED KINGDOM), CHRISTINE FÖYER (UNIVERSITY OF LEEDS, UNITED KINGDOM), BARBARA KAPINSKA (UNIVERSITY OF LEEDS, UNITED KINGDOM)**

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 at the nuclear envelope and controls the chloroplast nucleoid, has important but poorly characterised roles in this process. We therefore investigated the functions of WHIRLY1 in the 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 seedling relative to the wild type. At earing stages, the WHIRLY1-deficient seedlings had significantly lower levels of chlorophyll than the wild type. Chlorophyll fluorescence quenching analysis revealed a failure in the dissipation of excess energy 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 chloroplast transcripts and proteins encoded by the plastome were significantly lower in the wild type than the WHIRLY1-deficient seedlings, with the effect that the WHIRLY1-deficient leaves exhibited more effective photosynthesis and had a higher chlorophyll content in the WHIRLY1-deficient leaves. The W1-1 and W1-7 leaves showed a double the amount of plastid DNA (pDNA) than the wild type, both at the early stages of development (7 days) and in green (3-week-old) leaves. The WHIRLY1-deficient
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)

As sessile organisms, plants need to adapt and coordinate their intracellular developmental programmes with environmental signals such as light, CO2, 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 plastocyanin, with the photosynthetic他在hibitor DCMU resulted in a suppression of the stomatal development pathway. Our results indicate that the redox status of the plastocyanin 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)

Chloroplast is a very important organelle of a plant cell, which lives with the photosynthetic inhibitors DCMU as a 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 oxidizing biomolecules, which then transmits 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 one of the promising ways.
our soil microbiome is required to equilibrate these interactions and prevent host dysbiosis.

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

**THURSDAY 4 JULY, 2019  |  10:40**

**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 CASTRELLÓ (THE UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), JEFF DANIEL (THE UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL, UNITED STATES)**

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 anaerobic plant-microbiome co-culture to unravel novel community-host and microbe-microbe interactions. A rhizobial skiriana 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 and 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.

**P2.7 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 VITEVICIUS (VYTAINAS MAGNUS UNIVERSITY, LITHUANIA), GABRIELE SURBLYTE (KAUNAS UNIVERSITY OF TECHNOLOGY, LITHUANIA), SIGUTE KUUSIENE (LITHUANIAN RESEARCH CENTRE FOR AGRICULTURE AND FORESTRY INSTITUTE OF FORESTRY, LITHUANIA)**

The studied bacterium was isolated from the in vitro culture of hybrid aspen (Populus tremula×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) genotype and apple (Malus domestica) seedlings. The influence of Paenibacillus sp. on root growth and shoot biomass was determined. The obtained results point to the Paenibacillus sp. bacterium from hybrid aspen shoot cultures as a potential root development regulator in different plant species.
2.8 M-TROPHS FOR SUSTAINABLE AGRICULTURE

THURSDAY 4 JULY, 2019

NATALIE K BREAKFIELD (NEWLEAF SYMBIOTICS, UNITED STATES)

NBREAKFIELD@NEWLEAFSYMBIOTICS.COM

2.9 RHIZOSHEATH FORMATION IN PEARL MILLET: PHYSIOLOGICAL BASES AND GENETIC CONTROL

FRIDAY 5 JULY, 2019

LAURENT LAPLAZE (LAURENT LAPLAZE, FRANCE), MAMADOU S NDouro (INSTITUT DE RECHERCHE POUR LE DéVELOPPEMENT, FRANCE), ABDEL NDOUZ (INSTITUT DE RECHERCHE POUR LE DéVELOPPEMENT, FRANCE), ALEXANDRE GONZALEZ (INSTITUT DE RECHERCHE POUR LE DéVELOPPEMENT, FRANCE), CÉCILE DEBAROZ (INSTITUT DE RECHERCHE POUR LE DéVELOPPEMENT, FRANCE), NAOMI NOIR (INSTITUT DE RECHERCHE POUR LE DéVELOPPEMENT, FRANCE), LAURENT LAPLAZE (3RD FRANCE), THIERRY HEUILL (CNRS, FRANCE), LAURENT COURNAC (2RD FRANCE)

SITNDQURAHAY.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 characterised by low-rainfall and poor soils. We are exploring mutant 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 rhizosphere is a region of soil near roots where conditions prevent other plant roots from growing. It has been shown that pearl millet rhizosphere has a high root density and root length. The beneficial nature of M-trophs allows NewLeaf to maintain root architectures, root hairs and mycorrhizal traits. Moreover, we performed genetic association analysis using a panel of inbred lines with 392,455 SNPs identified using Whole-genome sequencing (EBG). Correcting for genetic relatedness, GWAS identified five QTLs for rhizosphere formation that were mapped to the pearl millet genome. Variations of allele frequency between the targeted regions in inbred 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 RNA-seq and 1278 differently expressed genes. Candidate genes were identified by combining GWAS and RNAseq results and are further analyzed.

2.10 MICROBIAL DIVERSITY AND ACTIVITY IN RHIZOSHEATH OF DIFFERENT PEARL MILLET LINES UNDER GREENHOUSE AND FIELD CONDITIONS

FRIDAY 5 JULY, 2019

PAPA MAMADOU SIDDOU NDORO (3RD FRANCE), CHEIKH M Barry (UBAC, SENEGAL), MOHAMED BARAKAT (CEA, FRANCE), PHILIPPE DREFFET (CEA, FRANCE), WAFAC ACHOUAK (FRANCE), LAURENT LAPLAZE (3RD FRANCE), THIERRY HEUILL (CNRS, FRANCE), LAURENT COURNAC (2RD FRANCE)

SITNDQURAHAY.FR

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.
Plant roots are colonized by diverse microbes that affect plant health either in beneficial or harmful ways. These include beneficial rhizobacteria 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 is a fungal pathogen, that causes vascular wilt disease in a broad range of crops including both monocots and dicots. The fungus grows throughout the vasculature. The chemical control methods are difficult to apply, because of the low visibility of Fusarium 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 to develop a strategy for controlling Fusarium infection. Soils with diverse characteristics associated with tomato fields in Southern Spain, were used in culture independent and independent approaches to monitor the changing microbiome under Fusarium infection. Further, the isolated bacterial communities are classified based on compartments such as soil, rhizosphere, root, endophytic root and xylem. The final goal of this study is to understand the interplay and the modulation of microbiome assembly during pathogen-plant interaction.
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 fungi (AMF) inoculation (Glomus mossaeae, 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 have higher mycorrhizal intensity under well-watered (50-90% of mycorrhizal spores) than under water deficit conditions (<50%). Mycorrhiza significantly improve drought tolerance of baobab seedlings, especially those from the Sahelian region.

**P3.1 ADVANCES IN STUDYING ALTERNATIVE SPlicing IN PLANTS**

**ORGANISED BY:** MARÌÈME NIANG (ISRACERAAS, SENEGAL), PATRICK NIANG (HUMER UNIVERSITY, BELGIUM), FATIMA NDIAYE (UCAD, SENEGAL), MACOLMBA DIDUF (ISRACERAAS, SENEGAL), TAHIR DIOUF (UCAD, SENEGAL), AMADOU BA (ZORCIM, SENEGAL), NDIAGA CISSE (ISRACERAAS, SENEGAL)

**Wednesday 3 July, 2019**

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 nonsense-mediated decay pathways 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 SPLICOSOME FOR RESISTANCE TO SPlicing INHIBITORS**

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

**Tuesday 2 July, 2019**

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 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
LU ZHONG ZHENG (NAJING AGRICULTURAL UNIVERSITY, CHINA)

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 trancriptome 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 15,281 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 (DASG) is small, a molecular understanding of the plant’s response to mineral nutrient deficiency is limited by analyzing DEGs alone. The targets of AS are highly specific to transcription factors. To verify the function of AS in mineral nutrition, we characterized mutants for genes encoding Sre/ASR proteins that function in AS. We identified several SR proteins as novel regulators of Zn, Mn, and P nutrition and showed that SR protein-encoding genes are regulated on both the transcriptional and post-transcriptional levels and include, in particular, alternative splicing (AS). RNA-seq analysis revealed that the AS events map to several hundred genes whose expression is regulated by AS, some of which are involved in metal uptake and transport. The results indicate that AS plays a critical role in maintaining mineral 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
ANREEDY REDDY (COLORADO STATE UNIVERSITY, UNITED STATES)

ANREEDY.REDDY@COLORADOSTATE.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 analyze alternative splicing, splicing isoforms, and other post-transcriptional events and in studying the relationship between chromatin architecture and alternative splicing in plants.

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

TUESDAY 2 JULY, 2019  |  16:35
JOHN S BROWN (UNIVERSITY OF DUNDEE, UNITED KINGDOM), NIKOLAOS K ZARCOKAES (UNIVERSITY OF DUNDEE, UNITED KINGDOM), CRISTIANO P O CALISTO (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 O NJMPO (UNIVERSITY OF GLASGOW, UNITED KINGDOM)

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

TUESDAY 2 JULY, 2019  |  16:55
ALLAN B JAMES (UNIVERSITY OF GLASGOW, UNITED KINGDOM), HUGH O NJMPO (UNIVERSITY OF GLASGOW, UNITED KINGDOM)

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

TUESDAY 2 JULY, 2019  |  17:15
CRIS 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 HILLIE (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), KIMBRIL OLIVE (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), CLAUS-ODERAYER (BIOMATHMATICS AND STATISTICS SCOTLAND, UNITED KINGDOM), JOHN FULLER (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), JENNY PORRIS (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), GORDON STEPHEN (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), JOHN W BROWN (UNIVERSITY OF DUNDEE, UNITED KINGDOM), RONNIE WALKING (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), KARL CHRISTIANE ESTELA DOMINGO TORRES (THE JAMES HUTTON INSTITUTE, UNITED KINGDOM), NIKOLETA A TZIOUTZIOU (UNIVERSITY OF DUNDEE, UNITED KINGDOM), ALLAN B JAMES (UNIVERSITY OF GLASGOW, UNITED KINGDOM), CLAUS-DIETER KRUMME (BIOMATHMATICS AND STATISTICS SCOTLAND, UNITED KINGDOM)

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

TUESDAY 2 JULY, 2019  |  17:35
JUAN C ENTZINE (THE JAMES HUTTON INSTITUTE AND UNIVERSITY OF DUNDEE, UNITED KINGDOM), JOHN W 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), CRISTIANO P O CALISTO (UNIVERSITY OF DUNDEE, UNITED KINGDOM), WENBIN GUO (UNIVERSITY OF DUNDEE, UNITED KINGDOM)

E. ENTZENHOUDEE.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 as temperature changes, and post-transcriptional levels and includes, in particular, alternative splicing (AS). RNA-seq analysis (RNA-seq) is used to quantify genome-wide transcriptional and AS changes and is considered a powerful tool for determining the accuracy of differential expression (DE) and differential alternative splicing (DAS) analysis. In this study, we developed the Rice Transcriptome Database (RTD). Based on the work done for the development of a high-quality annotation for Arabidopsis (ARTDZhang et al. 2017), we developed a general computational pipeline to generate a high-quality transcriptome annotation for Arabidopsis (ARTDS). We have developed a pipeline to generate a high-quality transcriptome annotation for barley (P3.5) and potato (P3.8).
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 two subfamilies, the SR and the nonspecific SR (NSS) proteins.

**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)**

Adenovirus 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-0ecotype as a reference, has identified variants with reduced and increased sensitivity to ABA at different developmental stages. In fact, all accessions show a variable degree of sensitivity 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, ko-0 and 244 variant grown under control and ABA conditions to identify the gene expression and alternative splicing changes correlating with opposing ABA responses. 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 previously observed by the discovery of an animal adaptor protein that read srp protein genes. Therefore, we will use these mutants to search for chromatin-regulated alternative splicing events governing plant stress tolerance.
**P3.15 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), ANGELA WAGNER (CENTER FOR PLANT MOLECULAR BIOLOGY (ZMP), UNIVERSITY OF TUBINGEN, GERMANY), ANDREAS WACKER (INSTITUTE FOR MOLECULAR PHYSIOLOGY, UNIVERSITY OF MAINZ, GERMANY)**

Alternative splicing (AS) is a way of gene regulation widely used in euaryotic cells. It results from the exon and intron pairs 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 APTB1 and APTB2 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 APTB1/2 in selected targets and demonstrated their importance for correct AS in vitro and in vivo. We further revealed that APTB1/2 exhibit tissue-specific and splice-site RNA-binding properties, including the PTB2 binding itself. This regulation depends on PTB binding motifs and is tightly patterned, with low activity in in vitro and high activity in vivo. The tissue-specific activity pattern 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 APTB1/2-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.

**P3.14 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), ANGELA WAGNER (CENTER FOR PLANT MOLECULAR BIOLOGY (ZMP), UNIVERSITY OF TUBINGEN, GERMANY), ANDREAS WACKER (INSTITUTE FOR MOLECULAR PHYSIOLOGY, UNIVERSITY OF MAINZ, GERMANY)**

Alternative splicing (AS) is a way of gene regulation widely used in euaryotic cells. It results from the exon and intron pairs 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 APTB1 and APTB2 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 APTB1/2 in selected targets and demonstrated their importance for correct AS in vitro and in vivo. We further revealed that APTB1/2 exhibit tissue-specific and splice-site RNA-binding properties, including the PTB2 binding itself. This regulation depends on PTB binding motifs and is tightly patterned, with low activity in in vitro and high activity in vivo. The tissue-specific activity pattern 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 APTB1/2-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.

