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PLANT BIOLOGY
ABSTRACTS

P1 FROM GENOTYPE TO PHENOTYPE

ORGANISED BY: WOLFGANG BUSCH (SALK INSTITUTE, UNITED STATES) AND CHRIS TOPP (DONALD DANFORTH PLANT SCIENCE CENTER, UNITED STATES)

P1.1 FROM GENOTYPE TO PHENOTYPE IN LEAF DEVELOPMENT AND EVOLUTION

MONDAY 3 JULY, 2017 **09:00**

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A key challenge in biology is to understand how diversity in organismal form is generated. Genetic analyses in model systems have identified key regulators that sculpt the body plans of metazoa and seed plants. However, less is known about how the action of such regulators produces particular organ shapes, or how the balance of conservation versus divergence of such form regulating pathways generated the tremendous morphological diversity of multicellular eukaryotes. One impediment to answering these questions is the relative paucity of experimental platforms where genetic tools can be utilized to unambiguously study morphogenesis and its evolution in a genome-wide, unbiased fashion. To circumvent this problem we developed the Arabidopsis thaliana relative Cardamine hirsuta into a versatile system for studying morphological evolution. We aim to understand the molecular mechanisms through which leaf morphology evolved in these species, resulting in simple, undivided leaves in A. thaliana and dissected leaves with distinct leaflets in C. hirsuta. This presentation will discuss our progress towards understanding the morphogenetic pathways that specify dissected versus entire leaf shapes and that regulate the number, position and timing of leaflet production. It will also detail how studies in C. hirsuta have helped understand to what degree pathways underlying morphological variation between and within species overlap.

P1.27 LINKING ECOPHYSIOLOGICAL MODELLING WITH GWAS TO DESIGN IMPROVED WATER DEFICIT STRESS RESILIENT RICE (ORYZA SATIVA L.)

MONDAY 3 JULY, 2017 **09:40**

XINYOU YIN (WAGENINGEN UNIVERSITY, NETHERLANDS), NITEEN KADAM (WAGENINGEN UNIVERSITY, NETHERLANDS), KRISHNA SV JAGADISH (INTERNATIONAL RICE RESEARCH INSTITUTE, PHILIPPINES), PAUL C STRUIK (WAGENINGEN UNIVERSITY, NETHERLANDS)

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Genotype-phenotype relationships are often modelled using statistical genetics approaches. However, growing evidence has shown that genetic markers can be used in combination with ecophysiological models to predict the performance of genotypes in given environments, especially for complex phenotypic traits at crop scale. We explore the use of crop models to design markers and ideotypes for improving yields of rice (Oryza sativa) under field water-deficit stress. Using the model GECROS (Genotype-by-Environment interaction on CROp growth Simulator), crop yield was dissected into several easily measured parameters. SNP loci for these parameters were identified via GWAS for an indica rice panel of ~275 accessions differing in water-deficit tolerance. SNP-based values of accessions for each of these parameters were calculated from estimated effects of the loci, and were fed to the model to simulate yields of the accessions grown under well-watered and water-deficit conditions and to design virtual ideotypes for those conditions. Genetic variation in some parameters had more significant effect on yield than that of other parameters. Using the SNP-based parameter values, GECROS also simulated yield variation among the accessions in independent experiments. The GECROS-based dissection approach detected more SNP loci than the analysis using only yield per se. Model-based sensitivity analysis ranked all SNP loci for their importance in determining yield differences among the accessions. Virtual ideotypes based on SNPs identified by modelling had higher yield than those based on SNPs for yield per se. Ecophysiological modelling is a powerful tool for crop design for improved rice yields under contrasting conditions.

P1.3 APPROACHING THE GENETIC AND MOLECULAR BASES OF ENVIRONMENTAL ROOT GROWTH REGULATION

MONDAY 3 JULY, 2017 **09:55**

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To grow and survive plants need access to nutrients and water: resources that are not evenly distributed in the soil environment. Plants have evolved complex, often highly branched root systems that allow them to explore and forage the soil to acquire these resources. At the same time, a multitude of environmental signals are processed in order to continuously adjust root growth. Interestingly, growth responses to environmental signals differ not only between species, but also within species. However, little is known about which genetic components are responsible for determining genotype-specific differences in root growth and its response to environmental signals.

We aim to identify genes, gene networks, and their molecular functions that are responsible for these different responses. We use custom phenotyping pipelines that enable us to capture quantitative root phenotypes from a very large number of individuals, GWAS to identify the associated loci in the genome, and systems-biology driven approaches to identify networks of interacting genes and pathways that provide the molecular and cellular context in which the underlying genes quantitatively regulate root growth. Using these approaches, we have identified novel regulators and regulatory modules of genes that shape root growth in *Arabidopsis thaliana*. These include a cluster of genes encoding for *LEUCINE-RICH RECEPTOR-LIKE-KINASES* that interact at the protein level, constituting a novel molecular signaling module for root growth regulation. Overall, our systems-genetics approach enables us to approach the complex genetic and molecular bases for the determination of root growth by environmental signals.

P1.4 ARABIDOPSIS LEAF GROWTH ANALYSIS FOR THE SEARCH OF GROWTH-REGULATING GENES AND GENE NETWORKS

MONDAY 3 JULY, 2017 **10:25**

NATHALIE GONZALEZ (INRA, FRANCE), DIRK INZÉ (VIB-PSB, BELGIUM)

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Plant growth is a quantitative, dynamic, and multi-factorial trait regulated by numerous genetic and environmental factors. The study of this complex machinery requires the integration of multiple approaches, at different scales (plant, organ, cell) including genetics, physiology, quantitative phenotyping, and various -omics technologies in order to obtain a holistic image of the molecular regulation of organ growth.

Arabidopsis leaf growth consists of a complex sequence of interconnected events involving cell division and cell expansion, and requiring multiple levels of genetic regulation. To identify the molecular players involved in leaf size control, we combine different phenotypic and molecular approaches. First, with classical genetics, we have identified and functionally characterised regulators involved in distinct cellular processes governing leaf growth. Second, since genetic background can influence the expressivity of a phenotype caused by a specific mutation, we have explored the natural variation response, at morphological and molecular level, after perturbation of the expression of known regulators, in Col-0 background, of leaf growth. Finally, since only a tight co-ordination between the numerous molecular players can support the formation of a functional organ, we have studied the connections between the components of the network through gene-stacking approaches.

Despite these advances in the understanding of leaf growth control, the picture of the regulatory network is far from complete. The use of high-throughput phenotyping technologies to study large numbers of natural accessions or mutants will allow for further identification of additional players that constitute the leaf growth regulatory networks.

P1.5 THE BLESSINGS OF DIMENSIONALITY

MONDAY 3 JULY, 2017 **14:00**

DAVID HOULE (FLORIDA STATE UNIVERSITY, UNITED STATES)

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With genomes in hand, we are all in the business of studying how the genomes affects the traits that we all care about, whether we like it or not. This is the genotype-phenotype map problem. The map is inherently multidimensional, meaning that it requires attention to many biological attributes simultaneously. From the viewpoint of the genome, each change may affect many phenotypes; from the viewpoint of a single phenotype, many parts of the genome are likely to affect it. Despite this, many biologists still study the genotype-phenotype map as a very large set of one-to-one mappings between a single SNP and a single trait. Part of the reason that biologists are often stuck in this mode is the claimed "curse of dimensionality" where measuring more and more becomes less and less useful. I argue that the curse is an artifact of our limited imaginations; dimensionality is a blessing, not a curse. Directly approaching the many-to-many relationships in the map will speed our progress towards understanding the map. I illustrate this claim with data from our studies of the development and evolution of wings in fruit flies.

P1.6 THE ADDED VALUE OF NATURAL VARIATION IN THE ELUCIDATION OF QUANTITATIVE TRAIT REGULATION

MONDAY 3 JULY, 2017 **14:40**

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Over the last decade genome wide association (GWA) mapping has rapidly become a major tool for the identification of natural polymorphisms explaining observed population variation. Especially in Arabidopsis the field has rapidly developed and contributed to many aspects of modern biology. Here, we will highlight some of the advancements made and illustrate this with recent case studies. GWA mapping has been instrumental in identifying novel regulators of complex traits. As such, it has contributed to our further understanding of physiological traits, plant metabolism and adaptation and evolution. Now that many studies have appeared it is becoming increasingly clear that natural variation at specific loci can have strong pleiotropic effects on multiple traits. This is especially noticeable in the coregulation of plant metabolism, where often hotspots of trait associations are found. In addition, many examples of epistatic genetic regulation can be seen, further adding to the complexity of quantitative trait regulation. Nonetheless, GWA mapping has allowed the identification of many novel players in the pathway topology of many traits. Some of these show strong signatures of evolution, such as selective sweeps or balancing selection. This is often reflected in the geographical distribution of allelic variation and thus provides indications for ecological adaptation. We will provide examples to demonstrate the contribution that GWA mapping has made to our understanding of the evolution and regulation of quantitative trait variation.

