CONFÉRENCES JACQUES-MONOD

Roscoff (France), 4-8 juin 2008

Régulations fines des voies de signalisation chez les plantes

Fine Tuning of Plant Signalling Pathways

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Rapport sur la Conférence

Conference Report

RESUME DU RAPPORT

Conférence Jacques Monod intitulée : Régulations fines des voies de signalisation chez les plantes

Roscoff, 4-8 juin 2008

Historique de la conférence:

La récente conférence qui s'est tenue à Roscoff du 4 au 8 juin 2008, est la suite d'une série de conférences Jacques Monod dédiée de façon générale aux " Voies de signalisation chez les plantes". La première fut organisée par Jean Guern and Dieter Klambt in 1989, et traitait des mécanismes de perception et d'action de l'homorne végétale auxin. La deuxième conférence eut lieu en 1992, orgnanisée par Dieter Klambt, Michel Caboche and Michel Delseny. Elle concernait les mécanismes de régulation de l'expression des gènes par les différentes hormones. La troisième conférence organisée par Michel Caboche, Michel Delseny and Richard Hooley en 1995, se concentrait sur les mécanismes moléculaires régulant le développement embryonnaire et le déloppement précoce de la plantule. La quatrième, organisée par Richard Hooley and Jérôme Giraudat in 1998 décrivait les nouvelles découvertes relatives à la caractérisation des gènes de biosynthèse d'hormone et l'élaboration des voies de signalisation hormonales. La cinquième conférence organisée par Jérôme Giraudat and Malcolm Bennett se déroula en 2001 et concernait essentiellement les voies de signalisations dans le context du développement de la plante. La sixième organisée en 2004 par Malcolm Bennett et Catherine Bellini fut consacrée à l'intégration des multiples voies de signalisations au cours du développement de la plante et son adaptation à l'environnement. Cette dernière conférence organisée par Catherine Bellini et Nicholas Harberd du 4 au 8 Juin 2008 à Roscoff a été consacrée aux différents niveaux de régulation et aux mécanismes impliqués dans les régulations fines de diverses voies de signalisations.

Contexte scientifique

Les plantes perçoivent et répondent aux signaux endogènes et environnementaux de manière à assurer une croissance et un développement optimal. Les cellules végétales doivent intégrer ces myriades de signaux intrinsèques et extrinsèques par des réseaux de voies de transduction qui produisent les réponses adaptatives. Les phytohormones et les composants de leurs voies de signalisation occupent une place centrale dans ces réseaux de transduction du signal, agissant fréquemment en conjonction avec d'autres signaux morphogénétiques et développementaux pour contrôler de façon coordonnée la croissance et le développement. Les plantes sont des organismes sessiles et nécessitent de fait la mise en place de mécanismes régulateurs extrêmement efficaces capables de réagir et de s'adapter très rapidement au moindre changement environnemental. De nombreux points de contrôle existent au niveau transcriptionnel, post-transcriptionnel et post-traductionnel. Au cours des dernières années d'importants progrès ont permis de mieux comprendre comment les plantes coordonnent de façon fine différentes voies de signalisation. Par exemple, la récente identification des principaux récepteurs d'hormones a permis de mieux comprendre comment ces petites molécules organiques sont perçues par les cellules végétales. De plus la démonstration de l'importance des complexes SCF et du "turnover" des protéines comme éléments centraux dans la réponse précoce à l'auxine ou à l'acide gibbérellique suggère que la protéolyse de molécules répresseurs est un mécanisme important dans la signalisation hormonale chez les plantes. La découverte de petits ARNs impliqués dans la régulation de l'accumulation d'ARN messagers est un autre fait marquant des trois dernières années. En réalité de nombreux processus de

développement et de signalisation sont régulés par la dégradation ciblée par les microARNs d'ARN messagers.
Cette Conférence Jacques Monod vient dans la continuité d'une série de conférences dont le thème général est " La transduction du signal chez les plantes". La thématique sera consacrée aux différents niveaux de régulation et aux mécanismes associés impliqués dans la coordination fine des différentes voies de signalisation.

