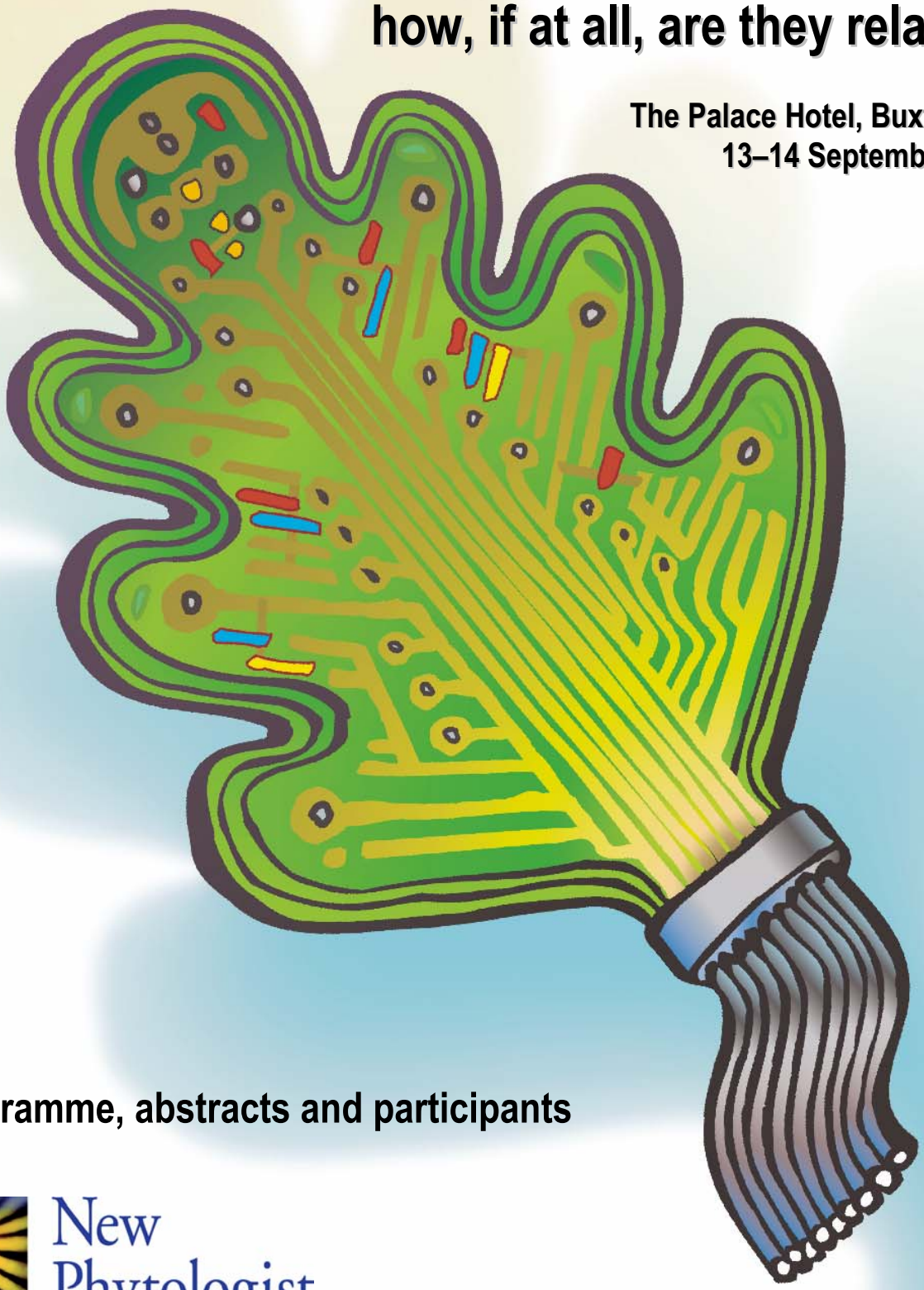
17th *New Phytologist* Symposium

Systems Biology and the Biology of systems: how, if at all, are they related?

