

Speaker Abstracts

The responses of stomata to environmental signals

L01

Monday 9:05-09:45

Stomata are pores found on the surfaces of plant leaves. They control the uptake of carbon dioxide for photosynthesis and the loss of water vapour during the process of transpiration. The aperture of the stomatal pore is governed by the state of turgor of the two guard cells that surround the stomatal pore. When the guard cells are fully turgid the pore gapes open allowing gas exchange and conversely stomatal closure is associated with a loss of turgor. A wide range of environmental signals and plant hormones contribute to the control of stomatal development and aperture. Underlying changes in guard cell turgor and hence stomatal movements is a complex intracellular signalling network. An increase in the concentration of guard cell cytosolic free calcium ions has been shown to be involved in the response to many different signals. This lecture will discuss evidence that guard cell signalling is organised on a network basis and consider recent data related to how guard cells couple environmental signals to changes in stomatal aperture and development.

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Reference

Hetherington AM and Woodward FI (2003) The role of stomata in sensing and driving environmental change. *Nature*, 424, 901-908

A high light responsive chloroplast-to-nucleus retrograde signalling pathway in *Arabidopsis* involves discrete H₂O₂ sources linked by ABA and is regulated by leaf water status

L02

Monday 9:45-10:15

In *Arabidopsis* leaves exposed to a moderate increase in light intensity, bundle sheath cell (BSC) chloroplasts are one of the most prominent sites of hydrogen peroxide (H₂O₂) accumulation. The H₂O₂ is formed by the reduction of oxygen at photosystem I in a process driven by changes in linear photosynthetic electron flux (LEF). BSC-produced H₂O₂ does not promote oxidative stress, but has been shown to participate in signalling that leads to both local and systemic induction of the expression of ASCORBATE PEROXIDASE2 (APX2) and altered responses to further changes in the environment. In both plant and animal cells, a key factor in H₂O₂-mediated signalling may be its containment at discrete sub-cellular sites by surrounding antioxidant systems. Therefore, a distinction can be made between H₂O₂ implicated in eliciting oxidative stress where containment may fail, and spatially discrete H₂O₂-mediated signalling that leads to recovery from and acclimation to adverse conditions. In a model of BSC chloroplast-to-nucleus retrograde signalling in the high light exposed leaf, containment of H₂O₂ predicts that a non-ROS molecule must convey a signal out of the chloroplast. In this communication, evidence will be presented that a H₂O₂-stimulated synthesis of abscisic acid (ABA) in BSC is an essential part of this signalling pathway. In all ABA biosynthesising tissues, the pathway is split between the chloroplast and the cytosol. Thus stimulation of ABA biosynthesis by H₂O₂ would deliver a chloroplast-originated signal to the cytosol. We propose that xanthoxin, the precursor of ABA, synthesised in and exported from the chloroplast, provides a conduit for this retrograde signal. Increased levels of ABA may stimulate a BSC-specific ABA signalling network, which is directed to produce H₂O₂ at the plasma-membrane. This leads to an observed accumulation of H₂O₂ in the apoplast between BSC and the vascular strand and provides a possible explanation for the known requirement for an extracellular source of H₂O₂ for the expression of APX2. The ABA signalling to the plasma-membrane may involve the coordinated action of the ABI1 protein phosphatase 2C (PP2C), the OST1 SNF-related protein kinase, the heterotrimeric G protein complex and AtrbohD/F-encoded NADPH oxidases. Once a plasma-membrane source of H₂O₂ is established, then the remaining steps to the activation of APX2 expression may involve an ABI2-PP2C regulated protein phosphorylation cascade and transcription factors that bind to consensus ABRE cis motifs present in the APX2 promoter. Importantly, the operation of this retrograde signalling pathway is contingent on leaf water status as determined by the prevailing humidity around the leaf. High humidity completely blocks all aspects of this pathway. Thus this paper will discuss how a water status signal that must be transmitted to the chloroplast may control a retrograde signal that exits the chloroplast.

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Light and temperature crosstalk in plant environmental adaptation

L03

Monday 10:15-10:35

Light and temperature are amongst the most important environmental signals regulating plant development. One of the greatest threats to plant survival in natural communities is light limitation through vegetational shading. Light reflected from and transmitted through living vegetation is depleted in photosynthetically active red (R) and blue wavelengths and enriched in green and far-red (FR) wavelengths. Plants detect the presence of neighbouring vegetation through monitoring the ratio of R to FR wavelengths (R:FR) in ambient light. Reductions in R:FR are perceived by the photoreversible phytochrome family of plant photoreceptors and initiate a suite of developmental responses termed the shade avoidance syndrome. These include increased elongation growth of stems and petioles, phenotypes that often correlate with reductions in leaf area, leaf thickness and plant biomass. Such responses serve to elevate leaves within a canopy and enable plants to over-top competing vegetation. We have observed that plant adaptation to the threat of vegetational shade is highly plastic and modulated by the integration of multiple signalling pathways. At lower temperatures and permissive photon fluences, plants forage for light by dramatically increasing leaf area, leaf thickness and dry biomass a strategy, which correlates with expression of the 'CBF regulon', a suite of genes involved in cold acclimation and enhancement of plant freezing tolerance.

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Signalling and gene expression in response to low temperature

L04

Monday 11:00-11:30

Our work on the molecular basis of plant responses to low temperature has focussed upon the second messenger calcium and the protein SFR6, both components in the cold acclimation response leading to freezing tolerance. We have shown that a cold-induced calcium signal is necessary for the induction of many genes associated with cold acclimation. Most notably, calcium regulates the CBF/DREB1-controlled regulon, which is arguably the most important gene regulon involved in cold acclimation. We have demonstrated that the level of regulation is post-translational and are currently identifying the specific mechanism by which this occurs. We have shown that the SFR6 gene product is necessary for the correct functioning of the CBF/DREB1 regulon: *sfr6* mutants show greatly reduced expression of *CBF/DREB1* target genes, and consequently reduced ability to cold acclimate. SFR6 regulates CBF transcription factors at the post-translational level. We have recently cloned *SFR6* and are using proteomic approaches to understand its function at the molecular level.

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Biochemical scanning of combinatorial peptides to deduce optimal phosphorylation sites of protein kinases

L05

Monday 11:30-12:00

Reversible protein phosphorylation is one of the most versatile mechanisms in integrating molecular messages in the cell. In Arabidopsis, there are over 1000 predicted or confirmed kinase genes. Learning about their functions in a physiological context requires, at least in part, identification of their physiological substrates. Several experimental techniques already exist to aid identifying potential targets for protein kinases, including two-hybrid or the more recently developed *in vitro* phosphorylation of proteins fixed onto a solid phase. Powerful as they may be, verification of hundreds of putative targets by other corroborating evidence can be time-consuming. With this in mind, we have implemented an innovative technology that can accurately predict kinase targets providing that the genome is adequately annotated. This method combines informatics and phosphorylation of semi-degenerate peptides to mathematically deduce a hierarchy of optimal phosphorylation motifs. These motifs are then used to search for their corresponding proteins. In collaboration with Ben Turk [Hutti *et al.*, (2004) Nat. Meth.1, 27-29], we have used this technology to predict targets for the Arabidopsis OPEN STOMATA1 (OST1) kinase, which is involved in drought and ABA signalling. We have predicted that the "preferred" motifs of OST1 exist in the b-ZIP class of transcription factors, for which some ABA-insensitive mutants are already known. This innovative approach, in principle, should expediate the accurate prediction of targets for virtually any kinase at the genome scale.