Le programme

La conférence s'est articulée sur 5 sessions :

Session 1 : Régulation de l'expression des gènes - Remodelage de la chromatine - Facteurs de transcriptions
Modérateurs: Catherine Bellini - Javier Paz-Ares

Session 2 : Régulation post-transcriptionnelle de l'expression des gènes miANRs - métabolisme des ARNs
Modérateurs: Nicholas Harberd - Salomé Prat

Session 3 : Stabilité des proteins – Dégradation
Modérateurs: Robert Hill - Catherine Rechenmann

Session 4 : Signalisation longue distance - Nouveaux signaux
Modérateurs: Yka Helariutta - Ida Ruberti

Session 5 : Signalisation hormonale et développement des plantes I
Modérateurs: Pascal Genschik - Petra Stirnberg

Le programme était partagé 25 en longues (30 min) et 13 courtes (15 min) communications orales. Les communications courtes ont été sélectionnées parmi les 54 résumés proposés pour des présentations par affiches. La moitié de ces courtes interventions étaient présentées par des collègues français dont 5 femmes. Ce qui a permis de rééquilibrer au moins partiellement le ratio femmes/hommes qui s'est retrouvé être de 30%
En plus des présentations orales 41 posters étaient à la disposition des participants pendant toute la durée de la conférence, ce qui avec les 2 sessions posters d'une 1h30 chacune offert d'amples possibilités de discussion.

Cette conférence a été très appréciée par l'ensemble des participants qui d'un commun accord ont décidé de poursuivre la série. De fait le vice président Nicholas Harberd a accepté de présider la prochaine conférence avec l'aide du nouveau vice-président Patrick Achard, élu à la fin de la conférence

CONFERENCE REPORT

Final report from the Jacques-Monod Conference entitled *Fine-tuning of plant signalling pathways*

Roscoff, 4-8 June 2008

Historical background to the conference series

The recent conference in Roscoff continued a series of Jacques Monod conferences devoted to the general theme of "Signal Transduction in Plants". The first of these was organised by Jean Guern and Dieter Klambt in 1989, and focused on the mechanisms of perception and action of the plant hormone auxin. The second conference took place in 1992 and was organised by Dieter Klambt, Michel Caboche and Michel Delseny. It concentrated on the mechanisms by which various hormones regulate gene expression. The third conference organised by Michel Caboche, Michel Delseny and Richard Hooley was focussing on the molecular genetic analysis of embryogenesis and early development. The fourth on was organised by Richard Hooley and Jérôme Giraudat in 1998. It concentrated on recent advances in the characterisation of hormone biosynthetic genes and in elaboration of components of hormone signal transduction pathways. The fifth conference organised by Jérôme Giraudat and Malcolm Bennett took place in 2001 and dealt with signalling processes in the context of plant development. The sixth conference was organised in 2004 by Malcolm Bennett and Catherine Bellini and focussed on the integration of various signalling pathways involved in building a plant and in its adaptation to the environment. The present conference organised by Catherine Bellini and Nicholas Harberd took place from June 4 to 8 2008 in Roscoff and focussed on the different regulatory levels and the corresponding mechanisms involved in fine-tuning the various signalling pathways.

Background to the Roscoff conference thematic area held in June 2008

Plants sense and respond to environmental cues and endogenous signals to ensure optimal growth and development. Plant cells must integrate these myriad extrinsic and intrinsic signals via a network of transduction pathways that produce adaptive response outputs. Phytohormones and their signalling components occupy a central position within this transduction network, frequently acting in conjunction with other environmental and morphogenic signals, to co-ordinately regulate plant growth and development. Impressive strides have been made to dissect the molecular basis of signal cross talk in plants. Plants are sessile organisms and need to set up efficient regulatory mechanisms that allow reacting and adapting rapidly to any environment change. Several regulatory check points exist at the transcriptional, post-transcriptional and at the protein levels. In the last few years comprehensive progress have been made in the understanding how plants fine-tune different signalling pathways. For example the recent identification of the major plant hormones' receptors gave more insights in how these simple organic molecules are perceived by the plant cells. In addition the identification of the SCF complexes and protein turnover as central to early auxin and GA signalling events suggests that the proteolysis of repressor proteins is an important hormone signal transduction mechanism in plants. Another important issue in the last three years was the discovery of microRNAs used for regulating mRNA accumulation. Indeed several developmental process and signalling pathways are regulated by miRNA-guided degradation of target mRNAs.

The conference untitled "Fine-tuning of plant signalling pathways" aimed at giving an overview of the latest discoveries relative to different levels of regulation of signalling pathways in plants.

Report on the meeting proceedings

The meeting was divided into five sessions, each addressing distinct levels of regulation of signalling pathways. Nevertheless, due to last minute changes in the participation and/or arrival time of invited speakers, the final programme has sometime changed compared to initial programme and sessions as homogenous as they were supposed to be. However, the high quality of the presentations the conference overcame this little defect.

