



	<p>2nd EPSO Conference – In honour of Jeff Schell “Interactions in Plant Biology: cells, plants and communities”</p> <p>Ischia, Italy - October 2004 http://www.epsoweb.org/catalog/conf2004.htm</p>	
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Sunday 10 October 2004	
From 13:00	Registration
15:00 – 18:00	<p>Opening Chair: Karin Metzloff, EPSO, Gent, BE & Paolo Costantino, Rome, IT</p> <p>Plant Science in Europe Chair: Marc Zabeau, Gent, BE Co-Chair: Mauro Cresti, Siena, IT</p> <p>Posters related to this session: P 001 – P 003</p>
	<p>Speakers: Karin Metzloff and Paolo Costantino (20 min) <i>Executive Director of the European Plant Science Organisation</i> <i>Istituto Pasteur Fondazione Cenci Bolognetti, Università La Sapienza, Rome.</i> Welcome from EPSO</p> <p>Gioacchino Fonti, Rome, IT (20 min) <i>Director General for the Development and Internationalization of Science - Ministero dell'Instruzione, dell' Università e della Ricerca (MIUR)</i> Welcome from the Italian Ministry of Education, Universities and Research</p> <p>Speakers: Chris Patermann, European Commission (30+10 min) Director DG Biotechnology, Agriculture and Food S 001 Current Developments and Outlook on European Science Discussion</p> <p>Federico Mayor, Madrid, ES (30+10 min) S 002 <i>President of the ERC Expert Group</i> Europe needs a European Basic Research Fund Discussion</p> <p>Marc Zabeau, Gent, BE (20+10 min) S 003 <i>Chairman of the EPSO Board</i> The European Technology Platform “Plants for the Future” Discussion</p> <p>Wilhelm Gruissem, Zürich, CH (20+10 min) S 004 <i>“European Plant Science: A Field of Opportunities”</i> The scientist's long-term vision for European plant science Discussion</p>
18:00	Break
19:00 – 20:30	<p>Keynote in Honour of Jeff Schell Chair: Michael Bevan, Norwich, UK</p>
	<p>Speaker: Marc Van Montagu, Gent, BE (60+15 min) S 005 Perspectives in Plant Science</p>
20:30	Welcome Reception
Monday 11 October 2004	
8:30 – 10:30	<p>Interactions within cells I: Ubiquitin Chair: Jean-Marc Neuhaus, Neuchatel, CH Co-Chair: Giorgio Morelli, Roma, IT</p> <p>Posters related to this session: P 004, P 142</p>
	<p>Speakers: Jean-Marc Neuhaus, Neuchatel, CH (30+5 min) S 006 Protein traffic in the secretory pathway</p> <p>Crisanto Gutierrez, Madrid, ES (25+5 min) S 007 Cell Cycle Regulation and proteolysis</p>