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Rapid hormonal responses in the Arabidopsis shoot apex during light-triggered leaf initiation.

L06

Monday 12:00-12:20

Dark-grown seedlings exhibit repressed shoot apical meristem activity, and arrested, incipient leaf primordia. Following the first exposure to light, leaves rapidly expand and differentiate. An in-depth examination of this transition should allow the uncovering of phenomena at very early stages in leaf development. We dissected shoot apices of Arabidopsis seedlings grown in the dark, and over a time course following the transfer to light, and carried out microarray analysis using Affymetrix ATH1 arrays. We compared the shoot apical gene expression programme with that of cotyledons. Among early transcriptional responses observed, those associated with plant hormones and with ubiquitination processes were, unexpectedly, most noticeable. Extraction of gene expression signatures associated with the response to the main plant hormones revealed an early shoot apex-specific down-regulation of the response to auxins and ethylene, and an elevation of gibberellin and cytokinin action. The cytokinin action signature followed the drop in auxin response and coincided in time with a highly synchronous initiation of cellular growth and cell cycle activity. These early hormonal responses were transient, with auxin responses becoming again elevated at the time of leaf primordia expansion, and the expression of Auxin Response Factors in successive waves being apparent. We are currently trying to understand the exact location, within the meristem or the primordia, of these changes, and their functional significance in the control of early leaf differentiation and growth.

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A key role for Arabidopsis circadian clock genes in temperature sensing and the control of seed germination

L07

Monday 12:20-12:40

Plant can sense the temperature of their environment and use the information to regulate diverse developmental responses. Yet genetic evidence for the early steps in plant temperature signalling remains elusive. Circadian clocks can be entrained to temperature signals and are therefore temperature-responsive, a key feature of a temperature sensor. Here we show that normal circadian clock function is essential for temperature sensing in plant seeds. Seeds are an excellent model system for plant temperature signal transduction because they show quantitative germination responses across the entire biological temperature range, and also respond specifically to alternating temperatures. We show that different clock gene mutants show germination defects in response to low temperature, ambient temperature and alternating temperatures, and that the clock also controls the germination response to dry after-ripening. We show that the transcriptional clock is arrested in an 'evening'-like state in dry seeds, but in contrast to recent reports, rapidly entrains to light/dark cycles in ambient temperatures upon imbibition. Consistent with a role for the clock in dormancy control, the amplitude of clock-gene expression is strongly affected by dormancy-breaking temperatures and after-ripening, and the control of seed hormone metabolism is perturbed in clock gene mutants. Interestingly, we show that germination is timed to occur at dawn in 12 hour light/dark cycles and that this timing requires clock gene function. We conclude that the circadian clock has a key role in the integration of environmental signalling controlling germination and growth.

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Regulatory network of MicroRNA399 and *PHO2* by systemic signaling

L08

Monday 13:30-14:00

Recently, we showed that microRNA399s (miR399s) control inorganic phosphate (Pi) homeostasis by regulating the expression of *PHO2* encoding a ubiquitin-conjugating E2 enzyme (UBC24). Arabidopsis plants overexpressing miR399 or the *pho2* mutant overaccumulate Pi in shoots and displayed Pi toxicity symptoms. Pi toxicity was caused by increased Pi uptake and translocation of Pi from roots to shoots, and retention of Pi in the shoots. The association of Pi translocation and co-expression of miR399s and *PHO2* in vascular tissues suggests their involvement in long-distance signaling. Reciprocal grafting between wild-type and miR399-overexpressing transgenic plants suggests the movement of miR399 from transgenic scions to wild-type rootstocks where *PHO2* expression is suppressed. Suppression of *PHO2* with miR399b or c was less efficient than that with miR399f. Of note, findings in grafted Arabidopsis were also found in grafted tobacco plants. The analysis of the *pho1* mutant provides additional support for systemic suppression of *PHO2* by the movement of miR399 from Pi-depleted shoots to Pi-sufficient roots. We propose that the long-distance movement of miR399s from shoots to roots is crucial to enhance Pi uptake and translocation during the onset of Pi deficiency. Moreover, *PHO2* siRNAs mediated by the cleavage of miR399s may function to refine the suppression of *PHO2*. The regulation of miR399 and *PHO2* via long-distance communication in response to Pi deficiency will be discussed.

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The only constant is change – the yin and yang of nutrient availability and root growth behavior

Nutrient distribution in the soil is very heterogeneous, and root growth behavior, which involves changes to apical growth rates, rates of branching, cell expansion and growth and patterning of root hairs, changes specifically in response to differences in their environment. Mineral nutrients cannot be considered just as signals, as a material requirement for them in metabolism also provides direct mechanistic feedback restraints that prevent extreme imbalances between resource availability and growth activities. We are interested in the molecular mechanisms that couple the perception of mineral nutrients to growth behavior. In phosphate (Pi) - limited plants, continued root growth is required for Pi acquisition from new sources, yet meristem activity consumes Pi translocated from the shoot. Thus, the timing, pattern and magnitude of root growth responses have evolved under constraints of 'cost' and 'benefit'. This implies the evolution of a sophisticated growth regulatory network controlling adaptive behavior, which we aim to dissect. We are also dissecting growth responses at the cellular level: When plants are Pi-limited, enhanced root or shoot growth exacerbates, whereas growth inhibition suppresses Pi starvation responses. Our results show that inhibition of cell-cycle activity specifically reduces Pi starvation-responsive gene expression. We propose that cell-cycle activity is the ultimate arbiter for Pi demand in growing organs, and that other factors that influence levels of PSR gene expression do so by affecting growth through modulation of meristem activity. We will present results of our recent spatial and temporal analysis of phosphate-responsive growth control networks.