P1.7 THE GENETIC BASIS FOR *LOTUS JAPONICUS* COLD ADAPTATION AND COLONIZATION OF JAPAN

MONDAY 3 JULY, 2017 **15:10**

STIG U ANDERSEN (AARHUS UNIVERSITY, DENMARK), NIRAJ SHAH (AARHUS UNIVERSITY, DENMARK), TOMOMI WAKABAYASHI (KYOTO UNIVERSITY, JAPAN), YASUKO KAWAMURA (TOHOKU UNIVERSITY, JAPAN), MING-ZHUO WANG (TOHOKU UNIVERSITY, JAPAN), VIKAS GUPTA (AARHUS UNIVERSITY, DENMARK), HAOJIE JIN (AARHUS UNIVERSITY, DENMARK), SHOHEI KUSAKABE (TOHOKU UNIVERSITY, JAPAN), MADS SØNDERGAARD (AALBORG UNIVERSITY, DENMARK), KAARE L NIELSEN (AALBORG UNIVERSITY, DENMARK), KORBINIAN SCHNEEBERGER (MAX PLANCK INSTITUTE FOR PLANT BREEDING RESEARCH, GERMANY), JENS STOUGAARD (AARHUS UNIVERSITY, DENMARK), SHUSEI SATO (TOHOKU UNIVERSITY, JAPAN)

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The Japanese archipelago is separated from mainland Asia by the Japan sea, which acts as a natural barrier for plant colonization. Furthermore, the archipelago shows large variation in climatic conditions, challenging plant adaptation. *Lotus japonicus* (Lotus) has overcome these challenges and can be found throughout Japan. To understand the genomic history of *Lotus* in Japan and decipher the genetic events that underpin colonization and adaptation, we carried out a population genetic analysis based on re-sequencing of 133 Lotus japonicus accessions. We found evidence of a population-wide selective sweep overlapping with a seed-expressed transcription factor, suggesting a possible requirement for a specific seed dormancy phenotype during the establishment of the Japanese population. Our data indicated that *Lotus* first appeared in the south of Japan, migrating to the north while losing genetic diversity and separating into three sub-populations with different population histories. This indicated a three-stage colonization of Japan in step with global temperature fluctuations, and with the northernmost Hokkaido Island only very recently colonized. Based on winter hardiness field data, we found two significant signals in a genome-wide association scan, suggesting that *Lotus* has exploited both standing variation and *de novo* mutation for successful migration and cold adaptation. Our results indicate that a few key genetic adaptations have allowed *Lotus* to colonize a very geographically diverse archipelago in a short period of time, suggesting that great phenotypic versatility does not necessarily require extensive genetic polymorphism.

P1.18 THE WONDROUS CYCLES OF POLYPLOIDY IN PLANTS

MONDAY 3 JULY, 2017 **16:10**

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One of the signal realizations of the genomics era is that all flowering plants are multiply polyploid, varying in the number and relative antiquity of their episodic, whole-genome doubling events. *Gossypium*, the cotton genus, exemplifies this recurrent, episodic polyploidization, with both ancient polyploidy and more recent neoallopolyploids that originated following a biological reunion 1-2 MYA of divergent diploids from different hemispheres. This most recent serendipitous merger between diploid genomes that varied two-fold in size generated myriad genomic and transcriptomic responses, which serve as illustrative models for understanding evolutionary processes following allopolyploidy. These include gene silencing, intergenomic gene conversion, and novel cytonuclear interactions. Allopolyploid formation also induces complex transcriptomic responses, including genome-wide modification of genic expression and co-expression patterns and variable cis- and trans-control of duplicate gene expression. Cyclical, recurring polyploidy occurring over time scales ranging from hundreds to millions of years sets in motion processes that lead to genome downsizing, genomic fractionation, and chromosomal diploidization. This polyploidy-induced dynamism, observed in *Gossypium*, is episodically and variably reiterated throughout the angiosperms. A major challenge is to connect these long and short-term processes to our understanding of the genotype-to-phenotype equation, and hence the adaptive role of polyploidy and its importance to the generation of biodiversity and to agriculture.

P1.19 ADAPTATION OF MEIOTIC RECOMBINATION AFTER WHOLE GENOME DUPLICATION

MONDAY 3 JULY, 2017 **16:40**

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Whole genome duplication (WGD) has important implications for adaptation, speciation, and agriculture. But doubling the number of homologous chromosomes in a genome poses challenges to meiotic chromosome segregation. Newly formed polyploids often have low fertility attributable to defects such as multivalent associations among the available homologs, or failures in pairing that result in univalents. These challenges are, however, evolutionarily surmountable - many polyploid species have stable diploid-like chromosome segregation – but the mechanism underlying this has remained mysterious. To investigate the mechanistic basis of meiotic stabilization in polyploids, we use Arabidopsis arenosa, an outcrossing relative of A. thaliana with extant natural diploid and autotetraploid populations. The autotetraploid has cytologically diploidized meiosis, reduced crossover rates, and increased terminalization of crossovers relative to the diploid – a pattern seen in a wide range of polyploids. In a genome scan for

selection we identified six functionally connected meiosis genes as being under strong selection in tetraploids. The products of these genes are structural proteins that function collaboratively to coordinate chromosome pairing, synapsis, and the number and distribution of crossovers. We show for three genes that the tetraploid alleles indeed reconfigure crossovers and promote polyploid meiotic stability. Our work has led us to favor a model in which stabilization of chromosome segregation in autopolyploids is achieved by modifying both placement and number of crossovers, likely through increased strength of crossover interference.

P1.20 HOW TODAY'S PHENOTYPING TECHNOLOGIES CAN SPEED UP GAINS IN AGRICULTURAL PRODUCTIVITY

TUESDAY 4 JULY, 2017 **10:30**

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A goal of plant science is to find new solutions to increasing productivity, to provide affordable food to the world's population and conserve land, water and chemical inputs. Productivity arises from the combination of crop Genotype, Environment, and soil inputs and Management (G x E x M). Links among plant science, genomics for breeding and input technologies and soil management can be strengthened to enhance G x E x M productivity. Phenotyping can measure the result of combining G x E x M. Today's phenotyping technologies use automation to allow the dynamics of plant and crop development to be tracked non-destructively in fields and greenhouses using a wide range of wavelengths and imaging methods to select beneficial growth and physiology traits. A rapidly advancing area of phenotyping is that of the crop root systems. This allows quantification of root growth, soil interactions and function, and the contributions from genotype, environment, and management. Phenotyping can measure whole-plant phenotypes (root, rhizosphere and shoot traits) and hence productivity traits can be much more accurately quantified than in the past. This talk will present examples to support how today's plant and crop phenotyping technologies can be better integrated into G x M x E selection strategies to enhance the efficiency of gains from seed genomics and input technologies to increase crop productivity.

P1.21 WHAT'S GOING ON IN THERE? IMAGING TECHNOLOGIES AND ANALYSIS FRAMEWORKS TO INVESTIGATE THE HIDDEN PARTS OF PLANTS

TUESDAY 4 JULY, 2017 **11:10**

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The Topp Lab is interested in crop root system growth dynamics and function in response to environmental stresses such as drought, rhizosphere interactions, and as a consequence of artificial selection for agronomically important traits such as nitrogen uptake and high plant density. Studying roots requires the development of imaging technologies, computational infrastructure, and statistical methods that can capture and analyze morphologically complex networks over time and at high-throughput. The lab uses several imaging tools (optical, X-ray CT, PET, others) along with quantitative genetics and molecular biology to understand the dynamics of root growth and physiology. We aim to understand the relationships among root traits that can be effectively measured both in controlled laboratory environments and in the field, and to identify genes and gene networks that control root, and ultimately whole plant architectural features useful for crop improvement.

P1.22 BUILDING A LEAF WITH CELLS OR VICE VERSA - ANALYSING AND MODELLING THE RELATIONSHIPS BETWEEN TRAITS

TUESDAY 4 JULY, 2017 **11:40**

CHRISTINE GRANIER (INRA MONTPELLIER, FRANCE)

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Plant organ growth results from a combination of cellular processes. The number of cells is increased by mitotic cycles, cell size increases through cytoplasmic growth and turgor-driven cell-wall extension. In addition, in many plant species, the endocycle, is used to increase cellular DNA contents without cell division and is associated with cell enlargement. Many molecular actors controlling each process have been identified within plant leaves during the last decades. However, reverse genetics approaches have failed in many cases to elucidate how these cellular processes are coordinated together, with contradictory conclusions from a study to another. Many reasons can explain these apparent contradictions including the low consideration of gene redundancy, environmental effects, developmental phases,...