The Palace Hotel, Buxton, UK
13–14 September 2007



Programme, abstracts and participants

New Phytologist

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Organizing committee

Sid Thomas (*IGER, UK*)

Helen Ougham (*IGER, UK*)

Alan Gay (*IGER, UK*)

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Programme, abstracts and participant list compiled by Helen Pinfield-Wells. Systems illustration by Sam Day, www.samday.com

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Speaker Abstracts

Session 1:
Chairperson: Helen Ougham IGER, Aberystwyth, UK

1.1 Unwinding the circadian clock with systems biology
ANDREW MILLAR
University of Edinburgh, UK

1.2. Tracking plant growth and form
J. ANDREW BANGHAM
School of Computing Sciences, University of East Anglia, UK

To quantify the growth and form of a leaf requires detailed measurements of movement throughout the growing organ. Fluorescent paint or fluorescent gene products generate feature points that can be tracked through series of time-lapse, two or three dimensional, images. Implicit in the analysis are assumptions about how the features could reasonably move and the results are sets of growth tensors. These can directly control growth models implemented with, for example finite elements, and these models form a common framework in which hypothesis on gene action can be compared with experimental observation.

1.3. Real world genomics
STEFAN JANSSON
Umeå Plant Science Centre, Department of Plant Physiology, Umeå University, SE-901 87 Umeå, Sweden

What are the challenges and opportunities when molecular biology and high-throughput techniques like transcriptomics and metabolomics are used to study plants in their natural environment? Will uncontrolled variation in biotic and abiotic factors introduce so much experimental noise that reliable data acquisition and analysis is impossible? In addition, to what extent is genetic variation influencing our results? In this contribution data from several experiments will be presented, all involving studies on plants grown in the field. For example, we have investigated responses to excess light, global patterns of gene regulation, responses to biotic stress and how the tree knows that it is autumn. The take home message will be that, despite the challenges involved, it will be necessary to study plants grown in natural environments in order to understand the most important parts of plant biology.

Session 2:
Chairperson: Alan Gay, IGER, Aberystwyth, UK

2.1. Rational design of a plant sentinel

JUNE MEDFORD[1], HOMME HELLINGA[2], KEVIN MOREY[1], MAURICIO ANTUNES[1], AND J. JEFF SMITH[2]
[1]Department of Biology, Colorado State University, Fort Collins CO 80523, USA; [2]Department of Biochemistry, Duke University Medical Center, Durham, NC 27710, USA

Because plants have evolved to continuously monitor their environment, the ability to develop plants that sense and response to ligands of interest has been a long sought goal. A plant sentinel requires development of two traits: a sensing-transmitting system and a readout system. For the sensing system we utilized computer-designed receptors so plants could sense ligands of interest (e.g., explosives, terrorist agents, environmental pollutants). Upon ligand reception, a synthetic signal transduction system, based on well-characterized histidine kinase pathways, is activated. The signal is transmitted to the nucleus and triggers a degreening gene circuit that causes plants to turn white, which provides a simple readout system that is easily recognized by the public. In laboratory conditions, plants sensed 23 parts per trillion of an explosive and turned white within 24–48 hours with remote detection capacity within a few hours. Plants regreen upon removal of the ligand providing a biosensor with a reset capacity. Concurrent efforts have allowed development of automated recognition algorithms so machines can recognize these changes. These data suggest plants can be produced that will serve as simple monitors for explosives, terrorist agents and environmental pollutants.

2.2. Can the properties and goals of systems biology be useful for investigating the ecology of a symbiosis at the ecosystem level?

ANDY F.S. TAYLOR
Department of Forest Mycology and Pathology, PO Box 7026, Swedish University of Agricultural Sciences, Uppsala, SE 750 07 Sweden

The ectomycorrhizal (ECM) symbiosis is an obligate association formed between a species-rich and taxonomically diverse group of soil fungi and the roots of a range of woody perennial plants. At first glance the idea of using systems biology to examine a multilayered, complex biological phenomenon such as the ectomycorrhizal symbiosis at an ecosystem level is daunting and perhaps naive. But a closer examination reveals many parallels between the approaches, concepts and ideas used in systems biology and those used within ecosystems ecology. For example, biological robustness in systems biology and ecosystem resilience or stability are comparable expressions that share several components (e.g. redundancy and modularity). Graceful and catastrophic system degradations are also equally applicable concepts at both scales. Given these similarities, is it possible to develop new strategies and insights into ECM ecology by considering those properties identified within systems biology as crucial for our understanding of any system? This question will be examined with reference to recent work in which we have been using a mechanistic approach to explain the dramatic response of ECM fungal communities to the addition of N to boreal forest ecosystems.