		Pascal Genschik , Strasbourg, FR (25+5 min) S 008 EIN3-dependent regulation of plant ethylene hormone signaling by two Arabidopsis F-box proteins: ESF1 and ESF2	
		Csaba Koncz , Cologne, DE (15+5 min) S 009 Interactions of AMP-activated protein kinases with proteasome and SCF complexes	
10:30	Coffee Break		
11:00 – 13:00	Interactions within cells II: Signal Transduction Chair: John Mundy , Copenhagen, DK Co-Chair: Alessandro Vitale , Milano, IT	Speakers: John Mundy , Copenhagen, DK (30+5 min) S 010 MAP kinase 4 & systemic immunity	
	Posters related to this session: P 005 – P 028, P 140	Jen Sheen , Boston, USA (25+5 min) S 011 Arabidopsis MAPK Signaling Networks	
		Montserrat Pagès , Barcelona, ES (25+5 min) S 012 Nuclear trafficking of the ABA response protein Rab17 from maize	
		Yasunori Machida , Nagoya, JP (15+5 min) S 013 The MAP kinase cascade that positively regulates the formation of cell plates during plant cytokinesis	
13:00	Lunch		
15:00 – 17:00	Interactions within plants I: Development Chair: Ben Scheres , Utrecht, NL Co-Chair: Paola Vittorioso , Rome, IT	Speakers: Ben Scheres , Utrecht, NL (30+5 min) S 014 The roots of Arabidopsis stem cells	
	Posters related to this session: P 029 – P 046, P 137, P 141	Martin Hülskamp , Cologne, DE (25+5 min) S 015 Analysis of Epidermal Patterning in Arabidopsis	
		Liam Dolan , Norwich, UK (25+5 min) S 016 Using hairs to define polarity	
		Patrick Laufs , Versailles, FR (15+5 min) S 017 MicroRNA regulation of the CUC genes is required for boundary size control in Arabidopsis meristems	
17:00	Coffee Break		
17:30 – 19:30	Interactions within plants II: Hormones Chair: Nicholas Harberd , Norwich, UK Co-Chair: Ida Ruberti , Roma, IT	Speakers: Nicholas Harberd , Norwich, UK (30+5 min) S 018 Relief of DELLA-restraint: integration of multiple signal input to the control of plant growth	
	Posters related to this session: P 047 – P 057	Klaus Palme , Freiburg, DE (25+5 min) S 019 Role of auxin in plant development	
		Jeff Leung , Gif-sur-Yvette, FR (25+5 min) S 020 Mouthing off: Genetic dissection of drought tolerance	
		Remko Offringa , Leiden, NL (15+5 min) S 021 A PINOID-dependent binary switch in apical-basal PIN polar targeting directs auxin efflux	
19:30 – 20:30	Poster Session	19:30 – 20:00 Even posternumbers will be attended 20:00 – 20:30 Uneven posternumbers will be attended	
Tuesday	12 October 2004		
8:30 – 10:30	Multidisciplinary Science: Modeling / Systems Biology Chair: Enrico Coen , Norwich, UK Co-Chair: Carlo Soave , Milano, IT	Speakers: Enrico Coen , Norwich, UK (45+5 min) S 022 Genes and Shape	Spons. by 
	No Posters related to this session	Andrew Millar , Warwick, UK (30+5 min) S 023 Interacting feedbacks and the design of circadian clocks	

		Przemyslaw Prusinkiewicz , Calgary, CAN (30+5 min) Multiscale modeling of plants: from molecules to plant architectures	S 024
10:30	Coffee Break		
11:00	Excursion		
17:30 – 19:30	Breakthroughs in Life Sciences Chair: Gerd Jürgens , Tübingen, DE Co-Chair: Enrico Pè , Milano, IT	Speakers: Gerd Jürgens , Tübingen, DE (20+5 min) Apical-basal pattern formation in Arabidopsis embryogenesis	S 025
	Posters related to this session: P 058	Gloria Coruzzi , New York, USA (20+5 min) A systems approach to CN sensing in Arabidopsis	S 026
		Maria Clauss , Jena, DE (20+5 min) Ecological and Evolutionary Functional Genetics of Plant Defense	S 027
		Giorgio Bernardi , Napoli, IT (20+5 min) Plant Genomics	S 028
19:30	Break		
21:00 – 23:00	Plant Science and society Chair: Chiara Tonelli , Milano, IT	Speakers / Panelists: Chiara Tonelli , Milano, IT (Introduction, 5 min) Introduction	
	No Posters related to this session:	Massimiano Bucchi , Trento, IT (15 min) Why are people hostile to biotechnologies? Life Sciences, Democracy and the Governance of Innovation	S 029
		Leonardo Vingiani , Milano, IT (15 min) Communicating agricultural biotechnology: the experience of the Agrobio-industry in Italy	S 030
		Ann Van Gysel , Gent, BE (15 min) Bioscience Communications ... a vital challenge !	S 031
		Dario Frisio , Milano, IT (15 min) A view from an economist	S 032
		Discussion (55 min)	
Wednesday	13 October 2004		
8:30 – 10:30	Plant science and its manifold use Chair: Cathie Martin , Norwich, UK Co-Chair: Luigi Monti , Portici, IT	Speakers: Cathie Martin , Norwich, UK (30+5 min) Engineering natural products in plants for improved foods.	S 033
	Posters related to this session: P 059 – P 064	Eva Stoger , Aachen, DE (25+5 min) Utilizing the storage properties of cereal seeds for the production of recombinant proteins	S 034
		Toni M. Kutchan , Halle, DE (25+5 min) Improving one of mankind's oldest medicinal plants, the opium poppy.	S 035
		Josef Glössl , Vienna, AT (15+5 min) Modulation of the N-Glycosylation Pathway in Plants	S 036
10:30	Coffee Break		
11:00 – 13:00	Interactions between organisms I: Pathogens / Symbionts Chair: Jeff Dangl , North Carolina, USA Co-Chair: Felice Cervone , Roma, IT	Speakers: Jeff Dangl , North Carolina, USA (30+5 min) Perception of Bacterial Virulence Factors by Plants Disease Resistance Proteins	S 037

