11TH EUROPEAN PLANT SCIENCE RETREAT

8TH- 10TH JULY 2019
NOTTINGHAM UK

University of Nottingham Future Food

New Phytologist

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Contents

Welcome

Welcome to the 11th European Plant Science Retreat at the University of Nottingham. We are so excited to welcome you all!

The EPSR is a free Plant Science congress organised by PhD students for PhD students. This year's retreat is organised by a group of PhD students in Plant and Crop Science at Nottingham. During the congress we will hear from 8 keynote speakers, multiple students and have 2 poster sessions. We will provide refreshments and food for 3 days as well as two evening events. The EPSR is the perfect occasion to discuss, share and network with students across Europe.

There's plenty to see and do in Nottingham while you are here. Nottingham hosts the oldest pub in England, has an extensive network of caves running under the city and is home to Robin Hood. We are also located close to the Peak District, one of England's most beautiful national parks.

This leaflet includes information about the venue, speaker abstracts, poster numbers and a list of all attendees.

If you have any questions please get in touch at epsr2019@nottingham.ac.uk or on twitter @epsr2019.

If you need to speak to the committee urgently whilst you're in England you can phone Dimitra 07561831327 or Carlos 07712803716.

Meet the Committee

Jason Banda

Jordan Robson

Johanna Astrand

Cindy Callens

Alexander Bridgen

Emily Morris

Dimitra Aggelopoulou

Martina Franchini

Carlos Robles

We've been hard at work organising this EPSR for you!
To learn more about who we are and what research we do check out epsr2019.wordpress.com/committee

Our Sponsors

To make this event possible we have received support from a range of sponsors. We are very grateful for their generous contributions to EPSR 2019. Check out epsr2019.wordpress.com/sponsors for more information.

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EPSR 2019

How to get to Nottingham

If you're coming to Nottingham by plane the closest airport is **East Midlands Airport**, located just outside of Nottingham with good connections to the rest of Nottingham via the Skylink bus (https://www.trentbarton.co.uk/services/skylinknottingham).

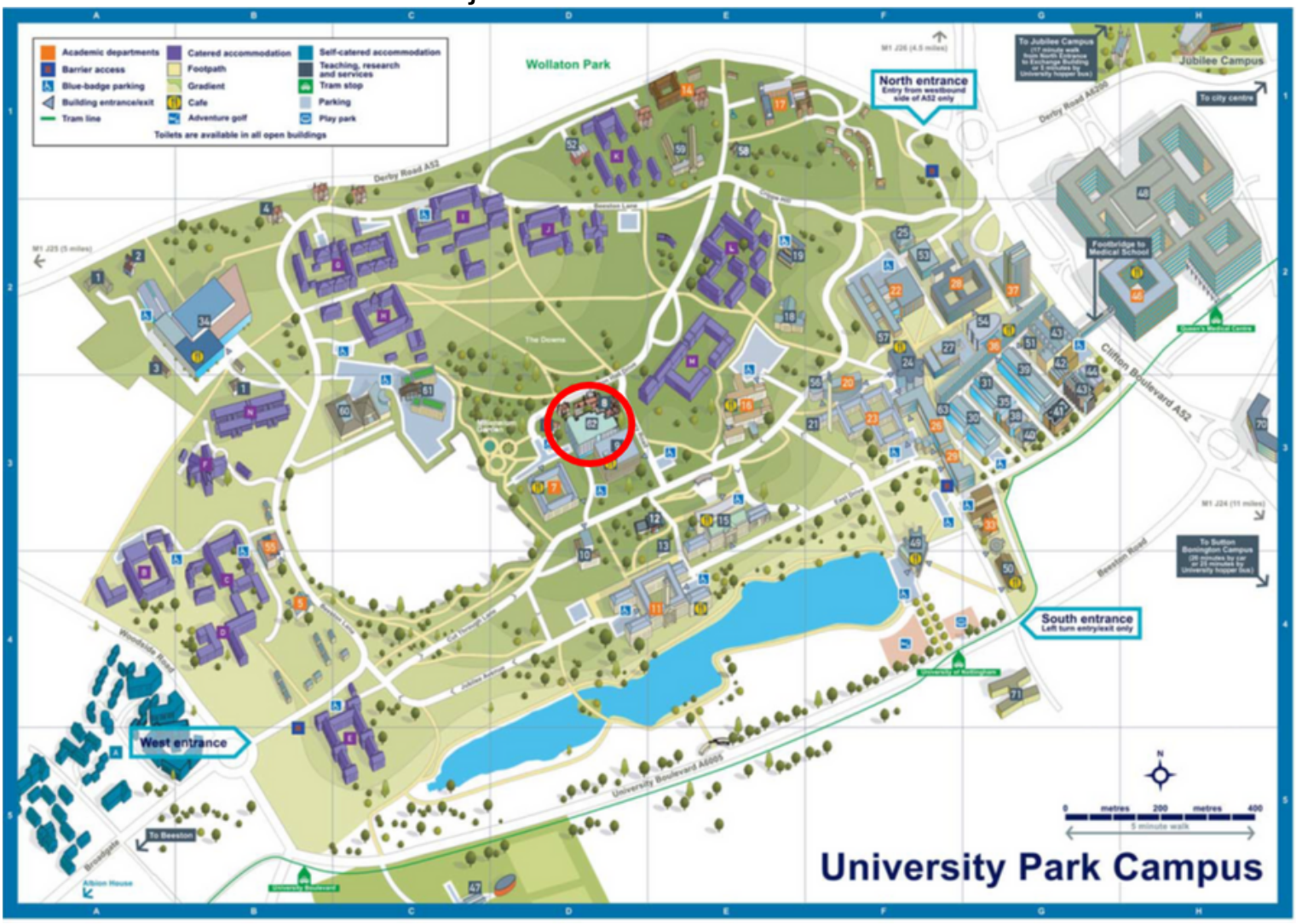
Other airports with great connections to Nottingham are Manchester Airport, Birmingham Airport, and London Luton Airport. Other London airports are also accessible but the journey to Nottingham will take slightly longer. There are plenty of buses and trains available from these airports to **Nottingham Station**.

Useful links for getting around in England:
By train: www.thetrainline.com
By bus: www.nationalexpress.com/en and https://uk.megabus.com/

EPSR 2019

The Venue

The retreat will be held at the **University Park Campus (UP)** at the University of Nottingham. The seminars will take place in the lecture theatre (A03) in the **Teaching and Learning Building** (number 62, circled in red, on the map below). The registration desk will be in the Atrium on A floor. Posters, lunch and refreshments will be set up in the Atrium just outside of the seminar room.