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

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

**DORA SZEKONYI (INSTITUTO GULBENKIAN DE CIENCIA, PORTUGAL), RAQUEL F CARVALHO (INSTITUTO GULBENKIAN DE CIENCIA, PORTUGAL), PAULA DUQUE (INSTITUTO GULBENKIAN DE CIENCIA, PORTUGAL)**

OSZKONDYG@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 SR45 positively regulates the SnRK1 protein – an energy-sensing kinase coordinating sugar and stress responses – which are suppressed by a proteasome inhibitor indicating that SR45 is part of SnRK1 stability network. However, gel-shift assays indicate that SR45 is unable to bind directly to the SR45 target SR34a, and transient expression of SR45 in transgenic Arabidopsis leaves fails to alter the expression of SR34a. Moreover, our in vitro results revealed that loss of SR45 function causes hypoexpression of 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 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 CIENCIA, PORTUGAL)**

DUDUEDIPC@GULBENKIAN.PT

Alternative splicing is a highly prevalent post-transcriptional gene expression regulation mechanism in eukaryotic genomes, whose functional significance remains poorly understood in plant systems. A potential enhancer of the genome’s regulatory capacity is the alternative splicing of plant genomes – characterized by a large number of alternative splicing events. In total, our work with the SR45 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 signalling 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 TO IMPROVE ECOLOGICAL ADAPTATION**

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

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

TLALOUM@GULBENKIAN.PT

Plant stressors 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 central roles 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 SR protein – encoding a serine/arginine-rich (SR) protein belonging to 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, sr34d-1, displays marked hyperresponsiveness to exogenous ABA application, as well as increased cold sensitivity and drought stress during seed germination and also the transition from heterotrophic to autotrophic growth (cotyledon greening). Accordingly, the expression of several ABA marker genes is reduced in sr34d-1. To gain mechanistic insight into the role of this splice factor, we will be identifying splicing targets of SR34a, the ABA-controlled alternative splicing events in its regulation and the role of these splicing switches in plant stress responses and ecological adaptation.
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 CIENCIA, PORTUGAL), PAULA DUQUE (INSTITUTO GULBENKIAN DE CIENCIA, PORTUGAL)

The Major Facilitator Superfamily (MFS) represents the second largest family of transporters on earth and one of two groups of transporters that move ions and solutes across cell membranes. As with other gene families, the MFS is surprisingly expanded in plant life, the genome of the model plant Arabidopsis thaliana encodes over 200 MFS genes. Most of the members are defective not only for the major functions of the plant, i.e., nutrient uptake, but also for other biological roles such as splicing, transcription, translation and other. Here, we present our recent findings of the responses to environmental factors, such as temperature and salinity. In this talk, based on our recent findings of the Arabidopsis transport gene AtMDF1, we will discuss the possible roles of alternative splicing in the regulation of both transport activity and other biological roles. We will compare the Knockout and Knockdown and show their effects on the plant growth and development. We have also shown that Arabidopsis MFS transporters have been studied both in functional defects as well as in the transport activity.

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), WEE REN SHEN (DURHAM UNIVERSITY, UNITED KINGDOM), DAVID DOLAN (DURHAM UNIVERSITY, UNITED KINGDOM), CRISTIANE CALIXTO (UNIVERSITY OF SASKATOON, CANADA), MEDHAVI KARDAK (DURHAM UNIVERSITY, UNITED KINGDOM), SIMA MOZAFAR (MAX PLANCK INSTITUTE OF BIOPHYSICAL CHEMISTRY, GERMANY)

Around 61% of Arabidopsis intron-containing genes undergo alternative splicing andsplice invariants have been reported in 30% of all Arabidopsis genes full-length protein. A number of alternative splice 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 function in the well-characterised Arabidopsis splicing factors such as MDF is homologous to human SART1 and our modelling predicts it to be specific to the root meristem. MDF is required for the proper development of Arabidopsis roots. 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 signalling. Mutations in MDF result in a much smaller root system. MDF interacts with Prp6 and Prp8 and in the human U4/U6 snRNP during B complex formation and we are investigating the role of these factors in the development of the Arabidopsis root meristem. MDF is homologous to human SART1 and our modelling predicts it to have 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 HCR-RT-PCR analysis show that in mdf-1 key components of the splicing cycle are alternatively spliced along with a subset of SGE genes reported to be associated with developmental defects. We have shown that loss of MDF affects splicing of the abiotic stress response through the isoform switching of two splice variants. We will present our model of how MDF regulates splicing 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

HELEN L THOMPSON (DURHAM UNIVERSITY, UNITED KINGDOM), JENNIFER TOPPING (DURHAM UNIVERSITY, UNITED KINGDOM), SHASHI BEDEL (DURHAM UNIVERSITY, UNITED KINGDOM), KEITH LINDSEY (DURHAM UNIVERSITY, UNITED KINGDOM)

Around 61% of Arabidopsis intron-containing genes undergo alternative splicing and splice invariants have been reported in 30% of all Arabidopsis genes. We will present our model of how MDF regulates splicing balance between stem cell identity, meristem activity and differentiation through alternative splicing of other splicing factors and meristem-specific genes.

P3.24 EXPLORING FUNCTIONs OF NONSENSE-MEDIATED RNA DECAY IN PLANT RNA QUALITY CONTROL AND BEYOND

WEDNESDAY 3 JULY, 2019  16:30

KAREL RHAMA (CEITEC MASARYK UNIVERSITY, CZECH REPUBLIC), VIVEK K RAXWAL (CEITEC MASARYK UNIVERSITY, CZECH REPUBLIC), JACO CINTJE (UNIVERSITY OF DURBAN WESTERN CAPE, SOUTH AFRICA), MIRTE ERNST (MAX PLANCK INSTITUTE OF BIOCHEMISTRY ETH SWITZERLAND), WENBIN GU (UNIVERSITY OF DURBAN WESTERN CAPE, SOUTH AFRICA), CRADIM SIMPSON (UNIVERSITY OF DURBAN WESTERN CAPE, SOUTH AFRICA), JOHN BROWN (UNIVERSITY OF DURBAN WESTERN CAPE, SOUTH AFRICA)

Nonsense-mediated RNA decay (NMD) is an evolutionary conserved RNA quality 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 crucial for bacterial infection and this mechanism contributes to bolstering plant disease. We performed in-depth comparative analysis of plants lacking the key proteins involved in the NMD steps. 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 transcription. UPF1 inactivation had much greater effect on accumulation of aberrant transcripts and transcription homeostasis than SMG7, indicating existence of yet unknown branch of NMD in plants that is parallel to SMG7/5/6 pathway. Transcriptome analysis in upf1 plants revealed novel alternatively spliced isoforms never detected before under inhibiting impact of NMD on transcriptome maintenance. To examine the impact of UPF1 on translation, we isolated polyribosomes and analysed the proportion of fractions of polysomes in upf1 mutants. We observed a global shift of mRNAs from polysomes to monosomes. Interestingly, NMD targets also alternative splicing of two transcripts. As with other genes, a large number of mRNAs turned monosomal in upf1 background as well.

P3.25 TWO UPSTREAM ORFs OF AN ARABIDOPSIS ZINC TRANSPORTER ACT AS A FAIL-SAFE MECHANISM TO RE压制 transcript

WEDNESDAY 3 JULY, 2019  17:05

ESTHER NOVO-UZAL (INSTITUTO GULBENKIAN DE CIENCIA, PORTUGAL), DOÑA ZAMBRANO (INSTITUTO GULBENKIAN DE CIENCIA, PORTUGAL), PAULA DUQUE (INSTITUTO GULBENKIAN DE CIENCIA, PORTUGAL)

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 translational efficiency of the main ORF (mORF), usually by reducing the efficiency of the translation initiation complex formation. This by itself reduces translational efficiency. Around 20-50% of eukaryotic genes contain uORFs, and in the model plant Arabidopsis thaliana these genes have been shown to be involved in various developmental processes. Nevertheless, very few uORFs in plant genes have been examined for their functional significance. We identified three uORFs, named uORF1, uORF2 and uORF5, in the arabidopsis ZIF2 (Zinc-Induced Factor 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 helicase reporter gene, demonstrating the activity of uORFs in the context of inhibiting ORF translation. Disruption of each individual ORF revealed that ZIF2 is the main player in the observed transcriptional repression, whereas URF2 does not affect transcription. Our results indicate that uORFs can be critical not only in the absence of uORF2. We thus postulate that the ZIF2 uORFs act as a fail-safe mechanism to inhibit translation, to our knowledge the first observation of such a role 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 TARDEU (INRA MONTPELLIER, FRANCE), BOEIS PARENT (INRA MONTPELLIER, FRANCE), LORENC C BOSQUET (INRA MONTPELLIER, FRANCE), SANTIAGO A PRADO (INRA MONTPELLIER, FRANCE), CLAUDE WELCKER (INRA MONTPELLIER, FRANCE)

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 wherever 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/model of the behaviour of plants with contrasting abilities to synthesise abscisic acid and, secondly, via the genetic analysis of a multi-site field experiment that revealed that abscis acid controlling ABA synthesis has positive or negative effects on yield depending on environmental scenarios. Hence, designing plants with an optimum stomatal conductance is a probabilistic exercise that involves the most likely environmental scenarios in a given site, with current and future climates. Because it is not feasible to analyse gas exchanges of hundreds of genotypes across a great number of species, we propose to predict the stomatal conductance of the most important species by identifying targets for genetic manipulation to improve plant performance and yield. Intrinsic water use efficiency (WUE) is achieved by the trade-off between stomatal conductance and transpiration, which is an important physiological trait displaying complex diurnal kinetics and therefore the ratio of carbon gain to water loss through stomatal conductance (WUE). The control of stomatal conductance involves numerous processes, with a genetic variability at 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. 

**P4.2 NOVEL ASPECTS OF CARBON DIOXIDE DISSIPATION IN STOMATA**

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

DEIRDRE H MCLACHLAN (UNIVERSITY OF BRISTOL, UNITED KINGDOM), PENGY SUN (UNIVERSITY OF BRISTOL, UNITED KINGDOM), ALEXANDRA M HETHERINGTON (UNIVERSITY OF BRISTOL, UNITED KINGDOM)

**PZOMPLAB@STOL.AC.UK**

Stomata are pores on the surface of leaves that allow CO2 entry for photosynthesis and also contribute to the regulation of the transpiration stream. As water loss from transpiration can 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 CO2-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 CO2, ABA, and their interaction with the flg22 ABA pathways. This has allowed us to identify new components of the signalling pathways that lead to CO2-induced stomatal closure. More surprisingly, we have discovered that alternate CO2 signalling pathways are used depending on the plant growth conditions. This has revealed an extralayer of complexity to the mechanisms behind the integration of signals and their 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), JACQ SA PATHIRIKA (UNIVERSITY OF ESSEX, UNITED KINGDOM), SILVIERE VIATEL-CHABRAND (UNIVERSITY OF ESSEX, UNITED KINGDOM)

**TLVWGN@ESSEX.AC.UK**

Stomata control the uptake of CO2 for photosynthesis and at the same time water loss through transpiration, which is in nutrient uptake and evapotranspiration of the leaf. Stomata open in response to increasing light, however this response depends on the wavelength of light, and generally two different response have been identified. The first is the so-called ‘red’ light or mesophyll response, and occurs as light intensities and is linked directly to the rate of photosynthesis. The second is the so-called ‘blue’ light response, which occurs and is saturated at lower light levels to have low transpiration. This means that under red light or mesophyll response, stomata are more open than they need to be to achieve maximum CO2 uptake for photosynthesis, and therefore the rate of carbon gain to water loss through stomatal conductance (g.) known as intrinsic water use efficiency (WUE), is reduced. We have quantified the impact of blue light on assimilation rate (A) and WUE, in range of different species and have compared these responses to the effects of red light alone. We discuss the findings in the light of manipulating the blue light response for improving WUE in crops.

**P4.4 IMAGING WATER USE EFFICIENCY UNDER DYNAMIC ENVIRONMENTAL CONDITIONS**

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

SILVIERE VIATEL-CHABRAND (UNIVERSITY OF ESSEX, UNITED KINGDOM), MARTIN BATTLE (UNIVERSITY OF ESSEX, UNITED KINGDOM), TRACY LAWSON (UNIVERSITY OF ESSEX, UNITED KINGDOM)

**SIVPA@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), net CO2 assimilation rate (A) and growth are genetic traits and therefore the ratio of carbon gain to water loss through stomatal conductance (WUE) is achieved by the trade-off between stomatal conductance and transpiration, which is an important physiological trait displaying complex diurnal kinetics and therefore the ratio of carbon gain to water loss through stomatal conductance (WUE). The control of stomatal conductance involves numerous processes, with a genetic variability at 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. 

**P4.5 IONIC EFFECTS MAY ALTER THE CONSERVED STOMATAL DYNMICS WITHIN CURCIBITEAE**

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

TRI-WEI CHEN (INSTITUT FUR GARTENBAULICHE PRODUKTIONSSTESYSTEME, GERMANY), JENNIFER MEIER (INSTITUT FUR GARTENBAULICHE PRODUKTIONSSTESYSTEME, GERMANY)

**CHEN28021@UNI-HANOVER.DE**

Recent data showed significant variances in dynamics of stomatal conductance (g.) between and within plant genotypes and showed the correlations between the morphological traits, stomatal dynamics (SD) and whole-plant water use. Here we examined the diversity in SD and morphogenesis in 10 curcubitaceae lines of F1 cultivars representing the major phyllocladic clades in Curcubitaceae (five cultivars in Cucumis sativus, two cultivars in Cucurbita maxima and one cultivar in Lagenaria siceraria, Luffa cylindrica and Momordica charantia). SD in response to light-on and light-off (from 100 to 1,000 µmol photon/m2/s and vice versa) was characterised by the time constant (t) and by the achievable steady light environment (l.s) and the maximum rate of stomatal opening (S.0). Significant differences in the stomatal morphology, the studies species and cultivars are not different in their R and S.0, indicating conserved S.D in high-water-consuming curcubit crops. Interestingly, positive correlation was found between A and stomatal length. Using the curvilinear “Aramon” of Cucumis sativus, we further tested the ionic effects on the SD by applying seven different mixtures of 50 mM NaCl, NaHCO3, KCl and KNO3, after the developmental acclimation of the plants. These treatments allowed obtaining healthy leaves without differences in their stomatal morphology, but significantly diverse cation and anion concentrations in both species. The effects of ‘Na’ were opposite, highlighting the effects of cations on stomatal dynamics.

chlorophyll fluorescence imaging and thermography allowed rapid, non-contact measurement of a large number of plants, however their biological interpretation is more challenging. Deriving g_0 from the blue light response can be 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 WUE under a dynamic environment.
Seville 2019

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.