	Posters related to this session: P 065 – P 092, P 136, P 143	Jonathan Jones , Norwich, UK (25+5 min) S 038 Spons. by: Mechanisms of disease resistance	
		Jens Stougaard , Aarhus, DK (25+5 min) S 039 Recognition of symbionts: receptor and signal transduction	
		Cyril Zipfel , Basel, CH (15+5 min) S 040 RLKs as watchdogs of innate immunity in plants	
13:00	Lunch		
15:00 – 17:00	Interactions between organisms II: Allelochemicals Chair: Ian Baldwin , Jena, DE Co-Chair: Amadeo Alpi , Pisa, IT	Speakers: Ian Baldwin , Jena, DE (30+5 min) S 041 Plant-Insect signaling in the Real World Chris Bowler , Naples/Paris, IT/FR (25+5 min) S 042 Exploring the molecular secrets of marine diatoms Jorge Vivanco , Colorado, USA (25+5 min) S 043 Allelopathy and exotic plant invasion: from molecules and genes to species interactions Andy Phillips , Rothamsted, UK (15+5 min) S 044 Putting insects off the scent: modifying plant semiochemistry to disrupt plant-insect interactions.	
	Posters related to this session: P 093 – P 094, P 139		
17:00	Coffee Break		
17:30 – 19:30	Interactions within cells III: Chromatin and transcription factors Chair: Javier Paz-Ares , Madrid, ES Co-Chair: Angelo Viotti , Milano, IT	Speakers: Javier Paz-Ares , Madrid, ES (30+5 min) S 045 Genetics and genomics approaches towards unravelling transcriptional control of phosphate starvation responses in Arabidopsis Vincent Colot , Evry, FR (25+5 min) S 046 Arabidopsis heterochromatin Wilhelm Gruissem , Zürich, CH (25+5 min) S 048 Arabidopsis RBI1 and MSI1 integrate cell cycle and epigenetic regulation of female gametophyte and seed development Giovanna Benvenuto , Naples, IT (15+5 min) S 047 The DET1/DDB1 complex regulates photomorphogenesis in plants and interacts with chromatin	
	Posters related to this session: P 095 – P102, P 138		
21:00	Conference Dinner		
Thursday 14 October 2004			
8:30 – 10:30	Interactions within Plants III: Abiotic Stress Chair: Kazuo Shinozaki , Tsukuba, JP Co-Chair: Roberto Tuberosa , Bologna, IT	Speakers: Kazuo Shinozaki , Tsukuba, JP (30+5 min) S 049 Global analysis of gene networks in abiotic stress responses and tolerance Lutz Nover , Frankfurt am Main, DE (25+5 min) S 050 A network of chaperones and transcription factors controls the plant heat stress response Jian-Kang Zhu , Riverside, California, USA (25+5 min) S 051 Genetic analysis of plant responses to salt, drought and cold stresses. Teun Munnik , Amsterdam, NL (15+5 min) S 052 Phospholipid Signalling Pathways in Abiotic- and Biotic Stress	
	Posters related to this session: P 103 – P 104		
10:30	Coffee Break		