2.3. Integrating computational modelling of regulatory networks and plant development

JAN KIM
University of East Anglia, School of Computing Sciences, University Plain, Norwich, Norfolk, NR4 7TJ, UK

Biological systems are comprised of multiple levels of organisation, including the genomic, the morphological, the ecological and the evolutionary level. A global and integrated

understanding of biological systems is a central objective of systems biology. Tools, such as formal computer languages, to formally represent the principles governing complex biological systems, play a central role in working towards this objective. The transsys framework is built on the basis of a computer language for modelling regulatory gene networks (RGNs). RGNs are modelled by objects called transsys programs. These can be used as components to build integrated computer models of biological systems. This enables construction of computer models that integrate the RGN and other levels, such as development and morphogenesis. All RGN models involve substantial amounts of numeric parameters which need to be fitted or matched to empirical measurements. The transsys framework provides optimisation tools which fit parameters on a global, system level. This approach focuses on the ability of the entire system to capture the gene expression dynamics measured empirically, without requiring individual measurements of each numeric parameter in isolation. A risk in this approach is overfitting: If the RGN model is too complex given the size of the empirical data set, a good fit to the data may not be related to an adequate capture of the true RGN's dynamical structure by the model. Therefore, statistical tests are applied to assess significance of parameter optimisation results. This approach has been applied to a partial model of the RGNs that mediate the response to wounding in Arabidopsis.

Parameter optimisation can also be applied to explore the potential of a RGN model to organise empirically observed processes of development and morphogenesis. As a next step towards systems modelling that integrates more than one level of biological organisation, the combination of these optimisation approaches to produce models that jointly represent the dynamics of gene expression and of development will be explored.

Session 3:
Chairperson: TBA

3.1. Genericness, modularity, and mutual embedding of programming paradigms for improved Functional-Structural Plant Modelling

WINFRIED KURTH, OLE KNIEMEYER, REINHARD HEMMERLING, JAN VOS& GERHARD H. BUCK-SORLIN,
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Functional-Structural Plant Modelling (FSPM) is a relatively recent discipline that combines botanical, agronomical and silvicultural information from different sources (morphology, ecophysiology, biophysics) and perspectives (cellular, organ, individual, stand) in order to gain improved insights into basic growth and development processes, usually with the aim to improve commercial plant production. In this way, FSPM could be termed as the upscaled equivalent of Systems Biology. A typical FSPM is individual-based, represents some sort of spatial structure and dynamics, and exhibits rules for growth and development, which are locally applied yet globally integrated. Ideally, FSPM should also have a modular structure, thereby enabling a certain degree of genericness (easy exchange of parameters, methods and rules).

Three programming paradigms have been used in the past in plant modelling: the procedural, the object-oriented, and the rule-based paradigm. Each one has disadvantages, which could be overcome by combining them. Embedding one paradigm into the other has widened the range of natural processes that can be modelled as we will show using examples created in the XL language, a modelling language combining the rule-based paradigm (relational growth grammars operating on graphs) with the object-oriented and procedural language Java. Limits of the new approach (e.g. increased model complexity) are discussed and some generic system archetypes for FSPMs are proposed.

3.2. Biological Systems Analysis: Useful and Useless

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[1] *International Rice Research Institute, DAPO 7777, Metro Manila, Philippines*
[2] *Department of Animal and Plant Sciences, University of Sheffield, Sheffield S10 2TN, UK*

A system can be defined as a number of interacting elements existing within a boundary which is surrounded by an environment. Biological systems are hierarchical in the sense that they can be described at different levels of detail stretching from molecular to organismal. The success of an operation at any level depends on the successful integration of processes at the lower levels. However, it is important to bear in mind that when the system is viewed as a whole, it is expected that the whole delivers more than the simple sum of its parts. The nature of the emergent properties of the product determine the value added to the inputs and ultimately the efficiency of the system. Modelling involves building caricatures of systems using set of equations, the most important and critical features are included and fine detail is often ignored. Empirical models describe and mechanistic models seek to explain. Progress in understanding the behaviour of complex natural systems begins with observations at the whole system level and progresses as our understanding of the component parts increases at all levels. When information concerning the output is used to control the inputs or behaviour of the system that information is described as feedback. Feed forward can be found in 'intelligent' systems and is the use of information concerning consequences of change in the environment to guarantee survival. Biological systems depend on control mechanisms, although they are often ill understood at a mechanistic level. In this paper, we will describe discoveries made using systems modelling in our research on nitrogen fixation, photosynthesis, crop management and yield limits.