L09

Monday 14:00-14:30

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Post-embryonic cell fate changes of *Arabidopsis* rhizodermic cells in response to phosphate deficiency

L10

Monday 14:30-14:50

Acclimation of plants to the prevailing environmental conditions is achieved by reprogramming metabolism and gene expression, gaining new functions of particular cell type(s). The decision of a root epidermal cell to form a hair is dependent on bidirectional signaling circuits among neighboring cells and on positional information from the underlying tissue. In addition, environmental signals are perceived and integrated into the cell specification process and may interact with, or overrule intrinsic programs. In particular, suboptimal availability of phosphate, iron, and manganese causes re-differentiation of rhizodermic cells. The spatial expression of genes determining the cell fate during embryogenesis was found to be unaffected by nutrient signals. Mutants harboring defects in cell specification genes were still responsive to phosphate deficiency, but the mutations affected the number and position of the hairs. We put forward the hypothesis that during post-embryonic development a novel second mechanism becomes dominant over the basic patterning mechanism, conferring cellular plasticity. This supposition is supported by mathematical modeling assuming an inhibitor-activator mechanism downstream of the WER patterning cascade that is sensitive to environmental signals. Candidate genes and processes involved in the change of root hair patterning were investigated by forward genetic mutant screening. The *perfect* mutant is defective in phosphate sensing and shows a phenotype typical of P-deficient plants in the presence of phosphate. P-deficient perfect plants formed very short root hairs and were impaired in their response to phosphate starvation. *PERFECT* encodes a ubiquitin-specific protease, underlining the importance of protein turnover in the adaptation to available phosphate.

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Temporal regulation of root hair development by *RHD6* family genes

L11

Monday 14:50-15:10

While many genes that participate in root hair development have been identified, the transcriptional regulation of hair initiation and tip growth is still poorly understood. Previously, we showed that two bHLH transcription factors, *RHD6* and *RSL1*, are required for root hair initiation. Here, we describe four paralogues of *RHD6* that form a sister clade to the *RHD6* clade. The genetic analysis shows that the sister clade genes function downstream of *RHD6* and *RSL1* in root hair development. One gene controls both hair initiation and tip growth while the other three members control tip growth in the hair. The expression of *RHD6* family genes follows a temporal pattern that reflects the timing of their roles during development. We also showed that the internal (auxin and ethylene) and external (phosphate availability) factors regulate root hair development through these genes that lie downstream of *RHD6* and *RSL1*. In summary, we found a subgroup of key regulator genes in the same bHLH subfamily form a regulatory network to integrate the internal and external signals for root hair initiation and tip growth.

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Analysis of natural variation for mineral concentration in *Arabidopsis thaliana*

L12

Monday 15:30-16:00

Tight regulation of mineral homeostasis is crucial to growth and development of plants. Plants require more than fifteen mineral elements. These include macronutrient elements like P, K, Ca and micronutrient elements, such as Zn, Fe, Mn and Mg. All of these nutrients are taken up by roots, translocated through the plant and used or stored for later use. Plants or plant derived products can be important sources of essential elements as dietary nutrients for humans and animals. Therefore, knowledge of the genes controlling mineral uptake and distribution in plants will increase our understanding of the mineral homeostasis process and may facilitate the improvement of plant nutrient content with potentially beneficial effects on human and/or animal health as well as on crop yield and quality. We examined the natural variation for seed, leaf and root mineral content in several recombinant inbred line (RIL) populations of *Arabidopsis thaliana* such as Landsberg erecta (Ler) x Kondara (Kond), Ler x Cape Verde Islands (Cvi), Ler x Antwerp (An) and Ler x Erinsboda (Eri). Plants were grown in several replicates on hydroponic solution or in soil. A quantitative trait loci (QTL) approach was used to identify and unravel the genetic loci controlling seed, leaf or root concentration of P, K, Ca, Mg, Mn, Fe and Zn. For each mineral several QTL were identified in each population. Co-localization of some QTL suggested single loci to be involved in the accumulation of multiple minerals. In many cases, QTL for seed mineral concentration identified in plants grown on soil did not co-localize with QTL for seed mineral concentration identified in plants grown hydroponically, suggesting a strong effect of environment on these traits. Such effect was further genetically examined in plants exposed to abiotic stress conditions, such as induced drought and Zn deficiency. Analysis of the *CRY2* and *ERECTA* loci showed that in addition to environment also plant development has a significant effect on seed mineral status.

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Characterisation of the APS kinase gene family in *Arabidopsis thaliana*

L13

Monday 16:00-16:20

Upon assimilation in higher plants, sulphur is partitioned into components of primary and secondary metabolism. The branching point is the metabolism of adenosine 5'phosphosulphate (APS). APS can be reduced to sulphite by APS reductase, and after further reduction incorporated into cysteine and other components of primary metabolism, or phosphorylated by APS kinase (APK) to form PAPS. PAPS is the sulphate donor for sulphotransferase enzymes which catalyse the transfer of the sulphate group onto free hydroxyl groups of acceptor molecules. Such sulphated secondary metabolites include the glucosinolates and sulphated hormones, which play important roles in defence against biotic and abiotic stress. How the partitioning of sulphur between primary and secondary metabolism is controlled in plants is poorly understood. By investigating the *APK* gene family in *Arabidopsis* we hope to gain insight into the mechanism and control of sulphate partitioning. There are four isoforms of *APK* in *Arabidopsis*, which we are characterising using a combination of tools including reverse genetics, web-based and SQRT-PCR expression analysis, promoter::GUS / GFP reporter lines, biochemical analysis and metabolic profiling. Different expression patterns and subcellular localisation suggests distinct roles for individual isoforms within the family. Characterisation of single and multiple knockout mutants of *APK* is confirming this, with particular attention being paid to the metabolite profiles of the double mutants.

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***EZ-Rhizo*: Integrated software for fast and accurate measurement of Arabidopsis root system architecture**

L14

Monday 16:20-16:40

The root system is essential for the growth and development of plants. In addition to anchoring the plant in the ground it is the site of uptake of water and minerals from the soil. Plant root systems show an astonishing plasticity in their architecture, which allows for optimal exploitation of diverse soil structures and conditions. The signalling pathways that enable plants to sense and respond to changes in soil conditions, in particular nutrient supply, are a topic of intensive research, and root system architecture (RSA) is an important and obvious phenotypic output. At present, quantitative description of RSA is labour-intensive and time-consuming, even using currently available software, and the lack of a fast RSA measuring tool hampers forward and quantitative genetics studies. We have developed *EZ-Rhizo*, a Windows-integrated and semi-automated computer program designed to detect and quantify multiple RSA parameters from plants growing on a solid support medium. The method is non-invasive, enabling the user to follow RSA development over time. Faster and more accurate measurement of RSA will permit a fine dissection of environmental and genetic control of root traits. *EZ-Rhizo* was applied to investigate Arabidopsis natural variation using principal component analysis of non redundant RSA parameters. This study underscored the importance of measuring different RSA parameters to fully describe RSA variation and allowed us to identify novel RSA determinants.

