



## Society for Experimental Biology Annual Main Meeting 28th June – 1st July 2009, Glasgow, UK

### P6 – MODELLING PLANT SYSTEMS: CELL TO AGRO-ECOSYSTEMS

#### P6.1

09:05 Sunday 28th June 2009

#### Constraints of space in plant development

Przemyslaw Prusinkiewicz (University of Calgary)

Like all forms in nature, living organisms are subject to the properties of space. On the one hand, these properties provide the most fundamental link between growth and form: local growth rates determine curvature. On the other hand, they put strict limits on what is possible: no point in space can be occupied by several organs at once. Plants employ several strategies to develop within these limits, including symmetric or self-similar tiling of space, competition for space, and escape to another dimension. These strategies are combined with developmental and evolutionary constraints to produce the observed diversity of patterns and forms.

An interesting question is the nature of the constraints that determine the forms of trees. The dominating point of view, originating in the architectural analysis of tropical trees, is that their forms are determined by specific branching patterns, tightly controlled by the underlying genetic mechanisms. An alternative point of view is that the forms of trees, especially those found in temperate climates, emerge from self-organizing processes, in which competition of branches for space plays a dominant role. Computer models and simulations show that the latter viewpoint is more likely to capture the key patterns of temperate-climate tree development. Further analysis indicates that self-similarity can originate in a variety of processes, which may explain its prevalence among plants. Our results also put in focus open questions regarding the relation between bud activation and light.

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#### P6.2

09:45 Sunday 28th June 2009

#### Meristematic fronts: A new model of the plant architectural development?

Lionel Dupuy (Scottish Crop Research Institute), Philip J. White (Scottish Crop Research Institute), Blair McKenzie (Scottish Crop Research Institute), Matthieu Vignes (BIOSS)

#### Introduction

Plant architectures result from the functioning of meristems. Meristems develop in a sequence of cell proliferation and differentiation events, and the final plant architecture is due to the precise patterns of the meristematic activity. Polarity is central to this process. Newly created tissues expand and become rigid as cells differentiate, and meristematic regions, pushed by this indeterminate self-organized process, tend to propagate through space forming fronts.

#### Results

In this study, we have used these principles to develop a new approach to modelling plant morphogenesis. Differential imaging was used to illustrate the process both at a cellular and whole plant level. Computational models of root and shoot architectural development showed wave-like proliferation of meristems at the whole plant level, and mathematical models showed the morphologies of the waves of meristems are inherent to local developmental processes, namely expansion, initiation of new primordia and tropic responses.

#### Conclusion

Our work has demonstrated that the plant development can be viewed as a propagating wave of meristems, where the overall plant architecture is the footprint of this process. Not only are waves visual and understandable concepts they also provide simplified quantitative objects to build models and dissect species and their developmental strategies.

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#### P6.3

10:30 Sunday 28th June 2009

#### Model-assisted integration of genetic and environmental constraints in the design of root system architecture for optimal water capture

Xavier Draye (Université catholique de Louvain), Mathieu Javaux (Université catholique de Louvain)

Increasing attention is being devoted to root system architecture in drought tolerance studies and breeding. Surprisingly, while the explicit consideration of architecture is a key to system-wide approaches of water dynamics in the soil–plant continuum, plant biologists often take soil water distribution as an external given, which leads to such expectations that deep roots warrant improved access to soil water resources. This view may underemphasize the influence of root architecture on soil moisture and nutrient distributions at the macroscopic to the plant scales. In addition, although the impact of one-dimensional root distributions on the profile of depletion of soil water content has been shown in numerous studies, horizontal water content variability may arise due to contrasting uptake by different root segments and redistribution processes, even with uniform horizontal soil hydraulic properties. In this paper, we highlight the importance of addressing the dynamics of the soil matrix in plant biology, to understand how water fluxes driven by soil and plant processes affect water availability and uptake throughout a growth cycle. From early modeling efforts focusing on one-dimensional effective root water uptake, two- and three-dimensional models that involve a higher level of complexity in the description of root structure and related soil and plant processes are now being developed. We anticipate that coupling such water dynamics models with QTL-based structure–function plant models will better allow the integration of environmental and genetic constraints to support model-assisted design of plant architectures susceptible to improve yield under given drought scenarios.

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#### P6.4

##### 11:10 Sunday 28th June 2009 Towards a virtual meristem

Christophe Godin (INRIA)

This talk will present an overview of the progress that has been made recently in the modeling of shoot apical meristem functioning and growth at cell resolution. I will present the different ingredients that need to be assembled to build a virtual meristem. This includes reconstruction of 3D-geometry of meristems based on *in vivo* microscopy images, transport models of hormones, mechanical models of cell–cell interaction, cell growth and division and models of gene regulation. The presentation will briefly sketch these modeling approaches and emphasize the main barriers that are currently being faced by modelers and biologists in designing and assembling such components. Different illustrations of how the use of such a systems biology approach can help biologists to elaborate hypotheses, integrate them in a coherent system and test them against real data will be given throughout the talk.

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#### P6.5

##### 11:50 Sunday 28th June 2009 A functional–structural model of nitrogen distribution within the wheat culm during grain filling

Bruno Andrieu (INRA UMR 1091 EGC), Jessica Bertheloot (INRA UMR 1091 EGC), Christian Fournier (INRA UMR 759 LEPSE), Pierre Martre (INRA UMR 1095 GDEC)

Nitrogen is an important resource for both the vegetative and the reproductive apparatus of plants. Within a dense vegetative canopy,

specific lamina nitrogen mass is distributed vertically and follows the light gradient. This has often been interpreted as a way for plants to maximize their carbon gain. During grain growth, most of nitrogen stored in the vegetative modules is remobilized toward grains. How this takes place impacts carbon gain and the protein content of grains. In this study we present a model of N distribution within a wheat culm after anthesis. Experiments allowed quantifying the spatio-temporal patterns of nitrogen dynamics after anthesis: Nitrogen mass per unit tissue area decreased with canopy depth, but was homogeneous within each individual lamina or sheath. Nitrogen dynamics were identical at all phytomer position except for a scale factor. In the period of no root nitrogen uptake, those dynamics followed a first order kinetics. Based on these results, we developed a functional–structural model of nitrogen dynamics within the culm botanical structure. The model expresses the turnover of the proteins of the photosynthetic apparatus, with the assumption that the different entities of the culm share a common pool of mobile nitrogen. The model was able to simulate the dynamics of nitrogen observed for a contrasted range of conditions. Nitrogen–light relationships were simulated as an emerging property of processes described at a local scale. This work paves the way for simulating the regulation of nitrogen dynamics in individual-based models of plant population.

