00 01

## Defense genes and proteins in barley

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A large number of homogenous barley proteins has been screened for their ability to inhibit bacterial and fungal pathogens *in vitro*. Putative defense proteins thus selected have been further investigated to identify complementary and synergistic effects resulting from the combination *in vitro* of components from different protein families. Genes encoding proteins of interest have been cloned and used for transgenic expressiOn in tobacco. Transgenic plants have been challenged with appropriate pathogens to test the defense potential of the proteins *in vivo*. Gene-specific probes, obtained from the cloned barley genes, have been used to study their developmental and pathogen-induced expression in bacterial and fungal compatible/incompatible interactions. A combinatorial model is proposed to account for the plasticity of the plant response to the different situations and the independent regulation of the genes.

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00 02

## Global change effects: modelling crop growth, and experimentation

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"Global Change" is an ambiguous term, encompassing many factors. The empirical study of the effects of just temperature and $CO_2$ on crop growth and development has been of enormous value. Yet, crop growth is a dynamic process of interaction of many factors, and it is often difficult to extrapolate the experimental results to variable real-world conditions. Simulation modelling is the appropriate tool for this extrapolation, by providing a scientifically sound framework for combining experimental data and scientific hypotheses, and evaluating their dynamic interaction during the time that the crop grows. The model results should be tested with real-world data. The requirement of an accurate control of the external conditions is then replaced by that of careful monitoring. Within the Core Project GCTE (Global Change of Terrestrial Ecosystems) of IGBP (International Geosphere-Biosphere Program), crop research is grouped into a few crop-specific networks. Within each network both modelers and experimenters participate. For wheat and rice the networks are in full operation, for potato and cassava they are in their starting phase. A major effort is underway to compare model results for more than 10 different crop growth models that exist around the world. The preliminary results show a rather large range of model results, even for supposedly similar conditions. These findings indicate once more that models should be properly described and tested, both for internal consistency and for real world conformity.

00 03

## Integration of developmental processes

W.P. JACOBS
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The role of plant growth substances in the integration of development is critically examined in the light of recent experimental results, with emphasis on the movement of gibberellins. The research of the Brno school on axillary outgrowth and hormones and of the Princeton group on *Coleus blumei* will be discussed in more detail.

00 04

## Is there a common "GAS" (general adaptation syndrome) response to different types of physiological stress?

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This talk will deal with the possibility that the classic Selyean GAS mammalian stress coping hypothesis applies to plants as well. According to the basic tenets of this approach, if indeed pertinent to plants, different types of environmental stress, *e.g.* heat, cold, drought, salinity, flooding, *etc.* at a basic level, would induce the same stress-adaptation mechanisms. Drawing upon examples of stress coping involving oxy-free radical scavenging, osmoregulants, molecular chaperonins, phytohormomes, heat shock proteins and surface tension related biophysical changes in membranes and also upon specific anatomical adaptations, the pros and cons of the GAS hypothesis will be discussed.

00 05

## From light perception to gene activation: phytochrome mediated signal transduction pathway in plant

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We have previously used single-cell assays in a phytochrome-deficient tomato mutant to demonstrate that phytochrome signalling involves heterotrimeric G proteins, calcium and calmodulin. Whilst G protein activation could stimulate full chloroplast development and anthocyanin pigment biosynthesis, calcium and calmodulin could not induce anthocyanins and were only able to stimulate the development of immature chloroplast lacking cytochrome $b_6f$ and photosystem I core components. We now report that cyclic GMP alone is able to trigger the production of anthocyains and that a combination of cyclic GMP with calcium can induce the development of fully mature chloroplast containing all the photosynthetic machinery. Furthermore, using reporter genes for these different pathways (*cab-gus*, *chs-gus*, and *fnr-gus*) we demonstrate that cGMP and calcium act primarily by modulating gene expression.

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00 06

## Molecular analysis of flower induction and development of *Antirrhinum majus*

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In recent years, isolation of several genes affecting flower development in *Antirrhinum majus* made this species a major model system to study this important developmental process. Genes like *SQUAMOSA* and *FLORICAULA* are involved in determination of the floral meristem. Their mutation result in the development of bract forming shoots at positions where normally flowers would develop. The phenotypes obtained upon mutation of the genes found to affect floral organogenesis fall into three major categories. In each category, it is always the floral organs in two adjacent whorls which become homeotically transformed. Based on this observation a simple genetic model has been proposed to explain the establishment of floral organ identity in the four concentric whorls of the flower. The model hypothesizes the independent induction of two developmental pathways specifying floral organ identity after the formation of sepals as the basic type of organ following induction of a floral meristem. One of these pathways is under the control of the *PLENA* gene, the other is controlled by the *DEFICIENS* and *GLOBOSA* genes. These genes, as well as *SQUAMOSA*, encode transcription factors sharing a conserved DNA binding domain: the MADS-box. *In vitro* DNA-binding studies complemented with molecular genetic analysis of the respective mutants show that the DEF and GLO proteins may act together in the form of a heterodimer in the regulation of their target genes as well as in autoregulation. The possible interactions between other MADS-box proteins and their role in flower development is under current investigation.