Session 1 *Regulation of gene expression - Chromatin remodelling - transcription factors*

Polycomb-group genes regulate many key developmental transitions in plants, including seed development, seed maturation and flower development. They act by repressing the expression of their target genes, which include many of the transcription factors and other key regulators of developmental patterning. **Justin Goodrich** (Edinburgh Univ., UK) described the approaches they have developed to identify targets of Polycomb genes that are still largely unknown. He described the genome wide distribution of epigenetic marks conferred by Polycomb-group genes using chromatin immunoprecipitation, and he presented the results from a large-scale genetic screen for modifiers. The characterization of the ZOUPHI gene, which encodes a bHLH transcription factor and acts during early seed development and is needed for normal epidermal development has been discussed. Heterochomatin participates in numerous nuclear processes, including centromere function, gene silencing and nuclear organization. Its formation requires conserved pathways of histone and DNA modifications and it was recently shown that the RNA-interference pathway (RNAi) is implicated in heterochromatin assembly and gene silencing. **Thierry Lagrange** (Perpignan Univ., France) discussed the role of two forms of a fourth type of DNA-dependent RNA polymerase, Pol IVa and Pol IVb, that mediate siRNA accumulation and DNA methylation-dependent silencing of endogenous repeated sequences. He showed that Arabidopsis expresses two evolutionarily related forms of RNAPIV (Pol IVa and Pol IVb). RNAPIVb is the most abundant form of RNAPIV in Arabidopsis. Selective disruption of either form of RNAPIV indicates that RNAPIVa-dependent siRNA accumulation is not sufficient per se to drive robust silencing at endogenous loci and that high levels of DNA methylation and silencing depend on siRNA that are accumulated through a pathway involving the concerted action of both RNAPIV forms.

To conclude the "chromatin" aspects of the session **Donna Bond** (CSIRO, Cambera, Australia) gave a short presentation on the role of *VERNALIZATION INSENSITIVE 3 (VIN3)* gene in stress responses. *VIN3* is a chromatin remodelling PHD finger protein, which is essential for the vernalization response in Arabidopsis. **D Bond** showed that *VIN3* is induced in response to anaerobic conditions in Arabidopsis but is not altered in response to heat, high salt or drought conditions, suggesting that *VIN3* is essential for the anaerobic response in Arabidopsis.

The second part of this session was dedicated to transcriptional regulation. **Loic Lepiniec** (INRA-Versailles, France) gave an overview of the role of transcription factors belonging to three different classes (MYB, bHLH and WDR) in the regulation of complex regulatory network controlling accumulation of both storage and secondary metabolites during seed maturation in Arabidopsis. He highlighted the relationships between these different regulators that provide a fine-tuned regulation of the network. This was completed by a short presentation given by **Martine Devic** (Perpignan Univ., France) who described the genetic interaction of three B3-type transcription factors (FUS3, ABI3 and LEC2). She highlighted the importance of a partial redundancy between these 3 genes for fine-tuning the proper embryo development and seed maturation process in Arabidopsis. **Ida Ruberti** (CNR, Rome, Italy) analysed the role of bHLH transcription factors such as PIL1 or HFR1/ SICS1 in the shade avoidance response mechanisms. The shade avoidance response is a strategy of major adaptive significance to plants in natural communities. It is highly

widespread in the angiosperms, and depends on the ability of the plant to perceive the presence of neighbors. A plant grown under canopies perceives the reduction in the ratio of red (R) to far-red (FR) light as a warning of competition, and enhances elongation growth in an attempt to overgrow its neighbors. **I Ruberti** reported that the same low R/FR signal that induces hypocotyl elongation also triggers a rapid arrest of leaf primordium growth, ensuring that plant resources are redirected into extension growth. The growth arrest induced by low R/FR depends on auxin-induced cytokinin breakdown in incipient vein cells of developing primordia, thus demonstrating the existence of a previously unrecognized regulatory circuit underlying plant response to canopy shade. **Céline Charon** (Univ. Paris Sud-Orsay, France) ended this session with a short presentation on the role of the 2 RNA -binding proteins Terminal Ear 1-like (TEL1) in the regulation of vegetative growth and floral transition in Arabidopsis.

Session 2 *Post-transcriptional regulation of gene expression - miRNAs - RNA metabolism*