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#### P6.6

##### 13:30 Sunday 28th June 2009 Modelling the effects of genes and QTLs on the plant sensitivity to environmental conditions

Francois Tardieu (INRA), Boris Parent (INRA), Claude Welcker (INRA)

The genetic analysis of adaptive processes, e.g. transpiration rate or growth rate, faces the problem of a high genotype×environment interaction. Modelling can greatly help this analysis, with different possible roles for models. A first purpose is to identify stable and heritable traits which account for the apparent variability of time courses under fluctuating environmental conditions. One seeks to get stable parameters calculated from time courses, for instance half times of responses, parameters of response curves or maximum rates. These traits are then used to detect QTLs or to carry out association genetics. We argue that mechanistic models are not appropriate here, first because they are based on physiological hypotheses which may or may not be compatible with the genes whose polymorphisms will be eventually be identified, second because mechanistic models use too many parameters for a genetic analysis. A second purpose is to evaluate the consequences, at the whole plant level, of the effect of a QTL or of an allelic series which affects specific functions of the plant. In this case, mechanistic models are essential, over-parametrisation does not necessarily cause major problems provided that most parameters are kept common among the tested genotypes. Examples of each type of models will be discussed for their usefulness and possible drawbacks.

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#### P6.7

##### 14:10 Sunday 28th June 2009 Modelling the crop: From system dynamics to systems biology

Xinyou Yin (Centre for Crop Systems Analysis Department of Plant Sciences Wageningen University), Paul C. Struik (Centre for Crop Systems Analysis Department of Plant Sciences Wageningen University)

There are strong inter-plant competitions in a crop stand for various resources and complex compensation and regulation mechanisms along the developmental cascade of the whole crop. As a result, crop productivity under any environment cannot be predicted simply from the performance of individual plants grown in isolation. Principles in system dynamics (e.g. feedback control) have thus been applied in crop science in the form of quantitative simulation models. In view of potential values of these models added to classical quantitative genetics, model-input parameters are increasingly considered to represent certain genetic characteristics—thereof also called 'genetic coefficients'. The advent of functional genomics and systems biology engenders excellent opportunities to enable the 'genetic coefficients' of these models being really genetic. A number of case studies, in which the effects of quantitative trait loci have been incorporated into existing ecophysiological models, have shown promise of using models in analyzing genotype-to-phenotype relationships of some crop traits. For further progress, crop models must be upgraded based on understandings at lower organizational levels for enigmatic phenomena such as sink formation in response to environmental clues, sink feedback on source activity, and physiological acclimation to prevailing environment. Within this context, we believe that the recently proposed 'crop systems biology', which explores complementary roles of modern genomics and traditional physiology and biochemistry in crop improvement, will ultimately realize the expected roles of *in silico* modelling in narrowing genotype-to-phenotype gaps. This paper summarises findings and opinions to provide an integrated perspective for modelling genotype-by-environment interactions on whole crop processes.

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#### P6.8

14:50 Sunday 28th June 2009

#### Multiscale modelling of gas exchange in fruit tissues

Pieter Verboven (K.U. Leuven), Bart M. Nicolai (K.U. Leuven), Bert Verlinden (VCBT vzw), Metadel Abera (K.U. Leuven), Solomon Fanta (K.U. Leuven), Quang Tri Ho (K.U. Leuven)

A multiscale gas exchange model was developed to perform *in silico* experiments to evaluate the effect of external conditions, fruit size and maturity on the intra-cellular respiration and risks of occurrence of physiological disorders in pear fruit. The approach combines models of gas transport and respiration at the macro- and microscales. The macroscale model consisted of a three-dimensional diffusion-permeation-respiration intact fruits. The microscale model was developed to solve cellular gas exchange and respiration mechanisms using 2D and 3D micrographs and tessellation models of the cellular architecture of the fruit tissues. Next, multiscale analysis allowed to compute the fruit response to different external gas conditions and determines the regions that were more susceptible to physiological disorders caused by anoxia and high CO<sub>2</sub> partial pressure. The microscale model was applied to compute the corresponding intra-cellular metabolic gas concentration. The *in silico* study revealed that O<sub>2</sub> concentration of optimally picked pear stored at typical controlled atmosphere condition (2.5 kPa O<sub>2</sub>, 0.7 kPa CO<sub>2</sub> at -1 °C) were higher than the Michaelis-Menten constant (K<sub>m</sub>) for cytochrome *c* oxidase, the rate limiting enzyme of the respiration pathway. In contrast to small pears, large pears and extreme low O<sub>2</sub> storage conditions lead to O<sub>2</sub> concentrations well below the K<sub>m</sub>. This most probably leads to fermentation and physiological disorders which have been observed under such conditions. Ripening of the fruit increased the risk of physiological disorders since increased respiration resulted in anoxia in the fruit center even at the typical storage conditions.

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#### P6.9

15:40 Sunday 28th June 2009

#### New genotype to phenotype models at the intersection of genetics, physiology and statistics

Fred Van Eeuwijk (Biometris-Applied Statistics)

The prediction of phenotypic responses from genetic and environmental information is an area of active research in genetics, physiology and statistics. Rapidly increasing amounts of information become available on the phenotype as a consequence of high throughput phenotyping techniques, while more and cheaper genotypic data follow from the development of new genotyping platforms. In between genotype and phenotype, a wide array of -omics data can be generated. Continuous monitoring of environmental conditions has become an accessible option. This wealth of data requires a drastic rethinking of the traditional quantitative genetic approach to modeling phenotypic variation in terms of genetic and environmental differences. Where in the past a single phenotypic trait was partitioned in a genetic and environmental component by analysis of variance techniques, we nowadays desire to model multiple, and often time dependent, phenotypic traits as a function of genes (QTLs) and environmental inputs, where we would like to include intermediate genomic information as well. As soon as genomic data enter the modeling, the number of genomic and genetic predictors typically starts to exceed the number of individuals (observations), thereby invalidating classical statistical approaches based on least squares principles. In this paper, statistical modeling strategies will be presented that are able to identify the genetic basis of complex traits across environments, with special attention for the modeling of genotype by environment interactions in dependence on physiological environmental characterizations. The problem of the number of predictors being larger than the number of observations will also be discussed. It will be shown how physiological insights can be integrated with advanced statistical modeling techniques to arrive at more reliable phenotypic predictions and optimal use of the abundant genetic and genomic information.

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#### P6.10

16:20 Sunday 28th June 2009

#### Stem diameter variations analysed by a validated mechanistic model describing sugar and water transport in trees

Veerle De Schepper (Ghent University), Kathy Steppe (Ghent University)

In trees, water and carbohydrates are transported by respectively xylem and phloem conduits which are hydraulically linked. A simultaneous study of both flows is physiologically interesting, since they concurrently influence processes such as stomatal regulation and radial growth. Some mathematical models are already developed to investigate the influence of these two coupled flows. However, none of them was validated with real field data. To validate this kind of models, continuous measurements of stem diameter variations could be very useful, since they reflect both the water and sugar transport.