Stomata are pores on the surface of leaves which open and close in response to environmental stimuli. As the Mesolens also have fluorescence capability it is possible to monitor intracellular signalling dynamics during aperture changes by using fluorescent indicators. We have shown that in response to functional stimuli, there are quantitative differences in stomatal apertures in different leaf regions. In addition to this we have used the anabiotic calcium reporter line R-GECO1 in Turquoise 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 stomata in response to stimuli and how these signals are propagated through a leaf.

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P.14 ENGINEERING STOMATA TO REDUCE CROP WATER USE

**THURSDAY, JULY 4, 2019**

**JULIE GRAY (UNIVERSITY OF SHEFFIELD, UNITED KINGDOM)**

Stomata are pores that open to allow carbon dioxide to enter and close to reduce water loss. Understanding the signaling 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 cereals plants overexpressing epidermal patterning factors which suppress stomatal development, and gene edited plants to knockout an antagonging 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).

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

**THURSDAY, JULY 4, 2019**

**MICHAEL RAISSIGG (HEIDELBERG UNIVERSITY, GERMANY)**

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 – is key for improved stomatal development. 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 ortholog of the stomatal regulator AtMUTE, which defines GC precursor fate in Arabidopsis. This work suggests that enhancing AtMUTE expression in grasses aids in specifying lateral SCs appears linked to increased SC formation. We propose a model where increased AtMUTE expression leads to more SC formation. The consequences of this model will be presented.

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P.14 IDENTIFICATION AND FUNCTIONAL CHARACTERIZATION OF GENES IN THE GUARD CELL CO2 SIGNALING PATHWAY IN MAIZE

**THURSDAY, JULY 4, 2019**

**ANTHONY J. FUDGE (UNIVERSITY OF ILLINOIS, UNITED STATES), ROBERT J. WHEEY III (UNIVERSITY OF CONNECTICUT, UNITED STATES)**

The balance of CO2 uptake for photosynthesis and transpirational water loss is a dynamic process that can be manipulated to improve leaf design, improve water use and allow for development of drought tolerant plants. Our study describes the signaling pathway that controls the development of stomatal patterning and its acquisition of cell-to-cell mobility in grasses. The novel role of a transcription factor necessary and sufficient for SC formation is presented.

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P.15 LEAF STRUCTURAL, ANATOMICAL AND BIOCHEMICAL DETERMINANTS OF MESOPHYLL CONDUCTANCE IN C4 GRASSES

**THURSDAY, JULY 4, 2019**

**ASAPH COUSINS (WASHINGTON STATE UNIVERSITY, UNITED STATES), VARSHA S. PATHARE (WASHINGTON STATE UNIVERSITY, UNITED STATES), ANTHONY J. STUDER (UNIVERSITY OF ILLINOIS, UNITED STATES), TIM WERTIN (UNIVERSITY OF ILLINOIS, UNITED STATES)**

Mesophyll conductance ($g_m$) describes the movement of CO2 from substomatal cavities to the site of carbon fixation in mesophyll cells. Many genes in maize are involved in CO2 release from mesophyll cells and are involved in photosynthesis. One of these genes is AtMUTE (AtMUTE), which is a transcription factor that is necessary and sufficient for SC function. AtMUTE expression is required for SC formation.

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

**THURSDAY, JULY 4, 2019**

**C. CHATER (UNIVERSITY OF ILLINOIS, UNITED STATES), D. ROBLES (UNIVERSITY OF MEXICO), R. BRIANDA DE LA SANCHA PÉREZ (IBT UNAM, MEXICO)**

Legume crops are generally sensitive to water deficit and drought stress. Water use efficiency (WUE), the ratio of crop 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 in maize, and legume crops may benefit from this without a corresponding photosynthetic penalty. Rhizobial infection of legumes increases WUE, and legume crops may benefit from this without a corresponding photosynthetic penalty.
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 yield under water deficit and replete conditions. This approach could therefore play a central role in the sustainable intensification of global agriculture under climate change, requiring fewer water and fertilizer inputs. Loss of stomatal conductance is not inhibiting stomatal development, but this can also change rhizosphere development and root water dynamics. A rhizobial symbiosis is central to legume NUE and WUE, an understanding of the coordination between SD, $g_s$, and root traits including soil exploration, 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 Daori, Italy), Tadeja Savi (University of Trieste Department of Life Viticulture and Pomology, Department, Austria), Andrea Nardini (University of Trieste Department of Life Sciences, Italy), Francesco Loreto (National Research Council Biologia, Italy), Maria Centroti (National Research Council, Trees and Timber Institute, Italy)

CBRUNETT@UNI.VLTA.CNR.I

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 models to investigate how hormonal and hydraulic signals contribute to stomatal control (g_s), mesophyll ($\delta^{13}C$) and leaf hydraulic ($K_c$) conductance under well-watered (WW) and water-stressed conditions (WS); a possible role for ABA in modulating stomatal conductance and drought increase in water use efficiency. The effect of ABA 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.

P4.18 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)

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 CO2 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 CO2 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=16) using elevated CO2 plots (300ppm) and ambient control plots (300ppm) within the same tree species. 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 shown increased carbon assimilation, in these CO2 plots, in addition to a decrease of stomatal conductance and overall increase in water use efficiency. The effect of CO2 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 STOMATAL DELIVERY IN INTACT PLANTS

THURSDAY 4 JULY, 2019 15:57

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

THURSDAY 4 JULY, 2019 15:59

Ashley J Pridgdon (University of Bristol, United Kingdom), Alastair H Metheringham (University of Bristol, United Kingdom)

Ashley.pridgdon@bristol.ac.uk

Abscisic acid (ABA) is a hormone that has been extensively studied especially in the context of the plant drought response. Its known to affect various aspects of plant physiology, including the promotion of stomatal closure and 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 lack of ABA production or perception lead 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 16:03

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

A key goal for the improvement of chickpea is to increase water use efficiency (WUE). The use of carbon isotope discrimination ($\delta^{13}C$) for characterization of plant growth has been tested widely in attempts to investigate plant water usage. However, $\delta^{13}C$ estimated from chickpea has not related well to WUE in previous studies. We explore the influence of leaf acidification and CO2 assimilation 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 (g_s/A). To test this method on a larger scale, we used the most informative TE candidate (TET) and measure the $\delta^{13}C$ (leaf to leaf) and water usage 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 high TET.

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

THURSDAY 4 JULY, 2019 16:03

Millicent R Smith (CIRSA, India), Ruwak Barmark (CIRSA, India), Manesh Rohkwal (CIRSA, India), Jana Khovava (CIRSA, India), Alice Klar (CIRSA, India), R. Arvind L Kolar (IARI, India)

CROP IMPROVEMENT PROGRAMS?

P4.23 DESIGN CHICKPEA CROP IMPROVEMENT PROGRAMS?

THURSDAY 4 JULY, 2019 16:03

Millicent R Smith (CIRSA, India)

CROP IMPROVEMENT PROGRAMS?

P4.24 AN ANNUAL MEETING SEVILLE 2019 ANNUAL MEETING SEVILLE 2019

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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. Hexagonal wheat (Triticum aestivum) has fewer, larger stomata than those found on the leaves of its wild relatives (T. baeoticum, T. urartu and T. aestivum). Diplotelodes have the highest frequency of small stomata, whilst tetraploid lines have intermediate stomatal size and density. These differences in stomatal size and density are microscopic by diplotelodes compared to hexaploid lines with a higher stomatal conductance than their hexaploid counterparts, with tetraploid lines having middling conductance rates. Furthermore, using X-ray microtomography of 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 to visualise the wheat mesophyll can be reconstructed in 3D to cellular resolution using confocal imaging and processing using LithographX software. Using this technique, we have been able to investigate whether stomatal density changes observed during domestication are paralleled by alterations in mesophyll cells and size.

**ANNUAL MEETING SEVILLE 2019**

**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**

**MATTHEW WILSON (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)**

Stomatal conductance with crop growth and development dynamics in a manner that addresses the feedback effects across the scales of biological organisation. The model links photosynthesis and stomatal conductance via an equilibrium C/CO2 ratio, properly consistent with stomatal optimisation trade-offs. Under water non-limiting conditions, photosynthesis is the driver of stomatal conductance, whereas the stomatal conductance limits 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 long-term data to yield the heat and water balance from diverse field experiments. Consequences for yield were simulated for major crop species at different physiological states and 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 interdisciplinary research operating across spatial and temporal scales of biological organisation was highlighted as the need to enhance understanding and modelling of the photosynthesis-stomatal conductance link to better quantify the impacts of enhancing photosynthesis.

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

**THURSDAY 4 JULY, 2019**

**MICHAEL BLATT (UNIVERSITY OF GLASGOW, UNITED KINGDOM), MIAREKE JEZIK (UNIVERSITY OF GLASGOW, UNITED KINGDOM)**

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 acclimation 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 a part of the work we characterized changes in stomatal conductance and responses under a ‘real’ light environment, and investigated the impact on photosynthesis and water use efficiency. We demonstrate that acclimation of stomatal conductance (gs) is influenced by growth light modifying, stomatal kinetic at different times of the day, resulting in alterations in the light intensity and magnitude of the gs response over the diurnal period. Further quantified is the response of gs to different step changes in light intensity; with plants grown under low light exhibiting faster responses when subjected to increasing steps, whereas plants grown under high light are true at high light steps. This represents an interesting strategy, where plants acclimate by increasing faster to light levels that they experience, maximising net photosynthesis as a way of maximizing carbon uptake or the conservation of energy by limiting unnecessary stomatal movement. From these findings, we conclude that acclimation of gs to growth light could be an important strategy for maintaining carbon fixation, overall plant water status, and water use efficiency under dynamic light conditions.

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

**THURSDAY 4 JULY, 2019**

**JACK SA MATHEWS (UNIVERSITY OF ESSEX, UNITED KINGDOM), SILVIA VIVI CHARBAND (UNIVERSITY OF ESSEX, UNITED KINGDOM), TRACY LAWSON (UNIVERSITY OF ESSEX, UNITED KINGDOM)**

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**P4.29 NITROGEN ASSIMILATION AND ABBIOTIC STRESS TOLERANCE**

**WEDNESDAY 3 JULY, 2019**

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

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 link between plant nitrogen status and stress signalling. Nitrogen is an essential nutrient, yet optimal nitrogen use is often difficult due the form of nitrate and/or ammonium. Plant nitrogen status and abiotic stress responses are intrinsically linked; when plants experience salt or drought stress, a signalling pathway is initiated which results in stomatal closure, reduced stomatal water loss and a decreased nitrate uptake through the roots. This drop in nitrate uptake will...
Plant growth is as much the product of the plants as much as it is the product of the soil into which they are growing. A properly balanced plant nutrition plan can help to reduce the negative effects of soil deficiencies and increase the overall health of plants. The nutrient balance in the soil should be maintained at the right levels to ensure optimal plant growth and development. The soil should be regularly tested to determine the nutrient content and adjust the nutrient balance as needed. This approach can lead to healthier and more productive plants, as well as reduced costs associated with nutrient imbalances and soil deficiencies.
to assess differences in root tips transcriptome (RNaseq) and develop two large F2QTL populations. QTLin F2 populations were analysed using bulked pools of lines with extreme phenotype ±p. The combination of GWAS, gene expression analysis and bulk segregant analysis revealed interesting QTLs and candidate genes in 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

DAFIMAR VAN DUSSCHOTEN (2BO–FORSCUNGSZENTRUM JUELICH, GERMANY), YANNICK MUELLERS (2BO–FORSCUNGSZENTRUM JUELICH, GERMANY), JANNEK KOCHS (2BO–FORSCUNGSZENTRUM JUELICH, GERMANY), DANIEL PFISSELBERG (2BO–FORSCUNGSZENTRUM JUELICH, GERMANY), HENDRICK FOERSTER (2BO–FORSCUNGSZENTRUM JUELICH, GERMANY), JOHANNES A POSTMA (2BO–FORSCUNGSZENTRUM JUELICH, GERMANY), D. VAN. DUSCHOTENMPFZ–JUELICH.DE

Local root water uptake (RWU) is dependent on shoot transpiration rates as well as several root characteristic and the surrounding soil water content (B). 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 several plants in a few minutes to determine total change of water in the column (ml/ plant water uptake) as well as the local changes in W with a precision of 2e-2 cm/s/ cm2 at a 1D resolution in the order of mm. Due to the sensors’ high precision and fast dynamics we can derive local RWU variations 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/(m2*s)). Before and after scanning, the root length distribution was determined using magnetic resonance imaging (MRI). We used the SWaP tomometer 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 VITIENNE (UNIVERSITY OF TURIN, ITALY), CLAUDIO LOVISOLO (UNIVERSITY OF TURIN, ITALY), ANDREA SCHUBERT (UNIVERSITY OF TURIN, ITALY)

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 acclimatization to drought in several plant species, mostly because it promotes stoma closure in abscisic acid (ABA)-dependent and independent ways. In tomato (Solanum lycopersicum L.) and rice, SL also regulates shoot development, and thereby promotes stoma closure to limit water losses. 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 stoma closure. Alternatively, recent studies demonstrate the importance of root–shoot responses to increased atmospheric VPD. The surgical technique of girdling (removal of stem phloem tissue) suppresses shoot-to-root signalling, allowing the independence of root-to-shoot and shoot-to-root signalling to be evaluated at gene expression, biochemical and physiological levels.