How to get to the venue

Getting to the venue from the City Centre:
University Park campus is well connected to the City Centre and surrounding areas via a regular Tram service. **The nearest tram stop is the University of Nottingham**, which is a 10-15 minute walk from the Teaching and Learning Building. Information about times and tickets can be found here: www.thetram.net/

There are also multiple buses that run to the University of Nottingham University Park Campus from the City Centre. The **University 34 bus** takes you directly onto campus, stopping at East drive, a 5 minute walk from the Teaching and Learning Building. Other good options include the 18, 20 or the Indigo, which follow a similar route but drop you off on the edge of the campus. Nottingham Bus Service information: www.nctx.co.uk/services or www.trentbarton.co.uk/nottsunimap

Social Events

We've organised two great evening events for all EPSR attendees.

Monday:
16.30- After the first day's sessions end we will lead a walk to **Wollaton Park** (featured as Batman's house in The Dark Knight Rises!)
18.30- **Networking BBQ** (sponsored by GARNet) and drinks outside the Teaching and Learning Building

Tuesday:
19.00- Dinner and drinks at **Via Fossa** in the city centre (www.greeneking-pubs.co.uk/pubs/nottinghamshire/via-fossa)

Where to stay in Nottingham

There are plenty of options in Nottingham. You can either stay close to the campus or in the city centre. Here are a few options.

University Park Campus:
Travelodge Nottingham Wollaton Park
www.travelodge.co.uk/hotels/474/Nottingham-Wollaton-Park-hotel

City Centre:
Mercure
www.mercurenottingham.com/

ibis Nottingham Centre Hotel
www.accorhotels.com/gb/hotel-6160-ibis-nottingham-centre/index.shtml

Igloo Backpackers hostel
www.igloohostel.co.uk/

Midtown Hostel Nottingham
https://midtown-hostel-nottingham.hotelmix.co.uk/

Explore Nottingham

If you have time to explore Nottingham here are some of our favourite things to see.

Robin Hood Tours- For an insight into the legend behind Robin Hood and a tour of the major sites in the city.
www.ezekialbone.com

City of Caves- A huge network of caves lie underneath Nottingham and you can take a tour.
www.nationaljusticemuseum.org.uk/venue/city-of-caves

Ye Olde Trip to Jeruselum- This pub claims to be the oldest in England and is half buried into Castle Rock.

Peak District National Park- If you have time to get out of the city then the Peaks are a must-see for nature lovers.Trains run from Nottingham Station into the Peaks.

Programme

	Monday 8th July
9.00	Registration and coffee
10.00	Welcome by Committee & Malcolm Bennett
10.30	**Plenary Session- Prof. Dame Caroline Dean**
11.30	Break
11.45	**Session I: Development**
	Keynote: Prof. Zoe Wilson
12.30	*Jorge Zamora Zaragoza*
12.50	*Mhairi L H Davidson*
13.10	*Pierre Gautrat*
13.30	Lunch
14.30	**Session II: Signalling**
	Keynote: Prof. Joop Vermeer
15.15	*Alvaro Montiel Jorda*
15.35	*Matthew Johnston*
15.55	*Sophie Mogg*
16.15	Group photo
16.30	Optional Tour of Wollaton Park
18.30	**Networking BBQ**

Programme

	Tuesday 9th July
8.30	Hang posters (even numbers)
9.00	**Session III: Plant-Microbe Interactions**
	Keynote: Prof. Sofie Goormachtig
9.45	*Besma Bouznif*
10.05	*Liam Walker*
10.25	*Tijmen van Butselaar*
10.45	Break
11.00	**Session IV: Abiotic Stress**
	Keynote: Dr. Daniel Gibbs
11.45	*Anne-Claire Talhouet*
12.05	*Félix de Carpentier*
12.25	*Valérie Hoogers*
12.45	Lunch
13.45	**Session V: Food Security**
	Keynote: Dr. Matthew Reynolds
14.30	*Aleyda Sierra-Gonzalez*
14.50	*Naveen Kalluri*
15.10	*Rosa Castillo Bravo*
15.30	**Poster Session I (until 17.00)**
19.00	**Dinner & Drinks at Via Fossa**

Programme

	Wednesday 10th July
9.45	Hang posters (odd numbers)
10.15	**Session VI: Plant Physiology**
	Keynote: Prof. Erik Murchie
11.00	*Marina Muñoz Triviño*
11.20	*Natalia Hurtado Castano*
11.40	*Sarah Courbier*
12.00	Lunch
13.00	**Session VII: Phenotyping**
	Keynote: Dr. Saoirse Tracy
13.45	*Angela Romero Vergel*
14.05	*Olivia Cousins*
14.25	*Riccardo Fusi*
14.45	**Poster Session II**
15.45	Break & Vote
16.00	Evaluation
	Location for EPSR 2020
	Awards Ceremony
17.00	End of Meeting

Poster Prizes will be available, kindly sponsored by NEB

Keynote Speakers

Prof. Dame Caroline Dean

John Innes Centre, Norwich, UK

Chromatin regulation and non-coding transcription are now seen as major factors regulating gene expression in most eukaryotic genomes. Through the study of how plants time developmental transitions, we have discovered that Arabidopsis floral repressor FLC is an excellent system in which to dissect how non-coding transcription and chromatin mechanisms regulate gene expression. FLC expression is quantitatively modulated by an antisense-mediated chromatin mechanism that coordinately influences transcription initiation and elongation. Expression is then epigenetically silenced through a cold-induced, cis-based, Polycomb switching mechanism. The talk will describe our latest understanding of these conserved mechanisms and how they have been modulated during adaptation.

Prof. Zoe Wilson

University of Nottingham, UK

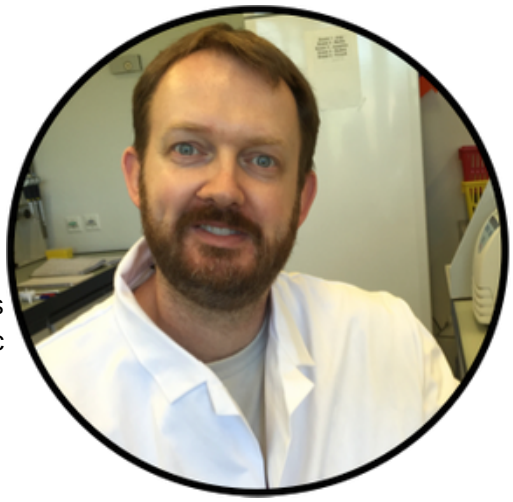
I am interested in how the plant controls the production of pollen and the regulatory gene networks that are involved in this pathway. We have been working with a number of transcription factors that are expressed in the maternal tapetum tissue of the anther, which control the formation of the pollen wall and regulate the progression of pollen development. These gene networks are highly conserved across species and we have translated this knowledge from Arabidopsis to crops such as rice, barley and wheat. The aims of this are to characterise the reproductive processes in the crops so that we can develop effective breeding systems for hybrid development to improve crop yields. Of particular interest is the impact of abiotic stress on pollen development and the damaging effect that it can have on crop fertility and thus yield. Abiotic stress can result in failure of pollen development, which results in significant losses in yield and productivity. This is therefore a major future challenge to maintain crop yields alongside climate change and extremes in weather.

