INTERNATIONAL PLANT MOLECULAR BIOLOGY 2018

PROGRAM ABSTRACTS – ORAL PRESENTATIONS

Sunday, August 5th

Mechanisms of Biotic Interactions
Keynote Speaker - Pamela Ronald

Abstract Title: ENGINEERING RICE FOR DISEASE RESISTANCE, FLOOD TOLERANCE AND ENHANCED NUTRITION

Primary Author(s) and Institution(s): PAMELA RONALD; UC Davis

Abstract

By the year 2100, the number of people on Earth is expected to increase by ~50%, placing increasing demands on food production in a time when;a changing climate change is predicted to compromise;crop yields. Feeding this future world requires scientifically informed innovations in agriculture. Throughout human history, genetic improvement of plants has led to the development of food crops that are useful to farmers and that are nutritious/pleasing to consumers. I will describe how the discovery and characterization of the rice XA21 immune receptor, which confers resistance to the Gram-negative bacterium Xanthomonas oryzae pv. oryzae (Xoo), has led to insights into the molecular mechanisms controlling the plant immune response. I will also explain how introduction of the Submergence tolerance 1A (Sub1A) gene into rice, a staple food for half the world's people, has helped farmers in South and Southeast Asia mitigate rice crop failure during prolonged flooding. I will show how we have used CRISPR-Cas9 genome editing to generate rice plants with insertion of a 5.2kb carotenoid biosynthesis cassette into a genomic safe harbor. This proof of concept study shows that marker-free targeted gene insertion can be obtained at relatively high efficiencies in rice. These studies reveal how international teams of scientists can use knowledge of basic plant biology to address major agronomic challenges faced by farmers and society. Despite these successes, it seems likely that the debates surrounding crop bioengineering will continue. For these reasons, plant scientists may wish to seize opportunities to describe their research to non-scientists. Such conversations will ensure consumers are engaged in the important challenge of helping farmers produce nutritious food in a productive and ecologically-based manner.

Natural Variation and Adaptation
Keynote Speaker - Detlef Weigel

Abstract Title: Evolution in response to the environment – as scientist and as a plant

Primary Author(s) and Institution(s): WEIGEL, DETLEF Max Planck Institute for Developmental Biology, Tübingen, Germany, weigel@weigelworld.org; Max Planck Institute for Developmental Biology

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Abstract

During my undergraduate and PhD work, I was trained as a Drosophila developmental biologist. Seeing how crowded this field was getting, I switched to the study of plants as a postdoc. Work on the initiation of flowers in my own lab then led to an interest in the control of flowering time. Since flowering at the right time of year is of essence for survival in nature, this made us think much more generally about questions of adaptation and evolution. My lab thus became one of the first to exploit natural genetic variation for understanding how the environment affects plant development. In recent years, much of our work has focused on plant immunity and epigenetics. In addition to hypothesis-driven research, my group has a long history of providing new technologies and resources to the community. This has culminated in an effort to sequence the genomes of over 1,000 natural A. thaliana strains (The 1001 Genomes Project). In my presentation, I will discuss adaptation over multiple time scales, from short-term transgenerational adaptation involving transient epigenetic changes to medium-term adaptation to climate change.

Monday, August 6th

Plenary Speaker - Lucie Strader

Abstract Title: Regulation of Auxin Response Factors

Primary Author(s) and Institution(s): Lucie Strader; Washington University in St. Louis. USA

Abstract

The phytohormone auxin is a central regulator of plant growth and development. The AUXIN RESPONSE FACTOR (ARF) family of transcription factors mediates transcriptional responses to auxin and alteration of ARF activity often leads to severe developmental consequences. Using a combination of structural, molecular, and cell biology, we have identified a mechanism to regulate cellular competence to respond to auxin, based on ARF activity.

Plenary Speaker - Raphael Mercier

Abstract Title: Unleashing meiotic crossovers, from Arabidopsis to crops

Primary Author(s) and Institution(s): Raphael Mercier; INRA

Abstract

Meiotic crossovers shuffle parental genetic information, providing novel combinations of alleles on which natural or artificial selection can acts1. However, meiotic crossovers are relatively rare, typically one to three per chromosome2, limiting the efficiency of the breeding process and related activities such as genetic mapping. Using a forward genetic screen, we identified a series of genes that limit meiotic recombination in Arabidopsis, defining three anti-crossover pathways3–8. We analyzed recombination in Arabidopsis plants in which one, two, or all three of these pathways were disrupted in both pure line and hybrid contexts9. The greatest effect was observed when combining recq4 and figl1 mutations, which increased the hybrid genetic map length from 389 to 3,037 cM9. This corresponds to an unprecedented 7.8-fold increase in crossover frequency. However, it remained to be demonstrated whether crossovers could also be increased in crop species hybrids. We then explored the effects of mutating these pathways on recombination in three distant crop species, rice (Oryza sativa), pea (Pisum sativum) and tomato (Solanum lycopersium). We found that the single recq4 mutation increases crossovers ~three-fold in these crops, suggesting that manipulating RECQ4 may be a universal tool for increasing recombination in plants.

Plenary Speaker - Rainer Hedrich

Abstract Title: Venus flytrap – an excitable carnivorous plant

Primary Author(s) and Institution(s): Rainer Hedrich

Abstract

Charles Darwin over 100 years ago recognized that the Venus flytrap Dionaea muscipula living on nutrient poor soil is capturing animals. When small animals visit the trap surface and touch the trigger hairs the trap gets excited and after firing two action potentials closes. Trying to escape the encaged prey keeps on exciting the capture organ and thereby glands covering the inner trap surface trigger secretion of a digestive fluid. During prey decomposition the animal-derived nutrients are ingested. Although the concept of botanical carnivory is known since Darwin's time, due to the entire lack of genomic information, the molecular processes providing for animal feeding remain still unknown. To bridge that gap, we sequenced the genome together with transcriptome expressed in different organs of Dionaea and assembled a backbone transcriptome of the carnivorous plant. Given that with Dionaea leaves only the bi-lobed tip but not the petiole develops into a sophisticated capture organ, we focused on trap genes that become active upon contact with the animal victim. Special attention we gave to trigger hairs and glands engaged with i) generation of the action potential, ii) secretion of hydrolases, and iii) uptake of nutrients extracted from the digested animal. Serving the latter function, we spotted ion channels and transporter. Following expression of the Dionaea gland-expressed nutrient transporter genes in Xenopus oocytes, ion selective voltage changes and currents were recorded. Our studies indicate that Dionaea glands operate selective, high capacity channels and transporters to provide nutrients and osmotic potential while the feeding on a decomposing victim. During the seminar the molecular nature and mechanism of the hunting cycle of the most exciting green carnivore will be discussed.

Flower and Seed development

Plenary Speaker - Doris Wagner

Abstract Title: DEVELOPMENTAL REPROGRAMMING FOR FLOWER PRIMORDIUM FORMATION

Primary Author(s) and Institution(s): Jun Xiao 1 , Yuhee Chung 1 , Yang Zhu 1 , and DORIS WAGNER 1 1 University of Pennsylvania, Department of Biology, Philadelphia PA 19104, USA & University of Pennsylvania

Abstract

Plant development and survival is tuned in response to endogenous and environmental cues in the context of chromatin. My lab is particularly interested in the series of events that lead from cue perception to transcriptional, epigenetic and cellular reprogramming during the spatiotemporal control of flower formation. The stereotypical arrangement of flowers on the primary inflorescence stem determines the species-specific inflorescence architecture, reproductive fitness and yield. Cues that

direct initiation of flower primordia include plant hormones such as auxin and gibberellin, photoperiod, temperature, nutrient sensing, stress and more. How this multitude of possible cues is interpreted to trigger the vital (and frequently irreversible) developmental transition to making flowers remains poorly understood. I will discuss new mechanistic insight into the question how photoperiod and auxin tune the timing and positioning of flower primordium formation, respectively.

Mechanisms of Biotic Interactions
Concurrent Chair - Bart Thomma

Abstract Title: ADAPTIVE GENOME EVOLUTION IN A FUNGAL PLANT PATHOGEN

Primary Author(s) and Institution(s): Bart Thomma Wageningen University;

Abstract

Fungi cause severe crop losses and threaten food security worldwide. The soil-borne fungal pathogen Verticillium dahliae causes vascular wilt disease on hundreds of plant species, and disease control is challenging because resistance in plants is rare. Moreover, V. dahliae has a flexible genome allowing it to escape host immunity and maintain aggressiveness. Through comparative population genomics we try to unravel mechanisms to establish genomic diversity that is essential for adaptive genome co-evolution during the continued arms race with host plants. These analyses have revealed lineage-specific regions within V. dahliae genomes that are important for virulence. Interestingly, these regions are enriched for in planta-expressed effector genes encoding secreted proteins that enable host colonization. Some of these effectors enable host specificity.

Mechanisms of Biotic Interactions
Invited Speaker - Wenbo Ma

Abstract Title: INDUCTION OF PLANT SMALL RNAs WITH ANTIMICROBIAL ACTIVITY AND THEIR SUPPRESSION BY PHYTOPHTHORA EFFECTORS

Primary Author(s) and Institution(s): WENBO MA 1 , YINGNAN HOU 1 , YI ZHAI 1 , WENWU YE 2 , JINBIAO MA 3 , JIXIAN ZHAI 4; Center for Plant Cell Biology, Department of Microbiology and Plant Pathology, University of California Riverside, Riverside, CA 92521 USA. 2 Department of Plant Pathology, Nanjing Agricultural University, Nanjing 210095, China. 3 State Key Laboratory of Genetic Engineering, Department of Biochemistry, Institute of Plant Biology, School of Life Sciences, Fudan University, Shanghai 200438, China. 4 Institute of Plant and Food Science, Department of Biology, Southern University of Science and Technology, Shenzhen, China.; University of California, Riverside

Abstract

Plants have evolved complex defense mechanisms that must be defeated by pathogens to establish infection. The destructive eukaryotic pathogen Phytophthora encodes RNAi suppressors, but it remains unknown whether they target a specific host RNAi pathway that confers resistance. We show that Phytophthora infection induces the production of diverse secondary small interfering RNAs (siRNAs) in Arabidopsis hosts. Instead of regulating endogenous genes, some of these siRNAs silence target genes in Phytophthora during natural infection. Introduction of a plant siRNA in Phytophthora leads to developmental deficiency and reduced virulence while Arabidopsis mutants defective in secondary

siRNA biogenesis pathway exhibit enhanced disease susceptibility. Notably, a Phytophthora RNAi suppressor PSR2 specifically inhibits secondary siRNA biogenesis in Arabidopsi s, thereby enhancing plant susceptibility. These findings together reveal RNAi as an antimicrobial mechanism targeting eukaryotic pathogens and establish a new paradigm of plant-pathogen arms race including both defense and counter-defense components.

Mechanisms of Biotic Interactions
Concurrent Speaker - Hye-Young Lee

Abstract Title: MONITORING OF BACTERIAL TYPE III EFFECTOR DELIVERY IN PLANT CELLS USING SPLIT FLUORESCENT PROTEIN SYSTEM

Primary Author(s) and Institution(s): Hye-Young Lee 1 , Jongchan Woo 3 , Savithramma P. Dinesh-Kumar 2 , Doil Choi 1 , Eunsook Park 1 1 Department of Plant Science, College of Agriculture and Life Science, Seoul National University, Seoul 08826, Republic of Korea 2 Department of Plant Biology and the Genome Center, College of Biological Sciences, University of California, Davis, CA USA 95616 3 Department of Bioindustry and Bioresource Engineering, Sejong University, Seoul 05006, Republic of Korea

Abstract

Pathogenic gram-negative bacteria deliver effector proteins (T3E) into host cells to attenuate the host immune responses using the type III secretion system (T3SS). Localization of several T3Es at various subcellular compartments have been shown in several studies, providing clues of their molecular mechanism to modulate biological processes of the host cells. We recruited an engineered self-assembling split super-folder green fluorescent protein (sfGFP OPT) system to monitor the subcellular localization of the T3Es, which are delivered through the bacterial T3SS into plant cells. The T3E fused to 11th β-strand of sfGFP secreted from Pseudomonas syringae into plant cells can be assembled with sfGFP1-10 fragment (sfGFP1-10 OPT) expressed in plant cell. Consequently, the reconstituted sfGFP led to fluorescence emission at the specific target compartment of the T3E. We will introduce a number of Arabidopsis thaliana transgenic lines expressing sfGFP1-10 OPT in the various subcellular compartments to facilitate the localization of sfGFP11-tagged effectors delivered from bacteria. The versatile split sfGFP OPT system will facilitate a better understanding of dynamic plant-microbe interaction in plant immunity.

Mechanisms of Biotic Interactions
Concurrent Speaker - Tatsuya Nobori

Abstract Title: TRANSCRIPTOME LANDSCAPE OF BACTERIA UNDER PLNAT IMMUNITY

Primary Author(s) and Institution(s): TATSUYA NOBORI and KENICHI TSUDA Max-Planck Institute for Plant Breeding Research; Max-Planck Institute for Plant Breeding Research

Abstract

Since the 1950s, extensive studies have revealed the mechanisms of plant immune activation against pathogens. However, it is largely unknown how plant immunity affects global metabolisms of pathogens

to inhibit their growth. In case of bacterial pathogens, a major bottleneck is a difficulty in determining the global bacterial transcriptome and metabolic responses in planta . Here, using the model plant Arabidopsis thaliana and the foliar bacterial pathogen Pseudomonas syringae , we developed a pipeline that allows for in planta high-quality bacterial transcriptome analysis with RNA-seq. We examined a total of 27 combinations (100 samples) of plant immunity and bacterial virulence mutants to gain an unprecedented insight into the bacterial transcriptomic responses in planta . The data let us identify specific bacterial transcriptomic signatures that are linked to bacterial growth inhibition during plant immune activation. Among them, we found a P. syringae gene that plays an important role in bacterial growth restriction under plant immunity. This study illuminates the enigmatic mechanisms of bacterial growth inhibition by plant immunity. We will also discuss the in planta transcriptomes of a wide variety of commensal bacteria naturally associated with Arabidopsis , shedding light on the commonalities and differences in the impact of plant immunity on different bacterial species.

Mechanisms of Biotic Interactions
Concurrent Speaker - Kirankumar Mysore

Abstract Title: INSERTIONAL MUTAGENESIS OF MEDICAGO TRUNCATULA AND ITS UTILIZATION TO IDENTIFY NOVEL SOURCES OF RESISTANCE AGAINST ASIAN SOYBEAN RUST

Primary Author(s) and Institution(s): KIRANKUMAR S. MYSORE, UPINDER GILL, YASUHIRO ISHIGA, SRINIVASA RAO UPPALAPATI, JIANGQI WEN Noble Research Institute, LLC.; Noble Research Institute

Abstract

Tobacco retrotransposon, Tnt1 , has been used to mutagenize and tag the whole genome of a model legume, Medicago truncatula . Tnt1 is very active and transpose into, on average, 50 different locations during M. truncatula tissue culture. Mutations induced by Tnt1 insertion are stable during seed to seed generation. We have generated over 20,000 independent Tnt1 -containing lines encompassing ~500,000 insertion events. Over 400,000 Tnt1 flanking sequence tags (FSTs) have been recovered and a database has been established. The range and diversity of mutant phenotypes obtained to date suggest that M. truncatula offers a great opportunity to dissect symbiotic and developmental pathways for comprehensive understanding of legume biology. A forward genetics approach using Tnt1 tagged M. truncatula lines has been established (Fig. 1) to identify genes that confer nonhost resistance to Asian Soybean Rust pathogen, Phakopsora pachyrhizi. Several M. truncatula Tnt1 mutants with altered response to P. pachyrhizi have been identified and being characterized. Characterization of some of these mutants will be presented. For example, an irg1 (i nhibitor of r ust g erm-tube differentation 1) mutant, which has a mutation in a Cys(2)His(2) zinc finger transcription factor, inhibited pre-infection structure differentiation of P. pachyrhizi and several other biotrophic pathogens.

Coding and Decoding Calcium Signals
Concurrent Chair - Sheng Luan

Abstract Title: REGULATION OF NUTRIENT HOMEOSTASIS BY THE CBL-CIPK CALCIUM DECODING NETWORK

Primary Author(s) and Institution(s): Sheng Luan, University of California at Berkeley; UC Berkeley

Abstract

Plants constantly monitor nutrient status in the soil and maintain nutrient homeostasis by controlling ion transport across the plasma membrane (PM, for uptake) and vacuolar membrane (tonoplast, for storage). However, the signaling mechanism linking nutrient status in the soil and membrane transport in plants is largely unknown. Our lab discovered CBL-CIPK calcium signaling network that functions in a number of cellular pathways including nutrient sensing. In addition to the CBL-CIPK pathway that targets a voltage-gated K-channel in PM in response to low-K status, our more recent work further identified a complex CBL-CIPK network that regulates vacuolar transport of a number of mineral nutrients. These studies have thus connected the CBL-CIPK signaling mechanism to the regulation of transport activities across both PM and tonoplast, the two most important sites for nutrient homeostasis in plant cells. We will present data to establish a major theme in cell signaling in the context of plant nutrition: a large

network of “CBL-CIPK-transporter” interactions couples the environmental signals (changes in nutrient status) to the regulation of membrane transport and nutrient homeostasis in plant cells. The specific data will include study of the CBL-CIPK network for the regulation of AKT1 K-channel in the root hair model in response to K-deficiency; the CBL-CIPK pathways controlling Mg vacuolar sequestration under high Mg condition; and the coordination between the PM and vacuolar pathways in the regulation of nutrient homeostasis. The presented work aims to deliver audience a comprehensive view on the integration of signaling network and the transport network to control the nutrient distribution and utilization in plants to allow them to adapt to the constantly changing nutrient status in the soil.

Coding and Decoding Calcium Signals
Invited Speaker - Myriam Charpentier

Abstract Title: Role of Nuclear Calcium Channel Beyond Symbioses

Primary Author(s) and Institution(s): Myriam Charpentier John Innes Centre, Cell and Developmental Biology Department, Colney Lane, NR47UH, Norwich, UK; John Innes Centre

Abstract

Nuclear calcium signalling is known to be essential in legumes to promote associations with nitrogen fixing bacteria and phosphate delivering arbuscular mycorrhizal fungi. Using a wide range of approaches, we have discovered a number of ion channels located at the nuclear envelope that are responsible for symbiotic nuclear calcium release. Among them, we defined the first plant nuclear-associated calcium channels encoded by cyclic nucleotide gated channels (CNGC15s). The CNCG15s sit at the nuclear envelope in a complex with a potassium permeable channel (DMI1), also required for the generation of the symbiotic nuclear calcium signals. Interestingly, CNGC15s and DMI1 are conserved across all land plants, including non-symbiotic species, strongly suggesting that they have other functions during plant development. The function of this nuclear calcium channel complex beyond root legume symbioses will be presented.

Coding and Decoding Calcium Signals
Concurrent Speaker - Michael Wudick

Abstract Title: CORNICHON SORTING AND REGULATION OF GLR CHANNELS UNDERLIES POLLEN TUBE CALCIUM HOMEOSTASIS

Primary Author(s) and Institution(s): MICHAEL M. WUDICK 1,3 , MARIA TERESA PORTES 1,3 , ERWAN MICHARD 1,3 , PAUL ROSAS-SANTIAGO 2 , MICHAEL A. LIZZIO 1 , CUSTÓDIO OLIVEIRA NUNES 1,3 , CLÁUDIA CAMPOS 3 , DANIEL SANTA CRUZ DAMINELI 1 , JOANA C. CARVALHO 3 , PEDRO T. LIMA 3 , OMAR PANTOJA 2 , JOSÉ A. FEIJÓ 1,3 1 University of Maryland Dept. of Cell Biology and Molecular Genetics, 0118 Bioscience Research Building, 4066 Campus Drive, College Park, MD 20742-5815, USA 2 Instituto de Biotecnología, Universidad Nacional de Autónoma de México, Cuernavaca, Morelos 62250, México 3 Instituto Gulbenkian de Ciência, Rua da Quinta Grande 6, Oeiras, 2780-156, Portugal; University of Maryland

Abstract

Compared to animals, evolution of plant Ca 2+ physiology has led to a loss of proteins for influx and small ligand-operated control of cytosolic Ca 2+ , leaving many Ca 2+ mechanisms unaccounted for. Here, we show a mechanism for Glutamate Receptor-Like (GLR) sorting and activation by CORNICHON HOMOLOG (CNIH) proteins by means of reverse genetics, microscopy and electrophysiology. Single mutants of pollen-expressed At GLRs showed growth and Ca 2+ flux phenotypes expected for plasma membrane Ca 2+ channels. However, higher order mutants of At GLR3.3 revealed phenotypes contradicting this assumption. These discrepancies could be explained by sub-cellular At GLR localization and we explored the implication of At CNIHs in this sorting. We found that At GLRs interact with At CNIH pairs, yielding specific intracellular localizations. At CNIHs further trigger At GLR activity in mammalian cells without any ligand. These results reveal a regulatory mechanism underlying Ca 2+ homeostasis by sorting and activation of At GLRs by At CNIHs.

Coding and Decoding Calcium Signals
Concurrent Speaker - Massimiliano Corso

Abstract Title: CCX2 PLAYS A PIVOTAL ROLE IN THE REGULATION OF ER AND CYTOSOL CA2+ DYNAMICS UPON OSMOTIC STRESS IN ARABIDOPSIS

Primary Author(s) and Institution(s): MASSIMILIANO CORSO 1 , FABRIZIO G. DOCCULA 2 , J. ROMÁRIO F. DE MELO 1 , ALEX COSTA 2,3 , NATHALIE VERBRUGGEN 1 1;Laboratory of Plant Physiology and Molecular Genetics, Université Libre de Bruxelles, 1050 Brussels, Belgium; 2 Department of Biosciences, University of Milan, 20133 Milan, Italy; 3 Institute of Biophysics, Consiglio Nazionale delle Ricerche, 20133 Milan, Italy

Abstract

Given the lack of a nervous system in plants, Ca 2+ signals are of vital importance for perceiving environmental stimuli and adaptive responses to environmental stresses. We recently characterized the endoplasmic reticulum (ER)-localized Arabidopsis thaliana CATION/Ca 2+ EXCHANGER2 (CCX2) . AtCCX2 knockout and overexpressing mutants were respectively less and more tolerant to osmotic stress than the wild-type (WT). In addition, AtCCX2 partially suppresses the Ca 2+ sensitivity of the low-affinity Ca 2+ uptake K667 yeast triple mutant, hence supporting its role in Ca 2+ transport. Moreover, NES-YC3.6 and CRT-D4-ER Cameleon Ca 2+ sensors revealed that the absence of AtCCX2 activity results in decreased cytosolic and increased ER Ca 2+ concentrations in comparison with WT and the gain-of-function mutants upon osmotic stress. Our results suggested that AtCCX2 is directly involved in the control of Ca 2+ fluxes between the ER and the cytosol and plays a key role in the ability of plant to cope with osmotic stresses. This work sheds light on an as-yet uncharacterized and key player that tunes intracellular Ca 2+ homeostasis, with particular significance for plants under salt stress.

Coding and Decoding Calcium Signals
Concurrent Speaker - Valérie Cotelle

Abstract Title: CROSS-REGULATION BETWEEN THE CALCIUM-DEPENDENT PROTEIN KINASE CPK3 AND 14-3-3 PROTEINS DURING SPHINGOLIPID-INDUCED CELL DEATH IN ARABIDOPSIS

Primary Author(s) and Institution(s): VALERIE COTELLE 1 , MELANIE ORMANCEY 1 , AGNIESZKA PAWELEK 2 , EUGENIE ROBE 1 , CAROLE PICHEREAUX 3 , CHRISTIAN BRIERE 1 , SABINE GRAT 1 , PATRICE THULEAU 1 , CHRISTIAN MAZARS 1 1 Laboratoire de Recherche en Sciences Végétales, UMR 5546 CNRS Université de Toulouse UPS, BP 42617, F-31326, Castanet-Tolosan, France 2 Nicolas Copernicus University, Chair of Plant Physiology and Biotechnology, Lwowska St. 1, PL 87-100 Torun, Poland 3 Fédération de Recherche 3450 Agrobiosciences Interactions et Biodiversité, Plateforme Protéomique Génopole Toulouse Midi- Pyrénées, CNRS, UMR 5089, Institut de Pharmacologie et de Biologie Structurale, BP 64182, F-31077, Toulouse, France; Laboratoire de Recherche en Sciences Végétales Université de Toulouse CNRS

Abstract

Calcium-dependent protein kinases (CDPKs) are calcium sensors that play pivotal roles in plant development and stress responses. They have the unique ability to translate intracellular Ca 2+ signals

into reversible phosphorylation events of various substrates. Recent studies have revealed roles for the coordinated action of CDPKs and 14-3-3 proteins in regulating diverse aspects of plant biology. Our previous work showed that CPK3, an Arabidopsis CDPK, is associated in vivo with 14-3-3 proteins. We further demonstrated that CPK3 is a positive regulator of programmed cell death (PCD) mediated by two sphingoid long chain bases (LCBs), dihydrosphingosine (dDHS) and phytosphingosine (t18, PHS) in Arabidopsis. During this process, PHS induces activation of CPK3, which phosphorylates its partners, the 14-3-3s, on a conserved serine residue located at the dimer interface. This phosphorylation which is likely to induce 14-3-3 monomerization leads to the disruption of the CPK3/14-3-3 complex and to CPK3 cleavage. While modulation of this complex has been observed during LCB-mediated PCD, the molecular mechanisms underlying CPK3 association with 14-3-3 proteins are still unknown. Using biochemical approches, we show here that CPK3 directly binds to Arabidopsis 14-3-3s with various affinities in a calcium- and phospho-dependent manner.

Integrative System Biology
Concurrent Chair - Rodrigo Gutierrez

Abstract Title: The transcriptional landscape of the nitrate response of Arabidopsis roots

Primary Author(s) and Institution(s): Rodrigo A. Gutiérrez; Millennium Institute for Integrative Biology. FONDAP Center for Genome Regulation. Molecular Genetics and Microbiology Department. Facultad de Ciencias Biológicas. P. Universidad Católica de Chile.

Abstract

Understanding how plants sense and respond to changes in nitrogen (N) availability is important for biotechnological applications to improve nitrogen-use efficiency. Plants can adjust their capacity to acquire and use different forms of N in a range of concentrations by adjusting expression and function of a myriad of genes. Nitrate is a potent nutrient signal that regulates expression of hundreds of genes in Arabidopsis thaliana. Integrating mRNA profiling, genome-wide RNA polymerase II (RNPII) ChIP-Seq and DNase-seq we established the relationship between RNPII occupancy and chromatin accessibility in response to nitrate in Arabidopsis root organs. Genome-wide mapping of DNase I hypersensitive sites (DHSs) and genomic footprinting allowed us to identify regulatory elements controlling gene expression in response to nitrate. Integrated analyses of the data lead us to discover new nitrate cis-elements, map key TF regulatory interactions and describe the intricate transcriptional wiring evoked by nitrate treatments. We identified new mechanisms, regulatory genes as well as positioned the contribution of known regulatory factors in gene networks mediating changes in gene expression, metabolic and developmental adaptations in response to nitrate.

Integrative System Biology
Concurrent Speaker - Blaise Pascal Muvunyi

Abstract Title: Comparative genome and functional analysis of polyamine and ethylene pathway genes, implication for crop improvement

Primary Author(s) and Institution(s): BLAISE PASCAL MUVUNYI, Fan Wu, Jiyu Zhang; Wang Yanrong; Lanzhou University

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Abstract

Both polyamine (mainly putrescine, spermine and spermidine) and ethylene pathway genes are intrinsically involved in the regulation of plant abiotic and biotic stress responsive mechanism. However, the two pathways compete for the same substrate, Synthase Methionine (SAM) and Synthase Adenosyl Methionine Decarboxylase (SAMDC) for the activity of their respective genes and enzymes. We conducted a comparative wide genome survey and functional analysis of the key genes from both pathways to elucidate their relationship under evolutionary and functional aspects. In total, we characterized from Cleistogenes songorica 76 genes involved in the biosynthesis pathway of ethylene and polyamines, and grouped them into eight clades based on their conserved protein domain nature. Motif and conserved domain analysis revealed striking signatures of plant abiotic stress tolerance mechanism in genes from both pathways. Multiple sequence alignment did not indicate any consensus amino acid residue among the two pathways, but within the same gene families. The up-stream promoter region analysis of key genes found polyamine genes slightly richer into drought responsive (MBS), Abscisic acid responsive (ABRE) and LTR (low temperature) cis -regulatory elements compared to ethylene genes. More, expression analysis and validation with quantitative RT-PCR of these key genes from both pathways showed that only polyamines genes are induced by both drought and ABA, while ethylene genes are only responsive to drought in roots and leaves tissues. Further, Arabidopsis lines expressing CsSAMDC2 showed enhanced salt and drought resistance as well as an improved activity of gene from both pathways. Surprisingly, exogenous application of ABA under salt stress did not affect the expression ethylene pathways. This study provides a comprehensive outline of C. songorica polyamine and ethylene pathway genes, and novel insights into the expansion and the function of genes from this family.

Integrative System Biology

Concurrent Speaker - Kallyne Ambrosio Barros

Abstract Title: DIURNAL PATTERNS OF GROWTH AND TRANSIENT RESERVES OF SINK AND SOURCE TISSUES ARE AFFECTED BY COLD NIGHTS IN BARLEY PLANTS

Primary Author(s) and Institution(s): KALLYNE A BARROS 1 , ALBERTO A ESTEVES-FERREIRA 1 , MASAMI INABA 1 , RONAN SULPICE 1 1 National University of Ireland -Galway, Ryan Institute; Plant AgriBiosciences Research Centre, Plant Systems Biology Lab, Galway, Ireland

Abstract

Transient carbon reserves are crucial for night maintenance of growth. The main carbohydrate reserve for most plants is starch, however, barley can also accumulate sucrose malate and fructans. To understand how the carbon is utilized in response to cold, barley plants were grown in a combination of cold days and/or nights. Contrary to Arabidopsis, elongation rates were affected by both day and night temperatures. Most carbon reserves used at night were stored in both young and mature blades and not in the sheaths. Sucrose and fructan contents were increased by cold during the day, but cold nights did not affect their accumulation. Fructans contributed little to night growth. Sucrose was the main carbohydrate supplying growth (30-60%) in all conditions, followed by starch (10-25%) and malate (10-30%). Starch synthesis and degradation were strongly inhibited by cold in the daytime, but surprisingly also under warm day and cold night. It suggests that the inhibition of growth observed during cold nights repressed starch synthesis during the day. Altogether our data suggest that, contrary to Arabidopsis, barley growth machinery is sensitive to cold night, and that it negatively feedback on the accumulation of transient carbon stores during the day.

Integrative System Biology

Concurrent Speaker - Camila Rodriguez

Abstract Title: IDENTIFICATION OF DEVELOPMENT-REGULATED MICRORNA/TARGET MODULES IN ARABIDOPSIS THALIANA ROOTS

Primary Author(s) and Institution(s): RODRÍGUEZ-MONROY CAMILA 1 . RIQUELME, A FERNANDO 2 ., SAAVEDRA, GABRIELA 2 ., LARRAIN, LUIS F 1 ., ELENA, VIDAL A 1 .,; Universidad Mayor

Abstract

1 Millennium Institute for Integrative Systems and Synthetic Biology (MIISSB), Universidad Mayor, Santiago, Chile. 2 Centro de Genomica y Bioinformatica, Facultad de Ciencias, Universidad Mayor. The plant root system senses, explores and uptakes nutrients from the soils. At a given time, root system architecture (RSA) is the result of the integration of external cues experienced by the plant into intrinsic developmental programs. Thus, plasticity of RSA is a dynamic process that changes during plant life cycle according to specific plant requirements to optimize growth in heterogenous and changing environments. Despite the importance of roots for plant growth and productivity, little is known on root plasticity regulators and their impact during different stages of plant development. This is of paramount importance for developing biotechnological applications that target the improvement of root systems

for growth in stress conditions such as limiting nutritional conditions. Post-transcriptional gene silencing by small RNAs (sRNAs) is a key determinant of plant developmental processes. To date, the patterns of expression of some sRNAs have been studied in detail during Arabidopsis development in shoot tissue and have been shown to be crucial for timing of phase change. Although root-expressed sRNAs controlling primary and lateral root growth have been identified, their role during specific stages of plant development, the gene regulatory networks (GRNs) that they control, or their role in adaptation to environmental conditions have not yet been identified. In this work, we predicted Arabidopsis microRNA targets using bioinformatics programs and experimental data from available degradome-seq analyses and we analyzed their developmental expression patterns using root transcriptomics datasets. In addition we were able to obtain transcriptomic analyses from our own Arabidopsis root sRNA-seq data, thus allowing us to identify and experimentally confirm diverse development-regulated microRNA/TARGET modules in roots. Using available interactomics data, together with our results, we generated miRNA-controlled GRNs expressed at different developmental time points in the root.
FONDECYT #1170926, Millennium Institute for Integrative Systems and Synthetic Biology (MIISSB).

Crop genomics and genome editing
Concurrent Chair - Ksenia Krasileva

Abstract Title: Identifying genome editing targets to enhance plant immunity

Primary Author(s) and Institution(s): Elisha Thynne 1 , Andrew Deatker 1,2 , Erin Baggs 2,3 , KSENIA V KRASILEVA 1,2,3 1 The Sainsbury Laboratory, Norwich NR4 7UH, United Kingdom 2 Department of Plant and Microbial Biology, University of California, Berkeley, CA 94720 USA 3 Earlham Institute, Norwich NR4 7UZ, United Kingdom; Earlham Institute

Abstract

P athogens manipulate plant cells to establish infection by suppressing plant immunity and creating a favourable nutrient-rich environment. All plant pathogens secrete effector molecules that target and modify plant proteins. In turn, plants monitor for the presence of effectors either directly or indirectly. Identification and manipulation of plant susceptibility components can provide a long-lasting solution against pathogens. A major class of plant immune receptors is Nucleotide Binding Leucine Rich Repeat domain (NLR) family proteins. A recent breakthrough - the identification of NLRs with integrated exogenous domains (NLR-IDs) that serve as 'bait' for the pathogens - opened new ways of identifying plant susceptibility components through bioinformatics screens that look for homologs of IDs. We have analyzed 65,000 NLRs from flowering plants and identified over 3,000 putative NLR-IDs. We mapped the homologs of IDs to the genomes of Arabidopsis, Brachypodium, tomato, rice, and wheat to identify genes and pathways potentially targeted by the pathogens. The pathways enriched in potential pathogen baits included sugar and lipid metabolism, as well as hormones and secretion. We also identified multiple genes involved in PAMP-triggered immunity to be fused to NLRs. These genes and pathways represent prime targets for modification by genome editing to produce disease resistant crops.

Crop genomics and genome editing
Invited Speaker - Brian Staskawicz

Abstract Title: GENOME EDITING AGRICULTURAL CROPS FOR SUSTAINABLE DISEASE RESISTANCE

Primary Author(s) and Institution(s): BRIAN STASKAWICZ Department of Plant and Microbial Biology and the Innovative Genomics Institute, University of California, Berkeley, USA; University of California, Berkeley, CA 94720 USA

Abstract

In our laboratory, we are developing genomic strategies are part of a multi-pronged approach to develop durable disease resistance in agricultural crops. I will discuss our current data on the identification of host susceptibility genes in several crop species and present our recent results on the use of genome editing tools to create mutations in host susceptibility genes that give rise to disease resistant crops. Furthermore, I will discuss our efforts to employ DNA-free genome editing and our strategies to increase the frequency of homologous recombination in both plant protoplasts and immature embryos of wheat and rice. Finally, I will present an integrated approach to develop durable disease resistance in agricultural crops that employs multiple mechanisms of resistance .

Crop genomics and genome editing
Concurrent Speaker - Goetz Hensel

Abstract Title: SITE-DIRECTED MUTAGENESIS USING RNA-GUIDED CAS9 ENDONUCLEASE TO ALTER IMPORTANT TRAITS OF BARLEY

Primary Author(s) and Institution(s): GOETZ HENSEL 1 , POUNEH POURAMINI 1 , STEFAN HIEKEL 1 , PHILLIP REUTER 2 , STEFFEN BAIER 2 , SEBASTIAN MÜLLER 3 , KLAUS PILLEN 3 and JOCHEN KUMLEHN 1 1 Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben, Plant Reproductive Biology, Seeland/OT Gatersleben, Germany 2 Friedrich-Alexander-University, Division of Biochemistry, Department Biology, Erlangen, Germany 3 Martin Luther University Halle Wittenberg, Institute of Agricultural and Nutritional Sciences, Halle, Germany; Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)

Abstract

Barley represents one of the major crops grown worldwide and is utilized for the production of feed, food and drinks. It has been used as genetic model system because of its true diploidy along with the similarity of its genome to those of other small-grain cereals. Targeted genome modification triggered by customizable endonucleases offers novel possibilities for the elucidation of gene function and the improvement of crop performance. RNA-guided Cas9 endonuclease-mediated mutagenesis has been established in many crop species and is now being routinely used to produce knock-out lines. After establishment of an efficient pipeline for target motif selection and the pre-validation of guide-RNA/Cas9 constructs, we have altered genes which are essential for barley malting quality, flowering time and spike architecture. Beside indels in the target motifs, also precise deletions between two guide-RNA target sites were detected. The typically multiple mutant alleles present in primary gRNA/Cas9 transgenics were efficiently resolved and fixed via production of doubled haploids using embryogenic pollen cultures. Either phenotypic or enzymatic analyses mostly revealed the expected consequences of mutant alleles at the plant level. The improvement of malting quality which was first obtained in the model cultivar Golden Promise was then extended to elite malting barley.

Crop genomics and genome editing
Concurrent Speaker - Jae-Young Yun

Abstract Title: PRECISION GENOME ENGINEERING THROUGH ADENINE BASE EDITING IN PLANTS

Primary Author(s) and Institution(s): YOUJIN SHIN, JAHEE RYU, MINKYUNG CHOI, BEUM-CHANG KANG, SANG-TAE KIM, JIN-SOO KIM, and JAE-YOUNG YUN **Article in press (Nature Plants) regarding this study Affiliations for all listed authors: Center for Genome Engineering, Institute for Basic Science, Daejeon, Republic of Korea.

Abstract

CRISPR genome editing in plants holds promise as a revolutionary tool for basic research and biotechnology. Canonical CRISPR nucleases cleave DNA in a targeted manner resulting in small indels at target sites. In plant research, however, inducing point mutations rather than indels remains a challenge, although point mutagenesis is one of the key strategies to achieve crop improvement and to decode natural genomic variations. The recent development of adenine base editors (ABEs), composed of the Cas9 nickase and engineered tRNA adenosine deaminases, has enabled efficient programmable A/T-to-G/C base conversions in eukaryotic cells. For in planta ABE applications, we tested ABEs with several plant-specific expression systems. We found that a plant-compatible ABE system can be successfully applied to Arabidopsis plants via agrobacterium-mediated transformation to obtain organisms with desired phenotypes. For example, targeted precise A-to-G substitutions generated a single amino-acid change in the FT protein or mis-splicing of the PDS3 RNA transcript with germline transmission of such edited alleles, and we could thereby obtain transgenic plants with late flowering and albino phenotypes, respectively. Taken together, we demonstrate 'proof-of-concept' in planta ABE applications that can lead to induced neo-functionalization or altered mRNA splicing, opening up new avenues for plant genome engineering and biotechnology. **Article in press (Nature Plants) regarding this study

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Crop genomics and genome editing
Concurrent Speaker - Tianwang Wen

Abstract Title: TWO LINKAGE LOCI AFFECT THE COLOUR AND AGRONOMIC TRAITS OF BROWN FIBRE (GOSSYPIUM HIRSUTUM)

Primary Author(s) and Institution(s): TIANWANG WEN 1 , MI WU 1 , CHAO SHEN 1 , BIN GAO 1 , DE ZHU 1 , XIANLONG ZHANG 1 , CHUNYUAN YOU 2 and ZHONGXU LIN 1 . 1 National Key Laboratory of Crop Genetic Improvement, College of Plant Science and Technology, Huazhong Agricultural University, Wuhan, China 2 Cotton Research Institute, Shihezi Academy of Agriculture Science, Shihezi, Xinjiang, China; Huazhong agricultural university

Abstract

Brown fibre cotton is an environmental-friendly resource that plays a key role in the textile industry. However, the fibre quality and yield of natural brown cotton are poor, and fundamental research on brown cotton is relatively scarce. To understand the genetic basis of brown fibre cotton, we constructed

linkage and association populations to systematically examine brown fibre accessions. We fine-mapped the traditional brown fibre region, Lc1, and dissected it into 2 linkage loci, qBFA07-1 and qBF-A07-2. The qBF-A07-1 locus mediates the initiation of brown fibre production, whereas the shade of the brown fibre is affected by the interaction between qBF-A07-1 and qBFA07-2. Gh_A07G2341 and Gh_A07G0100 were identified as candidate genes for qBF-A07-1 and qBF-A07-2, respectively. Haploid map of Lc1 region showed that most tetraploid modern brown cotton accessions exhibit the introgression signature of Gossypium barbadense. We identified 10 quantitative trait loci (QTLs) for fibre yield and 19 QTLs for fibre quality through a genome-wide association study (GWAS) and found that qBF-A07-2 negatively affects fibre yield and quality through an epistatic interaction with qBFA07-1. This study sheds light on the genetics of fibre colour and lint-related traits in brown fibre cotton, which will guide the elite cultivars breeding of brown fibre cotton.