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

Wednesday 3 July 2019 11:30

PEDRO CASTRO (LANCASTER UNIVERSITY, UNITED KINGDOM), JAIMÉ PUÉRTOLAS (LANCASTER UNIVERSITY, UNITED KINGDOM), IAN C DOOD (LANCASTER UNIVERSITY, UNITED KINGDOM), YANG HAO (HONG KONG, HONG KONG), JIANMIA ZHANG (HONG KONG BAPTIST UNIVERSITY, HONG KONG)

P.CASTRO@ALD.CANTUS.LANCASHIRE.AC.UK

Soybean is an important global crop for human and animal nutrition, but its production is affected by environmental stresses such as drought. Crop adaptation to these stresses are produced by 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 leaves, thereby promoting stoma closure to limit water losses. 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 stoma closure. Alternatively, recent studies demonstrate the importance of root–shoot responses to increased atmospheric VPD. The surgical technique of girdling (removal of stem phloem tissue) suppresses shoot-to-root signalling, allowing the independence 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 ROOT ACCOUNTS FOR DIFFERENTIAL SALT TOLERANCE IN QUINOA ACCESSIONS

Wednesday 3 July 2019 11:45

NADJA BAZHIZHINA (UNIVERSITÀ DEGLI STUDI DI FIRENZE, ITALY), STEFANO MANCUSO (UNIVERSITÀ DEGLI STUDI DI FIRENZE, ITALY), SERGEY SHABALA (UNIVERSITY OF TAMPA, AUSTRALIA)

NADJA.BAZHIZHINA@KLU.ET

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 gene expression data indicate that reductions in photosynthetic rates were due to stomatal limitations rather than biochemical changes. This suggests that, in the tolerant accession, improved responses at the root level due to the inhibition of water flux across cell membranes thereby explaining their improved gas exchange. Confirming the greater root adaptivity at low level of accessions compared with the tolerant accession 68, we found a decline in cell viability and an increase in H2O2 production in both the apical and mature root zones following salinity stress. As signaling 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, independent of shoot based tolerance mechanisms (including EBC density), improved signalling in the tolerant accession, based on OH− -activation of K+ channels, elicited modulated metabolic processes. This is 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 KERAPHYTA SCHLECHTERI AND EGRAGOSTIS KINNAND

Wednesday 3 July 2019 12:00

MARIAP ANILIA (UNIVERSITY OF CAPE TOWN, SOUTH AFRICA), JILL FARRANT (UNIVERSITY OF CAPE TOWN, SOUTH AFRICA), HENN WILHELMS (NAGENGAN UNIVERSITY RESEARCH, NETHERLANDS)

MARIAP.ANILIA@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 of 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 Keraphyta schleichteri, we examined the effect of exogenous NaCl on growth and gene expression. To enrich the pathological analysis cross talk of salinity and drought, we fed plants with 150mM NaCl, followed by 150mM NaCl and 150mM NaCl. The method employed to analyze the expression changes in response to salinity and drought included by RNA-Seq analysis. Transcriptomic data was analyzed using the R environment. This approach led to the identification of genes related 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 13:40

TOM BUCKLEY (UNIVERSITY OF CALIFORNIA DAVIS, UNITED STATES)

TNBEEKLEYUCDAVIS.EDU

Recent work has clarified the role of hydraulic mechanisms driving stomatal responses to changes in VPD, hydraulic conductivity and soil moisture, but has also identified mechanistic 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 MOLDING APPROACH TO QUANTIFY THE INFLUENCE OF STOMATAL BEHAVIOUR AND SALINITY STRESS ON WATER USE EFFICIENCY OF CUCUMBER PLANTS

**WEDNESDAY 3 JULY, 2019**

**DANY ROJALIU-NGANQUE** (LEIBNIZ UNIVERSITÄT HANNOVER, GERMANY)  
**ROULANGEL@UNI-HANNOVER.DE**

Water use efficiency (WUE) is driven mainly by leaf traits that reduce transpiration and improve water use efficiency. Foliar salinity leads to a decrease of water use efficiency. 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 dynamic model. The model combines the dynamics of the canopy stomatal conductance with the model 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 impact of stomatal response will be computed at each time point, and using the current values of stomatal conductance, the effective value of the net assimilation will be derived together with the transpiration rate using the Penman-Monteith equation. Comparison of WUE under different light conditions will reveal the dynamics of WUE on cloudy and sunny days. WUE with respect to stomatal parameters and salinity stress will be presented for different scenarios of sunny and cloudy days.

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

**WEDNESDAY 3 JULY, 2019**

**ANTONIO DIAZ-ESPRILO** (CHUÑAS CSC, SPAIN), IAN C DODD (LANCASTER UNIVERSITY, UNITED KINGDOM), JAIME PUERTAS (LANCASTER UNIVERSITY, UNITED KINGDOM)

Recent years have seen a change in the paradigm for the main source of ABA involved in regulating stomatal responses. Most evidence now consists of 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 doubted 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 aims to assess to what extent this leaf-exogenous ABA plays a major role in regulating stomatal conductance. Since its very difficult to empirically separate ABA according to its origin, reciprocal- and self-grafts of wild-type (WT) and ABA-deficient (Bar) barley were grown and compared 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 flaccar 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 increase evaporative demand.

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

**WEDNESDAY 3 JULY, 2019**

**JAIME FLEKAS** (INAGA, SPAIN), ALICIA PERERA-CASTRO (INAGA, SPAIN), MARC CARRIOQUI (INAGA, SPAIN), JAIVIER GUILLAS (INAGA, SPAIN), MIGUEL NADAL (INAGA, SPAIN)

**JAIME.FLEKAS@ES**

Mesophyll conductance to CO2 (g m ) is as much limiting for photosynthesis as stomatal conductance and, in some organisms, even more. The maximum g m of a given species is determined by the specific anatomical arrangements of the mesophyll, with a dominant role of cell wall thickness (CW) and the fraction of mesophyll cells covered by chloroplasts (CC). Significant and important differences in g m exist between phylogenetically distant plant groups. Specifically, a decreasing trend for CW and an increasing trend for S/C 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 plains 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.

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

**WEDNESDAY 3 JULY, 2019**

**ANTONELLA GORI** (DAORG - DEPARTMENT OF AGRICULTURAL FOOD PRODUCTION AND ENVIRONMENTAL SCIENCES, ITALY), ANATOLY P SOBOLEV (CNR - ISTITUTO DI METODOLOGIE CHIMICHE E HEDONISTECA LABORATORI DI RISORSA MAGNETICA “ANNALURA SEGRE, ITALY), ANATOLY P SOBOLEV (CNR - ISTITUTO DI METODOLOGIE CHIMICHE E HEDONISTECA LABORATORI DI RISORSA MAGNETICA “ANNALURA SEGRE, ITALY), ANATEL GORI@UNIFI. IT

**ANTONELA.GORI@UNIFI.IT**

These results provide a framework for better understanding metabolic analysis integrated into physiological models and drought focused breeding endeavours.

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

**WEDNESDAY 3 JULY, 2019**

**BASILY M KRETLER** (LANCASTER UNIVERSITY - LANCASTER ENVIRONMENT CENTRE, UNITED KINGDOM), IAN C DODD (LANCASTER UNIVERSITY - LANCASTER ENVIRONMENT CENTRE, UNITED KINGDOM), ELIZABETH CAMILLI-SPOLAS (LANCASTER UNIVERSITY - LANCASTER ENVIRONMENT CENTRE, UNITED KINGDOM)

**KRETLERBAILEY@GMAIL.COM**

The UK summer of 2018 was particularly hot with the months of June to August being, on average, 6°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 future conditions, since summer mean air temperatures in the UK are predicted to increase by 2-3°C by 2050, with a concomitant decrease in rainfall. During this summer, a factorial field experiment was conducted to measure drought focused breeding endeavours.

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

**WEDNESDAY 3 JULY, 2019**

**KATHARINA HUNTBURG** (LANCASTER UNIVERSITY, UNITED KINGDOM), MARK A STALHAM (NEAB CUP, UNITED KINGDOM), IAN C DODD (LANCASTER UNIVERSITY, UNITED KINGDOM)

**K.HUNTBURG@LANCASTER.AC.UK**

The UK summer of 2018 was particularly hot with the months of June to August being, on average, 6°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 such extreme conditions are predicted to increase by 3°C by 2050, with a concomitant decrease in rainfall 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 (< 25 mm soil moisture deficit) produced smaller shoots and lower yield than plants 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 pressurised 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 07:45**

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

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 different bulk densities (1.4 vs 1.74 g/cm³), 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 isopentenyl adenine, 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), NORMITSU HAMAKA (KYUSHU UNIVERSITY, JAPAN), MARI IWAYA-INDUE (KYUSHU UNIVERSITY, JAPAN), YUSHI ISHIBASHI (KYUSHU UNIVERSITY, JAPAN)

Cowpea (Vigna unguiculata (L.) Walp) is one of the legume crops cultivated in semi-arid area, and have the characteristics of highly drought tolerant. In general, deep root system enables plants to absorb water from deep soil layer. It is now that typical upland rice cultivars have deeper rooting system than lowland ones, suggesting that the deep rooting characteristic may be one of ways to improve their drought resistance. We, therefore, focused on deep root 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 root 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 contribute to its drought tolerance through enhanced water uptake from deep soil layer.

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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), LINFLING ZHOU (AUSTRALIAN NATIONAL UNIVERSITY, AUSTRALIA), ODHRAN D’SULLIVAN (AUSTRALIAN NATIONAL UNIVERSITY, AUSTRALIA), MARY A HESKELL (MACALESTER COLLEGE, UNITED STATES), KEITH J BLOOMFIELD (IMPERIAL COLLEGE LONDON, UNITED KINGDOM), LASANYA K MERRASIMNE (UNIVERSITY OF PERADENIYA, SRI LANKA), MARK O JUOEKER (WESTERN SYDNEY UNIVERSITY, AUSTRALIA), PETER R REICH (UNIVERSITY OF MINNESOTA, UNITED STATES), KEVIN S DRIPFIN (COLUMBIA UNIVERSITY, UNITED STATES), VAUGHAN HURBY (SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES, SWEDEN), PATRICK MEIR (COLUMBIA UNIVERSITY, UNITED STATES), HESKEL (MACALESTER COLLEGE, UNITED STATES), KEITH J BLOOMFIELD (IMPERIAL COLLEGE LONDON, UNITED KINGDOM), E. CARMO SIILVA (LANCASTER UNIVERSITY, UNITED KINGDOM).

High-temperature variability in plants is important in a warming world, with extreme heat waves potentially leading to lethal heating of leaves. To assess this variability, we measured the changes in photosynthetic performance at high temperatures in 40 species of plants from different habitats. We found that the photosynthetic response to high temperature varied widely among species, with some species showing a significant decline in photosynthetic performance, while others were able to maintain high photosynthetic rates even at temperatures above 30°C. This variability highlights the need for further research on heat tolerance in different plant species to improve crop productivity in a changing climate.

P6.2 OPTIMISING THE REGULATION OF CO₂ ASSIMILATION TO ENHANCE THE STABILITY OF WHEAT GRAIN YIELDS IN THE CHANGING CLIMATE

FRIDAY 5 JULY, 2019 09:30

ELIZABETH CARMO-SILVA (LANCASTER UNIVERSITY, UNITED KINGDOM).

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 source of carbohydrate to fill the grain. The enzyme RuBisCO (ribulose-1,5-bisphosphate carboxylase/oxygenase) is responsible for the initial step in CO₂ assimilation. It is not very efficient 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 an inactive conformation. It is hypothesised that, under optimal conditions, maintaining RuBisCO highly active contributes to greater rates of CO₂ assimilation leading to higher grain yields; conversely, conditions of stress, particularly at elevated temperatures, RuBisCO inhibitors may protect the enzyme from protolytic breakdown and enable fast recovery of CO₂ assimilation rates upon relief from stress. Progress in testing these hypotheses have used transgenic approaches to modify Uncoupling Protein 1 (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 photosynthetic sink during abiotic stress, resulting in enhanced drought resilience and increased yield.

P6.3 POLLEN DEVELOPMENT THE WEAKEST LINK – DEVELOPING RESILIENCE TO 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 TIVY (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), P BARRETO (UNIVERSITY OF CAMPINAS, BRAZIL), P ARRUDA (UNIVERSITY OF CAMPINAS, BRAZIL).

Pollen formation is high 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 is generally vegetative and 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 is resilience to reproductive stress stress is not developed. We have been using various approaches to identify the changes associated with heat stress during pollen development in a rapeseed, 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 Protein (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 photosynthetic 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 MORELL (UNIVERSITY OF READING, SCHOOL OF AGRICULTURE POLICY AND DEVELOPMENT, UNITED KINGDOM), TESS DILKS (ROTHAMSTED RESEARCH, PLANT SCIENCES DEPARTMENT, UNITED KINGDOM), CHEAN SUA (UNIVERSITY OF LEEDS, SCHOOL OF EARTH AND ENVIRONMENT, UNITED KINGDOM), HERMAN DEGOONING (SCOTLAND’S RURAL COLLEGE, DEPARTMENT OF LAND ECONOMY, ENVIRONMENT AND SOCIETY, UNITED KINGDOM), SANDRA S. SAMALASKINE (LANCASTER UNIVERSITY, LANCASTER ENVIRONMENT CENTRE, UNITED KINGDOM), BENJAMIN E SIECK (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), RODRIGUEZ-COSTA (INTERNATIONAL CENTER FOR TROPICAL AGRICULTURE (CIAT), AGROBIODIVERSITY (BEAN PROGRAM), COLOMBIA), CAN ODD (LANCASTER UNIVERSITY, LANCASTER ENVIRONMENT CENTRE, UNITED KINGDOM), ANDRIAN BARNES (SCOTLAND’S RURAL COLLEGE, DEPARTMENT OF LAND ECONOMY, ENVIRONMENT AND SOCIETY, UNITED KINGDOM), ARRUDA (UNIVERSITY OF CAMPINAS, BRAZIL), ORTEGA (UNIVERSITY OF READING, SCHOOL OF AGRICULTURE POLICY AND DEVELOPMENT, UNITED KINGDOM), DONALD H O’SULLIVAN (UNIVERSITY OF READING, SCHOOL OF AGRICULTURE POLICY AND DEVELOPMENT, UNITED KINGDOM).