Recent advances in plant phenotyping technologies and the development of whole pipeline of analyses have increased the capacity to measure and analyse many morphological and physiological traits on large number of individuals. By combining quantitative genetics, modelling and statistics, we recently disentangled how leaf growth-related traits are embedded in networks of dependencies and independencies. Analysing the relationships between biochemical, physiological, tissular, organ and whole shoot developmental traits and how these are affected by genetics and environment gave new insight into multi-scale leaf growth controls and its plasticity.

P1.23 ASSESSMENT OF PLANT PERFORMANCE TRAITS IN CONTROLLED ENVIRONMENTS AND TRANSLATION TO THE FIELD

TUESDAY 4 JULY, 2017 **12:10**

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To meet the challenges in global food security requires the development of strategies towards the optimization of yield formation and resource efficiency of crop plants under future climate scenarios. To enable this, a deeper understanding of processes underlying plant acclimation to changing environments is necessary. Using high throughput automated plant phenotyping systems at IPK, the dynamics of plant growth and photosynthetic efficiency have been studied in accession panels of Arabidopsis and the maize IPK Genebank collection under controlled conditions. This led to the identification of Arabidopsis and maize candidate accessions with different acclimation strategies to high light and variations in biomass yield and photosynthetic efficiency, respectively. To evaluate and enhance the prospects of lab-to field translation, candidate maize accessions have furthermore been phenotyped for root- and shoot traits under different cultivation conditions in the glasshouse and in the field. Modification of the standard cultivation procedures improved the lab-to-field translation of phenotypic trait expression which will be further optimized in the Plant Cultivation Hall currently being erected at IPK. This building will enable to run specifically designed and reproducible cultivation scenarios that mimic field conditions. In this way, trait expression similar to that in the field will be triggered and monitored using automated phenotyping installations. Investigations involving precise variation of environmental parameters will yield a deeper understanding of acclimation processes and underlying molecular mechanisms and genetic determinants and will support the prediction of idiotypes with improved performance under future climate scenarios.

P1.24 COMPLEX TRAIT GENETICS BEYOND ADDITIVITY

TUESDAY 4 JULY, 2017 **13:40**

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Genetic studies of complex traits often rely on the statistical genetics models, methods and tools developed in quantitative genetics. The theory and assumptions within this framework were largely formed before molecular genetics and genomics provided the ability to study how individual genotypes contributed to the variation in complex traits. Much genetics, genomics and functional data has now shown that the biological mechanisms determining such quantitative traits are often non-additive. I will use several empirical examples to illustrate the importance of non-additive allelic effects for the regulation of complex trait phenotypes in natural and experimental populations. I will then show how the revealed non-additive allelic effects often contribute much additive genetic variance in populations. The examples illustrate the limitations of the classic quantitative genetics models for making inferences about the importance of additive and non-additive genetic mechanisms for complex trait variation. The present analysis paradigm in quantitative genetics was not designed to unravel the mechanisms contributing to complex traits. By realizing the limitations of using these models for this purpose, alternative analytical strategies can be developed that makes better use of the powerful data generated in genetics today.

P1.25 PUBESCENCE IN MEXICAN HIGHLAND MAIZE IS DRIVEN BY GENE FLOW FROM WILD RELATIVES

TUESDAY 4 JULY, 2017 **14:20**

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Maize was domesticated 9000 BP from balsas Teosinte *(Zea mays subsp. parviglumis)* in the basin of the Balsas river in Mexico. Once it was domesticated, maize dispersed to the highlands of central Mexico. In this new niche maize encountered and hybridized with Chalco teosinte *(Zea mays subsp. mexicana)* resulting in gene flow from mexicana into maize. Chalco teosinte and Mexican highland maize share intense stalk pigmentation and a high density of macro-hairs around the sheath, traits absent from both balsas teosinte and maize from the mexican lowlands, suggesting that the presence of these traits in maize results from gene flow from chalco teosinte. QTL mapping of sheath pubescence using a recombinant inbred line mapping population, derived from the cross of the Mexican highland landrace Palomero Toluqueño and reference inbred B73, identified a major QTL on chromosome chromosome 9, which co-localizes with a previously reported region of introgression from Chalco teosinte. This is compelling evidence that this trait, which is present in the majority of mexican highland maize, was derived from Chalco teosinte, and could potentially represent an important adaptation to the highland environments.

P1.26 MODEL-ASSISTED ESTIMATION OF THE GENETIC VARIABILITY OF TOMATO GROWTH PHYSIOLOGICAL PARAMETERS UNDER CONTRASTED WATER CONDITIONS

TUESDAY 4 JULY, 2017 **14:35**

DARIO CONSTANTINESCU (INRA, FRANCE), MOHAMED M MEMMAH (INRA, FRANCE), GILLES VERCAMBRE (INRA, FRANCE), MICHEL GÉNARD (INRA, FRANCE), VALENTINA BALDAZZI (INRA, FRANCE), NADIA BERTIN (INRA, FRANCE)

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Drought stress is a major abiotic stress threatening plant and crop productivity. Understanding mechanisms governing water and carbon accumulations and identifying genes, QTLs and phenotypes that will enable trade-offs between fruit growth and quality under Water Deficit (WD) condition is a crucial challenge for breeders and growers.

In the present work, 117 recombinant inbred lines of a population of *Solanum lycopersicum* were phenotyped under control (C) and WD condition. Data of plant water status, fruit growth, and composition were used to calibrate a process-based model describing water and carbon fluxes in growing fruit, in order to analyse the principal mechanisms involved in the plant adaptation to WD.

Eight model genotypic parameters were estimated and their variability was analysed, permitting to explore diverse genetic strategies in response to WD.

The model was then applied to design ideotypes (i.e. ideal plants) producing fruits with high dry matter content in C condition and low fresh mass loss in WD condition. The ideotypes were then confronted with the existing recombinant lines, confronting the processes involved in the WD resistance.

P1.2 LINKING THE ARABIDOPSIS BIOLOGICAL CLOCK MODEL TO THE 1001 GENOMES PROJECT

TUESDAY 4 JULY, 2017 **14:50**

URIEL URQUIZA-GARCÍA (THE UNIVERSITY OF EDINBURGH, UNITED KINGDOM), NACHO MOLINA (IGBMC - CNRS, FRANCE), ANDREW J MILLAR (THE UNIVERSITY OF EDINBURGH, UNITED KINGDOM)

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24-hour biological rhythms driven by the circadian clock control plant processes from elongation growth, to metabolism and seasonal flowering. Mathematical models of the clock gene circuit have been fundamental for integrating heterogeneous data into quantitative theories for circadian rhythms in Arabidopsis thaliana. We show that recasting a clock model into absolute units (molecules per cell) provides a first step in linking mechanistic models to the 1001 Arabidopsis genomes.

Successive plant clock models have increased in complexity by incorporating newly-identified biochemical components and links. While real units of time have been central, the mass scale has been left in arbitrary units. We therefore rescaled the P2011 clock model to match publically-available data with absolute mass units, in order to test whether the model's predicted kinetics were biochemically reasonable. The results for RNA and protein concentrations will be discussed, locating potentially problematic dynamics of specific clock components. Experimental, absolute quantification of key circadian clock proteins is crucial to test these hypotheses. This process revealed an approach to link circadian oscillator dynamics to transcriptomic profiles, not only within a single ecotype but also in the context of the Arabidopsis 1001 genomes project. We exemplify the process for a key clock component. Our results promise a mechanistic link from SNPs in genomic DNA sequence to gene expression dynamics that control multiple, physiological phenotypes.