Hence, we developed a model that enables simulation of stem diameter variations driven by the water and the carbohydrate flow. Stem diameter variations are calculated as volume changes of both the xylem and the phloem tissue. These volume changes depend on: (i) the water transport according to the cohesion–tension theory, (ii) the transport of carbohydrates according to the Münch hypothesis, (iii) loading and unloading of carbohydrates and (iv) irreversible turgor-driven growth. The model tree is subdivided in three compartments: crown, stem and roots. To validate the model, we conducted double girdling experiments on young oak (*Quercus robur* L.) trees in growth rooms. During these experiments, data was collected of stem diameter variations, photosynthesis and xylem sap flow for both manipulated and non-manipulated trees. In addition to these plant variables, the micro-climate was also monitored. A good agreement was found between simulated and measured data. Hence, the model is a realistic representation of the processes observed in reality.

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#### P6.11

10:30 Monday 29th June 2009

#### Sharing efforts for modelling plant systems: from publications to reusable software components

Christian Fournier (INRA), Christophe Pradal (CIRAD), Michael Chelle (INRA), Frédéric Boudon (CIRAD), Gaëtan Louarn (INRA), Corinne Robert (INRA), Didier Combes (INRA), Thomas Cokelaer (CIRAD), Jessica Bertheloot (INRA), Kai Ma (INRA), Sébastien Saint-Jean (INRA), Alban Verdenal (INRA), Abraham Escobar-Gutiérrez (INRA), Bruno Andrieu (INRA), Christophe Godin (CIRAD)

Plant models become increasingly complex and their implementation often implies the use of advanced techniques in computer science. This evolution has been accompanied by the production of dedicated plant modelling tools, such as simulation platforms, that facilitate research in this field. However, much less sharing is observed for plant models themselves, that is for computer programs produced by scientists to address their specific questions. Yet, these programs could be highly valuable for other researchers, to avoid redundant development of similar code or to help non-specialists to simulate parts of a complex system. Model descriptions found in academic publications, even combined with code sources, are generally not sufficient for model reuse. Most difficulties come from the heterogeneity of language used, the structure of the programs, the download and installation procedures, the accessibility to the source code of the model, and the availability of documentation. The OpenAlea initiative (<http://openalea.gforge.inria.fr>) has been launched to address these problems by providing plant modellers with collaborative tools and guidelines to increase software quality, hence re-usability of their models. The Alinea pilot project further tested these concepts in a sample community of ecophysicists and biophysicists. Based on this experience, we illustrate pros and cons of the approach and discuss future direction of progress. We foresee three steps towards a better re-usability of models: a better interoperability of existing tools and simulation platforms, the emergence of design patterns for plant modelling, and the definition of standardised data structures.

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#### P6.12

11:10 Monday 29th June 2009

#### Designing the sorghum crop model in APSIM to simulate the physiology and genetics of complex adaptive traits

Graeme L. Hammer (The University of Queensland), Erik Van Oosterom (The University of Queensland), Greg McLean (Queensland Department of Primary Industries and Fisheries), Scott Chapman (CSIRO Plant Industry)

Progress in crop improvement generally and in molecular approaches to plant breeding particularly are limited by our ability to predict plant phenotype based on its genotype, especially for complex adaptive traits. However, the capacity of crop growth and development models to bridge this predictability gap is questionable if the models rely on algorithms that describe key aspects of crop growth and development too simply, or if they delve too far into detailed process specification requiring extensive and sophisticated parameterisation. Here we outline a generic cereal crop growth and development model designed to retain good predictive skill at crop level while also introducing sufficient physiological rigour that complex phenotypic responses become emergent properties of the model dynamics, thus facilitating effective gene-to-phenotype links. The generic template has been constructed in the APSIM software platform, which facilitates on-going and collaborative development. We detail experiments underpinning development and testing of the sorghum crop model implemented in this template. The approach is focussed around quantifying capture and use of radiation, water, and nitrogen. We present an example of how introducing genetic variation in plant height can generate emergent simulated phenotypic differences in green leaf area retention associated with nitrogen dynamics. The relevance of this capability for complex trait dissection and plant breeding is discussed.

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#### P6.13

11:50 Monday 29th June 2009

#### Scaling root growth responses from seedlings to field

A.G. Bengough (Scottish Crop Research Institute), Tracy A. Valentine (Scottish Crop Research Institute), Ian J. Bingham (SAC), Blair M. McKenzie (Scottish Crop Research Institute)

Good root system development is essential for optimum plant growth, especially in soils where water and nutrients are limiting. Climate change offers the likelihood of increased rainfall variability resulting in soils that are either too wet or too dry for good root growth. Soil physical limitations to root growth may decrease seedling root extension rates to 40% or less of their unimpeded rate if soil strength exceeds 2 MPa penetrometer resistance, air-filled porosity is less than 0.10, or if matric potential approaches  $-1.5$  MPa. Our field and lab measurements in sandy-loam soil indicate that such physically limiting conditions occur for much of the growing season, and vary greatly with depth, time, and soil cultivation. We have evidence that physically limiting conditions, particularly soil strength, are often present in arable soils throughout Eastern Scotland. In the light of these results, we will discuss some major uncertainties underlying our ability to predict root growth in the field: namely the relation between seedling root growth and the growth of older plants, and the plasticity of root systems in responding to heterogeneous soil environments.

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**P6.14****13:30 Monday 29th June 2009****Functional–structural plant modelling: A new paradigm in crop science**

Jan Vos (Wageningen University), Jochem B. Evers (Wageningen University), Gerhard H. Buck-Sorlin (Wageningen University), Andrieu Bruno (UMR1091 Environnement et Grandes Cultures Thiverval-Grignon F), Chelle Michael (UMR1091 Environnement et Grandes Cultures Thiverval-Grignon F), Pieter H. De Visser (Plant Research International-WUR NL)

Since the 1960s so-called ‘process-based’ crop models were developed. These explain crop performance by simulating resource flows (radiation, carbon, water, nutrients). However, plants react to their environment and to management interventions not only by adapting their functions (processes such as photosynthesis) but also by adapting their structure (architecture). In the last decade it became technically feasible to develop functional–structural plant models (FSPM), combining the adequate representation of both the three-dimensional (3D) plant structure and plant function. This adds a dimension to crop modelling and shows promise in several applications, including decision support.

An FSPM consists of an architectural part (plant structure) intimately connected to a process part (plant functioning). The architectural part deals with (i) the types of organs that are initiated and the way these are connected (topology), e.g. the branching pattern, (ii) organ expansion dynamics, and (iii) geometrical data, such as leaf angles and leaf curvature. The process part can contain any physiological or physical process that affects plant growth and development. Examples are photosynthesis, carbon allocation, nutrient uptake and transport, but also plant hormone synthesis or mechanical rules for branch bending.