11:00 – 13:00	<p>Interactions between organisms III: Natural variation / diversity Chair: Francesco Salamini, Cologne, DE/IT Co-Chair: Michele Stanca, Fiorenzuola d'Arda, IT</p> <p>Posters related to this session: P 135</p>	<p>Speakers:</p> <p>Francesco Salamini, Cologne, DE/IT (30+5 min) S 053 Wild species, genes and geographic areas relevant for wheat domestication</p> <p>Ed Buckler, Ithaca, NY, USA (25+5 min) S 054 Using Natural Variation to Dissect Complex Traits in Maize</p> <p>Beat Keller, Zürich, CH (25+5 min) S 055 Molecular diversity and evolution of disease resistance loci in wheat</p> <p>Françoise Védèle, Versailles, FR (15+5 min) S 056 Nitrogen use efficiency in Arabidopsis Thaliana: functional genomic and quantitative genetic approaches</p>
13:00 – 13:15	<p>Closing Karin Metzlaff, Gent, BE & Paolo Costantino, Rome, IT</p>	
13:15	<p>Departure</p>	

We would like to thank our committee and secretariat members for organizing this conference:

Members of the organising committee: **Michael Bevan, Chris Bowler, Paolo Costantino (coordinator), Mauro Cresti, Denes Dudits, Helene Lucas, Karin Metzlaff, Kirsi-Marja Oksman-Caldentey, Mark Stitt, Chiara Tonelli, Roberto Tuberosa, Pierre de Wit, Marc Zabeau.**

Conference secretariat: Katrien Molders and Margherita Groeben

Session: Plant Science and Society

Follow in the footsteps of your best tradition, opening yourselves to all the developments of the technological era, but jealously safeguarding the perennial values that characterize you.

This is also the way to give a hope-filled future to the world of agriculture.

(John Paul II, Jubilee of the Agricultural World, 11 November 2000)

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In developed countries public opinion and policy decision makers are worried about the role and the scope of plant research in itself. The concern regards several controversial issues:

- a) There is still a need of agricultural innovation in developed countries?
- b) Is innovation going to be under constraint?
- c) Is private research going to be sole?
- d) What is the role of public research? Is it still independent and trustworthy?

Technical innovations to enhance crop production have been controversial also in the past. Some critics argued that the “Green Revolution” was biased against the poor, making the rich richer and the poor poorer, others still point out its weaknesses and the new problems created somewhere, forgetting its strengths and the problems partially solved, like famine.

The sources that inspire the critics of the “Gene Revolution” are quite different from those in the past (European consumers were afraid of food security, now are in trouble with food safety, Green lobbies have more power, etc.). There are, also, some similarities between the dynamics of public perception of the impacts of these two crop revolutions. In both cases, prior to and following introduction of the technologies, a critical literature succeeded in creating confusion about the potential economic benefits for farmers and consumers.

In the last decades, there was however a substantial change in agricultural research that produces a new kind of controversy: the role of private research combined with changes in controls of intellectual property rights.

Worldwide, public investments in agricultural research nearly doubled in real terms from 1976 to 1995, but in many parts of the world, this growth slowed dramatically during the 1990s.

Private investments in agricultural research are not new, but rose substantially in the last decades. Pardey and Beintema estimated that, by the mid-1990s, about one-third of the \$33 billion total investment in agricultural research worldwide was private.

Most of the agricultural technologies were free of proprietary claims and substantially available to all. By the 1980s, the scope of intellectual property was extended to biological material, particularly in agbiotech area, so biological innovations attracted more private investment than before.

Nevertheless, the performances of agricultural technologies is site-specific and strongly affected by agroecological conditions, then agricultural R&D still relies on significant amounts of public support and is likely to continue to do so. This is true in developing countries, but also in developed countries. In Italy, for example, there is a need of agbiotech innovations related to typical foods that are threatened by biotic and abiotic stresses.