P1.29 SHAPE UP - STUDY OF NATURAL VARIATION IN ROOT-SHOOT RATIO UNDER SALT STRESS REVEALS GENES INVOLVED IN EARLY SALT STRESS RESPONSES

TUESDAY 4 JULY, 2017 **16:00**

MAGDALENA M JULKOWSKA (KING ABDULLAH UNIVERSITY OF SCIENCE AND TECHNOLOGY, SAUDI ARABIA), ARTHUR KORTE (UNIVERSITY OF WUERZBURG, GERMANY), RACHID AIT HADDOU (KING ABDULLAH UNIVERSITY FOR SCIENCE AND TECHNOLOGY, SAUDI ARABIA), CHRISTA TESTERINK (UNIVERSITY OF AMSTERDAM, NETHERLANDS), MARK A TESTER (KING ABDULLAH UNIVERSITY FOR SCIENCE AND TECHNOLOGY, SAUDI ARABIA)

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High soil salinity is one of the major factors limiting crop yield. Shoot sodium exclusion is an important contributor to salinity tolerance, but it is not always correlated with salinity tolerance, indicating importance of other traits. Notably, salt stress rapidly impacts the growth and development of different plant organs to different extents, leading to alterations in plant development. In Arabidopsis Col-0 genotype, reduction in main root growth is more severe than reduction in lateral root growth or development, resulting in altered root architecture. Other alterations to plant development, such as root : shoot ratio are likely to be also contributing to salinity tolerance. In this study, we describe salt stress and hormone induced changes in root : shoot ratio in Arabidopsis plants grown on agar plates, by quantifying the dynamics of root and shoot growth in different conditions. We developed a tool that enables estimation of increases in root and shoot mass through quantification of green and white pixels and automated fitting of growth curves. We identified genetic components underlying salt stress-induced changes in root:shoot ratio by studying natural variation in the Arabidopsis “HapMap” population and performing association genetic analyses to identify candidate genes specific to stress conditions. Further validation of candidate genes will provide more insight into signals regulating stress-induced alterations in plant development and their role in overall salinity tolerance.

P1.30 MAKING SPACE TO BREATHE: THE ROLE OF THE CELL WALL IN DETERMINING STOMATAL AND MESOPHYLL CONDUCTANCE

TUESDAY 4 JULY, 2017 **16:30**

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Photosynthetic carbon uptake is dependent on developmentally and dynamically regulated gas flux through the stomatal pores and complex underlying airspace. The cell wall must be important in stomata and mesophyll formation, yet our understanding of its role remains limited. An immunological screen of Arabidopsis leaves indicated that differential methylation of pectic homogalacturonan (HG) is associated with differentiation of both the mesophyll and the stomata. In the mesophyll, esterified HG is most abundant at the corners of airspaces, whereas joined cell walls contain an abundance of de-esterified HG, suggesting a role for pectin modification in regulating cell separation and determining porosity. In stomata, guard cells lack methyl-esterified HG. Our previous work which identified a pectin methyl-esterase with a specific role in guard cell function showed that gain of methyl-esterified HG in the guard cell wall compromises stomatal function. In addition, we show that stomatal poles have a specific pattern of methyl-esterified HG. Probing guard cell stiffness by atomic force microscopy suggests that this polar pattern of methyl-esterified HG leads to altered mechanical properties and function of the guard cells. Finally this project aims to examine how mesophyll airspace formation is coordinated with stomatal positioning to form sub-stomatal cavities. By examining cellular architecture by microCT scanning, and measuring gas exchange in mutants with altered stomatal density or reduced stomatal function, we will investigate the coupling of these two developmental processes.

P1.31 MAPPING THE EARLY RESPONSES TO SALT STRESS IN *ARABIDOPSIS THALIANA*

TUESDAY 4 JULY, 2017 **16:45**

MARIAM AWLIA (KING ABDULLAH UNIVERSITY OF SCIENCE AND TECHNOLOGY, SAUDI ARABIA), ARTHUR KORTE (UNIVERSITY OF WÜRZBURG, GERMANY), KLÁRA PANZAROVÁ (PHOTON SYSTEMS INSTRUMENTS (PSI), CZECH REPUBLIC), SÓNIA NEGRÃO (KING ABDULLAH UNIVERSITY OF SCIENCE AND TECHNOLOGY (KAUST), SAUDI ARABIA), MARK TESTER (KING ABDULLAH UNIVERSITY OF SCIENCE AND TECHNOLOGY (KAUST), SAUDI ARABIA), MAGDALENA M JULKOWSKA (KING ABDULLAH UNIVERSITY OF SCIENCE AND TECHNOLOGY (KAUST), SAUDI ARABIA)

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Salt stress reduces plant growth very rapidly after salt exposure. This reduction occurs prior to toxic ion accumulation in the shoot and the early responses to salt stress are part of the osmotic component of salinity tolerance. In this study, we examined the natural variation in the early salt stress responses of Arabidopsis accessions from the HapMap population using high-throughput non-destructive phenotyping. RGB images of rosettes and kinetic measures of chlorophyll fluorescence were captured daily for seven days from the time of salt application. Traits associated with rosette growth and chlorophyll fluorescence, such as rosette area, rosette greenness and non-photochemical quenching, were quantified non-invasively using the PSI PlantScreen phenotyping system. The natural variation observed was employed for the identification of candidate genes using genome-wide association studies (GWAS) and 10M SNP markers. In addition to the common single-trait GWAS model, we also used a multi-trait mixed model to determine salt stress-specific associations. We identified genetic associations that are unique for individual time points and traits, but also associations recurring through time and across different traits. Validating candidate genes underlying the observed associations and performing molecular characterisation of the allelic variation will improve our understanding of the genetic control of rapid growth rate reductions caused by salt stress. Gaining insight into genes affecting the early responses to salt stress, and their contribution to overall salinity tolerance, will aid crop salinity research and facilitate cultivation of plants in arid and saline conditions globally.

P1.8 IDENTIFICATION OF A PROLINE RICH FAMILY PROTEIN THAT IS NEGATIVELY CORRELATED WITH ETIOLATED *ARABIDOPSIS THALIANA* HYPOCOTYL GROWTH

TUESDAY 4 JULY, 2017 **POSTER SESSION**

MALGORZATA ZDANIO (UNIVERSITY OF ANTWERP, BELGIUM), AGNIESZKA K BORON (UNIVERSITY OF ANTWERP, BELGIUM), DARIA M BALCEROWICZ (UNIVERSITY OF ANTWERP, BELGIUM), MARIOS N MARKAKIS (UNIVERSITY OF ANTWERP, BELGIUM), GRÉGORY MOUILLE (INRA CENTRE DE VERSAILLES-GRIGNON, FRANCE), DMITRY SUSLOV (SAINT-PETERSBURG STATE UNIVERSITY, RUSSIA), HERMAN HÖFTE (INRA CENTRE DE VERSAILLES-GRIGNON AGROPARISTECH INSTITUT JEAN-PIERRE BOURGIN, FRANCE), KRIS VISSENBERG (UNIVERSITY OF ANTWERP, BELGIUM)

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Growth of the etiolated Arabidopsis hypocotyl is biphasic. During the first phase all cells elongate slowly and synchronously. At 48hrs after imbibition, cells at the hypocotyl base undergo a growth acceleration. Subsequently, this rapid elongation propagates through the hypocotyl from base to top. It is largely unclear what regulates the switch from slow to fast elongation. Micro-array analysis performed before, during and after growth acceleration identified many differentially expressed genes. Reverse genetics-based screening for hypocotyl phenotypes identified three independent mutant lines of At1g70990, a proline-rich family protein, with shorter etiolated hypocotyls during the slow elongation phase. Dark-grown hypocotyls of those mutants start to elongate faster compared to wild type at 72hrs after imbibition. Mature 8-day-old dark-grown hypocotyls were significantly longer than wild type. Analysis of transgenic seedlings bearing a promoter::GFP construct indicated expression in the root, that was confined to the endodermis and pericycle. In 2-days-old dark-grown seedlings expression was especially strong in the basal part of hypocotyl, whilst mature seedlings exhibited expression throughout this organ. The protein encoded by At1g70990 was localized to the cytoplasm in C-terminal protein-GFP fusion lines using confocal microscopy. Fourier Transformed Infrared (FT-IR) Microspectroscopy identified subtle changes in cell wall composition. In addition, altered cell wall biomechanics were detected in the mutant lines using constant load extensiometry. Although the precise working mechanism remains unknown, our results suggest that the proline-rich family protein is required during the first phase of elongation and regulates the moment and extent of the growth acceleration by regulating cell wall extensibility.

P1.9 GENOME-WIDE ASSOCIATION STUDY REVEALS THE GENETIC ARCHITECTURE OF GRAIN CALCIUM ACCUMULATION IN FINGER MILLET

TUESDAY 4 JULY, 2017 **POSTER SESSION**

SWATI PURANIK (INSTITUTE OF BIOLOGICAL ENVIRONMENTAL AND RURAL SCIENCES ABERYSTWYTH UNIVERSITY, UNITED KINGDOM), HENRY OJULONG (INTERNATIONAL CROPS RESEARCH INSTITUTE FOR THE SEMI-ARID TROPICS (ICRISAT), KENYA), RATTAN YADAV (INSTITUTE OF BIOLOGICAL ENVIRONMENTAL AND RURAL SCIENCES ABERYSTWYTH UNIVERSITY, UNITED KINGDOM)

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Calcium (Ca) is an essential macromineral and required in relatively large dietary quantities for maintaining a sound overall health. Therefore, significant progress is needed for biofortification of staple crops to enhance grain Ca content. Among all cultivated cereals, finger millet [*Eleusine coracana* (L.) Gaertn.], has the highest concentration of Ca (350mg/100g) in its grains and can serve as an excellent sustainable candidate for Ca biofortification. With the aim to identify genomic loci underlying grain Ca content, we performed genome-wide association (GWA) analysis utilizing a world collection of finger millet germplasm. Grain Ca contents showed very high variability among the collection with distinct differences observed among African, Asian, European and American genotypes. Large-scale genotyping-by sequencing was employed and 154238 bialleleic, polymorphic SNPs with a MAF $\geq 1\%$ across the genotypes were employed for GWA mapping. Associations were done by fitting three statistical models. After correction for population structure and family relatedness, loci showing strong associations with grain Ca content have been identified. This is the first GWA study based on large-scale SNP genotyping in finger millet for grain Ca content. The novel genomic loci identified can facilitate positional cloning of underlying causal genes. These results will facilitate further improvement of finger millet and also other staple crops. Such crops will be a tremendous boost for smallholder farmers, agriculture sectors, and food industries which will help to reduce the burden of Ca deficiency.