This paper answers the following questions (i) how are FSPM constructed and (ii) for what purposes are they useful? The spectrum of applications of FSPM in crop production encompasses e.g. yield prediction of field or greenhouse crops, ornamental quality, plant–weed competition, plant–pathogen interactions, biocide spraying, remote sensing and exploring the significance of genetic variation in particular traits.

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**P6.15****14:10 Monday 29th June 2009****Using a turbid medium approach to estimate light interception by individual plants**

Didier Combes (INRA-URP3F), Abraham J. Escobar-Gutiérrez (INRA-URP3F), Michaël Chelle (INRA-EGC), Alban Verdenal (INRA-URP3F)

Grasslands are complex system for which individual plant modeling within the canopy is a key approach to understand their functioning and dynamics in relation to management and environmental factors. Light radiation plays a major role at the individual plant scale acting on major processes such as photosynthesis, which in turn could alter the acquisition of other resources. Light interception by phytoelements within canopies has been widely estimated based on the Beer–Lambert law by assuming the system as a series of turbid medium layers. In parallel, light models have been developed to accurately estimate the light interception at local scales using virtual plants with 3D representation of plant architecture. In this work, we analyzed light interception by individual isolated plant and by individual within a

vegetal canopy using 3D virtual plants and the turbid medium approach. The results show that the approximation of the canopy into horizontal layers gives rise to a supplementary clumping between layers. However, the results show that the accuracy of the calculations depend on the plant development stage and the direction of illumination. This method to estimate light interception could be used to simulate light within a vegetal canopy with large number of entities.

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**P6.16****14:30 Monday 29th June 2009****Can we use evolutionary algorithms to outdo evolution? A computational approach to increasing crop photosynthetic productivity**

Stephen P. Long (University of Illinois), Xin-Guang Zhu (Chinese Academy of Sciences, Max Planck Society)

Global atmospheric change, an increase in population to 8 billion and increasing land use pressure require an accelerated rate of improvement in the yield potential ( $Y_p$ ) of our crops, especially the major grains. Large increases in  $Y_p$  over the past 50 years are from increased partitioning of biomass to grain and production of canopies that intercept most available radiation during the growing season. These strategies have been so successful that they're both now close to their theoretical maxima, with little room for further improvement. By contrast photosynthesis has been improved little and realized efficiencies of solar energy conversion are far short of the theoretical potential. Photosynthesis is perhaps the best understood plant process, from genes to crop stands. Mechanistic dynamic models describing the >100 discrete biophysical and metabolic steps through linked differential equations have been developed. These successfully simulate the behavior of crop leaves *in vivo*. Evolutionary algorithms were applied to this system to determine: a) if investment of resources within the photosynthetic apparatus is optimal for productivity; b) how investment should be re-optimized for rising  $CO_2$ . Results suggest that altered investment, could increase photosynthetic efficiency by 60%. Results are consistent with recent transgenic manipulations. Why has this re-optimization not occurred as a result of natural evolution? The answer, at least in part, may be increased vulnerability to extreme events and failure to adapt to the increase in  $CO_2$  that has already occurred.

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**P6.17****15:30 Monday 29th June 2009****Use and misuse of modelling for projections of climate change impacts on crops and pastures**

Jean-François Soussana (INRA UR0874 UREP Grassland Ecosystem Research F-63100 Clermont-Ferrand, France), Francesco N. Tubiello (Joint Research Centre European Commission Ispra, Italy), Anne-Isabelle Graux (INRA UR0874 UREP Grassland Ecosystem Research F-63100 Clermont-Ferrand, France)

Projections of climate change impacts on global food supply are largely based on crop and pasture modelling. The consistency of these models with experimental data and their ability to simulate the effects of elevated  $CO_2$  and of increased climate variability has been debated. It

has recently been argued that most models tend to overestimate the CO<sub>2</sub> response of crops compared to Free Air Carbon dioxide Enrichment (FACE) data. In addition, the effects of high temperatures, of increased climate variability and of several limiting factors such as nutrients, air quality, pests and weeds, may reduce the effects of elevated CO<sub>2</sub> and such interactions are neither well understood nor well implemented in leading models. We discuss possible improvements in crop and pasture models based on fundamental knowledge at the plant and plot level. We conclude by making recommendations for current and future research needs, with a focus on stable and increased support for long-term studies and multi-factor experiments, explicit inclusion of biodiversity, disturbance, and extreme events in experiments and models and increased support for model-model and model-experiment comparisons.

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#### P6.18

16:10 Monday 29th June 2009

#### Meta-phenomics: Building a unified framework for interpreting plant growth responses to diverse environmental variables

Hendrik Poorter (Utrecht University), Achim Walter (Research Center Juelich), Fabio Fiorani (VIB Crop Design), Uli Schurr (Research Center Juelich), Ülo Niinemets (University of Tartu)

A tremendous but non-systematic effort has been made during the past 60 years to characterize the response of an array of plant species to their environment. This has happened at various levels, such as biochemistry, physiology, anatomy as well as at the level of whole-plant carbon budget and growth. As a result, a large number of phenotypic data are publicly available. Unfortunately, this information is not unified in a quantitative and structured way which allows for a comparative analysis. We aim to fill this important gap by building a large database containing the environmental responses of circa 40 growth-related variables for a range of plant species. In this talk we discuss 4 questions:

1. How can we generalize across different experiments and species?
2. How do plants respond to 12 of the most important environmental constraints? That is: what is the form of the response curve and to what extent can we order the magnitude of the responses for the various environmental factors?
3. Are there systematic differences between groups of species in the response curves (either among functional groups of species or between families)?
4. Can we get a handle on the interactions between various environmental variables in their effect on plants?

This approach—that we refer to as ‘meta-phenomics’—not only will serve as a benchmark for future and comprehensive phenotyping efforts, but it will also represent a very valuable tool per se in understanding the integrated response of plants to their environment.

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#### P6.19

#### Poster Session – Monday 29th June 2009 Modelling plasticity in plant architecture

Jochem B. Evers (Wageningen UR), Jan Vos (Wageningen UR), Paul C. Struik (Wageningen UR)

Plant plasticity is the ability of a plant of a particular genetic make-up to adjust its phenotype in response to environmental signals. Environmental signalling and the response in terms of plant plasticity comprise a wide and active field of mainly experimental research. The role of modelling has been fairly limited. With the introduction of the functional-structural plant modelling (FSPM) methodology, this is gradually changing.

A well-known example of plasticity in plant architecture is the shade-avoidance syndrome, a set of plastic responses to competition for light that the plant is likely to experience in the near future. Plants invest more biomass in height, display more erect leaves, and reduce outgrowth of axillary buds. The FSPM methodology provides the facilities to capture key aspects of shade avoidance: (I) plant architectural aspects (geometry and optical properties of leaves, stems, etc.); (II) light interception and scattering within a canopy and the resulting changes in intensity and spectral composition; (III) acquisition and allocation of carbon and nitrogen; (IV) synthesis and transport of plant hormones and other compounds that act as signals; (V) changes in the various sink/source relations; (VI) the resulting plastic response in plant development.