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The molecular basis of cell-cell communication during double fertilization in *Arabidopsis*

L15

Tuesday 9:00-09:40

Research in our laboratory focuses on the developmental genetics of plant reproduction. Our studies have shown that both genetic and epigenetic mechanisms play a key role in plant reproduction. In this seminar I will focus on cell-cell interactions during double fertilization. We have isolated a female gametophytic mutant, *feronia*, which disrupts double fertilization: in *feronia* mutant embryo sacs the pollen tubes, even if wild-type, are unable to release the sperm cells to effect fertilization. This phenotype suggests that the female gametophyte plays a crucial role in pollen tube reception and, thus, controls the behavior of the male gametophyte. The *feronia* mutant defines novel signaling processes between the male and female gametophytes in the process of double fertilization. *FERONIA* was shown to encode a receptor-like kinase of a plant-specific subfamily. I will report on the molecular and biochemical characterization of *FERONIA* and on our search for additional components of this signal transduction process using genetic and biochemical approaches. Interestingly, some interspecific crosses result in phenotypes that are very similar to those observed in the *feronia* mutant. The evolutionary implications of these findings will be discussed.

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Genetic control of male germ line development in flowering plants

L16

Tuesday 9:40-10:10

Pollen grains represent the highly reduced haploid male gametophyte generation in spermatophyte plants. In flowering plants their role is to nurture and deliver a pair of sperm cells to the embryo sac for double fertilisation. Recent advances in our understanding of landmark events in pollen development are largely based on progress achieved using genetic and transcriptomic approaches. Genome-wide analysis has revealed complex patterns of gene expression during male gametophyte development in *Arabidopsis* (1). There is also evidence for extensive germ cell gene expression in maize and lily (2,3) and several male germ cell-specific promoters have been characterized in *Arabidopsis* (4-7). These datasets and molecular tools complement progress in genetic analyses that is beginning to uncover the molecular mechanisms that pattern pollen development. A central outstanding question in pollen development is how the vegetative cell exits the cell cycle and differentiates to form the pollen tube, while the germ cell divides to form functional twin sperm cells? The identification of a non-germ cell repressor protein, Germline Restrictive Silencing Factor, in lily suggests the involvement of transcriptional derepression in male germ cell specification (8). The analysis of a suite of *Arabidopsis* mutants that block male germ cell division provides further insight. Cyclin Dependent Kinase (CDK) and Chromatin Assembly Factor (CAF1) pathway mutants show that germ cell division can be uncoupled from gamete specification (9,10). Recent progress involves the identification of an F-box protein that forms an SCFFBL17 complex in germ cells that targets the CDK inhibitor protein KRP6 for proteasome-dependent degradation. SCFFBL17 acts as a male germ cell proliferation licensing factor, but is also not involved in cell differentiation. However the R2R3 Myb transcriptional regulatory protein DUO15, coordinates these processes by activating germ line-specific gene expression and Cyclin B1:1 to commit differentiating germ cells to mitosis. DUO1 is therefore a key male germ cell fate determinant that regulates twin-sperm cell production and germ cell-specific genes including GCS16, which is essential for gamete fertility and double fertilization. Further progress in understanding the essential switch between germ and non germ cell lineages will continue to benefit from the integration of genetic and genomic technologies, offering new opportunities to build complex functional models of male gametophyte development.

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Post-genomics approaches to understand mechanisms regulating the completion of germination

L17

Tuesday 10:10-10:30

Post-genomics approaches, in combination with classical genetics and physiology have been used to analyse how genotype and environment interact to regulate genome expression and phenotype during germination. Novel genetic screens (1) have been used to identify components required for the completion of germination in *Arabidopsis thaliana*, and this information has been used to study the genetics of 'candidate genes' in barley. Physiological analyses have revealed transcriptome components responsive to after-ripening (AR) in *Arabidopsis* (2,3), and demonstrate that AR capacity is a developmental process that does not require ABA (2). Key regulators underlying the molecular network linking after-ripening status with Abscisic Acid (ABA) function in the imbibed mature seed have been uncovered. Analysis of genome expression responsive to these regulators demonstrates how AR and ABA influence endosperm rupture prior to the completion of germination. These and other approaches are being used to inform research projects addressing the physiological disorder Pre-Harvest Sprouting in wheat (4).

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From Arabidopsis to rice: pathways in pollen development

L18

Tuesday 11:00-11:30

We have characterised the Arabidopsis *MALESTERILITY1* (*MS1*) gene and shown that it plays a fundamental role in tapetal development and the production of fertile pollen. In the absence of *MS1* no viable pollen is formed and the plants are fully male sterile, although female fertility is unaffected. *MS1* is expressed in a highly regulated manner both at the transcriptional and post-translational level in the anther tapetum after microspore meiosis. We have been establishing the Arabidopsis *MS1* network and have shown that it regulates large numbers of genes, particularly those associated with pollen wall formation. We have taken this network information from Arabidopsis and applied it to rice. We have identified the equivalent *MS1* orthologous gene in rice and demonstrated that it has a conserved function. The network of gene expression in the anther during the late stages of pollen development and the role of *MS1* in Arabidopsis and rice will be discussed.

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Cell fate determination by genetic and hormonal patterning in fruits

L19

Tuesday 11:30-12:00

The fruit of flowering plants provides an excellent system to study cell differentiation and tissue specification, since it is divided into discrete sections with juxtaposed cell types that are dramatically different from each other. The *Arabidopsis thaliana* fruit has been used extensively as a model to investigate how fruits are formed and several of the key regulators of the process have been identified. Patterning the *Arabidopsis* fruit involves formation of polarity along the proximo-distal and medio-lateral axes. Getting it right is crucial for proper development and much of the information has been laid down well before fertilisation. The plant hormone auxin plays important roles in organogenesis and tissue patterning. Polar auxin transport ensures regulation of local auxin concentrations, which mediate specification of organ outgrowths, polarity within organs or formation of specific cell types. Although significant leaps have been made in the understanding of auxin distribution and responses, not much is known about the upstream events that are likely to be specific to individual tissues. Our results show that auxin distribution is tightly regulated throughout *Arabidopsis* fruit development and that the valve margin identity factor INDEHISCENT (IND) negatively regulates polar auxin transport leading to the formation of a local auxin-response minimum and anticlinal cell division. Consistent with these data, ectopic production of auxin specifically in valve margin cells results in inhibition of the specification programme and lack of valve margin formation. Our results firmly embed auxin dynamics within the established regulatory pathway of *Arabidopsis* fruit patterning.

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The *Solanum lycopersicum* auxin response factor 7 (*SIARF7*) regulates auxin signaling during Tomato fruit set and development

L20

Tuesday 12:00-12:20

Auxin Response Factors (ARFs) are encoded by a gene family of transcription factors that specifically control auxin-dependent developmental processes. A tomato *ARF* gene, homologous to Arabidopsis *NPH4/ARF7* and therefore designated as *Solanum lycopersicum ARF7 (SIARF7)*, was found to be expressed at high level in the unpollinated mature ovaries. More detailed analysis of tomato ovaries showed that the level of *SIARF7* transcript increases during flower development, remains at a constant high level in mature flowers, and is down-regulated within 48 hours after pollination, suggesting that this ARF has a regulatory role in fruit set. Transgenic plants with decreased *SIARF7* mRNA levels formed seedless (parthenocarpic) fruits. These fruits were heart-like shaped and had a rather thick pericarp due to increased cell expansion, as compared to the pericarp of wild type fruits. The expression analysis, together with the parthenocarpic fruit phenotype of the transgenic lines, suggest that in tomato *SIARF7* acts as a negative regulator of fruit set until pollination and fertilization have taken place, and moderates the auxin response during fruit growth.