P1.10 LINKING TRANSCRIPTOME TOPOLOGY TO PHENOTYPE TO IDENTIFY CANDIDATE TRANSCRIPTS DRIVING IMPORTANT CROP TRAITS IN POTATO

TUESDAY 4 JULY, 2017 **POSTER SESSION**

ERIK ALEXANDERSSON (DEPARTMENT OF PLANT PROTECTION SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES, SWEDEN), SANDEEP KUSHWAHA (DEPARTMENT OF PLANT BREEDING SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES, SWEDEN), ERIK ANDREASSON (DEPARTMENT OF PLANT BREEDING SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES, SWEDEN)

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Potato is the third most consumed crop in the world. It has a very high yield potential and constitute an almost irreplaceable part of many countries' cuisines. To gain better understanding of *Phytophthora infestans* resistance and other important crop traits, 34 progeny lines in a crossing population obtained from a resistant breeding line and a susceptible cultivar (SW93-1015*Desiree) were phenotyped for 37 different traits in the field and controlled environments. In addition to *P. infestans* resistance these included yield, tuber greening and Dickeya and Alternaria susceptibility. By Illumina Hiseq 2000 sequencing, a master transcriptome was constructed based on all 34 crossing lines by *de novo* assembly. After this, gene expression and phenotypic data for all lines were analyzed by different similarity indices and correlation coefficients. With a correlation cutoff (Pearson corr > 0.5 and p-value < 0.05) we found transcript putatively associated to, for example, traits such as yield (17 transcripts), high laying tubers (8 transcripts), tuber blight (27 transcripts), *P. infestans* leaf resistance (34 transcripts), above-ground growth rate (35 transcripts), tuber greening (14 transcripts) and early flowering (24 transcripts). The most highly transcript expression correlation was associated to *P. infestans*, and several of these transcripts are annotated as disease resistance factors. In this work we explore new ways of relating transcript expression levels to phenotypes using a crossing population. We believe that several of the transcripts we have identified to have highly correlated expression with certain traits affect these traits. However, this needs to be confirmed by further experiments.

P1.11 IDENTIFICATION AND CHARACTERIZATION OF *APOLLO*, AN ARABIDOPSIS THALIANA MUTANT WITH INCREASED HYPOCOTYL ELONGATION

TUESDAY 4 JULY, 2017 **POSTER SESSION**

MALGORZATA ZDANIO (UNIVERSITY OF ANTWERP, BELGIUM), AGNIESZKA K BORON (UNIVERSITY OF ANTWERP, BELGIUM), MARIOS N MARKAKIS (UNIVERSITY OF ANTWERP, BELGIUM), NORA GAAL (UNIVERSITY OF ANTWERP, BELGIUM), DMITRY SUSLOV (SAINT-PETERSBURG STATE UNIVERSITY, RUSSIA), IRMA ROIG-VILLANOVA (CENTRE FOR RESEARCH IN AGRICULTURAL GENOMICS, SPAIN), JAUME F MARTÍNEZ-GARCÍA (CENTRE FOR RESEARCH IN AGRICULTURAL GENOMICS, SPAIN), GRÉGORY MOUILLE (INRA CENTRE DE VERSAILLES-GRIGNON, FRANCE), HERMAN HÖFTE (INRA CENTRE DE VERSAILLES-GRIGNON AGROPARISTECH INSTITUT JEAN-PIERRE BOURGIN, FRANCE), KRIS VISSENBERG (UNIVERSITY OF ANTWERP, BELGIUM)

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We isolated a mutant with increased hypocotyl growth in the light and named it *apollo*. Adaptor-PCR revealed that the T-DNA was inserted in the intergenic region between two anti-parallel genes. One of them codes for a transcription factor, named ORPHEUS, that is normally down-regulated upon light perception. *Apollo* had a more than 40% increase in etiolated hypocotyl length and a striking 420% increase when grown in the light versus the wild type. Cellular measurements confirmed that this was due to increased cell elongation. In addition, petiole length of leaf 1 and 2 was increased by more than 80%, seed area by 20%, embryo area by 23% and the rosette area was 30% smaller. Although increased thinning of the walls could cause the observed increase in etiolated hypocotyl elongation, cell wall thickness of fully elongated wild type or apollo cells did not differ significantly. Cell wall extensibility, on the other hand, was enhanced in etiolated hypocotyl segments of *apollo*. FT-IR analysis of *apollo* and wild type hypocotyl cell walls revealed no changes in cell wall composition. The shade-avoidance-like phenotype of *apollo*, defective response to simulated shade and altered de-etiolation under continuous red/far-red light suggest a potential deficiency of the phytochrome chromophore phytochromobilin. Genomic *apollo* DNA sequencing excluded a mutation in the phytochromobilin synthase (HY2) gene, although the expression level of HY2 was decreased in the mutant. We suggest that the T-DNA deregulates the transcriptional control of the ORPHEUS transcription factor and that this leads to defective responses upon light perception.

P1.12 USING STRUCTURAL MODELS TO VALIDATE AND IMPROVE ROOT IMAGE ANALYSIS PIPELINES

TUESDAY 4 JULY, 2017 **POSTER SESSION**

GUILLAUME LOBET (FORSCHUNGSZENTRUM JUELICH, GERMANY), MANUEL NOLL (UNIVERSITÉ DE LIÈGE, BELGIUM), IKO T KOEVOETS (UNIVERSITY OF AMSTERDAM, NETHERLANDS), LOIC PAGÈS (INRA AVIGNON, FRANCE), PATRICK E MEYER (UNIVERSITÉ DE LIÈGE, BELGIUM), PIERRE TOCQUIN (UNIVERSITÉ DE LIÈGE, BELGIUM), CLAIRE PÉRILLEUX (UNIVERSITÉ DE LIÈGE, BELGIUM)

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Many structural root models have been developed, either generic or for specific species, and these have repeatedly been shown to faithfully represent the root system structure, as well as being able to output ground-truthed data for every simulation and image, independent of root system size. However, they have almost never been used as validation tools for image analysis procedure. Here we will show that structural root models can be used in combination with image analysis pipelines to assess and improve their overall performance. First, we will show that an in-depth analysis of root image analysis pipelines using such models reveals strong limitations in their ability to measure complex root systems. Secondly, we will present an innovative strategy that combines root models and machine-learning algorithms (random-forests), that has the ability to increase the measurement accuracy.

P1.13 USING ASSOCIATION MAPPING AND ARTIFICIAL SELECTION TO DISSECT THE GENETICS OF SHOOT BRANCHING PLASTICITY IN ARABIDOPSIS

TUESDAY 4 JULY, 2017 **POSTER SESSION**

HUGO TAVARES (SAINSBURY LABORATORY CAMBRIDGE UNIVERSITY, UNITED KINGDOM), MAAIKE DE JONG (SAINSBURY LABORATORY CAMBRIDGE UNIVERSITY, UNITED KINGDOM), URSZULA KANIA (SAINSBURY LABORATORY CAMBRIDGE UNIVERSITY, UNITED KINGDOM), REBECCA BUTLER (SAINSBURY LABORATORY CAMBRIDGE UNIVERSITY, UNITED KINGDOM), ALICE THOMAS (SAINSBURY LABORATORY CAMBRIDGE UNIVERSITY, UNITED KINGDOM), JULIE AFFLECK (SAINSBURY LABORATORY CAMBRIDGE UNIVERSITY, UNITED KINGDOM), RACHEL BURROWS (SAINSBURY LABORATORY CAMBRIDGE UNIVERSITY, UNITED KINGDOM), GILU GEORGE (SAINSBURY LABORATORY CAMBRIDGE UNIVERSITY, UNITED KINGDOM), KATYA KOZHEVNIKOVA (SAINSBURY LABORATORY CAMBRIDGE UNIVERSITY, UNITED KINGDOM), HAYLEY MCCULLOCK (SAINSBURY LABORATORY CAMBRIDGE UNIVERSITY, UNITED KINGDOM), RAJ PASAM (SAINSBURY LABORATORY CAMBRIDGE UNIVERSITY, UNITED KINGDOM), ANNE READSHAW (SAINSBURY LABORATORY CAMBRIDGE UNIVERSITY, UNITED KINGDOM), SALLY WARD (SAINSBURY LABORATORY CAMBRIDGE UNIVERSITY, UNITED KINGDOM), LISA WILLIAMSON (SAINSBURY LABORATORY CAMBRIDGE UNIVERSITY, UNITED KINGDOM), OTTOLINE LEYSER (SAINSBURY LABORATORY CAMBRIDGE UNIVERSITY, UNITED KINGDOM)