Common beans (Phaseolus vulgaris L.) are widely proposed as a highly nutritious and marketable crop for ex-combatants in Colombia, but high temperatures may represent a major threat. Two major knowledge gaps undermine the efficiency of current breeding for heat tolerance. First, the physiological mechanisms underlying existing genetic variation in heat resistance are poorly understood; second, current breeding programs and crop–climate models may not reflect the predicted future changes in temperature and precipitation. We address these gaps by characterising the impacts of precisely timed heat/drought stresses in development, photosynthesis and reproduction through the precise phenotyping of sensitive stages and temperature thresholds through the growing season. Genotype previously identified as heat tolerant possess a high degree of repeatability and are used for the development of new cultivars.

J. MIRRETBARRIO@READING.AC.UK

J.FRIBERG@READING.AC.UK

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P.6.5 NOVEL CYTOKININ ANTAGONISTS AS A TOOL FOR CROP ENHANCEMENT UNDER ABIOTIC STRESS CONDITIONS

FRIDAY 5 JULY, 2019 10:46

BRITANNY HEEP (LANCASTER UNIVERSITY, UNITED KINGDOM)

GABRIELLA TOLEDO-ORTIZ (LANCASTER UNIVERSITY, UNITED KINGDOM), MARTIN NOIR (LANCASTER UNIVERSITY, UNITED KINGDOM)

B. HEAP@LANCASTER.AC.UK

In recent years, abiotic stress conditions over account for 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 yield. 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 woody crop species. As chlorophenylalanine and Orcinol, cytokinin is a class of plant hormones that regulate cell division and differentiation in plants; they play an opposing role in the rooting ability of seedlings. Upon application of the compounds, the decrease 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-fertiliser, not only increasing the plants resilience to abiotic stress. The role of the novel cytokinin antagonist in promoting root growth and parameters related to nutritional uptake will be discussed.

P.6.6 GENE ACTION OF Drought TOLERANCE AND ACHEIVE YIELD RELATED TRAITS IN SUNFLOWER (HELIANTHUS ANNUUS L.)

FRIDAY 5 JULY, 2019 10:47

HUMERA RAZZAQ (UNIVERSITY OF AGRICULTURE FAISALABAD, PAKISTAN)

HUMERARAZZAQ4040@GMAIL.COM

Sixty sunflower accessions were evaluated under polyethylene glycol (PEG-6000)-mediated drought stress. Selection criteria for drought tolerant accessions were measured 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 017578 and testers HA-133 and 017577 were the best general combiners under normal and drought-stress treatments. Results of SCA indicated that A-23 x 017577, A-79 x 017578, A-49 x 017578, A-79 x 017578 and A-79 x 017578 were the best specific combiners. Crossovers G-61 x HA-124 and A-48 x 341 had midparent, heterobelt 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 number of flowers while the other characteristics were observed for non-additive gene action. The association of traits based on correlation and path analysis suggested that seedling fresh weight, dry weight and hundred seed weight might be used as criteria for selecting sunflower for drought tolerance and high achene yield.

P.6.7 TASTING THE SPOTLIGHT: THE PATH OF THE SUN TRIGGERS DIURNAL 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 PAIT (AMERICAN JORDAN UNIVERSITY, JORDAN) (AARON PAIT UNIVERSITY OF THE NEGEV RESEARCH BEN-GURION UNIVERSITY OF THE NEGEV, ISRAEL)

NRA4446@CORNELL.EDU

Micrometeorological conditions such as solar irradiance and temperature were 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 stress-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 acclimation, 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 v gradient of irradiance levels in the fruit zone by harnessing the strong and stable solar irradiance in the Negev desert. The role of fulvic light and explains grape composition was analysed by using the three-dimensional structure of the grape cluster and integrating berry-level metabolomics and microbiomeology. In addition, the impact of sun path on the diurnal metabolic processes in the grape were analyzed for the composition of the grape cluster and integrating berry-level metabolomics and microbiomeology. Taken together, these evidence indicate that radiation management is essential to improving fruit quality and homogeneity and mitigating the detrimental consequences of warm and arid conditions.

P.6.8 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)

HINASALEEM093040@GMAIL.COM

Climate change is a major issue worldwide due to global warming. Abiotic stress, especially 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 genetic and biological effects 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 the local research group and were hybridized 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 (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 midparent combining ability was greater than that of general combining ability in all drought stress treatments, and that there was additive gene action. Line + tester analysis had more proportional contribution under T0=63.69, T1=61.45, T2=51.92 followed by lines T0x82.62, T1=43.10, T2=47.66, testers T0x76.69, T1=71.09 and T2=6.11. Cross Zm+5=Rainbow performed best in normal and drought conditions.

P.6.9 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), KRISTEN FRENCH (UNIVERSITY OF WOLLONGONG, AUSTRALIA)

ALISON.HAYNES@UOW.EDU.ON.NET

As organisms experience the environment at their own scale of time, seeking a leaf or an acorn useful when determining the rates 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 isolation and water. At larger scale, urbanisation of fringe 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 (nanotopography) and texture (smooth vs. textured). I planted 100 species fixed them to 15 panels which 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 from within this study region. Measurements of light and temperature were taken seasonally. Overall, tiles with more ruggedness and a niche (concave) design are expected to promote moss establishment; too shady sites without rocks are not suitable for both. Larger scale processes such as population fragmentation detering establishment. Initial results show decreased moss establishment with increasing urbanisation and higher establishment in ‘niches’ (concave) tiles. This experiment will further us our understanding of the effects of urbanisation on plant microclimate and contribute to research on urban green.
However, there is little information on the regulation of inorganic ion transport at the whole-plant level. In this regard, more attention has been paid to the isocitric macronutrients K⁺, N⁺, and CO₂ while Na⁺ has traditionally been considered non-toxic to crops. But unlike Na⁺, plants make an important use of metabolic energy to accumulate Cl⁻. Apart from being an essential nutrient, we have described Cl⁻ as a biologically macronutrient, playing specific roles in maintaining plant growth and water balance. Macronutrient Cl⁻ levels reduce stomatal conductance without a concomitant decrease of the net photosynthesis rate. Since stomate-mediated water loss through transpiration is inherent in the need of C₃ plants to capture CO₂, increased leaf water use is inherent in the need of C₃ plants to capture CO₂. Thus, increased leaf water use is a key factor in drought acclimation responses like the rapid turgor recovery of leaf and root cells, and the stomatal closure.

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

FRIDAY 5 JULY, 2019 10:57

SANJA ASHRAF (UNIVERSITY OF AGRICULTURE FAISALABAD, PAKISTAN)

SANAJMALIK350290MAIL.COM

Climate change is a global challenge that has no borders and to combat it, requires coordinated work by all countries. Average global temperature rise has been observed and it shows that these changes have occurred over many decades, and this warming over the years has increased the threat of extreme events. The impact of climate change poses a serious threat to agriculture, and its effects are visible in the form of drought, heat waves, and the spread of various diseases. In this paper, we report the strategy for inducing mutations in sunflower plants using gamma rays and UV-C irradiation to produce drought resistant plants.

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

FRIDAY 5 JULY, 2019 11:30

JOSE M COLPEN-JONES (INSTITUTO DE RECURSOS NATURALES Y AGROBIOLÓGIA (CSIC), SPAIN), JUAN D FRANCISCO-NAVARRO (INSTITUTO DE RECURSOS NATURALES Y AGROBIOLÓGIA (CSIC), SPAIN), TORAIS MAIERHOFER (INSTITUTO DE BIOPHYSICS (UNIVERSITY OF WURZBURG), GERMANY), DIETER GEISLER (INSTITUTO DE RECURSOS NATURALES Y AGROBIOLÓGIA (CSIC), SPAIN), MANUEL A ROSALES (INSTITUTO DE RECURSOS NATURALES Y AGROBIOLÓGIA (CSIC), SPAIN), SIBEL ECEGUER (INSTITUTO DE RECURSOS NATURALES Y AGROBIOLÓGIA (CSIC), SPAIN), ANTONIO DÍAZ-ESPEJO (INSTITUTO DE RECURSOS NATURALES Y AGROBIOLÓGIA (CSIC), SPAIN)

CHEMEKHINE@CSIC.CS

At the cellular level, homeostatic mechanisms have been described by which inorganic ion fluxes, particularly K⁺, N⁺, Cl⁻, and Na⁺ play key roles in drought acclimation responses like the rapid recovery of leaf and root cells, and the stomatal closure.

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.UA

The non-protein amino acid γ-aminobutyric acid (GABA) has been proposed as a prebiotic messenger for cell communication conserved across kingdoms. GABA has well-defined signaling roles in animals; however, whilst GABA accumulates in plant tissue under stress, and can regulate plant tissue growth, it has not been determined how and when GABA acts as an endogenous plant signaling molecule. Here, we establish that endogenous GABA is a bona fide plant signaling by demonstrating it antagonises stomatal movement in response to opening and closing stimuli, and modulates plant growth exchange through the direct inhibition of plasma membrane and apoplastic-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 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.

P6.14 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, UNIVERSITY WURzburg, GERMANY), DIETMAR GEISLER (MOLECULAR PLANT BIOLOGY AND BIOPHYSICS, UNIVERSITY WURzburg, 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 CO₂ uptake and transpirational water loss were optimised by the acquisition of grass specific stomatal complex. 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 differentiation in the major cereal crop barley. Upon feeding barley to a crop of an intact barley leaf, stomata closed a nitrate dependent manner. This process was initiated by activation of guard cell SLAC1-type anion current channels. HvSLAC1 expressed in Xenopus oocytes give rise to t-type anion currents that increased several fold upon stimulation with nitrate. We identified tandem amino acid residues motifs that were conserved in the SLAC1 channels from different barley varieties and 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 ABIS TRANSCRIPTION FACTOR IN DROUGHT RESPONSE

FRIDAY 5 JULY, 2019 16:30

ANNA COLLIN (DEPARTMENT OF GENETICS, UNIVERSITY OF SILESIA IN KATOWICE, POLAND), ANNA SABORUKA (DEPARTMENT OF GENETICS, UNIVERSITY OF SILESIA IN KATOWICE, POLAND)

ANNA.SABORUKA@MAIL.COM

ABA INSENSITIVE 5 (ABIS) 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 ABIS gene using TILLING strategy. The HvABIS 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 Tunder drought stress. We performed the global expression analysis (Barley Agilent Microarrays) of HvABIS and WT under drought and we identified 2,926 differentially expressed genes (DEGs) between both genotypes. With the aim of hunting the potential HvABIS targets within the list of DEGs, we performed the analysis of the DEG promoter sequences and we identified 179 putative HvABIS targets. We further analyzed the expression of selected putative HvABIS targets under drought and eight of them under ABA treatment in both HvABIS and its WT. Four genes associated with chlorophyll biosynthesis (Geranylgeranylflavones, Geraniol) have been described in barley as playing key roles in drought acclimation responses like the rapid turgor recovery of leaf and root cells, and the stomatal closure.

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), MEHEDI HASAN (UNIVERSITY OF TASMANIA, AUSTRALIA), SERGEY SHABALA (UNIVERSITY OF TASMANIA, AUSTRALIA), L. SHABALAKAITUS, EDU

Drought stress in 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 larger 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 trials. Barley seedlings were grown initially to severe drought by withholding irrigation for 30 days under glasshouse conditions and the drought tolerance score based on the degree of the leaf wilting, fresh and dry biomass and relative water content. The characteristics were related to stomatal conductance, stomatal density, residual transpiration and leaf sap Na, K, Cl contents measured in leaves. 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 genotypes. In a follow-up work, we assessed various screening methods for their suitability to breeders for rapid and reliable evaluation of drought tolerance in barley genotypes. Selection of different drought treatments were evaluated by measuring transpiration rate, quantum yield of PSI (chlorophyll fluorescence of Fv/Fm ratio), and differentially expressed genes (DEGs) that were highly correlated with ABA expression level, drought and ABA treatment. Physical interaction between their promoters and HvABIS 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 HvABIS. This work was supported by National Science Center Poland, project 2017/26/N/ZDA/014. "The role of HvABIS transcription factor in their barley (Hordeum vulgare L.), response to drought stress", 2018-2020.
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 future. 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 overly affected 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 was also revealed both tissue and varietal specific expression differences. Overall, the current study has generated a knowledge base on mechanisms that are utilised by sorghum plants in drought stress adaptation.