This work presents studies on plasticity in the structure of wheat plants, in terms of the dynamics of axillary bud outgrowth. Results show that bud outgrowth behaviour in response to environmental signals such as light intensity and spectral composition can be simulated using FSPM, exemplifying the potential of modelling plastic plant responses to environmental factors.

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#### P6.20

Poster Session – Monday 29th June 2009

#### Does canopy architecture play a role in the effect of plant density and sowing date on epidemics of *Septoria tritici* in wheat crops?

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*Septoria tritici* is one of the most damageable wheat foliar diseases in Europe. It has been suggested that sowing date and plant density influence its epidemics. The aim of this study is to better understand these effects and to evaluate the hypothesis that they result from changes in canopy architecture. Indeed, several field studies have pointed out that canopy architecture may influence *S. tritici* development. However because interactions between canopy structure and pathogen are numerous and change constantly during the growing season, field data analyses are complicated. To overcome these difficulties, the approach here combines modelling and experiments.

In 2007 and 2008, field trials in three locations were set up in which sowing date and density were varied. Disease assessments on the upper leaves showed that these treatments resulted in a wide range of epidemic's levels. The effect of sowing date and density on epidemics varied with the year and the location with a strongest effect of the sowing date. Canopy architecture also showed variation in organs dimensions, phyllochron and tillering dynamics. We used Septo3D, a wheat architectural model coupled with a *S. tritici* model to simulate the

time course of leaf area index and crop architecture in each treatment. We used these results to evaluate the hypothesis that change in canopy architecture is determinant for the change in epidemics between treatments.

Our approach appears of interest for evaluating the role of crop architecture in epidemic development and could thus aid in identifying beneficial agricultural practice combinations.

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## P6.21

Poster Session – Monday 29th June 2009

### Unbalancing global resources: Will plants be edible in a high CO<sub>2</sub> world?

Roslyn Gleadow (Monash University), Tim Cavagnaro (Monash University), Natalie O'Donnell (Monash University), John Evans (Australian National University), Alan Neale (Monash University), Cecilia Blomstedt (Monash University), John Hamill (Monash University)

Predicting the impact of changes in atmospheric CO<sub>2</sub>, and the concomitant changes in climate on plant growth and composition, are essential if we are to anticipate the changes required in plant breeding and agricultural practice to ensure on-going food security. The results presented here focus on cyanogenic glycosides, secondary metabolites that break down to release toxic cyanide (HCN) when plant tissue is damaged. Three cyanogenic crops were compared (*Trifolium repens*, *Sorghum bicolor*, *Manihot esculenta*, cassava) under different climate scenarios. The concentration of both cyanogenic glycosides and phenolics increased in leaves of plants suffering water stress. Genes governing cyanogen synthesis in sorghum (CYP79A1, CYP71E1) were moderately up-regulated but the change in concentration may also, in part, be a passive consequence of reduced growth rates. In elevated CO<sub>2</sub>-grown C3 plants, foliar cyanogenic glycoside concentration increased but protein levels decreased. Surprisingly, tuber yield decreased in eCO<sub>2</sub>-grown cassava, possibly as a consequence of the role of cyanogens play in nitrogen transport in this species. Partitioning of resources between primary and secondary metabolites is incorporated into our models of the effect of climate change on food security. We predict increases in cyanogenic compounds, decreases in protein and increases in all measures of C-based defence, with a consequent reduction in the nutritional value of many plants in the coming century.

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## P6.22

Poster Session – Monday 29th June 2009

### Imaging the 3D kinematics of circumnutation in maize roots

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#### Introduction

Although plant roots maintain consistent growth directions during development, they rarely follow linear trajectories. Root tips tend to oscillate perpendicularly to the main axis of growth, describing ellipses of various types. As root tips advance, their trajectories follow spirals, and this movement is known as circumnutation.

#### Results

We set up a new system to analyze the circumnutation movement of maize roots in 3D. Seedlings were placed in squared cuvettes two days after germination and allowed to grow vertically in humid air. A motorized stage was designed to image the samples using a standard fluorescent microscope from four perpendicular orientations. Time lapse imaging was performed every 2 min and during a 4 h period. We used Particle Image Velocimetry to track the displacement of patches placed along the root axis and combined the analysis on the different faces to reconstruct the kinematics of circumnutation e.g. expansion, torsion and bending deformations along the root.

#### Conclusion

Using this new imaging system, it was possible to obtain accurate quantitative description of the 3D growth kinematics. Although it was applied to describe circumnutation on maize roots, the system could be applied to characterize growth kinematics in various conditions.

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## P6.23

Poster Session – Monday 29th June 2009

### Drought and ABA effects on aquaporin content translate into changes in hydraulic conductivity and leaf growth rate: A trans-scale approach

Francois Tardieu (INRA), Boris Parent (INRA), Charles Hachez (UCL), Thierry Simonneau (INRA), François Chaumont (UCL)

The effects of abscisic acid (ABA) on aquaporin content, root hydraulic conductivity ( $L_{pr}$ ), whole-plant hydraulic conductance and leaf growth are controversial. We addressed these effects via a combination of experiments at different scales of plant organisation, and tested their consistency via a model. We analysed under moderate water deficit a series of transformed maize (*Zea mays* L.) lines, one sense and three antisense, affected on the *NCED* gene expression and which differed in the concentration of ABA in the xylem sap. In roots, the mRNA expression of most aquaporin *PIP* genes was increased in S plants and decreased in AS plants. The same pattern was observed for the protein contents of 4 PIPs. This resulted in more than 6-fold differences between lines in  $L_{pr}$  under both hydrostatic and osmotic gradients of water potential. This effect was probably due to differences in aquaporin activity because it was nearly abolished by an H<sub>2</sub>O<sub>2</sub> treatment, which blocks the water channel activity of aquaporins. The recoveries of leaf water potential and elongation upon rehydration differed between lines and were accounted for by the experimentally measured  $L_{pr}$  in a model of water transfer. A sensitivity analysis of the model shows that, in addition to hydraulic conductivity, leaf volume plays an essential role in the rate of recovery.