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Dissecting the genetics of complex quantitative traits remains a challenge, even in the era of genomics. This is particularly true if traits are controlled by many loci of small effect and/or by multi-allelic loci. Furthermore, traits might be plastic, such that an individual's phenotype depends on the environment. Here, we try to dissect the genetics of shoot branching in Arabidopsis by using complementary approaches: association (QTL) mapping and an evolve-and-resequence artificial selection experiment. We predict that this trait has a broad-sense heritability in the order of 20%-30%, and is considerably plastic in response to nutrient availability. This plasticity is partially genetic, with different genotypes responding differently to Nitrate availability. Despite this heritability, it proved challenging to identify QTL to explain it. By doing association mapping in a multi-parent mapping population (the Arabidopsis MAGIC lines), we hypothesize that part of the challenge is related with multi-allelic loci controlling the trait, which are not captured when using conventional (bi-allelic) SNP-based mapping. Furthermore, we have evidence that this trait might involve multiple (small effect) loci spread across the genome, which were revealed in an evolve-and-resequence experiment, where we artificially selected individuals with high number of branches in replicate randomly mating populations. We found several putative selective sweeps in these populations, which we believe are not due to drift, as randomly selected (control) populations did not show the same pattern of variability. Our study suggests that shoot branching is a canonical example of a complex trait, controlled by many loci with multiple functional alleles.

P1.14 GENETIC AND MOLECULAR MARKERS FOR REDUCED AGGRESSION IN ATLANTIC SALMON (SALMO SALAR L.)

TUESDAY 4 JULY, 2017 **POSTER SESSION**

JOHANNA AXLING (UPPSALA UNIVERSITY, SWEDEN), LEIF ANDERSSON (UPPSALA UNIVERSITET, SWEDEN), SVANTE WINBERG (UPPSALA UNIVERSITET, SWEDEN)

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As other vertebrates, teleost fish display divergent stress coping styles ('personality traits'), similar to what has been described as proactive and reactive stress coping in rodents. The routine based behaviour of proactive fish should be an advantage in the confined environment of aquaculture. Aggression, which is often a serious problem in commercial aquaculture, is also part of the proactive behavioural profile. This project aims at identifying genetic markers for proactive stress coping and aggression, markers that could allow selective breeding for non-aggressive salmon. We have performed a large scale study to evaluate behavioural assays to be used for screening stress coping styles of individual salmons. Behavioural tests were done on 1800+ individuals and of those 170 were tested twice in order to more accurately derive a true behavioural profile of each individual. Relationships between neuroendocrine stress responses and behavioural profiles will be investigated.

P1.15 PHENOTYPING AND GENOTYPING TO ENABLE GENOMIC ESTIMATED BREEDING VALUES IN POTATO

TUESDAY 4 JULY, 2017 **POSTER SESSION**

CATJA SELGA (SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES, SWEDEN), AAKASH CHAWADE (SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES, SWEDEN), MARIETTE ANDERSSON (SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES, SWEDEN), RODOMIRO ORTIZ (SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES, SWEDEN)

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Table potato, the third most important staple crop in the world, suffers from a number of diseases that requires multiple applications of pesticides to prevent tuber yield losses. The most economically detrimental late blight disease is caused by the oomycete Phytophthora infestans, which can affect both the foliage and tubers of the potato plant. The main targets for potato breeding in Sweden are to develop a cultivar with host plant resistance to P. infestans, high tuber yield and quality. We are pursuing a breeding method called genomic selection (GS) that could save the time and resources used in potato breeding. Phenotypic data were taken for host plant resistance, tuber yield-related traits, and flowering date on 1882 individuals from a training population (TP) based on eight bi-parental crosses. Host plant resistance was the most heritable trait and was significantly higher in all eight crosses compared to reference clones included in the field trial. Late blight also affected significantly tuber yield. GS is based on the use of genomic estimated breeding values (GEBVs), which are calculated through genotype calling of all 1882 clones included in the TP together with the phenotypic data. The genotypes are determined through Kompetitive Allele Specific Polymorphism (KASP) genotyping based on 2000 single nucleotide polymorphisms (SNPs) selected from a 12K SNP array of 88 randomly selected individuals from the TP and four parental lines. This research reinforces the need for appropriate phenotyping to assist on developing reliable GEBVs.

P1.16 GUARD CELL WALL STRUCTURE IN EUDICOTS AND MONOCOTS

TUESDAY 4 JULY, 2017 **POSTER SESSION**

SARAH CARROLL (THE UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), SAM M J AMSBURY (THE UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), ALICE L BAILLIE (THE UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), JULIE E GRAY (THE UNIVERSITY OF SHEFFIELD, UNITED KINGDOM), ANDREW J FLEMING (THE UNIVERSITY OF SHEFFIELD, UNITED KINGDOM)

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Stomata are controllable pores on the leaf surface formed by pairs of guard cells. These have a specialised cell wall structure which allows them to repeatedly expand and contract to control stomatal aperture, thus regulating gas exchange for photosynthesis and transpiration. Excessive transpiration results in detrimental water loss, thus stomatal aperture must be rapidly adjusted to ensure optimum water use. It has been proposed that the mechanics of the system may limit the speed of stomatal adjustment, yet we have little idea of how this is set, other than that the cell wall is likely to be of central importance. We have investigated the structure of the guard cell wall in *Arabidopsis thaliana*, a eudicot species, and more recently in *Brachypodium distachyon*, a model monocot species with reported similarities to *Hordeum vulgare* and *Triticum aestivum*. Immunohistochemistry and functional assays show that pectin is highly influential in regulating stomatal movement in both plants, yet the form of pectin involved varies. We aim to identify the genes in *Brachypodium* which regulate pectin biosynthesis and create mutant lines over-expressing or suppressing these genes. We will then assess these lines for stomatal function, as well as for whole plant physiological traits such as water use efficiency.

P1.17 DESIGNING RESILIENT AND PRODUCTIVE GRASSES WITH PLASTICITY TO EXTREME WEATHER EVENTS

TUESDAY 4 JULY, 2017 **POSTER SESSION**

DIMITRA A LOKA (NATIONAL PLANT PHENOMICS CENTRE IBERS ABERYSTWYTH UNIVERSITY, UNITED KINGDOM), DYLAN GWYNN-JONES (NATIONAL PLANT PHENOMICS CENTRE IBERS ABERYSTWYTH UNIVERSITY, UNITED KINGDOM), JOHN SCULLION (NATIONAL PLANT PHENOMICS CENTRE IBERS ABERYSTWYTH UNIVERSITY, UNITED KINGDOM), ALAN GAY (NATIONAL PLANT PHENOMICS CENTRE IBERS ABERYSTWYTH UNIVERSITY, UNITED KINGDOM), JOHN HARPER (NATIONAL PLANT PHENOMICS CENTRE IBERS ABERYSTWYTH UNIVERSITY, UNITED KINGDOM), DAGMARA GASIOR (NATIONAL PLANT PHENOMICS CENTRE IBERS ABERYSTWYTH UNIVERSITY, UNITED KINGDOM), ALISON KINGSTON-SMITH (NATIONAL PLANT PHENOMICS CENTRE IBERS ABERYSTWYTH UNIVERSITY, UNITED KINGDOM), ROSALIND DODD (BANGOR UNIVERSITY ENVIRONMENT CENTRE WALES, UNITED KINGDOM), DAVID CHADWICK (BANGOR UNIVERSITY ENVIRONMENT CENTRE WALES, UNITED KINGDOM), PAUL HILL (BANGOR UNIVERSITY ENVIRONMENT CENTRE WALES, UNITED KINGDOM), DAVID ROBINSON (BANGOR UNIVERSITY ENVIRONMENT CENTRE WALES, UNITED KINGDOM), DAVID JONES (BANGOR UNIVERSITY ENVIRONMENT CENTRE WALES, UNITED KINGDOM), GINA MILLS (CENTRE FOR ECOLOGY AND HYDROLOGY ENVIRONMENT CENTRE WALES, UNITED KINGDOM), FELICITY HAYES (CENTRE FOR ECOLOGY AND HYDROLOGY ENVIRONMENT CENTRE WALES, UNITED KINGDOM), MIKE HUMPHREYS (NATIONAL PLANT PHENOMICS CENTRE IBERS ABERYSTWYTH UNIVERSITY, UNITED KINGDOM)