3.3. Integrating crop modelling and functional genomics: towards crop systems biology

XINYOU YIN & PAUL C. STRUIK
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Plant systems biology, as currently defined, seems to be the privilege of scientists working on molecular, sub-cellular or cellular levels. To emphasize the importance of systems biology for understanding and manipulating phenotypes relevant to the real-world challenges for agriculture, we have proposed the 'crop systems biology' concept. This complementary approach uses crop simulation models to investigate whole-crop physiology and honours the inter-dependence of modern genomics and conventional biochemistry and physiology in improving crop yield and resource use efficiencies. The first case studies, in which molecular marker-based quantitative trait loci information was incorporated into existing crop models, showed that current knowledge in crop modelling already shows promise in supporting genetic analyses of complex traits. These case studies include (i) dissection of complex traits into component traits based on ecophysiological insight, (ii) physiological phenotyping of developmental traits, and (iii) better resolution of genotype-by-environment interactions. For further progress, crop models must be upgraded to allow gene- or transcription-level understandings to be incorporated, thereby, bringing the information from 'omics' up to the crop. We expect that this crop systems biology approach will narrow the gene-to-phenotype gaps, enhance 'plant breeding by design', and result in an integrated knowledge base of plant biology and crop science.

3.4. Strategies for predicting the movement and fitness of transgenes in wild plant communities

MIKE J. WILKINSON, JOEL ALLAINGUILLAUME & CAROLINE S. FORD
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Predicting the ecological consequences of gene flow from genetically modified crops to their wild relatives represents a huge scientific challenge. Achieving this goal requires integration of information relating to the crop, agricultural systems in which it is grown, spatial distributions of the crop and the recipient populations, crop-recipient hybrid fitness, genetics and cytogenetics of introgression, population-level gene exchange, identifying traits, genes and genome regions that contribute to ecological fitness of the non-transgenic recipient in its natural community, of how the transgene will change the ecological behaviour of the recipient and an understanding of which associated species are most likely to be detrimentally perturbed by any changes to the wild recipient. We therefore describe progress towards developing a landscape-scale model to predict the ecological consequences of gene flow from genetically modified oilseed rape (*Brassica napus*) to its closest wild relatives (*B. rapa* and *B. oleracea*) occupying natural and semi-natural habitats across the United Kingdom. In order to provide data for model parameterisation, emphasis is placed on exploiting information gained on the fate of loci from conventional crops after gene flow into a relative and on characterising the selection pressures experienced by the wild recipients and their community associates.

Poster Abstracts

Listed alphabetically by first author, presenting author is underlined

1. Metabolite regulation of gene expression during the heterotrophic to autotrophic transition in developing seedling of Arabidopsis

ALLEN, ELIZABETH[1], MOING, ANNICK[2], EBBELS, M. TIMOTHY[3], MARCOURT, MICKAEL [2], TOMOS, DERI A.[1], ROLIN, DOMINIQUE [2] & HOOKS, A. MARK[1]*

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Seed germination and development represents a unique stage of plant development where metabolic programs that are geared initially towards catabolism of stored carbon reserves (heterotrophy) undergo a transition to permit fixation of inorganic carbon into organic compounds by photosynthesis (autotrophy). This transition involves a transcriptional reprogramming to dismantle catabolic and produce the photosynthetic machinery. Because this transcriptional programming revolves around metabolic changes, a key question is the role of metabolic signals in regulating this process. Expanding on our work on acetate regulation of gene expression during seedling development, we are taking a holistic approach to identify other potential signalling metabolites. Using ^{1}H-NMR, we have profiled a group of metabolites in samples from imbibed seeds to seedlings 8 days after imbibition. We have also profiled expressed genes at corresponding time points using microarrays. We have calculated correlations among differentially expressed genes and metabolite levels in order to determine potential metabolic signals for future study. Interestingly, Spring Embedding models of metabolite and gene expression networks have shown that metabolite profiles from day 2 samples group with profiles from day 0 (imbibed seeds) and day 1, but that gene expression profiles from day 2 samples group with those from day 3 to day 8. This suggests that metabolic programming of embryos within seeds establish a pattern that may precede reprogramming of gene expression.