Cell Walls

Concurrent Chair - Ying Gu

Abstract Title: Regulation of cellulose synthesis through exocytosis and endocytosis

Primary Author(s) and Institution(s): YING GU, Shundai Li, Xiaoyu Zhu Department of Biochemistry and Molecular Biology, Pennsylvania State University, University Park, PA 16802; Pennsylvania State University

Abstract

Cellulose is synthesized at the plasma membrane by cellulose synthase complexes (CSCs). By a combination of proteomic, live-cell imaging, and genetic approaches, we set out to decipher how the steady level celluose synthase can be regulated by endocytosis, exocytosis, and recycling. Here we report that the de novo secretion of CSCs is mediated by cooperation among a recently identified cellulose synthase interacting protein 1 (CSI1), exocyst complex, and a plant-specific protein PATROL1 in Arabidopsis thaliana . Upon delivery of CSCs to the plasma membrane, they synthesize cellulose microfibrils in a direction mirroring the underlying cortical microtubule in a CSI1-dependent manner. The retrieval of CSCs from the PM depends on clathrin-mediated endocytosis by two separate complexes: Adaptor complex (AP2) and TPLATE/TSET complex. Cellulose synthase protein represents a cargo protein that is not present in yeast and mammalian cells. Therefore, plants offer unique opportunities to characterize the function of endocytosis and exocytosis that may provide insights into the evolution of protein trafficking in eukaryotes.

Cell Walls

Invited Speaker - Simon Turner

Abstract Title: The role of protein modification by S-Acylation during cellulose synthesis

Primary Author(s) and Institution(s): SIMON TURNER , MANOJ KUMAR, PAUL CARR The University of Manchester; University of Manchester

Abstract

Cellulose is synthesised at the plasma membrane by a very large membrane-bound protein complex, the cellulose synthase complex (CSC). The process is characterised by the unique way the CSC moves

through the plane of the plasma membrane as it generates the cellulose microfibrils while maintaining the integrity of the membrane. This complex contains at least 18 subunits, the CESA proteins that constitute the catalytic subunits. We have recently shown that the CESA proteins are extensively modified by S-acylation that involves the addition of fatty acid chains onto cysteine residues. This modification profoundly increases the hydrophobicity of the CSC and is likely to contribute to locking the complex within the plasma membrane. In order to better understand the function of S-acylation, we have been characterising the modification sites in both CESA proteins and in other proteins associated with cellulose synthesis such as the endoglucanase Korrigan. We will report our latest findings on the number and position of S-acyl modifications and how these modifications affect the assembly and trafficking of the CSC and the interaction between CESA proteins and other proteins required for cellulose synthesis.

Cell Walls

Concurrent Speaker - Markus Pauly

Abstract Title: IN VITRO SYNTHESIS OF PLANT CELL WALL HEMICELLULOSES

Primary Author(s) and Institution(s): MARKUS PAULY , BALAKUMARAN CHANDRASEKAR, NIKLAS GAWENDA, FABIAN STRITT, CATALIN VOINICIUC Instiute for Plant Cell Biology and Biotechnology, Heinrich-Heine University Düsseldorf, Germany; HHU

Abstract

Plant cell walls represent complex, sophisticated materials that encapsulate all plant cells. The dominant component of these walls are polysaccharides among them various hemicelluloses. In recent years many enzymes involved in the synthesis of this class of polysaccharides have been identified [1,2]. However, many basic questions remain unanswered such as what determines the degree of polymerization of the nascent polysaccharides or how is the degree of substitution determined during synthesis? To address these questions we chose a synthetic biology approach by reconstituting the biosynthetic machinery in a heterologous (non-hemicellulose containing) host – yeast. For this purpose, a large number of plant polysaccharide biosynthetic genes were transformed into yeast including not only glycosyltransferases, but also potential co-factors. Our results indicate that we are indeed able to synthesize plant hemicelluloses in yeast, albeit with a different structure than those observed in plants. Fine-tuning of the plant biosynthetic machinery in yeast allows us to modify the hemicellulose structure. [1] Pauly M, Keegstra K, Biosynthesis of the plant cell wall matrix polysaccharide xyloglucan, Annual Review of Plant Biology, 2016 , 67(1): 235-259 [2] Pauly M, Gille S, Liu L, Mansoori N, de Souza A, Schultink A, Xiong G, Hemicellulose biosynthesis, Planta, 2013 , 238 (4), 627-642

Cell Walls

Concurrent Speaker - June Kwak

Abstract Title: CELLULAR PRECISION FOR CELL SURFACE INTEGRITY AND PLANT FITNESS

Primary Author(s) and Institution(s): YUREE LEE, 1 TAEK HAN YOON, 1 JIYOUN LEE, 1 SO YEON JEON, 1 JAE HO LEE, 1 MI KYOUNG LEE, 1 HUIZE CHEN, 1 JU YUN, 1 SE YUN OH, 1 XIAOHONG WEN, 2 HUI KYUNG CHO, 1 HYUNGGON MANG, 1 AND JUNE M. KWAK 1,2 1 Center for Plant Aging Research, Institute for Basic Science, Daegu 42988, Republic of Korea 2 Department of New Biology, DGIST, Daegu 42988, Republic of Korea

Abstract

The cell wall, a defining feature of plants, provides a rigid structure critical for bonding cells together. To overcome this physical constraint, plants must process cell wall linkages during growth and development. However, little is known about the mechanism guiding cell-cell detachment and cell wall remodeling. Here, we identify two neighboring cell types in *Arabidopsis*that coordinate their activities to control cell wall processing, thereby ensuring precise abscission to discard organs. One cell type produces a honeycomb structure of lignin, which acts as a mechanical 'brace' to localize cell wall breakdown and spatially limit abscising cells. The second cell type undergoes transdifferentiation into epidermal cells, forming protective cuticle, demonstrating *de novo*specification of epidermal cells, previously thought to be restricted to embryogenesis. Loss of the lignin brace leads to inadequate cuticle formation, resulting in surface barrier defects and susceptible to infection. Altogether, we show how plants precisely accomplish abscission.

Cell Walls

Concurrent Speaker - Holly Allen

Abstract Title: EXPLOITING TREE PATHOGENS TO ALTER PLANT CELL WALL COMPOSITION

Primary Author(s) and Institution(s): HOLLY ALLEN, Simon Turner The University of Manchester; The University of Manchester

Abstract

Plant secondary cell walls are an ideal feedstock for producing biofuels since they constitute the majority of plant biomass and they do not compete with biomass allocated to food production. However, efficiently converting cell walls into commercially viable bioethanol is hampered by lignin, a phenolic polymer which makes the cell wall resistant to enzymatic digestion. Secondary cell walls with severely reduced lignification naturally occur in the xylem of apple trees infected with apple rubbery wood (ARW) disease. However, how ARW alters the cell wall has not been described in detail . We have performed detailed histochemical and biochemical analyses of cell wall composition in symptomatic xylem that reveal ARW causes large increases in cellulose and hemicellulose deposition, but dramatically reduces lignin content of xylem fibres. RNA-sequencing analysis demonstrated that enzymes involved in cellulose and xylan biosynthesis are strongly upregulated in symptomatic branches, consistent with the cell wall analyses. Rather surprisingly, we find a dramatic increase in the lignin biosynthesis pathway, despite a reduction in lignin content. We are currently analysing the data to understand what might

cause the reduction in lignin. Elucidating the molecular basis of ARW symptoms may offer a novel approach for altering cell wall composition for feedstock improvement.

Grapes of Health
Concurrent Chair - Mario Pezzotti

Abstract Title: GXE IN GRAPEVINE: THE GENOMIC PERSPECTIVE

Primary Author(s) and Institution(s): MARIO PEZZOTTI , SILVIA DAL SANTO, SARA ZENONI, GIOVANNI BATTISTA TORNIELLI; University of Verona

Abstract

The phenotype of every organism is determined by a combination of its genotype (G), environment (E) and genotype-dependent responses to different environments, the latter being known as genotype × environment (G×E) interactions. Grapevine (Vitis spp., family Vitaceae) is characterize by a pronounced sensitivity towards the environment, and the metabolic composition of the berries is characterized by broad phenotypic plasticity, offering advantages such as the range of different wines that can be produced from the same cultivar and the adaptation of existing cultivars to different growing regions. The relevance of the interaction between varietal genotypes and the environment is best exemplified by the concept of terroir, which combines varietal attributes with the climate, soil and winemaking practices, plus all the possible interactions among them. Most grapevine G×E studies have focused on single traits using classical methods such as the analysis of quantitative trait loci. Here we illustrate the use of 'omics' approaches in open-fieldexperiments to unravel the phenotypic plasticity of grapevine berries of a single grapevine variety and G×E interactions in two grapevine varieties by analyzing their transcriptomes. In parallel, we also investigated genomic and epigenomic elements to provide a multilayered scientific definition of the formerly empirical basis of terroir. Finally, we applied correlation analysis to the transcriptomic and climatic data to unravel the molecular basis of G×E interactions.

Grapes of Health
Invited Speaker - Kristina Gruden

Abstract Title: MAPMAN ONTOLOGIES AND GOMAPMAN DATABASE AS A TOOL IN MULTILEVEL INTEGRATIVE STUDIES

Primary Author(s) and Institution(s): KRISTINA GRUDEN National Institute of Biology - Department of Biotechnology and Systems Biology Vecna pot 111, SI-1000 Ljubljana, Slovenia; NIB

Abstract

With the development of high-throughput data technologies and consequent rise in the amounts of experimental data available there is an increasing need for tools allowing easy biological integration of data. This is even more true if the experimental data are collected on different molecular levels. The MapMan ontology was developed due to the limited scope of prior existing biomedical ontologies for plant-related research, more specifically, to cover plant-specific pathways and processes. Using MapMan ontology one can visualize, analyze and interpret the experimental dataset on the level of biological processes (mapman.gabipd.org/mapmanstore). GoMapMan is a database where information about gene function from various resources is merged and visualized in the hierarchical tree of MapMan

ontology (www.gomapman.org). Several downloadable files are also available assisting the use of diverse analysis tools such as GSEA. GOMapMan now includes 11 different plant species besides the model plant Arabidopsis thaliana. To improve functional annotation in crops and synchronise individual curating efforts, annotation is consolidated between species through orthologue group information. A recent addition to GoMapMan are similar functional annotations of smallRNAs and metabolites. The combined use of protein, smallRNAs and metabolite annotations assists in interpretation of multilevel studies. We will show the advantages of using these tools for biological interpretation of complex datasets on the example of potato in interaction with viral pathogen and grapevine in interaction with phytoplasma.

Grapes of Health

Concurrent Speaker - Kelem Gashu Alamrie

Abstract Title: Topo climate effects on phenology and fruit metabolism of red and white wine grapevine cultivars under extreme desert conditions

Primary Author(s) and Institution(s): KELEM GASHU 1,* , ERAN HARCAVI 3 , ELYASHIV DRORI 4 , AMNON BUSTAN 2 , and AARON FAIT 1 1 Ben-Gurion University of the Negev, Jacob Blaustein Institutes for Desert Research, French Associates Institute for Agriculture Biotechnology of Drylands, Sede-Boqer 849900, Israel, e-mail: kelemg2007@gmail.com; 2 Desert Agriculture Research Center, Ramat Negev R D, Halutza D.N. 85515, Israel. 3 Ministry of Agriculture and Rural Development, Agricultural Extension Service - Shaham, POB 28, Bet-Dagan 50250, Israel; 4 Agriculture Research Department, Eastern Region Research and Development Center, Ariel 40700, Israel; Ben-Gurion University of the Negev

Abstract

Desert conditions are considered beyond the climate frame of traditional wine producing belts due to water scarcity, high temperatures and excess light/UV intensity, all negatively affecting fruit metabolism and wine quality. However the semiarid to arid regions are inevitably becoming wine grapevine growing area in Israel, the Negev desert offers diverse topo climate conditions, with altitudes ranging from 250 to 900 m asl. To identify cultivars with crop quality potentials under desert environments two experimental vineyards were setup in Ramat Negev R D Center, and Ramon, at 300 and 850m asl, respectively comprising 10 white, and 20 red cultivars. In the first two harvest years (2015 and 2016), Chenin Blanc and French Colombard among the white cultivars, and Petit Verdot and Malbec among the red ones, exhibited promising wine qualities, with some advantages to the relatively cooler region, Ramon. A consistent two-week difference in plant and berry phenology between the two vineyards was preserved from bud break to véraison, while the differences among cultivars at each site were small in 2017 growing season. The fruit ripening period, from véraison to harvest was on average 50% longer in the significantly warmer Ramat Negev vineyard, where a considerable number of fruit clusters shriveled before reaching the BRIX harvest threshold. Metabolic data of berry skin and pulp are being processed to assess environmental and varietal interaction on primary and secondary metabolism.

Grapes of Health

Concurrent Speaker - Charles Romieu

Abstract Title: NEW PHYSIOLOGICAL AND GENETIC APPROACHES TO BREED GRAPEVINES CHALLENGING CLIMATE WARMING

Primary Author(s) and Institution(s): CHARLES ROMIEU ANTOINE BIGARD , MATTHIEU BREIL, REZK SHAHOOD, ANNE PELEGRINO, AGNES DOLIGEZ, LAURENT TORREGROSA

Abstract

Global warming already induced a drift towards earlier ripening, higher sugars and lower pH in grapevine. R esilient cultivars should be selected everywhere this metabolic syndrome is detrimental to wine quality. Two major innovations may help to elucidate t he physiological and genetic bases of grapevine fruit response to warming: i) Reconsidering fruit ripening quantitative bases : R NA and metabolic profiles confirmed that berries at different stages coexist in clusters; circumventing artefacts of non-synchronous samples elucidated water and osmoticum fluxes and their respective timings ; a H+/sucrose exchange, consistent with VVHT6 activation, is induced at the tonoplast; sugar accumulation continues after malate breakdown completion without membrane energization; phloem loading stops around 26 days when sugar concentration continues by berry shriveling. ii) Microvine accelerates fruit genetics and breeding , due to the continuous production of reproductive organs and the lack of juvenile period. We have screened Vitis vinifera germplasm for fruit water and primary metabolite accumulation. Genotypes limiting sugars accumulation below 1 M at ripe stage were crossed to generate two microvine populations segregating for berry development and composition. GBS was performed to identify QTLs controlling fruit growth and primary metabolite accumulation, as new targets in breeding programs.

Grapes of Health

Concurrent Speaker - Stefania Pilati

Abstract Title: ABSCISIC ACID IS A MAJOR REGULATOR OF GRAPE BERRY RIPENING ONSET: NEW INSIGHTS INTO ABA SIGNALING NETWORK.

Primary Author(s) and Institution(s): PILATI STEFANIA a , Bagagli Giorgia a , Sonego Paolo a , Moretto Marco a , Brazzale Daniele a , Castorina Giulia b,c , Simoni Laura b , Tonelli Chiara b , Guella Graziano d,e , Engelen Kristof a , Galbiati Massimo b , Moser Claudio a a) Research and Innovation Centre, Fondazione Edmund Mach, via E. Mach 1, 38010 San Michele a/Adige (TN), Italy b) Dipartimento di Bioscienze, Università degli Studi di Milano, Via Celoria, 26 20133 Milano c) Present Address: Dipartimento di Scienze Agrarie e Ambientali - Produzione, Territorio, Agroenergia, Università degli Studi di Milano, Via Celoria, 2 20133 Milano d) Department of Physics, Bioorganic Chemistry Lab, University of Trento, Via Sommarive 14, 38123 Povo, Trento, Italy e) CNR, Istituto di Biofisica Trento, Via alla Cascata 56/C, 38123 Povo, Trento, Italy; Fondazione Edmund Mach

Abstract

The process of grape berry ripening is non climacteric and does not rely on the sole ethylene signal. Abscisic acid (ABA) is recognized as an important hormone of ripening inception and color development in ripening berries. To elucidate the effect of this signal at the molecular level, pre-véraison berries were

treated ex-vivo for 20 hours with 0.2 mM ABA and berry skin transcriptional modulation was studied by RNA-seq after the treatment and 24 hours later, in the absence of exogenous ABA. This study highlighted that a small amount of ABA triggered its own biosynthesis and had a transcriptome-wide effect characterized by the amplification of the transcriptional response over time. An extensive overlap with the genes modulated during physiological ripening proved the major role played by ABA in the regulation of berry ripening. The signaling network of ABA, encompassing ABA metabolism, transport and signaling cascade, has been analyzed in detail and expanded based on knowledge from other species. Four candidate genes have been experimentally assayed for their transcriptional regulation by ABA. This knowledge of the ABA cascade in berry skin at ripening onset might be useful to other areas of viticultural interest, such as bud dormancy regulation and drought stress tolerance.

Tuesday, August 7th

Protein Modification and Degradation

Plenary Speaker - Jean-Philippe Vielle-Calzada

Abstract Title: Apomixis: control, induction, and evolution of clonal seed formation

Primary Author(s) and Institution(s): Jean-Philippe Vielle-Calzada; Langebio CINVESTAV

Abstract

Several decades of theoretical studies have yet to provide a reasonable explanation for the evolutionary emergence of mechanisms that can give rise to seeds through asexual methods of clonal reproduction. Apomixis refers to a set of reproductive mechanisms that invariably rely on avoiding meiotically derived gamete reduction and fertilization of the egg cell. After being long considered a strictly asexual oddity leading to extinction, the integration of more than 100 years of embryological, genetic, molecular and ecological research have revealed its importance as a widely spread component of the dynamic processes that shape plant evolution through several flexible and versatile developmental pathways. I will review our current findings related to the mechanisms controlling unreduced gamete formation, haploid induction, and parthenogenesis, emphasizing similarities and differences between sexuality and apomixis, and highlighting their implications for its evolutionary emergence. On the basis of these comparisons, the developmental origins of apomixis appear related to a dynamic epigenetic landscape in which environmental fluctuations reversibly influence female reproductive development through mechanisms of hybridization and polyploidization.

Plenary Speaker - Christine Beveridge

Abstract Title: SHOOT BRANCHING - Role of strigolactones and interactions with other signals

Primary Author(s) and Institution(s): Christine Beveridge, François Barbier1, Tinashe Chabikwa, Stephanie Kerr, Fengxi Han, Franzi Fichtner, John Lunn; The University of Queensland, School of Biological Sciences

Abstract

Shoot branching occurs due to the regulation of the outgrowth of axillary buds which are embryonic shoots in the axil of leaves. Long-distance signaling is central to this regulation and mainly involves strigolactones, cytokinins, auxin and sugars. The sugar role may be at least partly due to sugar signalling and to involve trehalose 6-phosphate. It also appears that the growth of axillary buds from a state of very slow growth or dormancy, to sustained growth involves a number of stages during which the emerging shoots show differential sensitivity to growth stimulus and inhibition. For example, there are substantial differences in responses to different hormones at different periods after shoot tip removal. This could be due to differences in hormone signaling and downstream responses as well as due to changes in the vasculature of the growing buds. We will present our latest unpublished findings on the interaction of signals during bud outgrowth. In addition to providing a new mechanism for how plants respond to shoot tip removal, this work is provides a better understanding of how plants achieve diverse architecture in response to the environment.

Traficking

Plenary Speaker - Iris Meier

Abstract Title: A ROLE FOR PLANT LINC COMPLEXES IN POLLEN TUBES, GUARD CELLS, AND NODULATION

Primary Author(s) and Institution(s): IRIS MEIER; Ohio State University

Abstract

Nuclear movement is involved in cellular and developmental processes across eukaryotic life, driven by linker of nucleoskeleton and cytoskeleton (LINC) complexes, which bridge the nuclear envelope (NE) via the interaction of Klarsicht/ANC-1/Syne-1 Homology (KASH) and Sad1/UNC-84 (SUN) proteins. Arabidopsis LINC complexes are involved in nuclear movement and positioning in several cell types, including pollen tubes, guard cells, and root hairs. WPP domain-interacting proteins (WIPs) are one type of plant KASH proteins. Together with their binding partners, the WPP domain-interacting tail-anchored proteins (WITs), they are essential for nuclear migration during pollen tube growth. Loss-of-function mutations in WIT and/or WIP gene families result in impaired pollen nuclear movement, inefficient sperm cell delivery, and defects in pollen tube reception. Two different Arabidopsis KASH proteins, SINE1 and SINE2, modulate stomatal dynamics during abiotic stress, likely upstream of Ca 2+ signaling and an actin-remodeling event. In addition, we show that LINC complexes are conserved in legumes, and may contribute to the initiation of nodulation.

Natural Variation and Adaptation
Plenary Speaker - Christophe Maurel

Abstract Title: AQUAPORINS AND PLANT HYDRAULICS AS TARGETS AND PLAYERS OF ENVIRONMENTAL AND HORMONAL SIGNALING

Primary Author(s) and Institution(s): CHRISTOPHE MAUREL Biochemistry and Plant Molecular Physiology, CNRS, INRA, Montpellier SupAgro, Univ. Montpellier, F-34060 Montpellier, France

Abstract

Plant water transport is a key component of plant performance and adaptation to adverse environments. Aquaporins of the Plasma membrane Intrinsic Protein (PIP) subfamily mediate multiple controls of plant tissue hydraulics . New insights into the mechanisms at work in their regulation in roots, leaf veins and stomata will be presented. In particular, the PIP2;1 aquaporin contributes to auxin-regulated lateral root emergence and to stomatal closure in response to abscisic acid (ABA) or the bacterial elicitor flg22. Due to activation of its water and hydrogen peroxide (H 2 O 2) transport activities, PIP2;1 plays a dual hydraulic and signaling role in guard cells. Recently, the genetic bases of root hydraulics were explored using quantitative genetics approaches in Arabidopsis thaliana. These studies uncovered novel pathways for plant adaptation to stresses. For instance, a RAF-like MAP3 kinase named Hydraulic Conductivity of Root 1 (HCR1) was found to delineate a combinatorial signaling pathway integrating two soil signals, K + and O 2 availability. In all these studies, natural allelic variants provide useful genetic resources to understand and possibly manipulate the modes of plant adaptation to combined or opposing environmental stresses.

Mechanisms of Parasitic Plant Interactions
Concurrent Chair - Shelley Lumba

Abstract Title: MAPPING THE FUNCTIONAL LANDSCAPE OF STRIGOLACTONE RECEPTORS FROM STRIGA HERMONTHICA

Primary Author(s) and Institution(s): S. LUMBA 1 , S. SCHUETZ 1 , M. BUNSICK 1 , G. LY 1 , W. ZHAO 1 , Y. TSUCHIYA 2 , S. TOH 3, P. MCCOURT 1 1Dept. of Cell and Systems Biology, University of Toronto; 2Division of Biological Science, Nagoya University, Japan and 3Meiji University, Japan;

Abstract

In Africa, the parasitic weed, Striga hermonthica, infects major food crops which results in devastating yield losses for over 100 million subsistence farmers. Because Striga is an obligate parasite, it is essential for Striga seed to germinate in the vicinity of a plant host. Roots of hosts exude the hormone, strigolactones (SLs), which are perceived by Striga seed to indicate that a host is nearby and thereby germinate. Strigolactone receptors in Striga hermonthica (ShHTLs) can perceive picomolar concentrations of SL in the soil whereas the homologous HTL/KAI2 receptors from non-parasitic plants cannot. Instead, the HTL/KAI2 receptors perceive an unidentified endogenous ligand as well as smoke-derived compounds called karrikins. Based on alignments of parasitic and non-parasitic KAI2/HTLs and analyses of crystal structures, we identified eight key residues that we hypothesize would contribute to the increased sensitivity of ShHTL receptors to SL. To characterize the functions of these residues, we decided to change the identity of the eight amino acids in AtHTL/KAI2 to those of ShHTL7. We generated

constructs consisting of every combination of the mutations (28) resulting in 256 alleles. To test the function of these variants, we transformed them into an htl/kai2 mutant background. Based on large-scale quantitative datasets, we have begun to identify residues that contribute significantly to maintaining HTL/KAI2 function as well as residues that potentially lead to gain-of-function phenotypes. These results, as a whole, have led to a preliminary understanding of the mechanisms by which ligand binding pockets in ShHTLs could change to perceive specific ligands at high sensitivity.

Mechanisms of Parasitic Plant Interactions
Invited Speaker - Julia Scholes

Abstract Title: Novel resistance genes in rice provide broad spectrum resistance to the parasitic weed striga hermonthica

Primary Author(s) and Institution(s): JULIE SCHOLES1, EMILY BEARDON1, KIYOSUMI HORI2, MAMADOU CISSOKO1, ALEXIS MOSCHOPOULOS1, ARNAUD BOISNARD1, ALBERTO MARTIN-SANZ1, JON SLATE1, PEIJUN ZHANG1, MELANIE CRAZE3, SARAH BOWDEN3, EMMA WALLINGTON3, MASAHIRO YANO2, MATHIAS LORIEUX4

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Abstract

Rice plays a pivotal role in the national economies of sub-Saharan Africa and production is expanding faster than any other cereal. However, many upland rice varieties are susceptible to the obligate root parasitic weed,S. hermonthica,which causes yield losses from 20% to total crop failure. Striga-resistant cultivars are recognized as sustainable and cost effective for resource-poor farmers, but their use is limited by lack of knowledge of the molecular genetic basis of host resistance. Our work is focused on the discovery of novel resistance genes in rice to Striga, with the aim of breeding durable defence. We have mapped a highly significant Striga-resistance Quantitative Trait Locus (QTL) on chromosome 12. The QTL region is rich in genes encoding transposable elements, and contains a cluster of disease resistance proteins, which are key candidates for Striga resistance. A comparative analysis of the genomes of resistant and susceptible parental lines has revealed complex gene sequence rearrangements within the QTL region. We are investigating which of the candidate gene(s) is/are responsible for Striga-resistance by profiling their expression in resistance and susceptible rice varieties following infection with S. hermonthica and by down-regulating genes (by RNAi) to examine their effect on susceptibility to S. hermonthica.

Mechanisms of Parasitic Plant Interactions
Concurrent Speaker - Anna Kokla

Abstract Title: THE ROLE OF HOST HORMONES IN PARASITIC PLANT INFECTION

Primary Author(s) and Institution(s): ANNA KOKLA AND CHARLES W. MELNYK SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES(SLU), DEPARTMENT OF PLANT BIOLOGY Almas Allé 5, BioCentrum; Uppsala, Sweden; SLU

Abstract

Parasitic plants are devastating agricultural pests that account for ˜1% of all angiosperms. Parasitism in plants has evolved independently more than 11 times and despite independent origins, all parasitic plants form a multicellular invasive organ termed the haustorium that penetrates host tissues and connects to the host vasculature to withdraw water, nutrients and sugars. These vascular connections are known as xylem bridges and form between often distantly related hosts and parasites. Despite the biological and agricultural importance of plant parasitism, we know little about the developmental processes that occur in the host during haustorium and xylem bridge formation. Here, we study the interaction between the facultative root parasite Phtheirospermum japonicum and its host Arabidopsis thaliana. We developed an in vitroinfection assay that allows us to monitor in real time with confocal microscopy gene expression changes and xylem bridge formation at the haustorium. We furthermore test variousArabidopsis mutants in parasitic plant infection assays and identify several hormone mutants that form haustoria but fail to form xylem bridges. Together, these results indicate that host-derived developmental processes are important for successful parasitic plant infection.

Mechanisms of Parasitic Plant Interactions
Concurrent Speaker - Lucky Omoigui

Abstract Title: BREEDING COWPEA FOR RESISTANCE TO STRIGA GESNERIOIDES IN THE DRY SAVANNAS OF WEST AFRICA USING MARKER-ASSISTED SELECTION

Primary Author(s) and Institution(s): Breeding cowpea for resistance to Striga gesnerioides in the dry savannas of West Africa using marker-assisted selection LUCKY O. OMOIGUI1, 2*, Alpha Y. Kamara2, Catherine C. Danmaigona1, and Michael P. Timko3; International Institute of Tropical Agriculture (IITA)

Abstract

Striga gesnerioides is a parasitic weed which attaches to, and penetrates, the host root system. S. gesnerioides is widely distributed in Africa, causing significant loss of yield in cowpea and continuing to spread and intensify in some areas. Historically, conventional breeding has been the primary strategy used to develop a few Striga-resistant cowpea varieties currently grown in the Sahel of Western Africa. In this study, we have successfully developed and applied a marker-assisted selection strategy that employs a single backcross programme to introgress Striga resistance into farmer preferred varieties of cowpea for the Nigeria savannas. In this strategy, we have introduced the Striga resistance gene from the donor parent IT97K-49935 into an elite farmer preferred cowpea cultivar 'Borno Brown'. The selected 47 BC1F2 populations confirmed the recombinants with desirable progeny having Striga resistance gene(s). The 28 lines selected in the BC1F2:4 generation with large seed size, brown seed coat colour and carrying marker alleles were evaluated in the field for resistance to Striga resistance. This led to the selection of several desirable improved lines that were immune to Striga having local genetic background with higher yield than those of their parents and standard varieties.

Mechanisms of Parasitic Plant Interactions
Concurrent Speaker - Atsushi Okazawa

Abstract Title: METABOLISM OF A STORAGE CARBOHYDRATE IN OROBANCHACEAE SEEDS AS A POTENTIAL TARGET FOR THEIR CONTROL

Primary Author(s) and Institution(s): ATSUSHI OKAZAWA 1,2 , ATSUYA BABA 1 ,TAKUMI OGAWA 1 , YUKIHIRO SUGIMOTO 2,3 , DAISAKU OHTA 1 1 Grad. Sch. Life Environ. Sci., Osaka Pref. Univ., 2 SATREPS, JST/JICA, 3 Grad. Sch. Agric. Sci., Kobe Univ.

Abstract

Some species of Orobanchaceae cause serious damage on crop production. Despite the substantial efforts to establish a method to overcome the problem, ultimate countermeasures against these parasites have not been developed. The seed germination stage is fragile in their life cycle because they totally depend on the storage materials in the tiny seeds at this point. Comparing with the knowledge on the perception of strigolactones, metabolic processes after the perception of strigolactones are not fully understood. Previously, we revealed that planteose (Pla) is a storage carbohydrate in Orobanchaceae seeds and some chemicals can suppress the seed germination through the inhibition of Pla metabolism. Here we investigate the enzymes involved in Pla metabolism together with the enzymatic inhibitors. Pla is a galactosyl sucrose, so transcriptome data from germinating seeds of Orobanche minor were screened for α-galactosidases expressed during germination. A candidate gene, OmAGAL was expressed in Escherichia coli and tested for Pla hydrolytic activity. As a result, OmAGAL was revealed as an acidic α-galactosidase capable of Pla hydrolysis. Screening of a chemical library composed of 15,000 compounds discovered 28 OmAGAL inhibitors. Some OmAGAL inhibitors suppressed the O . minor germination suggesting Pla metabolism is a potential target for their control.

Hormone Signaling
Invited Speaker - Alexander Jones

Abstract Title: THE FORMATION AND FUNCTION OF GIBBERELLIN GRADIENTS IN VIVO

Primary Author(s) and Institution(s): ALEXANDER M JONES, ANNALISA RIZZA, ANKIT WALIA, LEAH BAND; Sainsbury Laboratory Cambridge University

Abstract

Regulated distribution of plant hormones across tissues and over time is fundamental to plant growth and development and optical biosensors for plant hormones are beginning to shed light on hormone distributions in planta . We have engineered an optogenetic biosensor for the plant growth hormone gibberellin, Gibberellin Perception Sensor 1 (GPS1), which detects nanomolar levels of gibberellin and can reveal gibberellin patterning at the cellular level. Analysis of Arabidopsis thaliana plants expressing a nuclear localised GPS1 revealed gibberellin gradients that correlated with gradients of cell length in rapidly elongating roots and dark-grown hypocotyls. It remains unclear how these gradients arise from the ensemble activities of gibberellin enzymes and transporters. In roots, accumulation of exogenously applied GA also correlated with cell length, suggesting that a root GA gradient can be established independently of GA biosynthesis. Indeed, gibberellin biosynthetic mutants supplemented with gibberellin also display gibberellin gradients as well as restored growth patterning. The effect of further

gibberellin enzyme and transport mutants on gibberellin patterning in roots will be discussed in the context of understanding how gibberellin gradients are determined and how they, in turn, influence patterning of plant cell growth.

Hormone Signaling
Concurrent Speaker - Thierry Heitz

Abstract Title: COMPLEX JASMONATE METABOLISM AND ITS IMPACT ON HORMONE SIGNALING

Primary Author(s) and Institution(s): VALENTIN MARQUIS 1 , EKATERINA SMIRNOVA 1 , JULIE ZUMSTEG 1 , LAURE POIRIER 1 , YANN AUBERT 1 , EMILIE WIDEMANN 1 , FRÉDÉRIC BELTRAN 2 , LAURENCE MIESCH 2 , ROZENN MENARD 1 and THIERRY HEITZ 1 1 Institut de Biologie Moléculaire des Plantes, CNRS, Université de Strasbourg, Strasbourg, France 2 Laboratoire de Chimie Organique Synthétique, Institut de Chimie, Université de Strasbourg, CNRS, France; IBMP-CNRS

Abstract

Jasmonates (JAs) regulate major sectors of immune responses and mediate also developmental processes like growth or fertility. Among many other possible metabolic fates, jasmonic acid (JA) gains its hormonal activity through conjugation into jasmonoyl-isoleucine (JA-Ile) that controls most responses when its perception triggers JAZ repressor elimination. Our aim is to elucidate new metabolic steps in the JA pathway that govern JA-Ile homeostasis and impact signaling output, by using co-regulation networks, reverse genetics/biochemistry combined with metabolic analysis and biological assays. We have characterized in Arabidopsis two integrated JA-Ile catabolic pathways that are stress-induced in leaves, concomitantly to JA biosynthesis and signaling. They consist in 1) two-step JA-Ile w -oxidation mediated by cytochromes P450 of the CYP94 subclade to gradually inactive derivatives and 2) the cleavage of JA-Ile and 12OH-JA-Ile by the amidohydrolases IAR3 and ILL6. Recently, we have characterized Jasmonic Acid Oxidases (JAO) of the 2-oxoglutarate family that oxidize directly JA to 12OH-JA. Inactivation of the specific JAO2 isoform identified an important metabolic diversion mechanism, where removal of a subpool of JA is needed to maintain repression of defenses in non-stimulated leaves. The strikingly different impact of deficiency in pre- and post- JA-Ile metabolic steps on defense signaling will be discussed.

Hormone Signaling
Concurrent Speaker - Javier Botto

Abstract Title: B-BOX TRANSCRIPTION FACTORS & PLANT DEVELOPMENT

Primary Author(s) and Institution(s): JAVIER BOTTO IFEVA-CONICET. Universidad de Buenos Aires. Buenos Aires, Argentina Universidad de Buenos Aires. Facultad de Agronomía. Cátedra de Fisiología Vegetal. Buenos Aires, Argentina; IFEVA-CONICET Agronomy Faculty University of Buenos Aire

Abstract

B-box (BBX) proteins are a class of zinc-finger transcription factors containing a B-box domain with one or two B-box motifs, and sometimes also feature a CCT domain as contain CONSTANS and CO-like proteins. BBX proteins are key factors in regulatory networks controlling growth and developmental processes including seedling photomorphogenesis, photoperiodic regulation of flowering, shade

avoidance, and responses to biotic and abiotic stresses. In this talk, I will describe the functional characterization of those members of zinc-finger transcription factors that contain two B-boxes (BBX). I will discuss the function of BBX proteins mediating transcriptional regulation and protein-protein interactions in plant signaling. I will also provide insights into the molecular mechanisms of their action in seedling de-etiolation, shade avoidance responses and in mature plants by the integration of hormonal and environmental signals. I will discuss the potential to use engineering crops with this technology to increase productivity.

Hormone Signaling

Concurrent Speaker - Jae-Ung Hwang

Abstract Title: ARABIDOPSIS THALIANA RAF22 PROTEIN KINASE MAINTAINS GROWTH CAPACITY DURING POST-GERMINATIVE GROWTH ARREST UNDER STRESS

Primary Author(s) and Institution(s): JAE-UNG HWANG 1 , SOJEONG YIM 1 , THANH HA THIDO 1, JOOHYUN KANG 1 , and YOUNGSOOK LEE 1,2 Department of Life Sciences, Pohang University of Science and Technology (POSTECH), Pohang, 37673, Republic of Korea 2 Division of Integrative Bioscience and Biotechnology, POSTECH, Pohang, 37673, Republic of Korea; POSTECH

Abstract

When seeds are exposed to drought and salinity during germination, newly germinated embryos stop growth and enter a quiescent state, called post-germinative growth (PGG) arrest. PGG arrest protects embryos from the stress, but it is not known how PGG is restored from the arrest when stress is eased. In this study, we show that, under stress- or ABA-induced PGG arrest conditions, Arabidopsis thaliana Raf-type protein kinase 22 (AtRaf22) overexpression accelerated photoautotrophic seedling establishment, whereas atraf22 knockout mutations enhanced the arrest. Furthermore, when the stress intensity was reduced subsequently, AtRaf22 overexpression plants resumed growth and accomplished photoautotrophic transition much faster than the knockout or wild-type plants. These results suggest that AtRaf22 activity is important for maintaining growth capacity during stress-induced PGG arrest, which is most likely critical for competitive growth when the stress subsides and plants resume growth. Such a factor has not been reported before.

Hormone Signaling

Concurrent Speaker - Jungmook Kim

Abstract Title: A DUAL MODE OF A POSITIVE FEEDBACK LOOP EXERTED BY LBD18 TO CONTROL ARF EXPRESSION AND TRANSCRIPTIONAL ACTIVITY IN ARABIDOPSIS

Primary Author(s) and Institution(s): JUN GMOOK KIM * , Shashank K. Pandey, Han Woo Lee, Min-Jung Kim, Nguyen Thu Hien , and Eunkyoo Oh

Abstract

The plant root system consists of a primary root derived from during embryogenesis and lateral roots and secondary roots that form post-embryonically. Lateral roots are a major determinant of root architecture, which is important for root anchoring and water and nutrient acquisition. Auxin plays major roles in every step of lateral root development. Gene regulatory networks controlling lateral root formation via auxin signaling, including the ARF7/ARF19- LBD16/LBD18 network via the AUX1/LAX3 auxin influx carriers, has been identified . However, their feedback regulation mechanisms are not known. We show that LBD18 binds a specific DNA motif in the ARF19 promoter to regulate its expression in vivo as well as in vitro . LBD18 interacts with ARFs including ARF7 and ARF19 via the PB1 domain of ARF to enhance ARF transcriptional activity, and competes with Aux/IAA repressors for ARF binding, overriding a negative feedback loop exerted by Aux/IAA repressors. These results suggest that LBD18 utilizes a dual mode of a positive feedback loop to regulate ARF expression and transcriptional activity in Arabidopsis , provid ing a robust feedback mechanism for sustained lateral root formation in response to auxin. This study was supported by grants from RDA (PJ031220) and NRF (2016R1A2B4015201 and 2017R1A4A1015620), Korea to J. Kim.

Protein interactomics in Plant Growth and Development

Concurrent Chair - Geert De Jaeger

Abstract Title: COMBINING TARGETED AP-MS WITH PHOSPHOPROTEOMICS MAPS THE TOR INTERACTOME.

Primary Author(s) and Institution(s): GEERT DE JAEGER , ASTRID GADEYNE, HAN CHAO, CAROLINE MATTHIJS, DOMINIQUE EECKHOUT, BERNARD CANNOOT, NANCY DE WINNE, GEERT PERSIAU, EVELINE VAN DE SLIJKE, IVE DE SMET, and JELLE VAN LEENE UGent-VIB Center for Plant Systems Biology, 9052 Ghent, Belgium; VIB-Ghent University

Abstract

The target of rapamycin (TOR) kinase is a central regulatory hub that translates environmental and nutritional information into permissive or restrictive growth decisions. Although the TOR pathway is conserved across eukaryotes, plants developed unique adaptations to this pathway to cope with their autotrophic and sessile nature. Overall, compared to other eukaryotic model species, the current knowledge of TOR signaling in plants is still scarce. Only few TOR pathway components are known and no phosphoproteome or interactome screens targeted to the TOR kinase have been performed. To fill

this gap, we combined a systematic phosphoproteome screen with an extensive state of the art protein complex analysis, generating for the first time a comprehensive TOR signaling network in plants. Integration of both networks significantly increased our understanding of plant TOR signaling, elucidating both evolutionarily conserved as well as novel plant-specific links, covering a broad range of biological processes such as protein and nucleotide biosynthesis, autophagy, auxin signaling, chloroplast development, lipid metabolism, and senescence.

Protein interactomics in Plant Growth and Development
Invited Speaker - Madelaine Bartlett

Abstract Title: PROTEIN-PROTEIN INTERACTIONS AND THE EVOLUTION OF GENE REGULATION OF FLOWER DEVELOPMENT

Primary Author(s) and Institution(s): MADELAINE BARTLETT 1 , AMANDA SCHRAGER-LAVELLE 1 , GRACE PISANO 1 , PUBUDU HANDAKUMBURA 2 , COURTNEY BABBITT 1 1 University of Massachusetts, Amherst, MA 01003 2 Pacific Northwest National Laboratories, Richland, WA 99354; University of Massachusetts Amherst

Abstract

The regulatory hypothesis proposes that the evolution of gene regulation is central in the evolution of plant and animal form. Gene expression patterns are determined by the combination of transcriptional regulators present at a particular cis- regulatory element at a particular time. Regulatory novelty has typically been sought in the evolution of these cis- regulatory elements. However, interactions between transcription factor proteins are also of profound importance in determining gene expression patterns. This is particularly true of the floral MADS-box transcription factors, which likely function as part of tetrameric protein complexes. Current models predict that the precise composition of these MADS-box tetramers determines downstream gene expression patterns and, in turn, floral organ identity. Arising from this model of MADS-box function is the evo-devo hypothesis that shifting MADS-box protein-protein interactions affect downstream gene regulation, and thus drive evolutionary change. To test this hypothesis, my lab has developed an experimental system in the grasses where we can manipulate MADS-box protein-protein interactions in an evolutionary context, and assess consequent impacts on global gene expression patterns and floral development. We have found widespread transcriptional changes downstream of altered protein-protein interactions. In contrast, floral morphology is very subtly affected. Our results have implications for understanding flower development and evolution, and for understanding the mechanisms driving the evolution of gene regulation more broadly.