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Senescence in *Arabidopsis* siliques: a comparison to senescence in other tissues and its role in seed development and nutrition

L21

Tuesday 12:20-12:40

Senescence of plant organs is a genetically controlled process that regulates cell death to facilitate nutrient recovery and recycling and frequently precedes, or is concomitant with, ripening of reproductive structures. In *Arabidopsis* the seeds are contained within a silique which undergoes a programme of senescence prior to dehiscence. A transcriptional analysis of the silique wall was undertaken to identify changes in gene expression during senescence and to correlate these events with ultrastructural changes. The study revealed that the most highly up-regulated genes in senescing silique wall tissues encoded seed storage proteins and the significance of this finding is discussed. Global transcription profiles of senescing siliques were compared with those from senescing *Arabidopsis* leaf or petal tissues using microarray datasets and metabolic pathway analyses. In all three tissues, members of NAC and WRKY transcription factor families were up-regulated whilst components of the shikimate and cell wall biosynthetic pathways were down-regulated. The expression of genes encoding ethylene biosynthesis and action had more similarity between senescing siliques and petals than with leaves. Genes involved in autophagy were highly expressed in the late stages of death of all plant tissues studied, but not always during the preceding remobilisation phase of senescence. Analyses showed that, during senescence, silique wall tissues exhibited more transcriptional features in common with petals than with leaves. The shared and distinct regulatory events associated with senescence in the three organs are evaluated and we present ongoing work exploring the potential for manipulating storage protein accumulation in seeds.

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Seasonal control of flowering in annual and perennial plants

L22

Monday 13:30-14:00

Arabis alpina, a member of the *Brassicaceae* that diverged from *Arabidopsis* around 30 million years ago. We have studied the effect of vernalization (exposure to low winter temperatures) on the life cycle of *Arabis alpina* and compare the mechanisms underlying vernalization response in this species with those of *Arabidopsis*. We propose that there is correlated selection of the vernalization response as species evolve from perennial to annual. The talk will present this comparative approach to study flowering-time control.

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The need for winter in the switch to flowering

L23

Tuesday 14:00-14:30

The Dean laboratory is studying the importance of prolonged cold (winter) for flowering, a process known as vernalization. We have used a molecular genetic analysis in the model plant *Arabidopsis thaliana* to identify genes involved in determining both the ability to vernalize and the need for vernalization. The pathways we study share a common downstream target, a gene encoding the repressor of flowering, *FLC*. Mutants attenuating the vernalization response revealed *FLC* expression is silenced during the cold and this repression remains epigenetically stable through the rest of the plant life-cycle. A Polycomb-based chromatin regulation involving conserved regulators and PHD finger proteins mediates this epigenetic silencing. The autonomous floral promotion pathway affects the need for vernalization. Recent work suggests this pathway links RNA processing, RNAi machinery and chromatin regulation to cause the down-regulation of *FLC*. It has also been shown to play widespread roles in the epigenetic silencing of the *Arabidopsis* genome. Functioning antagonistically to both the autonomous pathway and vernalization, *FRIGIDA* (*FRI*) causes plants to overwinter in the vegetative state by up-regulating *FLC* expression. *FRI* is the major determinant of flowering time variation in *Arabidopsis* and *FRI* loss-of-function alleles have been found to be the basis for the evolution of many rapid-cycling *Arabidopsis* accessions. The talk will describe our current understanding of these pathways and how they have changed in *Arabidopsis* variants adapted to different climates.

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Optimising flowering time in *Miscanthus* for improved biomass yield and quality

L24

Tuesday 14:30-14:50

The perennial C4 grass *Miscanthus* is a leading candidate for sustainable bioenergy production in Europe and N. America. *Miscanthus* has a broad natural geographical range that provides extensive and currently unexploited genetic diversity. *Miscanthus* is currently co-fired with coal to produce heat and electricity but may also be chemically converted to liquid fuel. Optimisation of flowering time has been identified as key to improving both the yield and quality of biomass. Early flowering associates with reduced yield and is therefore undesirable. However, as flowering is also a potential trigger for senescence and the subsequent remobilisation of nutrients to the underground rhizome it is important for crop sustainability. Senescence may also improve yield quality as downstream processing is detrimentally affected by residual nutrients in harvested biomass. Genotypes exhibiting late flowering coupled tightly with senescence could therefore optimise the yield, quality and sustainability of the crop. An F1 mapping population, based on a cross between early and late flowering genotypes of *M. sinensis*, is being used to identify quantitative trait loci associated with flowering time. In addition, homologues of genes controlling flowering time in other species are being identified in *Miscanthus*. Sequence information from these homologues will be used together with phenotypic data from a genetic collection with wide-ranging flowering times. This data will be used to perform association studies, where single nucleotide polymorphisms will be correlated with flowering phenotype, thereby facilitating marker assisted selection.

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Genetic basis of the link between senescence regulation and flowering time control

L25

Tuesday 14:50-15:10

In annual plants, leaf senescence is often linked to reproduction. However, no effect of sterility on senescence was found using mutants of *Arabidopsis*, suggesting that senescence in *Arabidopsis* is not regulated by the successful formation of fruits and seeds. Nevertheless, flowering time and senescence are correlated among different accessions of *Arabidopsis*, indicating that floral initiation and senescence are linked, although the causal relationship remained unresolved. Analysing the effect of sugar supply on senescence in recombinant-inbred lines (RILs) we found that while sugar treatment induced senescence in early-flowering lines, the effect was less pronounced in late-flowering lines. Microarray analysis revealed differences in the expression of flowering genes, such as *FLC* and *SOC1*, in the RILs. Quantitative trait locus (QTL) experiments were conducted to determine the genetic basis of this regulation. A major QTL mapped to the top of chromosome IV where *FRI*, an activator of the floral repressor *FLC* is localised. Since interaction of functional *FRI* and *FLC* alleles results in vernalisation dependent flowering, the effect of vernalisation on senescence was determined in early and late flowering lines. Whereas a clear correlation between flowering and senescence was found without vernalisation, vernalisation abolished differences between the lines, thus supporting the genetic link between the vernalisation-dependent pathway of flowering and senescence regulation revealed by the QTL analysis.