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## P6.24

Poster Session – Monday 29th June 2009

### PlaSMo: Making existing plant and crop mathematical models available to plant systems biologists

Christopher Davey (Aberystwyth University), Helen Ougham (Aberystwyth University), Andrew Millar (University of Edinburgh),

Howard Thomas (Aberystwyth University), Christopher Tindal (University of Edinburgh), Robert Muetzelfeldt (Simulistics Ltd)

Plant systems biologists have developed many mathematical models at the organ, cell and molecular scales. There is now a need to be able to incorporate these models into existing plant/crop models in order to access their effects at the plant, crop and landscape levels and under different climatic conditions. However, many of the plant/crop models are not readily available and the definitive model descriptions exist only as computer code often in legacy formats and so there is a real danger of them being lost altogether. This poster describes the PlaSMo project which is converting a set of the existing models into a *standardised open XML* format that will provide *full and unambiguous* descriptions of the models that users could implement in their own computational environments or use in packages designed to read the XML. To facilitate the conversion the models are being reimplemented in the graphical format used by the declarative modelling package Simile which can use the XML format. The XML versions of the models will then be made available from a specially designed web-portal which will also provide documentation, datasets and example output.

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## P6.25

Poster Session – Monday 29th June 2009

### Dynamic model of genetic control of plant development (on the example of *Arabidopsis thaliana*)

Olga A. Shulga (Centre), Vitaliy A. Rekrubratskiy (Centre Bioengineering RAS), Alexandr E. Korotkov (Moscow Physical Engineering Institute), Maria A. Korotkova (Moscow Physical Engineering Institute)

The model proposed investigates the influence of the environmental conditions and gene mutations presence upon the dynamics of plant growth and fertility. The gene network operation in the model provides for two states of a gene: active and inactive. Any mutation is considered as a strong mutation causing a complete loss of gene function. This assumption has enabled to use basic Petri nets for simulating of the gene network operation. All external environment impacts on plant development have an effect on the state of genes only. The simulation of the network operation determines flower initiation, flower organs identity in 4 concentric circles and plant fertility. The organs identity simulation is based on the analysis of several existing models of the organ determination. The software implementation of the developed model enables user to define mutant genes and environmental parameters dynamics for a simulation session. The plant development dynamics is then reflected and visualized by a three-dimensional model of the plant, a two-dimensional scheme of the flower (as the most important part of the plant) and gene network schemes. The model was used to define flower organ types for the known phenotypes of *Arabidopsis thaliana* plants with mutations in one, two or three genes to test the model correctness. The results have shown that the model has the high ability for the organ type prediction.

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## P6.26

Poster Session – Monday 29th June 2009

### Simulating the effect of light on greenhouse cucumber architecture

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Cucumber plants possess a phytochrome-B-dependent phototropic system that responds to R:FR ratio gradients created by asymmetric distributions of neighbours around the plant. They actively move leaf area into sunlit gaps in the canopy. Moreover, internode growth is influenced by PAR and the ratio of red to far-red light irradiance (R:FR) reflected from neighbour plants perceived at the stem. Gradients in the local R:FR on the individual leaf might trigger horizontal leaf movement. This in turn might alter the R:FR perceived at stem level and consequently feedback on internode elongation. Moreover, in greenhouse cucumber production systems, plant training and pruning additionally affect canopy architecture.

This work presents the concepts of a three-dimensional functional-structural plant model used to simulate the canopy architecture with respect to the effects of the interaction of PAR and R:FR perceived at stem level and gradients in the local R:FR on the individual leaf in greenhouse cucumber (*Cucumis sativus* L.). The dynamic structural plant model is based on a parametric Lindenmayer system, which interacts with a light model that provides local flux density of photosynthetically active radiation and red to far-red ratios. Two main model features mimic the light response of individual organs: Developmental plasticity allows for light-foraging by horizontal leaf movement through petiole bending and expansion of internodes in response to the light environment. Simulation outputs give realistic views on the effects of light on canopy architectures. Future model work will be discussed.

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## P6.27

Poster Session – Monday 29th June 2009

### Modelling temperature-compensated rates of development (an alternative to growing degree days)

Francois Tardieu (INRA), Boris Parent (INRA)

Temperature fluctuates rapidly, and affects all developmental and metabolic processes. We propose a method for calculating temperature-compensated rates of several developmental processes, based on the coordination of these processes. In a dataset comprising 41 experiments conducted in the greenhouse, growth chamber or the field, we compared the temperature responses in the range of 6–36 °C for different processes in maize, rice and *Arabidopsis thaliana*. Developmental processes like germination, cell division, expansive growth rate, leaf initiation and phenology showed coordinated temperature responses and followed common laws within each species. Arrhenius-like responses to rising temperature were observed until 18, 24 and 28 °C in *A. thaliana*, maize and rice, respectively, followed by a short quasi-linear response and then by a decline in rate at higher temperatures. This applied evenly to genotypes with temperate or tropical origins. We calculated temperature-compensated rates of development using the response equations corresponding to pooled developmental processes. The resulting rates remained remarkably stable under fluctuating temperature, and were able to unify the time courses of developmental processes over several experiments with different scenarios of temperature.

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**P6.28****Poster Session – Monday 29th June 2009****Crop modelling as an aid for environmental characterisation and crop improvement**

Karine Chenu (DPIF), Scott C. Chapman (CSIRO), Greg McLean (DPIF), Douglas Lush (DPIF), Graeme L. Hammer (University of Queensland), Fernanda Dreccer (CSIRO)

Genotype–environment interactions impede crop improvement for complex traits such as yield in water limited environments. Crop modelling is a powerful tool to characterise the nature of the environmental stresses experienced across locations, years, managements and genotypes. Simulation of the seasonal plant environment can aid in understanding genotype–environment interactions within and across trials and in identifying key adaptive traits specific to different environment types. An environmental characterisation has been undertaken for wheat in North East Australia. Simulations based on more than 100 years climatic data were conducted for representative sites, soils and management systems, for the cultivar Hartog. Five environment types based on patterns of crop water stress around flowering were identified and the frequency of occurrence of each environment type was determined in each site. Cultivars differing in maturity were simulated and their performance in the different environment types analysed. The simulations reproduced the expected genotype–environment interactions between genotype maturity and stress pattern, thus indicating the potential of this method to unravel more complex trait–environment interactions. Simulations also provided insight into the key adaptive traits associated with improved performance in each environment type, with flowering date and the amount of water use pre- and post-anthesis having a major role. Using crop modelling for environmental characterisation can help breeding programs to set up their trials and select for germplasm best adapted to the targeted regions.