Protein interactomics in Plant Growth and Development
Concurrent Speaker - Mee-Len Chye

Abstract Title: ARABIDOPSIS ACYL-COA-BINDING PROTEIN1 COORDINATES STEROL REGULATION IN PLANT DEVELOPMENT VIA PROTEIN–PROTEIN INTERACTION

Primary Author(s) and Institution(s): MEE-LEN CHYE , SHIU-CHEUNG LUNG, and PAN LIAO School of Biological Sciences, The University of Hong Kong, Pokfulam, Hong Kong, China; University of Hong Kong

Abstract

Acyl-CoA-binding proteins (ACBPs) play important roles in fatty acid metabolism by binding acyl-CoA esters. In Arabidopsis thaliana , six ACBP members are classified into four classes based on their molecular mass and domain architecture. Besides having the conserved acyl-CoA-binding domain, Class II ACBPs (AtACBP1 and AtACBP2) possess an ankyrin-repeat domain for mediating protein–protein interactions. The identification of protein partners of ACBPs will help elucidate their biological functions. Two forms of STEROL C4-METHYL OXIDASE1 (SMO1), SMO1-1 and SMO1-2, were demonstrated to co-express and interact with AtACBP1 by yeast two-hybrid, co-localization, pull-down, co-immunoprecipitation and β-glucuronidase assays. SMO1-1 or SMO1-2 knockdowns in the acbp1 mutant were used in phenotyping, gas chromatography-mass spectrometry and expression profiling. Lipid metabolism was impaired as revealed from the aberrant fatty acid and sterol compositions, which were linked to various developmental defects affecting the trichomes, seed coat mucilage and seed oil formation. ACBP1–SMO1 interaction appears to control the synthesis of lipid modulators that serve as cellular signals.

Protein interactomics in Plant Growth and Development
Concurrent Speaker - Cyrus Raja Rubenstein Sabbagh

Abstract Title: TOWARDS A GLOBAL INTERACTOMIC MAP BETWEEN THE RALSTONIA SOLANACEARUM SPECIES COMPLEX CORE TYPE III EFFECTORS AND THE TOMATO PROTEOME

Primary Author(s) and Institution(s): CYRUS RAJA RUBENSTEIN SABBAGH 1 , ARRY MOREL 1 , PATRICK BARBERIS 1 , STÉPHANE GENIN 1 , FABIENNE VAILLEAU 1,2 and NEMO PEETERS 1 . Institutions: 1 LIPM, Université de Toulouse, UMR INRA-CNRS 441-2594, 31326 Castanet Tolosan, France 2 INP, ENSAT, Université de Toulouse, 18 chemin de Borde Rouge, 31326 Castanet Tolosan, France; UMR INRA-CNRS 441-2594

Abstract

Abstract: The Ralstonia solanacearum species complex (RSSC) virulence strategy relies on type III effectors (T3Es) injected inside the plant cells via a type III secretion system. Thanks to the currently known genomic sequences of the different plant pathogenic strains of the RSSC, we have identified a list of 30 core T3Es [1]. As these core-T3Es have been conserved through the evolution of the highly diverse RSSC, with strains affecting different host plants, we hypothesize that they must be important for virulence. Our main objective is to identify putative tomato targets for all of these 30 core-T3Es using systematic Y2H screening against a tomato root cDNA library. Many candidate tomato targets, some of which are hubs (targets interacting with more than one effector), were identified from 14 screenings. These identified targets have been tested against all the 30 T3Es and other effectors from different pathogens and thanks to a Y2H-pairwise-matrix, we were able to increase the number of the identified hubs up to 17 candidates. Validation of some interactions in planta as well as reverse genetics for these hubs is currently carried on in order to reveal their contribution to the wilting disease. I will present our most recent results, exposing some interesting candidate tomato targets of Ralstonia T3Es. References : [1] Peeters N, Carrere S, Anisimova M, Plener L, Cazalé AC, Genin S. Repertoire, unified nomenclature and evolution of the Type III effector gene set in the Ralstonia solanacearum species complex. BMC genomics. 2013;14: 859. doi:10.1186/1471-2164-14-859

Protein interactomics in Plant Growth and Development
Concurrent Speaker - Petra Bauer

Abstract Title: THE MULTIPLE LAYERS OF IRON DEFICIENCY RESPONSE REGULATION

Primary Author(s) and Institution(s): Petra Bauer , Tzvetina Brumbarova, Regina Gratz, Jörg Kudla, Prabha Manishankar, Matias Zurbriggen, Rocio Ochoa-Fernandez

Abstract

The micronutrient iron is important for a diverse set of biological functions in plants. To balance essential and potentially deleterious effects of this metal, iron acquisition by plant roots and further allocation and cellular homeostasis in plants are strongly controlled and responsive to environmental and developmental signals. In an iron-deficient situation plants mobilize iron in the soil, thus render it more soluble and bio-available for uptake and allocation to different plant parts. New components of iron regulation are identified by a combined analysis of co-expression data and protein-protein interactions and subsequent physiological, genetic and biochemical analysis. We present our current understanding of the iron regulatory transcription factor cascade. The bHLH protein FIT is essential for root iron uptake and activated downstream of the iron regulatory cascade. FIT integrates via protein-protein interactions and phosphorylation environmental signals to adjust iron acquisition.

Diversity and Genetic Basis of Complex Traits
Concurrent Chair - Kang Chong

Abstract Title: Rice sensing cold signal and the potential in crop breeding

Primary Author(s) and Institution(s): Kang Chong; Key Laboratory of Plant Molecular Physiology, Institute of Botany, Chinese Academy of Sciences

Abstract

Abnormal environmental temperature caused by the global climate change, affects plant growth and threatens crop production. The mechanism underlying the adaptation to cold temperature provides the theory basis for molecular breeding. Thus dissecting the perception of cold signal and its signal transduction with genetic approach, as well as GWAS strategy is the key to solve this scientific problem. Rice is a sensitive to cold temperature for its survival which is useful character to easily identify the gene's function in cold tolerance. Comparatively, there is a significant difference in cold tolerance between indica (Xian) and japonica (Geng) rice which belong to subspecies of Asian rice.We used genetic population with indica (Xian 93-11) and japonica rice (Geng Niponbare) to isolate a key QTL gene COLD1 to enhance chilling tolerance in japonica (Geng) rice. COLD1 encodes a regulator of G-protein signaling. It interacts with the G-protein α subunit RGA1 to sense cold signal to activate the Ca2+ channel and the electric physiological signal for active defense system. Based on the genomic sequence analysis with 112 accessions of rice including cultivars and wild rice, we found that the chilling-tolerant allele was originated from the Chinese O. rufipogon populations and was subject to strong human selection during japonica domestication. The allele with specific SNP2 in COLD1 was used in molecular design for breeding with the tolerance to chilling. It is useful allele in improvement for the cold tolerance for breeding. Trade-off the opposite traits such as defense and development is a survival strategy under stress conditions. Therefore, it is a key issue for to explore the molecular switch in the molecular

network to balance the traits in chilling stress. It is a case that the rice MADS-box transcription factor OsMADS57 cooperating with its interaction protein OsTB1 regulated the cold tolerance and organogenesis of tiller in rice, which is depend on temperature changes during cold stress.

Diversity and Genetic Basis of Complex Traits
Invited Speaker - Xianran Li

Abstract Title: From complex to simple: dissecting genetic and environmental determinants advances phenotype prediction

Primary Author(s) and Institution(s): XIANRAN LI 1 , XIN LI 1 , TINGTING GUO 1 , and JIANMING YU 1 1 Department of Agronomy, Iowa State University, Ames, IA 50011; Iowa State University

Abstract

Phenotypic plasticity, the ability of plants to respond to diverse environments, is a well-recognized challenge for accurate trait prediction. With a wealth of knowledge from whole-plant physiology, genomics, molecular genetics, and quantitative genetics, one bottleneck of understanding and leveraging phenotypic plasticity is the quantification of relevant environmental stimuli from natural environments. We grew a sorghum population with 250 recombinant inbred lines (RILs) across 4 years at fields spanning latitude from 18˚ to 42˚ and observed complex patterns of flowering time dynamics. We discovered that photothermal time (PTT = GDD × day length) from a growth period (18-43 days after planting) can be used to quantify external stimuli of each environment as its high correlation with mean flowering time. Quantifying each environment with PTT allows us to develop a joint genomic regression analysis (JGRA) framework to model and predict flowering time of each RIL and the effects of key flowering time genes (Ma 1 , Ma 6 , FT , ELF3) through linear regression models with PTT. The power of in-season and on-target prediction through JGRA was empirically validated with data from next two seasons. The generality of this JGRA framework was further verified with a rice dataset deposited online from an independent lab. A rice bi-parental population was evaluated in nine rice environments (6 locations in 3 years). PTT from a similar period (8-45 days after planting) as sorghum quantifies the external stimuli of each environment for heading date and Hd1 , Hd2 , Hd5 , and Hd6 are key genes responding to the environmental stimuli. Cross-validation indicated that leveraging PTT enables accurate and on target prediction of rice flowering time. Encouraged by the successful application for bi-parental populations, we are expanding the applications of JGRA framework into in-season and on-target forecasting other traits for diverse and elite crop germplasm.

Diversity and Genetic Basis of Complex Traits
Concurrent Speaker - Carla de la Fuente Cantó

Abstract Title: IDENTIFICATION OF GENES CONTROLLING EARLY ROOT GROWTH IN PEARL MILLET (Pennisetum glaucum L.) BY COMBINING GWAS AND TRANSCRIPTOMICS

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GenomiX, Montpellier, France 4 ICRISAT, Niger 5 LMI LAPSE, Dakar, Senegal § Present address: UCL, Louvain-la-neuve, Belgium; IRD

Abstract

Early root growth plays a pivotal role for crop establishment and adaptation in low-input agricultural systems where water and nutrients are scarce. We studied primary root growth in pearl millet, a key staple crop for food security in arid region of sub Saharan Africa and India. We evaluated primary root length using a 2D pouch system in a large panel of 173 inbred lines representing the crop genetic diversity. Genome Wide Association Scan (GWAS) using 392.493 SNP markers revealed nine significant marker-trait associations for primary root growth. These markers were mapped to the newly released pearl millet genome (Varshney et al. , 2017). In parallel, we compared gene expression in the root tip of two inbred lines with very contrasted root growth phenotype using RNAseq. The combination of GWAS and gene expression data revealed some interesting candidate gene for the regulation of root growth in pearl millet. These candidates were assessed further in a new evaluation of primary root growth conducted in two large segregating F2 populations derived from crosses between contrasted inbred lines. Variations of allele frequency at the targeted genes in bulked pools of lines with extreme phenotypes provided the means for a cost-effective validation of our results.

Diversity and Genetic Basis of Complex Traits

Concurrent Speaker - Luis Fernando Revers

Abstract Title: APPLE FLC AND TBRR GENES REGULATE DORMANCY INTEGRATING HORMONAL STIMULUS AND MOLECULAR RESPONSES

Primary Author(s) and Institution(s): REVERS LF 1,2 , CATTANI AM 1,2 , SARTOR T 1,2 , SILVEIRA CP 1 , PASQUALI G 2 . 1 Centro Nacional de Pesquisa de Uva e Vinho, Empresa Brasileira de Pesquisa Agropecuária, Bento Gonçalves, RS, 95701-008, Brazil 2 Graduate Program in Cell and Molecular Biology, Centro de Biotecnologia, Federal University of Rio Grande do Sul, Porto Alegre, RS, 91501-970, Brazil Embrapa

Abstract

Type-B response regulators (TBRRs) act in the final steps of the cytokinin-signaling pathway. Previous studies revealed the presence of TBRR binding sites at the promoter region of MdoDAM1 and MdoFLC , important genes for apple dormancy regulation. The aim of this study is to understand the MdoDAM1/MdoFLC gene expression regulation through TBRRs in response to cytokinin stimulus. The transcript levels of the TBRR s, MdoFLC and MdoDAM1 genes were measured by RT-qPCR in 'Royal Gala' apple buds exposed to controlled chilling (3°C) and growth-promoting conditions (25°C). Results indicated that MdoFLC expression increases during chilling exposure, which contrasts with a drop in MdoDAM1 transcript levels. Two TBRR s have a peak expression during chilling accumulation, also contrasting with a decrease in MdoDAM1 expression. When buds were exposed to growth-promoting conditions, transcripts of other TBRR s increased, while at the same time MdoFLC expression dropped. The ability of TBRRs and MdoFLC to bind the MdoDAM1 promoter was evaluated by a transactivation assay using Arabidopsis thaliana protoplasts. Results showed that TBRRs and MdoFLC bind to the MdoDAM1 promoter, acting as repressor transcription factors. These findings suggest an important link

between cold exposure, hormonal stimulus, and molecular responses regulating dormancy and budbreak in apple.

Diversity and Genetic Basis of Complex Traits
Concurrent Speaker - Fu-Chun Liang

Abstract Title: GENERATION OF RICE CULTIVARS WITH IMPROVED NITROGEN USE EFFICIENCY

Primary Author(s) and Institution(s): FU-CHUN LIANG , YI-FANG TSAY Institute of Molecular Biology, Academia Sinica

Abstract

Nitrogen, an essential macronutrient in plant, influences the growth and yield of crops. However, excess nitrogen fertilizers left in the soil cause damage to our environment in many perspectives such as eutrophication and soil acidification, generation of green house gas. Rice is one of the most important crops in the world. We use rice mutants to find potential strategy of improving nitrogen use efficiency (NUE). Sodium azide-mutagenized lines of rice in IR64 (Oryza sativa L. ssp. indica) background were grown in hydroponic system with low, medium and high nitrogen. By analyzing biomass-related traits under these three nutrition conditions, 25 lines out of 1291 lines with distinct biomass phenotypes which might be due to altered NUE were picked up after five rounds of experiment and then subjected to field test. Consistent with their hydroponic biomass phenotypes, the field test results showed that at low N condition, AZ567 had more panicle while at high N condition, grain weights are enhanced in AZ1306 but decreased in AZ283, AZ358 and AZ1108. Several N-related properties, e.g. nitrate/nitrogen content, nitrate reductase activity, nitrogen uptake and partition, will be analyzed to find out the underlying mechanisms for the altered growth at particular N condition. Our ultimate goal is to identify novel genes that are vital for NUE in crop.

Flower and Seed development
Concurrent Chair - Xiangdong Fu

Abstract Title: Heterotrimeric G proteins determine grain size and shape via the regulation of MADS-domain transcription factors in rice

Primary Author(s) and Institution(s): Qian Liu, Ruixi Han, Kun Wu, Jianqing Zhang, Yafeng Ye, Xiangdong Fu State Key Laboratory of Plant Cell and Chromosome Engineering, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, 100101, China

Abstract

Although the genetic improvement of rice grain yield delivered by the exploitation of semi-dwarfism and heterosis over the past fifty years, a substantial increase in grain productivity is required to feed a growing world population. The prime breeding target is to increase both grain size and grain number, because they impact both on yield potential and its end-use quality. However, the simultaneous improvement of grain quality and grain yield is a major challenge because of the negative correlation between these two traits, all of which is controlled by quantitative trait loci and influenced by environmental changes. Here we show that a rice grain yield quantitative trait locus qLGY3 encodes a transcription factor OsMADS1, which acts as a key downstream effector of Gβγ dimers. The presence of an alternatively spliced protein OsMADS1 lgy3 is shown to be associated with formation of long and slender grains, resulting in increases in both grain quality and yield potential of rice. Gβγ dimers function as cofactors to enhance OsMADS1 transcriptional activity and promote the co-operative transactivation

of common target genes, thereby regulating grain size and shape. We also demonstrate that combining OsMADS1 lgy3 allele with dep1-1 allele represents an effective strategy for simultaneously improving both the productivity and end-use quality of rice.

Flower and Seed development

Invited Speaker - Toshiro Ito

Abstract Title: AUXIN-MEDIATED MULTISTEP TERMINATION OF FLORAL STEM CELL ACTIVITIES

Primary Author(s) and Institution(s): TOSHIRO ITO Nara Institute of Science and Technology Nara Institute of Science and Technology

Abstract

In flower development, the robust stem cell activities are terminated to produce a fixed number of floral organs and eventually seeds for the next generation. In Arabidopsis, the floral stem cell activity is sustained by expression of the homeo-domain transcription factor WUSCHEL (WUS). Expression of WUS is terminated by multiple genetic pathways including the floral homeotic protein AGAMOUS (AG). In order to reveal spatio-temporal-specific regulation of floral stem cell activities, we have studied downstream activities of AG and other transcription factors by molecular genetic approaches. AG induces two transcription factors KNUCKLES (KNU) and CRABS CLAW (CRC), which function to terminate WUS . While KNU directly represses WUS , CRC controls floral meristem determinacy through the regulation of auxin homeostasis, thus repressing WUS . The zinc finger transcription factor SUPERMAN (SUP) is also involved in negative regulation of WUS . SUP is expressed at the boundary regions of stamen and carpel primordia. SUP interacts with components of Polycomb repressive complex 2 (PRC2) and fine-tunes local auxin signaling by negatively regulating the expression of the auxin biosynthesis genes YUCCA1/4 (YUC1/4) . I will discuss how auxin flow is controlled in developing carpels, and thus controls floral meristem determinacy.

Flower and Seed development

Concurrent Speaker - Tobias Meitzel

Abstract Title: Activation of auxin biosynthesis by trehalose 6-phosphate is required for normal seed filling in pea (Pisum sativum)

Primary Author(s) and Institution(s): Tobias Meitzel , Ruslana Radchuk, Erin L. McAdam, Ina Thormählen, Regina Feil, Eberhard Munz, Peter Geigenberger, John J. Ross, John E. Lunn, Ljudmilla Borisjuk; Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)

Abstract

Seeds determine the reproductive capacity of plants and are vital to their existence. To ensure seed survival and nourishment of seedling growth upon germination, the embryo enters the maturation phase, which encompasses the accumulation of reserve compounds and the acquisition of desiccation tolerance . Trehalose 6-phosphate (T6P), which functions as a signal for sugar availability in plants, is believed to regulate storage processes in seeds, since disruption of T6P synthesis in Arabidopsis thaliana causes embryo abortion at the onset of the seed filling phase. To investigate the role of T6P during seed development, we modulated the T6P content in pea embryos by ectopic expression of the T6P synthase

(OtsA) or T6P phosphatase (OtsB) genes from E. coli . We show that T6P promotes cotyledon growth and starch accumulation in maturing seeds, and that this requires transcriptional induction of auxin biosynthesis . Thus, our data indicate that T6P integrates auxin levels with sugar availability to facilitate seed filling in pea.

Flower and Seed development

Concurrent Speaker - Lyudmila Borisjuk

Abstract Title: NEW NUCLEAR MAGNETIC RESONANCE IMAGING TOOLS FOR PLANT DEVELOPMENTAL BIOLOGY

Primary Author(s) and Institution(s): LYUDMYLA BORISJUK 1 ,EBERHARD MUNZ 1 ,2 , PETER JAKOB 2 , THOMAS NEUBERGER 3 1 Leibniz-Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany 2 Institute of Experimental Physics 5, University of Würzburg, Würzburg, Germany 3 Huck Institutes of the Life Sciences; University Park, PA, USA; Leibniz Institute of Plant Genetics and Crop Plant Research

Abstract

A major thrust of developmental biology is to understand how molecular and cellular processes produce 3D morphology. Nuclear Magnetic Resonance Imaging (MRI) has a great virtue in being non-invasive and therefore has the potential to monitor physiological processes in vivo. Especially in medical research, MRI became superior to other imaging options for structural, metabolic and gene expression studies. Our presentation provides clear expositions of these key topics in the field of plant biology plant and introduces new original MRI applications for seeds and flowers. We prime MRI for visualization and survey of flowers and seeds interior with close to cellular resolution. Currently, MRI application provides new insights by investigating genetically manipulated plants (barley, maize, tobacco) and mutants (pea, Arabidopsis) and by assisting breeding practices (canola, oat, wheat). In our hands, MRI is capable to capture the previously hidden growth and metabolism without seed destruction and thus allows us to monitor developmental processes. The introduction of functional imaging on living seed enables us to display nutrient supply during seed filling and uncover intimate events of the awakening of life during germination. Our study promotes NMR-imaging as a versatile analytic tool for developmental biology, potent for in vivo study of the inner life of plants.

Flower and Seed development
Concurrent Speaker - Johan Zicola

Abstract Title: Targeted DNA methylation represses two enhancers of FLOWERING LOCUS T in Arabidopsis thaliana

Primary Author(s) and Institution(s): Johan Zicola 1 , Liangyu Liu 2 , Petra Tänzler 1 , Franziska Turck 1 1 Max Planck Institute for Plant Breeding Research, Cologne, Germany 2. College of Life Sciences, Capital Normal University, Beijing, China

Abstract

FLOWERING LOCUS T (FT) plays a major role in regulating the floral transition in response to inductive long day (LD) photoperiod in Arabidopsis thaliana . Expression of FT in leaves is dependent on the distal transcriptional enhancer Block C , located 5 kb upstream of the transcriptional start site (TSS). We expressed an inverted repeat of Block C to induce local DNA methylation and heterochromatin formation, which lead to FT downregulation in inductive photoperiod. Using targeted DNA methylation as a tool to uncover additional regulatory regions at the FT locus, we identified Block E , located 1 kb downstream of the gene, as a novel enhancer of FT . Similarly to Block C , Block E is conserved across Brassicaceae and located in accessible chromatin. In combination with a minimal promoter, Block E drives phloem-specific expression of a reporter gene , indicating that Block E acts as transcriptional enhancer of FT .

Evolution and Domestication of Plant Specialized Metabolites
Concurrent Chair - Asaph Aharoni

Abstract Title: PLANT 'METABOLIC CARAVANS': FROM ANTI-NUTRITIONAL TO ANTI-PARKINSON ALKALOIDS

Primary Author(s) and Institution(s): ASAPH AHARONI ; Department of Plant Environmental Sciences, Faculty of Biochemistry, Weizmann Institute of Science, P.O.B . 26, Rehovot, 7610001, Israel;

Abstract

The regulation of metabolic pathways in plants is constantly tuned in order to suit the needs of development and fitness. Our main research objective is to unravel networks of genes and proteins which coordinate the activity of metabolic pathways, predominantly secondary metabolism, during plant development and stress response. An integrated investigation of several members of the Solanacea family (mainly tomato, potato and eggplant), rather than studying a single plant, provided us with unprecedented insights to metabolic biology in these species. Most if not all processes characterized, impact to a certain degree key quality, nutritional and post-harvest traits of these crop plants. Integrating cutting-edge transcriptomics, proteomics and metabolomics tools together with genes co-expression assays were of great value in making several key discoveries. In a recent example, combined co-expression analysis and metabolic profiling in tomato and potato led to the discovery of the multi-step, core pathway leading to the formation of the renowned Solanum alkaloids including the biosynthesis of their precursor, cholesterol. This class of molecules represent important anti-nutritional compounds in these crop plants. In the presentation, I will highlight several advanced technologies and genetic research tools and the invaluable knowledge on core metabolic traits obtained through

combining them in a single study. Most if not all could be applied in the coming years to the study of key traits in other, less studied plant species.

Evolution and Domestication of Plant Specialized Metabolites
Invited Speaker - Robert Last

Abstract Title: The tip of the trichome: evolutionary innovation in Solanaceae specialized metabolism

Primary Author(s) and Institution(s): ROBERT LAST , PENGXIANG FAN, BRYAN LEONG, YANN-RU LOU, DANIEL LYBRAND, GAURAV MOGHE, CRAIG SCHENCK; Michigan State University

Abstract

This work focuses on specialized metabolism in glandular trichomes of cultivated and wild tomatoes and other plants in the Solanaceae. Protective acylsugars – relatively simple metabolites typically composed of sucrose or glucose and C2 to C12 acylesters – are produced in the tip cell of the long hairs of domesticated and wild tomato. Despite being derived from simple chemical building blocks, tremendous variation in acylsugar structures is observed within and across species. Some of the changes in products and enzymatic activities occurred over remarkably short evolutionary timeframes. The talk will describe results documenting 'recruitment' of enzymes of carbon, amino acid and fatty acid metabolism into acylsugar biosynthesis, as well as studies of BAHD acyltransferase evolution. This work provides examples of how comparative biochemistry leads to insights into how gene duplication, neofunctionalization and gene loss contributed to the impressive acylsugar diversity observed in domesticated and wild tomato species. Work towards understanding the evolutionary history of this metabolic network over tens of millions of years of evolution of the Solanaceae will be described.

Evolution and Domestication of Plant Specialized Metabolites
Concurrent Speaker - Keiko Yonekura-Sakakibara

Abstract Title: UGT79B31 IS RESPONSIBLE FOR THE TERMINAL MODIFICATION STEP OF POLLEN-SPECIFIC FLAVONOID BIOSYNTHESIS IN PETUNIA HYBRIDA

Primary Author(s) and Institution(s): KEIKO YONEKURA-SAKAKIBARA EVA K NOCH SATOKO SUGAWARA TETSUYA MORI RYO NAKABAYASHI KAZUKI SAITO; RIKEN Center for Sustainable Resource Science

Abstract

Flavonoids are known to be involved in pollen fertility in petunia (Petunia hybrida) and maize (Zea mays). As a first step toward elucidating the role of flavonoids in pollen, we have identified a glycosyltransferase that is responsible for the terminal modification of petunia pollen-specific flavonoids. An in silico search of the petunia transcriptome database revealed four candidate UDP-glycosyltransferase (UGT) genes. UGT79B31 was selected for further analyses based on a correlation between the accumulation pattern of flavonol glycosides in various tissues and organs and the expression profiles of the candidate genes. Arabidopsis ugt79b6 mutants that lacked kaempferol/quercetin 3- O -glucosyl(1 → 2)glucosides, were complemented by transformation with UGT79B31 cDNA under the control of Arabidopsis UGT79B6 promoter, showing that UGT79B31 functions as a flavonol 3- O -glucoside: 2 ¢ ¢ - O -glucosyltransferase in planta . Recombinant UGT79B31 protein can convert kaempferol 3- O -galactoside/glucoside to kaempferol 3- O -glucosyl(1 →

2)galactoside/glucoside. UGT79B31 prefers flavonol 3- O -galactosides to the 3- O -glucosides and rarely accepted the 3- O -diglycosides as sugar acceptors. UDP-glucose was the preferred sugar donor for UGT79B31. These results indicated that UGT79B31 encodes a flavonoid 3- O -glycoside: 2 ¢ ¢ - O - glucosyltransferase. Transient expression of UGT79B31 fused to green fluorescent protein (GFP) in Nicotiana benthamiana showed that UGT79B31 protein was localized in the cytosol.

Evolution and Domestication of Plant Specialized Metabolites

Concurrent Speaker - Robert Schuurink

Abstract Title: Regulation of terpene biosynthesis and development of type VI glandular trichomes in tomato by a dual function transcription factor

Primary Author(s) and Institution(s): ROBERT SCHUURINK, JIESEN XU, MICHEL HARING; University of Amsterdam

Abstract

The glandular trichomes of tomato (Solanum lycopersicum) are biochemical factories capable of making a diverse array of (specialized) metabolites. Although the cultivated tomato lacks the chemical diversity of wild species, it makes a bouquet of volatile mono- and sesquiterpenes in the type VI glandular trichomes. Volatile terpenes are involved in the direct and/or indirect defense against herbivores. We have discovered a transcription factor (TSGT6) that not only regulates the transcription of terpene synthases in the mature type VI glandular trichome, but is also involved in initiating the development of the type VI glandular trichome. Downregulation of TSGT6 leads to a shorter stalk, reduced expression of monoterpene synthases and monoterpene production but not to a reduction in the production of other specialized metabolites. Interestingly, the terpene synthases in the type VI glandular trichomes on the leaf are differently regulated than in those on the stem. Whereas downregulation of STGT6 lead to reduced expression of sesquiterpenes in leave trichomes, this activated the transcription of certain sesquiterpene synthases in type VI glandular trichomes on the stem. Eliminating expression ofTSGT6 using CRISPR-Cas9 lead to tomato plants without type VI glandular trichomes both on stem and leaves while slightly affecting the density of the other trichomes. As predicted, herbivores performed better on these lines. We have thus identified a transcription factor with a dual function, regulating both terpene biosynthesis and the production site, the type VI glandular trichome.

Evolution and Domestication of Plant Specialized Metabolites
Concurrent Speaker - Ana Arruabarrena

Abstract Title: EXPLORING ALLELIC VARIATION FOR KEY CAROTENOID BIOSYNTHESIS GENES IN MANDARINS AND TOMATOES

Primary Author(s) and Institution(s): ANA ARRUABARRENA 1 , LÁZARO E. P. PERES 2 , FERNANDO RIVAS 1 , MATÍAS GONZÁLEZ-ARCOS 1 , SABINA VIDAL 3 , JOANNA LADO 1 1 Estación experimental INIA Salto Grande, Instituto Nacional de Investigación Agropecuaria, Salto, Uruguay 2 Escola Superior de Agricultura "Luiz de Queiroz",University of São Paulo, Piracicaba, Brazil 3 Facultad de Ciencias, Univesidad de la República, Montevideo, Uruguay

Abstract

There is an increasing demand for food with a high nutritional value, that can contain bioactive compounds and promote health and prevent diseases. The development of fruits with high amounts of bioactive compounds is of high interest in many research programs. Carotenoids comprise a large group of terpenoid compounds involved in several processes in plants. Some of them are powerful antioxidants. Mandarins and tomatoes are highly consumed worldwide and are major sources of carotenoids. Hence, these crops are good candidates to improve fruit nutritional value for human health. Here we analyzed the key steps of the carotenoid biosynthetic pathway in different mandarin and tomato genotypes throughout their fruit developmental stages. Expression pattern of different PSY and β CHX alleles from several mandarin varieties were characterized. All mandarin genotypes displayed changes in the expression of genes involved carotenoid biosynthesis (PSY and β CHX), which were reflected in carotenoid content during fruit ripening. For tomato, we explored the mRNA accumulation pattern of a putative new phytoene synthase gene in cultivated tomato and in the wild relative Solanum pimpinellifolium . We discussed the differences in allelic variation for carotenoid biosynthesis genes and its potential to improve food nutritional value.

Tropical and Mediteranean Plants
Concurrent Chair - Pierre Marraccini

Abstract Title: CREATING NEW COFFEE VARIETIES TO COPE WITH CLIMATE CHANGES: CURRENT KNOWLEDGE AND FUTURE CHALLENGES

Primary Author(s) and Institution(s): P. MARRACCINI1, S.O. DE AQUINO2, L.F. TORRES2, G.S.C ALVES2, J-C. BREITLER1, C. CAMPA3, S. LERAN1, L. VILLAIN1, F. GEORGET1, A. de KOCHKO4, V. PONCET4, A.C. ANDRADE5, H. ETIENNE1, B. BERTRAND1

1CIRAD, UMR IPME (Univ. Montpellier, CIRAD, IRD) F-34394 Montpellier, France 2Federal Univ. Lavras (UFLA), 37200 Lavras (MG), Brazil 3IRD, UMR IPME (Univ. Montpellier, CIRAD, IRD) F-34394 Montpellier, France 4IRD, UMR DIADE (Univ. Montpellier, IRD) F-34394 Montpellier, France 5EMBRAPA Café- INCT-Café/INOVACAFÉ, 37200 Lavras (MG), Brazil

Abstract

Like many other crops, coffee production is threatened by climate changes. Therefore, research on coffee adaptation to abiotic stresses as well as alternative faster breeding programs are priorities in

many coffee growing countries. During the last decade, studies have been focused on identifying the physiological, molecular and genetic determinisms of coffee drought-tolerance, mainly on C. canephora. By comparing drought-tolerant and -susceptible clones, several candidate genes (like CcDREB1D) were highlighted. Recent studies demonstrated that CcDREB1D promoter haplotypes differentially regulate the expression of this gene under drought (and other abiotic stresses), mainly in leaf guard cells. In order to predict the adaptedness of C. canephora populations to climate change, statistical analyses are in progress to associate SNPs found in such candidate genes with climate parameters. Regarding C. arabica, new F1 hybrids resulting from conventional varieties crossed with wild Ethiopia accessions were recently created. With high vigor and yield, these hybrids were proved to be better adapted to agroforestry (low light) and full-sun (high light) conditions than traditional cultivated varieties*. Even though the molecular mechanisms of heterosis in these hybrids are largely unknown, preliminary studies suggested higher homeostasis probably linked to a better regulation of genes involved in the circadian clock. *BREEDCAFS (BREEDing Coffee for AgroForestry Systems) project H2020-SFS-2016-2 supported by EU (www.breedcafs.eu)

Tropical and Mediteranean Plants
Invited Speaker - Bjorn Usadel

Abstract Title: Complex tomato genomes: Easy with Nanopores

Primary Author(s) and Institution(s): Bjorn Usadel; RWTH Aachen University, Institute for Biology I

Abstract

Recent updates in Oxford Nanopore technology have made it possible to obtain GBases of sequence data from one single flowcell. It has been demonstrated that this is very beneficial for microbial genome assemblies and can also be used to assemble human genome data. However medium to large plant genomes have been shown to often be recalcitrant to genome assemblies due to their repetitive nature. We therefore set out whether -and if so how- plant genomes can be tackled using long read nanopore data. We comprehensively evaluated different assembly strategies on full (ca. 100x coverage) and subsampled data sets for a genome featuring a size of slightly more than 1.1 Gbase. We showed that excellent N50 values and BUSCO completeness scores can be obtained using long read data alone. We will discussing implications for plant genome assemblies and their analysis.

Tropical and Mediteranean Plants
Concurrent Speaker - Jennifer Smith

Abstract Title: CREATING DROUGHT, HEAT, AND SALT TOLERANT COTTON BY CO-OVEREXPRESSING RCA AND AVP1

Primary Author(s) and Institution(s): JENNIFER SMITH, TEXAS TECH UNIVERSITY NARDANA ESMAEILI, TEXAS TECH UNIVERSITY PAXTON PAYTON, USDA-ARS JOHN BURKE, USDA-ARS HONG ZHANG, TEXAS TECH UNIVERSITY; TexasTech University

Abstract

Abiotic stress is a serious challenge we face in agriculture and our goal as molecular scientists is to create tolerant crop plants to stresses of drought, heat, and salt. Higher yielding crops are urgently

needed to sustain our increasing world population as we face more challenges of soil erosion, deforestation, and urban development the land use is also changing. Traditional breeding has been successful in developing crops over the last 50 years, but our efforts have plateaued. By using a genetic engineering approach to confer abiotic stress is something that we have not seen on the seed market. Genetic advances such as conferring herbicide resistance and controlling harmful insects are making great progress in the crop development field but we see abiotic stress factors come in various combinations. Therefore, by using transgenic technology we created cotton co-overexpressing genes for increased tolerance to abiotic factors of drought, heat and salinity. We have introduced a DNA construct that contains two genes, the vascular H + -pyrophosphatase gene, AVP1 , and a Rubisco activase gene, RCA , into cotton. Overexpression of AVP1 would lead to increased drought and salt tolerance in transgenic plants, while the overexpression of RCA is expected to increase heat tolerance. We expect that co-overexpression of AVP1 and RCA will lead to increased tolerance against three stresses: drought, salt and high temperatures. Our most recent physiological data on analyzing transgenic cotton plants co-overexpressing AVP1 and RCA in the field, greenhouse, and heat chamber conditions will be presented at the meeting.

Tropical and Mediteranean Plants

Concurrent Speaker - Mehtap Çevik

Abstract Title: Expression Analysis of NAC Transcription Factors in Response to Drought Stress in Different Citrus Rootstocks

Primary Author(s) and Institution(s): MEHTAP ŞAHİN-ÇEVİK 1 , BETÜL GÖNÜLKIRMAZ 1 AND BAYRAM ÇEVİK 2 1 Department of Agricultural Biotechnology, Faculty of Agriculture, Süleyman Demirel University, 32260 Isparta, Turkey 2 Department of Plant Protection, Faculty of Agriculture, Süleyman Demirel University, 32260 Isparta, Turkey; Süleyman Demirel University

Abstract

Drought stress reduces the yield and productivity of agriculturally important plants including Citrus in many regions. Genome-wide expresssion analysis in plants revealed that hundreds of genes with a variety of functions were induced in response to drought stress. Among these genes, transcription factors (TFs) constitute an important group of genes. NAC TFs involved in the regulation of gene expressions during stress response in plants. Analysis of Citrus genome revealed that the presence of 145 of NAC TFs, whose functions have not been explored in detail yet. In this study, ten NAC TFs showing homology with NAC genes involved in drought stress response in the other plants, were selected from Citrus genome. The expressions of these NAC genes were analyzed in response to 14-day of drought stress in different Citrus rootstocks, including Rangpur lime (Citrus x limonia), Carrizo (Citrus sinensis X Poncirus trifoliata), sour orange (Citrus aurantium) and Poncirus trifoliata . For this purpose, drought stress was applied to these rootstocks and leaf samples were collected from these plants and control plants at 0, 1, 7, 9, 11 and 14 days of stress treatment. Total RNA was isolated from collected leaf samples using Trizol RNA isolation solution. Expression levels of these NAC TFs were determined in drought treated and control plants using total RNAs by real-time RT-PCR. Changes in the expression levels of these NAC genes were observed from different Citrus rootstocks during different stages of drought stress. This study was supported by TÜBİTAK project number 215O444.

Tropical and Mediteranean Plants

Concurrent Speaker - Patricia Fernandes

Abstract Title: MECHANISMS INVOLVED IN THE PMEV COMPLEX-CARICA PAPAYA INTERACTION THAT LEADS TO THE DELAYED STICKY DISEASE SYMPTOMS

Primary Author(s) and Institution(s): ANTUNES TFS 1 , MADROÑERO J 1 , CARMINATI L 1 , MARASTONI M 1 , QUADROS O 1 , RODRIGUES SP 1,2 ,VENTURA JA 1,3 FERNANDES AAR 1 FERNANDES PMB 1 . 1Núcleo de Biotecnologia, Universidade Federal do Espírito Santo, Vitória 29040-090, Espírito Santo, Brasil 2Núcleo Muldisciplinar de Pesquisa UFRJ – Xerém em Biologia, Universidade Federal do Rio de Janeiro, Duque de Caxias 25245-390, Rio de Janeiro, Brasil 3 Instituto Capixaba de Pesquisa, Assistência Técnica e Extensão Rural, Vitória, Espírito Santo, Brazil

Abstract

Papaya sticky disease (PSD) one of the major diseases of papaya, is caused by a dsRNA of approximately 8.8 kb, named papaya meleira virus (PMeV), and a ssRNA of approximately 4.5 kb, PMeV2. PMeV and PMeV2 are encapsidated in particles formed by the PMeV capsid protein. The presence of both PMeV and PMeV2 was confirmed in field plants showing typical symptoms of PSD, but PMeV was detected alone in asymptomatic plants, indicating that PSD is associated with double infection by PMeV and PMeV2, or PMeV complex. PMeV complex resides in papaya laticifers, where it changes potassium levels and the osmotic balance, leading to rupture of the cell. A proteomic approach revealed the modulation of 26S proteasome-, photosynthesis- and cell-wall remodeling-associated proteins. Global gene expression analysis indicates host stress responses associated to the tolerance to PSD symptoms at pre-flowering stage. At pre- and post-flowering stages, 633 and 88 differentially expressed genes were altered, respectively. At pre-flowering, genes related to stress and transport were up-regulated while metabolism-related genes were down-regulated. SA signaling likely operates at the pre-flowering stage of PMeV complex-infected C. papaya inhibiting the development of PSD symptoms, but the induction of its negative regulators prevents the full-scale and long-lasting tolerance.

Wednesday, August 8th

Hormone Signaling

Plenary Speaker - Sean Cutler

Abstract Title: ENGINEERING PLANT SIGNAL TRANSDUCTION FOR WATER SMART CROPS

Primary Author(s) and Institution(s): SEAN R. CUTLER , Aditya S. Vaidya, Sang Youl Park, Jonathan Helander, Dezi Elzinga, Wim Dejhonge. Department of Botany and Plant Sciences, Institute of Integrative Genome Biology, University of California, Riverside, California 92521, United States; UC-Riverside

Abstract

Plant hormones are a structurally diverse collection of small molecules that control plant growth, development, and environmental responses. Work over the past two decades has established that many plant hormones directly stabilize protein-protein complexes and act analogously to chemical dimerization agents, which were first described for the immunosuppressants rapamycin, FK506, and cyclosporin. Abscisic acid (ABA) stabilizes a complex between soluble ABA receptors and downstream phosphatases; the ABA-induced complex inhibits phosphatase activity, which in turn derepresses downstream kinases and activates signaling. I will describe my lab's work on this sensing module, our efforts to design synthetic ABA receptor agonists, and our development of engineered signaling modules. Specifically, I will describe a new non-sulfonamide agonist called opabactin (for overpowered ABA receptor activation) that possesses ~10x increased potency relative to ABA. This molecule was developed using a combination of computational screening and structure-guided optimization. Opabactin possesses substantially improved bioactivity relative to quinabactin in both wheat, tomato, and Arabidopsis and confirms the importance of subfamily III ABA receptors as key target sites for manipulating crop water use. I will additionally describe a new PYR1/PP2C-derived chemical-induced dimerization module that is insulated from endogenous signaling components due to surface mutations that establish an orthogonal PYR1-PP2C interaction as well as other mutations that eliminate PP2C catalytic activity and enable control by the agrochemical mandipropamid. This engineered dimerization module provides a simple platform technology for programming crops with agrochemical-controlled traits.

Plenary Speaker - Rob Martienssen

Abstract Title: Epigenetically activated small RNAs mediate chromosome segregation and dosage.