OR: 1088B 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 root or lettuce morphology, physiology, or drought tolerance. Combined exposure to blue and white blue light increased leaf area, specific leaf area, and dry matter production. The root length of the primed plants was shorter than that of the controls. The primed plants also had lower water use efficiency. Combined exposure to blue and white light increased water use efficiency and decreased stomatal conductance. The primed plants also had lower water use efficiency and decreased stomatal conductance. The primed plants also had lower water use efficiency and decreased stomatal conductance.
is agriculture. The effect of climate change is devasting due to increase in temperature combined with a decrease in rainfall which lead to increase in 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 REGAIANO (DEPARTMENT OF AGRICULTURAL SCIENCES, UNIVERSITY FEDERICO II OF NAPLES, ITALY), AMALIA BARONE (DEPARTMENT OF AGRICULTURAL SCIENCES, UNIVERSITY FEDERICO II OF NAPLES, ITALY), CARMEN ARENA (DEPARTMENT OF BIOLOGY, UNIVERSITY FEDERICO II OF NAPLES, ITALY).

C. ARENAKUZZA. 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 rich in antioxidant 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% (RI), 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, in R1, 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 ROS, a reactive oxidative stress. Photosynthetic capacity is reduced. Besides under severe water stress IL925 also exhibited a higher PSII photochemical efficiency associated with a lower non-photocatalytic quenching. In this genotype prolonged severe water stress induces the formation of fruits rich in antioxidant (polyphenols, 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), CHUN-YAO LI (DEPARTMENT OF AGRONOMY, NATIONAL CHUNG HSING UNIVERSITY, TAIWAN).

Edamame ( Glycine max L.) is a crop of economic importance with high nutritional value. Edamame beans are a good source of protein and nutritive elements. Kaohsiung No. 9 (KH9), Kaohsiung No. 11 (KH11) and Xiang No. (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 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 shelled beans and has associated with a reduction in edamame yield. We examined the aforementioned three cultivars under drought conditions during the blooming period. The soil water content was reduced by 10% of field capacity after 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 production differed between the three cultivars. In KH9, KH11, and XJ, after 10 days of the drought, 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 REPEPRODUCTION**

**WEDNESDAY 3 JULY, 2019 POSTER SESSION**

ALISON C TJOY (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM).

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% millions 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 BnaD.F5 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 underpin environmental stress losses by targeted breeding 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**

MIQUEL A ROSALES (CSIC, SPAIN), JUAN D FRANCO-NAVARRO (CSIC, SPAIN), PABLO SÁEZ-HERRA (CSIC, SPAIN), CARLOS RIVERO (CSIC, SPAIN), JAVIER BRÚMOS (ZVIA, SPAIN), ALFREDO RUBIO-CASAL (UNIVERSITY OF SEVILLE, SPAIN), ALFONSO DE CERES (UNIVERSITY OF SEVILLE, SPAIN), JOSE M COLUMENO-FLORES (CSIC, SPAIN).

Chloride (Cl) has recently been 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 tested for 30 days with three nutrient regimes: control and two biannual solutions: Cl (Cl5MmC), N (5mM nitrate, and S1 (2.5mM sulphate and 1.875mM 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 moderately drought (60% field capacity). Results showed that, in comparison to S1 and N treatments, Cl application (Cl treatment) increased stomatal conductance, transpiration rates and WUE under drought conditions. Interestingly, Cl-treated plants exhibited the strongest growth reduction during drought, showing higher stress symptoms caused by a significant decrease in 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**


L. HICKEY@UQ.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 closely associated with improved access to water and nutrients in deep soils during terminal drought. RSA, therefore is a drought-adaptive trait that can significantly increase water use efficiency. Here, GWAS for a terminal root angle (RSA) identified seven marker-trait associations clustered on chromosome 6A, representing a major water conserving QTL (secre6A-1A) which also displays high levels of pairwise LD (r^2 = 0.97). Subsequent haplotype analysis revealed significant differences between major groups. Candidate gene analysis revealed loci related to gravitropism, polar growth and cultivars with a wide range of RSA, therefore can be used for root biomass between lines carrying hap1 and hap2 for secret6A-1A, highlighting the opportunity to perform marker-assisted selection for the secret6A-1A locus and directly select for narrow RSA, without influencing root biomass. Our study revealed that the genetic predisposition for deep rooting was best expressed under water-limited yet the root system displayed plasticity in producing root growth in response to water availability in upper soil layers. We discuss the potential to deploy root architectural traits in cultivar improvement in yield stability in environments that have experience limited rainfall.

**P6.28 THE RESURRECTION PLANT CRATEROSTIGMA PUMILUM REVEALS IMPACTS OF CHLOROPHYLL 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 (NEUMANN INSTITUTE OF SCIENCE, ISRAEL), L. HICKEY@UQ.AU

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 homochlorophyllous 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 breakdowns 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** METABOLOMICAL ANALYSIS OF ZYGONEMA SP. VEGETATIVE AND PRE-AKINETE FIELD SAMPLES FROM SVALBARD

**WEDNESDAY 3 JULY, 2019 POSTER SESSION**

ANDREAS HOLZINGER (UNIVERSITY OF INNSBRUCK, AUSTRIA), ERLANN ARC (UNIVERSITY OF INNSBRUCK, AUSTRIA), ILSE KRANER (UNIVERSITY OF INNSBRUCK, AUSTRIA), MARTINA PICHTORVA (CHARLES UNIVERSITY PRAGUE, CZECH REPUBLIC)

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 pre-akinetes 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 model proteins are cysteine or glutamine were down-accumulated in pre-akinetes 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. Monosaccharides like mannose and ribose were down-accumulated in pre-akinetes, particularly galactinol. Most low-molecular-weight organic acids were down-accumulated in the pre-akinete samples. Among the detected metabolites, the abundance of amino acids and low-molecular-weight organic metabolites exist between vegetative cells and pre-akinetes. Monosaccharides like mannose and ribose were down-accumulated in pre-akinetes. Among the detected metabolites, the abundance of amino acids and low-molecular-weight organic metabolites exist between vegetative cells and pre-akinetes. Monosaccharides like mannose and ribose were down-accumulated in pre-akinetes, particularly galactinol.

**P7.1 THE TRANSCRIPTIONAL REGULATION OF SENESCEENCE IN WHEAT**

**WEDNESDAY 3 JULY, 2019 14:00**

PHILIPPA BORRILL (UNIVERSITY OF BIRMINGHAM, UNITED KINGDOM)

F. 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. 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)

N. NIKOLOSKI@MPI-MG..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 are 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 contexts 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 genomic data for improved performance.
corrections. This is problematic, as it means that studies are not multiple testing, including FDR (False discovery rate) and Bonferroni test used to detect segregation distortion, with some authors inheritance. This phenomenon is reported in a wide variety of crop derived from a biparental cross deviate from Mendelian ratios of Segregation distortion is the phenomenon in which progeny would provide the basis for improved adaptation of new germplasm an overview of similarities and differences among barley lines. The (PCA), kinship and phylogenetic relationship were performed to were distributed into two main groups based on threshold level variability in number of root traits under an established semi- 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 under studied 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 studies were undertaken based on 1598 RSsilicoDArT 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 divergence among lines was evaluated with routine statistics, principal component, linkage disequilibrium and neighbor joining tree. The patterns of linkage disequilibrium showed significant LD with r² =0.24. In population structure analysis, the barley lines were distributed into two main groups based on threshold level of 0.8 on membership coefficient. Principal component analysis (PCA), kinship and phylogenetic relationship were performed to understand interrelationships 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.

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

Wednesday 3 July, 2019 15:54

Dongun Yun (National Institute of Agricultural Sciences, Korea (South)), Sunghoo Oh (National Institute of Agricultural Sciences, Korea (South)), Anchel Chang (National Institute of Agricultural Sciences, Korea (South)), Gansu Lee (National Institute of Agricultural Sciences, Korea (South))

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 assessment 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 was placed in eight directions as pollen receivers. Five pollen receiver cultivars were Unbawong, Daebi, Saegeyirmi, 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 Unbawong, Daebi, Saegeyirmi, Nakdong, and Ilmi, respectively, which were planted around PAC GM rice. The GM-unGMhybrid birds were detected by repeated spraying of herbicide and PAT immunotrap assay. Finally, the hybrids were confirmed by PCR analysing 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-GM non-GM hybrids were located in two distance from the PAC GM rice zone.

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-Campos (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)

The circadian clock, the molecular mechanism that provides plants with the ability to sense, adapt and anticipate to 24 h 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 with the aim to understand 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 a rapidly accumulating omics 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 promote sequence of the corresponding genes. Topological analysis and network motifs identification together with GO and DNA motifs enrichment 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.

P7.5 SEGREGATION DISTORTION: FACT OR FICTION?

Wednesday 3 July, 2019 15:52

Alex Coulton (The University of Bristol, United Kingdom)

Segregation distortion is the phenomenon in which progeny 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, while others use corrections for multiple testing, including FDR (False discovery rate) and Benferroni 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 a silico-simulation of a biparental mapping population where we can apply selection pressure at an arbitrary locus to assess segregation distortion and evaluate which tests is
P7.9 GROWTH-DEFENCE TRADE-OFF IN WHEAT IS CONTROLLED BY A TRANSCRIPTIONAL MEMORY CIRCUIT

Wednesday 3 July, 2019  15:50

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

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 defense. Employing a multi-scale modeling approach, we reconstructed gene regulatory networks and discovered five stimulus-specific response modules that act in concert to balance the growth-defense 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-spectrum switches in the response of defined meta-modules to this primary stimulus. In stage 2, the experiments systemic immune responses were induced by infecting Xanthomonas oryzae. The primary immune response was suppressed in parallel by the secondary defense system to avoid interference. The implementation of this primed immunity in correlation with bi-stable toggle switches in the defense-associated meta-module, which via inter-molecular 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 defense-associated processes. The gene regulatory network within the defense meta-module provided insights into transcription factor binding sites that might act as central switches to secure both growth and defense 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 O LEWENBY (LA TROBE UNIVERSITY, AUSTRALIA), MARK ZANDER (SALK INSTITUTE FOR BIOLOGICAL STUDIES, UNITED STATES), JOSEPH R ECKER (SALK INSTITUTE FOR BIOLOGICAL STUDIES, UNITED STATES), SHAO-DIAN CAROL HUANG (UNIVERSITY OF WASHINGTON, UNITED STATES), RENIAN O'MALLEY (DOE JOINT GENOME INSTITUTE, UNITED STATES), MINJANG XIE (CIBUS, UNITED STATES), SHELLY TRIGO (UNIVERSITY OF WASHINGTON, UNITED STATES), SIDDHARTH JAIN (CAREER MEWNEL UNIVERSITY, UNITED STATES), ROBERTO SOLANO (CENTRO NACIONAL DE EDICIONAL-CIES, SPAIN), ZIV Bar-Joseph (CAREER MEWNEL UNIVERSITY, UNITED STATES)

We have investigated the genomic regulatory program that controls the responses to the hormone jasmonate in etiolated seedlings. There is much interest currently in understanding the systems-levels of transcription factors. However, such studies can provide greater biological insights if fused in the context of the natural signaling pathway that initiates gene expression changes and achieves a functional and phenotypical response to the signal. We have conducted an integrated analysis of the response to jasmonate, spanning from signal perception and transcription, through activity of effectors and secondary regulatory transcription factors, to chromatin remodelling and gene expression outputs. Wemakeuse of genome-wide target maps for hundreds of transcription factors, dynamic histone modification analysis, massively multiplexed protein-protein interactome data and time series transcription 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-GOLC (UNIVERSITY OF SILESIA IN KATOWICE, POLAND), ANNA COLLIN (UNIVERSITY OF SILESIA IN KATOWICE, POLAND), JAN MARCIN ZUBER (UNIVERSITY OF SILESIA IN KATOWICE, POLAND)

CBP (Cap-Binding Complex) consisting of two subunits— CBP20 (Cap-Binding Protein 20) and CBP60—was identified over 20 years ago. However, CBP20 were identified in different temperature and oxidative stress conditions. CBP20 encodes a small subunit of CBP that directly binds the cap, however actual binding requires the presence of the CBP80 responsible for the

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 WAK KIM (NATIONAL INSTITUTE OF CROP SCIENCE, KOREA (SOUTH)), CHUL OH CHO (NATIONAL INSTITUTE OF CROP SCIENCE, KOREA (SOUTH)), JAE BUN CHUN (NATIONAL INSTITUTE OF CROP SCIENCE, KOREA (SOUTH)), MI SUK SEO (NATIONAL INSTITUTE OF CROP SCIENCE, KOREA (SOUTH)), NAM HEE JONG (NATIONAL INSTITUTE OF CROP SCIENCE, KOREA (SOUTH)), MI JUN JIN (NATIONAL INSTITUTE OF CROP SCIENCE, KOREA (SOUTH))

The maize was mutated with ethyl methanesulfate (EMS) to enhance its genetic variability including disease resistance, abiotic and biotic stress resistance. 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 mutated maize generated landscape of genetic variability and promising genotypes. This enables us to predict a genotype with good performance for drought and salt tolerance. These genotypes will be tested in the field. Ultimately, these findings will provide insights about genetic load and how they regulate specific aspects of starch biosynthesis and nitrogen usage for leaching in high water potential. This study will make it possible to develop rice-tolerant lines that can be used in the field in the future. The molecular analyses will provide valuable information for the breeding of improved rice varieties with higher stress tolerance.

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

Wednesday 3 July, 2019  18:20

MARTINA HUBER (UTRECHT UNIVERSITY, NETHERLANDS), ARDEBELI NEADERI (AGRICULTURAL RESEARCH INSTITUTE, PHILIPPINES), RASHMI SASIDHARAN (UTRECHT UNIVERSITY, NETHERLANDS), KAISA KAJALA (UTRECHT UNIVERSITY, NETHERLANDS), RONALD PIEK (UTRECHT UNIVERSITY, NETHERLANDS)

How do you cope with competition against neighbours if you cannot run away? Here a model of two rice plants growing next to each other in modern rice farming will be presented. Here, we present the first attempt of understanding the role of CBC under drought stress at the molecular level in plants.

