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Oral Communication Abstract - 6.01

TOWARDS A DYNAMIC MODEL OF THE *ARABIDOPSIS* SHOOT APICAL MERISTEM

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During the last decade an impressive body of knowledge concerning shoot apical meristem function has been generated.

This concerns information on the genes involved, their expression patterns, cell differentiation, cell division patterns, etc. The complexity of these data is such, that an integrated view of meristem function is not yet possible. Therefore, adapted mathematical and informatics approaches are now required to integrate the knowledge and to advance the level of understanding in the field. To formulate and test hypotheses on spatial aspects such as flows of signalling molecules between cells, strain within tissues, and the role of gene products in the spatial control of cell proliferation, we are creating a virtual meristem, that will integrate as much spatial, dynamic and quantitative information as possible.

Here, we will present the first results obtained on the mathematical modelling of auxin fluxes in the meristem, based on experimental data. This modelling framework, based on local interaction hypotheses between cells, suggests that phyllotaxy patterns may emerge due to auxin overflowing in the meristem centre in growing meristems.

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Oral Communication Abstract - 6.02

COMPLEX SYSTEMS AND ARTIFICIAL COGNITIVE PROCESSES IN PLANT GENETICS

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complex traits, self-learning processes, genetic algorithms, random forests

Linear models and distributive assumptions are the basis of the traditional dissection of complex phenotypes in Genetics: a sound example is the Fisher's infinitesimal model in the analysis and interpretation of quantitative traits. This simple but effective approach is based on a *black box strategy* in which unspecified natural functions associate the input (unknown) variables, the genes, to the output ones, the phenotypes. Decades of theoretical and experimental results support the effectiveness of the black box approach.

Nowadays the increasing knowledge on genomics, gene expression and metabolic networks strongly suggests the opportunity to open the black box and to fill it of sound interpretation of the relevant paths between genes and phenotype or its components. The number of available data at different level from DNA sequence to phenotypic expression is growing faster and faster and simple stochastic models are inadequate to efficiently manage them, even at a first approximation.

New analytical approaches are, for these reasons, required to mine the huge amount of genetic and phenotypic trait and to find the relevant core of information.

The class of artificial cognitive processes can be an appealing solution. More particularly, some procedures, based on computer simulations and Montecarlo methods, are available. They reach solutions by means of an iterative self-learning process based on the principles, for instance, of natural selection and evolution.

In particular the basics and the applications of two of these dynamical rule based systems, the *Genetic Algorithms* and the *Random Forests,* will be presented with examples based on experimental results in forest genetics.

The possibility of a joint analysis of traits with different distributive characteristics and the related information about the ranking of single trait on the basis of its relative importance in problem solving will be discussed in the frame of varietal identification in Poplar.

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Oral Communication Abstract - 6.03

ANALYSIS OF THE "METABOLIC GENOME" OF ARABIDOPSIS USING MICOARRAY DATA: IMPLICATIONS FOR PLANT BIOTECHNOLOGY

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Each microarray experiment is capable of producing measurements of transcript level for many thousands of genes. The analysis of such large amount of data is usually restricted to the comparison among experiments (time series or treated vs control). The reason for this is twofold: such results are easy to produce with little computation (i.e. identify the genes showing the largest variation among slides) and easy to grasp (induction or repression of single genes). In our approach we analyzed the genes coding for metabolic enzymes of *Arabidopsis thaliana* using two-gene scatter plots over all the publicly available data from a microarray database. The Pearson Correlation coefficient of each scatter plot was used as a measure of the co-regulation for each pair of transcripts. Software tools were constructed to calculate the Pearson coefficient i) of a gene against all the other genes present on the microarray chip and ii) of all possible gene pairs from a given list generating matrices of correlation coefficient. A graphical representation of such matrices was devised to allow a bird's eye view on the entire metabolic genome of Arabidopsis.

Analysis of the matrices reveals that, at the genomic level, the phenomenon of parallel activation is rather common in major pathways of plant metabolism, at least at the transcript level, thus suggesting that the best approach for metabolic engineering of endogenous pathways is the coordinate induction of enzymes (the so called 'universal method', see Morandini and Salamini, 2003 Trends Plant Sci. 8:70-5). It is mandatory to stress that the expression level for a gene does not coincide with the protein level, but can be used, in most cases, at least as a gross index for the activity.

Many predictions on the role of different enzymes isoforms in the carotenoid and sterol pathways, on the linking of metabolic pathways and on the function of several genes will be presented.

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Oral Communication Abstract - 6.04

THE BINDING ACTIVITY OF THE CHAPERONE BiP IN THE PLANT ENDOPLASMIC RETICULUM AND ITS ROLE IN THE SYNTHESIS OF SECRETORY PROTEINS

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molecular chaperones, endoplasmic reticulum, protein traffic and accumulation

The binding protein (BiP) is a member of the heat shock 70 chaperone family and a major resident of the endoplasmic reticulum (ER). BiP has been found in ATP-sensitive transient association with the newly synthesized forms of many secretory proteins and in more prolonged association with structurally defective polypeptides. Numerous experiments support a model in which BiP avoids improper interactions that can lead to irreversible misfolding and at the same time contributes to ER retention of not-yet mature proteins and targeting of permanently defective proteins for degradation, thus being a major actor of protein quality control within the ER. In vitro studies using random synthetic peptides indicate that BiP has affinity for sequences enriched in hydrophobic amino acids and thus exposed on the surface of proteins only before the tertiary and quaternary structures have been acquired. An algorithm based on these studies has been developed and used to predict BiP binding sites in secretory proteins. Along the sequence of the vacuolar protein phaseolin (the major storage protein of common bean) we have mapped a short domain that promotes in vivo interactions with BiP both in phaseolin and when added to reporter proteins. Consistently with the results of the above mentioned in vitro experiments with synthetic peptides and the model of BiP activity, this domain has an unusually high content of putative BiP binding sites as predicted by the BiP algorithm and is directly involved in phaseolin trimerization. However, by expressing these and other chimeric proteins in transgenic plants, we have found that mutated proteins that will eventually be degraded by quality control, or accumulate in large amounts in the ER or are delivered to the vacuole can have unusually extensive interactions with BiP when compared to wild type counterparts, suggesting that other interactions play a role in determining the final fate. Possibly, the selection of one destiny over the other depends on the degree of overall structural defects of the protein and the ability to form very large complexes.

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