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Climate change is projected to reduce the persistency of currently used forage grass varieties, thereby challenging global food security and compromising on their existing ecosystem functionality. Our objective is to identify morphological traits and monitor physiological responses from diverse and novel *Festulolium* (ryegrass spp. x fescue spp. Hybrids) grass populations that provide optimal combinations of good forage production together with resilience to multiple stresses. The grasses were: *Festulolium* variety Prior *(Lolium perenne x Festuca pratensis)*, shown to mitigate run-off and flooding; two advanced breeding populations of diploid *L. perenne* with genes for drought tolerance derived from the Mediterranean fescue species *F. arundinacea* and *F. glaucescens*; two tetraploid hybrid populations involving *L. perenne* in combination with *F. glaucescens* and *F. mairei* (from North Africa), respectively. As controls, *Festulolium* variety AberNiche and *L. perenne* variety AberWolf were used. Treatments consisted of: A) Control; plants maintained at optimum conditions, B) Drought; plants received limited quantity of water for 12 weeks, C) Flood; plants were fully submerged for 4 weeks and D) Ozone; plants were exposed to increased ozone concentrations (110 ppb) for 4 weeks. Root morphological traits and physiological responses were monitored and recorded before stress initiation and at the end of stress and recovery periods and the results were evaluated. Identifying and selecting reliable morphological and physiological traits associated with increased resistance to multiple abiotic stresses is a prerequisite to ensure future grasslands resilience.

P2 CARNIVOROUS PLANTS – PHYSIOLOGY, ECOLOGY, AND EVOLUTION

ORGANISED BY: SIMON POPPINGA (UNIVERSITY OF FREIBURG, GERMANY)

P2.1 TRAP DIVERSITY AND EVOLUTION IN CARNIVOROUS PLANTS

THURSDAY 6 JULY, 2017 **09:00**

ANDREAS FLEISCHMANN (BOTANISCHE STAATSSAMMLUNG MÜNCHEN, GERMANY)

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Carnivory has evolved at least ten times in flowering plants, resulting in 19 carnivorous plant genera containing at total of ca. 800 species. Five basic trap types are found among carnivorous plants (pitfall traps, adhesive traps, snap traps, eel traps, and suction traps), several of which have evolved in parallel in only distantly related groups. On the other hand, some trap types (especially active traps such as suction or snap traps) resulted from modification of passive trap types within the same evolutionary lineage. The evolution of trap types is discussed with a special focus on Nepenthales and Lamiales, which show the highest trap and species diversity among carnivorous plants.

P2.2 FACING THE GREEN THREAT: MORPHOLOGICAL REACTIONS OF DAPHNIIDS ON BLADDERWORT PRESENCE

THURSDAY 6 JULY, 2017 **09:40**

SEBASTIAN KRUPPERT (RUHR-UNIVERSITÄT BOCHUM, GERMANY), MARTIN HORSTMANN (RUHR-UNIVERSITÄT BOCHUM, GERMANY), LINDA C WEISS (RUHR-UNIVERSITÄT BOCHUM, GERMANY), ANNA WESTERMEIER (ALBERT-LUDWIGS-UNIVERSITÄT FREIBURG, GERMANY), SIMON POPPINGA (ALBERT-LUDWIGS-UNIVERSITÄT FREIBURG, GERMANY), THOMAS SPECK (ALBERT-LUDWIGS-UNIVERSITÄT FREIBURG, GERMANY), RALPH TOLLRIAN (RUHR-UNIVERSITÄT BOCHUM, GERMANY)

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Having a key position in many lentic ecosystems, waterfleas of the family Daphniidae are threatened by a wide diversity of predators. Daphniids counter this predation pressure by plastically developing adaptive morphological defence strategies. These increase their survival chances. In fact, a vast variety of such inducible defences has been described against a range of animal predators including larvae of the phantom midge *Chaoborus* (diptera), the backswimmer *Notonecta* (heteroptera), *Triops* (crustacea) and fish. However, next to animal predators daphniids are also exposed to predation by carnivorous plants such as the bladderwort, *Utricularia australis*. With its suction traps optimised to consume zooplankton prey and seasonally dependent large populations, it poses a serious threat to small daphniid species. Due to daphniid's high degree of plasticity towards animal predators, we here wanted to determine whether *Ceriodaphnia dubia* is also able to defend from *Utricularia* predation. For that, we performed a bioassay in conjunction with predation trials. We measured *Ceriodaphnia* morphology in 2D and 3D. We detected significant morphological changes. Morphologically adapted *Ceriodaphnia* were less susceptible to *Utricularia* predation in our predation trials.

In conclusion, we anticipate that this is a first description of an inducible morphological defence against a carnivorous plant.

P2.3 FACING THE GREEN THREAT: UNRAVELLING THE COMPLEX MORPHOLOGICAL REACTIONS OF DAPHNIIDS TO *UTRICULARIA*

THURSDAY 6 JULY, 2017 **09:55**

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Waterfleas of the genus *Daphnia* are abundant primary consumers and key species in freshwater ecosystems. Many studies have shown their high degree of phenotypic plasticity against a range of predators. Daphniids form so called ‘inducible defences’ that are temporally coherent to the occurrence of carnivorous animals, e.g. larvae of the phantom midge *Chaoborus* or fish. In addition to animal predators, freshwater ecosystems often also contain carnivorous plants, like the bladderwort *Utricularia* spec. and in fact, this plant species feeds on small daphniid species. However, up to now the development of inducible defences against *Utricularia* predation has not been shown. We chose to investigate the development of defences in *Ceriodaphnia dubia*, which we found coexisting with *Utricularia australis.* Actively preying *U. australis* induced morphological changes in *C. dubia*. We detected these changes by computing a 3D morphometric analysis. The head’s lateral width is increased, through the development of lateral fornices. The overall animal morphology becomes slender in dorso-ventral and lateral direction and the body length measured from the posterior ventral gap to the neck region increases. We anticipate that *C. dubia* benefits from developing such a quader-shaped body with an especially angular head region to outgrow the predator’s gape. Our data highly suggest a novel inducible defence strategy of a daphniid species against a carnivorous plant and again highlight the enormous degree of plasticity of this small freshwater crustacean.

P2.4 BLADDERWORT PREY CAPTURE: LESSONS FROM THE SMALLEST SUCTION FEEDERS

THURSDAY 6 JULY, 2017 **10:10**

ULRIKE K MULLER (CALIFORNIA STATE UNIVERSITY FRESNO, UNITED STATES), OTTO BERG (CALIFORNIA STATE UNIVERSITY FRESNO, UNITED STATES), MATTHEW BROWN (CALIFORNIA STATE UNIVERSITY FRESNO, UNITED STATES), JANNEKE M SCHWANER (UNIVERSITY OF IDAHO MOSCOW, UNITED STATES), GEN LI (CHIBA UNIVERSITY, JAPAN)

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Bladderwort, a carnivorous plant genus, are among the smallest and fastest suction feeders, catching zooplankton prey in millimeter-sized, underwater traps within less than 1 millisecond. Compared with larval fish, which are the main other group of small suction feeders, aquatic bladderwort generate much faster and briefer suction events, which ultimately result in higher capture success rates. We quantified the flow generated by bladderwort traps during manually triggered suction events. We found that the bladderwort traps generate inviscid flow: the generated flows outside and inside the mouth fit inviscid flow models. Flow speeds inside the mouth peak at 5 m/s, acceleration peaks at 50,000 m/s^2. Suction pressure in front of the mouth peaks early during the suction event. A computational analysis of the flow to explore how pressure magnitude and speed of pressure onset affect flow suggests that the high pressures generated by bladderwort help them to maintain inviscid flow conditions, which ensure high flow speeds. We found no strong effect of the onset duration on peak flow speed: slow onset does not strongly affects peak flow speed. We conclude that bladderwort maintain inviscid flow conditions through generating a strong sub-ambient pressure in their traps.