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

Thursday 4 July, 2019  08:00

COLLEEN DOHERTY (NORTH CAROLINA STATE UNIVERSITY)

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 response of abiotic stress responses can be 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 the identification of candidate targets to improve stress responses.
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 night time temperature sensitivity in rice.

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

**BOB SCHMIDT (UNIVERSITY OF GEORGIA, UNITED STATES)**

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 dataset 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 hot spots for genome rearrangements and agronomically important traits. We have developed a plant-specific chromatin signature that is indicative of cis-regulatory DNA elements. We are using this signature to identify 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**

**KATHERINE DENBY (UNIVERSITY OF YORK, UNITED KINGDOM), ELSPETH RAMSAY (UNIVERSITY OF YORK, UNITED KINGDOM), JULIA GEMAN (UNIVERSITY OF YORK, UNITED KINGDOM), GILL HIGDIS (UNIVERSITY OF YORK, UNITED KINGDOM), FABIAN VAISSTELJ (UNIVERSITY OF YORK, UNITED KINGDOM), CYRIL CARTER (UNIVERSITY OF YORK, UNITED KINGDOM)**

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 methods. We have generated high-resolution time series expression data from Arabidopsis leaves following infection with bacterial and fungal pathogens. These time series data sets allowed us to identify regulatory changes in gene expression and resolve the chronology of plant defence responses. We have generated transcription 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 the key regulatory genes were previously known to affect susceptibility to plant pathogens. We have applied this time-series based network analysis to gain a deeper understanding of the network underlying the 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 transcriptional changes in both host and pathogen to investigate how the plant defence response against these two pathogens is regulated, probe the molecular basis of plant-pathogen interaction and predict key regulators of virulence in the pathogen and resistance in the crop plant.

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

**AMY MARSHALL-COLON (UNIVERSITY OF ILLINOIS URBANA-CHAMPAIGN INSTITUTE OF AGRICULTURAL SCIENCE, UNITED STATES), YU WANG (UNIVERSITY OF ILLINOIS URBANA-CHAMPAIGN DEPARTMENT OF PLANT BIOLOGY, UNITED STATES), STEPHEN LONG (UNIVERSITY OF ILLINOIS URBANA-CHAMPAIGN CENTER FOR SUPERCOMPUTING APPLICATIONS, UNITED STATES), KAVYA KANNAN (UNIVERSITY OF ILLINOIS URBANA-CHAMPAIGN DEPARTMENT OF PLANT BIOLOGY, UNITED STATES)**

Current crop models can 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 varieties. We will highlight our efforts to generate virtual plant models that capture whole-system dynamics in response to key 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 crop macromolecules, photosynthesis, and crop 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: 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. We also carried out a series of in silico experiments to test the performance of different models under changing conditions. To make direct observations about crop phenotypic performance in response to varying scenario conditions. In silico exploration has the potential to help researchers target components of the underlying crop genotype and engineering to ultimately enhance crop yield and nutritional quality.

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

**AMY MCWILLIAMS, EDU**

Protein and nutrient content in wheat grains is highly influenced by the timing of senescence, yet we understand relatively little about the mechanisms underlying the regulation of this complex trait. NAC transcription factors (TF) (e.g. NAM-1, Uazy 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 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 is delayed in 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 network to identify putative shared downstream targets. NAM-1 and NAC-3 are known to affect several key transcription factors and to work together to regulate senescence. These transcription factors are known to affect cell cycle arrest, and we have shown that the NAC TF-NAC-3 acts as a positive regulator of senescence in wheat and may act in tandem with NAM-1.
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 Capsicum β-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, 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 (0.8 µg/g zeaxanthin, deep yellow), stBAK-PAC (1.4 µg/g ketocarotenoids, including astaxanthin, pinkish-red) and B-PAC×Ccs (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.

Soil salinity is one of the major environmental stress limits 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 LEE SWEETLOVE (OXFORD UNIVERSITY, UNITED KINGDOM)

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 modelling in which each discrete step of the process may be represented and studied in conjunction with biological and physical models of developing crop canopies. Application of optimization routines via high-performance computing, has predicted changes that could substantially improve photosynthetic efficiency in both C3 and C4 crops (Long et al., 2013). Some of these have 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).

P8.3 A NEW 3D SHOOT-ROOT MODEL FOR SIMULATING RHIZODEPOSITION PROCESSES IN THE CONTEXT OF WHOLE PLANT GROWTH
FRIDAY 5 JULY, 2019 09:45

FREDÉRIC REEES (UMR ECOSYS INRA, FRANCE), CLAUDE RICHEL (UMR ECOSYS INRA, FRANCE), CHRISTOPHE PRADAL (ADAP CIRAD INRA MONTPELLIER SUP AGRO), UNNE MONTPELLIER, FRANCE), LOÏC PÉRÈS (IR 1155 PSHA, FRANCE), CÉLINE RICHARD-MOLARD (UMR ECOSYS INRA, FRANCE)

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 whole plant model. After summarizing the current knowledge on the mechanisms and carbon-costs associated to rhizodeposition, we will present a 3D shoot-root model, ArchiSimple, a shoot-root model developed at the OpenAlea platform, which integrates a new rhizodeposition model, a shoot root architecture model (ArchSimple) and a model of C and N metabolism in the whole plant system. ArchiSimple is a highly adaptable framework can be used to gain mechanistic insight into the generation of observed root system architectures.

P8.4 AVERTING ROBO-BEES: INSECT POLLINATORS FROM MATHS TO FIELD
FRIDAY 5 JULY, 2019 10:00

ROS OGLEDON (MURRYS UNIVERSITY MELBOURNE, AUSTRALIA), ALAN DORIN (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), JIM HANAN (HORTICULTURAL SCIENCE GAVIT, UNIVERSITY OF QUEENSLAND, AUSTRALIA)

Food security and the sustainability of native ecosystems depend on plant-insect interactions in countless ways. Recently reported rapid and dimensens 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 insect pollinators might be replaced with free-flying robotic bees, an ecologically problematic notion. We argue instead that computer simulation of insect-plant interactions is a far more measured and ecologically sound application of robotic 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 which these flowers are grown 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 impact of Antropocene activity on the relationships between flowering plants and insects, and to mitigate against future where insects populations have crashed or been irrecoverably altered.

P8.6 DESIGNING SORGHUM CROPS FOR ADAPTATION TO THE DROUGHT AND HEAT RISKS ANTICIPATED IN FUTURE CLIMATES
FRIDAY 5 JULY, 2019 11:30

GRAPE HAMPER (UNIVERSITY OF QUEENSLAND, AUSTRALIA), GREG MCLEAN (QUEENSLAND DEPARTMENT OF AGRICULTURE AND FISHERIES, AUSTRALIA), ERIK VAN OOSTEROM (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), ANDREW OWENS (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), AL DOHERTY (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), BANGYOU ZHENG (CSIRO AGRICULTURE, AUSTRALIA), ALEX WU (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), AL DOHERTY (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA), G. HAMPER (THE UNIVERSITY OF QUEENSLAND, AUSTRALIA)

Climate risks pervade agriculture. They generate major consequences on crop production. We do not know what the next season will be like, yet alone the season 50 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 in 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 exist considerable knowledge of climate, both present and future, from climate records and climate models. This gives us insights into future variability and trends. We know that crop, 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 CO2, 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 as to provide the basis for efficient policy and management 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
P8.7 USING METABOLIC MODELLING TO UNDERSTAND THE LIMITATIONS TO PHOTOSYNTHESIS UNDER CHANGING ENVIRONMENTAL CONDITIONS

FRIDAY 5 JULY, 2019  12:00

HELENA A HERMANN (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 throughout this century, there will be a need to shift plant growth times of the year when temperatures are suboptimal or variable. In order to breed plants for a subsided growth season, we need to understand the limits on photosynthesis across different environmental conditions. We use both kinetic and constraint-based modelling techniques to understand the metabolic changes required for photosynthesis acclimation to changing environmental conditions. Using modelling and experimental data from the six different temperature conditions, we identify metabolic changes required for photoacclimation of Arabidopsis thaliana across its physiological temperature range.

FRIDAY 5 JULY, 2019  15:00

KINGONCHI ZHU (INSTITUTE OF PLANT PHYSIOLOGY AND ECOLOGY CHINESE ACADEMY OF SCIENCES, CHINA), TIANCHANG CHANG (INSTITUTE OF PLANT PHYSIOLOGY AND ECOLOGY CHINESE ACADEMY OF SCIENCES, CHINA)

ZHUKINGPICEE.ACN

On the face of the rapid advancements 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 Whole-Plant Carbon Nitrogen Interaction (WACNI), which predicts crop growth under various management conditions and at different grain yields. Systematic sensitivity analysis with WACNI was used to classify the 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 sink and transport related genetic manipulations on rice grain yields.

FRIDAY 5 JULY, 2019  15:35

ERNST D SCHAFER (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), MALCOLM J BENNETT (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), ETIENNE FAROC (INRA, UMR AGAP  UNIV. MONTPELLIER, FRANCE), SYLVIE CITERNE (INSTITUT JEAN-PIERRE BOURDIN CENTRE DE RECHERCHE INRA, INRA, UMR AGAP  UNIV. MONTPELLIER, FRANCE), FRÉDÉRIC GODIN (LABORATOIRE RÉPRODUCTION ET DÉVELOPPEMENT DES PLANTES, UNIV LYON ENS DE LYON, FRANCE), SOULAMIN BAR (INRA, INRA, ARAGOC-CROM-QUEST UNIVERSITÉ D'AUNIS, FRANCE, 4207 QUASAY, FRANCE)

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 existing ecosystems and the world’s food security. 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 a substantial improvement in crop yields under nutrient-poor conditions. Furthermore, this study predicted the way in which the change in soil nutrient system can be used to mitigate the dry weight loss of cultivars in the field. This shows the importance of developing new varieties that are suitable to meet future challenges.
Process-based crop simulation models are popular tools to understand how individual shoots grow in a stepwise approach to improve the management of free 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 interaction cannot be easily measured, making it difficult to analyze 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 during the in silico macadamia shoot growth. 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.

The environment surrounding leaves (phylloenvironment) determines the rate of photosynthesis, depending on the physiologic and morphologic traits of the leaf. Leaf phenotyping results from the exchange of energy, CO$_2$ and H$_2$O 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 light (i.e. thermomorphogenesis) leads to higher photosynthesis. A novel 3D computer program 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 the optimal temperature was particularly beneficial to photosynthesis under high light intensities and less so (or even detrimental) under low light intensities. However, thermomorphogenesis in Arabidopsis is not optimal for photosynthesis and that it may have a different ecological function, questioning the optimal photosynthetic acclimation theory.

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 water and trophic dynamics 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 trade-offs for contrasting soil resources, phylogenetic, 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 micromobility, and ecosystem function will create unprecedented opportunities to understand the interplay of plant genotype, phenotype, and environment, and to guide the development of the crops and cropping systems of the 21st century.
P8.18 COMPUTING A MORE EFFICIENT LEAF USING METABOLIC NETWORK MODELS

FRIDAY 5 JULY, 2019  17:45

LEE J SWEETLOVE (OXFORD UNIVERSITY, UNITED KINGDOM), SANI SHARMA (UNIVERSITY OF OXFORD, UNITED KINGDOM), R GEORGE RATCLIFFE (UNIVERSITY OF OXFORD, UNITED KINGDOM)

Metabolism underpins the growth of plants and in many circumstances limits its growth. Although primary metabolism in plants is 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 endogenous 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 metabolic properties in the context of efficiency of use of energy, nutrients and water.

P8.20 EVALUATING PHOTOSYNTHETIC INDUCTION USING GAS EXCHANGE DATA

THURSDAY 4 JULY, 2019  POSTER SESSION

S A Y L E H T (LANCASTER UNIVERSITY, UNITED KINGDOM), DOUGLAS J ORR (LANCASTER UNIVERSITY, UNITED KINGDOM), ELIZABETH CARR-WILKES (LANCASTER UNIVERSITY, UNITED KINGDOM), S TAYLORS@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 CO₂ assimilation responses and leaf growth. We have extended a photosynthesis limiting induction during which photosynthetic response curves and cuvette-level experiments can be used to measure induction responses. The ‘photosynematics’ 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 published gene expression data and a network of photosynthetic carbon gain components (e.g., 50% to leaves, 50% to stems, etc.) based on previous observations with proper training data, these will estimate long-term averages, but the model results 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 an arate 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 be extended to respond to environmental factors, such as day length and water status, which is comparable and easy to incorporate. The utilization model is more computationally difficult to solve than the partitioning model, but is likely more suitable for addressing many scientific questions.

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

WEDNESDAY 3 JULY, 2019  POSTER SESSION

MICHAIL SENYOV (ROTHAMSTED RESEARCH, UNITED KINGDOM), NIKI S A N P A R I (ROTHAMSTED RESEARCH, UNITED KINGDOM), MICHAIL.SEMENOV@ROTHAMSTED.AC.UK

Designing crop ideotypes is a key step to raising genetic yield potential in target environments. In the present study, we designed wheat ideotypes based on the Sirius process-based wheat model to increase 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) and potential (IP) conditions by exploring the full parameter ranges. A substantial increase in yield potential, 43–51%, over current cv. Claire, was predicted for IW, whereas a 51–62% increase was obtained for IP. The genetic yield potentials of wheat were 16% (2.6 tonnes/ha) and 33% (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 increases 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 roadmap for selection of the target traits for improvement and genetic adaptation to raise the genetic yield potential.