This second session was dedicated to the post-transcriptional regulation of gene expression and most of the presentations dealt with the recently discovered area of small RNAs. **Hevré Vaucheret** (INRA-Versailles, France) gave an overview of the small RNA pathways in plants that contain more ARGONAUTE (AGO), DICER-LIKE (DCL), DOUBLE-STRANDED RNA BINDING (DRB) and RNA-DEPENDENT RNA-POLYMERASE (RDR) proteins than any other eukaryote, resulting in increased complexity of the regulatory networks. **Martin Crespi** (CNRS-Gif sur Yvette, France) described the emerging class of riboregulators represented by long non-protein coding RNAs (npcRNA), which act either directly in this long form or are processed to shorter miRNA and siRNA. They performed a genome-wide bioinformatic analysis of full-length cDNA databases identified 76 Arabidopsis npcRNAs. One npcRNA expressed in root tissues corresponded to TAS3a, a trans acting small RNA (tasiRNA) precursor target of miR390. They showed that long npcRNAs and small RNAs may fine-tune the expression of regulatory genes in response to environmental stresses to regulate root developmental plasticity. **Javier Paz-Ares** (CSIC, Madrid, Spain) described the non-protein coding gene *IPS1* (*INDUCED BY PHOSPHATE STARVATION 1*) from Arabidopsis thaliana. IPS1 contains a motif with sequence complementarity to the phosphate (Pi) starvation-induced miRNA miR-399, but the pairing is interrupted by a mismatched loop at the expected miRNA cleavage site. They showed that IPS1 RNA is not cleaved but instead sequesters miR-399 and by this way regulates its availability. By using artificial target mimics they showed that target mimicry can be generalized beyond the control of Pi homeostasis, and could be a way to regulate miRNA activity. Two short presentations followed. One by **Manuel Echeverria** (Perpignan Univ., France) who described the identification and characterisation of novel miRNAs, which control development and growth in rice. He mostly discussed the role of osa-miR827, which is implicated in phosphate homeostasis in rice. osa-miR827 targets the cleavage of an mRNA encoding an SPX-domain containing protein, predicted to be implicated in phosphate or nutrient transport. They demonstrated demonstrate that osa-miR827 is induced by Pi deprivation in both leaves and roots. In situ hybridisation confirms that osa-miR827 is localised in vascular tissues. The second was presented by **Andreas Niebel** (INRA-Toulouse, France) who described the regulation of the expression of *MtHAP2-1*, a transcription factor (TF) involved in early stages of nodulation in the model legume Medicago truncatula. MicroRNA169 restricts MtHAP2-1 to the meristematic zone of nodules in a process that is essential for proper nodule growth. In addition the first intron of MtHAP2-1 is alternatively spliced in increasing amounts during nodule development. This negatively regulates MtHAP2-1 expression. This novel regulatory mechanism involves a small peptide, called uORF1p that is produced by an upstream ORF present in this first intron of MtHAP2-1. They suggest that miR169 and uORF1p play essential, sequential and non-redundant roles in regulating MtHAP2-1 expression in the nodule meristematic zone.

The day after, the session continued with **Vincent Colot** (ENS-Ulm, CNRS, Paris France) who gave an overview on DNA methylation, which plays a role in silencing transposable elements and controlling gene expression in plants and mammals. In plants however, accidental loss or gain

of DNA methylation can be transmitted through meiosis, leading to the notion that plants do not reset DNA methylation patterns at each generation, unlike mammals. **Colot** and collaborators have recently discovered that in fact, loss of DNA methylation in Arabidopsis is corrected efficiently over numerous sequences. Remarkably, RNAi-mediated corrective DNA remethylation requires one passage through meiosis to be initiated and is progressive over several generations. This progressive and differential correction of epigenetic defects may increase adaptive opportunities while preserving genome stability. **Catherine Bellini** (UPSC, Umeå Sweden) described the recent findings in her group regarding the molecular mechanisms regulating adventitious root formation in Arabidopsis. They showed that the auxin response factors *ARF6* and *ARF8* that are targets of microRNA mir167 are positive regulator of adventitious rooting whereas *ARF17*, target of mir160, is a negative regulator. They regulate each other's expression at the transcriptional and post-transcriptional level by modulating the activity of mir160 and mir167. *ARF6* and *ARF8* are positive regulators of the auxin-induced genes *GH3-3*, *GH3-5* and *GH3-6* whereas *ARF17* is a negative regulator.