Primary Author(s) and Institution(s): Robert A. Martienssen; Howard Hughes Medical Institute, Cold Spring Harbor Laboratory

Abstract

Chromosome dosage plays a significant role in reproductive isolation and speciation in both plants and animals, but underlying mechanisms are largely obscure. We have found that a highly conserved microRNA in plants, miR845, targets the tRNAMet primer-binding site (PBS) of LTR-retrotransposons in Arabidopsis pollen, and triggers the accumulation of 21 to 22-nucleotide small RNA in a dose dependent fashion via RNA polymerase IV. We show that these epigenetically activated small-interfering RNAs

(easiRNAs) mediate hybridization barriers between diploid seed parents and tetraploid pollen parents ("the triploid block"), and that natural variation for miR845 may account for "endosperm balance" allowing formation of triploid seeds. Targeting the PBS with small RNA is a common mechanism for transposon control in mammals and plants, and provides a uniquely sensitive means to monitor chromosome dosage and imprinting in the developing seed. In mutants which lose both DNA methylation and RDR6-dependent easiRNAs from pericentromeric regions fertility defects can be traced to the centromeric region of chromosome 5, and can be rescued by either an ectopic increase in DNA methylation at a pericentromeric retrotransposon, or by directing artificial siRNAs to that locus. Loss of easiRNAs in DNA methylation mutants results in severe mitotic chromosome mis-segregation, strongly reminiscent of similar mutants in S.pombe, which also lacks DNA methylation.

Plant Microbiome
Concurrent Chair - Corné Pieterse

Abstract Title: THE SOIL-BORNE SUPREMACY

Primary Author(s) and Institution(s): CORNÉ M.J. PIETERSE 1 , GIANNIS STRINGLIS 1 , KE YU 1 , GILLES VISMANS 1 , YANG SONG 1 , ELINE VERBON 1 , PAULINE TRAPET 1 , KIRSTIN FEUSSNER 2 , IVO FEUSSNER 2 , RONNIE DE JONGE 1 , ROELAND L. BERENDSEN 1 , AND PETER A.H.M. BAKKER 1 . 1 Plant-Microbe Interactions, Department of Biology, Science4Life, Utrecht University, the Netherlands 2 Plant Biochemistry, Albrecht von Haller Institute, University of Göttingen, Germany; Utrecht University

Abstract

Plants nurture a large community of root-associated microbiota, which provide them with essential services, such as enhanced nutrient uptake, growth promotion, and protection against pathogens. Our research is focused on understanding plant-beneficial functions encoded by the root microbiome and the role of plant genes facilitating these functions. We demonstrated that upon foliar pathogen infection, Arabidopsis roots recruit a consortium of synergistic microbes to their rhizosphere that in turn trigger an induced systemic resistance (ISR) that is effective against a broad spectrum of pathogens (ISME J : 10.1038/s41396-018-0093-1; Cell 172: 1178-1180). Using the Arabidopsis- Pseudomonas simiae WCS417 model system, we identified the root-specific transcription factor MYB72 as a central regulator in the onset of ISR. Metabolome analysis revealed that MYB72 controls the biosynthesis of the iron-mobilizing coumarin scopoletin, which is excreted in the rhizosphere where it aids in iron uptake (PNAS : 10.1073/pnas.1722335115). Scopoletin also has antimicrobial activity to which WCS417 is insensitive. Microbiome analysis of coumarin-deficient mutants revealed that scopoletin functions in rhizosphere community assembly, possibly to promote recruitment of ISR-inducing rhizobacteria. Understanding the mechanistic basis of early root-microbiome interactions will provide a firm knowledge basis for the sustainable development of improved crop systems that maximize profitable functions from the root microbiome.

Plant Microbiome
Invited Speaker - Cara Haney

Abstract Title: Mechanisms in microbial regulation of plant growth and defense

Primary Author(s) and Institution(s): Cara H. Haney; The University of British Columbia

Abstract

Plant root-associated microbial communities (“rhizosphere microbiome”) influence plant growth and defense. Closely-related bacteria can have dramatically different effects on plant growth and range from pathogenic to mutualistic. As a result, function of a community cannot be predicted by taxonomic (e.g. 16S rRNA sequencing) methods alone. Using beneficial Pseudomonas sp. and Arabidopsis as a tractable rhizosphere microbiome model, we are using a combination of comparative genomics and functional assays to correlate microbiome function with the presence of certain genes in the plant microbiome. Using these approaches, we have identified the genetic basis of 1) Pseudomonas modulation of plant immunity and 2) that Pseudomonas can transition from an opportunistic pathogen through gain and loss of genomic islands via homologous recombination. We have identified closely-related strains (>97% identical by 16S rRNA) of P. fluorescens that induce systemic resistance (ISR) or susceptibility (ISS) to foliar pathogens. Using a combination of comparative genomics and functional assays we have identified a bacterial spermidine synthase (speE) gene that is uniquely present in ISS strains. We have deleted the speE gene and found that it is necessary for the ISS phenotype, and purified spermidine can phenocopy ISS strains. This indicates that single bacterial genes can underlie effects on host immunity. In addition to bacterial genes involved in modulation of systemic defense, we have identified P. fluorescens genes that are involved in transition from pathogenic to commensal lifestyles within P. fluorescens . Using the same comparative genomics platform, we have found that this transition is mediated by homologous recombination leading to gain and loss of horizontally transferred genomic elements. This work suggests that homologous recombination may be an evolutionary mechanism driving lifestyle changes in closely-related bacteria. Collectively, this work will inform our understanding of bacterial transitions from free living to host-associated, and how the plant microbiome affects plant health.

Plant Microbiome

Concurrent Speaker - Heike Seybold

Abstract Title: INFECTION WITH ZYMOSEPTORIA TRITICI RENDERS WHEAT SUSCEPTIBLE TO NON-ADAPTED PLANT PATHOGENS

Primary Author(s) and Institution(s): Heike Seybold 1,2 , Tobias Demetrowitsch 3,4 , AMINE HAssani 1,2 , Carla Krone 1 , Karin Schwarz 3,4 , Eva H. Stukenbrock 1,2 1 Environmental Genomics, Botanical Institute, Christian-Albrecht-University of Kiel, Germany 2 Max Planck Institute for Evolutionary Biology, Plön, Germany 3 Institute of Human Nutrition and Food Science, Christian-Albrecht-University of Kiel, Germany 4 Spectromics: Network of Analytical Spectroscopy and Mass Spectrometry, Kiel

Abstract

The specialized fungal wheat pathogen Zymoseptoria tritici is the causal agent of Septoria tritici Blotch (STB), a major threat to wheat production in Europe and temperate climates worldwide. A symptom-free and presumably biotrophic phase of fungal growth is followed by a lifestyle switch to necrotrophic growth. We aimed to elucidate the nature of the symptom-free infection phase and the range of putative immune suppression during biotrophic fungal growth. In addition to wheat cultivars of varying STB susceptibility, we used different pathovars of Pseudomonas syringae bacteria to study the physiological responses of wheat to Z. tritici infections . During the biotrophic infection phase, we observed that non-adapted P. syringae strains were able to infect wheat. This effect was not limited to the fungal infection site, but also detected in adjacent leaf areas. Remarkably, after Z. tritici infection of wheat cultivars carrying STB resistance genes, we observed systemic acquired resistance also towards adapted P. syringae strains . We further measured plant-produced metabolites and found supporting evidence of fungus-mediated resistance suppression during colonization of susceptible wheat. Our findings suggest that virulent Z. tritici infections of wheat (I) cause systemic acquired susceptibility allowing colonization by non-adapted phytopathogens and (II) the fungal infection impacts leaf microbiome dynamics.

Plant Microbiome

Concurrent Speaker - Cécile Vriet

Abstract Title: UNRAVELING THE IMPORTANCE OF SUGAR TRANSPORT IN PLANT-BENEFICIAL RHIZOBACTERIA INTERACTIONS

Primary Author(s) and Institution(s): Cécile Vriet , Antoine Desrut, Pierre Coutos-Thévenot UMR-CNRS 7267 EBI, 86000 Poitiers, France.; UMR7267 EBI

Abstract

Plant Growth Promoting Rhizobacteria (PGPR) are able to confer to plants an improved growth and/or tolerance to various biotic and abiotic stresses. Understanding the molecular mechanisms involved in these biological processes should help develop novel and environmentally friendly strategies for crop protection and productivity improvement and contribute to the rise of a more sustainable agriculture system. A growing body of evidence demonstrates the importance of sugar transport in plant pathogen resistance and in plant-microorganism mutualistic symbioses. In contrast, the role and regulation of sugar transporter activities in plant-PGPR interactions remain to be investigated. To address this issue,

we have set up an in vitro experimental system that allow a detailed study of the different PGPR modes of action and mechanisms involved in their beneficial effects on plant growth and development. Using this system, the model plant Arabidopsis thaliana , and a collection of PGPR strains, we have carried out a comprehensive targeted gene expression analysis (by quantitative RT-PCR). From this work, we have identified several plant sugar transporter genes whose expression is induced or repressed by the PGPR strain(s). We are currently studying the function of some of these candidate genes by a reverse genetic approach.

Hormone Transport
Concurrent Chair - Youngsook Lee

Abstract Title: G SUB-FAMILY MEMBERS OF ABC TRANSPORTERS TRANSPORT VERY IMPORTANT MOLECULES IN PLANTS

Primary Author(s) and Institution(s): YOUNGSOOK LEE, THANH HA THI DO, JIE ZHANG, JAE-UNG HWANG; Division of Integrative Bioscience and Biotechnology, POSTECH, 77 Cheongam-Ro, Pohang, 37673, South Korea

Abstract

ABC transporters exist in all living organisms, and are particularly enriched in terrestrial plants. We have been studying many members of ABCG sub-family in Arabidopsis, and found that they transport diverse compounds including plant hormones, hydrophobic surface coating materials, and secondary metabolites. Some of them are highly specific for substrates, others are not. Some of them exhibit transport activities in heterologous systems, but others do not. Thus, more studies are necessary to fully understand their mechanism of function. We will report the approaches we are taking to obtain better understanding on these transporters, and also, a new member of this sub-family which has a unique structure and a very important function.

Hormone Transport
Invited Speaker - Eilon Shani

Abstract Title: ROBUSTNESS AND SPECIALIZATION AMONG HORMONE TRANSPORTERS: REINFORCING FUNCTIONAL REDUNDANCY TO UNDERSTAND PLANT GROWTH

Primary Author(s) and Institution(s): EILON SHANI School of Plant Sciences and Food security, Tel Aviv University, Israel; Tel Aviv University

Abstract

Gibberellins (GAs) are plant hormones that promote plant growth and are commonly used in agriculture. While GA perception is well understood, little is known about the process of GA transport or the regulation of GA distribution in the plant. We have utilized a unique bioactive fluorescently-labeled GAs to screen for Arabidopsis mutants deficient in GA transport and identified NPF3 that efficiently transports GA across cell membranes both in vitro and in vivo. NPF3 belongs to an evolutionarily conserved but strongly expanded and diversified family of transporters with 53 members

in Arabidopsis and 90 in Tomato. Plant genomes are highly redundant as over 80% of all protein-coding genes belong to families with at least two members. In order to reinforce functional redundancy, we have developed transportom-scale amiRNA and CRISPR based multiplexing screens that aim to close the current gap in knowledge regarding the robust and specialized mechanisms used by plants to transport hormones. Our screens revealed multiple novel functionally redundant putative plant hormone transporters, among them the NPF and ABC families. On this basis, we propose that functionally redundant but specialized activity of the NPF and ABC families drive hormone distribution, activity and growth in Arabidopsis and Tomato.

Hormone Transport

Concurrent Speaker - Sumin Lee

Abstract Title: IDENTIFICATION OF A FAMILY OF ACC TRANSPORTERS IN ARABIDOPSIS THALIANA

Primary Author(s) and Institution(s): SUMIN LEE AND MOON-SOO SOH Division of Integrative Bioscience and Biotechnology, Sejong University, Seoul 05006, Republic of Korea; Sejong University

Abstract

1-aminocyclopropane-1-carboxylic acid (ACC), a biosynthetic precursor of ethylene, has long been proposed to act as a mobile messenger in higher plants. However, little is known about the transport system of ACC. Recently, our genetic characterization of an early-senescence mutant revealed that LYSINE HISTIDINE TRANSPORTER1 (LHT1) functions as a transporter of ACC. As amino acid transporters might have similar molecular selectivity, we hypothesized that other amino acid transporters including LHT1 paralogs might preserve the ACC-transporter activity. As a proof-of-concept, in this study, we took gain-of-function approach by transgenic complementation of lht1 . When we introduced overexpressing transgene into lht1 knock-out mutant, we found that transgenic expression of selected members of LHT and AMINO ACID PERMEASE (AAP) can restore not only ACC-resistance phenotype but also early-senescence syndrome of lht1 mutant. Taken together, these results provide genetic evidence that some, if not all, of amino acid transporters in Arabidopsis function as ACC transporters like LHT1 and we propose that multiple transporters of ACC have been evolved, contributing to various aspects of biological processes, such as attenuation of leaf senescence.

Hormone Transport

Concurrent Speaker - Chloe Beziat

Abstract Title: TRANSCRIPTIONAL AND POST-TRANSCRIPTIONAL REGULATIONS OF PILS INTRACELLULAR AUXIN CARRIERS MEDIATING NUCLEAR AUXIN SIGNALLING

Primary Author(s) and Institution(s): CHLOE BEZIAT 1,2 , ELKE BARBEZ 1,2 , MUGUREL IOAN FERARU 1 , DORIS LUCYSHYN 1 , JÜRGEN KLEINE-VEHN 1,2 1 Department of Applied Genetics and Cell biology, University of Natural Resources and Life Sciences (BOKU), Muthgasse 18, 1190 Vienna, Austria. 2 Department of Plant Systems Biology, VIB and Department of Plant Biotechnology and Bioinformatics, Ghent University, Technologiepark 927, 9052 Gent, Belgium

Abstract

The phytohormone Auxin is a central growth regulator involved in a multitude of developmental aspects. We identified in silico a novel putative auxin carrier family called PIN-LIKES (PILS), whose members are localized at the endoplasmic reticulum (ER). PILS facilitate intracellular auxin accumulation at the ER, which interferes with the nuclear availability and signaling of auxin. We used the apical hook as a model for differential growth control and reveal that PILS guard nuclear auxin signaling and de-repression of growth during apical hook opening. PILS gene activity is under the control of the light sensitive transcription factor PHYTOCHROME INTERACTING FACTOR 5 (PIF5). Thereby, light perception modulates PILS-dependent auxin signaling, integrating environmental information into the growth program. Moreover, to unravel additional molecular components, we conducted a forward genetic screen, identifying a post- transcriptional regulator of PILS turnover at the ER.

Hormone Transport

Concurrent Speaker - Michał Jasiński

Abstract Title: MTWBC20 IS AN ABA EXPORTER ACTING IN ROOTS AND SEEDS OF MEDICAGO TRUNCATULA.

Primary Author(s) and Institution(s): ALEKSANDRA PAWELA Department of Plant Molecular Physiology, Institute of Bioorganic Chemistry, Polish Academy of Sciences, Poznan, Poland JOANNA BANASIAK Department of Plant Molecular Physiology, Institute of Bioorganic Chemistry, Polish Academy of Sciences, Poznan, Poland WANDA BIAŁA Department of Plant Molecular Physiology, Institute of Bioorganic Chemistry, Polish Academy of Sciences, Poznan, Poland ENRICO MARTINOIA Department of Plant and Microbial Biology, University of Zurich, 8008 Zurich, Switzerland. MICHAŁ JASIŃSKI Department of Plant Molecular Physiology, Institute of Bioorganic Chemistry, Polish Academy of Sciences, Poznan, Poland Institute of Bioorganic Chemistry, Polish Academy of Sciences, Poznan, Poland

Abstract

Abscisic acid (ABA) is a ubiquitous plant hormone and signaling molecule. It controls plant growth and development and modulates the response to environmental stressors. As a phytohormone, ABA also controls germination under unfavorable conditions. In Arabidopsis thaliana , members of the ATP-binding cassette (ABC) family have been shown to be involved in ABA transport. Intriguingly, almost nothing is known about the ABA translocation and ABA transporters in legumes. Here, we describe a Medicago truncatula MtWBC20, as an ABA exporter that fulfills novel roles in roots and germinating

seeds. In seeds, MtWBC20 was found in the hypocotyl-radicle transition zone of the embryonic axis. Heterologous expression in Arabidopsis thaliana provided evidence that MtWBC20 is a plasma membrane protein that is likely to form homodimers. Moreover, export of ABA from Nicotiana tabacum BY2 cells expressing MtWBC20 was faster than in the BY2 control line. Mtwbc20 plants produced fewer lateral roots and more nodules than wild-type plants in conditions mimicking drought stress. Seeds of mtwbc20 were more sensitive to ABA upon germination, and the ABA translocation within mtabcg20 embryos was impaired. National_Science_Centre Grant 2013/10/M/NZ3/00260

Synthetic biology
Concurrent Chair - Nicola Patron

Abstract Title: TAILORING PLANTS FOR BIOMANUFACTURING

Primary Author(s) and Institution(s): NICOLA J PATRON; Earlham Institute

Abstract

Synthetic biology has already demonstrated that microorganisms can be reprogrammed to produce valuable molecules from simple inputs like sugars. Plants provide the potential for the rapid production of complex molecules from water and light but, until recently, we lacked the tools and data necessary for the complex engineering required to optimise purity and yield. In our lab, we use comparative genomics and systems biology approaches to understand how the primary sequence of regulatory elements relates to function and to understand how plants respond to, and attempt to detoxify foreign molecules. We use this information to design and write and edit DNA sequences to tailor plants as biomanufacturing platforms and to engineer traits related to nutrition and yield. Our work is underpinned by applying the principles of engineering to biology. This enables up to undertake high-throughput experimentation at nanoscales. Rapid testing of the relationship between sequence and function is enabled by automated fabrication of DNA assemblies coupled to transient ratiometric gene expression assays.

Synthetic biology
Invited Speaker - Diego Orzaez

Abstract Title: A TOOLBOX OF MODULAR ELEMENTS FOR ORTHOGONAL CONTROL OF GENE EXPRESSION IN PLANTS

Primary Author(s) and Institution(s): DIEGO ORZAEZ , JOAN BERNABÉ, SARA SELMA, ALFREDO QUIJANO, BORJA DIEGO, JAVIER MANCHEÑO, MARÍA AJENJO, ASUN FERNÁNDEZ-DEL-CARMEN, ANTONIO GRANELL, MARTA VÁZQUEZ Instituto de Biología Molecular y Celular de Plantas Consejo Superior de Investigaciones Científicas (CSIC) Universitat Politècnica de València; IBMCP-CSIC

Abstract

The effective control of gene expression in plants require new orthogonal regulatory elements that facilitate the design of complex gene circuits. We report our advances in the design of two types of genetic devices: a reversible toggle switch based on PhiC31 integrase-mediated DNA recombination, and a number of programmable transcriptional regulators based on CRISPR/cas9 architecture. The recombinase-based switch was analysed using register constructs that alternate Luciferase and GFP

expression in ON and OFF conformations respectively. Registers´ functionality was tested transiently in N. benthamiana , showing effective transition from ON to OFF states and vice versa in the presence of PhiC31 with or without its Reversibility Factor. Later, registers were stably transformed N. benthamiana and shown that functionality of the switch is retained in the context of the plant genome. On the other hand, a number of programmable transcriptional factors (PTF) were constructed based on CRISPR/Cas9 architecture combined with transcriptional activation domains and using SAM and Sun-Tag strategies to maximize cooperativity. PTF activity was tested transiently and stably in N. benthamiana using luciferase constructs driven by standard promoter regions as reporters. An optimal design of PTFs and gRNAs resulted in activation rates that reached up to 80 fold in the case of a reporter construct carrying the tomato dehydroxy flavonol reductase (DFR) promoter.

Synthetic biology

Concurrent Speaker - Jonathan Tremblay

Abstract Title: A LOOP REPLACEMENT DESIGN APPROACH FOR THE DEVELOPMENT OF PLANT CYSTATINS HIGHLY SPECIFIC TO HERBIVOROUS ARTHROPOD DIGESTIVE PROTEASES

Primary Author(s) and Institution(s): Jonathan TREMBLAY 1 , Marie-claire GOULET 1 , Vanessa MERCURE GODIN, Charles GOULET 1 and Dominique MICHAUD 1 1 Centre de recherche et d'innovation sur les végétaux, Université Laval, Québec QC, Canada; Université Laval

Abstract

Numerous studies have discussed the use of plant cystatins to implement pest resistance in transgenic crops. These proteins behave as pseudo-substrate inhibitors in the midgut of herbivorous arthropods to hinder the active site of digestive proteases and compromise protein digestion. A key goal at present to take full advantage of plant cystatins in pest control is to optimize their inhibitory profile towards arthropod proteases without altering the host plant's own proteases. The idea is to generate cystatin variants with both strong affinity for the pest proteases and weak affinity for the host plant proteases. We here performed protease inhibition assays with E. coli -produced forms of 20 phylogenetically distant plant cystatins and the proteases of selected plant–arthropod models to appreciate the extent of functional diversity among plant cystatins. We then used the most potent cystatins as 'donors' of structural elements to create arthropod-specific cystatin hybrids by a 'loop replacement design' protein engineering approach. Our results illustrate the wide variety of protease inhibitory profiles among plant cystatins and the usefulness of these proteins as a pool of discrete structural elements for the design of potent cystatin hybrids specific to target pest digestive proteases.

Synthetic biology

Concurrent Speaker - Anna Coll

Abstract Title: PLANT X-TENDER, A SYSTEM FOR THE ASSEMBLY, DELIVERY AND EXPRESSION OF MULTIGENE CONSTRUCTS IN PLANTS

Primary Author(s) and Institution(s): ANNA COLL 1 , TJAŠA LUKAN 1,2 , FABIAN MACHENS 3* ŠPELA BAEBLER 1 , KATRIN MESSERSCHMIDT 3 and KRISTINA GRUDEN 1 1 National Institute of Biology, Department of Biotechnology and Systems Biology, Ljubljana, Slovenia; 2 International Postgraduate School, Ljubljana, Slovenia; 3 University of Potsdam, Cell2Fab Research Unit, Potsdam, Germany; # Current address: University of Potsdam, Department Molecular Biology, Potsdam, Germany

Abstract

Cloning multiple DNA fragments for delivery of several genes of interest into the plant genome is one of the main technological challenges in plant synthetic biology. Despite several modular assembly methods developed in recent years, the plant biotechnology community has not widely adopted them yet, probably due to the lack of appropriate vectors and software tools. Here we present Plant X-tender, an extension of the highly efficient, scar-free and sequence-independent multigene assembly strategy AssemblX, based on overlap-depended cloning methods and rare-cutting restriction enzymes. Plant X-tender consists of a set of plant expression vectors and the protocols for most efficient cloning into the novel vector set needed for plant expression and thus introduces advantages of AssemblX into plant synthetic biology. The novel vector set covers different backbones and selection markers to allow full design flexibility. We have included ccdB counterselection, thereby allowing the transfer of multigene constructs into the novel vector set in a straightforward and highly efficient way. Vectors are available as empty backbones and are fully flexible regarding the orientation of expression cassettes and addition of linkers between them, if required. We optimised the assembly and subcloning protocol by testing different scar-less assembly approaches: the noncommercial SLiCE and TAR methods and the commercial Gibson assembly and NEBuilder HiFi DNA assembly kits. Plant X-tender was applicable even in combination with low efficient homemade chemically competent or electrocompetent Escherichia coli . We have further validated the developed procedure for plant protein expression by cloning two cassettes into the newly developed vectors and subsequently transferred them to Nicotiana benthamiana in a transient expression setup. Thereby we show that multigene constructs can be delivered into plant cells in a streamlined and highly efficient way. Our results will support faster introduction of synthetic biology into plant science.

Synthetic biology

Concurrent Speaker - Khanh Vuu

Abstract Title: ENGINEERING PLANTS WITH NOVEL METABOLIC PATHWAYS AS A PRODUCTION PLATFORM FOR BIO-PRODUCTS

Primary Author(s) and Institution(s): KHANH M. VUU 1,2 , AYMERICK EUDES 1,2 , PATRICK M. SHIH 1,2 1 Joint BioEnergy Institute, Emery Station East, 5885 Hollis St, 4th Floor, Emeryville, California 94608, USA. 2 Biological Systems and Engineering Division, Lawrence Berkeley National Laboratory, 1 Cyclotron Road, Berkeley, Berkeley, California 94720, USA.; JointBio Energy Institute

Abstract

A large portion of the U.S. energy supply relies on non-renewable natural resources of fossil fuels such as petroleum, coal, and natural gases. Inefficient practices and demand for more energy have increased the usage of fossil fuels. Therefore, it is critical and of high interest to develop alternative, renewable methods for biotechnological production processes before depleting the global supply. Advances in microbial systems, such as E. coli and yeast, have made it possible to engineer artificial pathways for chemical production, due to the ease of genetically manipulating and optimizing metabolic routes. However, with improvements in plant synthetic biology tools and increasing interest in leveraging plants as a bio-platform for production of biologics or industrially-relevant chemicals, we explore the potential use of plant-based manufacturing of the chemical, muconic acid—an intermediate molecule that can be derived into several bio-plastics. Here, we exploit primary plant metabolism to test and optimize various metabolic routes, enabling direct production of muconic acid (± 18.54 mg/g D.W.) via photosynthesis, and circumventing toxic byproducts of existing chemical processes. Plant-based metabolic engineering efforts may enable a more sustainable means of producing desirable chemicals and thereby decrease our reliance on current practices heavily dependent on petroleum feedstock.

DNA Damage and Repair
Concurrent Chair - Paula Casati

Abstract Title: ROLE OF CHROMATIN REMODELING PROTEINS IN DNA DAMAGE AND REPAIR AFTER UV-B EXPOSURE

Primary Author(s) and Institution(s): PAULA CASATI; CEFOBI

Abstract

Terrestrial life evolved only after the stratospheric ozone layer formed and could absorb most damaging UV-B (280-315 nm) in solar radiation. The strong absorption of UV-B by biological molecules, particularly DNA, makes this radiation extremely dangerous. Because plants must absorb photons to power photosynthesis, they are inevitably exposed to damaging UV-B. Chromatin remodeling in response to UV-B has been implicated in plants. In particular, the package of DNA in the chromatin affects the structure and accessibility of DNA, and therefore the velocity of formation and repair of damage in DNA molecules. Thus, we explored the role of chromatin proteins in DNA damage and repair after UV-B exposure. In particular, we investigated the role of histone acetylation and the participation of histone chaperones in DNA repair and UV-B damage responses, and the function of chromatin proteins in the regulation of the cell cycle after exposure. Our results indicate that chromatin remodeling is a key process in DNA repair after a UV-B treatment, and that lines deficient in this process are more sensitive to UV-B.

DNA Damage and Repair
Invited Speaker - Jean Molinier

Abstract Title: SMALL RNA-MEDIATED REPAIR OF UV-INDUCED DNA LESIONS

Primary Author(s) and Institution(s): JEAN MOLINIER , VALERIE COGNAT, STEFANIE GRAINDORGE Institut de biologie moléculaire des plantes du CNRS, 12 rue du Général Zimmer, 67000 Strasbourg, France.; IBMP-CNRS

Abstract

As photosynthetic organisms, plants need to prevent irreversible UV-induced DNA lesions. For this, several photolesions specific DNA repair pathways are activated such as Direct Repair and Nucleotide Excision Repair (NER). Recently we have uncovered a previously unrecognized interplay between NER and small interfering RNAs (siRNAs) in the recognition of DNA photoproducts. The biogenesis of photoproduct-associated siRNAs (21-nt) involves the non-canonical, concerted action of RNA POLYMERASE IV, RNA-DEPENDENT RNA POLYMERASE-2 and DICER-LIKE-4. Upon UV irradiation, the DNA DAMAGE-BINDING PROTEIN 2 (DDB2) and ARGONAUTE 1 (AGO1) of Arabidopsis thaliana form a chromatin-bound complex together with 21-nt siRNAs, which likely facilitates recognition of DNA damages in an RNA/DNA complementary strand-specific manner. The identification of this new pathway significantly extend the now emerging notion that complex interconnections between core siRNAs biogenesis factors exist. Using genetics and genome wide approaches we will present how UV-induced DNA damage, DNA methylation and small RNA-mediated processes interconnect and contribute to efficiently maintain genome and epigenome integrity.

DNA Damage and Repair

Concurrent Speaker - Janice de Almeida-Engler

Abstract Title: WEE1: A KEY CELL CYCLE REGULATOR INVOLVED IN PLANT-ROOT KNOT NEMATODE INTERACTION

Primary Author(s) and Institution(s): CABRAL DO NASCIMENTO, Danila (1), José Dijair Antonino de Souza Jr(2), ENGLER, Gilbert (1), Maria Fatima Grossi de Sa (2), Lieven De Veylder and DE ALMEIDA ENGLER, Janice (1) (1) INRA, Université Cote D'Azur, CNRS, UMR 1355-7254 Institut Sophia Agrobiotech. (2) Embrapa Recursos Genéticos e Biotecnologia. (3) Plant Systems Biology, VIB; Gent University.; Institut National de la Recherche Agronomique

Abstract

Plant parasitic nematodes are among the most destructive plant pathogens. Root-knot nematodes (RKN; Meloidogyne spp.) infect plant roots and trigger the formation of specialized feeding sites by substantial reprogramming root cell development. Both, the plant mitotic cycle and the endocycle, are essential targets for a successful susceptible interaction between the host plants and nematodes. Key cell cycle genes, as well as inhibitor genes are important components to allow the induction and maintenance of the nematode feeding site (NFS) development. Among them, WEE1 belongs to a family of protein kinases involved in the terminal phosphorylation and inactivation of cyclin-dependent kinase 1- cyclin B complex resulting in G2 cell cycle arrest in response to DNA damage in Arabidopsis . WEE1 is mainly expressed at early nematode infection stages most likely due to stress caused by nematode infection. Morphological analysis shows that the lack of WEE1 protein induces mitotic activity in galls. Functional analysis of the wee1-1 line illustrate cumulative mitotic defects possibly due to the lack of the appropriate timing for proper DNA replication and repair in giant cells. Our data suggest a conserved plant WEE1 function in galls triggering cell cycle arrest in response to DNA damage.

DNA Damage and Repair
Concurrent Speaker - Gideon Mmbando

Abstract Title: AFRICAN RICE SPECIES (O. GLABERRIMA, O. BARTHII AND O. SATIVA) EXHIBIT HYPERSENSITIVITY TO UVB RADIATION RESULTED FROM CPD PHOTOLYASE POLYMORPHISM

Primary Author(s) and Institution(s): GIDEON MMBANDO , MIKA TERANISHI, JUN HIDEMA Graduate School of Life Sciences,Tohoku University, Japan

Abstract

The sensitivity to UVB radiation varies widely among Asian rice (O. sativa L.) cultivars, and the activity of cyclobutane pyrimidine dimers (CPD) photolyase, which repairs UVB-induced CPD, is crucial factor for determining the UVB sensitivity. African rice is not of the same origin as Asian rice but rather is an entirely different species (i.e., O. glaberrima Steud., O. barthii). O. glaberrima is well adapted for cultivation in west Africa and possesses traits for increased tolerance to biotic and abiotic stresses. However, information about UVB sensitivity among African rice is largely unknown. Here, we investigate the relationship between UVB sensitivity and CPD photolyase activity in 15 Africa cultivated rice strains include O. glaberrima , O. barthii and tropical O. sativa from various geographical location. Rice strains were grown in growth chamber with or without supplementary UVB (1.2 W m -2). Africa rice cultivars exhibit hypersensitive phenotypes in comparison to Asian rice and the hypersensitivity is caused by new identified polymorphism. The activity of native African rice CPD photolyase was significantly reduced in cultivars possessing new polymorphism. Furthermore, the transcript level of CPD photolyase varies among Africa rice cultivars. Our results suggest that, new polymorphism largely affect UVB sensitivity.

Physiology and development of stomata guard cells
Concurrent Chair - Nathalie Leonhardt

Abstract Title: A GENETIC SCREEN TO IDENTIFY ARABIDOPSIS GENES INVOLVED IN TRANSPIRATION RATE, LEAF TEMPERATURE AND STOMATA REGULATION AND DEVELOPMENT

Primary Author(s) and Institution(s): N. LEONHARDT ; B. ROUX; H. JACQUET H; N. POCHON; S. CHIARENZA Laboratoire de Biologie du Développement des Plantes (LBDP) Institut de Biosciences et Biotechnologies d'Aix-Marseille (BIAM) UMR 7265 CNRS-CEA-Université Aix-Marseille II CEA Cadarache FRANCE; CEA

Abstract

In plants, the majority of water loss occurs through pores on the leaf surface, which are called stomata. The size of the stomatal pores varies and controls the rate of diffusion of water vapour out of the plant. In addition to controlling water loss, stomata allow CO 2 to diffuse into the leaf for photosynthesis. Thereby, stomata permanently control the trade-off between carbon uptake and water loss. Regulation of stomatal movements by guard cells in response to environmental stimuli and stress conditions is a primary factor in determining water use efficiency and productivity of crop plants. To identify new actors involved in guard cell signaling, a new genetic screen was performed taking advantage of the "open stomata" phenotype of the ost2-2D mutant. This mutant, due to the constitutive H + -ATPase activity, displays very high hyperpolarization values of the free-running potential of the guard cell plasma membrane. Using thermal imaging, we identified genes and mutations that suppress the "open

stomata" phenotype of the ost2-2D dominant mutant in response to light/dark transition. Finally, the use of the new high throughput DNA sequencing technologies, allows us the rapid identification of causal mutations at single-nucleotide resolution even in complex genetic backgrounds. Also, owing to the high-throughput nature and cost-effectiveness, sequencing-based methods for mutation identification replace recombination-based genetic mapping. Several mutants involved in the control of transpiration rate, stomatal regulation and development, or leaf temperature were identified. In addition , new elements involved in H + -ATPase regulation were discovered and their characterization will shed a new light on how these proteins drive crucial plant functions with potential major outcomes for crops.

Physiology and development of stomata guard cells
Invited Speaker - Diana Santelia

Abstract Title: Sugar transport to guard cells is required for stomatal opening and plant growth

Primary Author(s) and Institution(s): Arianna Nigro1, Klára Panzarová2, Diana Santelia1; Institute of Plant and Microbial Biology, University of Zurich, Switzerland

Abstract

CO2 for photosynthesis enters plants via stomata – small adjustable pores on the leaf surface. Stomatal opening is promoted by increase in the turgor pressure of the two flanking guard cells through accumulation of osmotically active inorganic (K+, Cl-) and organic (malate2- and sugars) solutes. Given that starch breakdown or CO2 fixation within guard cells can only provide a limited amount of carbon, symplastically isolated guard cells likely rely on external carbon sources to fulfil their metabolic needs. Here, we investigated the role of sugar import in stomatal opening in Arabidopsis thaliana. We show that the synergistic action amongst members of the plasma membrane monosaccharide/proton symporters STP family is required for stomatal opening and CO2 uptake driving photosynthesis and biomass production. Furthermore, we reveal that the uptake of apoplastic sugars into guard cells provides the main source of carbon for guard cell starch accumulation. Thus, at the start of the day, guard cell metabolism for stomatal opening relies predominantly on mesophyll-derived sugars imported into guard cells in the form of monosaccharides. This study highlights that a tight coordination between mesophyll and guard cell carbohydrate metabolism is critical to promote stomatal opening and plant growth.

Physiology and development of stomata guard cells
Concurrent Speaker - Noriane Simon

Abstract Title: HOW DO CIRCADIAN RHYTHMS INCREASE PLANT WATER USE EFFICIENCY?

Primary Author(s) and Institution(s): N.M. L. SIMON 1 , H. KUDOH 2 , A. M. HETHERINGTON 1 , A. N. DODD 1 1 UNIVERSITY OF BRISTOL, UK 2 KYOTO UNIVERSITY, JAPAN; University of Bristol

Abstract

Reduced soil water availability represents a serious threat to modern agriculture, causing significant decreases in crop yield worldwide. Therefore, it is a research priority to develop solutions for more sustainable use of water in agriculture. Circadian rhythms regulate stomatal opening and increase plant

water use efficiency (WUE), but the mechanisms underpinning this process and its contribution to plant performance remain unclear. I am examining the involvement of circadian regulation in the WUE of higher plants. I have identified several circadian oscillator components that make a key contribution to WUE. I have also performed targeted manipulations to the circadian oscillator to better understand the relationship between the circadian oscillator and stomatal aperture. I have identified specific and novel roles for the guard cell circadian oscillator in whole-plant physiology. Overall, this work is providing a deeper understanding of how circadian rhythms optimise plant WUE.

Physiology and development of stomata guard cells
Concurrent Speaker - Alexis De Angeli

Abstract Title: DYNAMIC MEASUREMENTS OF CYTOSOLIC PH AND [NO3-] REVEALS THE IN VIVO ACTVITY OF ANION CHANNELS AND TRANSPORTERS IN GUARD CELLS

Primary Author(s) and Institution(s): ALEXIS DE ANGELI 1 , ELSA DEMES 1 , LAETITIA BESSE 1 , BEATRICE SATIAT-JEUNEMAITRE 1 , SEBASTIEN THOMINE 1 1 Institute for Integrative Biology of the Cell (I2BC), CEA, CNRS, Univ. Paris - Sud, Université Paris - Saclay, 91198, Gif - sur - Yvette cedex, France; CNRS

Abstract

Anion transporters/channels of the plasma and intracellular membranes are key actors of guard-cells responses to environmental stimuli. Indeed, anion transport systems are necessary to mediate stomata movements. During stomata opening/closure, it is assumed that the guard-cells undergo massive H + -coupled fluxes of (an)ions (like Cl - and NO 3 -) between the apoplast, the cytosol and the vacuole. These fluxes induce a change of the guard-cell osmotic potential leading to changes of the cellular volume. All the ionic fluxes between the apoplast and the vacuole has to pass through the cytosol. This opens of the question of the regulation of the ionic gradients across the guard-cell plasma and the vacuolar membranes. To address this unexplored issue we developed the use of a fluorescent biosensor enabling to simultaneously measure the cytosolic pH and [NO 3 - , Cl -] in Arabidopsis guard-cells. Unexpectedly, we observed fast cytosolic pH and [NO 3 -] responses to extracellular conditions and stimuli. Further, we could visualize in vivo the impact of the activity of the vacuolar exchanger CLCa and of the plasma membrane channel SLAC1 on cytosolic pH and [NO 3 -]. Our results show that the activity of anion transport systems have a major impact on the cytosolic pH and [NO 3 -] homeostasis

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Physiology and development of stomata guard cells
Concurrent Speaker - Elsa Ronzier

Abstract Title: TWO CA2+-DEPENDENT PROTEIN KINASES (CPKS) OPPOSITELY REGULATE A UBIQUITOUS K+ CHANNEL IN ARABIDOPSIS THALIANA

Primary Author(s) and Institution(s): Elsa Ronzier 1 ,2 , Claire Corratgé-Faillie 1 , Frédéric Sanchez 1 , Christian Brière 3 , Jean-Baptiste Thibaud 1 and Tou Cheu Xiong 1 . 1: BPMP, 2 place Viala Bat 7, 34060 Montpellier cedex 1, France 2 MGH, HMS, 185 Cambridge Street, Suite 3201, Boston, MA 02114, USA 3 : LRSV, 24 chemin de Borde-Rouge. BP 42617 Auzeville, 31326 Castanet-Tolosan, France

Abstract

In plant cells, as regards both the electrical polarization of the plasma-membrane and the osmotic homeostasis, voltage-gated K + channels participate in transduction chains, often downstream Ca 2+ signals. Thus, worth considering is, among the range of post-translational modifications, that potentially regulate their activity, the phosphorylation of these so-called Shaker channels by Ca 2+ -dependent protein kinases (CPKs). We investigated the interactions between these two families of proteins by a combination of techniques: heterologous expression in Xenopus oocytes followed by electrophysiology recordings, in planta interaction by FRET-FLIM imaging, in vitro phosphorylation study using channel-derived peptide arrays, looking for overlap of expression patterns and characterization of gain- or loss-of-function mutants. Here we have identified several CPKs targeting and regulating the Shaker channel activities. Interestingly, we found that CPK13, a Ca 2+ -insensitive CPK, and CPK6, a Ca 2+ -strictly dependent CPK, respectively inhibits and activates the same Shaker channel, KAT2. In the context of (i) the large expression pattern of KAT2 (e.g. in leaf vasculature and in guard cells) and (ii) the documented ability of KAT2 to form heteromeric channels with the Shaker sub-units AKT2 and KAT1, we shall discuss the potential implication of KAT2 regulation by CPKs in phloem and stomata physiology.

Molecular Mechanisms of Autophagy
Concurrent Speaker - Richard Vierstra

Abstract Title: INTEGRATED MULTI-OMICS ANALYSES OF MAIZE REVEAL ROLES FOR AUTOPHAGIC RECYCLING IN PROTEOME REMODELING AND LIPID TURNOVER

Primary Author(s) and Institution(s): RICHARD D. VIERSTRA , FIONN MCLOUGHLIN, ROBERT C. AUGUSTINE, RICHARD S. MARSHALL, FAQIANG LI, AND LIAM D. KIRKPATRICK Department of Biology, Washington University in St. Louis, St. Louis, MO 63130; Washington University in St. Louis

Abstract

The turnover of cytoplasmic material via autophagic encapsulation and delivery to vacuoles is essential for recycling intracellular constituents, especially under nutrient-limiting conditions. To determine how cells/tissues rely on autophagy, we applied in-depth multi-omic analyses to study maize (Zea mays) autophagy mutants grown under nitrogen-replete and starvation conditions. Surprisingly, broad alterations in the leaf metabolome were evident in plants missing the core autophagy component ATG12 even without stress, particularly affecting products of lipid turnover and secondary metabolites, which were underpinned by substantial changes in the transcriptome and/or proteome. Cross-comparison of mRNA and protein abundances allowed for the identification of organelles, protein

complexes, and individual proteins targeted for selective autophagic clearance, and revealed several processes controlled by this catabolism. In particular, autophagic turnover of proteasomes (proteaphagy) in response to nutrient deprivation or inactivatlon, is regulated by multiple ubiquitylation and aggregation events that either help advance turnover or protect proteasomes for reuse when nutrient availability improves. Collectively, we describe a facile proteomic strategy to survey autophagic substrates, and show that autophagy has a greater than expected influence in sculpting plant proteomes and membranes both before and during nutrient stress. This work was supported by U.S. NSF-PGRP (IOS-1339325)

Molecular Mechanisms of Autophagy
Invited Speaker - Diane Bassham

Abstract Title: REGULATION OF AUTOPHAGY DURING ENDOPLASMIC RETICULUM STRESS

Primary Author(s) and Institution(s): DIANE C BASSHAM; Iowa State University

Abstract

Autophagy is a macromolecule degradation pathway in which cellular components are transported to the vacuole for recycling. It acts to mobilize nutrients during nutrient deficiency and senescence and to clear damaged molecules and organelles during environmental stress. Autophagy therefore contributes to cell survival during adverse environmental conditions. My lab is analyzing the function and regulation of autophagy in plants, including its role in degradation of the endoplasmic reticulum during ER stress. We found that ER stress induces autophagy in plants via an IRE1b-dependent pathway. IRE1b is a dual protein kinase and ribonuclease, and we determined that the ribonuclease domain, but not the kinase domain, is required for autophagy. We also identified several downstream factors whose mRNAs must be degraded by IRE1b to allow activation of autophagy. We hypothesize that IRE1b is a “licensing factor” linking ER stress to autophagy by degrading the RNA transcripts of factors that interfere with the induction of autophagy.