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Evolution of regulatory networks controlling floral organ identity: a MIKC blessing

L26

Monday 9:05-09:45

Flower development is controlled by gene regulatory networks (GRNs) that are dominated by MIKC-type MADS-box genes encoding transcription factors (1). Changes in these regulatory networks are underlying the morphological evolution of flowers and hence the generation of floral biodiversity. To better understand the link between the evolution of floral GRNs and the morphology of the flower we study MIKC-type genes and proteins in evolutionary informative spermatophytes. A special focus of our work is on the floral homeotic genes which encode proteins that form multimeric complexes ('floral quartets') specifying floral organ identity by activating and repressing the appropriate target genes during the development of floral organs (2). Studies in the gymnosperm *Gnetum* and in orchids indicate in more and more detail how the origin of new classes of MIKC-type genes by gene or genome duplications contributed to the establishment of morphological novelties, such as the floral perianth, or the orchid's lip (3, 4). Investigations on grasses such as maize (*Zea*) and orchids reveal that at least some classes of floral homeotic genes have been highly conserved throughout more than hundred million years of evolution, even though the organs they specify sometimes have been modified dramatically (3, 4). Studies in tulips (*Tulipa*) demonstrate that class B floral homeotic gene function is also conserved in petaloid monocots. Our findings demonstrate the importance of sub- and neo-functionalization of developmental control genes for the evolutionary origin of morphological novelties. The evolutionary relevance of heterotopic expression of developmental control genes resulting in homeosis, and of the modularity of genes and organisms, are recurrent themes in our investigations (3-5).

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Control of floral transition in maize

L27

Tuesday 16:00-16:20

Flowering time in plants is controlled by a number of environmental factors, among which photoperiod plays a key role. Maize ancestors are short-day (SD) plants, but breeding programs have selected genotypes whose flowering is largely autonomous and occurs after production of a constant number of leaves regardless of photoperiod. Only few flowering time genes have been identified in maize; one of them is *INDETERMINATE1 (ID1)*, cloned from a late-flowering mutant and encoding a zinc finger transcription factor. By contrast, the genetical control of flowering by photoperiod is best understood in the long-day (LD) dicot *Arabidopsis* and the SD monocot rice. A key regulator is the *CONSTANS* gene that mediates between the circadian clock, the time-keeper of the plant, and the synthesis of flowering signals. Here we report the analysis of a *CONSTANS* homolog in maize, *ZmCO*, in SD and in LD, and in different parts of the plant. Expression of *ZmCO* was found to be rhythmic and to be higher in young leaf primordia than in mature leaf blades. Striking coincidence was observed with expression of *ID1*.

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Hormonal control of shoot branching

L28

Wednesday 9:00-09:30

A unique feature of plant development is the ability to alter body plan in response to environmental conditions. The primary body axis of plants is laid down during embryogenesis with the establishment of the shoot apical meristem at one end and a root apical meristem at the other. Post-embryonically, the meristems elaborate this basic axis, but in addition secondary meristems arise in both the root and shoot, which give rise to new axes of growth- lateral branches. It is this ability to produce lateral branches that gives plants their spectacular plasticity of form. As a model for understanding the role of plant hormones in plant developmental plasticity, we are investigating the hormonal control of shoot branching. We are focusing on two hormones that inhibit branching-auxin, which has been known to regulate branching for 80 years; and a novel hormone, which has not yet been chemically defined. In Arabidopsis, the novel hormone came to light through the analysis of mutants at 4 loci, called *MAX1-MAX4*, with increased shoot branching. These genes define an additional pathway that interacts with auxin to mediate branch inhibition. Grafting studies have demonstrated that three of these loci are involved in the production of a long-range graft transmissible signal that inhibits bud growth, while the third acts locally in the transduction of this signal, and this is consistent with the molecular identities of these genes. The pathway appears to act by modulating auxin transport capacity in the main stem, suggesting an interesting indirect mechanism for apical dominance and its modulation. A third hormone, cytokinin, that promotes bud activation fits into this network and also interacts with auxin and its transport. Our progress in understanding the operation of this hormonal network in modulating shoot branching in response to the environment will be presented.

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To grow or not to grow

L29

Wednesday 9:30-10:00

The DELLA proteins (DELLAs) are a subfamily of the plant-specific GRAS family of putative transcriptional regulators that regulate plant growth in response to the phytohormone gibberellin (GA). The DELLAs restrain growth, and GA promotes growth by opposing DELLA function. Essentially, GA binds to a specific GA-receptor protein (GID1), thus stimulating a GID1-DELLA protein-protein interaction. This interaction itself promotes specific targetting of DELLAs for destruction in the proteasome via the SCFSLY1 E3 ubiquitin ligase. Additional signalling pathways, such as those associated with phytohormones other than GA, and environmental variables such as light, temperature and nutrient status, also influence plant growth via effects on the GA-DELLA growth-regulatory mechanism. The concept that the DELLAs are integrators of multiple plant growth regulatory signalling inputs will be explored, and the broader biological significance of DELLA function will be illustrated, with particular emphasis on the question of how the GA-DELLA growth-regulatory mechanism arose during land-plant evolution.

Recent publications:

Achard *et al.* (2006). *Science* 311: 91-94.

Achard *et al.* (2007). *Plant Physiology* 143: 1163-1172.

Achard *et al.* (2007). *Proceedings of the National Academy of Sciences (USA)* 104: 6484-6489.

Yasumura *et al.* (2007). *Current Biology* 17: 1225-1230.

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To divide or not to divide – How ABA affects root growth

L30

Wednesday 10:00-10:20

ABA is primarily known as a stress hormone that relays the plants responses to environmental signals such as drought, salt stress or cold. Increases in ABA concentration lead to inhibition of root growth but it is unclear what the underlying cellular mechanisms are. Detailed growth analyses and cell division markers such as *CycB1;1* revealed that ABA regulates root growth by influencing cell division rates. We are also interested where in the root the ABA signal is perceived and used a transactivation approach to investigate whether any root tissue in particular is important for ABA signal perception. Results will be presented that show that there are indeed differences in ABA sensitivity between the different root tissues. In addition, ABA appears to influence root architecture by antagonising auxin in the initiation of lateral roots. Using the same transactivation approach we could show that ABA inhibits the initiation of lateral root primordia in addition to its previously reported inhibitory effect on growth after lateral root emergence (1). In summary we show some of the mechanisms by which ABA integrates environmental responses into the root developmental growth program and thus shapes root growth in response to environmental cues.

References

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Root growth in *Arabidopsis* requires gibberellin/DELLA signalling in the endodermis

L31

Wednesday 10:50-11:20

Gibberellins (GAs) are key regulators of plant growth and development. They promote growth by targeting the degradation of DELLA repressor proteins; however, their site of action at the cellular, tissue or organ levels remains unknown. To map the site of GA action in regulating root growth, we expressed *gai*, a non-degradable, mutant DELLA protein, in selected root tissues. Root growth was retarded specifically when *gai* was expressed in endodermal cells. Our results demonstrate that the endodermis represents the primary GA responsive tissue regulating organ growth and that endodermal cell expansion is rate-limiting for elongation of other tissues and therefore of the root as a whole.