Prof. Joop Vermeer

University of Zurich, Switzerland

How is membrane identity regulated? How is this modified during development and upon stress responses? How are these responses integrated during development? How is differential growth regulated? How do cells communicate during this process? These questions have always driven my scientific curiosity. My research focusses on how plants integrate chemical and mechanical signals during plant development. My group combines live cell imaging with cell type specific manipulation of cellular properties and transcriptome sequencing to better understand organ formation in plants. Currently we are using Arabidopsis lateral root formation as a model system. The long-term goal of our work is to better understand how we can adapt root system architecture to increase plant production also under challenging environmental conditions.

I will talk about how we use cell type specific promoters as surgical blades to dissect lateral root development. Through development of novel genetic tools combined with 4D live cell imaging of cellular differentiation we are dissecting the interaction between different cell layers during lateral root formation. In parallel, we are using forward genetics and cell type specific transcriptome profiling to build an expression atlas describing the underlying regulatory network of this developmental process. Lastly, I will also show some recent results of some new branches of research where we try to get a better insight into how conserved the mechanism of cell shape regulation are in an evolutionary context.



Prof. Sofie Goormachtig

VIB, Ghent, Belgium

My research focusses on how interactions between plant roots and neighboring organisms influence plant growth. Initially, the emphasis was on the endosymbiosis between legumes and rhizobia, resulting in the formation of new root organs, the nodules, in which the rhizobia reside and fix atmospheric nitrogen for the plant.

Currently, my group study two rhizosphere related events. We study how strigolactones, important rhizosphere molecules, control parasitic plant germination. We pursue a combined proteomics, transcriptomics and genetic approach to elucidate the signaling components acting downstream of strigolactone perception by the parasitic plant seed. Secondly, we are interested in the mechanisms of plant growth promotion by rhizosphere bacteria in Zea mays (maize) and Arabidopsis thaliana. We are exploring the microbial community composition and its effects on plant growth regulating molecular networks in changing environmental conditions.

Dr. Daniel Gibbs

University of Birmingham, UK

Daniel Gibbs' research is focused on understanding how plants use targeted protein degradation (proteolysis) as a mechanism for sensing and responding to signals derived from their environment. His group utilises diverse molecular approaches to uncover new functions for proteolysis during plant growth and stress responsiveness. After completing his PhD (2009) on lateral root development with Dr Juliet Coates at the University of Birmingham (Gibbs et al 2014 New Phytologist), Dan joined the lab of Professor Michael Holdsworth at the University of Nottingham, where his postdoctoral work helped to delineate the molecular basis through which plants perceive and respond to low-oxygen stress and the signaling molecule nitric oxide (Gibbs et al 2011 Nature; 2014 Molecular Cell). In 2012 he began a Nottingham Advanced Research Fellowship, before moving to a tenure-tracked 5 year Fellowship position at the University of Birmingham in 2013, where he is currently a Senior Research Fellow. Current projects in Birmingham – funded by the BBSRC and an ERC starter grant – are investigating roles for co-translational protein degradation in plant development, and exploring how proteolytic control of chromatin modifying proteins regulates epigenetic responses to environmental change (Gibbs et al 2018 Nature Communications).

Dr. Matthew Reynolds

International Maize and Wheat Improvement Center (CIMMYT), Mexico

I have worked at the International Maize and Wheat Improvement Centre (CIMMYT) based in Mexico since 1989, where my professional goals are to develop and transfer technologies to improve wheat cropping systems worldwide. The challenge of using and improving our understanding of physiological processes in plants to improve crop productivity, especially in climate-challenged environments, has been the driving force for this research. Working at CIMMYT provides the opportunity to link basic plant research to farm level productivity via many disciplines, including phenomics, genomics, economics, exploration of genetic diversity and breeding. It has been a highly rewarding experience to be part of a global community of scientists, farmers and other stakeholders through collaboration and knowledge sharing. Impacts from the CIMMYT Wheat Physiology Lab include a new generation of advanced lines based on physiological breeding approaches to widen the wheat genepool, increased understanding of yield potential and adaptation of wheat to drought and heat stress, development of high throughput phenotyping methodologies, and capacity building. To further these goals I have been active in developing global collaborations to tap into the expertise of plant scientists worldwide –such as the International Wheat Yield Partnership https://iwyp.org/– and the Heat and Drought Wheat Improvement Consortium https://www.hedwic.org/. I also lead the community of practice on crop modelling for the CGIAR Big Data in Agriculture platformhttps://bigdata.cgiar.org/communities-of-practice/crop-modelling/, and am a board member of the Global Plant Council http://globalplantcouncil.org/.

Prof. Erik Murchie

University of Nottingham, UK

I'm fascinated by all aspects of plant life and especially how plants respond to the environment around them which occurs in surprisingly diverse and dynamic ways. My research concerns crop plants and the way they convert solar energy into food, fuel and materials for our consumption. Improving this process is the goal. I'd like to talk about the fascinating mechanisms that plants have evolved in this area and how we might use nature's existing diversity as a guide to improve agriculture sustainably.

My current research focuses on wheat and rice (the key food crops of our age) to examine how canopy architecture i.e the 3 Dimensional structure of plants affects the way in which they intercept and convert light into biomass. We like utilising novel approaches e.g. imaging and deep learning techniques to understand how plant motion contributes to this process. We collaborate with those using traits and genes from wild relatives of wheat to try and regain properties that may have been lost during domestication and breeding, such resources will be useful for producing crops that can deal with future climates that are likely to be challenging in comparison with today. And I said all that with barely a mention of the word 'photosynthesis' which is the process that my lab spends most of their time measuring.