The building of public acceptance of agbiotechnology and new trust on plant science is possible through the assumption of a clear Social Responsibility by research institutions, both private and public. This means: transparency in decision-making and funds finding, effective and realistic communications, clearness in the goals researched, easy access of developing countries to the technologies (knowledge, tools, but also education).

Appendix: The DET1/DDB1 Complex Regulates Photomorphogenesis in Plants and Interacts with Chromatin**Session: Interactions within Cells – Chromatin and transcription factors**

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Light provides a major source of information from the environment during plant growth and development. Plants perceive light through the action of several photoreceptors, including the UV-A/blue light receptor classes denoted cryptochromes and phototropins, and the red/far red light receptors known as phytochromes.

In order to obtain a better understanding of light signal transduction pathways in plants we are focusing on the tomato light hypersensitive mutants *high pigment-1* (*hp-1*) and *high pigment-2* (*hp-2*). Analysis of the *hp-2* mutant has previously revealed that it is mutated in the *DET1* gene. Mutations in the *DET1* gene were first identified as being responsible for the constitutively de-etiolated phenotype of Arabidopsis *det1* mutants. Recent findings show that the *hp-1* mutant is mutated in the homolog of vertebrate UV-Damaged DNA Binding Protein (DDB1). *hp-1/hp2* double mutants show an additive phenotype inferring that the two proteins interact within the same pathway. Recent results indeed demonstrate that DET1 and DDB1 are present within the same nuclear complex and that they interact physically.

The phenotypes of *hp-1* and *hp-2* mutants suggest that DET1 and DDB1 act as negative regulators of photomorphogenesis. Previous studies have ruled out that DET1 may directly bind to DNA or that it binds to the RNA polymerase holoenzyme. We have therefore investigated whether the influence of DET1 and DDB1 on photoregulated gene expression may be mediated by an epigenetic mechanism involving binding to histone tails. In a series of in vitro and in vivo experiments, we have found that this is indeed the case, specifically that the DET1/DDB1 complex binds to non-acetylated H2B tails within a nucleosome context. Consequently, this study infers that chromatin remodelling may play an important role in the control of photoregulated gene expression.

Erratum: Technical development for visualization of water distribution in the root and the hypocotyl of *Arabidopsis thaliana* using an NMR microscope
Session: Breakthroughs in Life Sciences

P 058

Nuclear Magnetic Resonance Imaging (MRI) technique is contact free and noninvasive one. This technique offers a potentially unique means of accessing structural, growth, and hydrodynamic information in intact tissue. Application of MRI technique to living (or intact) plant can provide very useful data for plant science. However, because of low spatial resolutions of MRI technique, it is difficult to apply this technique to small plant, such an *Arabidopsis thaliana*. Then, in order to enable us to apply the NMR microscopic imaging technique to a small model plant, *Arabidopsis thaliana*, we have developed a special preparation technique to grow a plant with a straight main root. In principle, MRI technique could reconstruct three dimensional distribution of water in plants if its spatial resolution of the microscope is high enough. Whereas our system satisfied this requirement, it takes too long time to obtain huge amount of voxel data and to process them to reconstruct overall image of the root. To overcome this difficulty, we have developed to get grow the plant with a straight main root in a sample tube (5mm in diameter) for an imaging probe. This development enabled us to obtain whole image of the root with the two dimensional imaging technique, which reduced the data acquisition time. The plant growing technique described above resulted in improving the signal to noise ratio of the image, too, which was absolute necessity to perform numerical analysis of water distribution and its dynamics. Actual procedure to grow the plant with the straight root was as follows: (1) we prepared an agar gel with hemi-columnar shape. (2) sowed an *Arabidopsis* seed on the flat surface of the hemi-column, and the column was held vertically, and (3) inserted it into a sample tube for MRI probe three days after germination. The root developed along the surface almost vertically, and was not embedded into agar gel. This nature of the root improved the S/N ratio and image contrast of the root markedly because water in agar did not contaminated the image data. Images with high S/N provided us reliable data of signals originated from free water distribution of the root. We are using image data to link among water distribution, water dynamics and molecular genetic study. A part of analysis will be presented elsewhere (Takase et al.) in this meeting.