Session 3 *Protein stability - degradation*

The ubiquitin proteasome system is a key regulator of many biological processes in all eukaryotes. This mechanism employs several types of enzymes, the most important of which are the ubiquitin E3 ligases that catalyse the attachment of polyubiquitin chains to target proteins for their degradation by the 26S proteasome. Among the E3 families, the SCF is the best understood; it consists of a multi-protein complex in which the F-box protein plays a crucial role by recruiting the target substrate. Strikingly, nearly 700 F-box proteins have been predicted in Arabidopsis, suggesting that plants have the capacity to assemble a multitude of SCF complexes, possibly controlling the stability of hundreds of substrates involved in a plethora of biological processes.
Three presentations were about the DELLA proteins (DELLAs) that are a subfamily of the plant-specific GRAS family of putative transcriptional regulators that regulate plant growth in response to the phytohormone gibberellin (GA) and the importance of their degradation trough the proteasome via the SCFSLY1 E3 ubiquitin ligase for a proper development and adaptation of the plant to different environments. **Nicholas Harberd** (Oxford Univ., Oxford, UK) presented the GA-DELLA mechanism from an evolutionary point of view. The interaction between GID1 and DELLA components from *Selaginella kraussiana* (a lycophyte) is stimulated by GA. In contrast, in the moss *Physcomitrella patens*, GID1-like (GLP1) and the DELLA components do not interact, suggesting that GA-stimulated GID1-DELLA interactions arose in the land-plant lineage after the bryophyte divergence. A DELLA-deficient *P. patens* mutant strain lacks the de-repressed growth characteristic of DELLA-deficient angiosperms, and both *S. kraussiana* and P. patens lack detectable growth responses to GA, indicating that early land-plant DELLAs do not repress growth in situ. On another hand, *S. kraussiana* and *P. patens* DELLAs function as growth-repressors when expressed in the angiosperm *Arabidopsis thaliana*. Therefore the GA-DELLA growth-regulatory mechanism arose during land-plant evolution and via independent stepwise recruitment of GA-stimulated GID1-DELLA interaction and DELLA growth-repression functions. **Salomé Prat** (CSIC, Madrid, Spain) described the role of the DELLA proteins during the GA-stimulated elongation of Arabidopsis in the light. A lack of DELLA function reverts the dark de-etiolated phenotype of GA-related mutants, implicating the DELLA repressors in this response. DELLAs were shown to interact with the PHYTOCHROME INTERACTING proteins PIF3 and PIF4 in a yeast 2-H system. **S Prat** reported on the central role of the nuclear transcription factor PIF4 in the positive control of genes mediating cell elongation and show that PIF4 is negatively regulated by the light photoreceptor phyB and by the DELLAs. Consistent with this model, intermediate hypocotyl lengths were observed in transgenic plants over-accumulating both DELLAs and PIF4. An interaction/destabilization cascade mediated by phyB, that destabilizes this factor in the light, and by DELLAs, that in the absence of GAs block its DNA binding ability, hence explains how plants integrate both light and GA signals to optimize their growth and development in response to

changing environments. **Patrick Achard** (CNRS, Strasbourg, France) concluded this session on the DELLA proteins by giving a short presentation in which he described that Arabidopsis DELLAs cause Reactive Oxygen Species (ROS) levels to remain low after either biotic or abiotic stress, thus delaying cell death and promoting tolerance. Stress-induced DELLA accumulation elevates the expression of genes encoding ROS-detoxification enzymes, thus reducing ROS levels. He also showed that DELLAs regulate root-hair growth via a ROS-dependent mechanism and proposed that environmental variability regulates DELLA activity and that DELLAs in turn couple the downstream regulation of plant growth and stress tolerance through modulation of ROS levels.

Michael Prigge (Bloomongton Univ., Indiana, USA) represented **Mark Estelle** who couldn't attend the conference. He described the evolution of the auxin signalling mechanisms among different land plants. By using comparative genomics, he found that components of the auxin-signaling pathway are widely conserved across land plants, with many of the corresponding gene families dramatically expanding later in the lineage leading to flowering plants. Genetic and biochemical analyses in moss provided the first evidence that the molecular mechanism of auxin perception is conserved outside of flowering plants and offers new insights into poorly understood aspects of the auxin signalling pathway. **Pascal Genschick** (CNRS, Strasbourg, France) discussed about the role of Cullin (CUL)-dependent ubiquitin ligases in the control of palnt development and hormonal pathways. These proteins form a class of structurally related multi-subunit enzymes that control the rapid and selective degradation of important regulatory proteins involved in cell cycle progression and development, among others. Arabidopsis genome contains two related CUL3 genes and 76 BTB-domain belonging to 11 major families. CUL3A and CUL3B genes are ubiquitously expressed in various plant organs and shows largely overlapping expression patterns suggesting possible functional redundancy The disruption of both the CUL3A and CUL3B genes causes embryo lethality demonstrating that CUL3 genes play an essential role during embryogenesis. The production of a week cul3a/cul3b double mutant called cul3w revealed an important role of CUL3 in the regulation of ethylene biosynthesis. Cullin3 forms a complex with the BTB protein, ETO1 and controls the degradation of ACS5 a rate-limiting enzyme involved in ethylene biosynthesis. To investigate the function of a family of BTB proteins called BPMs, Genschik's group adopted a reverse genetic approach using the artificial micro RNA strategy. They obtained multiple BPM knock down plants, which developmental defects indicate that this class of BTB play a role in developmental processes.