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**P6.29****Poster Session – Monday 29th June 2009****A new network model explains the evolution of plant-specific metabolic networks**

Zoran Nikoloski (Institute of Biochemistry and Biology University of Potsdam), Patrick May (Max-Planck Institute for Molecular Plant Physiology), Joachim Selbig (Max-Planck Institute for Molecular Plant Physiology)

For a set of metabolic pathways, we define six models of metabolic networks including all possible pairwise relationships between metabolites, enzymes, and reactions. The unified study of these models provides an accurate systematic framework for evolutionary interpretation of the salient network properties. Here, we analyze the network properties of plant-specific metabolic networks assembled from Biocyc for the following species: *Arabidopsis thaliana*, *Capsicum annum*, *Coffea canephora*, *Solanum lycopersicum*, *Solanum tuberosum*, *Sorghum bicolor*, *Medicago trunculata*, *Petunia hybrida*, *Nicotiana tabacum*, and *Oryza sativa*. In addition, we compare and contrast the obtained results with those from: *Escherichia coli*, *Synechocystis*, *Candida albicans*, *Saccharomyces cerevisiae*, *Dictyostelium discoideum*, *Chlamydomonas reinhardtii*, *Mus musculus*, and *Homo sapiens*. As a result of our empirical study, we propose a probabilistic growth model which (i) can explain the evolutionary characteristics of

metabolic networks, (ii) differs from the well-established scale-free network models, (iii) demonstrates scale-free behavior of the degree distribution in both tails. We argue that the theoretical and empirical analyses of the proposed model, in terms of few salient network invariants, can help identify the evolutionary role of enzymes and metabolites through their participation in reactions.

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**P6.31****Poster Session – Monday 29th June 2009****The dynamics of resource allocation during rice (*Oryza sativa*) seedling establishment**

Saritha Kappalla (University of Liverpool), Ghulam M. Subhani (University of Agriculture Faisalabad), N.K. Sathymoorthy (Tamil Nadu Agricultural University), Meriel G. Jones (University of Liverpool), Martin Mortimer (University of Liverpool)

Rice cultivar selection for improved seedling establishment and vigour is essential as direct seeding is increasing adopted to combat the water shortages faced in traditional rice transplanting. Seedling establishment in rice involves developmental morphogenesis from the embryo and the successive expression of a coleorhiza, coleoptile, radicle and plumule and subsequently root and shoot tissues. This transition from embryo to autotrophic seedling is highly sensitive to flooding induced stresses. We measured component changes during this transition and described the dynamics by non-linear regression. Endosperm utilization, prior to the onset of autotrophy, was found to vary noticeably across a cultivar range exhibiting adaptations to both saturated soil water environments (cvs IR72, IR64) and aerobic ones (cvs PSBRC09, Azucena). Cultivars differed in coleoptile responsiveness (extension rate and maximum length expressed) to timing and depth of flooding, as did the expression of root tissues. Whilst having similar initial seed weights, cultivars also differed in rates of endosperm mobilization and in proportional allocation of seed biomass to root and shoot. cv Azucena was able to sustain growth in darkness for a significantly longer duration than other cultivars, whilst being much more sensitive to early flooding. The transcriptomics of gene expression underlying these phenotypic responses is currently being investigated.

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**P6.32****Poster Session – Monday 29th June 2009****Improving the genome-scale metabolic network of *Arabidopsis thaliana***

Nils Christian (MPI of Molecular Plant Physiology), Oliver Ebenhöf (MPI of Molecular Plant Physiology), Patrick May (MPI of Molecular Plant Physiology)

The development of modern high-throughput technologies has enabled biologists to collect an immense amount of data characterizing the state of a cell or organism. The present challenge of systems biology is now to integrate this diverse information to develop a systems wide understanding of biological processes. We present a strategy that incorporates genomic sequence data and metabolite profiles into modeling approaches to arrive at improved gene annotations and more complete genome-scale metabolic networks.

We have applied our method to *Arabidopsis thaliana* and identify missing routes in its metabolic network inferred from the genome sequence. With the ability to derive testable hypotheses by integrating heterogeneous data and modeling approaches, our strategy demonstrates the strength of close collaboration between experimentalists and modelers.

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### P6.33

Poster Session – Monday 29th June 2009

#### Genotype specific modulation of flowering time by integrating environmental and QTL effects into flowering phenology models

Ralf Uptmoor (Leibniz Universität Hannover), Alexandra Brandt (Leibniz Universität Hannover), Hartmut Stutzel (Leibniz Universität Hannover)

The development of wide adaptation cultivars is often constricted by phenological responses of plants to environmental signals like photoperiod and temperature. The major goal of our work was to identify genotypes showing low responses to these environmental signals and to predict the effects of daylength and temperature on flowering time in bi-parental *Hordeum vulgare* and *Brassica oleracea* populations by coupling QTL-analysis and crop modelling. The populations were phenotyped under varying photoperiod and temperature conditions in climate chambers and QTL analysis was carried out on the parameters of flowering phenology models. In both species main QTL were detected on chromosomal regions on which known flowering genes are located. Independent trials revealed that flowering time was accurately predictable within the populations.

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### P6.34

Poster Session – Monday 29th June 2009

#### Integrated control of leaf growth by cell turgor in response to combinations of evaporative demands and aquaporin-mediated reductions in root hydraulic conductivity

Thierry Simonneau (INRA), Christina Ehlert (INRA), Christophe Maurel (CNRS), François Tardieu (INRA)

The water uptake capacity of plant roots (their hydraulic conductivity,  $L_{p_r}$ ) is largely determined by aquaporins, channel proteins that facilitate the diffusion of water across cell membranes. An early response of plants to water deprivation is a reduction in  $L_{p_r}$ , as mediated by down-regulation of aquaporins. We addressed the general significance of  $L_{p_r}$  regulation with respect to shoot growth, water potentials and water flux through maize plants grown in hydroponics.  $L_{p_r}$  was manipulated in three independent ways by means of aquaporin inhibitors (acid loads or  $H_2O_2$ ) or oxygen deprivation.  $L_{p_r}$  was reduced by all treatments by 31 to 63%, with half times of about 15 min, and partially recovered when treatments were removed. Cell turgor measured in the elongating zone of leaves decreased synchronously with  $L_{p_r}$ , and leaf elongation rate closely followed these changes across all treatments. The results support that leaf growth response was mediated through changes in turgor. Furthermore, turgor and elongation of leaf cells were more sensitive than stomates to rapid reductions in  $L_{p_r}$  and therefore can be impacted by

changes in root aquaporin activity, even without change in transpiration. The proposed mechanism was formalized through a modeling of whole plant hydraulics that integrates a control of expansion growth based on Lockhart's equation. Data obtained with aquaporin inhibitors were used to calibrate the model which was further validated from the effects of anoxic stress. Also consistent with model outputs, we observed that increasing the evaporative demand dramatically sensitised leaf growth to changes in  $L_{p_r}$ .