Dr. Saoirse Tracy

University College Dublin, Ireland

Dr. Tracy's research interests include using X-ray Computed Tomography (CT) to understand the response of roots to the soil physical environment. She applies her skills and experience of X-ray CT, soil science, hydrology, plant biology and image analysis to answer further questions about the rhizosphere and plant function. Dr. Tracy's group research root:soil interactions using non-destructive imaging. Dr. Tracy is Director of the UCD X-ray CT facility and founded and chairs the Irish Plant Phenotyping Network. She moved to UCD to take up a position as Assistant Professor in Applied Plant Biology in 2015 after completing 3 years as a Research Fellow at the University of Nottingham, U.K. Dr. Tracy completed her PhD in 2012 at the University of Nottingham, U.K and investigated the response of root system architecture to soil compaction.

PhD Speakers

Development

Deciphering the master's code: phosphorylation-dependent regulation of the retinoblastoma-related1 protein functions

Jorge Zamora Zaragoza, Wageningen University, Netherlands

Plants are sessile and have non-motile cells. As a consequence, many plant responses to the environment require changes in cellular development. For this, signals from the environment need to be integrated into the developmental program. The RETINOBLASTOMA-RELATED (RBR) protein is a central hub protein that integrates developmental and environmental cues into cell division, stem cell differentiation and Programmed Cell Death (PCD) programs. Thus, RBR is a master regulator of cell responses, making it a potential target to improve traits related to the response of plant growth to the environment. Therefore, in this work I aim to understand but how can a single protein control so many processes? What are the molecular mechanisms underlying RBR function? In brief, how is the master regulator regulated?

RBR binds and represses transcription factors (TFs) that in turn control cell processes. An emerging paradigm hypothesizes the existence of a so-called "phosphorylation code": Combinatorial phosphorylation on 16 sites, spread throughout its structure, fine-tunes RBR interactions, providing a mechanism to differentially control RBR networks. Such mechanism allows RBR to spatio-temporally coordinate cell fates with clockwork precision. Despite the extensive research on RBR, this hypothesis has never been proven.

Using the model plant Arabidopsis thaliana, I generated and characterised transgenic lines for 15 RBR phospho-variants which introduce clusters of phospho-mutants and phospho-mimetics. Complementation analysis demonstrates that specific RBR-controlled processes (such as PCD, cell division and stem cell maintenance) can be uncoupled by specific phospho-sites combinations. Moreover, Yeast 2-hybrid screenings and a suppressor mutation provide biochemical basis to understand RBR functions. This results strongly support the phosphorylation code hypothesis and constitutes a big first step to decipher it.

Investigation of the role of the transcriptional regulator TZP in blue-light mediated hypocotyl elongation in Arabidopsis thaliana

Mhairi L H Davidson, University of Glasgow, UK

Introduction: Light is essential for plant growth and development. Tandem-Zinc-finger-Plus3 (TZP) is a transcriptional regulator that plays a major role in integrating light, hormone and clock signalling networks to promote plant growth in response to endogenous and environmental stimuli. Photomorphogenesis is a major transition early in plant development when hypocotyl (embryonic stem) elongation is inhibited, cotyledons (embryonic leaves) open, and greening occurs. TZP is a positive regulator of blue-light-mediated hypocotyl elongation and regulates expression of growth promoting genes (Loudet et al., 2008; Perrella et al., 2018). In addition, TZP localises to the nucleus in dynamic, transcriptionally active nuclear bodies (Kaiserli et al., 2015).

Methods: To further understand how TZP acts as a transcriptional regulator, structure-function analysis is essential. TZP contains a unique C-terminal structure with tandem zinc-fingers (ZF) directly adjacent to a Plus3 domain. Both domain types can interact with nucleic acids and other proteins. Deletion analysis of TZP in vivo and phenotypic assays were used to investigate the role of these domains in hypocotyl elongation.

Results and Discussion: Confocal imaging has shown that neither ZF nor Plus3 is required for the nuclear localisation of TZP. Furthermore, Plus3 alone and ZF-Plus3 lose nuclear specificity and can also be observed in the cytosol. Preliminary data suggests that TZP ZF-Plus3 is sufficient for TZP-mediated hypocotyl elongation in response to low blue light. The next step is to assess if the ZF-Plus3 domains of TZP are sufficient to associate with and regulate the expression of TZP target genes.

Conclusions: This project aims to investigate the molecular mechanism of TZP transcriptional regulation and to further understanding of the interactions among the transcriptional regulator TZP, photoreceptors and other light signalling components.

At the crossroads of local and systemic pathways involving signaling peptides to regulate nodulation in the Medicago truncatula model legume

Pierre Gautrat, University of Paris-Saclay, France

Plants have a high developmental plasticity to adapt to environmental constraints and to optimize their nutrition. Under limiting nitrogen conditions, legumes are notably able to form new root organs besides lateral roots, the nodules, thanks to an interaction with atmospheric nitrogen-fixing symbiotic bacteria called Rhizobia (Gamas et al., 2017). Nodulation is energetically costly and therefore tightly regulated by various local and systemic (long distance) signaling pathways. We recently identified in the model legume Medicago truncatula (Gautrat et al., 2019), that the two closest orthologous genes to the Lotus japonicus root F-Box TOO MUCH LOVE (TML), are a downstream effector of the Autoregulation of Nodulation (AON) systemic pathway negatively regulating nodulation. AON involves the perception of root-produced CLE (CLAVATA3/ESR-related) peptides by the SUNN (SUPER NUMERIC NODULES) receptor in shoots (Mortier et al., 2010). TML transcripts are targeted by the miR2111 microRNA which regulation by rhizobium depends on the AON. In addition, another systemic pathway positively regulating nodulation involves the perception of root-produced C-terminally ENCODED PEPTIDES (CEP) by the COMPACT ROOT ARCHITECTURE 2 (CRA2) receptor in shoots (Huault et al., 2014; Mohd-Radzman et al., 2016). This pathway also affects the miR2111/TML regulatory module. Finally, local miR2111-independent hormonal regulations of MtTML transcripts accumulation will be reported.

Signalling

Characterization of BML1, a novel protein linking brassinosteroid signaling with microtubules

Alvaro Montiel Jorda, University Paris-Sud, France

Plant hormones regulate many developmental and adaptive procuresses. Among them, brassinosteroids are of special importance for plant growth, as evidenced by the extreme dwarfism of mutants lacking this pathway. To find new regulators of the brassinosteroid signaling pathway, we search for new BRI1-interacting proteins. By performing a yeast-two-hybrid screen using BRI1 kinase as bait, we identified three novel proteins of unknown function named BMLs. Phylogenetic analyses revealed that orthologs of BMLs are present in lower plants such as liverworts and moss but absent in algae. We have cloned the three Arabidopsis BMLs (AtBML1-3) and chose to focus on BML1. We confirmed the interaction with BRI1 in yeast by Split Ubiquitin assays and in planta by BiFC and Co-IP. The BML1 protein was localized to microtubules, including cortical microtubules in close proximity to the plasma membrane. Interestingly, single bml knockouts display altered brassinosteroid responses, pointing to their functional importance. Overall, we have uncovered a new unexpected link between brassinosteroid signaling and cortical microtubules in the regulation of plant growth.