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

J U S T I N M MOGRATH (UNIVERSITY OF ILLINOIS-URBANA-CHAMPAIGN, UNITED STATES), S PETER LONG (UNIVERSITY OF ILLINOIS-URBANA-CHAMPAIGN, UNITED STATES)

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 can not 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 results 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 an arate 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 be extended to respond to environmental factors, such as day length and water status, which is comparable and easy to incorporate. The utilization model is more computationally difficult to solve than the partitioning model, but is likely more suitable for addressing 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

C H R I S T O P H E R  K BLACK (PENNSYLVANIA STATE UNIVERSITY, UNITED STATES), E R N S T  D SCHÄFER (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), J O N A T H A N  P L Y N C H (PENNSYLVANIA STATE UNIVERSITY, UNITED STATES)

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 root difficult to observe or sample, so many experiments rely on observations from roots grown 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 OpenVPhy, we have updated the soil parameterization to account for spatially heterogeneous soil properties. We have added grit for traction that are generated from walking tracks, and simulated a range of maize growth predictions. We have added grit for traction to multiple root models and the results indicate viable effects on leaf shape for all factors. In a next step, L-Cucumber simulations with an environment-sensitive dynamic leaf shape model were compared to the original model to determine, whether detected shape changes will significantly affect simulation results.
P9.1 WHEN DO TREES GROW?
ENVIRONMENTAL SIGNALS WHICH START AND STOP GROWTH IN DOUGLAS-FIR
(PSEUDOSUCA MENZIESII)

TUESDAY 2 JULY, 2019 09:00
CONSTANCE A HARRINGTON (USD PACIFIC NORTHWEST RESEARCH STATION, UNITED STATES)

Douglas-fir has several traits of meristem capable of 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 a obligate chilling requirement (both chilling and forcing temperatures during the dormancy season are required for bursting of the terminal bud). Non-terminating vegetative buds and stem vascular meristems will resume growth in the spring more quickly after chilling but its 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. As long 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 physiology 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 photosynthesis and temperature of Douglas-fir with the greatest variation among genotypes in the timing of terminal bud burst. This timing influences responses such as avoiding frost, completing substantial growth prior to summer and the severity of needle cast diseases associated with avoiding frost, completing substantial growth prior to summer.

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

TUESDAY 2 JULY, 2019 09:30
DALILA TRUPIANO (DEPARTMENT OF BIO SCIENCES AND TERRITORY - UNIVERSITY OF MOLISE, ITALY), ELENA DE ZIO (DEPARTMENT OF BIO SCIENCES AND TERRITORY - UNIVERSITY OF MOLISE, ITALY), ANTONIO MONTAGNOLI (DEPARTMENT OF BIOTECHNOLOGY AND LIFE SCIENCE - UNIVERSITY OF INSIURIA, ITALY), GABRIELLA S. SCICPIA (DEPARTMENT OF BIO SCIENCES AND TERRITORY - UNIVERSITY OF MOLISE, ITALY), KARIN LJUNG (SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES, SWEDEN), DONATO CORDATE (DEPARTMENT OF BIOTECHNOLOGY AND LIFE SCIENCE - UNIVERSITY OF INSIURIA, ITALY), GABRIELLA SFERRA (DEPARTMENT OF BIO SCIENCES AND TERRITORY - UNIVERSITY OF MOLISE, ITALY)

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 (Dellengan et al., 2008; Richter et al., 2012). Moreover, woody roots are still poorly investigated due to intrinsic difficulties in excision and sampling. By using a single experimental system, we previously found that waving of Arabidopsis roots explored the range of bending and compression forces in bent 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 CKx in the concave side support their involvement in RW production, whereby ABa could mediate the adaptation to the deforming conditions generated by bending, while CKx could act in synergy with ABa 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
DIAN NAGEL (UNIVERSITY OF CALIFORNIA RIVERSIDE, UNITED STATES)

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 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 PRR5 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 contribute to a circadian phase defect. The findings from this study will provide new mechanistic insights into how TRTF-C regulates and integrates temperature signals to the circadian clock, and potential 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 ZUTH (MAX PLANK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY), STEPHANIE SCHAARSDMIDT (MAX PLANK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY), ANS FISCHER (MAX PLANK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY), ALEXANDER ERBAN (MAX PLANK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY), KARL UTZEL (DEPARTMENT OF CHEMISTRY AND BIO SCIENCE, AALBORG UNIVERSITY, DENMARK), UMAHAH MUBEEN (MAX PLANK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY), DAIN WALSTER (MAX PLANK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY), PATRICK GAVAILLASSO (MAX PLANK INSTITUTE FOR BIOLOGY OF AUER, GERMANY), JOACHIM KOPKA (MAX PLANK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY), MEIKE SPRENGER (F1E-USENT CENTER FOR PLANT SYSTEMS BIOLOGY, BELGIUM), DIK K. HINCHA (MAX PLANK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY)

Plants from temperate regions increase their freezing tolerance during exposure to cold priming and experience increased cold acclimatization and hardening which is an adaptive response to 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 priming 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 metabolic composition (GC-MS). Unique differentially expressed genes after triggering were more represented 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, Col-0 accessions were accumulated with proposed functions in signaling or as precursors of jasmonic acid. The more freezing tolerant N14 maintained levels of cold-induced metabolites during the lag phase, whereas accumulation occurred in the less freezing tolerant Col-0 after triggering to point genetic differences of transcriptional 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.
P9.6 UNRVAELING THE MOLECULAR MECHANISMS UNDERLYING PLANT CLOCK FUNCTION

TUESDAY 2 JULY, 2019  14:00

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

P9.7 ARABIDOPSIS JMJD5/JMJD30 ACTS INDEPENDENTLY OF LUX ARRHYTHMO CLOCK TO ENABLE TEMPERATURE COMPENSATION

TUESDAY 2 JULY, 2019  14:30

MATT A JONES (UNIVERSITY OF ESSEX, UNITED KINGDOM), KENSO HINAISHI (TOKYO UNIVERSITY OF SCIENCE, JAPAN), ERIC GROTEWOLD (MICHIGAN STATE UNIVERSITY, UNITED STATES), STACEY L HARMER (UNIVERSITY OF ESSEX, UNITED KINGDOM)

MATTHEW.JONES@ESSEX.AC.UK

The circadian system ensures that plants respond appropriately to environmental change by predicting regular transitions that occur during diel and seasonal cycles. In order to be 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, a group that is thought to be important for maintaining the circadian system during stress. Interestingly, we find that LUX, but not the Evening Complex components, is dispensable for clock function at low temperatures. Further genetic analysis suggests that JMJD5 acts in a parallel pathway to LUX within the circadian system. Although intact [37]MJCAT1/cycb9 is required for rhythmicity within the clock, our findings suggest that JMJD5 does not directly regulate H3K36 methylation at circadian loci. Such data refine our understanding of how JMJD5 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 plant pathogens 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 life cycle (i.e., infection, disease development, and sporulation) can only occur within a thermal window, whereby optimum temperature is bounded by a minimum and maximum temperature. As temperature deviates from optimum, the stress on the pathogen increases from maximum to toward zero. Hence, optimum temperature and maximum temperature collectively referred to as cardinal temperature (CT) – define a pathogen’s temperature response, for a given stage of its life cycle. CT can be influenced by biogeography and resultant crop risk, both in space and time, by restricting pathogen to areas of climatic suitability. Here, we characterized CTs calculated for >600 plant pathogen and fungi species. Using this dataset, we first test the hypothesis that temperature has a 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 specialize in niches. Third, we test the hypothesis that the evolutionary capacity of pathogen 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 the “temperature niche” of species and how temperature influences the pathogen plant host 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 JAOGDISH (KANSAS STATE UNIVERSITY, UNITED STATES)

KJHODGDIHKSETU.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 phylogenetic, metabolic and genetic 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), RÔMULO SOBRAL (UNIVERSIDADE DO MINHO, PORTUGAL), HELENA SILVA (UNIVERSIDADE DO MINHO, PORTUGAL)

MÁRICA.COSTA@UNINOVO.PT

Several plant species display a temporal separation of the male and female flower 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, cDNA microarray analysis and comparison of protein coding sequences provide evidence of co-expression patterns that are shared among species and how temperature affects flowering pattern. Our results indicate that female flowers are induced before male flowers and that flowering in Q. suber may be preceded by temporarily separated induction events. Female flowers are mostly induced during the vegetative phase 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, showing a long period of anthesis that spans the dormant period. The results portray a genetic mechanism highly dependent on environmental 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 (KYOUSHU UNIVERSITY, JAPAN)

AKIKO.SATAKE@KYUDAI.JP

The intermittent and synchronized production of large volumes of flowers and seeds is a hallmark of the oak family. In Fagus, a family of flowering plants that includes typical mast-bearing species such as beech, oak, and tanbark oak. Applying recent advances in molecular and genetic studies about flowering time control and mast production, we established approaches to investigate how the circadian system and its interaction with the local environment regulates flowering and mast production in Fagus. We demonstrate that an evening-phased protein, the putative histone demethylase JMJD5, contributes to temperature compensation.

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

WEDNESDAY 3 JULY, 2019  11:30

BENÉDICTE WENDEN (UM 1322 BFP, INRA, UNIV. BORDEAUX, FRANCE), NÜÜN VIMONT (INRA, AGRO INNOVATION INTERNATIONAL - CENTRE MONDIAL D'INNOVATION - GROUPE ROULLIER, FRANCE), MATHIEU FOUCHÉ (INRA, FRANCE), NOÉMIE VIMONT (INRA, AGRO INNOVATION INTERNATIONAL - CENTRE MONDIAL D'INNOVATION - GROUPE ROULLIER, FRANCE), JEAN-CLAUD VYHN (AGRO INNOVATION INTERNATIONAL - CENTRE MONDIAL D'INNOVATION - GROUPE ROULLIER, FRANCE), PHILIP WIGE (THE SAINSURY LABORATORY, UNIVERSITY OF CAMBRIDGE, UNITED KINGDOM), ELISABETH CEDMANNER (INRA, FRANCE), SANDRA CORTOJ (THE SAINSURY 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 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 time course transcriptional analysis of sweet cherry (Prunus avium L.) flower buds from budbreak until the end of bud dormancy using next-generation sequencing. We observed big transcriptional changes during bud dormancy, which are associated with the main cherry tree flower bud dormancy stages. Our results indicate that transcriptional changes happening during dormancy are robust and conserve between different sweet cherry cultivars. Our work opens up avenues for the development of future molecular phenology models.

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

WEDNESDAY 3 JULY, 2019  15:00

CAPILLA CALDANA (MAX PLANCK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY), MARINA CM MARTINS (UNIVERSITY OF SÃO PAULO, BRAZIL), ATSUO SAKATA (YOKUHAM UNIVERSITY, JAPAN), PATRICE DEESE (KU CHRISTIAN UNIVERSITY, JAPAN), ALEX WEBB (UNIVERSITY OF CAMBRIDGE, UNITED KINGDOM), ANTHONY ARTINS (MAX PLANCK INSTITUTE OF MOLECULAR PLANT PHYSIOLOGY, GERMANY)

CALDANAPPP@GURU.MPO.DE

As sessile organisms, plants have a great plasticity to adapt to fluctuating environmental conditions adjusting their growth and development. To test this, our group is interested in understanding how the circadian oscillator responds to endogenous sugar signals. We will describe new data that demonstrates that the circadian oscillator responds to sugar signals. We conducted a fine tunable temporal transcriptomic analysis of sweet cherry (Prunus avium L.) flower buds from budbreak until the end of bud dormancy using next-generation sequencing.

The circadian clock is a fundamental molecular mechanism that regulates growth and development, affecting many aspects of plant physiology and behavior. It is a master oscillator that controls the organisms' circannual, circadian, and infradian rhythms, ensuring the proper timing of physiological processes. The circadian clock is also a crucial regulatory network for the integration of external signals, such as light, temperature, and nutrient availability. Understanding the mechanisms by which the circadian clock integrates information from the environment with the internal state of the plant is essential for improving crop productivity and plant health.

The circadian oscillator is a robust and flexible system that responds to a wide range of signals, including light, temperature, and nutrient availability. It has been shown that the circadian oscillator is a key regulator of carbohydrate metabolism, with rhythms in starch and sucrose levels being well documented. New evidence suggests that the circadian oscillator also plays a critical role in the integration of carbohydrate signals with photosynthesis and nutrient uptake.

In this study, we aimed to investigate the role of the circadian oscillator in the integration of carbohydrate signals with growth and development. We used time-course transcriptomic analyses of sweet cherry flower buds from budbreak until the end of bud dormancy. Our results revealed that the circadian oscillator is a key regulator of carbohydrate metabolism, with rhythms in starch and sucrose levels being well documented. New evidence suggests that the circadian oscillator also plays a critical role in the integration of carbohydrate signals with photosynthesis and nutrient uptake.

The circadian clock is a fundamental molecular mechanism that regulates growth and development, affecting many aspects of plant physiology and behavior. It is a master oscillator that controls the organisms' circannual, circadian, and infradian rhythms, ensuring the proper timing of physiological processes. The circadian clock is also a crucial regulatory network for the integration of external signals, such as light, temperature, and nutrient availability. Understanding the mechanisms by which the circadian clock integrates information from the environment with the internal state of the plant is essential for improving crop productivity and plant health.

The circadian oscillator is a robust and flexible system that responds to a wide range of signals, including light, temperature, and nutrient availability. It has been shown that the circadian oscillator is a key regulator of carbohydrate metabolism, with rhythms in starch and sucrose levels being well documented. New evidence suggests that the circadian oscillator also plays a critical role in the integration of carbohydrate signals with photosynthesis and nutrient uptake.

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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^+ locus in Triticum monococcum (Alvarez et al., 2016) and an orthologue of LUX ARRHYTHMO/PHYTOCLOCK 1 (LUX) underlies the Eps-3A 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 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.

P8.19 FISH IN A BIOGEOCHEMICAL BARREL: TAKING AIM AT THE EVOLUTIONARY CONSEQUENCES OF NUTRIENT CO-LIMITATION IN FRESHWATER

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

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.