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In plants, stem cells are maintained and regulated in meristems. The cambium and procambium are meristematic tissues that generate the xylem and phloem which are specialised organs for water and nutrient transport. Furthermore, cambial meristems are the main source of plant biomass and as such their regulation has come under increasing scrutiny as biomass is likely to play an increasing role in generation of renewable energy. One regulator of vascular meristems is PXY, a receptor-like kinase that is required for polar cell divisions within the procambium which are essential for organised vascular tissue development. We have recently identified additional components of the PXY signalling pathway. Over expression of a single PXY dependant component is sufficient to generate dramatic increases in vascular cell number and increase the proportion of undifferentiated cells. Furthermore, over-expression of multiple pathway components results in ectopic vascular tissue development and early onset of secondary growth. The data has identified multiple roles for PXY-dependent signalling. In addition to its role in setting the division plane, PXY forms part of a signalling network that regulates the rate of cambial cell divisions and as a result, the balance between dividing (undifferentiated) and differentiated cells.

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Auxin influx carriers are involved in apical hook development

L33

Wednesday 11:40-12:00

During skotomorphogenic growth, dicotyledonous plants form an apical hook at the top of the hypocotyl to protect the apical meristem and the cotyledons during growth through soil or mulching. Hook formation, maintenance and exaggeration are supposedly caused by an auxin gradient that induces differential growth. In *Arabidopsis*, the accumulation of DR5 auxin reporter signal on the concave side of the hook suggests an auxin maximum in this region. The gradient is established by active auxin transport, that is NPA sensitive and auxin efflux regulator dependent. We have found a significant role for a subset of auxin influx carriers in the development of the apical hook. While LAX3 is important for hook development in general, AUX1 is a prerequisite for ethylene induced exaggeration of the hook. Mutant analysis revealed that among the auxin influx regulators these two are playing an important role in steering hook development.

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Plant endomembrane system and chemical genomics

L34

Wednesday 13:00-13:30

Chemical genomics is an exciting new technology for studying gene functions in the context of living organisms or cell systems. The approach complements existing molecular and genetics tools (e.g. mutagenesis, RNAi) by allowing fine-tunable in vivo modulations of protein functions and cellular processes. For example, lethality and redundancy are common and challenging descriptors in genetic studies of the endomembrane system. Chemical genomics can be used to overcome these challenges and study protein trafficking mechanisms. We have performed a few chemical genomics screens and identified several useful compounds. Effect of these compounds on various markers of the endomembrane system was assessed. Analogs of these chemicals were tested to identify the chemical structures that are responsible for bioactivity of these molecules. Screens for resistant and hypersensitive mutants were carried out with the goal of identifying putative targets or to identify components of the pathway. Information about these targets and pathways will be discussed.

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The cytoskeleton in plant cell morphogenesis and development

L35

Wednesday 13:30-14:00

The plant cytoskeleton governs plant cell morphogenesis and it is composed of microtubules and actin filaments, and a plethora of associated proteins that serve to anchor, cross-bridge or otherwise regulate this fibrous network. These associated proteins are involved in competitive and/or cooperative interactions within cells to adjust the organisation of the cytoskeleton to the cells needs. These associated proteins are often stimulus responsive and are the effectors in signal transduction cascades. This system has evolved so that normally sedentary plant cells can respond to developmental and environmental cues in order to proliferate and grow, to maximise energy production, to take up nutrients from the soil, to reproduce and to protect from pathogen invasion. In all these cases the cytoskeleton has to respond to signals and reorganise so that cells can divide and expand, generate organelle movement, polarise cell growth and thicken the cell wall. Here, some of the main players in the control of cytoskeletal organisation in plant cells will be discussed.

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Novel compounds that disrupt actin filaments identified by chemical genetic screen for impairment of the Arabidopsis circadian clock

L36

Wednesday 14:00-14:20

To study the Arabidopsis circadian clock a forward chemical genetic screen was performed to identify small molecules that impair circadian rhythms. Here we describe the identification of two small molecules causing shortening of circadian period length. Additionally, the plants treated with the compounds exhibit growth phenotypes associated with microfilament defects. Short treatment with the compounds results in altered actin organization, but does not affect the tubulin filaments. A similar result was obtained in animal cells, indicating that the target of the compounds is highly conserved between the animal and plant Kingdoms. Well-characterized actin inhibitors triggered similar changes in the circadian clock showing that the altered circadian rhythmicity is the result of the impaired actin network. Actin inhibitors have specific, light-dependent effects on circadian oscillations suggesting that the role of actin filaments in the clock is predominantly linked to input pathways.

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Intramembrane protein dynamics in the ER and plasma membrane is affected by the actin cytoskeleton

L37

Wednesday 14:20-14:40

Proteins within plant cell endomembranes are highly mobile. Their mobility can be quantified using the confocal microscopy technique of photoactivation. What does a description of the speed of membrane protein dispersion tell us? Our initial observations lead us to believe that the structure of ER and plasma membranes is quite different. To mark the membranes, we use known protein transmembrane domains that target respective organelles fused to photoactivatable GFP (PAGFP). The ER is marked by calnexin-PAGFP and the plasma membrane is marked by Low Temperature Inducible protein 6B (LTI6B)-PAGFP. Neither of these proteins is predicted to interact with others and so are useful as a control for non-interacting protein mobility. The ER is a highly dynamic interconnected network of tubules and cisternal sheets. Its motion is actin-cytoskeleton dependant. When the actin is depolymerised by application of latrunculin B, bulk flow and remodelling of the ER ceases but calnexin continues to diffuse. Overexpression of the tail region of a myosin XI also results in cessation of ER movement but has a limiting effect on calnexin diffusion. LTI6B-PAGFP in the plasma membrane moves very slowly when photoactivated. The plasma membrane appears significantly different from the ER in this respect. Interestingly, there is evidence that when the actin cytoskeleton is depolymerised LTI6B becomes unconstrained and can diffuse more quickly within the membrane. This might point to the existence of actin corrals that contribute to protein-domain formation and these domains might be important regulatory structures for plant cells.

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The gene regulatory network for root epidermal cell differentiation

L38

Wednesday 15:00-15:30

A fundamental aspect of plant development is the specification and differentiation of distinct cell types. The position-dependent formation of the root-hair and non-hair cell types in the *Arabidopsis* root epidermis is useful as a simple model for studying plant cell differentiation. Cellular, molecular, genetic, and genomic approaches have defined genes and their corresponding proteins involved in this process. By studying these, we have found that transcriptional feedback loops acting within and between adjacent cells are important in establishing the cell type pattern. Specifically, the WER MYB-type protein, the GL3/EGL3 bHLH-type proteins, and the TTG WD-protein appear to interact in a transcriptional complex to positively regulate the *GL2*, *CPC*, *TRY*, and *ETC1* genes. The *GL2* homeodomain transcription factor regulates genes that generate the non-hair cell type. The *CPC*, *TRY*, and *ETC1* proteins are structurally-related small MYB transcription factors that appear to move to neighboring cells and inhibit the WER-GL3/EGL3-TTG complex; representing a type of lateral inhibition. In another regulatory loop, the GL3/EGL3 proteins negatively affect their own genes' expression and likely move to cells in the opposite direction. The position-dependent pattern relies on a LRR-RLK (SCRAMBLED (SCM)), that appears to cause an unequal distribution of the transcriptional regulators in the N and H cell positions. Currently, systems-based approaches and mathematical modelling are being used to construct and analyze the gene regulatory network that controls root epidermal cell patterning and differentiation. These studies are likely to provide insights into the logic of gene regulatory networks and mechanisms of cell specification during development.