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Erratum: How sedentary endoparasitic nematodes manipulate plant cell differentiation: cellular and molecular aspects**Session: Interactions between organisms – Pathogens / Symbionts****Godielieve Gheysen**

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Sedentary endoparasitic nematodes are an important problem in agriculture and their complex relationship with the plant host is still not very well understood. From a scientific viewpoint the ability of these sedentary nematodes to induce specialized feeding sites in plant roots is one of the most fascinating aspects of this plant-parasite interaction. Cyst nematodes generate syncytia by cell wall degradation, accompanied by endoreduplication and root-knot nematodes induce giant cells by mitosis without cytokinesis. By using cell cycle blockers, DNA synthesis and progression through G2 phase, or mitosis, were shown to be essential for gall and syncytium establishment. Analysis of the cytoskeleton by immunolocalization of the actin and tubulin proteins and by the use of gfp-fusions revealed that the cytoskeleton was strongly disrupted in syncytia. In giant cells, although disturbed compared to normal root cells, actin and microtubular fibres are visible. As nematode feeding involves the retrieval of large volumes of cytoplasm, a degree of cytoskeleton fragmentation may facilitate the uptake during nematode feeding.

Many efforts have been put into the identification of plant genes that are upregulated by nematode infection, especially during the early phases of the interaction. One of the early upregulated plant genes in syncytia and giant cell is an auxin-inducible transcription factor from the WRKY family. We have constructed plants overexpressing or producing RNAi for this transcription factor. They develop fairly normal except for some effects on root development indicating a common step in root and feeding site development. Nematode infection assays are being performed.

An important question in the plant-nematode interaction is how these changes in gene expression and cell differentiation are induced by the nematode. Several strategies are being employed to characterise the nematode pharyngeal gland secretions. We are currently analysing the possible role of a secreted ubiquitin-extension protein in the plant-nematode interaction by performing RNAi on the beet cyst nematode *Heterodera schachtii*, and by analysis of transgenic plants. Transgenic plants have been constructed that express the ubiquitin expression protein as a fusion with gfp with a nucleolar localisation as result. We are currently analysing possible effects of this protein on plant cells.

Erratum: The chromatin remodelling complex FACT associates with actively transcribed regions of the *Arabidopsis* genome

Session: Interactions within Cells – Chromatin and transcription factors

P 097

The compaction of the DNA provided by chromatin represses the transcription of genes by restricting the access of DNA binding regulatory factors to their DNA target sites, and by inhibiting the progression of RNA polymerases. Since both initiation and elongation of transcription by RNA polymerase II are inhibited in the chromatin context, the packaging of the genomic DNA into chromatin represents an important level of gene regulation. Numerous nuclear activities have been identified, which can help to overcome the repressive effects of chromatin.

In yeast and mammals, a nuclear complex termed FACT (facilitates chromatin transcription) consisting of the SSRP1 and Spt16 proteins was recently found to assist transcription through chromatin by remodelling nucleosomes in the path of RNA polymerase II without requirement for ATP hydrolysis. Here, using co-immunoprecipitation we have demonstrated the existence of the FACT complex in *Arabidopsis* cells. *Arabidopsis* FACT consists of the 120-kDa Spt16 and the 71-kDa SSRP1 proteins. Indirect immunofluorescence analyses revealed that both FACT subunits co-localise to nuclei of the majority of cell types in embryos, shoots and roots, whereas FACT is not present in terminally differentiated cells such as mature trichoblasts or cells of the root cap. A similar distribution was observed for the histone H3 variant methylated at Lys4, which is characteristic of transcribed euchromatin. In the nucleus, Spt16 and SSRP1 are found in the cytologically defined euchromatin of interphase cells independent of the status of DNA replication, but the proteins are not associated with heterochromatic chromocenters and condensed mitotic chromosomes. FACT can be detected by chromatin immunoprecipitation (ChIP) over the entire transcribed region (5'-UTR, coding sequence, 3'-UTR) of actively transcribed genes, whereas it does not occur at transcriptionally inactive heterochromatic regions and intergenic regions. FACT localises to inducible genes (*PR-1*) only after induction of transcription, and the association of the complex with the genes (*HSP70*) correlates with the level of transcription. Collectively, these results indicate that FACT assists transcription elongation through plant chromatin.