Molecular Mechanisms of Autophagy
Concurrent Chair - Tamar Avin-Wittenberg

Abstract Title: STUDYING THE INTERPLAY BETWEEN AUTOPHAGY AND PLANT CENTRAL METABOLISM

Primary Author(s) and Institution(s): TAMAR AVIN-WITTENBERG, Hebrew University of Jerusalem, Department of Plant and Environmental Sciences, Jerusalem, Israel SALEH ALSEEKH Max-Planck-Institut für Molekulare Pflanzenphysiologie, Department of Molecular Physiology, Potsdam, Germany JOSÉ VALLARINO Max-Planck-Institut für Molekulare Pflanzenphysiologie, Department of Molecular Physiology, Potsdam, Germany ALISDAIR R. FERNIE Max-Planck-Institut für Molekulare Pflanzenphysiologie, Department of Molecular Physiology, Potsdam, Germany; The Hebrew University of Jerusalem

Abstract

Plants usually produce their own energy source by photosynthesis. However, under some conditions, such as during the development of non-photosynthetic tissues or abiotic stress, in which photosynthesis is downregulated, there is a shortage of carbon supply. Therefore, plants use other resources to meet

their energy demands, partially degrading cellular components. This degradation results in notable metabolic changes. Autophagy is a conserved eukaryotic degradation process. The targets of autophagy vary and include soluble proteins, protein aggregates, whole organelles, and lipids. The hallmark phenotype of autophagy-related mutants (atg mutants) is higher sensitivity nutrient starvation. However, the direct impact of autophagy on cellular metabolism has not been well studied. Our group studies nutrient remobilization in plants, focusing on autophagy as a model system for this process. We investigate the role of autophagy during different stages in plant life in which nutrient remobilization is crucial. We observed distinct morphological differences between WT and atg mutant plants, suggesting delayed growth and early senescence. We employed high-throughput analyses to elucidate the underlying causes of the morphological phenotype. We were able to show that autophagy has a global effect on central metabolism under conditions in which nutrient remobilization is necessary.

Molecular Mechanisms of Autophagy
Concurrent Speaker - Jongchan Woo

Abstract Title: DISCOVERY OF CHEMICAL MODULATORS FOR AUTOPHAGY BIOGENESIS IN DIVERSE SPECIES USING BIOLUMINESCENCE RESONANCE ENERGY TRANSFER (BRET)-BASED SYNTHETIC SENSORS

Primary Author(s) and Institution(s): JONGCHAN WOO 1,2 , EUNSOOK PARK 3 , and S.P. DINESH-KUMAR 2 1 Department of Bioindustry and Bioresource Engineering, Sejong University, Seoul, Republic of Korea, 05006. 2 Department of Plant Biology and the Genome Center, College of Biological Sciences, University of California, Davis, California, USA. 3 Department of Plant Science, College of Agriculture and Life Science, Seoul National University, Seoul, Republic of Korea, 08826.; SEJONG UNIVERSITY

Abstract

Autophagy is a dynamic process during which double membrane-bound vesicles called autophagosomes enclose cytoplasmic materials and target them to the vacuole/lysosome for degradation or recycling. Recent studies have revealed that autophagy participates in diverse biological processes including cellular differentiation and development, cell and tissue homoeostasis, nutrient remobilization, senescence, innate and adaptive immunity, and programmed cell death (PCD). Autophagy biogenesis involves the conjugation of the ubiquitin-like autophagy protein ATG8 with the lipid, phosphatidylethanolamine (PE), after ATG4-mediated processing of ATG8. We have recently demonstrated that the BRET-based synthetic substrate of AtATG8a mimics endogenous AtATG8a in Arabidopsis . ATG8-PE lipidation processes are indispensable for autophagosome biogenesis and therefore are excellent targets for identification of modulators of autophagy. Currently, due to lack of specific autophagy modulators, we aim to characterize new chemical modulators capable of controlling autophagy biogenesis. Using the BRET-based synthetic ATG8 sensors, we have optimized high-throughput screening to identify chemical modulators in diverse species and characterized species-specific autophagy modulators for the evolutionally conserved maturation of ATG8s.

Molecular Mechanisms of Autophagy
Concurrent Speaker - Yasin Dagdas

Abstract Title: Role of autophagy in phenotypic plasticity responses in plants

Primary Author(s) and Institution(s): YASIN DAGDAS

Abstract

Autophagy is an evolutionary conserved recycling mechanism that plays important roles in stress tolerance and cellular reprogramming. One of the major challenges is to understand how autophagy contributes to cellular homeostasis in different cell types, and how this translates into overall organismal performance. Plants provide unique opportunities to tackle this question in depth. As sessile organisms, they heavily rely on quality control mechanisms for environmental adaptation. To tolerate environmental heterogeneity, they have evolved highly plastic body plans, which requires efficient resource allocation and cell state switching mechanisms. Functional tools to investigate distinct cell lineages in growing intact organisms are readily available. Also, ATG8 gene family has expanded, potentially allowing compartmentalization of the autophagy responses. To develop a comprehensive understanding of the autophagy responses in plants, we hypothesized that ATG8 gene family expansion drives functional diversification of the autophagy responses. To test this hypothesis, we performed affinity proteomics for different ATG8 isoforms and obtained biochemical evidence supporting functional specialization of ATG8s. ATG8 interactome data also revealed a new selective autophagy receptor that is highly conserved in metazoans and contributes to endoplasmic reticulum homeostasis during ER stress. Here, I will present our latest findings on the new selective autophagy receptor and tissue specific autophagy responses. I will also discuss our efforts to inducibly manipulate autophagy in different cell types to dissect tissue specific cell autonomous and non-cell autonomous autophagy responses in plants.

Plant Receptors - Mediators of the Interaction with the Environment
Concurrent Chair - Thomas Kroj

Abstract Title: Pathogen effector recognition by paired NLR immune receptors and decoy domains

Primary Author(s) and Institution(s): Stella CESARI 1 , Karine de GUILLEN 2 , Liwei GUO 3 , Véronique CHALVON 1 , Léa MAMMRI 2 , You-Liang PENG 3 , Junfeng LIU 3 , André PADILLA 2 and Thomas KROJ 1 1 BGPI, Univ Montpellier, CIRAD, INRA, Montpellier SupAgro , Montpellier, France 2 CBS, Univ Montpellier, CNRS, INSERM, Montpellier, France 3 Key Laboratory of Pest Monitoring and Green Management, MOA and College of Plant Protection, China Agricultural University, Beijing, People's Republic of China

Abstract

Nucleotide-binding domain and leucine-rich repeat containing proteins (NLRs) are important receptors in plant immunity and allow specific recognition of pathogen effectors. Based on our work on the detection of the Magnaporthe oryzae effectors AVR-Pia and AVR1-CO39 by the rice NLR RGA5, we recently developed the hypothesis that some NLRs recognize effectors by integrated decoy domains. By detailed structure-function analysis we deciphered the molecular details of the binding of AVR-Pia and AVR1-CO39 to the integrated heavy metal-associated (HMA) decoy domain of RGA5. This demonstrated that the direct RGA5-HMA/effector binding is strictly required for effector recognition but only of

moderate affinity and acts in concert with the association of the effectors to additional sites in RGA5. This combination of integrated decoy domains with additional independent effector-NLR interactions seems to confer robust effector recognition that is resilient to effector mutations. I will also present first results on how knowledge on the molecular details of effector recognition by integrated decoy domains can be exploited for the modification of the recognition spectrum of NLRs.

Plant Receptors - Mediators of the Interaction with the Environment
Invited Speaker - Yusuke Saijo

Abstract Title: PATTERN RECOGNITION RECEPTORS IN FLUCTUATING ENVIRONMENTS

Primary Author(s) and Institution(s): TAEHONG LEE, ELIZA PO-IIAN LOO, MIDORI TANAKA, YURI TAJIMA, TAISHI HIRASE, KOHJI YAMADA, SHIGETAKA YASUDA, KEI HIRUMA, YUSUKE SAIJO Nara Institute of Science and Technology, Japan; Nara Institute of Science and Technology

Abstract

Plants are in nature colonized by a rich diversity of microbes, which provide a key basis for plant health and homeostasis. However, it remains poorly understood how plants integrate microbial and abiotic cues to deal with these microbes that can be beneficial or harmful in a context-dependent manner under fluctuating environments. Recognition and management of microbes rely on pattern recognition receptors (PRRs), which detect microbe- and host damage-associated molecular patterns (MAMPs and DAMPs, respectively) and thereby mount pattern-triggered immunity (PTI). With a particular focus on PRRs, we pursue the hypothesis that plants modulate immune responses according to the nature of microbes encountered and changes in environmental factors. In Arabidopsis thaliana, we show that PRRs are differentially influenced under inorganic phosphate (Pi) deficiency, when plant growth often relies on beneficial microbes. By exploiting the root-colonizing plant growth promoting fungus Colletotrichum tofieldiae and its pathogenic relative, C. incanum, we show that the interplay between Pi starvation response (PSR) and DAMP pathways underlies the retention of effective pathogen resistance during beneficial association with mutualistic fungi. Moreover, we also report a previously unsuspected role for PRRs in salt stress tolerance.

Plant Receptors - Mediators of the Interaction with the Environment
Concurrent Speaker - Lei Li

Abstract Title: ACTIVATION MECHANISM OF RPP7/RPW8 IN PLANT AUTOIMMUNITY

Primary Author(s) and Institution(s): LEI LI , EUNYOUNG CHAE, RUI WU, ANA-CRISTINA BARRAGAN LOPEZ, WANGSHENG ZHU, REBECCA SCHWAB, DETLEF WEIGEL; Max Planck Institute for Developmental Biology

Abstract

Plants have evolved sophisticated mechanisms to recognize non-self molecules, allowing them to deploy effective immune reactions against a myriad of pathogens. Sometimes, however, plants mistakenly identify their own molecules as foreign and induce autoimmunity, causing severe growth defects including plant death. Autoimmunity is a hallmark of a syndrome that is seen in certain intra- and interspecific hybrids and that is known as hybrid necrosis. A particularly interesting case in Arabidopsis

thaliana is that of the RPP7 and RPW8 loci, where three different pairs of alleles from different wild strains interact in F1 hybrids to cause hybrid necrosis. RPP7, which confers resistance against oomycetes, encodes members of canonical CC-NLR (coiled-coil, Nucleotide-Binding Leucine-Rich-Repeat) immune receptors. The biochemical function of the RPW8 only coiled-coil domain proteins that primarily confer resistance to fungi is less well understood than that of NLRs. Here we showed the mechanisms by which interactions between RPP7 and RPW8 proteins activate immune responses by taking advantage of the allele-specificity of these interactions. We found RPP7 have intra- and intermolecular self-interaction. RPW8 disrupt RPP7 intramolecular interaction, but weakly affect RPP7 intermolecular self-association. P-loop of RPP7 is required for RPW8/RPP7 complex activation. This study advances our view on two arms of the plant immune system that have not been previously linked, NLRs and the enigmatic RPW8 proteins, through hybrid incompatibilities.

Plant Receptors - Mediators of the Interaction with the Environment
Concurrent Speaker - Jorge Lozano-Juste

Abstract Title: CHEMICAL ACTIVATION OF SETARIA VIRIDIS ABA RECEPTORS

Primary Author(s) and Institution(s): JORGE LOZANO-JUSTE , IRENE GARCIA-MAQUILON, ALFREDO MANICARDI, STTEFANY ROSARIO, ANDREA CHINI, ARMANDO ALBERT, PEDRO RODRIGUEZ; IBMCP

Abstract

Drought is the most important stress affecting crop yield worldwide. The plant hormone abscisic acid (ABA) coordinates multiple responses to tolerate reduced water soil content. The PYR/PYL/RCAR family of ABA receptors are responsible for ABA perception and activation of ABA responses and have been described in detail in the eudicot model plant Arabidopsis thaliana . However, the information about this protein family in crop plants remains scant. Setaria viridis (setaria) has emerged lately as a great model system for C4-monocot crops like maize or sorghum. Here, we describe the identification and characterization of S. viridis ABA receptors. Additionally, we have leveraged this knowledge to design a drug discovery approach to identify small molecules able to activate setaria ABA receptors and stress tolerance. We have found one molecule, IRE1, able to engage and activate SvPYL1 in vitro and in vivo . Additionally, we also report on the identification of a second small molecule, IRE2, able to trigger ABA responses by inhibiting HAB1, a key negative regulator of ABA signalling. Finally, we have also developed a genome-editing pipeline to generate mutants that will help us to understand ABA signalling and the effect of ABA agonists in Setaria viridis . Future work is proposed for the improvement of IRE1 and IRE2 in order to use them as agrochemicals to control stress tolerance in the field.

Plant Receptors - Mediators of the Interaction with the Environment
Concurrent Speaker - Yoshitake Desaki

Abstract Title: OsCERK1 regulates LPS-induced immune signaling in rice

Primary Author(s) and Institution(s): YOSHITAKE DESAKI 1,4 , YUSUKE KOUZAI 2 , YUSUKE NINOMIYA 1 , RYOSUKE IWASE 1 , YUMI SHIMIZU 1 , KEITO SEKO 1 , ANTONIO MOLINARO 3 , EIICHI MINAMI 2 , NAOTO SHIBUYA 1 , HANAE KAKU 1 , YOKO NISHIZAWA 2 1 Dept. Life Sciences, Sch. Agriculture, Meiji Univ. 2 Inst. Agrobiological Sciences, NARO 3 Dept. Chemical Sciences, Univ. of Naples Federico II 4 Present address: Dept. Biology Science and Technology, Tokyo University of Science

Abstract

Plants have the ability to recognize microbe/pathogen-associated molecular patterns (MAMPs/ PAMPs) through their pattern recognition receptors (PRRs) and initiate various defense responses. OsCERK1, a LysM-RLK in rice, plays a key role to initiate chitin-triggered immunity and AM symbiosis (1) . In this study, we found that the rice OsCERK1 knockout mutants (oscerk1) mostly lose the activities of the lipopolysaccharide (LPS)-induced ROS generation and gene expression (2) . We showed that OsCERK1 plays a crucial role in the immune responses to LPS. LPS is one of the cell wall components of gram-negative bacteria and recognized as a typical MAMP by both animals and plants. While the LPS perception systems are well characterized in mammals, those in plants are poorly understood. LORE, a bulb-type lectin S-domain-1 receptor-like kinase (SD1-RLK), was the only plant LPS receptor/co-receptor identified in Arabidopsis (3) . However, we found that several LORE-like proteins of rice and all the LysM-RLKs/receptor-like proteins of Arabidopsis do not participate in LPS-induced immune responses, indicating that the mechanisms of LPS perception system of rice and Arabidopsis are significantly different. (1) Miyata et al., 2014; (2) Desaki et al., 2018; (3) Ranf et al., 2015

Response to Climate Change
Concurrent Chair - Pedro Rodriguez

Abstract Title: Regulation of the turnover of ABA receptors and PP2Cs

Primary Author(s) and Institution(s): Pedro L. Rodriguez 1, Borja Belda-Palazon1, Maria Angeles Fernandez1, Jose Julian1, Alberto Coego1, Jorge Lozano-Juste1, Sabrina Iñigo2, Lesia Rodriguez1, Alain Gooseens2 1Instituto de Biología Molecular y Celular de Plantas, Consejo Superior de Investigaciones Científicas-Universidad Politécnica de Valencia, 46022 Valencia, Spain 2Department of Plant Systems Biology, VIB, Technologiepark 927, B-9052 Gent, Belgium; CSIC

Abstract

Studies that address the turnover of core ABA signaling components have opened new avenues of research in ABA signaling. Degradation of clade A PP2Cs through different E3 ligases, e.g. PUB12/13 and RGLG1/5, is a complementary mechanism to PYR/PYL/RCAR-mediated inhibition of PP2C activity to relieve repression of ABA signaling. ABA receptor proteins, e.g. PYR1, PYL4 and PYL8, can be degraded via an ubiquitination-dependent mechanism through monomeric and multimeric E3 ligases. We have identified a 10-member family of single-subunit E3 ubiquitin ligases, named RFA for RING finger ABA-related, acting as E3 ligases of the PYR/PYL/RCAR ABA receptors in different subcellular locations. RSL1/RFAs are structurally characterized by the presence of three domains in tandem, named as RING1-

IN BETWEEN RING (IBR)-RING2, and accordingly they belong to the RBR (RING between RING fingers) E3 ligase family. We provide evidence that RFA4 interacts with ABA receptors in the nucleus and promotes their ubiquitination and degradation in vivo. Additionally, we have identified the cognate nuclear E2 interacting with the RFA4 E3 ligase. Altogether, our results reveal a sophisticated targeting of ABA receptors at different subcellular locations, which involves at least the monomeric RBR E3 ligases and the multimeric CRL4 complex.

Response to Climate Change
Invited Speaker - Ebe Merilo

Abstract Title: STOMATAL REGULATION OF CEREALS: GRASSES FACE CLIMATE CHANGE

Primary Author(s) and Institution(s): Merilo Ebe; University of Tartu

Abstract

Stomata regulate photosynthetic CO2 uptake and water loss by transpiration and as such, represent a constant dilemma for plants and plant breeders. On the one hand, stomatal conductance of crops has inadvertently increased during breeding in the 20th century. On the other, higher stomatal conductance increases the vulnerability to drought. Here, we present the results of field and laboratory experiments with cereals showing different aspects of their stomatal regulation. In 3-year field experiment with malting barley genotypes, a positive correlation between gas exchange traits (stomatal conductance and net assimilation rate) and grain yield was detected only in climatically unfavourable year characterized by hot and dry period during tillering. Pooling all years, higher water use efficiency was associated with higher grain yield. Laboratory experiments with the same malting barley genotypes revealed that: 1) Barley leaves may function with more than optimally open stomata in well-watered conditions, as the drought-induced stomatal closure was much more extensive than the drought-induced photosynthetic reduction; 2) Well-watered barley plants are less sensitive to ABA compared to Arabidopsis in terms of stomatal closure, while, surprisingly, barleys subjected to soil water deficit do not respond at all to exogenous ABA with stomatal closure. We also compared the stomatal sensitivities of wheat and maize to CO2 concentration, exogenous ABA and ozone and found that maize stomata responded significantly to CO2 concentration, but were less sensitive to ABA and ozone. Our results indicate that as regards stomatal regulation, there are differences between crops and model plants.

Response to Climate Change
Concurrent Speaker - Stefano D'Alessandro

Abstract Title: ß-cyclocitral-mediated acclimation to high light exploits the xenobiotic detoxification response

Primary Author(s) and Institution(s): STEFANO D'ALESSANDRO , Aix Marseille University, CEA Cadarache, 13108 Saint Paul les Durance BRIGITTE KSASCEA Cadarache, 13108 Saint Paul les Durance MICHEL HAVAUX, CEA Cadarache, 13108 Saint Paul les Durance; CEA Cadarache / Aix Marseille University

Abstract

Because agriculture is inherently sensitive to climate variability, climate changes and extreme climatic events directly influence crop productivity and hence food availability. In fact, when exposed to unfavorable environmental conditions, plants can absorb light energy in excess to their photosynthetic capacities, with the surplus of energy leading to the production of reactive oxygen species and to photooxidative stress. Subsequent lipid peroxidation generates toxic reactive carbonyl species whose accumulation culminates in cell death. ß-cyclocitral, an oxidative by-product of ß-carotene generated in the chloroplasts, mediates a protective retrograde response that limits oxidative damages to intracellular components. In this study, we elucidate the molecular mechanism induced by ß-cyclocitral and show that the xenobiotic detoxification response intervenes with the tolerance to excess light energy. Excessive light is the first described physiological stimulus eliciting the xenobiotic response, suggesting a possible origin for this pathway. Furthermore, we establish the hierarchical structure of the ß-cyclocitral-dependent pathway, which involves the GRAS protein SCL14 and ANAC transcription factors. This pathway controls several enzymes of the xenobiotic detoxification response, the role of which has been previously reported in the protection of plants under stressful conditions.

Response to Climate Change

Concurrent Speaker - Anthony Guihur

Abstract Title: QUANTITATIVE PROTEOMICS, A WAY TO BETTER UNDERSTAND MECHANISMS INVOLVED IN LAND PLANT ACQUIRED THERMOTOLERANCE

Primary Author(s) and Institution(s): ANTHONY GUIHUR 1 , ANDRIJA FINKA 2 , BRUNO FAUVET 1 , MANFREDO QUADRONI 3 , PERRE GOLOUBINOFF 1 1 Department of Plant Molecular Biology, University of Lausanne, Switzerland. 2 Department of Ecology, Agronomy and Aquaculture, University of Zadar, Croatia. 3 Protein Analysis Facility, University of Lausanne, Switzerland.; University of Lausanne

Abstract

Global warming causes daily heat stresses to plant organisms and since plants are sessile and cannot escape stress, they need to somehow cope with these environmental changes. Heat can cause protein denaturation and aggregation, which leads to loss of protein activity and compromised membrane integrity. Exposure to a sublethal temperature triggers an adaptive response, called acquired thermotolerance (AT), which involves a molecular reprogramming that allows plants to synthetize new proteins (heat-shock proteins, HSPs) to survive noxious temperatures. By improving protein annotation and using a label-free LC-MS/MS proteomics approach, we identify, quantify and know the ratio between chaperones and others HSPs occurring in various cellular compartments after a mild heat treatment (2 hours at 38°C) leading to AT. We found that most of the degraded proteins are into the chloroplast and are involved in photosystem II, photosynthetic electron transfer, and lipid metabolism. Surprisingly, the classical response involving molecular chaperones, which have a key role in mitigating the effects induced by heat stress, occurs in the cytosol through a substantial increase of small HSPs. In addition, this study gave us new insights about molecular crowding in subcellular compartments and we are now addressing the protective and stabilizing effect during heat stress.

Response to Climate Change
Concurrent Speaker - Aditya Nayak

Abstract Title: MOLECULAR MECHANISMS OF AMBIENT TEMPERATURE SENSING IN ARABIDOPSIS THALIANA

Primary Author(s) and Institution(s): ADITYA NAYAK 1 CATARINA S. SILVA 1,2 and CHLOE ZUBIETA 1 1 Laboratoire de Physiologie Cellulaire and Végétale, Univ. Grenoble Alpes/CNRS/CEA/INRA/BIG, 17 rue des Martyrs, 38054 Grenoble, France. 2 European Synchrotron Radiation Facility, Structural Biology Group, 71 Avenue des Martyrs, F-38000 Grenoble.

Abstract

In Arabidopsis thaliana , robust circadian rhythms are generated through a multi-looped transcriptional circuitry of core clock genes. The circadian clock also integrates ambient temperature signals into the clock transcriptional circuitry to regulate clock functions .The Evening Complex (EC) composed of LUX ARRHYTHMO (LUX), EARLY FLOWERING 3 (ELF3) and ELF4, is a key circadian clock component, repressing multiple genes in the morning, central and evening loops. Temperature- and circadian clock-dependent flowering pathways are fine-tuned through EC based repression of PHYTOCHROME INTERACTING FACTOR 4 (PIF4) and PIF5. This work was aimed at understanding mechanisms of EC based repression of PIF4 and developing plants that could survive at higher ambient temperature. We performed structural, biochemical and in planta studies to understand the mechanisms of EC formation and activity. Further to understand the importance of EC binding site on PIF4 promoter, CRSIPR/Cas9 based gene editing was used to generate different Arabidopsis thaliana plant lines that had either attenuated susceptibility to higher ambient temperature or reduced EC repression at lower ambient temperature. The crystal structure of DNA-binding MYB domain of LUX was determined in complex with a 10-mer DNA to 2.1Å. The amino acid residues important in DNA binding were assessed from the crystal structure and probed by mutagenesis. DNA binding affinity was determined by EMSA for wildtype protien and mutants. Further to validate the structural and biochemical studies in planta , lux mutants were transformed with LUXR146A and LUX phenotypes were studied in terms of flowering, hypocotyl length and petiole elongation.

Conserved principles of plant development
Concurrent Chair - Olivier Hamant

Abstract Title: Conserved principles in the mechanical control of development

Primary Author(s) and Institution(s): Olivier Hamant; Université de Lyon, ENS de Lyon, UCBL, INRA, CNRS,

Abstract

Mechanical forces are present in all living organisms; interactions between physics and biology are inevitable during development. Thanks to ongoing developments in live imaging and modeling, this field of study has been rejuvenated: the relation between mechanics and shape changes can now be addressed more comprehensively, notably in plants in which morphogenesis is mainly determined by cell walls. In past work, we showed that shape- and growth-derived forces act as signals that orient plant microtubules. This response channels key biological features, such as cell shape, cell division plane

orientation and final organ shape. Beyond microtubules, such forces also contribute to cell polarity and to the expression patterns of master regulators of meristem maintenance. We are now addressing two major bottlenecks in the field: first, to formally challenge the role of mechanical signals in development, the relevant mechanotransduction pathways need to be identified; second, forces being invisible in essence, mechanical stress patterns in tissues need to be assessed experimentally, beyond computational model predictions.

Conserved principles of plant development
Invited Speaker - Nick Monk

Abstract Title: Bioattractors: understanding biological process through dynamical systems

Primary Author(s) and Institution(s): Nick Monk; University of Sheffield, UK

Abstract

Living systems are fundamentally dynamic, but many approaches to representing biological phenomena rely on essentially static conseptul structures. A key challenge is to understand the nature of the genotype-phenotype map. I will discuss how dynamical systems approaches can be used to characterise these maps, and how the features of this approach – phase portraits, attractors and bifurcations – define the regulatory and evolutionary potential of systems. This provides a formal setting for a processual view of life, and a natural framework in which to capture the active, self-organizing role of the environment in phenotypic dynamics and evolution. This approach yields mechanistic explanations that go beyond insights based on the simulation of evolving regulatory networks alone.

Conserved principles of plant development
Concurrent Speaker - Sarah Robinson

Abstract Title: Stress induced microtubule reorientation promotes hypocotyl elongation

Primary Author(s) and Institution(s): SARAH ROBINSON , Cris Kuhlemeier University of Bern; Institute of Plant Science

Abstract

Morphogenesis in plants is controlled by the spatial pattern of the mechanical properties across the tissue. During growth, internal mechanical stresses can develop and also serve as an important determinant of plant development. To investigate the mechanical properties and responses to mechanical stress in the developing tissues of the model plant Arabidopsis we developed an automated confocal micro-extensometer (ACME). ACME enables forces to be applied to tissues, while they are imaged with a confocal microscope. These images were analysed to extract 3D cellular strain measurements; revealing spatial gradients in mechanical properties that correlate with the pattern of growth. We also used ACME to investigate responses to mechanical stress. We combined finite element modelling with imaging of the outer and internal layers while applying mechanical stress. We saw that when a relative compressive force was applied the pattern of tissue stress changed, leading to a reorientation of the microtubules in the epidermis but not the inner layers. As the epidermis usually restricts growth, this reorientation led to growth increasing in these samples. This may mimic the

response of a seedling whose growth is restricted as it pushes through the soil and responds with an increase in growth.

Conserved principles of plant development
Concurrent Speaker - Michael Considine

Abstract Title: THE ROLE OF DEVELOPMENTAL HYPOXIA IN THE BUD BURST OF GRAPEVINE.

Primary Author(s) and Institution(s): KARLIA MEITHA, 1 PATRICIA AGUDELO-ROMERO, 1 SANTIAGO SIGNORELLI, 1 DANIEL J. GIBBS, 2 JOHN A. CONSIDINE, 1 CHRISTINE H. FOYER, 1,3 MICHAEL J. CONSIDINE . 1,3 1. School of Molecular Sciences, The University of Western Australia, Perth, 6009, Australia. 2. School of Biosciences, University of Birmingham, Birmingham B15 2TT, UK 3. Centre for Plant Sciences, University of Leeds, Leeds, West Yorkshire LS2 9JT, UK; University of Western Australia

Abstract

Dormant or quiescent buds of woody perennials are often dense and in the case of grapevine (Vitis vinifera L.) have a low tissue oxygen status. The precise timing of the decision to resume growth is difficult to predict, but once committed, the increase in tissue oxygen status is rapid and developmentally regulated. Here, we show that more than a third of the grapevine homologues of widely conserved hypoxia-responsive genes and nearly a fifth of all grapevine genes possessing a plant hypoxia-responsive promoter element were differentially regulated during bud burst, in apparent harmony with resumption of meristem identity and cell-cycle gene regulation. We then investigated the molecular and biochemical properties of the grapevine ERFVII homologues, which in other species are oxygen labile and function in transcriptional regulation of hypoxia-responsive genes. Each of the 3 VvERF-VIIs were substrates for oxygen dependent proteolysis in vitro, as a function of the N-terminal cysteine. Collectively, these data support an important developmental function of oxygen-dependent signalling in determining the timing and effective coordination bud burst in grapevine. In addition, novel regulators, including GASA-, TCP-, MYB3R-, PLT-, and WUS-like transcription factors, were identified as hallmarks of the orderly and functional resumption of growth following quiescence in buds.

Conserved principles of plant development
Concurrent Speaker - Ankit Walia

Abstract Title: CHEMICAL AND PHYSICAL SIGNALS IN CONTROL OF DIFFERENTIAL GROWTH IN ARABIDOPSIS

Primary Author(s) and Institution(s): ANKIT WALIA , ROSS CARTER, HENRIK JÖNSSON and ALEXANDER JONES

Abstract

A major challenge in plant biology is to understand how multicellular plants integrate dynamic developmental and environmental inputs to drive cellular responses. We are using photomorphogenic hypocotyls as a model to elucidate how changes in hormonal levels and mechanical properties of the cell wall are altered to drive differential cellular growth associated with apical hook opening. Our preliminary analysis indicates that cells on the inner side of the hook show maximum increase in cell volume and cell length, and 2D biophysical models are being generated to map the stress and strain patterns as well as stress anisotropy in a pressurized hooked object. Growth rate maps are now being used to build 3D models of mechanical stress and strain patterns. Since hormones and the microtubule-cytoskeleton play fundamental role in promoting growth anisotropy, I am quantifying auxin cellular levels and microtubule orientations during apical hook opening to test the hypothesis that auxin-induced changes in biomechanical properties of the cell wall could dynamically feedback on mechanical stress patterns and microtubule orientations to trigger and sustain differential growth and hook opening.

Epigenetic and Genome Function
Invited Speaker - Frederic Berger

Abstract Title: Histone variants impact on the chromatin landscape

Primary Author(s) and Institution(s): FREDERIC BERGER , Bhagyshree Jamge, Elin Axelsson, Zdravko Lorkovic, and Chulmin Park Gregor Mendel Institute; Gregor Mendel Institute

Abstract

In addition to histone modification and DNA methylation, chromatin composition varies with localized enrichment in variant of H3 and H2A core histones. We are studying the function and properties conferred by these variants to nucleosomes and specific domains of chromatin. Patterns of gene expression through the cell cycle requires prompt restoration of epigenetic marks after the dilution caused by DNA replication. We showed that the variant H3.1 is essential for maintenance and propagation of the transcriptional repressive mark histone H3 lysine 27 trimethylation (H3K27me3), illustrating the important role played by histone variants in epigenetic regulation of transcription (Jiang and Berger, 2017). New data will be presented on the role of H3 variants in reprogramming transcription.

Epigenetic and Genome Function
Concurrent Speaker - Amit Kumar

Abstract Title: POLYCOMB GROUP PROTEIN StMSI1 REGULATES POTATO DEVELOPMENT VIA PHOTOPERIOD DEPENDENT PATHWAY

Primary Author(s) and Institution(s): AMIT KUMAR, KIRTIKUMAR KONDHARE, ANJAN K. BANERJEE Biology Division, IISER-Pune, Maharashtra, Pin - 411008, India; Indian Institute of Science Education and Research Pune

Abstract

Phenotypic plasticity is a crucial survival strategy of plants. This often involves regulated gene expression mediated by chromatin modifiers such as Polycomb group (PcG) proteins. Solanum tuberosum ssp. andigena is a potato variety in which tuberization is strictly controlled by the duration of light. We selected this sub-species of potato to understand the role of PcG protein in controlling tuber development in response to different photoperiodic conditions. We have noted a differential expression of the PcG genes in potato stolons under long day v/s short-day photoperiod conditions. Overexpression of PRC2 complex genes, StMSI1 and StEz2 resulted in severe developmental aberrations in overall plant phenotypes. Moreover, both overexpression lines exhibited a drastic reduction in tuber yield. Additionally, upon short day (SD) photoperiodic induction, OE lines produced aerial stolons and tubers. Many of these phenotypes are known to be regulated by genes involved in plant growth hormone signaling, which were found to be differentially expressed in these overexpression lines. We further observed that the levels of miRNA156 increases in StMSI1 OE lines, suggesting a possible of miR156 by PcG proteins in potato. In summary, our results suggest that Polycomb Group Proteins play an important role in regulating overall potato development.

Epigenetic and Genome Function
Concurrent Speaker - Anjar Wibowo

Abstract Title: TRANSCRIPTIONAL AND EPIGENETIC PROFILES OF ROOTS ARE STABLY INHERITED UPON ASEXUAL PROPAGATION

Primary Author(s) and Institution(s): WIBOWO A 1,2 , BECKER C 2,3 , WEIGEL D 2 , GUTIERREZ-MARCOS J 1 1 School of Life Sciences, University of Warwick, UK 2 Max Planck Institute for Developmental Biology, Tübingen, Germany 3 Present address: Gregor Mendel Institute of Molecular Plant Biology, Vienna, Austria; Max Planck Institute for Developmental Biology

Abstract

Plant differ from most animals in their ability to regenerate whole individuals from differentiated cells. This property has been exploited by humans for the clonal propagation of many economically important plants, including tuber and root crops, as well as fruit and forest tress. However, clonally propagated plants often display variant phenotypes, a phenomenon known as somaclonal variation. Random genetic and stochastic epigenetic modifications induced during the regeneration process have been associated with this phenomenon. In this work, we investigated the fate of the epigenome after asexual propagation by generating clonal individuals from differentiated somatic cells through the manipulation of a zygotic transcription factor. We provide evidence that in Arabidopsis thaliana , cell-specific epigenetic marks are incompletely reset during regeneration. We observed that plants regenerated from roots inherit many aspects of root specific methylation and gene expression patterns – not just in

roots, but also in leaves. These epigenetic profiles and the resulting macroscopic and molecular phenotypes are stably inherited for at least four self-crossing generations. Our findings demonstrate that plants with novel methylation and gene expression patterns, as well as phenotypes, could be created using tissue specific regeneration. This provides us with novel technology to create stable epigenetic diversity within species.

Epigenetic and Genome Function
Concurrent Speaker - Ryan Austin

Abstract Title: Active chromatin and metabolic changes in the Arabidopsis root responding to cold stress.

Primary Author(s) and Institution(s): RYAN S. AUSTIN 1,2 SHAWN HOOGSTRA 2 , FIONA BERGIN 1,2 , KEEGAN LECKIE 2 , MANA CROFT 1,2 , JUSTIN RENAUD 2 , MARK SUMARAH 1,2 1. London Research Development Centre, Agriculture Agri-Food Canada. London, Ontario, Canada. 2. Western University, London, Ontario, Canada.; Agriculture & Agri-Food Canada

Abstract

DNAse-seq methods have emerged as a powerful genomic tool for identifying open chromatin, enhancer sites and even chromatin structure. At the same time, more studies are adopting cell-type specific genomic methods in order to facilitate a higher resolution of study of systems biology. Using a rapid and effective “direct-to-sequencing” DNAse-seq (DNAse-DTS) protocol we developed for single cell-type nuclei isolations, we mapped regions of differentially accessible chromatin in the genome of epidermal and endodermal cells of cold acclimated Arabidopsis plants. Our DNAse-DTS approach uses tagged-nuclei isolations, enzymatic based sequencing, and custom software to robustly identify regions of active chromatin. Integrating these data with results from untargeted metabolic profiling experiments performed in parallel, along with a priori transcription factor binding site mapping, and gene expression data, identified patterns in regulatory DNA that suggest MADS-box dependent remodelling of cold responsive gene promoters governs the accumulation of various polyamine and derivative molecules; including a 13-fold accumulation of a precursor to the abiotic stress molecule 4-aminobuteryate (GABA). Genome editing strategies for using this systems level understanding of cold response to manipulate native metabolites in the interest of abiotic stress tolerance will be discussed.

Epigenetic and Genome Function
Concurrent Speaker - Julie Law

Abstract Title: LOCUS-SPECIFIC CONTROL OF THE DE NOVO DNA METHYLATION PATHWAY IN ARABIDOPSIS BY THE CLASSY FAMILY

Primary Author(s) and Institution(s): JULIE A. LAW 1 , MING ZHOU 1 , ANA MARIE S. PALANCA 1 1 Salk Institute for Biological Studies

Abstract

Cytosine DNA methylation plays crucial roles in gene regulation, transposon silencing, and diverse developmental processes. Although the generation of specific DNA methylation patterns is critical for these processes, how methylation is regulated at individual loci remains unclear. In Arabidopsis , DNA methylation is established via the RNA-directed DNA methylation (RdDM) pathway, wherein RNA POLYMERASE-IV (Pol-IV), initiates biogenesis of 24-nucleotide small interfering RNAs (24nt-siRNAs) that guide methylation at cognate genomic loci. Using a combined genetic and genomic approach, we show that four Pol-IV-associated factors, CLASSY (CLSY) 1-4, act individually as locus-specific regulators of RdDM and together control the production of essentially all 24nt-siRNAs, demonstrating they are the master regulators of Pol-IV function. Mechanistically, the CLSYs function in connection with H3K9 and CG methylation to facilitate Pol-IV chromatin association and show a striking division of labor, with specific CLSY pairs preferentially regulating loci in the chromosome arms versus pericentromeric heterochromatin. These findings reveal an unanticipated layer of complexity within the RdDM pathway that enables locus-specific control of DNA methylation patterns. Given the conservation between methylation systems in plants and mammals, analogous pathways likely operate in a broad range of organisms.

Root Function and Development
Concurrent Chair - Niko Geldner

Abstract Title: Root damage and immune responses at cellular resolution

Primary Author(s) and Institution(s): Niko Geldner; University of Lausanne

Abstract

The study of the molecular mechanisms that underlie plant damage and immune responses is among the most active areas of plant research. Yet much of the paradigmatic models in this field have been developed working on aerial tissues and there is reason to assume that roots have significantly different ways of integrating and responding to cellular damage, perception of microbe-associated molecular patterns (MAMP) and other stresses. We have previously developed transcriptional, live-imaging reporters for stress and immune responses, covering ethylene (ET), jasmonic acid (JA), salicylic acid (SA) and MAMP responsive genes. Using single cell laser ablations, we show that such a restricted damage of root cells already leads to local surface depolarisation, ROS induction and Calcium increases, yet only causes a transcriptional response to ET, but not to JA, in contrast to laser-induced damage of leaf cells. Since roots are able to produce and respond to JA, this indicates that translation of cell damage into hormonal responses is very different from leaves. Using our MAMP-responsive markers, we confirmed previous reports that root responses to MAMPs are restricted to the elongation/late division zone. We

could demonstrate that this is largely controlled by receptor presence, since expressing a MAMP receptor in non-responsive tissues installed responsiveness in those cell layers in many cases. Intriguingly, laser-induced cell ablation could “unlock” MAMP-responsiveness in neighboring cells, associated with an upregulation of the MAMP receptor. Neither damage nor PAMP treatment alone were able to induce a MAMP response, suggesting that root cells perceive and combine cellular damage and MAMPs as two distinct signals. A similar “unlocking” of PAMP responsiveness was observed in cortical cells surrounding an emerging lateral root, although root emergence is not consistently associated with cell death and thus MAMP-responsiveness in these cells might be due to other factors, such as lateral root-produced peptides, small molecule signals or mechanical/cell wall stresses.

Root Function and Development
Invited Speaker - Veronica Grieneisen

Abstract Title: Developmental Homeostasis: unearthing the fast dynamics underlying root growth and optimal nutrient uptake

Primary Author(s) and Institution(s): Verônica A. Grieneisen; John Innes Centre

Abstract

We analyze the developing plant as a system in which information flows are coordinated through tissue polarity and relayed via phytohormones and nutrients to achieve higher level robustness as well as plasticity. Combining different systems biological to molecular-genetic interferences and imaging, we have elucidated an important mechanism by which root meristem size can be sustained or quickly altered. Moreover, by adopting a morphoengineering view on plant-nutrient uptake, we could find hidden and universal dynamical constraints that operate in transport system of polarized tissues, to avoid traffic-jam phenomenon of flows. Together, our work helps better understand how mechanisms underlying developmental robustness can also explain fast time-scale adaptations, and the importance of considering intrinsic instabilities when striving to make plants more efficient in their nutrient uptake capacity.