2. Integration of plant transcriptomic and metabolomic data in a systems biology context

BYLESJÖ, MAX[1], ERIKSSON, DANIEL [2], KUSANO, MIYAKO [2,3], MORITZ, THOMAS[2], TRYGG, JOHAN[1]

[1] Research group for Chemometrics, Department of Chemistry, Umeå University, SE-901 87 Umeå, Sweden; [2] Umeå Plant Science Centre, Department of Forest Genetics and Plant Physiology, Swedish University of Agricultural Sciences, SE-901 83 Umeå, Sweden; [3] RIKEN Plant Science Center, 1-7-22 Tsurumi, Yokohama City, Kanagawa, 230-0045, Japan

The progresses in technologies employed in life science applications have enabled compilations of practically limitless amounts of data. By gathering data from multiple analytical platforms (e.g. monitoring transcriptomic, metabolomic or proteomic events) one hopes to answer biological questions. This can be seen as a 'systems biology' approach to understand network interactions between different parts of biological systems to facilitate interpretations of the data. In the present material, the utility of employing the O2PLS multivariate regression method for combining 'omics' data types is demonstrated. The O2PLS method separates systematic joint variation across analytical platforms from platform-specific (orthogonal) systematic variation. This strategy has the potential to provide additional insight into the problem of integrating data from multiple sources; in particular concerning the interpretation of the subsequent results. An investigation of short-day

induced effects at transcript and metabolite levels for hybrid aspen (*Populus tremula* × *P. tremuloides*) is employed to demonstrate the strengths of the methodology. Statistical validation, interpretation to identify biologically applicable events and comparison to a pair-wise univariate correlation approach will be elaborated.

3. Biomolecular network discovery from multiple post-genomic multivariate data series

DROOP, ALASTAIR[1,2], GRAHAM, IAN. A.[1] & CAVES, LEO[2]
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[2]*York Centre for Complex Systems Analysis, University of York, Heslington, York, UK*

Systems biology studies can generate vast quantities of multivariate data from a range of post-genomic technologies. However, due to the difficulties of integrating data, analysis is often restricted to data from a single source.
We are developing methods for the analysis of series data (e.g. time course microarray experiments) based upon cross correlation analysis - matching signal patterns rather than their absolute values. This approach allows signals from different sources (e.g. transcriptomic, metabolomic and proteomic data) to be directly compared, provided that the data series represent equivalent time points or biological states. Correlations are tested for significance against a null distribution modelled from the data, that captures the implicit dependencies between points in the series [1]. Significant correlations (representing putative biomolecular associations) can then be used to generate hypotheses for further experimentation.
Analysis of correlation data can be performed in two ways: global and targeted. A targeted approach starts with a known subset of entities and iteratively constructs networks of correlation out from this starting point. Conversely, a global approach performs cross correlation analysis on the complete data set, allowing for a data mining approach.
To date, the work has focused on using linear (cross-) correlations; however the approach is not limited to using this metric. For example, many transcription factor to effector interactions will not be captured using linear correlations and in order to capture these associations, novel matching functions must be devised, and can be plugged into the existing analysis framework.
We present the methods and tools, as well as examples of their use on both an E. coli diauxic shift transcriptomic data set [2] and a combined Arabidopsis transcriptomic [3] and fatty acid metabolite data set.

[1] S Kruglyak & HX Tang (2001) J Comp Biol 8(5):463-470 [2] MF Traxler, DE Chang, & T Conway (2006) PNAS 103(7):2374-2379 [3] M Schmid, et al. (2005) Nat Gen 37(5):501-506

4. From local processes to whole plant functioning, using the functional-structural plant modelling approach

EVERS, JOCHEM, B. & VOS, JAN
Crop and Weed Ecology, Plant Sciences Group, Wageningen University, the Netherlands

In Poaceae, the outgrowth of axillary buds is suppressed by a low ratio of red and far-red light (R:FR). R:FR declines within a plant canopy from the top downwards as a result of higher absorption of red light by surrounding plant tissues than of far-red light. Here we present a functional-structural plant modelling (FSPM) approach to simulate effects of R:FR on tillering in spring wheat (*Triticum aestivum* L.). This type of modelling combines plant functioning (*i.e.* physiological processes) and plant structure (*i.e.* architecture).
In the model, bud break was related to R:FR as perceived by the plant. Simulations were done for three plant population densities. In accordance with experimental observations fewer tillers per plant were simulated for higher plant population densities. It was discussed

that a model based on relatively simple relations can be used to simulate the degree of bud break.
This study showed that the FSPM approach is a promising tool to analyse crop morphological and ecological research questions in which the determining factors act on the level of the individual plant organ. With the inclusion of physiological processes on the cell and tissue level, FSPM can contribute to narrowing the gap between systems biology and whole-plant functioning.