Session 3 on protein degradation ended with 2 short talks. The first one presented by **Severine Lorrain** (Lausanne Univ., Switzerland) was about the importance of the stability of phytochrome interacting proteins and their degradation through the proteasome for a proper regulation of light signalling pathways. She showed that PIF4 and PIF5 act early in the phytochrome signaling pathways to promote elongation growth during the shade avoidance responses. She proposed that in dense vegetation, which is rich in far-red, the shade avoidance is triggered, at least partially, as a consequence of reduced phytochrome-mediated degradation of transcription factors such as PIF4 and PIF5. The second short talk was presented by **Eike Rademacher** (Wageningen Univ., The Neterlands), who described the role of ARF transcription factors and their Aux/IAA inhibitors during embryo development in Arabidopsis. IAA10 expression is limited to suspensor cells, and gain of function iaa10 mutations specifically interfere with suspensor and hypophysis. ARF9 and 13 are co-expressed in the suspensor. Double knock-out lines of these ARFs showed that both genes redundantly control suspensor development. Interestingly, the suspensor-specific IAA10/ARF13/ARF9 auxin response machinery is functionally distinct from the embryo-specific IAA12/ARF5 machinery, as evidenced from miss-expression and promoter-swap experiments.

Session 4 *Long distance signalling - new signals*

In Arabidopsis a circadian-clock regulated pathway promotes flowering specifically in response to the longer day lengths of spring and early summer. This pathway includes the GIGANTEA (GI),

CONSTANS (CO) and FT proteins, which act in the vascular tissue of the leaves to promote synthesis of a systemic signal that triggers flower development at the shoot meristem. **Georges Coupland** (MPI, Cologne, Germany) desccribed how transcriptional regulation by the circadian clock and alterations in protein stability triggered by acute responses to light combine to confer day-length responsiveness on this pathway. The FLAVIN-BINDING, KELCH REPEAT, F-BOX 1 (FKF1), and GIGANTEA (GI) proteins regulate CO transcription in Arabidopsis. The timing of this interaction regulates the timing of daytime CO expression. CYCLING DOF FACTORS (CDF1, 2 and 5) are transcription factors from the DOF family that repress CO expression. FKF1 function is dependent on GI, which interacts with CO repressors (CDF), and controls their stability. GI, FKF1, and CDF proteins associate with CO chromatin. FKF1-GI complex forms on the CO promoter in late afternoon to regulate CO expression. **G Coupland** also described the differences in response to cold temperatures for flowering induction between Arabidopsis alpina (perennial) and Arabidopsis thaliana (annual). Interestingly in A. alpina not all the vegetative meristems of a given plant respond the same way. While some are subjected to phase transition other remain vegetative, allowing the plant to survive several years. The pep1 mutant of A. alpina makes more side shoot flowers and for longer time than the WT. PEP1 was cloned and shown to encode an ortholog of FLC.

Markus Schmid (MPI, Tuebingen, Germany) described the effects of SCHLAFMUTZE (SMZ) on FT expression. SMZ encodes an AP2-like transcription factors that represses flowering in long days. SMZ belongs to a clade of AP2-like genes containing 5 members that are regulated by miR172. 35S:miR172 lines are early flowering and this phenotype correlates with an increased expression of FT in the leaves. Transgenic lines expression a mir172 resistant form of SMZ never flower and the expression of FT is inhibited. Results from these experiments indicate that miR172/SMZ contribute to the induction of flowering by regulating the expression of FT in leaves.
A mutation in TOE1 (one of the 5 AP2-like genes) induces early flowering. Mutation in the other members does not give any phenotype, nevertheless *toe1toe2* double mutant flower earlier than the single mutant and the phenotype is even stronger in triple mutants suggesting than the 5 genes are most probably required for the regulation of flowering time. **M Schmid** also described that FRUIT FULL-like and SEPALATA-like that are flower identity genes are likely to be direct targets of FD.

Peter McCourt's (Toronto Univ, Toronto, Canada) presentation was about strigolactones that has been isolated as seed-germination stimulants for root parasitic weeds (Striga and Orobanche) and shown to act as a chemical signal for arbuscular mycorrhizal fungi during presymbiotic stages. He showed that strigolactones play an important role in germination and early seedling growth and development also in the model plant Arabidopsis. Moreover, it appears that functional light and/or retrograde signaling is required for strigolactone synthesis. Germination defects of mutants lacking phytochromes such as *hy1* or *hy2* are rescued by exogenously applied strigolactones. **P McCourt** suggested that strigolactones could be a new class of plant hormones. This presentation from **P McCourt**, prompted **Catherine Rameau (INRA-Versailles, France)** to change the topic of her presentation and she and her collaborator **Christine Beveridge** (Univ. of Queensland, Australia) decided to reveal that the novel signal controlling branching in pea and Arabidopsis was a strigolactone. They showed that the phenotype of the pea mutant *rms1,* which is defective in carotenoid biosynthesis enzymes acting upstream the biosynthesis of a so far unidentified signalling molecule, can be restored by very low concentration (10 nM) of exogenously applied GR24, which is an analogue of strigolactone. They also showed that the *rms1* mutants lacks strigolactones. This was the first public announcement of the discovery of this so far unidentified signal moving acropetally in the plant and regulating branching. The identification of this signal has been a challenge during the last 10 years for many research groups and this presentation represented the "scoop" of the conference. **Petra Stirnberg** (York Univ., UK) represented **Ottoline Leyser** who unfortunately couldn't attend the conference as previously planned. She gave an overview of the *MAX/RMS* pathway in Arabidopsis. She mainly focussed on the role of *MAX2*, which encodes a Fbox protein that is part of a SCF ubiquitination complex. A screen for suppressors of the max mutant phenotype was undertaken. A suppressor of *max2* was identified and the corresponding gene