Root Function and Development
Concurrent Speaker - Carlos Hernán Barrera Rojas

Abstract Title: SPL10 DE-REGULATION POSITIVELY IMPACTS PRIMARY ROOT LENGTH BY REDUCING CYTOKININ RESPONSE IN Arabidopsis thaliana

Primary Author(s) and Institution(s): BARRERA CARLOS. State University of Sao Paulo, Botucatu, Sao Paulo, Brazil; POLVERARI LAURA. Laboratory of Functional Genomics and Proteomics of Model Systems, Dipartimento di Biologia e Biotecnologie, Università La Sapienza, Rome, Italy; SABATINI SABRINA. Laboratory of Functional Genomics and Proteomics of Model Systems, Dipartimento di Biologia e Biotecnologie, Università La Sapienza, Rome, Italy; NOGUEIRA FABIO. Laboratory of Molecular Genetics of Plant Development, Department of Biological Sciences, Escola Superior de Agricultura ‘Luiz de Queiroz’, University of Sao Paulo, Piracicaba, Sao Paulo, Brazil

Abstract

Root system (RS) is important for anchorage and for supplying plants with nutrients and water. Several factors regulate RS; among them, auxin-cytokinin ratio determines root length (RL), and the genetic pathway controlled by microRNA156 regulates lateral roots. How those pathways interact to control primary root (PR) is unknown. Therefore, we analyzed this interaction in Arabidopsis thaliana (Col-0). Using miR156-resistant plants, we analyzed PR length by measured RL; root meristem size by counting the cortex-cell number; cell division-expansion rates by qPCR and GUS reporters of CYCLINB1 and EXPANSIN7 ; and cytokinin-auxin responses by qPCR and GFP reporters. Among miR156-resistant plants, seedlings containing the SPL10 de-regulated (rSPL10) display longer PR and larger root meristem size than wild-type (WT). qPCR and GUS staining analysis demonstrated that CYCLINB1 expression was higher in rSPL10 while EXPANSIN7 expression was similar to WT. Cytokinin-response analysis showed that ARR1 expression was highly reduced in rSPL10, similarly to the reduced expression of nTCS:GFP and pARR5:GUS reporters, whilst ARR12 expression did not change. Analyses of PIN1 , PIN3 and PIN7 expression by qPCR and GFP reporters showed no difference between rSPL10 and WT. Our data suggests that SPL10 de-regulation positively impacts PR length by reducing cytokinin response.

Root Function and Development

Concurrent Speaker - Duy Chi Trinh

Abstract Title: PUCHI regulates Very Long Chain Fatty Acid synthesis during lateral root development

Primary Author(s) and Institution(s): DUY CHI TRINH 1,2,3 , JULIEN LAVENUS 2 , QUENTIN DROGUE 2 , VIRGINIE VAISSAYRE 2 , MIKAEL LUCAS 2 , TATSUAKI GOH 4 , UTE VOSS 5 , FRÉDÉRIQUE TELLIER 6 , PASCAL GANTET 1 , JEAN-DENIS FAURE 6 , YOHANN BOUTTÉ 7 , STÉPHANE DUSSERT 2 , HIDEHIRO FUKAKI 8 , MALCOLM J. BENNETT 5 , LAURENT LAPLAZE 2,* AND SOAZIG GUYOMARC'H 1 Author affiliations: 1 Université de Montpellier, Unité Mixte de Recherche "Diversité Adaptation et Développement des plantes" (DIADE), Montpellier 34394 Cedex 5, France 2 Institut de Recherche pour le Développement, Unité Mixte de Recherche "Diversité Adaptation et Développement des plantes" (DIADE), Montpellier 34394 Cedex 5, France; 3 Department of Pharmacological, Medical and Agronomical Biotechnology, University of Science and Technology of Hanoi, Vietnam Academy of Science and Technology, Hanoi, Vietnam; 4 Laboratory of Plant Developmental Signaling, Nara Institute of Science and Technology, 8916-5 Takayama, Ikoma, Nara, 630-0192, Japan; 5 Centre for Plant Integrative Biology, School of Biosciences, University of Nottingham, Nottingham LE12 5RD, UK; 6 Institut Jean-Pierre Bourgin (IJPB), UMR1318 INRA-AgroParisTech, Saclay Plant Science (SPS), INRA Centre de Versailles-Grignon, Route de St-Cyr, 78000 Versailles, France; 7 UMR 5200 Membrane Biogenesis Laboratory, CNRS-University of Bordeaux, Ba ˆtiment A3 - INRA Bordeaux Aquitaine, 71 Avenue Edouard Bourlaux - CS 20032, 33140 Villenave d'Ornon, France; 8 Department of Biology, Graduate School of Science, Kobe University, Kobe, 657-8501 Japan.; IRD Montpellier

Abstract

Post-embryonic lateral root organogenesis plays an essential role in defining plant root system architecture, and therefore plant growth and performance. In Arabidopsis , the AP2/EREBP transcription factor PUCHI is involved in controlling cell proliferation and morphology of lateral root primordia; however, its targets are unknown. Here, we used a transcriptomic dataset of lateral root formation to identify potential targets of PUCHI . We found that genes coding for proteins of the very long chain fatty acid (VLCFA) biosynthesis machinery are activated downstream of PUCHI during lateral root

development, as revealed by gene expression level and expression pattern analyses. In addition, puchi-1 mutant shows enhanced callus formation in auxin-rich callus induction medium, consistent with the role of VLCFAs during callus formation (Shang et al., 2016). Moreover, a mutant perturbed in VLCFA biosynthesis (kcs1-5) shows similar lateral root development defects as does puchi-1 . Altogether, our results indicate that PUCHI positively regulates the expression of VLCFA biosynthesis genes during lateral root development, and further support the hypothesis that lateral root and callus formation share common genetic regulatory mechanisms.

Root Function and Development
Concurrent Speaker - Karen Sanguinet

Abstract Title: FUNCTIONAL CHARACTERIZATION OF THE BUZZ KINASE IN ROOT DEVELOPMENT

Primary Author(s) and Institution(s): KAREN A. SANGUINET, Thiel A Lehman, Rhoda AT Brew-Appiah, Zara York, Ying Wu, Tetyana Smertenko, Tobias I Baskin, Andrei Smertenko

Abstract

Root development and architecture is crucial for plant adaptation and reproductive success in diverse environments. To gain insight into the molecular and genetic cues involved in modulating root development and architecture in temperate grasses, we identified a roothairless mutant in Brachypodium distachyon termed buzz . The buzz mutant displays a root hairless phenotype with a dramatic increase in root growth rate. We used an NGS approach to identify SNPs associated with the buzz mutant phenotype. We identified a SNP in putative cell division kinase, which leads to an amino acid substitution in the kinase domain. Moreover, we identified a second buzz allele in with a roothairless phenotype suggesting the original EMS allele is a functional null. The buzz phenotype is root-specific and BUZZ expression can only be detected in root tips. To determine the functional conservation of the BUZZ kinase, the putative BUZZ ortholog in A. thaliana was identified and then characterized using two independent T-DNA lines. We describe further cell biological and biochemical of the BUZZ kinase, which will shed light on signaling events driving root hair development in grasses as well as dicots.

Protein Modification and Degradation
Concurrent Chair - Jean Colcombet

Abstract Title: MKK3 module: a conserved translation-dependent signaling mechanism in plants?

Primary Author(s) and Institution(s): CECILE SÖZEN, SEBASTIAN T. SCHENK, CAMILLE CHARDIN, ANNE KRAPP, MARILIA ALMEIDA-TRAPP, AXEL MITHÖFER, HERIBERT HIRT, JEAN COLCOMBET Institute of Plant Sciences Paris-Saclay IPS2, Centre National de la Recherche Scientifique, Institut National de la Recherche Agronomique, Université Paris-Sud, Université Evry, Université Paris-Saclay, Orsay, France Institute of Plant Sciences Paris-Saclay IPS2, Paris Diderot, Sorbonne Paris-Cité, Orsay, France Institut Jean-Pierre Bourgin, INRA-AgroParisTech, CNRS, Université Paris Saclay, 78000, Versailles, France Department of Bioorganic Chemistry, Max Planck Institute for Chemical Ecology, Jena, Germany Center for Desert Agriculture, King Abdullah University of Science and Technology, Thuwal, Saudi Arabia; IPS2

Abstract

Since its first descriptions in 1995 and its first functional characterization 12 years later, plants MKK3-type MAP2Ks have emerged as an important integrator in plant signaling. If it does not count among the major stress-dependent MAPK actors in plant, recent works shed light on important roles in plant adaptation to environment. Our previous work (Danquah et al 2014) showed that together with MAPKs of clade C and MAP3K17/18, MKK3 constitutes a functional module which is activated by abscisic acid (ABA) and drought. Surprisingly, this activation requires a strong transcriptional regulation of MAP3K genes, which are virtually not expressed in resting conditions, the protein accumulating upon stimulation. Consequently, C-clade MAPK activation by ABA is rather slow. We present here new piece

of data suggesting that MKK3 interacts strictly with a sub-clade of 8 MAP3Ks (including MAP3K17/18) and are activated by other stresses through transcriptional regulation. As example we characterize in more detail the wounding triggered activation of MKK3 module and show its connection with jasmonic acid (JA) biosynthesis. Taken together, this data breaks the textbook message that MAPK modules define fast responsive signaling pathways and suggest that MKK3 module could be a more general responsive signaling mechanism in plants, controlling a second layer of responses remaining to be identified.

Protein Modification and Degradation
Invited Speaker - Ari Sadanandom

Abstract Title: SUMO and plant stress signalling

Primary Author(s) and Institution(s): Ari Sadanandom; Durham University

Abstract

Plants adapt to heterogeneous soil conditions by altering their root architecture. For example, roots branch when in contact with water using the hydropatterning response. We report that hydropatterning is dependent on auxin response factor ARF7. This transcription factor induces asymmetric expression of its target gene LBD16 in lateral root founder cells on the side of the root in contact with water. This differential expression pattern is regulated by post-translational modification of ARF7 with the SUMO protein. SUMOylation negatively regulates ARF7 transcriptional activity. ARF7 SUMOylation is required to recruit the Aux/IAA repressor protein IAA3. Blocking ARF7 SUMOylation disrupts IAA3 recruitment and hydropatterning. We conclude that this new form of auxin regulation controls root branching pattern in response to water availability.

Protein Modification and Degradation
Concurrent Speaker - Jorge Zamora Zaragoza

Abstract Title: DECIPHERING THE MASTER'S CODE: PHOSPHORYLATION-DEPENDENT REGULATION OF THE RETINOBLASTOMA-RELATED1 PROTEIN FUNCTIONS

Primary Author(s) and Institution(s): JORGE ZAMORA ZARAGOZA . Wageningen University Research, Wageningen, the Netherlands. BEN SCHERES. Wageningen University Research, Wageningen, the Netherlands. Rijk Zwaan Department of Biotechnology, Fijnaart, the Netherlands Wageningen University and Research

Abstract

Spatio-temporal balance of cell growth, division and differentiation is crucial for plant development. This balance is regulated by RETINOBLASTOMA-RELATED1 (RBR), which integrates internal and environmental cues and control genetic programs to give a coordinated cell response. Stem Cell (SC) maintenance, asymmetric cell division, DNA damage response and cell death are also RBR-controlled processes. Despite the extensive research on RBR, how can a single protein coordinate such processes remains unknown. RBR protein interacts with and regulates Transcription Factors (TF) required for cell fate decisions. RBR-TF interactions are in turn controlled by RBR phosphorylation. An emerging paradigm hypothesizes the existence of a so-called "phosphorylation code": specific combinations of

phospho-sites control specific RBR-TFs interactions, allowing RBR to spatio-temporally coordinate cell fates with clockwork precision. My work aims to elucidate the mechanisms governing RBR activity that ultimately lead to an integrated cell output. By systematically mutating RBR phosphosites in various combinations, complementation analysis shows that RBR-linked phenotypes could be separated. Moreover, since RBR research mainly include knocking down/out or overexpressing the gene, new exciting phenotypes arose. My results strongly support the phosphorylation code hypothesis and constitutes a big first step to decipher it.

Protein Modification and Degradation
Concurrent Speaker - Gunjan Sharma

Abstract Title: UNDERSTANDING NOVEL SUBSTRATES OF CYS-ARG/N-END RULE PATHWAY AS POTENTIAL O2 SENSORS FOR HYPOXIA SURVIVAL RESPONSE

Primary Author(s) and Institution(s): Gunjan Sharma , Tinne Boeckx, Sophie Berckhan, Cristina Sousa Correia, JORGE VICENTE, Michael J. Holdsworth Division of Plant and Crop Sciences, University of Nottingham, Sutton Bonington Campus, Loughborough, LE12 5RD, UK Division of Plant and Crop Sciences, University of Nottingham

Abstract

Oxygen (O 2) plays essential roles in a variety of plant biochemical and physiological processes. A reduction in available oxygen, for example during submergence leads to a hypoxia responsive survival strategy. Sensing of O 2 (and also nitric oxide, NO) is mediated by Cys2-initiating Group VII Ethylene Response transcription factors (ERFVIIs) via the oxygen-sensing capacity of the Cys-Arg/N-end rule pathway of ubiquitin-mediated proteolysis. In silico analysis revealed the presence of 246 Arabidopsis proteins that like ERFVIIs initiate with Met1-Cys2, suggesting that non-ERFVII proteins may also function as O 2 /NO sensors. We analysed the capacity of selected proteins with diverse predicted functions to be substrates of the Cys-Arg/N-end rule pathway in vitro and in vivo . Our results suggest that a group of these are N-end rule substrates in vitro and that in vivo they have a very short half-life regulated by the 26S proteasome. Like ERFVIIs, these proteins promote hypoxia survival of the root tip. In conclusion, we demonstrate the existence of a diverse set of oxygen sensor proteins that are dynamically regulated by the N-end rule pathway and together enhance survival of hypoxia.

Protein Modification and Degradation
Concurrent Speaker - Wei Lan

Abstract Title: THE FUNCTIONAL ANALYSIS OF ATUPL3 DURING ARABIDOPSIS LEAF AGING

Primary Author(s) and Institution(s): WEI LAN , Weibo Ma, Shiyou Qiu, Ying Miao Center for Molecular Cell and Systems Biology, College of Life Sciences, Fujian Agriculture and Forestry University, Fuzhou 350002, China

Abstract

The homologous to E6-AP carboxy terminus ubiquitin-protein ligases (HECT E3s) family is one of E3s family existed in eukaryotes. In Arabidopsis thaliana , there are 7 members in HECT E3s family, from UPL1~UPL7. The previous research has reported that UPL3 is involved in the trichome development; UPL5 can disorder the process of senescence by ubiquitinating AtWRKY53, a key senescence-associated transcription factor, and then promoting its degradation via 26S proteasome. To address the regulatory function of UPL3 in post-translation level during plant development, ProUPL3::GUS transgenic plant was produced. The GUS histochemical staining of ProUPL3::GUS plants show that in juvenile plant GUS gene highly express in young leaf from base to tip, in mature plant the promoter of UPL3 shows high activity from young to old leaf, especially high expressed in trichome. Meanwhile, the upl3 mutants delay senescence compare to wildtype plants. Thus, UPL3 may also play a role in the process of leaf senescence, but an opposite role of UPL5. Further, comparative ubiquitination-proteomics analysis showed that more than 75 lysine sites of 73 substrate proteins are altered their ubiquitination levels. Interestingly, among them the core-histones of chromatin are found. It hints that UPL3 plays regulatory function in histone ubiquitination during plant development.

The Plant Immune System
Concurrent Chair - Jane Parker

Abstract Title: AN NLR RECEPTOR SIGNALING CIRCUIT IN EFFECTOR-TRIGGERED IMMUNITY

Primary Author(s) and Institution(s): JANE E PARKER HAITAO CAI JINGDE QIU DEEPAK BHANDARI DMITRY LAPIN; Max-Planck Institute for Plant Breeding Research

Abstract

A crucial plant immunity layer against host-adapted pathogens is mediated by intracellular nucleotide-binding domain/leucine-rich-repeat (NLR) receptors which recognize pathogen-delivered effectors in various host cell compartments. Two major plant NLR receptor sub-classes differ principally in their N-terminal domains: CC-NLRs (CNLs) have a coiled-coil domain and TIR-NLRs (TNLs), a Toll-Interleukin1-Receptor signaling (TIR) domain. These NLR types utilize the defense network in various ways to transcriptionally mobilize anti-microbial pathways, often associated with host cell death. We are interrogating TNL receptor downstream signaling mechanisms in Arabidopsis . Our aim is to understand how activated TNLs link up molecularly and functionally with other components, such as EDS1 complexes which mediate TNL transcriptional reprogramming, and identify which transcriptional sectors are important for stopping pathogen growth. I will describe a signaling circuit in TNL effector-triggered immunity (ETI) in which EDS1 complexes antagonize MYC2, a transcriptional master regulator of jasmonic acid (JA) signaling. Antagonism of MYC2 works independently of ICS1-generated salicylic acid

(SA). The genetic, molecular, protein structural and pathogen infection data suggest that this ETI signaling circuit serves both to protect and bolster SA-mediated defense. We reveal a new intersection between ETI and the plant stress hormone network which contributes to pathogen resistance.

The Plant Immune System
Invited Speaker - Hailing Jin

Abstract Title: Cross-Kingdom RNAi and small RNA trafficking between plants and fungal pathogens

Primary Author(s) and Institution(s): Qiang Cai 1 , Lulu Qiao 1,2 , Ming Wang 1 , Baoye He 1 , Feng-Mao Lin 3 , Jared Palmquist 1 , Hsien-Da Huang 3 , and HAILING JIN 1, * 1 Department of Microbiology Plant Pathology, Center for Plant Cell Biology, Institute for Integrative Genome Biology, University of California, 900 University Ave., Riverside, CA 92521, USA. 2 Department of Plant Protection, Nanjing Agriculture University, Nanjing, 210095, China. 3 Department of Biological Science and Technology, National Chiao Tung University, Hsin-Chu 300, Taiwan.;

Abstract

Cross-Kingdom RNAi and small RNA trafficking between plants and fungal pathogens Qiang Cai 1 , Lulu Qiao 1,2 , Ming Wang 1 , Baoye He 1 , Feng-Mao Lin 3 , Jared Palmquist 1 , Hsien-Da Huang 3 , and HAILING JIN 1, * 1 Department of Microbiology Plant Pathology, Center for Plant Cell Biology, Institute for Integrative Genome Biology, University of California, 900 University Ave., Riverside, CA 92521, USA. 2 Department of Plant Protection, Nanjing Agriculture University, Nanjing, 210095, China. 3 Department of Biological Science and Technology, National Chiao Tung University, Hsin-Chu 300, Taiwan. Small RNAs (sRNAs) are a class of short non-coding RNAs that mediate gene silencing in a sequence-specific manner. We have demonstrated that some sRNAs from eukaryotic pathogens, such as Botrytis cinerea , the fungal pathogen that causes grey mold disease on more than 1000 plant species, could be translocated into host plant cells and suppress host immunity genes for successful infection (Weiberg et al., Science 2013). Recently we have found that transgenic plants expressing hairpin RNAs that targeting Botrytis Dicer1 and Dicer2 genes could effectively block the generation of fungal sRNA effectors and suppress grey mold disease (Wang et al,, Nature Plants, 2016). These findings demonstrate an important role of bidirectional cross-kingdom RNAi in host – pathogen interactions. To examine whether host endogenous sRNAs are delivered into fungal cells, we developed a sequential protoplast preparation protocol to isolate pure fungal cells from the infected tissue, then profiled sRNA populations from the isolated B. cinerea cells. We also observed a drastic increase of extracellular vesicles (EVs) at the fungal infection sites, which led us to isolate EVs from the infection tissue and perform small RNA-seq analysis . We identified a panel of plant endogenous miRNAs and siRNAs that are secreted by EVs and transferred into fungal cells. These sRNAs induce cross-kingdom RNAi of fungal genes involved in pathogenicity. Furthermore, we discovered two Arabidopsis exosome markers that are induced by B. cinerea inoculation. Mutation in these exosome marker genes leads to reduced host sRNA trafficking and enhanced plant susceptibility. These data support that exosome-like extracellular vesicles are one of the major pathways to deliver host sRNAs into fungal cells and induce cross-kingdom RNAi of fungal virulent genes (Cai et al., Science 2018). Furthermore, we also discovered that B. cinerea can take up double-stranded RNAs and sRNAs from the environment. Applying sRNAs or dsRNAs that target Botrytis Dicer genes on the surface of fruits, vegetables and flowers significantly inhibits grey mold disease (Wang et

al,, Nature Plants, 2016). Such pathogen gene-targeting RNAs represent a new generation of fungicides that are durable and environmentally-friendly.

The Plant Immune System
Concurrent Speaker - Maya Bar

Abstract Title: Tomato NRC4a NB-LRR receptor activates plant immunity, linking extracellular and intracellular immune perception

Primary Author(s) and Institution(s): MAYA BAR 1 , MEIRAV LEIBMAN-MARKUS 2 , LORENA PIZARRO 2 , SILVIA SCHUSTER 2 , ZJ DANIEL LIN 3 , OFIR GERSHONY 1 , GITTA COAKER 3 and ADI AVNI 2 1 Department of Plant Pathology and Weed Research ARO, The Volcani Center, Rishon LeZion, 7505101, Israel 2 School of Plant Sciences and Food Security, Tel Aviv University, Tel Aviv, 69978, Israel 3 ; Department of Plant Pathology, University of California, Davis, California 95616, USA; ARO, Volcani Center

Abstract

Plant recognition and defense against pathogens employs a two-tiered perception system. Surface localized pattern recognition receptors (PRRs) act to recognize microbial features, while intracellular nucleotide binding leucine-rich repeat receptors (NLRs) directly or indirectly recognize pathogen effectors inside host cells. We identified an NLR that can associate with the PRR LeEIX2, termed SlNRC4a (NB-LRR Required for HR-associated Cell death-4). Co-immunoprecipitation demonstrates that SlNRC4a is able to associate with different PRRs. Physiological assays with specific elicitors revealed that SlNRC4a alters PRR-mediated responses. SlNRC4a overexpression enhances defense responses while silencing SlNRC4 reduces plant immunity. We found Tomato plants possessing elevated NRC4a expression to be resistant to a variety of pathogens. We propose that SlNRC4a acts as a non-canonical positive regulator of immunity mediated by diverse PRRs, linking both intracellular and extracellular immune perception.

The Plant Immune System
Concurrent Speaker - Yoji Kawano

Abstract Title: OsGAPC1 ACTS AS A NO SENSOR TO CONTROL HISTONE ACETYLATION TO INDUCE RICE IMMUNITY

Primary Author(s) and Institution(s): KEN-ICHI KOSAMI and YOJI KAWANO, Shanghai Center for Plant Stress Biology, Chinese Academy of Sciences; Chinese Academy of Sciences

Abstract

Plants dramatically change their redox state and epigenetic marks to organize their immunity in response to pathogen. The second messenger nitric oxide (NO)and post-translational modifications of histones play key roles in modulating immunity-related gene activity. However, signaling pathways leading to histone modification during plant immunity remain largely unknown. We have previously revealed that the small GTPase OsRac1 acts as a key regulator in rice immunity. Here we identified the glycolytic enzyme OsGAPC1 as a novel OsRac1 interactor, and found thatOsGAPC1 is a positive regulator of disease resistance to rice blast fungus. OsRac1 controlled chitin-induced NO production, thus triggering ofS-nitrosylationand nuclear translocation of OsGAPC1. OsGAPC1 associated with

the histone deacetylaseHDT701, and increased the acetylation level of histone H4K5 and the expression of defence genes. These results indicate that OsGAPC1 acts as a NO sensor that regulates defence gene expression through histone acetylation during rice immunity.

The Plant Immune System
Concurrent Speaker - Po-Yuan Shih

Abstract Title: DIFFERENTIAL ROLES OF GLUCOSINOLATES AND CAMALEXIN AT DIFFERENT STAGES OF AGROBACTERIUM-MEDIATED TRANSFORMATION

Primary Author(s) and Institution(s): PO-YUAN SHIH 1,3,4 , SHU-JEN CHOU 1 , CAROLINE M Ü LLER 6 , BARBARA ANN HALKIER 7 , ROSALIA DEEKEN 2 , and ERH-MIN LAI 1,3,5* 1 Institute of Plant and Microbial Biology, Academia Sinica, Taipei, Taiwan 2 Molecular Plant Physiology and Biophysics, Julius-von-Sachs-Institute for Biological Sciences, University of Wuerzburg, Wuerzburg, Germany 3 Molecular and Biological Agricultural Sciences Program, Taiwan International Graduate Program, Academia Sinica, Taipei, Taiwan 4 Graduate Institute of Biotechnology, National Chung-Hsing University, Taichung, Taiwan 5 Biotechnology Center, National Chung-Hsing University, Taichung, Taiwan 6 Chemical Ecology, Bielefeld University, Germany. 7 DynaMo Center, Department of Plant and Environmental Sciences, University of Copenhagen, Denmark.

Abstract

Aims: Agrobacterium tumefaciens can cause crown gall disease via transforming T-DNA into plants. To understand how plants respond to Agrobacterium infection, we used the Arabidopsis to reveal the gene expression profiles, and study how secondary metabolites regulate transformation efficiency. Methods: Arabidopsis seedlings were used to study the plant responses to Agrobacterium infection by gene expression and secondary metabolite profiling followed by functional studies. Transient transformation in seedlings and tumorigenesis assays on inflorescence stalks were used to study the impacts of glucosinolates and camalexin on Agrobacterium -mediated transformation. Results: Transcriptome analysis revealed Agrobacterium infection activated the indole glucosinolates (iGSs) modification and camalexin biosynthesis, but suppressed the aliphatic glucosinolates (aGSs) biosynthesis. The results in Arabidopsis mutant studies, metabolite profiling and chemical treatment assays showed that iGS hydrolysis played an inhibitory role in Agrobacterium- mediated transient transformation efficiency on seedlings, and camalexin accumulation was a key factor inhibiting tumor development on inflorescence stalks. We suggest the iGSs hydrolysis are used by Arabidopsis to defend Agrobacterium at early stage, and camalexin inhibits tumor development at the later stages. In addition, the differential effects of certain GS hydrolysis on Agrobacterium transformation may be used to control crown gall diseases or to modulate the transformation efficiency.

Long Distance Signaling
Concurrent Chair - Patrick Achard

Abstract Title: GA12 ACTS AS LONG DISTANCE GROWTH SIGNAL IN PLANTS

Primary Author(s) and Institution(s): PATRICK ACHARD 1 , LUCIE CAMUT 1 , THOMAS REGNAULT 1,2 , LALI SAKVARELIDZE-ACHARD 1 , JEAN-MICHEL DAVIÈRE 1 , THEODOR LANGE 3 . 1 Institut de Biologie Moléculaire des Plantes, UPR2357, associé avec l'Université de Strasbourg, 67084 Strasbourg, France. 2 Department of Plant Systems Biology, 85354, Freising, Germany. 3 Institut for Plant Biology, Braunschweig University of Technology, D-38106 Braunschweig, Germany.; Institut de biologie moléculaire des plantes, CNRS

Abstract

Plants live in fixed location and survive adversity by integrating growth responses to multiple environmental signals. For example, plants are highly responsive to subtle changes in ambient temperature and have evolved efficient mechanism to coordinate their growth accordingly. Like all multicellular organisms, this coordination requires communication mediated by signal molecules including phytohormones that move between distant organs of the plant. Gibberellins (GAs) are a large family of tetracyclic diterpenoid compounds controlling major aspects of plant growth and development. Although previous studies suggested the existence of a transport of GAs in plants, the nature and properties associated with this transport were unknown. By mixing old-style grafting with modern molecular genetics in Arabidopsis, we showed that the GA12 precursor, although biologically inactive, is the chemical form of GA undergoing long-distance transport across plant organs. Furthermore, our recent work shows that long-distance transport of GA12 enables plants to adjust their growth in response to change in ambient temperature.

Long Distance Signaling

Invited Speaker - Hitoshi Sakakibara

Abstract Title: A ROLE OF LONG-DISTANCE TRANSPORT OF CYTOKININS TO FINE-TUNE SHOOT GROWTH IN RESPONSE TO NITROGEN NUTRIENT CONDITIONS

Primary Author(s) and Institution(s): HITOSHI SAKAKIBARA 1,2 , ASAMI OSUGI 1 , MIKIKO KOJIMA 2 , TAKATOSHI KIBA 1,2 1 Graduate School of Bioagricultural Sciences, Nagoya University, Nagoya 464-8601, Japan 2 RIKEN Center for Sustainable Resource Science, Yokohama 230-0045, Japan; Nagoya University

Abstract

Cytokinin (CK) plays a pivotal role in regulation of plant growth and development, and its action is finely controlled by various steps including biosynthesis and metabolism, transport, and signaling. We have demonstrated that IPTs, CYP735As, and LOGs, which are key genes for de novoCK biosynthesis, are expressed in various parts during growth, and regulate synthesis of N6-(Δ2-isopentenyl)adenine (iP) and trans-zeatin (tZ). Studies on CYP735Asmutants show that tZ is important for the normal growth of shoot rather than that of root, suggesting amechanism that modulates physiological function of CKs by side-chain modification. This regulation is one of the qualitative controls of CK action regulating shoot growth by root-borne signal. The biosynthesis and transport genes are regulated by nutritional conditions for linking its status to growth regulation. Furthermore, recent studies suggest root-to-shoot transport of tZ and its precursor controls different set of shoot traits. These findings suggest that complex action of long-distantly transported CKs could be organized by the side chain structure and the dependency of the activation pathway. We will outline our recent progress in physiological significance of regulation of CK action to optimize growth and development for nitrogen nutrient conditions at whole plant level.

Long Distance Signaling

Concurrent Speaker - Archana Kumari

Abstract Title: ROLE OF PROTON PUMPS IN WOUND-INDUCED PLASMA MEMBRANE DEPOLARIZATION AND DEFENSE RESPONSES.

Primary Author(s) and Institution(s): ARCHANA KUMARI ,AURORE CHETELAT AND EDWARD E. FARMER; Univesity of Lausanne

Abstract

Wounded leaves generate electrical signals that initiate the synthesis of jasmonate, a potent regulator of wound-induced defense responses (Mousavi et al., 2013). Plasma membrane proton pumps (AHAs) are electrogenic pumps, that generate electrical potential differences across the plasma membrane. Since electrical signals consist of transient plasma membrane depolarization, it has been hypothesized that proton pumps play important role in electrical signal transmission. Indirect electrophysiological and pharmacological evidence suggests transient inhibition of proton pumps during electrical signaling. However, genetic evidence for this phenomenon is still lacking. Molecular studies have shown that the C-terminal, regulatory domain of proton pumps is a target for regulation in response to diverse environmental conditions that activate/inhibit proton pumping (Falhof et al ., 2016). In this study, proton pumps (AHAs) mostly expressing in vascular-bundle were modulated by deletion of auto-inhibitory C-terminal domain and used as tool to investigate the electrical signal and jasmonate pathway activity in specific cell types. Our data indicates that cell-type-specific modulation of AHAs can play an important role in wound signaling and defense responses.

Long Distance Signaling
Concurrent Speaker - Doron Shkolnik

Abstract Title: Perception of moisture gradient by roots is transmitted to the elongation zone by an asymmetric calcium signal in the phloem

Primary Author(s) and Institution(s): DORON SHKOLNIK , ROYE NURIEL, MARIA CRISTINA BONZA, ALEX COSTA, HILLEL FROMM; Tel Aviv University

Abstract

Ever since Darwin postulated that the tip of the root is sensitive to moisture differences across the root, and that it “transmits an influence to the upper adjoining part, which bends towards the source of moisture”, two important questions remained to be answered in order to explain the response of roots to uneven distribution of water in their microenvironment; which longitudinal signal transmits hydro-perception from the root tip to the elongation zone, where bending occurs, and which cross-root asymmetric lateral signal confers differential cell elongation on different sides of the root, resulting in root bending toward the water source. Here we show that an osmotic stress gradient applied across the root tip generates a slow long-distance asymmetric cytosolic Ca 2+ signal in the phloem, which peaks at the elongation zone, where it is dispersed laterally and asymmetrically to peripheral cells, where cell elongation occurs. Moreover, we demonstrate that the MIZ1 protein, which is indispensable for root curvature towards water, directly inhibits the activity of ECA1, an endoplasmic reticulum Ca 2+ transporter. This inhibition is required for generating the long-distance cytosolic Ca 2+ signal upon hydrostimulation.

Long Distance Signaling
Concurrent Speaker - Sandrine Ruffel

Abstract Title: INTERACTION BETWEEN SYSTEMIC NITROGEN SIGNALING AND HORMONES, IN ARABIDOPSIS

Primary Author(s) and Institution(s): SANDRINE RUFFEL a ARTHUR POITOUT a , AMANDINE CRABOS a , IVAN PETRIK b , ONDREJ NOVAK b , GABRIEL KROUK a , BENOIT LACOMBE a a BPMP, INRA, CNRS, Univ Montpellier, Montpellier SupAgro, Montpellier, France b Laboratory of Growth Regulators, Centre of the Region Haná for Biotechnological and Agricultural Research, Institute of Experimental Botany CAS and Faculty of Science of Palacký University, CZ-78371 Olomouc, Czech Republic

Abstract

Rapid adjustment of plant physiology and development to external fluctuations is critical for sessile organism, giving a singular interest to network signaling controlling these mechanisms. Among many adaptation processes, root plasticity is primordial to optimize nutrient acquisition but relies on a complex network integrating local and systemic (root <-> shoot) signaling. Indeed, locally, plants invest resource in soil area where nutrients are available and systemically they adjust nutrient acquisition to the whole plant demand. Our main goal is to decipher systemic signaling underlying the perception of nitrate heterogeneous provision, in Arabidopsis. Using the split-root system, in which physically isolated root systems of the same plant were challenged with different environments, we previously demonstrated that cytokinin biosynthesis constitutes one critical component of root-shoot-root communication. By combining the use of cytokinin mutants with hormone measurements, transcriptomic analysis, nitrate uptake assays, and root growth measurements, we show that root to shoot trans -zeatin (t Z) translocation is likely crucial for long distance signaling controlling rapid sentinel gene regulation and long-term functional acclimation to heterogeneous nitrate supply. Interestingly, shoot transcriptome profiling revealed that glutamate/glutamine metabolism is likely a target of t Z root-to-shoot translocation, prompting an interesting hypothesis regarding shoot-to-root communication. Finally, this study also highlights t Z-independent pathways triggered by variation into nitrogen supply.

Light and Shade
Concurrent Chair - Carlos Ballare

Abstract Title: INTERACTION OF PHYTOCHROME AND JASMONATE SIGNALING IN THE REGULATION OF GROWTH AND DEFENSE RESPONSES

Primary Author(s) and Institution(s): CARLOS L. BALLARE IFEVA, University of Buenos Aires and CONICET; IFEVA, University of Buenos Aires-CONICET

Abstract

Plants detect and respond to the proximity of competitors using light signals perceived by informational photoreceptors. A low red to far-red (R:FR) ratio in the canopy light is a signal of competition that is sensed by phytochrome B (phyB). Low R:FR ratios increase the synthesis of growth-related hormones, including auxin and gibberellins, which allows plants to rapidly elongate their shoots and avoid being shaded by their neighbors. Recent research demonstrates that phyB is also an important modulator of

the two principal hormonal pathways that regulate plant immunity against herbivores and pathogens, i.e. the jasmonic-acid (JA) and the salicylic-acid pathways (SA). Low R:FR ratios down-regulate JA-induced defense responses. This down-regulation is thought to help the plant to efficiently redirect resources from defense to rapid growth under conditions of intense competition. In this presentation, I will discuss recent advances in the understanding of the mechanisms that link phyB with JA signaling and metabolism, and explore their functional implications. Unveiling the molecular links between photoreceptors and the hormonal regulators of plant immunity is important to generate a mechanistic framework to understand how plants deal with resource allocation trade-offs under natural conditions.

Light and Shade
Invited Speaker - Salomé Prat

Abstract Title: PIF4-induced BR-synthesis is critical to diurnal and thermomorphogenic growth

Primary Author(s) and Institution(s): CRISTINA MARTÍNEZ, ANA ESPINOSA-RUÍZ, MIGUEL DE LUCAS, SALOMÉ PRAT

Abstract

The plant PIF4 and BES1/BZR1 factors antagonize light signaling by facilitating co-activated expression of a large number cell-wall loosening and auxin-related genes. While PIF4 activates these target genes, activity of BES1and BZR1 switches from a repressive to an activator function, depending on interaction with TOPLESS (TPL) and other families of regulators, like PIFs. Combinatorial complexity of this regulation is, however, little understood. Here, by using a protein array hybridization, we show that BES1, PIF4, and the BES1-PIF4 complex recognize different DNA elements, thus revealing a distinctive cis -regulatory code beneath BES1 repressive (BRRE- and G-box) and PIF4 co-activation (PBE-box) function. BES1 homodimers bind to conserved BRRE- and G-box elements in the BR-biosynthetic promoters and inhibit their expression during the day, while elevated PIF4 competes for BES1 homodimer formation, which results in peak BR levels at dawn. High ambient temperatures were shown to stabilize PIF4 and lead to auxin biosynthesis and response gene activation. We demonstrate that in addition to auxin, PIF4 plays a central role in the control of BR synthesis, induction of BR levels being essential to thermomorphogenic hypocotyl elongation.

Light and Shade
Concurrent Speaker - Johanna Krahmer

Abstract Title: Regulation of plant growth and metabolism by phytochrome signalling

Primary Author(s) and Institution(s): JOHANNA KRAHMER, Institute for Molecular Plant Sciences, University of Edinburgh DANIEL SEATON, EMBL-EBI AMMAD ABBAS, Institute for Molecular Plant Sciences, University of Edinburgh HIROFUMI ISHIHARA, Max Planck Institute for Plant Physiology MARK STITT, Max Planck Institute for Plant Physiology KAREN HALLIDAY, Institute for Molecular Plant Sciences, University of Edinburgh; The University of Edinburgh

Abstract

Phytochromes are plant photoreceptors, which, upon activation by red light, initiate vast transcriptional changes. While early phytochrome signalling events have been intensively studied, mostly in seedlings,

less is known about post-transcriptional or metabolic roles and phytochrome action in older rosettes. Metabolomics experiments on mature rosettes have uncovered remarkable metabolic mis-regulation in phytochrome mutants, including excess accumulation of sugars, amino acids and organic acids. Using 13C labelling, we have investigated which processes may contribute to these changes and how they may connect with stress signaling pathways. We have also studied the relationship of metabolite accumulation with growth since phytochrome mutants have severely reduced biomass, using growth curve analysis, carbon uptake measurements, 13C labeling of the cell wall and mathematical modeling. We showed that relative growth rate is impaired in phytochrome mutants until about 2.5 weeks, but equivalent to the WT thereafter, and this can be explained by their smaller cotyledon size. We found that metabolic mis-regulation occurs only at the later vegetative growth stages when phytochrome mutants grow at the same rate as the WT, while the opposite is the case in younger plants. Our study indicates that phytochrome signaling has intricate and pervasive effects on plant growth and metabolism.

Light and Shade

Concurrent Speaker - Stephan Wenkel

Abstract Title: VASCULAR TRANS-DIFFERENTIATION IS UNDERLYING SHADE-INDUCED GROWTH

Primary Author(s) and Institution(s): ESTHER BOTTERWEG-PAREDES 1,2 , ANKO BLAAKMEER 1,2 , SHIN-YOUNG HONG 1,2 , YAKUN XIE 3 , EDOUARD PESQUET 4 AND STEPHAN WENKEL 1,2,3 1 Copenhagen Plant Science Centre, University of Copenhagen, Thorvaldsensvej 40, 1871 Frederiksberg C, Denmark. 2 Department of Plant and Environmental Sciences, Faculty of Science, University of Copenhagen, Copenhagen, Denmark 3 Centre for Plant Molecular Biology (ZMBP), University of Tübingen, Auf der Morgenstelle 32, 72076 Tübingen, Germany 4 Arrhenius Laboratories, Department of Ecology, Environment and Plant Sciences (DEEP), Stockholm University, 160 91 Stockholm, Sweden; University of Copenhagen

Abstract

Transcription factors of class III homeodomain leucine zipper (HD-ZIPIII) and KANADI (KAN) families control polarity establishment in shoots and roots. Using a combination of ChIP-seq and mRNA-seq we identified sets of direct target genes. Surprisingly, the set of HD-ZIPIII/KAN shared target genes shows a significant enrichment for known components of the shade avoidance response. While we showed recently that some of these shade factors play fundamental roles in leaf patterning (Merelo et al., PNAS, 2016), an involvement of the upstream patterning factors in mediating shade growth remained opaque. Our current work has uncovered a shade-induced vascular patterning module: by directly impinging on WOX4, a master regulator of vascular differentiation, plants induce trans-differentiation of xylem elements inside the vascular cylinder leading to an increase in tracheary elements (TEs). Plants carrying mutations in either HD-ZIPIII/KAN or WOX4 fail to increase the number of TEs when shaded and are also impaired in their ability to induce elongation growth. In agreement with these findings we see that shade-insensitive mutants or mutants with a constitutive shade-avoidance response have similar TE expansion defects. Our results thus set the stage for a deeper understanding of how growth and patterning are coordinated in a dynamic environment.