5. A systems biology approach to model tomato fruit growth dynamics

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Yield prediction models rarely incorporate information at scales below the plant organ level. Recent research on tomato elucidates the genetic basis of fruit growth and quality, but knowledge on the interaction with the environment is still lacking. In this study we aim firstly to understand how tomato fruit growth, modeled as the integration cell division and cell expansion, is affected by gene regulation, temperature and carbohydrate metabolism and secondly, to use the effects of fruit cell dynamics to improve model-based genotype-specific yield and quality prediction. A modeling concept on gene-regulated cell cycles will be developed and incorporated in a module on cell division derived from project partners. The resulting cell number will be input to an existing fruit expansion model simulating the expansion process according to the Lockhart approach on turgor driven growth, combined with an equation on sugar import. The expansion model will be coupled to an existing crop growth model to receive data on assimilate supply per fruit. Experiments will be conducted to determine the relationship between processes at cellular and organ level and to investigate the effects of gene expression on fruit cell dynamics.

6. Establishing a proteomics-based platform for systems biology analysis of soybean seed development

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A combination of fresh weight measurements and color was used to delineate eight stages of soybean seed development. Storage protein, oil, and starch were quantified at each stage, and the morphological plus biochemical characteristics were combined to establish a first-stage model of seed development. The steady-state level of a cyclin-dependent protein kinase transcript was used to define the period of cotyledonary cell division. A protein fraction was isolated from seeds of each developmental stage, and separated on two-dimensional gels. Difference gel electrophoresis was used to target proteins that changed in abundance between the stages of seed development. Mass spectrometry was used to identify the targeted proteins, which were grouped according to function. The patterns of change in abundance of target proteins were analyzed by a unique application of hierarchical clustering plus multidimensional scaling and model building. More than 95% of the identified proteins could be accommodated by five expression patterns. Systems cartography was used to display relationships between and among proteins of differing functional and developmental groups. Our results establish a platform from which to further

elaborate systems biology-analysis of soybean seed development. Each aspect of this platform is suitable for expansion as additional data are accumulated.

7. Functional assays of PhoB in plants

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Our lab is developing plant sentinels to detect and respond to substances. To accomplish this, we have designed a synthetic signaling system to link input from computationally designed receptors to a response. The system starts when the receptor binds a substance, in the model case trinitrotoluene (TNT) and develops affinity for an extracellular histidine kinase domain, activating the kinase. The activated kinase transmits a high energy phosphate to an adapted bacterial response regulator, PhoB, which translocates to the nucleus and activates transcription. Evidence suggests that the adapted-PhoB also interacts with plant histidine kinase signaling components. One approach to reduce or eliminate this cross-talk is to test mutations in amino acid residues believed to be involved in interaction with plant signaling components. Each mutated form is tested for functionality with input from either cytokinin and/or TNT to determine if improvements can be made on the nuclear shuttling process and/or transcriptional activation process. To further demonstrate the utility of our system, we are also producing plant sentinels for the environmental pollutant, methyl tertiary-butyl ether (MTBE) by changing the modular receptor. Our vision is for plants to serve as simple widespread monitors for explosives and/or environmental pollutants.

8. Mathematical model of the Aux/IAA response to Auxin

MIDDLETON, A.M.[1], OWEN, M.[1], KEPINSKI, S.[2], GUILFOYLE, T.[3], BENNETT, M.[2] & KING, J. R.[2]
[1]*Centre for Plant Integrative Biology, School of Biosciences, University of Nottingham, Sutton Bonington Campus, Loughborough, LE12 5RD, UK.*
[2]*Centre for Plant Sciences, Faculty of Biological Sciences, University of Leeds, Leeds, LS2 9JT, UK.*
[3]*Biochemistry, 117 Schweitzer Hall, University of Missouri-Columbia, Columbia, MO 65211.*

The hormone Auxin is implicated in regulating a diverse range of processes in developing Arabidopsis roots, including cell division, elongation and differentiation. Auxin functions in part by mediating the activation of the so-called Aux/IAA family of genes, comprising 29 members. We have developed a model of a single Aux/IAA gene's response to an Auxin stimulus. The model encompasses the time evolution of the following molecule concentrations: Aux/IAA protein and mRNA, ARF protein and components of the Aux/IAA ubiquitination pathway, including the interaction between SCF-TIR1 and Auxin. We find that the model is in good qualitative agreement with current data.