Pulling at Plasmodesmata

Matthew Johnston, John Innes Centre, UK

Multicellular organisms require communication between cells, be that for growth, defence or development. Plants have a unique solution to this: plasmodesmata (PD). PD are membrane-lined pores that connect plant cells through the cell wall. Many molecules, from metabolites to proteins, can pass through PD. However, PD are not passive structures. The permeability of the pore can change in response to many stimuli, such as when pathogens are detected during defence.

When a plant is under attack from a pathogen, flux through PD is transiently restricted. This is due to the deposition of the macromolecule callose blocking movement through the PD. PD closure is triggered by chitin, a major component of fungal cell walls, as part of PAMP triggered immunity. Chitin mediated PD closure is dependent on three LysM receptors. Confocal microscopy shows that while one of the proteins clearly accumulates at PD, two have an even plasma membrane localisation when tagged with eGFP. To determine the presence of the plasma membrane localised LysM proteins at PD, I developed a PD purification protocol to extract PD from mature leaf tissue. Using this method, I showed that these two LysM proteins differentially associate with PD, identifying that PD chitin responses depend on complex associations between LysM proteins.

I am further using this method to explore PD signalling in other contexts such as the PD association of the C4 protein from Tomato yellow leaf curl virus that regulates the cell-to-cell movement of small interfering RNAs, and the flagellin responsive protein CML41. For these proteins I have further developed co-immunoprecipitation methods for PD fractions and will identify interactors to determine novel components of the PD signalling machinery.

A Phytozome-Wide Screening of CLE Proteins and the Functional Analysis of Multi-CLEs

Sophie Mogg, University of Manchester, UK

Our understanding of the importance of peptide hormone signalling in the growth and development of plants has improved in recent years with the identification of several protein families that regulate cell division and differentiation within a variety of meristematic tissues. One family in particular, known as CLAVATA3/ESR-RELATED (CLE) proteins, has been shown to be a diverse functioning family controlling differentiation of the xylem and phloem from the cambium and affecting root development. Previously CLE proteins were thought to contain a single CLE peptide at the C-terminal end however through bioinformatic investigation using a combination of BLAST and MEME FIMO we have identified several proteins that contain between four and fifteen CLE peptides in a tandem array separated by a conserved spacer region. These Multi-CLE peptide proteins have been identified across a variety of agriculturally important crop species but are not present in species such as Arabidopsis thaliana. Expression of the Gossypium raimondii Multi-CLE peptide protein in A. thaliana alters vascular tissue organisation in the hypocotyl, indicating that the protein is functional in vivo. Presumably protein cleavage occurs to release the individual CLE peptide(s) which are then recognised by native receptors and downstream effectors are activated or inhibited to alter cell division and differentiation. Further experiments are being conducted to elucidate the function of individual peptides within the multi-CLE protein and subsequently identify if cleavage does occur.

Plant - Microbe Interactions

Phylogenetic diversity of the Bradyrhizobium spp. associated with peanut, Arachis hypogaea

Besma Bouznif, University Paris-Sud, France

Nitrogen-fixing symbiosis is a key factor for the development and growth of most legume plants, many of which are known for their ecological and economic importance. Several cultivated legume species have been brought far from their native geographic range along human migrations. In this study, we review the different scenarios of nodulation of crop legumes in their zones of introduction, either by co-introduction of the bacterial partner, through nodulation by a local rhizobium that jumps from a local legume, or in a mixed scenario where horizontal gene transfer occurs between original nodulators and local rhizobia. We then focus on peanut (Arachis hypogaea), an oilseed legume native to South America and largely cultivated all over the world, and its nodulators in the different regions of the world through a phylogeographical approach. At a more regional scale, we currently conduct a study of bacterial diversity of peanut nodulators in northern and southern Tunisia, where contrasted climatic conditions and different history of peanut cultivation may affect the type of scenario of nodulation of this legume crop. Our study also aims at identifying interesting strains to develop bacterial inocula to improve and promote peanut cultivation in the south of Tunisia.

Molecular changes underpinning friend vs. foe recognition in legumes

Liam Walker, University of Warwick, UK

Leguminous plants possess the almost unique ability to form symbioses with soil-dwelling, nitrogen fixing bacteria called rhizobia. This symbiosis (nodulation) cumulates in the formation of specialized structures on the plant root called root nodules which are then colonized by rhizobia. Within these nodules, rhizobia assimilate atmospheric nitrogen into compounds which can be utilized by the host plant.

As nodulation requires invasion of the host plant by a microorganism, suppression of defence responses that would normally occur is a prerequisite of successful symbiosis. However, the plant must also maintain its ability to form robust defence responses to bona fide pathogens. Therefore, nodulation places competing demands on symbiotic and defence responses.

Using the model legume Medicago truncatula, we aim to identify genes that might be responsible for mediating the transition between defence and symbiosis responses in legumes roots. We will induce nodulation by treating plants with a strain of Sinorhizobium medicae associated with highly efficient nitrogen fixation in M. truncatula. We will also treat plants with the broad-spectrum root pathogen Ralstonia solanacearum to provoke defence responses.

Using samples at a range of timepoints that correspond to early stage plant-microbe interactions up to nodule formation or late stage pathogenesis we will be able to monitor how these responses vary through time. We will use RT-qPCR to assay the expression of markers of nodulation and putative markers of defence responses from these samples before using RNA sequencing to identify regulators of these processes.