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### P6.35

Poster Session – Monday 29th June 2009

#### Impact of tropospheric ozone on food and feed quality of Brassica species

Maarten De Bock (University of Antwerp), Yves Guisez (University of Antwerp), Reinhart Ceulemans (University of Antwerp), Nele Horemans (SCK), Karine Vandermeiren (CODA)

The impact of tropospheric ozone on *Brassica* species is important to understand economical and health consequences of climate change. Ozone is the third most important greenhouse gas and its concentration is still increasing. *Brassica napus* is very important for oil-production and as feed, *Brassica oleracea* is an important source of antioxidants for humans and has some interesting anticarcinogenic properties. Physiological measurements have been used to detect an early senescence in *Brassica napus*, which ultimately results in a reduction of oil-quantity after harvest. Glucosinolate content slightly increased due to ozone treatment in *Brassica oleracea*, an increase in the anticarcinogenic aliphatic glucosinolates is responsible. The toxic indolglucosinolates show a tendency to decrease. Shifts in vitamin concentration are examined to link with gene expression data. Eventually this should give a better understanding in the path that leads from ozone uptake to leaf development and ultimately to differences in yield.

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### P6.37

Poster Session – Monday 29th June 2009

#### Revealing the yield impacts of organ-level quantitative trait loci associated with drought response in maize—A gene-to-phenotype modelling approach

Karine Chenu (DPIF), Scott C. Chapman (CSIRO), Francois Tardieu (INRA), Greg McLean (DPIF), Claude Welcker (INRA), Graeme L. Hammer (University of Queensland)

Substantial genotype–environment (G×E) interactions make crop improvement for drought tolerance a major challenge for plant breeding. As part of understanding and exploiting G×E interactions for yield, we propose a modelling approach to bridge the gene-to-phenotype gap and evaluate the influence of quantitative trait loci (QTL) for two key processes (leaf and silk elongation) that influence crop growth, water use and grain yield in maize.

The yield of hypothetical recombinant inbred lines (RIL) was simulated for a range of climatic and drought conditions. QTL for faster leaf elongation increased crop yield under well-watered or pre-flowering deficit conditions, but reduced yield in terminal stress environments, as such genotypes prematurely exhausted their water supply. The QTL

impact on yield was substantially enhanced when the potential pleiotropic effects on silk elongation were included.

Simulations with this relatively simple model demonstrated the difficulty of interpreting the genetic control of yield at crop level. The results highlight the potential of integrative modelling for gene-to-phenotype prediction and for understanding G×E interactions for complex traits such as drought tolerance.

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### P6.38

Poster Session – Monday 29th June 2009

#### Modelling the interaction between rhizome and aboveground growth dynamics of *Miscanthus x giganteus*

Goetz M. Richter (Rothamsted Research), Richard J. Murphy (Imperial College), Andrew B. Riche (Rothamsted Research), Muhammad B. Umer (Imperial College), March Castle (Rothamsted Research)

Rhizome size and quality are well-known criteria for the success of new plantings affecting tillering, growth rate and tiller survival of *Miscanthus*. These relationships are not well known but important for the dynamic simulation of growth and yield formation modelling sink-source interaction. The purpose of this paper is to identify (a) patterns of carbon allocation and growth, (b) indicators of growth and vitality and (c) interactions with environmental factors.

Rhizome samples of different field sites and different planting age and fertility or fertilizer application were characterised by means of physical, chemical and biological methods and morphological indicators. Sub-samples were classified according to age using architectural traits (branching, internode counts, etc.) and carbohydrate content.

The distribution of morphological indicators gave insight into the annual growth rate in terms of internode number (13 to 22) and rhizome length (65 to 85 mm), number of branches, active and failing growing buds. Total rhizome dry matter varied between 7 and 16 t/ha in different plots, nitrogen application doubling it. The average annual allocation ranged between 1.5 and 3.5 t/ha. Rhizome recovery declined in samples older than four years and old material was not tractable under low nitrogen. The relationship between in-field shoot and rhizome dry matter was weak on the basis of single-year segments; however, a glasshouse study showed a significant effect of rhizome weight on shoot number and total shoot length. We discuss these findings in terms of improving the parameterisation of our process-based model.

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### P6.39

12:10 Monday 29th June 2009

#### Modelling N nutrition impact on plant functioning and root architecture in various genotypes of *Arabidopsis thaliana*

Céline Richard-Molard (INRA-groParisTech UMR1091 EGC), François Brun (INRA-groParisTech UMR1091 EGC), Michaël Chelle (INRA-groParisTech UMR1091 EGC), Bertrand Ney (INRA-groParisTech UMR1091 EGC)

Screening pertinent breeding traits for crop adaptation to low N supply remains difficult because plant response is a set of interacting processes, displaying a wide genetic and environmental variability. To integrate processes, a whole-plant structure-function model was devel-

oped on *A. thaliana*. Based on interactions between N/C fluxes, it offers an explicit and dynamic description of root system and leaf area growth.

The model was used to estimate in what extend homogeneous limiting N supply affects root architecture via the decrease in carbon availability, due to leaf area reduction. *A. thaliana* plants were grown in rhizotrons on a combination of C x N levels. Only 12 parameters, kept to the same values for all C x N datasets, were needed to satisfyingly simulate contrasted responses of root system architecture under our steady-state conditions, indicating that the major effect of global N availability on root system architecture was mediated by modifications of C fluxes.

Then, the root part of the model was simplified to characterize genetic variability of plant response and to identify the key parameters determining plant efficiency toward low N nutrition. We used this model to interpret the behaviour of five RILs and one mutant impaired on high affinity nitrate uptake. We found that the main source of variation relied on nitrogen uptake and carbon assimilation efficiencies, indicating that these parameters were the major determinants of plant response variability to steady-state N supply. The determining role of the AtNRT2.1 gene was also confirmed.

This work highlights how few key-mechanisms and related genes identified through modelling impact whole-plant phenotype.

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### P6.40

Poster Session - Monday 29th June 2009

#### Light phylloclimate within growth chambers: a modeling approach.

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Plant modeling and phenotyping require accurate data on plant growth and on their interaction with environment. Such data come mainly from experiments carried out in growth chamber; a spatially homogeneous climate being necessary to strictly compare results from different treatments or genotypes. Unlikely, a large variety of growth chambers is used and the within-chamber light field is often spatially heterogeneous. The effect of the light heterogeneity on the plant population would be higher for small plants (small specie (*Arabidopsis thaliana*); seedling) than for tall plants. For tall plants, the light variability would perturb studies at organ scale. Overcoming the “growth chamber” effect could be achieved by estimating the light phylloclimate, that is the light perceived by an individual organ.

Routine measurement of light phylloclimate could not be done due to sensor perturbations. Previous work proposed various modeling approaches. However, their models suffer from limitations, e.g., homogeneity approximation, limitation to PAR, etc. To overcome these limitations, we propose a modeling approach based on a 3D description of the growth chamber, its lighting system, and plants and relying on the Monte Carlo ray tracing. The SEC2 model has been successfully validated regarding the spatial distribution of irradiance within two different empty growth chambers. Moreover, it has simulated the light distribution on plants and plant organs. Results focus on the inter-plant and intra-plant variability of light.

Finally, the SEC2 model would illuminate virtual plant models and thus enable a better understanding of the interactions between genes and light (quantity and quality) resulting in phenotypes.

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