Light and Shade

Concurrent Speaker - Seong Wook Yang

Abstract Title: LIGHT SIGNALING PATHWAY INVOLVES IN THE REGULATION OF MICRORNA BIOGENESIS

Primary Author(s) and Institution(s): SEOK KEUN CHO 1 , MOON YOUNG RYU 1 , SUK WON CHOI 1 , ANDRAS VICZIAN 2 , ATTILA MOLNA 4 PABLO MANAVELLA 3 , FERENC NAGY 2,4 , AND SEONG WOOK YANG 1, 5 1 Department of Systems Biology, College of Life Science and Biotechnology, Yonsei University, Seoul, 120-749, Korea 2 Institute of Plant Biology, Biological Research Centre (BRC) of the Hungarian Academy of Sciences, H-6726 Szeged, Temesvári krt. 62. 3 Instituto de Agrobiotecnología del Litoral (IAL) Centro Científico Tecnológico Santa Fe (CCT), Santa Fe, Argentina 4 Institute of Molecular Plant Science, School of Biological Sciences Kings Buildings, University of Edinburgh, EH9 3JH, UK 5 Department of Plant and Environmental Sciences, Faculty of Science, University of Copenhagen, Thorvaldsensvej 40, DK-1871 Frederiksberg, Copenhagen, Denmark

Abstract

Constitutive photomorphogenic 1 (COP1) is a RING-finger E3 ligase that plays a central role in photomorphogenesis by destabilizing many light-regulated transcription factors and photoreceptors. Previously, we revealed a novel function for COP1 E3 ligase in controlling global miRNA biogenesis in Arabidopsis thaliana. In cop1 mutants, the level of miRNAs is dramatically reduced because of the diminution of HYPONASTIC LEAVES 1 (HYL1), an RNA-binding protein required for precise miRNA processing. Under dark condition, HYL1 is rapidly destabilized by a protease, HSP1 which specifically cleaves the N-terminal region from HYL1, thus neutralizing its function. Our results further show that the cytoplasmic partitioning of COP1 under light is essential to protect HYL1 against protease HSP1. As a next step, we further investigated whether the other major miRNA processing components - Dicer-like 1 (DCL1) and SERRATE (SE) - are also regulated by dark-to-light transition. DCL1 and SE are constitutively degraded by yet unknown proteolytic pathways in etiolated seedlings but dramatically stabilized in de-etiolated seedlings. Interestingly, the levels of many miRNAs are not correlated to the highly up-regulated microprocessor proteins. These results imply that miRNA processing can be differentially regulated by dark-to-light transition. Based on detailed molecular and biochemical analyses, we discuss a new regulatory crosstalk between light signaling and miRNA biogenesis.

Transcriptional and Post-Transcriptional Gene Silencing

Concurrent Chair - Xuemei Chen

Abstract Title: BIOGENESIS AND ACTIVITIES OF PLANT MICRORNAS - THE "WHERE" AND "HOW"

Primary Author(s) and Institution(s): Bailong Zhang and Xuemei Chen Department of Botany and Plant Sciences, University of California, Riverside, CA 92521, USA; University of California, Riverside

Abstract

MicroRNAs (miRNAs) impact nearly all biological processes by serving as sequence-specific regulators of gene expression. The biogenesis of miRNAs is a multi-step process involving the transcription of MIR genes into primary miRNAs (pri-miRNAs), the processing of pri-miRNAs into pre-miRNAs and then to miRNA/miRNA* duplexes, and the loading of miRNAs into an effector argonaute (AGO) protein. The miRNA-AGO complex regulates gene expression through degradation or translation repression of target

mRNAs. Although major players mediating miRNA biogenesis or miRNA activities have been uncovered, where miRNAs are synthesized or act in the cell and how the subcellular sites affect miRNA activities are poorly understood. I will discuss our recent findings that implicate the nuclear pore and endoplasmic reticulum in the biogenesis/activities of plant miRNAs.

Transcriptional and Post-Transcriptional Gene Silencing
Invited Speaker - Herve Vaucheret

Abstract Title: Distinct components of the RdDM pathway contribute to sense transgene PTGS initiation and PTGS-induced DNA methylation in Arabidopsis

Primary Author(s) and Institution(s): Christelle Taochy, Agnès Yu, Nathalie Bouteiller, Taline Elmayan, Hervé Vaucheret; Institut Jean-Pierre Bourgin, UMR1318 INRA, AgroParisTech, CNRS, Université Paris-Saclay

Abstract

During sense-transgene post-transcriptional gene silencing (S-PTGS), DNA methylation is established in the transgene transcribed portion, but its role remains unclear. Here, we show that the upstream components of the RNA-directed DNA methylation (RdDM) pathway, CLSY1, NRPD1, RDR2 and DCL3, are not required for S-PTGS-induced DNA methylation, whereas the downstream RdDM components NRPE1, DRD1 and DRM2, as well as the core S-PTGS component RDR6, are required, suggesting that RDR6-dependent siRNAs trigger S-PTGS-induced DNA methylation in an NRPE1-, DRD1- and DRM2-dependent manner, similar to de novo DNA methylation of reactivated transposons. Nevertheless, none of these RdDM components are required for induction of spontaneous S-PTGS, or for silenced tissue to transmit a systemic S-PTGS signal, suggesting that DNA methylation is a consequence, not a cause, of S-PTGS. However, NRPD1 and RDR2 are required for induction of S-PTGS upon grafting of nonsilenced scions onto silenced rootstocks, suggesting that NRPD1 and RDR2 promote systemic S-PTGS in recipient tissues.

Transcriptional and Post-Transcriptional Gene Silencing
Concurrent Speaker - Daai (Anna) Zhang

Abstract Title: A new RNAi transgene design for reduced transcriptional self-silencing and increased systemic gene silencing in plants

Primary Author(s) and Institution(s): DAAI (ANNA) ZHANG (University of Wollongong; Commonwealth Scientific and Industrial Research Organisation) CHENGCHENG ZHONG (Northwest Agricultrue and Forestry University; Commonwealth Scientific and Industrial Research Organisation) NEIL SMITH (Commonwealth Scientific and Industrial Research Organisation) REN ZHANG (University of Wollongong) MING-BO WANG (Commonwealth Scientific and Industrial Research Organisation); University of Wollogong & CSIRO

Abstract

Hairpin RNA (hpRNA) transgene-induced RNA interference (RNAi) has proven to be a powerful tool in gene function studies and crop improvement in plants. However, conventional hpRNA transgenes are subject to self-induced transcriptional silencing due to RNA-directed DNA methylation (RdDM),

compromising the efficiency of target gene silencing and long-term stability of the RNAi effect. To overcome this problem, we developed a new RNAi transgene design that can avoid self-induced RdDM. We demonstrate that this design induces more stable and uniform RNAi than conventional hpRNA transgenes against multiple target genes in plants. In a typical experiment, around 90-95% of independent transgenic lines containing the new construct show strong target gene silencing, in contrast to around 55-65% with the conventional hpRNA construct. Importantly, this new transgene design generates a unique profile of siRNA that favours posttranscriptional and systemic RNAi, as indicated by enhanced long distance gene silencing, but prevents RdDM hence transcriptional self-silencing of the transgene. DNA methylation analysis using bisulfite sequencing and McrBc-digestion PCR confirms that transgenes of the new design generally show little or no DNA methylation in the proximal promoter region, whereas all tested transgenic lines containing the conventional hpRNA construct display DNA methylation in the promoter region.

Transcriptional and Post-Transcriptional Gene Silencing
Concurrent Speaker - Jose Luis Reyes

Abstract Title: LEGUME-SPECIFIC MICRORNAS INVOLVED IN THE RESPONSES TO WATER DEFICIT IN PHASEOLUS VULGARIS (COMMON BEAN)

Primary Author(s) and Institution(s): JOSE LUIS REYES , CARLOS DE LA ROSA, ALEJANDRA COVARRUBIAS INSTITUTO DE BIOTECNOLOGIA, UNIVERSIDAD NACIONAL AUTONOMA DE MEXICO; Instituto de Biotecnologia-UNAM

Abstract

To contend with environmental adversities such as drought, plants have developed different mechanisms at the physiological, cellular and molecular levels. We have focused our work on the study of microRNAs as regulators of this response at the post-transcriptional level. We have identified microRNAs in common bean (Phaseolus vulgaris) that are expressed under water deficit conditions, including several legume-specific microRNAs. To aid in their study we have combined bioinformatical prediction of target transcripts, biochemical analysis of the AGO1 protein and of its interacting RNAs, and high-throughput sequencing analyses of cleaved mRNAs and sRNAs. Among the microRNAs found, here we describe a unique case where the conserved miR398a is encoded in the same gene locus as the legume-specific miR2119 present in common bean and other legumes. In common bean, mature miR398 and miR2119 are repressed in response to water deficit and we demonstrate that they target the mRNAs for COPPER-DEPENDENT SUPEROXIDE DISMUTASE 1 (CSD1) and ALCOHOL DEHYDROGENASE 1 (ADH1), respectively. Accordingly, the CSD1 and ADH1 mRNAs are up-regulated in response to water deficit. Furthermore, miRNA down-regulation was also observed when common bean plants were exposed to flooding, suggesting that reactive oxygen species and fermentation must be closely modulated under different adverse conditions.

Transcriptional and Post-Transcriptional Gene Silencing
Concurrent Speaker - Isabel Fredes

Abstract Title: IDENTIFYING THE ROLE OF ARGONAUTE1 PHOSPHORYLATION IN THE NITRATE RESPONSE OF ARABIDOPSIS THALIANA

Primary Author(s) and Institution(s): ISABEL FREDES 1 Andrea Vega 1 , Cristopher Hernández, 1 Xuemei Chen 2 and Rodrigo A. Gutiérrez 1 . 1 Center for Genome Regulation. Millennium Institute for Integrative Systems and Synthetic Biology. De partment of Molecular Genetics Microbiology, Faculty of Biological Sciences. Pontificia Universidad Católica de Chile. 2 Department of Botany and Plant Sciences and Institute of Integrative Genome Biology, University of California, Riverside.

Abstract

ARGONAUTE1 (AGO1) is a key component of the RISC complex and has an essential role in post-transcriptional control of gene expression in plants. We found AGO1 is differentially phosphorylated in Arabidopsis roots in response to nitrate treatments. Although, this phosphorylation has been identified in several independent phospho-proteome studies in Arabidopsis, there are no reports describing the impact of this phosphorylation on AGO1 function. We sought to address the role of AGO1 phosphorylation for control of gene expression and its impact on plant development and the nitrate response. We evaluated morphological and molecular phenotype of AGO1 phospho-null and phospho-mimic mutants plants subjected to various nitrate conditions. Our analysis showed that AGO1 phosphorylation/dephosphorylation balance is required for normal AGO1 function. Both mutants only partly complemented ago1 null mutants and exhibited distinct developmental phenotypes. To investigate the molecular impact of this post-translational modification on AGO1 function, we evaluated sRNA and mRNA abundance, AGO1 miRNA-loading and, AGO1 slicer activity. Interestingly, we did not find alteration on miRNA biogenesis or loading, but an altered miRNA-target regulation. Our results point to AGO1 phosphorylation as an important regulatory mechanism of AGO1 function with a role for regulation of gene expression and nitrate responses in plants.

Shoot Architecture
Concurrent Chair - Yonghong Wang

Abstract Title: Molecular mechanism underlying rice tiller angle

Primary Author(s) and Institution(s): Ning Zhang a,c , Hong Yu a , Yueyue Cai a,c , Jiyao Wang a,c , Guifu Liu a , Yundong Yuan a , Yan Liang a , Jiayang Li a,c , and Yonghong Wang a,b,c;

Abstract

Tiller angle in cereals is a key trait of shoot architecture that strongly impacts grain yield. Studies in rice (Oryza sativa L.) have implicated shoot gravitropism in the regulation of tiller angle. Previous studies have identified the rice LAZY1 (LA1) gene, which functions as a negative regulator of polar auxin transport (PAT). Loss-of-function of LA1 enhances PAT and thus alters the endogenous IAA distribution in shoots, leading to the reduced gravitropism and thus the tiller-spreading phenotype. To elucidate the mechanism of LA1 in the regulation of shoot gravitropism and thus tiller angle, we carried out a genetic screen to identify the suppressors of la1 , and identified several suppressors of LA1 that are components in the strigolactones (SLs) biosynthetic or signaling pathway. Further study revealed that SLs can inhibit

auxin biosynthesis and attenuate rice shoot gravitropism mainly through decreasing the local IAA content. Moreover, we conducted a large-scale transcriptome analysis of rice shoots in response to gravistimulation and identified two new nodes of a shoot gravitropism regulatory gene network that controls rice tiller angle. We demonstrate that HEAT STRESS TRANSCRIPTIONAL FACTOR 2D (HSFA2D) is an upstream positive regulator of the LA1-mediated asymmetric auxin distribution pathway. We also show that two functionally redundant transcription factor genes, WUSCHEL RELATED HOMEOBOX6 (WOX6) and WOX11 , are expressed asymmetrically in response to auxin to connect gravitropism responses with rice tiller angle. Next, we will identify genes to improve grain yields by facilitating the optimization of plant architecture.

Shoot Architecture

Invited Speaker - Klaus Theres

Abstract Title: REGULATION OF AXILLARY MERISTEM FORMATION IN TOMATO AND ARABIS ALPINA

Primary Author(s) and Institution(s): KLAUS THERES , UDHAYA PONRAJ, GREGOR SCHMITZ, HERNAN LOPEZ; Max Planck Institute for Plant Breeding Research

Abstract

Variation in shoot architecture of flowering plants is largely based on their ability to form new axes of growth throughout their life span. Shoots initiate from groups of pluripotent cells, called axillary meristems (AMs), established in the boundary zone between leaf and stem. In Arabis alpina, AM initiation is regulated by different mechanisms during vegetative and reproductive development. Knock-down of the regulator LATERAL SUPPRESSOR abolishes AM formation in the vegetative phase, but not in the reproductive phase. In the t omato mutant super determinant (sde) , axillary meristem development is compromised during all stages of vegetative development. Genetic analysis revealed two mutations, one on chromosome 4 (sde1), which contribute to the sde phenotype. Yet, in the WT accession VF36, the sde phenotype segregates as a single mendelian locus. Using a combination of classical mapping and RNAseq analysis we have mapped the sde1 mutation to a gene closely related to the RING components of the PRC1 complex (BMI1 and RING1). We confirmed the identity of Sde1 by complementation experiments and targeted knockout s using CRISPR/cas9 technology. Currently, we are analyzing Sde1 in the context of a putative epigenetic regulation layer and integrate it with the classical AM initiation pathways regulated by Ls and Bl ind .

Shoot Architecture

Concurrent Speaker - Jazmine Humphreys

Abstract Title: NOVEL GENETIC NETWORKS IN SHOOT BRANCHING REGULATION

Primary Author(s) and Institution(s): JAZMINE HUMPHREYS, School of Biological Sciences, University of Queensland MILOS TANURDZIC, School of Biological Sciences, University of Queensland; University of Queensland

Abstract

Branches develop from axillary buds established in the axils of leaves. Axillary buds are kept dormant by the actions of the plant hormone strigolactone (SL), while cytokinins (CK) and sugars are needed for bud

release from dormancy and for its outgrowth. We explored transcriptional responses to strigolactone (SL) and sucrose (SUC) in Arabidopsis, using a combination of transcriptomics, forward and reverse genetics, and systems biology approaches. Our results show that SL and SUC signalling is only partly convergent on the key branching regulator, transcription factor BRANCHED1 (BRC1). We discovered BRC1 -independent SL and SUC-regulated pathways that affect branching patterns in Arabidopsis involving members of Homeobox- and TCP-domain transcription factor gene families. We identified direct targets and downstream effects of these new branching regulators using a combination of RNA-seq, ChIP-seq and in vivo expression experiments. We further explored the dependence of SL- and SUC-elicited transcriptional responses on chromatin remodellers SPLAYED (SYD) and BRAHMA (BRM) and found that chromatin remodelling by SYD and BRM indeed plays a role in SL and SUC signalling. Taken together, these results expand existing and propose novel genetic networks involved in the transcriptional regulation of bud outgrowth, while highlighting the involvement of chromatin remodelling in this process.

Shoot Architecture

Concurrent Speaker - Franziska Fichtner

Abstract Title: TREHALOSE 6-PHOSPHATE INDUCES SHOOT BRANCHING IN ARABIDOPSIS

Primary Author(s) and Institution(s): FRANZISKA FICHTNER 1 , MARIA GRAZIA ANNUNZIATA 1 , FRANCOIS F. BARBIER 2 , REGINA FEIL 1 , MARK STITT 1 , CHRISTINE A. BEVERIDGE 2 and JOHN E. LUNN 1 1 Max Planck Institute of Molecular Plant Physiology, 14476 Potsdam-Golm, Germany, 2 School of Biological Sciences, The University of Queensland, St. Lucia, QLD 4072, Australia; Max-Planck-Institute of Molecular Plant Physiology

Abstract

Trehalose 6-phosphate (Tre6P) is a sucrose signalling metabolite in plants with influence over many metabolic and developmental processes. It was recently demonstrated that sucrose supply, rather than auxin, is the primary trigger for release of axillary bud dormancy after decapitation of pea plants, and that bud Tre6P levels rise rapidly after decapitation and correlate with bud outgrowth. To identify the sites and role of Tre6P signalling in shoot branching, we generated Arabidopsis (Arabidopsis thaliana) plants with altered Tre6P levels in the vasculature or in axillary buds. Increased Tre6P in the vasculature gave a bushy phenotype with plants having more primary rosette branches, while plants with less Tre6P had fewer branches. Lowering Tre6P in axillary buds strongly delayed bud outgrowth in long days, and inhibited branching under short day conditions. Combinatorial mutant analyses indicated that the effect of high Tre6P on shoot branching is dependent on FLOWERING LOCUS T and strigolactone signalling, but is at least partly independent of BRANCHED1. These results provide compelling evidence that Tre6P is a major player in shoot branching, and offer the first insights into how Tre6P-signalling is integrated with hormonal and other signalling pathways that regulate this process.

Shoot Architecture

Concurrent Speaker - Alice Vayssières

Abstract Title: Flowering commitment in cold determines shoot architecture of Arabis alpina

Primary Author(s) and Institution(s): ALICE VAYSSIERES 1 , PRIYANKA MISHRA 1 , ADRIAN ROGGEN 1 , KARIN LJUNG 2 , MARIA ALBANI 1 1 Botanical Institute, University of Cologne, Germany , 2 Umeå Plant Science Centre, Department of Forest Genetics and Plant Physiology, Swedish University of Agricultural Sciences, Umea, Sweden

Abstract

Perennial plant architecture is characterized by the maintenance of different meristems organized in zones within the plant. This special architecture is crucial for maintaining vegetative growth for several years. The perennial Brassicaceae model species Arabis alpina shows differential behavior of axillary meristems organized in zones: flowering branches, vegetative branches and dormant buds. Flowering in A. alpina is initiated during a prolonged vernalization period. P hysiology experiments with plants that experience cold but are not flowering and a mutant that does not require cold to flower demonstrate that commitment to flower in cold regulates perennial shoot architecture including maintenance of the dormant buds. To understand the molecular mechanisms regulating maintenance of dormant buds, an RNAseq experiment comparing meristem in different zones was carried out at the end of cold and shortly after. Results revealed (1) a difference between meristems in cold and (2) a reactivation of dormancy after cold in the dormant zone. IAA in stems within the dormant bud zone have been quantified and showed a transient increased after return to warm temperatures correlating with their inability to outgrow. With these results, we would like to suggest a model where the life strategy of A. alpina determines its shoot architecture.

Stem cells

Concurrent Chair - Kenneth Birnbaum

Abstract Title: Cell Division and Cellular Reprogramming During Regeneration

Primary Author(s) and Institution(s): KENNETH D. BIRNBAUM, New York University Ramin Rahni, New York University Marcela Hernandez Coronado, New York University Nicholas DelRose, New York University; New York University

Abstract

The widespread ability of plant cells to regenerate involves the alteration of existing tissue into a new type of tissue. Frequently, a damaged meristem will initiate a process that allows specified cells to alter their fate to recreate a new meristem. In the root regeneration system we use, cells in the most mature part of the meristem can give rise to new distal cell types, like columella, quiescent center, lateral root cap, which were all completely removed by injury. Do plant cells need to divide to change their fates? I will present our latest data on this important question, which we explore using live imaging techniques and single-cell RNA-seq analysis. I will dedicate some time to go over the evolution of techniques in single cell RNA-seq analysis, from plate-based methods to Chromium 10x to show how this data can be used to provide new insights into classic questions in plant biology. I will present how single-cell analysis shows some subtle changes in the cell cycle of regenerating plants. In addition, I will present our results

on coordinating our data from live imaging with single cell RNA-seq analysis. The working model is that fate transitions occur extremely rapidly but, surprisingly, so do cell divisions. Thus, cells might not need to divide to begin reprogramming but division appears to be necessary to finish the process. I will present the details of this model and our latest data on the mechanisms that operate during the cell cycle to mediate cell fate transitions.

Stem cells

Invited Speaker - Bert De Rybel

Abstract Title: DOF2.1 CONTROLS VASCULAR CELL PROLIFERATION DOWNSTREAM OF TMO5/LHW

Primary Author(s) and Institution(s): WOUTER SMET 1,2,3 , IRIS SEVILEM 4,5 , MARIA ANGELS DE LOUIS BALAGUER 6 , BRECHT WYBOUW 1,2 , ELIANA MOR 1,2 , MARK BOEKSCHOTEN 7 , GUIDO HOOIVELD 7 , ROSANGELA SOZZANI 6 KÄ HELARIUTTA 4,5,8 and BERT DE RYBEL 1,2,3 1 Ghent University, Department of Plant Biotechnology and Bioinformatics, Technologiepark 927, 9052 Ghent, Belgium 2 VIB Center for Plant Systems Biology, Technologiepark 927, 9052 Ghent, Belgium 3 Wageningen University, Laboratory of Biochemistry, Stippeneng 4, 6708 WE Wageningen, the Netherlands 4 Institute of Biotechnology, University of Helsinki, Viikinkaari 5d, 00014 Helsinki, Finland 5 Department of Biological and Environmental Sciences, University of Helsinki, 00014 Helsinki, Finland 6 Department of Plant and Microbial Biology, North Carolina State University, Raleigh, NC, 27695, USA 7 Wageningen University, Division of Human Nutrition and Health, Nutrition, Metabolism and Genomics group, Stippeneng 4, 6708 WE Wageningen, the Netherlands 8 Sainsbury Laboratory, University of Cambridge, Bateman Street, Cambridge CB2 1LR, UK; VIB

Abstract

As plant cells are fixed within their tissue context, a precise control of cell division orientation is crucial to generate complex three-dimensional organs. The transcription factor complex formed by TARGET OF MONOPTEROS5 (TMO5) and LONESOME HIGHWAY (LHW) triggers a change in cell division orientation leading to radial expansion, at least in part by activating local cytokinin biosynthesis. However, it remains unclear how cytokinin controls these oriented cell divisions. To unravel how the TMO5/LHW complex regulates cell proliferation, here we analyzed the transcriptional responses upon simultaneous induction of both TMO5 and LHW with high temporal resolution. Using inferred network analysis, we identified; AT2G28510/DOF2.1 as a cytokinin-dependent downstream target gene of the TMO5/LHW complex. We further showed that DOF2.1 is specifically required and sufficient for vascular cell proliferation without inducing other cytokinin-dependent effects such as the inhibition of vascular differentiation. In summary, we identified DOF2.1 as a TMO5/LHW target gene, specifically responsible for controlling vascular cell proliferation leading to radial expansion.

Stem cells

Concurrent Speaker - Margot Smit

Abstract Title: IDENTIFYING NEW REGULATORS OF VASCULAR IDENTITY ESTABLISHMENT DURING ARABIDOPSIS EMBRYOGENESIS

Primary Author(s) and Institution(s): MARGOT E SMIT 1 , HENRIETTE VAN BEIJNUM 1 , DARIA NOVIKOVA 1,2,3 , DOLF WEIJERS 1 1. Laboratory of Biochemistry, Wageningen University 6708 WE,

Wageningen, The Netherlands 2. Novosibirsk State University, Russian Federation 3. Institute of Cytology and Genetics, Russian Federation; Wageningen University

Abstract

Vascular tissues in plants are responsible for fluid transport and mechanical support. The developmental pathway leading up to mature vascular transport elements starts with unspecified cells acquiring vascular identity during early embryogenesis. While auxin signaling mediated by MONOPTEROS (MP) plays a key role, its activity is not limited to vascular cells, and hence additional factors must be involved in specifying vascular identity. To find such factors we performed genome-wide Yeast One Hybrid screens on early vascular promoters. We used our Arabidopsis embryo transcriptome atlas (www.albertodb.org) to select new vascular genes, and analyzed expression patterns of 45 genes in root and embryo. Together with previously described marker genes we selected 16 vascular genes. After screening these promoter sequences against an extensive TF collection, we selected 23 transcription factors for further analysis. One of these, GBF2, was identified as an interaction partner of MP. Using BiFC we showed that GBF1, a close homolog of GBF2, could indeed interact with the DNA-binding domain of ARF proteins. Evidence of AuxREs and G-boxes co-occurring in the genome supports the hypothesis that ARFs and GBFs might either bind DNA together or compete for binding. I will present our progress in characterizing these potential vascular regulators.

Stem cells

Concurrent Speaker - Weibing Yang

Abstract Title: CONTROL OF GENE EXPRESSION AND CELL CYCLE PROGRESSION BY mRNA NUCLEAR SEQUESTRATION IN PLANT STEM CELLS

Primary Author(s) and Institution(s): WEIBING YANG , 1 RAYMOND WIGHTMAN, 1 ELLIOT M. MEYEROWITZ 1,2 1 Sainsbury Laboratory, University of Cambridge, Bateman Street, Cambridge, CB2 1LR, UK 2 Howard Hughes Medical Institute and Division of Biology and Biological Engineering, California Institute of Technology, 1200 East California Boulevard, Pasadena, CA 91125, USA; Sainsbury Laboratory University of Cambridge

Abstract

In plants, active division and differentiation of stem cells and their progenitors in the shoot apical meristem (SAM) and the root apical meristem (RAM) lead to continuous formation of new tissues and organs, ensuring developmental plasticity in a changing environment. To gain more insight into the molecular mechanism underlying cell division in the SAM, we have carried out comprehensive RNA fluorescence in situ hybridization (FISH) analysis and identified a number of cell wall synthesis and cell cycle regulatory genes that are expressed exclusively in meristem dividing cells. In particular, two mRNAs, CDC20 and CCS52B (CDH1 ortholog), were found to be specifically sequestered inside the nucleus. CDC20 and CDH1 function as co-activators of the E3 ligase complex anaphase-promoting complex/cyclosome (APC/C) to trigger cyclin B (CYCB) degradation. We show that CDC20 and CCS52B are highly co-expressed with their target CYCB genes during mitosis. CYCB transcripts can be exported and translated; however, CDC20 and CCS52B mRNAs are confined to the nucleus at prophase, and the cognate proteins are not detected until after nuclear envelope breakdown (NEBD) at prometaphase. Mitotic expression of CDC20 and CCS52B enables the timely and rapid activation of APC/C; while their

mRNA nuclear sequestration at prophase inhibits protein translation and APC/C activation thus protecting cyclins from precocious destruction. Although non-coding RNAs have been shown to distribute primarily in the nucleus, nuclear localization of protein coding mRNAs has been considered rare in both animals and plants. Our results suggest that mRNAs can also be retained inside the nucleus, and this nuclear sequestration may provide a new mechanism for the control of gene expression and stem cell division.

Stem cells

Concurrent Speaker - Dongbo Shi

Abstract Title: CHARACTERIZATION OF CAMBIUM STEM CELL ACTIVITY DURING LATERAL GROWTH IN THE HYPOCOTYL OF ARABIDOPSIS.

Primary Author(s) and Institution(s): DONGBO SHI , VADIR LÓPEZ-SALMERÓNS, IVAN LEBOVKA, PABLO SANCHEZ, THOMAS GREB Department of Developmental Physiology, Centre for Organismal Studies (COS), Heidelberg University, Im Neuenheimer Feld 230, 69120 Heidelberg, Germany

Abstract

The presence of areas with low cell division rates is considered as a widespread feature of stem cell niches which ensures integrity of genetic information during somatic development. Radial growth of plant shoots and roots is a stem cell-driven process fundamental for the mechanical and physiological support of enlarging plant bodies. In most dicotyledonous species, the underlying stem cell niche, the cambium, generates wood (xylem) inwards and bast (phloem) outwards. Despite its importance and intriguing dynamics, however, the functional characterization of cambium stem cells is hampered by the lack of experimental tools for accessing distinct cambium sub-domains and for demonstrating stemness. Here, we use the hypocotyl of Arabidopsis thaliana to identify stem cell activity in the proliferating cambium. Combining pulse-labeling using the thymidine analogue EdU (5-ethynyl-2´-deoxyuridine) with genetically encoded lineage tracing, we find that a single bifacial stem cell generates xylem and phloem cell lineages. This stem cell is characterized by the combined activity of the PHLOEM INTERCALATED WITH XYLEM / TRACHEARY ELEMENT DIFFERENTIATION INHIBITORY FACTOR RECEPTOR (PXY/TDR), SUPPRESSOR OF MAX2 1-LIKE PROTEIN 5 (SMXL5) and the WUSCHEL HOMEOBOX RELATED 4 (WOX4) genes. Furthermore, in contrast to other plant stem cell niches, we observe that predominantly stem cells divide and not tissue-specific progenitors. Our analysis provides a cellular fate map of radial plant growth, and suggests that quiescent centers are no general prerequisite for a life-long tissue production.

Thursday, August 9th

Plenary Speaker - Yi-Fang Tsay

Abstract Title: NITRATE TRANSPORT, SIGNALING AND UTILIZATION EFFICIENCY

Primary Author(s) and Institution(s): YI-FANG TSAY, KUO-EN CHEN, HUI-YU CHEN; Institute of Molecular Biology, Academia Sinica

Abstract

Nitrate is not only a primary nitrogen source for plants, but also a signaling molecule that coordinates nutrient availability with plant growth. We are interested in revealing the regulatory mechanism of nitrate homeostasis and nitrate sensing by characterizing the nitrate transporters and nitrate transceptors of the NRT1/PTR family (NPF). Most nitrate transporters in the NPF family are low-affinity nitrate transporters, except for CHL1 (NRT1.1/NPF6.3) that is a dual-affinity transporter. Using the dual-affinity binding and phosphorylation switch, CHL1, which functions as a transceptor (i.e. a transporter with receptor function), can help plants to monitor a wide range of nitrate concentration changes in the soil and elicit proper expression levels of N-related genes. Research on CHL1 has revealed that the proline 492 residue, which is conserved in most NPF transporters, is essential for nitrate transport but is dispensable for nitrate sensing. NRT1.13 that lacks this conserved proline residue in the corresponding position is expressed in parenchyma cells next to xylem in the major leaf veins and the nodes of inflorescent stems. Phenotypes of nrt1.13 mutant and properties of NRT1.13 indicate that nitrate levels in the xylem are monitored by NRT1.13 to regulate flowering time, shoot architecture and lateral nitrate allocation via a nitrate-dependent mechanism. We will discuss strategies for employing NRT1 transporters to enhance nitrogen utilization efficiency.

Plenary Speaker - Jean-Philippe Combier

Abstract Title: Regulation of expression and activity of microRNAs

Primary Author(s) and Institution(s): Jean-Philippe Combier; CNRS, Université de Toulouse, UPS, UMR5546, Laboratoire de Recherche en Sciences Végétales, 31326 Castanet-Tolosan, France

Abstract

MicroRNAs (miRNAs) are small regulatory RNA molecules that inhibit expression of specific target genes by binding to and cleaving their messenger RNAs or otherwise inhibiting their translation into proteins. Whereas the role of miRNAs in biology begins to be well documented, the regulation of miRNA expression and activity is poorly understood. Using plants as model, we deciphered this topic and identified different layers of regulation of miRNA expression and activity. We have shown that plant primary transcripts of miRNAs contain short ORFs that encode miPEPs, which are regulatory peptides (Lauressergues et al., 2015). These peptides enhance the accumulation of their corresponding mature miRNAs, resulting in downregulation of their target genes. In parallel, we have shown the existence of natural protective miRNAs, which have a mismatch at their cleaving site, leading to protect the target gene against the degradation by other members of the same miRNA family (Couzigou et al., 2017).

Finally, whereas the Target Mimicry (or miR sponge in animals) was known to involve non-coding RNAs, we have shown that lots of coding genes can buffer miRNA activity (Guillotin et al., submitted).

Signaling in Plant Biotic Interaction
Concurrent Chair - Xinnian Dong

Abstract Title: Translation in plant immune responses

Primary Author(s) and Institution(s): XINNIAN DONG a , GUOYONG XU a , MENG YUAN b , GEORGE GREENE a , HEEJIN YOO a , CHAOREN AI b , LIJING LIU a , EDWARD ZHUANG a , SARGIS KARATYAN a , JORGE MARQUES a , JONATHAN MOTLEY a , KAROLINA MUKHTAR a , WEI WANG a , SHIPING WANG a a Howard Hughes Medical Institute-Gordon and Betty Moore Foundation, Department of Biology, Duke University, Durham, North Carolina 27708, USA b National Key Laboratory of Crop Genetic Improvement, National Centre of Plant Gene Research (Wuhan), Huazhong Agricultural University, 430070 Wuhan, China Duke University

Abstract

A major consequence of pathogen infection is perturbation of host metabolism, including protein synthesis. However, little is known about how host cells may respond to such perturbations and selectively synthesize defense-proteins to mount immune responses. My lab showed that TBF1, a transcription factor controlling the growth-to-defense transition in plants, is tightly regulated at both transcriptional and translational levels. The TBF1 mRNA contains two upstream open reading frames (uORFs) besides the main ORF. Translation of TBF1 is normally inhibited by these uORFs, which presumably cause dissociation of the ribosome from the mRNA before it reaches the downstream TBF1 ORF. Upon induction of both pattern-triggered immunity (PTI) and effector-triggered immunity (ETI), the inhibitory effects of uORFs are rapidly and transiently alleviated, leading to TBF1 protein translation. To elucidate the regulatory mechanisms, we performed global translatome profiling, using the recently developed ribosome footprinting technology, and identified several trans-acting regulators, a highly conserved RNA sequence (“R-motif”), and many new uORFs. Moreover, we used the pathogen-responsive TBF1 cassette to drive the production of defense proteins and provided the proof of concept, in Arabidopsis and in rice, that adding translational control to defense protein production is an effective new strategy for minimizing fitness costs associated with broad-spectrum disease resistance and reducing the selective pressure for resistant pathogens.

Signaling in Plant Biotic Interaction
Invited Speaker - Jonathan Jones

Abstract Title: Plant immune receptors; dissection, diversity and deployment

Primary Author(s) and Institution(s): JONATHAN JONES, The Sainsbury Laboratory, Norwich, UK Yan Ma, The Sainsbury Laboratory, Norwich, UK Kamil Witek, The Sainsbury Laboratory, Norwich, UK Hailong Guo, The Sainsbury Laboratory, Norwich, UK Zane Duxbury, The Sainsbury Laboratory, Norwich, UK Baptiste Castel, The Sainsbury Laboratory, Norwich, UK Hannah Brown, The Sainsbury Laboratory, Norwich, UK Pingtao Ding, The Sainsbury Laboratory, Norwich, UK Bruno Ngou, The Sainsbury Laboratory, Norwich, UK; Sainsbury Lab

Abstract

Diverse microbes cause plant disease, and plants have evolved a robust innate immune system that recognizes pathogen molecules and then activates defense. Immunity involves both cell surface transmembrane protein kinases and intracellular NLR immune receptors, often encoded by Resistance (R) genes. NLRs are modular proteins and usually carry an N-terminal signaling domain, followed by a nucleotide-binding domain and C-terminal LRRs. NLRs either directly or indirectly recognize pathogen effector molecules. Plants show extensive within- and between-species diversity in their NLR-encoding repertoires, which we investigate using sequence capture; polymorphism in NLR repertoires is important for their efficacy. I will report on our efforts to use these methods to recruit multiple genes for resistance to potato late blight caused by Phytophthora infestans . Some resistances require two NLR proteins. One (the sensor) detects effector action, while the other (helper) NLR transduces the signal. Arabidopsis RPS4 and RRS1 genes, encoding NLR proteins, are confer recognition of AvrRps4 or PopP2 bacterial effectors. RRS1 carries a C- terminal WRKY transcription factor domain targeted by AvrRps4 and PopP2, suggesting these effectors target other WRKY proteins. I will provide updates on how the RPS4/ RRS1 complex detects these effectors and then activates defense upon effector recognition.

Signaling in Plant Biotic Interaction
Concurrent Speaker - Lionel Navarro

Abstract Title: TRANSCRIPTIONAL CONTROL OF IMMUNE-RESPONSIVE GENES BY DNA METHYLATION AND DEMETHYLATION AND ITS RELEVANCE IN ANTIBACTERIAL DEFENSE

Primary Author(s) and Institution(s): LIONEL NAVARRO 1 , THIERRY HALTER 1 , JINGYU WANG 1 , DELASE AMESEFE 1 , EMMANUELLE LASTRUCCI 1 , ALVARO PÉREZ-QUINTERO 1 1 Institut de Biologie de l'Ecole Normale Supérieure (IBENS), 46 Rue d'Ulm CNRS UMR 8197–INSERM U 1024, F-75230 Paris, France

Abstract

In plants, small RNAs can guide DNA methylation of repeats and transposable elements. This phenomenon is referred to as RNA-directed DNA methylation (RdDM) and contributes to the transcriptional repression of some developmentally and stress-regulated genes that carry repeats in their vicinity. We have previously shown that the RdDM pathway negatively regulates the Arabidopsis immune response raised against a phytopathogenic Pseudomonas syringae strain. Accordingly, we have identified a subset of defense genes that are targeted and repressed by RdDM, presumably to prevent trade-off effects that would be caused by their constitutive expression and/or sustained induction. Some of these genes are also concomitantly demethylated in their promoters through an active DNA demethylation process, which ensures their rapid and pervasive induction upon pathogen detection. Here, I will present the extent to which the active demethylase ROS1 reprograms the Arabidopsis transcriptome during antibacterial defense and report on the specific steps of PAMP-Triggered Immunity that are regulated by this enzyme. I will also discuss the detailed mechanisms by which ROS1 facilitates the transcriptional activation of immune-responsive genes. Finally, I will show that modulation of active demethylation activity is likely essential to fine-tune the plant immune response in nature, presumably to promote adaptation to specific environment.

Signaling in Plant Biotic Interaction
Concurrent Speaker - Mary Beth Mudgett

Abstract Title: N-HYDROXY-PIPECOLIC ACID IS A MOBILE METABOLITE THAT INDUCES SYSTEMIC DISEASE RESISTANCE IN ARABIDOPSIS

Primary Author(s) and Institution(s): MARY BETH MUDGETT 1 , Yun-Chu Chen 1 , Eric C. Holmes 2 , Jakub Rajniak 2 , Jung-Gun Kim 1 , Sandy Tang 2 , Curt R. Fischer 3 and Elizabeth Sattely 2 1 Department of Biology, Stanford University, Stanford CA 94305-5020; 2 Department of Chemical Engineering, Stanford University, Stanford, CA 94305-5020; 3 Chemistry, Engineering Medicine for Human Health, Stanford University, Stanford CA 94305-5020 &; Department of Biology, Stanford University

Abstract

Plants lack circulating immune cells and instead rely on small molecule chemistry for local and long-distance defense signaling. Despite the importance of local and systemic immune responses in limiting and/or preventing pathogen infection, the chemical nature of plant sensors and priming agents is not fully understood. In this work, we used an untargeted metabolomics approach to determine the products of the FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1) gene, one of the most responsive

genes induced during biotic stress and required for systemic acquired resistance (SAR). We describe a novel metabolite, N -hydroxy-pipeclic acid (N -OH-Pip) and provide evidence that this molecule plays a role in initiating and amplifying SAR signal transduction in Arabidopsis thaliana . We show that FMO1 can synthesize N- OH-Pip from pipecolic acid in planta , and exogenously applied N- OH-Pip moves systemically in Arabidopsis can rescue the SAR-deficiency of fmo1 mutants. This work provides insight into the chemical nature of a signal for SAR and also suggests that the N- OH-Pip pathway is a promising target for metabolic engineering to enhance disease resistance.

Signaling in Plant Biotic Interaction
Concurrent Speaker - Keke Shangguan

Abstract Title: Lipopolysaccharides Trigger Two Successive Bursts of Reactive Oxygen Species at Distinct Cellular Locations

Primary Author(s) and Institution(s): KEKE SHANGGUAN, College of Agriculture and Biotechnology, Zhejiang University, Hangzhou 310058, China PING LI, College of Agriculture and Biotechnology, Zhejiang University, Hangzhou 310058, China YAN LIANG, College of Agriculture and Biotechnology, Zhejiang University, Hangzhou 310058, China; Zhejiang university

Abstract

Lipopolysaccharides (LPS) are major components of the outer membrane of gram-negative bacteria and are an important microbe-associated molecular pattern (MAMP) that triggers immune responses in plants and animals. A previous genetic screen in Arabidopsis (Arabidopsis thaliana) identified LIPOOLIGOSACCHARIDE-SPECIFIC REDUCED ELICITATION (LORE), a B-type lectin S-domain receptor kinase, as a sensor of LPS. However, the LPS-activated LORE signaling pathway and associated immune responses remain largely unknown. In this study, we found that LPS trigger biphasic production of reactive oxygen species (ROS) in Arabidopsis. The first transient ROS burst was similar to that induced by another MAMP, flagellin, whereas the second long-lasting burst was induced only by LPS. The LPS-triggered second ROS burst was found to be conserved in a variety of plant species. Microscopic observation of the generation of ROS revealed that the LPS-triggered second ROS burst was largely associated with chloroplasts, and functional chloroplasts were indispensable for this response. The lipid A moiety, the most conserved portion of LPS, appears to be responsible for the second ROS burst. Surprisingly, the LPS- and lipid A-triggered second ROS burst was only partially defective in lore mutants. LORE gene driven by its native promoter (LORE::LORE) complemented lore mutants defection in the lipid A-triggered biphasic ROS, however, LORE::LORE:HA transgene only complemented the second ROS burst, but not the first one. In addition, we found that lipid A could induce stomatal closure, and lore mutants are defective in this response. Interestingly, the stomatal phenotype was restored in LORE::LORE:HA/lore transgenic plants, suggesting that the second ROS burst might play a key role in lipid A-induced stomatal closure. Together, our findings provide insight on the LPS-triggered ROS production and stomatal immunity.