shown to be FHY3 (Far red elongated hypocotyl 3) which is required for the light-induced phyA nuclear accumulation and subsequent light responses.

Thierry Desnos (CEA, Cadarache, France) described the identification of a major QTL (LPR1 = Low Phosphate Response1), and its paralogue LPR2, two genes that reduce the primary growth when seedlings are on a phosphate-deficient medium. LPR1 and LPR2 encode multicopper oxidases (MCO), highlighting the essential role of MCO for plant development.

David Alabadi (CSIC-UPV, Valencia, Spain) gave a short presentation on the role of gibberellins in the light signalling pathway required for the control of de-etiolation in Arabidopsis. He showed that GAs modulate the activity of the light-signaling pathway by two distinct mechanisms, and identify the transcription factors HY5 and the PIF family as nodes of a regulatory network. This interaction occurs through distinct molecular mechanisms, based on the observation that GA signaling regulates HY5- but not PIF3- protein stability.

Session 5 *Hormone signalling and plant development*

Malcolm Bennett (Univ. of Nottingham, UK) dissected the mechanisms involved in the regulation of lateral root emergence, and more particularly the role of the gene *LAX3* that encodes an auxin influx carrier. Lateral roots originate deep within the parental root from a small number of founder cells at the periphery of the vascular tissues and must emerge through intervening layers of tissues. He showed that auxin originating from the developing lateral root acts as a local inductive signal, which reprograms adjacent cells. In particular LAX3 is induced in cortical and epidermal cells directly overlaying new primordia. Increased LAX3 activity reinforces the auxin-dependent induction of a selection of cell wall remodelling enzymes (AIR3, XTR6, EXPA), promoting cell separation in advance of developing lateral root primordial allowing their progressive emergence.

Catherine Perrot-Rechenmann (ISV, Gif sur Yvette, France) showed that the inactivation of ABP1 (Auxin binding protin 1) roots, results in an alteration of root meristem maintenance and subsequent arrest of root growth. In shoots, decreased ABP1 activity leads to severe growth retardation. The reduced leaf growth involves defect in cell division, an altered pattern of endocycle and a change in cell expansion. In addition, local repression of ABP1 activity in the shoot apical meristem revealed an additional role for ABP1 in cell plate formation and cell shape and a differential response depending on the region of the shoot apical meristem.

Martine Lemaire-Chamley (INRA Toulouse, France) showed that a tomato PIN gene was highly expressed in the ovary as well as in the locular tissue and columella of developing fruits. Reduced expression of this PIN gene induced altered ovary development and development of parthenocarpic fruits. Modifications of auxin metabolism were detected during the very early development of flowers in parthenocarpic lines. These observations were consistent with the deregulation of cell cycle and auxin signalling related genes during the development of young fruit**. Miguel Blázquez** (CSIC-PUV, Valencia, Spain) gave a short presentationon the role of hormone in the regulation of temperature-induced growth in Arabidopsis. He showed that temperature-related growth of the hypocotyl is not only mediated by auxin, but also by GAs and brassinosteroids (BRs). He proposed a model by which temperature would trigger a cascade of events involving the local increase in the levels of auxin, GAs and BRs, and crosstalk between the different hormones. The last short presentation was given by **Grégory Vert** (CNRS, Montpelier, France) who discussed the interconnection of the brassisteroid and auxin signalling in plants. He showed that the BIN2 kinase interacts with and phosphorylates the repressor Auxin Response Factor ARF2 to modify its binding to DNA and repressor activity, suggesting that BIN2 would increase expression of auxin-induced genes by directly inactivating repressor ARFs, leading to synergistic increases in transcription.