9. Involvement of calmodulin in expression of circadian clock and flowering time related genes in *Arabidopsis thaliana*

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In flowering plants, including *Arabidopsis,* changes in day length serve as important seasonal cues which are perceived and interpreted within the photoperiodic pathway. We have tested the hypothesis that calmodulin (CaM) is involved in transduction of the floral signal within the photoperiodic pathway.

A. thaliana seedlings at the ten leaf stage were treated daily for 14 days with the CaM antagonist W7 (N-(6-Aminohexyl)-5-chloro-1-naphthalene sulphonamide-HCL). Seedlings were then harvested every 4 h for a period of 28 h.
RT-qPCR analysis of the expression of, *TIMING OF CAB EXPRESSION 1* (*TOC1*), *CONSTANS* (*CO*) and *FLOWERING LOCUS T* (*FT*), revealed changes in phase and level of expression in CaM antagonist treated plants compared to controls.
These changes are most noticeable under short day conditions and provide evidence of the involvement of CaM in floral signature propagation.

10. Senescence – a suitable case for systems treatment

OUGHAM, HELEN J.[1], GAY, ALAN P.[1], ROBSON, PAUL R.[1], TAYLOR, JANET E.[1], DAVEY, CHRISTOPHER L.[2], THOMAS, HOWARD[2].
[1] *Institute of Grassland and Environmental Research, Plas Gogerddan, Aberystwyth, SY23 3EB, UK and* [2] *Institute of Biological Sciences, Aberystwyth University, Aberystwyth, SY23 2AX, UK*

When considering the application of systems biology to whole plants and cropping systems an inevitable consequence is the complexity and number of levels across which such a model must work. In this poster we consider the advantages of senescence as a process to which a systems biology approach could be applied. It has the significant advantage that the process is well defined in terms of its genetic and metabolic characterisation. Important collections of genetic material are available in plants such as maize that would allow the testing of system models. Also the linking crop models are available which would allow the practical consequences of the system models to be explored.

11. Gap- diversity and regeneration in old-growth seasonally dry deciduous *Shorea robusta* (Gaertn. f.) forest in Terai of Nepal

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Diversity and regeneration of woody species between two ecological niches viz. gaps and non-gaps of seasonally dry *Shorea* forest in Nepal were investigated. We related varieties of diversity measures and seedling attributes to gap characteristics. Significant recruitment variations in *Shorea* ($f = 34.8$; $p < 0.01$) and miscellaneous species ($f = 8.07$; $p < 0.05$) were observed between gaps and non-gaps. Though Shannon index showed Non-gaps (2.502) as more diverse than gaps (2.066), the Fisher's α index revealed the gaps (21.6) as more diverse than non-gaps (19.0). Larger gaps in our study could not explain most of seedling attributes. Gap created by multiple tree falls in different years showed higher recruitment of *Shorea* seedlings than gaps created by single and/or multiple tree falls in same year ($f = 6.6$; $p = <0.05$). The ratio of miscellaneous species to *Shorea* was highly related to number of tree falls in gaps ($r = 0.355$, $p = <0.01$) and their ages ($r = 0.268$; $p < 0.05$). In order to promote seedling recruitment in old-growth *Shorea* forests, the medium sized gaps (ca. <300 m^2) made up of successive tree removal are recommended. Ecological niche differentiation here verifies 'intermediate disturbance hypothesis', which enhances species co-existence.

WC, PS and MNG acknowledge scholarships from the Rajamangala University of Technology and the Mahasarakham University (Thailand) and CONACYT (Mexico), respectively. The Deutsche Bundesstiftung Umwelt financially supported the laboratory.