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Arranging biological resource information on the semantic web, an information platform towards genome design in Arabidopsis

L39

Wednesday 15:30-16:00

The Semantic Web is a standard framework for knowledge description and discovery by computer-aided inferences, based on the relationships represented as semantic links among resources including the complete genome sequence along with gene structure, gene products, metabolites, gene expression, resource lines, phenotypes, publications, and any information useful to the research community. As a tool to realize the semantic web, we have developed an internet-based system termed SWF (Semantic Web Folders) which is an information platform that allows people to develop collaboration communities on the semantic web, jointly build various databases, and make the databases available to the public through both the semantic web and the world-wide web. A person acquiring a power user account can set up a new community in SWF, and invite participants to the community to jointly produce a database on the framework of the semantic web, facilitating international collaboration and exchange of comments about individual data elements including annotations and ontology terms jointly defined in SWF. An SWF user can define ontology terms or classes, each of which plays a role as a database or a container of data records, which are connected to each other via semantic links to form an integrated database based on the semantic web. By using SWF we are developing a system allowing a wide range of users to download RIKEN's omics experimental data as huge as hundreds of terabytes to petabytes and to allow integrative browsing of omics data (1) along with predictions such as tiling-array-based predicted genes (2). We have established semantic links among Arabidopsis omics resources including the genome, genes and literature and have developed a system to generate inferences based on the data. The system is termed PosMed (Positional Medline), which instantaneously ranks instances of significantly related genes with functions mentioned in literature. This accomplishes not only a direct search but also an indirect search via SWF's semantic links (pathway relationship, orthologous relationship) for genes not directly related in literature (3). PosMed is used worldwide to select candidate genes for positional cloning, as it is possible to add a chromosomal interval to the search limiting the ranking to only those genes within the interval. Our future goal is to evolve the entire system into an expert system for genome design or synthetic genomics in Arabidopsis and other plants. Please visit our web site at <http://omicspace.riken.jp>.

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Reference

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A systems biology approach to identify transcription networks in Arabidopsis leaf senescence

L40

Wednesday 16:00-:16:30

Leaf senescence is a programmed event responding to a wide range of external and internal signals including those caused by development, age and environment. Senescence requires de novo gene expression and protein synthesis and is controlled in a tightly regulated manner. Identification of the genes that control senescence has been complicated by the complex combination of signalling pathways that appear to be involved in senescence. Cross talk exists between senescence and stress or pathogen responses and also the hormonal and nutrient signals that are implicated in the control of senescence. We are using Arabidopsis as a model, taking a systems biology approach, to study the genes involved with the control of leaf senescence. Extensive microarray analysis over a detailed time course of development is being used to identify transcriptional networks that operate to control gene expression during developmental leaf senescence. We have two developmental time series, in one the leaf enters senescence primarily due to developmental signals, in the other the leaf is induced to senesce by a combination of age and environment. Using these data sets we are characterising key genes and pathways involved in just one or in both processes. In addition, cross talk between stress related pathways and senescence is being elucidated by the use of mutants, treatments and comparative gene expression analysis. Functional analysis of selected senescence enhanced regulatory genes is underway to pinpoint the key regulatory points within the signalling network.

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Modelling dynamic biological systems at CSBE

L41

Wednesday 16:30-16:45

The Centre for Systems Biology at Edinburgh, CSBE, is a Centre for Integrative Systems Biology funded by the BBSRC and EPSRC and led by co-Directors, Professors Andrew Millar and Igor Goryanin. Modelling is central to systems biology, taking existing knowledge and through static and kinetic models in order to generate new knowledge. The key feature of CSBE is that we place this process at the centre of our endeavour. Through the work of the Centre we aim to make theoretical and practical developments to support all stages of the modelling process. This work is informed by three biological exemplar projects, which have been chosen to exercise all aspects of the modelling process: the circadian clock in *Arabidopsis*, RNA metabolism in yeast and Interferon signalling in macrophages. The projects represent a range of timescales, dynamics and numbers of biological components. I will use the circadian clock project to illustrate how CSBE's work is advancing the systems approach.

Firstly, we are establishing an informatics infrastructure that links diverse data types seamlessly to the tools required for modelling, named the Systems Biology Software Infrastructure, SBSI. The modular structure of SBSI will support several means to build models (including biologist-friendly network diagrams) and link the models to data, together with a suite of tools for model optimisation and model analysis. Such large-scale modelling frameworks have not previously been available in the academic setting.

Secondly, we are measuring the biochemical constants that are required to parameterise kinetic models, focussing on the assembly of protein-protein and protein-nucleic acid complexes, protein and RNA degradation and the acquisition of high-quality RNA timeseries. Information about the people and the projects can be found on our regularly updated website <http://csbe.ed.ac.uk>.

CSBE has members spanning multiple research institutions and representing diverse areas of research expertise. We also have strong links to industry via direct research partnerships, consultancy and our International Science Advisory Board. We welcome further opportunities for collaboration from both the public and private sectors. Our philosophy is strongly collaborative: open source and open access.

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Adopting an integrative biology approach to study root growth and development

L42

Wednesday 16:45-17:00

The Centre for Plant Integrative Biology (CPIB) at the University of Nottingham aims to create a *virtual root* which will serve as an exemplar for using Integrative Systems Biology (ISB) to model multi-cellular systems. CPIB brings together biologists, engineers, mathematicians and computer scientists to generate new data, biological resources and virtual models of plant roots that will aid understanding of how they grow and develop. The research programme involves multidisciplinary teams working simultaneously in sub-programmes at the molecular, cellular and organ levels. Our research activities are structured as three overlapping 3-year strands of increasing sophistication. Strand 1 focuses on modelling cell elongation during radicle emergence and primary root growth; Strand 2 focuses on the root apical meristem, the principal site for cell division during primary root growth; whilst Strand 3 will examine the initiation, patterning and emergence of lateral roots. Strand 4 will integrate these models at different physical scale across the first three strands. The output of the programme will be quantitative observational data, validated models constituting the prototype "virtual root" and proofs of concept, which will form the basis for further research programmes. Strand 1 started in March 2007. I will review progress made to date, highlighting the approaches, tools and results obtained so far.

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