The second part of this final session was held the last morning and comprised 3 invited presentations. The first one was by **Yka Helariutta** (Helsinki Univ. Finland) and dealt with the cell to cell signalling in the establishment of the vascular system in Arabidopsis. They have recently demonstrated that in Arabidopsis, cytokinin phytohormones negatively regulate protoxylem

specification, a “default” identity. AHP6, an inhibitory pseudophosphotransfer protein, counteracts cytokinin signaling in a spatially specific manner, allowing protoxylem formation in this domain. On the other hand, APL, a MYB coiled-coil-type transcription factor has a dual role in promoting phloem differentiation and in repressing protoxylem differentiation. In a screen for mutants altered in phloem development a mutant in the gene *PHABULOSA* was identified. The characterisation of this mutant as well as the expression of *PHABs* genes and mir166, which regulates their expression, allowed establishing their role during vascular development. **Robert Hill** (Manitoba Univ., Winnipeg, Canada) showed that FCA, a gene normally associated with the transition to flowering, is an ABA receptor. ABA interacts with FCA-δ, preventing its interaction with FY, resulting in a delay in the transition to flowering. ABAP1, another product of FCA after alternative splicing, also an ABA binding protein, regulates seed germination and dormancy via an ABA-dependent process.

At the end of the meeting the conference delegates elected a new Vice-President, Dr. Patrick Achard (IBMP, Strasbourg, France), whilst Prof. Nicholas Harberd (Oxford, UK) became the new President.

Final report from the Jacques-Monod Conference entitled:
"Fine-tuning of plant signalling pathways"
Roscoff 4-8 June 2008

Administrative report

Participation

A summary of the different categories of participants is presented in the table below.

	Non Europeans	European (non French)	French	Total
Invited speakers	4	11	10	25
Students	1	5	7	13
Post-docs	2	15	1	18
Senior Scientists	2	6	16	24

A total of 80 persons attended the conference. In May 2004, 82 participants (including 27 invited speakers) were present at the conference also held in Roscoff. Therefore the participation this year is very similar to that in 2004. We can see that the tendency has not evolved, and we did not manage to reach the participation to the conference in 2000, which has seen 101 participants.
This difference was mainly due to a reduction of the French participants (compared to 2000), which number did not increase this year. Indeed, the majority of the participants were still non-French (46 Non-French/34 French in 2008; 49 Non-French/33 French in 2004).

The different origins are listed in the table below:

Country	**n°**
Austria	2
Australia	2
Belgium	4
Canada	4
China	1
Finland	2
France	34
Germany	4
Israel	1
Italy	2
Japan	1
Norway	1
Spain	5
Sweden	3
Switzerland	2
The Netherlands	1
United Kingdom	10
United States	1

In 2004, 9 countries were represented whereas this time, representative of 17 countries were present.
In this respect, the meeting attracted delegates from most of the major Plant Biology laboratories in Europe and outside Europe.

The ratio male / female was 46 male participants and 34 females (43% female scientists).

The programme

The programme was divided in long talks (30 min, including the discussion time) and short talks (15 min, including the discussion).
The 25 invited speakers gave the long talks. We selected 13 participants, among the 54 who sent an abstract for poster presentation and give them the opportunity to present their work in a short oral communication. An average of two short communications per topic covered by the invited speakers, were selected. They were selected on the basis of scientific quality and to ensure the broadest possible representation of work from the various laboratories whose staff a students attended the meeting. Half of these short communications were given by French participants, 5 of them were female. This allowed re-equilibrate, at least partially the ratio between male and female speakers. We reached a ratio of 30% female speakers.

In addition, there were 41 posters presentations and we allowed ample time for viewing and discussion. Indeed, the posters were on during the entire conference and accessible at any time. Two poster sessions, of 1.5 hours long, were organised in order to promote discussion between the participants.

The venue

The conference took place in Roscoff where all the facilities are provided by the CNRS conference center. We wish to thank all the CNRS staff, supervised by Dominique Lidoreau, who helped and took care of the local practical organisation. Everything was perfectly organised from the registration and welcoming of the participants to the delicious food we could enjoy all along the conference. Dominique Lidoreau was also of extremely valuable help for the editing of the abstract book, and should be particularly thanked.
Nevertheless there are some limits in organising conferences in Roscoff. In particular the fact that the poster room is not located in the same building as the conference room make it more difficult to access the poster outside the poster sessions. The poster room is also too small since it can host only 40 posters at a time and therefore does not allow to have all the posters available during the entire conference.
In addition this year we had to walk 15/20 mn to go from the conference room to the Hotel Gulf Stream where the meals were taken. This, not only decrease the time allocated to presentations but might have been a problem in case of rain. This year, we have been particularly lucky because the weather has been fantastic so we enjoyed the walk to and from the hotel. This nice weather contributed a lot to the general good mood of the participants. It would certainly have been different in case of rain.