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Duroux, M., Houben, A., Ruzicka, K., Friml, J. and Grasser, K.D. (2004) The chromatin remodelling complex FACT associates with actively transcribed regions of the *Arabidopsis* genome. *Plant J.*, in press

Appendix: Visualization of phospholipids in legume protoplasts and root hairs

Session: Interactions within Cells - Signal Transduction

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R. Tobena
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Phospholipids are emerging as important signalling molecules in plants. They are involved in many processes such as defence responses, osmotic stress, endomembrane trafficking and tip growth. We study phospholipid signalling in living cells by fusing specific phospholipid binding domains, such as pleckstrin homology (PH) domains, to different variant of GFP. Here we show the results obtained using PH domains that bind specifically PI(4)P in Cowpea protoplasts and *M. truncatula* root hairs.

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Appendix: ARP2/3 mediates sugar responses in Arabidopsis

P 141

Session: Interactions within Plants - Development

In a screen for Arabidopsis mutants with higher sugar responses (hsr), we have identified genes that encode members of the ARP2/3 complex. This complex is involved in actin polymerisation and actin branching. The hsr3 and hsr4 mutants are allelic to distorted2 and distorted1 respectively and have similar cell morphology defects. Other KO mutants in components of the ARP2/3 complex also have higher sugar responses like hsr3/4, such as increased sugar induced growth, increased sugar induced gene expression, increased anthocyanin induction and reduced chlorophyll levels (Baier et al. 2004).

We are currently investigating this novel link between sugar responses and the plant cytoskeleton. Possibly the ARP2/3 complex regulates sugar transport or localisation of metabolic complexes.

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Appendix: High Sugar Response Mutant 5 encodes a F-box protein: A link between regulation of carbohydrate resource allocation and SCF ubiquitin ligase mediated protein degradation?

Session: Interactions within Cells - Ubiquitin

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Plants co-ordinate the processes of carbohydrate production, utilization for growth and storage in response to the availability of carbohydrates.

The mechanisms by which plants determine how much carbohydrates are available and how their allocation to the different processes is regulated remain largely unknown. In order to identify mutants with altered carbohydrate resource allocation a genetic screen was performed and several high sugar response mutants (hsr) were isolated (1). Here we report the characterisation and cloning of HSR5. The hsr5 mutant shows enhanced seedling growth in response to glucose and sucrose at low concentrations and is hypersensitive to arrest of seedling development caused by high sugar concentrations. When grown on 3 % sucrose the hsr5

seedlings accumulate 50% more starch and show reduced chlorophyll and elevated anthocyanin levels. These phenotypes are consistent with changes in expression levels of sugar responsive genes involved in starch, storage protein and anthocyanin biosynthesis, sugar transport and photosynthesis. When grown on soil the hsr5 mutant has a reduced growth rate, flowers later and produces bigger but fewer seeds. The hsr5 mutant shows unaltered responses to the plant hormones ABA, ethylene and cytokinin. These phenotypes suggest the hsr5 mutation effects the co-ordination of carbohydrate resource allocation directly or the plant fails to monitor its carbohydrate status correctly and therefore is unable to adjust the carbohydrate allocation in accordance with the available carbohydrates. We have cloned hsr5 by mapbased cloning and it

encodes a protein with a F-box motive. In a yeast two hybrid assay the HSR5 protein interacts via its F-box with ASK1/SKP1 subunit of ubiquitin ligase. Recently it has been reported that PRL1 competes with ASK1/SKP1 for the binding to plant Snf1-related protein kinases (SnRK) (2,3,4.)