Uncoupling Growth Inhibition from Plant Immunity in the Hyperresistant dmr6 dlo1 Mutant

Tijmen van Butselaar, Utrecht University, Netherlands

Plants have evolved an elaborate immune system to combat microbial pathogens. Resistance to biotrophic pathogens, which thrive on living host tissue, is predominantly mediated by the phytohormone salicylic acid (SA). Although SA stimulates immunity, it actively suppresses growth. This growth-immunity tradeoff exerts itself in SA-accumulating mutants, like the dmr6 dlo1 double mutant. Arabidopsis plants mutated in DMR6 and DLO1, which encode 2-oxoglutarate iron-dependent SA-oxygenases, are hyperresistant to biotrophs but show growth defects. Here, we use the resistance and growth phenotypes of the dmr6 dlo1 mutant to identify regulatory mechanisms that affect growth, but not immunity. In a forward genetics (EMS-mutagenesis) screen on the dmr6 dlo1 mutant, we identified 104 mutants with restored growth phenotypes at seedling and adult stages, similar to Col-0. Moreover, half of these restored growth mutants had high resistance levels to the downy mildew Hyaloperonospora arabidopsidis. The genomes of backcrossed lines have been sequenced to map causal genes (thereafter named MODIFIERS OF dmr6/dlo1-MEDIATED IMMUNITY (MDI)). We will present an update on the identification of MDI genetics and other phenotypes and responses in these EMS mutants. In conclusion, we have identified highly resistant Arabidopsis mutants with a reduced growth penalty. Finding the mode of action of the MDI genes in coupling growth and immunity will greatly aid to our understanding of the plant immune network.

Abiotic Stress

Methods of estimation of excess photosynthetic electron transport in two alpine plant

Anne-Claire Talhouet, University Paris-Saclay, France

Climatic conditions at high altitude are characterised by very high fluctuating photon flux densities (PFD), high UV radiation and temperature extremes. Soldanella alpina and Geum montanum, are two evergreen alpine plants. In winter, their leaves remain almost in darkness at temperatures around 0°C but receive PFDs of more than 2000 µmol photons m-2s-1 during snowmelt while melting snow keep the leaf temperature low. Interestingly, after cessation of snowmelt in the dry meadow and in full sunlight, leaf temperatures can rise up to 40°C. Low as well as high temperatures and high PFD are known to induce photoinhibition of photosynthesis and oxidative damage in most plants. Since neither strong photoinhibition, nor oxidative damage is observed in leaves of S. alpina and G. montanum, we postulate that both plants are able to (1)either efficiently dissipate absorbed light energy, (2) use it for carbon assimilation or photorespiration, or (3) apply alternative harmless electron transport pathways to consume excess energy. Absorbed light energy, which is not dissipated as heat or used for carbon assimilation and photorespiration, may generate reactive oxygen species which may cause oxidative damage. In my thesis I developed an experimental system to quantify the electrons which are in excess of carbon assimilation and photorespiration. Chlorophyll fluorescence and carbon assimilation techniques were applied to quantify the number of electrons transported at the level of PSII, to estimate the carbon respiration in light, to measure net carbon assimilation and to determine the specificity factor of Rubisco. With the help of these techniques and photosynthetic models, the number of electrons distributed to carbon assimilation and to photorespiration was quantified and the number of excess electrons could be calculated. All this were compared between leaves which were newly formed under favourable conditions and those taken out of the snow and after several weeks after snowmelt.

Stress-induced social behavior in Chlamydomonas reinhardtii

Félix de Carpentier, University Paris-Sud, France

The alga Chlamydomonas reinhardtii is a model organism for research in plant biology, mostly because of the power and speed of genetic approaches that can be developed. We use Chlamydomonas to try to understand how a unicellular organism adapts to survive in a hostile environment. Indeed, we have shown that facing a moderate stress, the cells aggregate forming a multicellular structure in which they can be protected from the toxic environment. We created and screened a library of insertional mutants in Chlamydomonas that allowed us to identify original mutants deregulated in the process leading to the aggregation. A multidisciplinary approach combining genetics, molecular biology, cell biology and proteomics is used to characterize the most promising mutants. In particular, the affected genes have been identified, the proteins involved have been quantified by the mass spectrometry tools we have developed in the lab. We have interesting candidates of genes involved in the aggregation in response to stress. Thereby we have a better understanding of the dialogue between unicellular organisms and the adaptation in a hostile environment. Aggregates could be intermediate between unicellular and multicellular states, we therefore acquire a some insight in the evolution of multicellularity.

Changes in root system architecture upon differences in light quality in the shoot in arabidopsis thaliana

Valérie Hoogers, Utrecht University, Netherlands

Plants have to adapt their growth strategies according to light quality and intensity. The perception of neighboring vegetation by a reduction in the ratio between red and far red light leads to changes in hypocotyl growth, petiole length and leaf angle. Furthermore, this change in light quality induces changes in root system architecture (RSA). However, thus far it remains unknown how these above-ground conditional changes are perceived by the roots. Shoot-to-root mobile compounds, like the transcription factor ELONGATED HYPOCOTYL5 (HY5), auxin and gibberellic acid (GA), play a role in the transduction of the signal, but their precise role and the interactions between different pathways are still to be fully understood. Grafting studies, phenotypic analysis of mutants and fluorescent reporter lines have revealed a role for HY5. In order to understand the transcriptomic changes induced by far-red light in the shoot, transcriptomic profiles will be generated of different root tissues. Furthermore, the aim is to understand how these changes in transcriptomic profiles in the root are regulated. In a broader perspective, this project aims to understand how the perception of a conditional parameter can induce changes in spatially separated organs.

Food Security

Genetic analysis of partitioning traits to increase yield, grain number and harvest index in a high biomass spring wheat panel

Aleyda Sierra-Gonzalez, University of Nottingham, UK

Strategies for achieving genetic gains in yield potential must combine enhanced above-ground dry matter as well partitioning to the grain (harvest index: HI). The present study N-IWYP700 aimed to identify grain partitioning traits to maximize grain yield in high biomass backgrounds.

A High Biomass Association Panel (HiBAP) comprised of 150 diverse spring wheat elite lines, landrace and synthetic derived genotypes was phenotyped in 2015-16 and 2016-17 in NW Mexico. Physiological traits measured included biomass, plant length (height, spike, awns, peduncle, internode 2 & 3), organ dry matter (DM) partitioning (spike, leaf lamina, true stem and leaf sheath) and fruiting efficiency (grain set per unit spike DM; FE) at anthesis (GS65+7 days) and biomass, grain yield, yield components and HI at harvest.

Cross-year field trials confirmed that the incorporation of landrace-derivate and synthetic-derivate background into elite lines resulted in a greater production of AGDM, radiation use efficiency, and grain weight (GW). However, no yield advantage was observed due to decreased HI and grain number per m2 (GN). The extra biomass was associated with higher lamina partitioning (LamPI) in landrace derived, and higher stem partitioning (StePI) in synthetic derived lines, resulting in both cases in less investment of DM in the spike (SPI). In this panel, SPI and FE were positively associated with HI and GN both, in turn, linearly related with grain yield. Higher SPI and HI were correlated with a shorter length of stem internode 2 (phytomer below peduncle) and reduced DM partitioning to stem internode 2. Detailed spike DM partitioning analysis at GS65+7d revealed that FE was associated with decreased awn DM partitioning and lower rachis DM partitioning with higher GW and grain yield. Therefore, selecting for these traits would contribute to maximizing SPI and FE and, therefore, HI and GN.