P2.5 CARNIVOROUS PLANTS ARE IDEAL MODEL SYSTEMS FOR EXPERIMENTAL RESEARCH

THURSDAY 6 JULY, 2017 **10:45**

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More than 600 carnivorous plants have evolved in at least six independent radiations within five angiosperm orders. Despite these independent origins, there is remarkable morphological convergence of carnivorous plant traps, physiological convergence of mechanisms for digesting and assimilating prey, and functional convergence in interspecific interactions between the plants and associated fauna. These convergent traits make carnivorous plants model systems for addressing questions in plant molecular genetics, physiology, ecology, and evolutionary biology. For example, the observation that carnivorous plant genera with morphologically complex traps have higher relative rates of gene substitutions than do those with simple sticky traps has suggested two alternative mechanisms for evolution and diversification of carnivorous plant lineages. Comparative physiological and morphological studies have revealed surface structures that facilitate prey capture and suggest new biomaterials. Experimental studies of pitcher-plants and their associated infauna provide compelling examples of convergent interactions that are being used to identify new symbioses in previously unexplored habitats. These microecosystems also are scalable models for identifying and manipulating rapid state changes in ecological systems. Finally, the widespread popularity of carnivorous plants among people of all ages and nationalities has led to the development of educational curricula and citizen-science initiatives that are advancing both botanical literacy and scientific discovery. Nearly 150 years after Charles Darwin first experimentally demonstrated that plants could attract, trap, eat, and digest insects, we continue to be surprised and fascinated by the knowledge gained from studying theses “most wonderful plants in the world”.

P2.6 THE TEASEL *(DIPSACUS FULLONUM)* AS A CANDIDATE FOR PROTO-CARNIVORY

THURSDAY 6 JULY, 2017 **11:25**

ANNEKE PRINS (MIDDLESEX UNIVERSITY, UNITED KINGDOM), DIRK WILDEBOER (MIDDLESEX UNIVERSITY, UNITED KINGDOM), STEVE KETT (MIDDLESEX UNIVERSITY, UNITED KINGDOM)

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Francis Darwin (1877) observed that insects drown and accumulate in the cup-like cavity formed by the leaves of *Dipsacus sylvestris*. He hypothesised that this could be an example of plant carnivory in its early stages. Since then, few studies other than Shaw and Shackleton's 2011 investigation have scrutinised this phenomenon. Their experimental feeding of *Dipsacus fullonum* (common teasel) did not result in increased non-reproductive biomass, but did cause a 30% increase in seed set and seed mass:biomass ratio. These data allied with a paucity of further data supporting potential carnivory in the teasel has sparked our curiosity. We posit that, in order for any plant to have evolved carnivory, its ancestors will have passed through stages of proto-carnivory. Thus, morphological and molecular traits that have evolved for one purpose might serendipitously provide secondarily advantageous proto-carnivory functions. Further selection may result in these adaptations acquiring primary function status as differential reproduction favours further enhancement of those traits. This study aims to determine whether *D. fullonum* leaf cups provide the plant with supplementary nutrients via capture, digestion and subsequent absorption of invertebrate prey. A population of *D. fullonum* established on urban waste ground will be studied, initially to determine aspects of morphology and molecular analysis of leaf cup water, whilst setting up a common garden experiment for more specific ecological energetic analyses.

P2.7 SLIP, TRIP AND TRAP: THE BIOMECHANICS OF PITCHER TRAPS, AND WHAT WE CAN LEARN FROM THEM

THURSDAY 6 JULY, 2017 **13:50**

ULRIKE BAUER (UNIVERSITY OF BRISTOL, UNITED KINGDOM)

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Carnivorous pitcher plants are increasingly turning into a model system to understand the functional morphology of plant surfaces, and their role in plant-insect interactions. Pitcher plants use antiadhesive surfaces to capture insects in fluid-filled pitfall traps. The principles underlying the slipperiness - micro-roughness, directionality and wettability of surfaces - are not unique to pitcher plants but are found across the plant kingdom where they play an important role in herbivore defence. However, pitcher plants are unique in that they commonly combine several slippery surfaces based on different biomechanical principles in the same plant organ. In addition, the digestive liquid at the bottom of the trap often has extraordinary physico-chemical properties that aid in prey retention. Conveniently for the experimental scientist, all captured prey is collected in the trap fluid, allowing for an easy and accurate quantification of trapping success. Together, these properties make pitcher plants an ideal model to study the function and effectiveness of antiadhesive plant surfaces, both in the lab and under natural conditions in the field. This talk will give an overview of the trap function, surface structure, and biomechanics of pitcher-prey interactions, with an outlook on recent discoveries and future avenues for research and technological innovations inspired by pitcher plants.

P2.8 KINEMATICS, BIOMECHANICS AND FUNCTIONAL MORPHOLOGY OF THE SNAP-TRAPS OF *ALDROVANDA VESICULOSA*

THURSDAY 6 JULY, 2017 **14:30**

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Within carnivorous plants, the worldwide distributed but rare Waterwheel plant *(Aldrovanda vesiculosa,Droseraceae)* is one of the scarcely investigated species. It possesses tiny underwater snap-traps and is sister to the well-known Venus flytrap *(Dionaea muscipula)*. However, the underlying movement principle is quite different. Whereas the trap closure (duration ~100-300 ms) in *Dionaea* relies i. a. on an elastic instability mechanism ('snap-buckling'), the Waterwheel trap (~20-50 ms) is regarded to function via movement amplification empowered by water displacement processes between cells and tissues. Theoretical approaches showed that the trapping motion of *Aldrovanda* falls in the range of purely hydraulically driven movements, yet, is so fast that it can be found at the transition zone to plant movements relying on elastic instabilities. Therefore, the question arose if *Aldrovanda* also incorporates pre-stresses as speed boost. Using a stereo high-speed camera setup, the comparative trap kinematics were analysed, validating that the closing movement of the trap lobes is coupled to the deformation of the midrib. Together with information obtained from trap manipulation experiments and Finite Elements computer simulations, we developed a physical trap model where pre-stresses clearly contribute to movement actuation. Furthermore, we found evidence for microevolution within monotypic *Aldrovanda vesiculosa* by comparing trap kinematics between temperate and tropical strains. First analyses with tracer particles also indicate how and where water displacement during trap closure proceeds, indicating consequences for prey capture and providing explanation for trap behaviour during snapping.

P2.9 HOW THE VENUS FLYTRAP SNAPS REVISITED

THURSDAY 6 JULY, 2017 **15:00**

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The Venus flytrap *(Dionaea muscipula)* is the most iconic carnivorous plant. Its (in)famous snap trap closes within ca. 100-300 ms, a motion which is driven by active hydraulic actuation in combination with an elastic instability (snap-buckling). *Dionaea* can withstand months-lasting submergence in its natural habitat, during which it is reportedly capable of trapping prey (e.g., newts). We comparatively investigated the snapping behaviour (trap closure durations) of traps in air and under water and found no significant difference. Moreover, we reveal three snapping modes: snapping with synchronous lobe movement, either with progressive snap-buckling or with sudden snap-buckling, and snapping with asynchronous lobe movement. *Dionaea* seedlings perform much slower trap movements as adults, indicating that slower prey may be caught in nature. For re-opening, traps of adult plant do not perform reverse snap-buckling. Our results highlight the functional resilience of the traps and the diversity of actions and actuation principles involved. Current investigations deal with the morphospace for fully functional traps by comparative investigations of trap kinematics and functional morphology in wild type plants and loss-of-function mutants.

P2.10 NO GUTS, NO GLORY? PLANT-MICROBE INTERACTIONS IN THE TRAPS OF THE ROOTLESS CARNIVOROUS *UTRICULARIA*

THURSDAY 6 JULY, 2017 **15:45**

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All higher eukaryotes live in a relationship with diverse microorganisms which colonize their bodily surfaces; plants are no exception. Plant-associated microorganisms have long been recognized as key partners in enhancing plant nutrient acquisition, mitigating plant stress, promoting growth, or facilitating successful defense mechanisms against pathogens or grazers. Apart from the well-studied and relatively 'simple' symbioses such as mycorrhizal and rhizobial interactions, there is a large pool of diverse microorganisms in varying degrees of association to different plant surfaces and tissues. The traps of carnivorous plants are good model systems to study these complex interactions: as sophisticated digestive systems, they represent interface environments between the supply and the demand for nutrients. We chose the miniature aquatic ecosystem found in the traps of aquatic carnivorous *Utricularia* plants as our study environment. By assessing the trap-associated microbial community structure, diversity, metabolic capabilities, as well as the nutrient regeneration potential by grazing protozoa, we gained an insight into the nutrient acquisition strategies of the *Utricularia* host plants. We conclude that the trap ecophysiological function is in many aspects highly analogous to that of the mammalian rumen and centers on the digestive mutualism involving complex consortium of diverse microorganisms which act in synergy to covert complex organic matter, often of algal origin, into a source of nutrients for plant growth.