12. Characterization of putative abscission related genes from A*rabidopsis thaliana*

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Abscission is a unique process of detachment of plant organs from the mother plant that may have adverse or beneficial effects on yield and quality. The precise cellular composition of this zone is difficult to ascertain and an analysis of the specific molecular changes associated with abscission is hampered by contamination from neighbouring non separating tissues. A unique and specific single cell abscission zone (AZ) library was created from Arabidopsis flowers; the cells were tagged using a specific AZ promoter fused to the reporter gene GFP (*$Pro_{At2g41850}$:GFP;* González-Carranza, *et al*., 2002) and then collected under a fluorescence microscope with the aid of micropipettes. A cDNA library was then generated and used to perform a microarray analysis and six genes were chosen to be studied on the basis of their expression profiles. The promoters from these genes were amplified and GUS and GFP reporter lines were obtained. These results will be discussed.

González-Carranza, *et al.,* (2002). *Plant Physiology*. 128: 534-543.

13. A genomic study of co-regulated genes in plants to reconstruct transcriptional regulatory networks

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Understanding how the behaviour of cells are controlled is one of the major challenges in biology. Through the past, the focus has been on characterization of individual gene/protein interactions. However, in reality changes are seldom caused by single isolated components. Rather they are the result of cellular networks interacting in the cell. The “omics” revolution has provided new technologies making it possible to study cell dynamics in complete new aspects. To be able to use the information generated using these technologies it is important to have access to high quality data based on good experimental design and robust statistical analysis.

We have created the public microarray database UPSC-BASE for storing and analyzing *Populus* microarray slides. This growing resource contains almost hundred different experiments from several different tissues and conditions making it an invaluable source of *Populus* transcription information. Genes with strongly correlated expression profiles are more likely to share common characterizations, like have their promoter regions bound by a common transcription factor. Our goal is to find the regulons of the dynamic transcriptional network to understand the complexity. Gene markers for those regulons will be used for high-trough put screening of *Populus* collections in a time and cost efficient manner.

14. Integrating physiological, transcriptional and genetic information to locate determinants of the genetic architecture of drought response in *Populus*.

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The two species *Populus trichocarpa* and *P. deltoids* have contrasting natural ranges within the USA and exhibit markedly different adaptive responses to drought stress with *P. trichocarpa* rapidly losing leaf area through leaf necrosis and shedding and *P. deltoides* undergoing controlled leaf senescence and entering dormancy. We have utilised an F_2 mapping population formed from a cross between these two species to map QTL for drought related physiological traits as well as for the expression of a subset of genes known to be

important in drought response. We have also conducted microarray experiments comparing the grandparental species and F_2 genotypes from the distribution extremes for drought response. The integration of these datasets is allowing us to identify both *trans* acting loci important in controlling drought response as well as *cis* acting loci for selected drought responsive genes. These genetic loci contain polymorphisms that are important in explaining adaptive species-level differences in drought response. Such loci can inform reverse genetics approaches to engineering drought resistance and can provide functionally and adaptively important candidate genes or genetic loci for use in association mapping experiments. The approach and methods used can easily be extended to the study of any complex quantitative trait.

15. The use of an interspecific cross between *Arabidopsis halleri* and *A. petraea* to investigate the relationship between metabolome and transcriptome

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Arabidopsis halleri and *A. petraea* are contrasting but closely-related species. *A. halleri* is a zinc and cadmium hyperaccumulator. They can be crossed to produce offspring that are intermediate in a wide range of characters. Since both species are related to *A. thaliana*, this cross provides a potential model for systems biology. In previous work, candidate zinc hyperaccumulation genes were identified by transcriptome and QTL analysis of F3 plants selected for low or high hyperaccumulation. This research aims to widen this approach and use the interspecific cross in the following ways. (a) Identify metabolite differences between the species and determine how the metabolome is inherited in F4 plants. (b) Identify genes that control metabolism/the metabolome by transcriptome analysis of F5 plants selected for specific metabolic traits. (c) Identify metabolic characters associated with zinc hyperaccumulation. Metabolite profiling will employ NMR, GC-MS and HPLC. Preliminary results of NMR metabolite profiling of the parent species and F4 plants will be presented

Participants

** S=speaker abstract; P=poster abstract*

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Bowen, Tessa	tabowen23@hotmail.com	Colorado State University	P7	plant molecular biology/synthetic singalling
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Bylesjo, Max	max.bylesjo@chem.umu.se	Umeå University	P2	multivariate data analysis, data integration, kernel methods, image analysis, visualization
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