Using the 35K Wheat Breeders Axiom array for the generation of SNPs (Single Nucleotide Polymorphism) and BLUEs (Best Linear Unbiased Estimators) from the cross-year analysis, a GWAS (Genome-Wide Association Study) was run. Novel marker-trait associations were identified for the grain partitioning traits at GS65+7d on chromosomes 5B (SPI), 6A (FESPI) and 7A (internode 3 length), and at harvest in 2B, 6B (HI), 2B, 3A (GN) and 5A, 6A, 7A (GY), explaining from 6-17% of the phenotypic variation.

The implementation of these results can benefit breeding programs through the exploration of genetic resources achieving genetic gains that would increase yield potential.

Exploring the almond genome for alleles useful in peach improvement

Naveen Kalluri, Centre for Research in Agricultural Genomics (CRAG), Spain

One of the main limitations in peach breeding is the low level of variability found in the commercial gene pool. Introgression of genetic variability from wild or cultivated Prunus species may provide new alleles useful to improve disease resistance or fruit quality. For that, we developed an approach, marker-assisted introgression (MAI), allowing the integration of a DNA fragment coming from a donor species (almond) in the background of a peach cultivar only two backcross generations after the hybrid. Additionally, a first survey of the genetics and map position of interesting major genes from the donor species can be done using a small subset of BC1 plants with a low number of introgressions (2-4). We have applied this method in a cross between peach ('Earlygold') and almond ('Texas'), where some interesting almond alleles providing powdery mildew resistance and red flesh color have already been identified. We are developing a introgression line collection of almond genomic fragments in the peach genome background. We already obtained a collection of lines with 2 or 3 introgressions covering the whole almond genome, and two sets of lines with one introgression in heterozygosis and homozygosis covering the 81% and 45% of the almond genome respectively. This collection will be a very useful tool for quantitative variation studies and can be considered as pre-breeding material to be used in peach breeding programs.

Identification of genome-dosage sensitive genes controlling seed size in Arabidopsis thaliana

Rosa Castillo Bravo, National University of Ireland Galway. Ireland

Heterosis (or hybrid vigour) refers to improvement in yield or other characteristics in the F1 offspring relative to parents. Heterosis is an essential tool for increasing yields per unit area for the world's crops. Despite its economic importance, the mechanistic basis of heterosis remains largely unknown. Heterosis for F1 seed size can occur when genetically different parental lines of Arabidopsis thaliana are crossed together. Heterosis-like genome dosage effects on F1 seed size can also be elicited by crossing genetically identical parental lines that differ only according to ploidy. However, the genes underlying such genome dosage effects on F1 seed size are largely unknown. To identify loci responsible for maternal genome dosage effects on triploid F1 seed size, a genome wide association study (GWAS) mapping experiment was performed with a diverse panel of F1 hybrid triploids. To generate the panel of 182 different F1 hybrid triploids, 182 Arabidopsis thaliana diploid (2x) accessions were used as pollen donors to pollinate a tetraploid (4x) tester line in a Ler-0 genetic background. Each of the 182 F1 hybrid triploid progeny had a maternal genome dosage excess consisting of 2 sets of maternal chromosomes and 1 paternal set (2m:1p). The Genome-Wide Association mapping conducted with the 182 F1 hybrid triploids identified a number of genomic regions that are being pursued by functional experiments to identify genome-dosage sensitive loci controlling F1 seed size.

Plant Physiology

Self-incompatibility induced Programmed Cell Death in plants: Identification of new physiological and molecular mechanisms

Marina Muñoz Triviño, Aberystwyth University, UK

Self-incompatibility (SI) is an important mechanism used by flowering plants to prevent self-fertilization, which would otherwise result in loss of plant fitness. In Papaver rhoeas (poppy), interaction between the female and male SI determinants, PrsS and PrpS, leads to pollen tube growth arrest and triggers a signalling pathway, ultimately leading to programmed cell death (PCD). Mechanistically, Papaver SI represents one of the best-characterized SI systems, helped by the availability of a well-established SI in-vitro bioassay. Recently, the transfer of both S-determinants to Arabidopsis, which is self-compatible, rendered Arabidopsis fully self-incompatible. Availability of this Arabidopsis SI system that functionally mimics that of Papaver, allows us to use genetic tools previously unavailable for studying Papaver SI.

We have optimized the SI bioassay for live-cell imaging using this Arabidopsis system. We have confirmed that the SI response in Arabidopsis pollen triggers key hallmark features of the Papaver SI-PCD signalling network, including a rapid cytosolic acidification, formation of punctate actin foci and generation of DEVDase/caspase-3-like activity. The ability to use genetically encoded markers allowed for detailed spatio-temporal evaluation of changes in pH and actin dynamics that are not possible in the Papaver SI system. Using vacuolar markers, we observed that the reticulated structure of the vacuoles started being disrupted within the first 30 minutes after SI induction, but after the initial drop of the cytosolic pH. Using the Yellow Cameleon (YC3.6) indicator, we confirmed that SI induces a rapid increase in cytosolic Ca2+ and also an increase of Ca2+ in the nucleus and rupture of the nuclear envelope at later stages . These data establish the robustness of these engineered Arabidopsis lines for studying SI induced cellular changes. In addition, we used this system to carry out a forward genetics screen and have identified a gene whose mutation results in recovery of seed-set.

Investigating the role of starch metabolism in CAM stomatal behaviour

Natalia Hurtado Castano, Newcastle University, UK

Starch is the most important storage carbohydrate in higher plants and its turnover supports different metabolic processes that include respiration, growth, development and energy production. Starch turnover has also recently been shown to play an important role in determining stomatal behaviour in the C3 model Arabidopsis. In many CAM plants, starch degradation in the leaf mesophyll supports nocturnal CO2 uptake and the synthesis of malate. The role of starch turnover in CAM guard cells however is relatively un-studied. The importance of starch in CAM stomatal behaviour was studied in Kalanchoë fedtschenkoi mutants that lack the enzyme phosphoglucomutase (PGM), which is required for starch synthesis. Data indicate that whilst starch mobilisation is not required for nocturnal (Phase I) opening of stomata, starch biosynthesis is required for day-time stomatal closure as was also indicated by failure of PGM stomata to remain closed under elevated CO2 concentration. Higher levels of soluble sugars in guard-cell enriched epidermal peels from PGM appear to curtail complete stomatal closure during the day. This data indicate that guard cell starch biosynthesis is an important sink for the mobilisation of organic solutes which lower guard cell turgor pressure and ensure day-time stomatal closure in CAM plants.