Since the prl1 mutant shows a hypersensitivity to glucose and sucrose which is remarkably similar to the hsr5 phenotype and Snf1 related kinases play a central role in the regulation of glucose signalling in yeast and animals we are tempted to speculate that HSR5 is part of a SCF complex that is regulated by SnRKs and PRL1.

References / Literature

1. Plant Physiol. 134: 81-91
2. Genes & Development 12: 3059-3073
3. PNAS 96: 5322-5327
4. EMBO 20: 2742-2756

Session: Interactions between organisms – Pathogens / Symbionts

Introduction

Berries are good sources of phenolic compounds, which often act as defence compounds in plants. In humans plant phenolics besides their other health-inducing effects have been found to possess antimicrobial activities. Our previous studies showed that phenolic berry extracts especially inhibited the growth of Gram-negative but not Gram-positive bacteria such as *Lactobacillus*. Especially cloudberry, raspberry and strawberry extracts proved to be strong inhibitors of the avirulent *Salmonella* (1).

Materials and Methods

Bilberry (*Vaccinium myrtillus*), lingonberry (*Vaccinium vitis-idaea*), cranberry (*Vaccinium oxycoccus*), raspberry (*Rubus idaeus*, var. Ottawa), cloudberry (*Rubus chamaemorus*), strawberry (*Fragaria ananassa* Senga Sengana), blackcurrant (*Ribes nigrum*, var. Öjeby) and sea buckthorn berry (*Hippophae rhamnoides*), were used in the study. For antimicrobial studies berries were freeze-dried and ground to fine powder. Phenolics were extracted from the berries by aqueous 70% acetone (2). Antimicrobial activity of freeze-dried grounded berries (2 or 10 mg/ml) and phenolic berry extracts (1 or 5 mg/ml) was analysed by determining the bacterial growth curves in liquid cultures (1). The bacterial strains used were *Listeria monocytogenes* VTT E-991205, *L. innocua* VTT E-981011, *Salmonella enterica* ser. Typhimurium VTT E-981151, *S. enterica* ser. Infantis VTT E-97738, *Staphylococcus aureus* VTT E-70045 and *Lactobacillus rhamnosus* VTT E-96666 (ATCC 53103).

Results

Salmonella strains were inhibited by all the berries. Cloudberry, raspberry, strawberry and bilberry extracts inhibited the growth during the first 12 h incubation. However, during the next 12 h the number of viable cells started to increase. Cloudberry extract was the best inhibitor showing strong antimicrobial effects. *Staphylococcus* strains were strongly inhibited by all the berries and berry extracts. The number of viable cells did not increase at the end of cultivation. The tested *Listeria* or *Lactobacillus* strains were not sensitive to berries or berry extracts, with the exception of cranberry, which showed inhibitory effects against *Listeria* bacteria.

Conclusions

The results showed that antimicrobial properties of the berry compounds aren't restricted to the avirulent *Salmonella* but inhibited also the virulent strains. The inhibition of the *Staphylococcus aureus* suggested that also the structure of Gram-positive bacteria is sensitive to the antimicrobial compounds of the berries. Bioactive berry compounds seem to inhibit the growth of pathogenic bacteria with several mechanisms. The difference in the antimicrobial properties of the berries and the berry extracts also suggested that other bioactive compounds are involved in the cell growth inhibition.

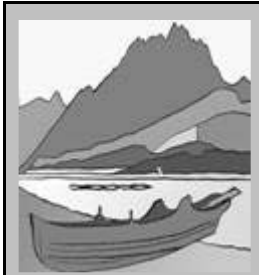
In the future, the most interesting berry extracts will be fractionated with the aim of identifying the antimicrobially active components. In addition the mechanism of action against gastrointestinal bacteria, especially intestinal pathogens, will be extensively studied. The results will be utilised in functional food development and in pharmaceutical applications.

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Appendix – Errata

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