Genes implicated in starch, sugar and malate metabolism and transport were selected based on their differential expression between mesophyll and guard cell-enriched epidermis tissue as presented in RNA-seq data for K. fedstchenkoi. Real-time PCR has been used to study the expression of some of these candidate genes in K. fedtschenkoi mutants lacking the enzymes PGM, BAM9 (β-amylase 9), PHS1 (Glucan phosphorylase 1) and the plastid glucose transport GlcT, respectively. These evaluations will help to elucidate if and how carbohydrate metabolism has been reprogrammed in CAM plants to allow their inverted stomatal behaviour.

FR light causes drastic transcriptome changes in tomato resulting in a dampening of defense responses against Botrytis cinerea

Sarah Courbier, Utrecht University, Netherlands

Plants are in constant need for an ideal light capture and availability. Red (R) and Blue (B) light are both used to fuel photosynthesis while Far-Red (FR) light is reflected towards neighboring vegetation. As plants experience high planting density, FR reflection from a plant to another leads to a dramatic decrease in the R:FR ratio. Low R:FR has been shown to increase plant susceptibility to pathogens known as the “FR-induced susceptibility”. By the use of RNA sequencing, we aimed to decrypt this phenomenon in a high impact crop species such as tomato. We investigated the effect of additional FR radiation as an early plant pretreatment preceding infection by Botrytis cinerea, a huge crop-devastating pathogen worldwide, on the tomato transcriptome. Our time series experiment unravels the chronology of the infection process and shows that FR perceived before inoculation strongly dampens jasmonic acid-mediated defense leading to a higher susceptibility. We also show that FR modulates the tomato sugar pool in such a way that the pathogen development is promoted within plant tissue. These findings aim to a better understanding of the FR-induced susceptibility in tomato to optimize plant resistance in greenhouse by the smart use of LED lighting.

Phenotyping

Modelling asparagus crop growing in Peru

Angela Romero Vergel, Aberystwyth University, UK

The aims of my PhD project are improve prediction of crop performance by linking remote sensing data of Sentinel 2 (optical) and Sentinel 1 (radar) to crop models for important crops in Peru and Colombia. Initially I am focussing on production of asparagus in Peru. It has been a major exporter of asparagus since 2001 (Fao, 2019) with 1.7 million cultivated hectares, being highly competitive exporting fresh and processed asparagus (Bhatti et al., 2006).

While low temperatures in Europe limit asparagus to a single harvest per year in South America higher temperatures allow continual production and multiple harvests per year. To model asparagus in Peru, we are developing a version of the Aspire model for asparagus based on the description and parameters in Wilson et al., (1997 and 2002). The model has two main phases: (1) spear growth and production during harvest with the consequential use of stored carbohydrate and (2) once spear harvesting ceases, canopy development and carbohydrate accumulation and storage for the next harvest.

The canopy can be senesced by withholding irrigation, and a further harvest started by restarting irrigation. Thus, modelling the accumulation of carbohydrates when the canopy is present is the key to forecasting production. Crop production, management and climate data from previous years being used to calibration under these conditions to validate predictions of future harvests. Field data collected, such as brix, dry matter of canopies and spears, and solar radiation interception are required. Carbohydrate content, canopy developing will be read from remote sensing data.

Preliminary results show simulated values of foliage weight, number of harvested spears and stem per plant are similar to those measured in field in Nov 2018.

This study is part of the EO4 cultivar project managed by Environment Systems funded by the UK Space Agency under the International Partnership Programme.

Architecture of roots: response of wheat to variable soil moisture and N

Olivia Cousins, University of Nottingham, UK

Plants have evolved traits which optimise water and nitrogen (N) uptake; however, the current climate is changing faster than plants' ability to adapt. Plant growth is affected by both quantity of water and frequency. Additionally, water variability directly affects N availability, therefore as climate change models predict rainfall to become more erratic, it is important to understand how the timing of rainfall will affect crop N supply.
We addressed how different soil moistures can affect biomass accumulation, allocation and root architecture within a soil system. Two wheat genotypes were subjected to two soil moisture regimes (wet, dry) and two N fertilisation rates (low, high N). The experiment was carried out at the Hounsfield Facility, where plants were subjected to X-ray Computed Tomography to analyse the root architecture response to the imposed water and N treatments. Results showed a greater root:shoot ratio under dry soil moisture conditions, with more root biomass under dry combined with low or high N. This, coupled with higher specific root lengths for dry soil moisture, suggests that N had a bigger impact on plant growth than water. In addition, there was a genotypic response between the two varieties.
Identifying root system adaptations to wet and dry soil moisture conditions and N will improve understanding of crop-environment interactions and encourage better management strategies for improved food production.

DEEPGENES: functional characterization of genes enhancing soil exploration in maize

Riccardo Fusi, University of Nottingham, UK

Root architecture and anatomy plays a key role in improving plant adaptation to stress conditions, which is crucial to face climate change constraints. Different root anatomical traits have been recently identified in maize to reduce carbon burden for soil exploration, which benefit plants' fitness and yield. In order to explore genetic diversity of these traits, a panel of >450 maize isolines was grown in South Africa and were sequenced using RNA-seq resulting in the 400K and 900K SNPs arrays. Root anatomical phenotyping was performed using shovelomics and a novel platform called 'Anatomics', respectively. This platform involves a high-throughput root sectioning using Laser Ablation Tomography (LAT) and trait measurements using softwares such as RootScan and CellSet. Further, Genome Wide Association Studies (GWAS) were performed for several root anatomical traits such as cortical cell number (CCN), cortical cell file number (CCFN), total cortical area (TCA), root cortical aerenchyma (RCA), revealing very interesting candidates. In order to functionally characterize these candidate genes, we are taking the advantage of novel gene editing tools such as CRISPR-Cas9, overexpression and reporter lines in maize and other grass model species such as Oryza sativa sp. and Brachypodium dystachyon sp. to assess the functional relevance of GWAS identified genes and to determine the molecular mechanisms underlying these genes across species. The final aim of the DeepGenes is to provide new tools for researchers and breeders to implement in maize and other cereal breeding programs.

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