Nutrient Transport and Sensing
Concurrent Chair - Gabriel Krouk

Abstract Title: Nitrogen Signaling Interactions

Primary Author(s) and Institution(s): ; Biochimie et Physiologie Moleculaire des Plantes (B&PMP) CNRS

Abstract

Plants need to adapt to a myriad of combined signals coming from i) their environment and ii) their own metabolism, to finely tune their development and phase transitions (1). Gene Regulatory Networks (GRNs) leading to these adaptations and signal integration are the central point of our research. Here, I will show that Hormones and Nitrogen interactions are quite central in the control of plant development (2, 3). I will also show that by focusing on Nitrate (NO3-) regulated transcription factors (TFs) and their genome wide activity, using a technique called TARGET (Transient Assay Reporting Genome wide Effect of Transcription factors(4)), we were able to identify several important signaling cross-talks between NO3-, Phosphate (PO43-) (5) and Reactive Oxygen Species (ROS) pathways (6). These studies open perspectives at the same time on i) applied biotechnology [since we discovered genotypes with an enhanced NO3- transport activity] (6), as well as on ii) basic understanding of large GRN function, dynamics (7), emerging properties, and topology in plants (8).1. G. Krouk, Hormones and nitrate: a two-way connection. Plant Mol Biol, (2016) 2. D. Ristova, C. Carre, M. Pervent, A. Medici, G. J. Kim, D. Scalia, S. Ruffel, K. Birnbaum, B. Lacombe, W. Busch, G. Coruzzi, G. Krouk, Combinatorial interaction network of transcriptomic and phenotypic responses to nitrogen and hormones in the Arabidopsis thaliana root. Sci Signal 9, (2016). 3. G. Krouk, B. Lacombe, A. Bielach, F. Perrine-Walker, K. Malinska, E. Mounier, K. Hoyerova, P. Tillard, S. Leon, K. Ljung, E. Zazimalova, E. Benkova, P. Nacry, A. Gojon, Nitrate-regulated auxin transport by NRT1.1 defines a mechanism for nutrient sensing in plants. Dev Cell 18, 927-937 (2010). 4. B. O. Bargmann, A. Marshall-Colon, I. Efroni, S. Ruffel, K. D. Birnbaum, G. M. Coruzzi, G. Krouk, TARGET: a transient transformation system for genome-wide transcription factor target discovery. Mol Plant 6, 978-980 (2013); 5. A. Medici, A. Marshall-Colon, E. Ronzier, W. Szponarski, R. Wang, A. Gojon, N. M. Crawford, S. Ruffel, G. M. Coruzzi, G. Krouk, AtNIGT1/HRS1 integrates nitrate and phosphate signals at the Arabidopsis root tip. Nature communications 6, 6274 (2015). 6. A. Safi, A. Medici, W. Szponarski, A. Marshall-Colon, S. Ruffel, F. Gaymard, G. Coruzzi, B. Lacombe, G. Krouk, HRS1/HHOs GARP transcription factors and reactive oxygen species are regulators of Arabidopsis nitrogen starvation response. BioRXiv https://doi.org/10.1101/164277, (submitted). 7. A. Para, Y. Li, A. Marshall-Colon, K. Varala, N. J. Francoeur, T. M. Moran, M. B. Edwards, C. Hackley, B. O. Bargmann, K. D. Birnbaum, W. R. McCombie, G. Krouk, G. M. Coruzzi, Hit-and-run transcriptional control by bZIP1 mediates rapid nutrient signaling in Arabidopsis. Proc Natl Acad Sci U S A 111, 10371-10376 (2014);. 8. C. Carre, A. Mas, G. Krouk, Reverse engineering highlights potential principles of large gene regulatory network design and learning. NPJ systems biology and applications 3, 17 (2017).

Nutrient Transport and Sensing

Invited Speaker - Terri Long

Abstract Title: IRONING OUT THE ISSUES: ELUCIDATING IRON HOMEOSTASIS REGULATORY PROCESSES IN PLANTS

Primary Author(s) and Institution(s): Terri A. Long Department of Plant and Microbial Biology, North Carolina State University, Raleigh, NC 27696; North Carolina State University

Abstract

Nutrient Transport and Sensing
Concurrent Speaker - Francois Barbier

Abstract Title: Sugar-induced shoot branching is mediated by multiple signalling pathways

Primary Author(s) and Institution(s): FRANCOIS BARBIER , FRANZISKA FICHTNER, CHRISTOPH WEISTE, FENGXI HAN, TINASHE CHABIKWA, SOULAIMAN SAKR, WOLFGANG DROGE-LASER, JOHN LUNN and CHRISTINE BEVERIDGE

Abstract

Sugars have recently emerged as important signals controlling the release of axillary buds from dormancy. However little is known about the molecular mechanisms involved in sugar signalling during the control of shoot branching. Using pea and Arabidopsis we identified different sugar signalling pathways involved in shoot branching. Triggering the HEXOKINASE 1 (HXK1) pathway of glucose signalling using sugar analogues promoted bud outgrowth in pea buds. In Arabidopsis, hxk1 null mutants have decreased shoot branching, but wild-type branching is restored by complementation with a catalytically inactive HXK1. Two other pathways more specific to sucrose are also involved. In pea, the onset of axillary bud outgrowth was accompanied by an increase in trehalose 6-phosphate (Tre6P), a sucrose signalling metabolite, and in Arabidopsis, over-accumulation of Tre6P triggered shoot branching. In both species, decapitation-induced bud outgrowth decreased the protein level and activity of the bZIP11 transcription factor, which is post-transcriptionally repressed by sucrose, while over-expression of bZIP11 in Arabidopsis inhibited bud outgrowth. Interestingly, both Tre6P and bZIP11 interact with SnRK1, which is a central growth regulator and is also involved in bud dormancy. In conclusion, shoot branching is governed by a complex signalling network involving both hexose and sucrose signalling pathways.

Nutrient Transport and Sensing
Concurrent Speaker - Sarah Lederer

Abstract Title: FUNCTION OF CDPK IN NITROGEN USE EFFICIENCY

Primary Author(s) and Institution(s): Sarah Lederer 1 , Fabian-Philipp Sylvester 1 , Philipp Schulz 1,2 , Anja Liese 1 , and Tina Romeis 1 1 Dahlem Centre of Plant Sciences, Freie Universität Berlin, Germany 2 Max Planck Institute of Molecular Plant Physiology, Potsdam, Germany; Freie Universität Berlin

Abstract

Nitrogen is an essential plant nutrient for growth and crop productivity. Nitrate has a dual function as nitrogen source and signaling molecule, which leads to rapid increase in cytosolic calcium-concentration and changes in gene expression pattern, large-scale metabolic adjustments as well as shaping root and shoot architecture of plants. We have identified a calcium-dependent protein kinase (CDPK) which is characterized by a higher nitrogen use efficiency (NUE) in Arabidopsis. CDPKs are mono-molecular Ca 2+ -sensor and kinase effector proteins which perceive Ca 2+ signals and translate them into target phosphorylation . Under nitrate starvation conditions, the overexpression of this CDPK isoform shows enhanced biomass and photosynthetic capacity compared to the wildtype, while single mutants show lower NUE. In vitro biochemical analysis implicates a high affinity calcium sensitivity for kinase activity. Enzyme variants that carry mutations in single EF-hand motifs are characterized by a reduced maximal

kinase activity and an altered calcium affinity. Current experiments aim for the linkage between the decoding of nitrogen-dependent intracellular calcium changes, CDPK in vivo activation, and plant growth and development in response to nitrogen availability.

Nutrient Transport and Sensing
Concurrent Speaker - Lucie Camut

Abstract Title: GIBBERELLIN FUNCTION IN NITRATE-MEDIATED GROWTH PROCESSES IN ARABIDOPSIS THALIANA

Primary Author(s) and Institution(s): Lucie CAMUT , Jean-Michel DAVIERE and Patrick ACHARD Institut de biologie moléculaire des plantes, CNRS, Université de Strasbourg, 12 rue du Général Zimmer, 67084 Strasbourg Cedex, France IBMP-CNRS

Abstract

Ensuring food security with minimal environmental damage is a major humanitarian challenge. Since the Green Revolution in the 1960's, the use of nitrogen (N) fertilizers associated with high-yielding semi-dwarf varieties led to impressive crop yield increases. Semi-dwarfing genes are known to interfere with the action or production of the plant growth hormone gibberellin (GA), and still today GA inhibitors are widely applied in cultivated lands. The resulting semi-dwarf stature prevents lodging. However, these yield increases have recently plateaued and excess of N-fertilizer applications accelerates eutrophication of rivers and acidifies soils. Hence, increasing grain yield and quality with reduced environmental costs, is one of the further challenges in plant research. Whereas various phytohormones have been implicated in the regulation of N deficiency responses, the role of GA remains largely unknown despite its role during the Green Revolution. We investigate molecular mechanisms controlling growth responses to change in nitrate (NO 3 -) availability, the main N sources. Using genetic and molecular approaches in Arabidopsis thaliana, we show that NO 3 - promotes growth by activating GA signaling. Building on this data, we are analyzing the contribution of GA signaling in the adaptive responses of plant root architecture to spatial NO 3 - -heterogeneity.

Genome Organization and Evolution
Concurrent Chair - Marie-Anne Van Sluys

Abstract Title: HIDDEN DIVERSITY PRODUCED BY TRANSPOSABLE ELEMENTS IN PLANT GENOMES.

Primary Author(s) and Institution(s): MARIE-ANNE VAN SLUYS (1); Geovani tolfo Ragagnin (1); Jonas W Gaiarsa (1); Sarah Oliveira (1,2); Andrew Leitch (2); Edgar Andres Ochoa-Cruz (1); Cushla Metcalfe (1); Nathalia de Setta (1); Claudia B Monteiro-Vitorello (3) (1) Universidade de Sao Paulo; GaTE Lab - Botânica – IB; 05508-090 São Paulo– SP; Brazil (2) Queen´s Mary University of London - UK
(3) Universidade de Sao Paulo; ESALQ, 54538, Departamento de Genética, Piracicaba, Sao Paulo, Brazil

Abstract

Plant genomes are known for extensive duplication events, however, evolutionary time in Land Plants (Embryophyta) seems short to explain over 350 thousand species described. Gene number in plants vary from 20,000 to 50,000 of which half are shared with another plant species. Also, comparative genomics using BUSCO and OrthoDB reveal more than 1440 genes that are highly conserved among

Magnoliophyta. Biodiversity is the visualization of “genotype to phenotype” expression through hierarchical steps of gene transcription, translation and, ultimately, function. In this scenario, genetic mobile elements are natural sources of gene amplification, reordering gene regulatory networks, producing epigenetic marks among other evolutionary substrates. We have depicted the presence and contribution to genome size of LTR-RT lineages in 10 plant genomes. We further narrowed the study to Saccharum clade revealing its mobile genome component and expression potential. Comparative analysis within Saccharum and closely related species uncover transposable elements commonalities in chromosome location. In addition, Saccharum LTR diversification results in lineage specific LTR-RT expression over time and under biotic stress conditions. Our results are in agreement with B McClintock statement that we know about the genome components but we still know little about how the cell instigate responses to adaptation and diversification. Financial support: The present work was supported by FAPESP (Brazil) grants 2008/52074-8 2016/17545-8 as well as CNPq (Brazil) 308197/2010-0and 310779/2017-0.

Evolution and Domestication of Plant Specialized Metabolites

Invited Speaker - C Robin Buell

Abstract Title: UNDERSTANDING THE EVOLUTION OF CHEMODIVERSITY THROUGH A PHYLOGENETIC-TRANSCRIPTOMIC-METABOLOMIC APPROACH IN THE LAMIACEAE

Primary Author(s) and Institution(s): Mint Evolutionary Genomics Consortium; Consortium Members: C. ROBIN BUELL 1 , Emily Crisovan 1 , Natalia Dudareva 2 , Nicolas Garcia 3 *, Grant Godden 1,3 , Laura Henry 2 , Mohamed O. Kamileen 4 , Heather Rose Kates 3 , Matthew B. Kilgore 2 , Benjamin R. Lichman 4 , Evgeny V. Mavrodiev 3 , Linsey Newton 1 , Carlos Rodriguez-Lopez 4 , Sarah E. O’Connor 4 , Douglas Soltis 3,5 , Pamela Soltis 3 , Brieanne Vaillancourt 1 , Krystle Wiegert-Rininger 1 , Dongyan Zhao 1; 1 Department of Plant Biology, Michigan State University, East Lansing, MI 48824, USA 2 Department of Biochemistry, Purdue University, West Lafayette, IN 47907-2063, USA 3 Florida Museum of Natural History, University of Florida, Gainesville, FL 32611, USA 4 The John Innes Centre, Department of Biological Chemistry, Norwich, NR4 7UH, UK 5 Department of Biology, University of Florida, Gainesville, FL 32611, USA; Michigan State University

Abstract

The evolution of chemical diversity has been a major driver of plant diversification, with novel compounds serving as key innovations across the Plant Kingdom. The Lamiaceae (mint family) is chemical diverse and produces an enormous variety of compounds that act as attractants and defense molecules in nature and are used widely by humans as flavor additives, fragrances, and anti-herbivory agents. To elucidate the mechanisms by which such diversity evolved, we combined leaf transcriptome data from 48 Lamiaceae species and four outgroups with a robust phylogeny and chemical analyses of three terpenoid classes (monoterpenes, sesquiterpenes, iridoids) that share and compete for precursors. Our integrated chemical-genomic-phylogenetic approach has revealed that multiple mechanisms contributed to the chemical diversity in extant Lamiaceae species. Furthermore, these datasets have identified a robust set of candidate genes for biochemical pathways of interest and in understanding metabolic flux in competing pathways.

Genome Organization and Evolution
Concurrent Speaker - Khalil Kashkush

Abstract Title: Transposable elements play a prominent role in wheat genome architecture

Primary Author(s) and Institution(s): KHALIL KASHKUSH , DANIELLE KEIDAR-FRIEDMAN, INBAR BARIAH Department of Life Sciences, Ben-Gurion University, Beer-Sheva 84105, Israel

Abstract

Wheat is considered one of the best models to study polyploidy due to multiple allopolyploidization events that occurred during its evolution and the relatively young age of the allohexaploid bread wheat. In addition, newly formed allopolyploids can be easily synthetized in laboratory. Following allopolyploidization process, the nascent allopolyploid genome reacts in a burst of genomic changes, including deletion of transposable elements (TEs) containing sequences. Yet, the mechanism of elimination of TE-containing sequencing following allopolyploidization events remains unknown. We have retrieved over 250,000 TE insertions from the most updated wheat genome drafts and have observed massive copy number variation among Triticum and Aegilops species. Over 50% of the retrieved TEs were associated with genes by creating allelic variation or intron retention. Comparative alignment of sequences flanking species-specific retrotransposon insertions from BB sub-genome of emmer wheat and bread wheat led to the identification of deletion breakpoints of eliminated sequences via, most probably, a mechanism of unequal intra-strand recombination involving TEs. Our data suggests a role for TEs in genome size reduction through recombination following allopolyploidization events. In addition, our data clearly indicates that TEs might play a prominent role in speciation by creating transcriptome variation.

Genome Organization and Evolution
Concurrent Speaker - Bárbara Hufnagel

Abstract Title: GENOME SEQUENCE OF WHITE LUPIN, A MODEL TO STUDY ROOT DEVELOPMENTAL ADAPTATIONS

Primary Author(s) and Institution(s): HUFNAGEL, BÁRBARA, BPMP, CNRS MARQUES, ANDRÉ, BPMP, CNRS MARANDE, WILLIAM, CNRGV, INRA SALLET, ERIKA, LIPM, INRA SORRIANO, ALEXANDRE, BPMP, CNRS ARRIBAT, SANDRINE, CNRGV, INRA BERGÈS, HÉLÈNE, CNRGV, INRA GOUZY, JÉRÔME, LIPM, INRA PÉRET, BENJAMIN, BPMP, CNRS; CNRS - BPMP

Abstract

White lupin (Lupinus albus ; 2n=50) stands out as a model legume species since it is the only crop producing cluster roots, one of the most outstanding developmental adaptations to nutrient-scarce environments. We report a high-quality chromosome-scale assembly of white lupin genome, together with an extensive transcriptome data from ten different organs of that species. We took advantage of single-molecule real-time technology, in combination with short-reads sequencing and optical and genetic maps in order to have a successful assembly. The final assembly size is 451Mb with a N50 of 17Mb. About 96% (434Mb) of the assembled genome is included on the 25 pseudo-chromosomes. The structural annotation identified 38 258 coding genes and 3129 ncRNA, being 97.3% genes anchored on the pseudo-chromosomes. A majority (94.6%) of the 1440 genes in the Plantae BUSCO dataset were

identified in the annotation, which is suggestive of a complete assembly and annotation. White lupin genome revealed to be laden with gene duplications and repetitive elements. It presents extensive duplication blocks inside its own genome and also a high degree of synteny with the close legumes species Lupinus angustifolious and Medicago truncatula . This genome is a valuable resource and represents a keystone for legumes genomics research.

Genome Organization and Evolution
Concurrent Speaker - Hyungtaek Jung

Abstract Title: THE GENOME SEQUENCE AND ASSEMBLY OF NICOTIANA BENTHAMIANA

Primary Author(s) and Institution(s): HYUNGTAEK JUNG 1 , AURELIANO BOMBARELY 2 , MICHAL LORENC 1 , EVA CHAN 3 , RUTH LYONS 3 , VANESSA HAYES 3 , JULIA BALLY 1 , CARA MORTIMER 1 , DIEGO ORZAEZ 4 , GIOVANNI GIULIANO 5 , PETER WATERHOUSE 1,6 , and EU HORIZON 2020 NEWCOTIANA 7 1 Centre for Tropical Crops and Biocommodities, Queensland University of Technology, Brisbane, Australia 2 Department of Horiculture, Virginia Tech, Blacksburg, USA 3 Genomics and Epigenetics Division, Garvan Institute of Medical Research, Sydney, Australia 4 Instituto de Biología Molecular y Celular de Plantas, Consejo Superior de Investigaciones Cientificas, Valencia, Spain 5 Casaccia Research Center, Italian National Agency for New Technologies, Energy and Sustainable Development (ENEA), Rome, Italy 6 School of Biological Sciences, University of Sydney, Sydney, Australia 7 Europeran Consortium Horizon 2020 Newcotiana Project, Europe and Australia; Queensland University of Technology

Abstract

Australian native tobacco plant, Nicotiana benthamiana , known as Pitjuri by indigenous Australians, is considered the ‘lab rat’ of the molecular plant world, and is used globally by geneticists and biotechnologists. It is increasingly becoming a biofactory to produce life-saving drugs and vaccines. Unfortunately, few resources are available to facilitate its genetic improvement. As an international consortium effort, including a Horizon 2020 Newcotiana project, here we report the assembly of a high-quality, chromosome-scale reference genome sequence for allotetraploid N . benthamiana , which was produced using short (Illumina) and long (Pacific Biosciences) read technologies in combination with optical (BioNano) and chromosome-contact maps (Hi-C). These genomic resources are an essential first step to facilitate the identification of the key agricultural-related key genes to guide the development of New Plant Breeding Techniques (NPBTs), which will open unprecedented opportunities in agriculture to dramatically improve plant species with desirable traits, the assembly requires considerable improvement.

Meiotic Recombination
Concurrent Chair - Emmanuel Guiderdoni

Abstract Title: MANIPULATION OF MEIOTIC RECOMBINATION IN RICE

Primary Author(s) and Institution(s): EMMANUEL GUIDERDONI 1 , DELPHINE MIEULET 1, IAN FAYOS 1, JULIE PETIT 1, ANNE-CECILE MEUNIER 1, AURORE VERNET 1, SERGI NAVARRO-SANZ 1, BRIGITTE COURTOIS 1, GAETAN DROC 1, CHRISTOPHE PERIN 1, GIACOMO BASTIANELLI 2, ALAIN NICOLAS 3, RAPHAEL MERCIER 4 1 Cirad, UMR AGAP, 34398 Montpellier Cedex 5 France and Université de

Montpellier, Cirad, Inra, Supagro, 34000 Montpellier, France 2 Meiogenix, 38 rue Servan, 75011 Paris, France 3 Institut Curie, UMR Dynamics of Genetic Information, 26 rue d'Ulm, 75248 Paris Cedex 05, France 4 Institut Jean-Pierre Bourgin, INRA, AgroParisTech, CNRS, Université Paris-Saclay, RD10, 78000 Versailles, France

Abstract

Meiotic recombination is hampered by the restricted number of crossovers (CO) between homologous chromosomes and an overall limitation of CO number, the CO homeostasis. Recombination frequency may also vary by 100 fold across regions in large genomes, limiting access to genes of interest in « cold » regions. Here, we present two approaches aiming at either enhancing or redistributing COs in the rice genome. It has been recently shown that FIGL1, FANCM and RECQ4 limit CO formation in Arabidopsis thaliana : Inactivating one or a combination of two of these anti-CO factors conducts to a 3 to 10-fold increase in CO frequency without affecting meiotic progression. RECQ4 and FANCM are highly conserved DNA helicases that resolves recombination intermediates into non CO in a minor CO pathway that normally accounts for 10% of the COs in Arabidopsis. Here, we demonstrate that an Osrecq4l -/- japonica hybrid exhibits an average 3.3-fold CO increase and exhibits normal meiosis progression and seed fertility. A similar approach in an OsfanCM mutant context conducted to a 2.2-fold CO enhancement. This work is being expanded to a distant hybrid background. SPO11 is an essential protein for triggering CO formation at the initiation of meiosis through its capacity to induce with several partners chromosomal double strand breaks (DSB). Based on a report in yeast, we determined whether the expression of the SPO11-1 coding sequence fused to the GAL4 binding domain (BD) -hereafter referred as SpiX1- can locally enhance CO frequency at GAL4 BD target sites in the rice genome. Genome wide recombination was examined in an aus x Spix1-japonica F2 population. The 4% intervals exhibiting the highest UAS density harbored a significant excess of recombinants in the Spix1 F2 population. Dense genotyping of 5 intervals exhibiting an excess of recombinants in the F2 population localized recombination break points in the vicinity of UAS sites. This approach is now being investigated in a spo11-1 mutant background. Progresses in targeting recombination through the use of a dCas9::SPO11 fusion will be also presented. Altogether, these results indicate that modulating recombination in rice is possible.

Meiotic Recombination

Invited Speaker - Ian Henderson

Abstract Title: Meiotic recombination landscapes in plant genomes

Primary Author(s) and Institution(s): IAN HENDERSON; University of Cambridge

Abstract

Plant genomes can be broadly divided in euchromatin and heterochromatin, which are cytologically defined, and generally correspond to gene versus transposon rich regions. We now appreciate that epigenetic modifications of the genome, for example DNA methylation, underlie differentiation of the genome into these different chromatin states. In addition to associating with different patterns of transcription, it is known that plant heterochromatin is typically also silenced for recombination during meiosis. In many of the large grass genomes, including wheat, the majority of the chromosomes consist of non-recombining expanses of heterochromatin, which can cause significant limitations for

breeding. Our research investigates the genetic and epigenetic factors that shape recombination in plant genomes. I will present new data where we have profiled Arabidopsis recombination factors genome-wide, which has revealed hotspots associated with genes and also, surprisingly, DNA transposons. I will discuss the implications of these finds for plant genome evolution and the relationship between genes and transposons. I will also present new work profiling chromatin states in the hexaploid wheat genome and show how this correlates with recombination. In summary I will explore the relationships between chromatin, transcription and recombination, with implications for the stability of plant chromosomes and how we improve crops via breeding.

Meiotic Recombination

Concurrent Speaker - Fatiha Benyahya

Abstract Title: LET'S HAVE A BREAK: HOW TO DECIPHER THE SPO11.2 FUNCTION IN THE POLYPLOID BREAD WHEAT?

Primary Author(s) and Institution(s): BENYAHYA FATIHA * , NADAUD ISABELLE*, GEORGES LUDOVIC*, LOUSSERT ALAIN*, LHOMMET ISABELLE*, SOURDILLE PIERRE* *UMR 1095 GDEC INRA, 5 Chemin de Beaulieu, 63039 Clermont-Ferrand Cedex 2

Abstract

Genetic variability is partly created during the meiotic recombination that reshuffles alleles position, regulation and function as well as crops fitness. This mechanism is initiated by the formation of double-strand breaks, by the Spo11 complex, which can be repaired through crossing-over. Studying the proteins involved in the recombination initiation allows the improvement of admixture efficiency. There is a lack of knowledge in this field for polyploid species such as bread wheat (2n = 6x = 42, A, B and D genomes) due to the difficulty of obtaining mutants. The objective of this work is to characterize spo11.2 (endonuclease) mutant behavior in a polyploid context to understand the role of each copy and the impact of the dosage effect. We isolated irradiation mutants from (cv Renan) knocking-out the copies of this proteins respectively on the A, B and D (simple mutation), AB, BD and AD (double mutation) and ABD (triple mutation) genomes. The mutant where characterized at several levels: 1) the general aspects of plants phenotypes 2) the cytological aspects analyzing the nuclei shape and viability, 3) the molecular level by studying the interaction between the ASY1 / ZYP1 proteins of the synaptonemal complex and the expression of the genes involved in the meiotic cascade.

Meiotic Recombination

Concurrent Speaker - Isabelle Colas

Abstract Title: Using Barley mutants to understand meiosis and recombination in cereals

Primary Author(s) and Institution(s): Isabelle Colas, Sybille Mittmann, Malcolm Macaulay, Luke Ramsay and Robbie Waugh; The James Hutton Institute

Abstract

A greater understanding of the control of recombination in crop plants would be particularly useful for crop species such as barley (and wheat) where a highly skewed distribution of meiotic crossover events means that up to half of the genes rarely, if ever, recombine. In these crops, substantial proportions of the chromosomes are inherited together as a large linkage block, preventing the generation of novel gene combinations and useful variation that could be exploited in breeding programmes. In order to improve our understanding of recombination in barley, and ultimately to be able to modulate recombination in barley, we are characterizing a collection of 14 non-allelic desynaptic (des) mutants that exhibit perturbed meiosis and semi-sterility compared to wild type. A number of these mutants have now been genetically mapped using the semi-sterility phenotype and cytologically characterized. In particular, 3D-SIM microscopy analysis reveals that each mutant is differently affected for synapsis, crossing over formation and meiosis progression. We will discuss results of some of these mutants,

showing the importance of the interplay between synapsis and recombination and the implication for the modulation of recombination for breeding purpose.

Meiotic Recombination
Concurrent Speaker - Rigel Salinas Gamboa

Abstract Title: NON-RESTRICTIVE EXPRESSION OF GENES AND PROTEINS ACTING DURING FEMALE MEIOSIS IN FLOWERING PLANTS

Primary Author(s) and Institution(s): RIGEL SALINAS GAMBOA 1 , MELANIE HAND 2 , MARTINA JURANIC 2 , NIDIA SÁNCHEZ 1 , ANNA M. KOLTUNOW 2 , and JEAN-PHILIPPE VIELLE-CALZADA 1 . 1 Grupo de Desarrollo Reproductivo y Apomixis, UGA Laboratorio Nacional de Genómica para la Biodiversidad, Cinvestav Irapuato, México. 2 Agriculture Flagship, Commonwealth Scientific and Industrial Research Organization, Private Bag 2, Glen Osmond, SA5064, Australia.; Langebio México

Abstract

Contrary to male meiosis in which all four meiotically derived microspores usually give rise to a viable pollen grain, female meiosis in most flowering plant species results in a single functional megaspore giving rise to the female gametophyte, while the rest of the haploid products degenerate without further division. In plants, the understanding of meiosis is gender-biased since almost all studies characterized the expression and subcellular localization on male meiocytes. By implementing whole-mount ovule procedures that allow in situ localization of mRNAs and proteins during megasporogenesis, we have initiated a systematic comparison of the patterns of expression of coding transcripts acting during meiosis and their corresponding proteins in Arabidopsis thaliana , Vigna unguiculata and Sorghum bicolor . Whereas in some cases their localization is confined to cells undergoing meiosis, other meiotic genes and proteins show expression in nucellar cells adjacent to the meiotic configuration, suggesting that a meiotic commitment is not exclusive to cells undergoing megasporogenesis. Our results suggest the existence of an unforeseen meiotic cross-talk occurring at the cellular intersection of the sporophytic and gametophytic generation.

Plant Reproduction
Concurrent Chair - Jose Feijo

Abstract Title: Ion signaling and reproduction: molecular basis and integrative mechanisms

Primary Author(s) and Institution(s): JOSÉ A. FEIJÓ University of Maryland Cell Biology and Molecular Genetics 0118 Bioscience Research Building 4066 Campus Dr. College Park, MD 20742-5815 Phone (301) 405-9746 Fax (301) 314-9489 Email: jfeijo@umd.edu; univ maryland

Abstract

Ion homeostasis has been implicated at various of reproductive success. We focus on Ca2+ and pH signaling on the pollen tube. Evolution of Ca2+ signaling in plants led to the apparent loss of molecular mechanisms for influx and small ligand-operated control of cytosolic Ca2+, leaving the diversity of Ca2+ signatures in plants largely unaccounted for. I will report on a novel mechanism by which Glutamate Receptor-Like (GLR) channels are sorted and activated by CORNICHON HOMOLOG (CNIH) proteins. We found evidence that AtGLRs localize to sub-cellular compartments by interacting with pairs of AtCNIHs,

leading to specific intracellular localizations for some of these channels. We further demonstrate that AtCNIHs trigger channel activity on AtGLRs when co-expressed in mammalian cells without any ligand. These results provide evidence for a new regulatory mechanism underlying Ca2+ homeostasis by sorting and activation of plant GLRs by CNIH proteins. Combined with quantitative studies of dynamics of protons in signaling and chemotropic responses, these results highlight the relevance of the ionic status of the pollen as fundamental for the perception and signaling of external cues and correct pollen tube targeting.

Plant Reproduction

Invited Speaker - Rita Gross-Hardt

Abstract Title: BUILDING AND BYPASSING PLANT POLYSPERMY BARRIERS

Primary Author(s) and Institution(s): THOMAS NAKEL 1 , DAWIT G TEKLEYOHANS 1 YANBO MAO 1 , GOLO FUCHERT 2 , DIEU VO 1 , RITA GROß-HARDT 1 1 University of Bremen, Department of Biology and Chemistry, Bremen, Germany, 2 Max-Planck-Institute, Plasma Physics, Greifswald, Germany equally contributed University of Bremen

Abstract

The ultimate goal for the survival of all species on earth is to reproduce. This uncompromising principle has triggered the evolution of numerous adaptations. One strategy commonly employed by sexually reproducing eukaryotes is the production of tremendous amounts of sperm to maximize the likelihood of an egg becoming fertilized. High sperm to egg ratios are, however, associated with an increased risk of polyspermy. To avoid potential harmful or deleterious consequences of supernumerary sperm fusion, many eukaryotes have evolved polyspermy barriers, which are implemented at different levels in the reproductive process. Here, we focus on polyspermy preventing mechanisms in flowering plants and discuss the developmental consequences associated with their failure.

Plant Reproduction

Concurrent Speaker - Leonor C. Boavida

Abstract Title: A FUNCTIONAL ROLE FOR HOMOTYPIC GAMETE INTERACTIONS IN DOUBLE FERTILIZATION

Primary Author(s) and Institution(s): LEONOR C. BOAVIDA 1 , CHANDRA C. MISRA 2 , NIKITA BHATNAGAR 1 and JORG D. BECKER 2 1 Purdue University, Deapartment of Botany and Plant Pathology, Purdue Center for Plant Biology, West afayette, Indiana, USA 2 Instituto Gulbenkian de Ciencia, Plant Genomics Lab, Oeiras, Portugal

Abstract

In flowering plants, two separate gametic fusions mark the fertilization process as one of the most impressive examples of heterotypic cell-cell recognition in plant development. Several core factors were identified to regulate male-female gamete adhesion, activation and fusion, but how homotypic cellular interactions between plant gametes of the same sex contribute to the success of double fertilization is still poorly understood. Tetraspanins (TETs) are conserved scaffold proteins with relevant functions in several important biological processes such as cell-cell adhesion, fusion, motility and signaling, but their functions in plants is poorly understood. In an earlier report, we provided the first evidences that in Arabidopsis AtTET11/AtTET12 accumulate in a stable adhesion microdomain at the interface of sperm cells (SCs) [1]. Using Y2H and BIFC we validated two plant-specific unknown proteins as TET-binding partners (TBPs). AtTBP8/AtTBP9 co-localize with AtTET11/AtTET12 at the SC-SC adhesion contact. In addition, we show that AtTBP8/AtTBP9 act as negative regulators of SC-SC adhesion. In the absence of AtTBP8/AtTBP9 , SCs exhibit a enhanced SC-SC adhesion and severe fertility defects caused by unbalanced fertilization events. These results support a critical biological function for SC TET-TBP complexes in facilitating a one-to-one gamete interaction in double fertilization. [1] Boavida et al. (2013), Plant Physiol., 163: 696-712.

Plant Reproduction

Concurrent Speaker - Jorge Muschietti

Abstract Title: RALF4/19 ARABIDOPSIS POLLEN PEPTIDES INTERACT WITH POLLEN LRX PROTEINS: AUTOCRINE CONTROL OF POLLEN TUBE GROWTH

Primary Author(s) and Institution(s): JORGE MUSCHIETTI 1,2 , MARTIN MECCHIA 1,3,4 , SOFÍA SOMOZA 1 , ANA SEDE 1 , GORKA SANTOS-FERNANDEZ 3 , DIEGO WENGIER 1 , JOSE ESTEVEZ 5 UELI GROSSNIKLAUS 3 . 1 Instituto de Investigaciones en IngenieríaGenética y Biología Molecular, Dr. Héctor Torres (INGEBI-CONICET),Vuelta de Obligado 2490, C1428ADN BuenosAires, Argentina. 2 Departamentode Biodiversidad y Biología Experimental, Facultad deCiencias Exactas y Naturales, Universidad de Buenos Aires. Ciudad Universitaria, Pabellón II,C1428EGA Buenos Aires, Argentina . 3 Department of Plant and Microbial Biology and Zurich-BaselPlant Science Center, University of Zurich, 8008 Zurich,Switzerland. 4 Center for Research in Agricultural Genomics (CRAG), Barcelona, Spain. 5 Fundación Instituto Leloir, IIBBA-CONICET,Buenos Aires, Argentina. INGEBI-CONICET-University of Buenos Aires

Abstract

Polarized growth involves the expansion of the cell tip, stimulating cell elongation in only one direction. In plants, it takes place in growing pollen tubes, root hairs and cotton fibers. Pollen tube growth is a highly-coordinated process, where actin cytoskeletal arrangement, vesicle mobility, reactive oxygen species (ROS) concentration, regulation of cell wall integrity and calcium (Ca 2+) dynamics are involved. Adequate signaling from the external cell wall to the pollen tube cytoplasm is necessary to sustain a proper growth. We have recently reported that two pollen R APIDAL KALINIZATION F ACTORs (RALFs),RALF4 and RALF19, act redundantly to regulate the pathway that controls growth and integrity of the pollen tubes.Furthermore, we have demonstrated that proteins of the LEUCINE-RICH EXTENSIN (LRX) family, that directly interact with the RALFs, regulate changes in cell wall integrity of pollen tubes. Comprehension of how these RALFs and LRXs control pollen tube growth will bring us closer to fully understand the mechanisms governing plant reproduction. The pollen tube is a highly suitable and affordable model to understand how autocrine and paracrine signals take part at different stages during pollination and how pollen tubes transduces that information in order to adapt its growth.

Plant Reproduction

Concurrent Speaker - Cora MacAlister

Abstract Title: IDENTIFICATION OF NEW POLLEN FERTILITY GENES THROUGH SUPPRESSION OF A POLLEN FERTILITY DEFECT IN HYDROXYPROLINE O-ARABINOSYLTRANSFERASE MUTANTS

Primary Author(s) and Institution(s): CORA A. MACALISTER STEVEN BEUDER ALYSSA CASTLE NIHARIKA RAJESH KEVIN NUDELL Molecular, Cellular and Developmenal Biology Department; University of Michigan; University of Michigan

Abstract

The ability of pollen tubes to deliver sperm nuclei to ovules relies on the highly polarized secretion of a compositionally unique pollen tube cell wall. Hydroxyproline O-arabinosylation (Hyp-Ara), the addition of short chains of arabinose sugars onto hydroxyproline residues is a strongly conserved plant-specific protein modification. A large number of cell wall-associated proteins are heavily Hyp-Ara modified, but the total breadth of target proteins and the function of this modification remain poorly understood. We have found that Hyp-Ara is required for full pollen fertility. Pollen lacking the arabinosyltransferase enzymes that initiate or extend this sugar chain fail to fertilize ~90% of available ovules leading to poor seed yield. The mutant pollen tubes show reduced total elongation in vitro , disrupted pollen tube morphology and meandering growth in vivo . To understand Hyp-Ara's role in pollen fertility, we carried out a genetic suppressor screen to identify mutants with improved seed set in an arabinosyltransferase mutant background. We identified 37 lines with phenotypes ranging from partial to full restoration of seed set. Whole genome sequencing of nine of these has revealed new alleles of known pollen fertility regulators as well as alleles of several genes not previously implicated in pollen fertility.

Plant Central Metabolism

Concurrent Chair - Yves Gibon

Abstract Title: System-oriented studies to link metabolism and plant performance

Primary Author(s) and Institution(s): Sophie Colombié 1 , Bertrand Beauvoit 1 , Jinliang Chen 2 , Léa Roch 1 , Coffi-Belmys Cakpo 3 , Isma Belouah 1 , Christine Nazaret 4 , Sylvain Prigent 1 , Pierre Pétriacq 1

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Abstract

A key objective for plant sciences is to understand what influences the growth and quality of plant products, with a view to improving them. Metabolism is an obvious target for improvement and understanding of the mechanisms that link it to phenotypes will help focus breeding strategies and/or improve agricultural practices. However, metabolism is extremely complex, with a number of highly intricate pathways that undergo extensive reprogramming throughout plant organ development, making it difficult to find the right targets for improvement. Systems biology represents a great opportunity to deal with this complexity. On the one hand, newly emerging top-down approaches enable highly predictive statistical models linking metabolome and plant performance. On the other hand, mechanistic modelling of metabolism has never been so easy thanks to significant advances in analytics and computing power. We have developed kinetic models consisting of sets of ordinary differential equations to study central metabolism as well as stoichiometric models describing larger areas of metabolism. The models were used to study tomato fruit metabolism throughout growth and development. In particular, they have revealed and explained the importance of carbon management in growing fruits and suggested strategies to improve yield. Modelling is currently being extended to other metabolic pathways including protein synthesis and degradation, integrated into ecophysiological models, and transferred to other fruit species.

Plant Central Metabolism

Invited Speaker - Jorg Schwender

Abstract Title: CENTRAL METABOLISM IN DEVELOPING OILSEEDS AND ITS CONTROL ON MULTIPLE LEVELS

Primary Author(s) and Institution(s): JöRG SCHWENDER Brookhaven National Laboratory, Upton, NY 11973, USA; Brookhaven National Laboratory

Abstract

During seed development, photoassimilate supplies are converted into seed storage compounds. Seed composition appears to be under tight genetic control in a species specific way. In various brassicaceae species mostly triacylglycerols and seed specific storage proteins are accumulated while starch accumulates transiently as well. The metabolic processes involved in carbon partitioning can be assumed to be controlled on multiple levels. The functioning and control of central metabolism in carbon partitioning in brassicaceae oil seeds is of major interest in my lab and different aspects will be presented. Applying a multi-omics approach with in-vitro cultured developing embryos of Brassica napus , an allosteric feedback control mechanism of carbon partitioning could be revealed which seems to dominate the process. The role of the Oxidative Pentose Phosphate Pathway in providing NADPH for fatty acid biosynthesis has been studied before based on different flux models. Now additional insights are obtained based on theoretical analysis of the redox balance of the conversion of sugars to oil.

Furthermore, recent progress in decoding the genetic control of oil synthesis in brassicaceae species based on a phylogenetic footprinting approach will be discussed.

Plant Central Metabolism

Concurrent Speaker - Ming-Hsiun Hsieh

Abstract Title: THE VITAMIN B1 BIOSYNTHETIC PATHWAY EXTENDS ACROSS MULTIPLE COMPARTMENTS IN ARABIDOPSIS

Primary Author(s) and Institution(s): MING-HSIUN HSIEH 1 , WEI-YU HSIEH 1 , JO-CHIEN LIAO 1 , HSIN-TZU WANG 1 , TZU-HUAN HUNG 2 , SHI-YUN WANG 1 , HSIN-MEI WANG 1 , CHING-CHIH TSENG 1 and TSUI-YUN CHUNG 1 1 Institute of Plant and Microbial Biology, Academia Sinica, Taipei 11529, Taiwan 2 Biotechnology Division, Taiwan Agricultural Research Institute, Taichung 41362, Taiwan

Abstract

Plants can synthesize thiamin diphosphate (TDP, vitamin B1) de novo , but its biosynthetic pathway has not been elucidated until recently. The Arabidopsis pale green1 (pale1) mutant contains higher concentrations of thiamin monophosphate (TMP) and less thiamin and TDP than the wild type. Supplementation with thiamin, but not the thiazole and pyrimidine precursors, rescued the mutant phenotype, indicating that pale1 is a thiamin-deficient mutant. Map-based cloning and whole-genome sequencing revealed that the pale1 mutant has a mutation in At5g32470 encoding a TMP phosphatase of the TDP biosynthesis pathway. Most plant TDP biosynthetic enzymes are located in the chloroplasts and cytosol, but PALE1-GFP localized to the mitochondria of the root, hypocotyl, mesophyll, and guard cells of the 35S:PALE1-GFP complemented plants. The subcellular localization of PALE1 suggests that the complete vitamin B1 biosynthesis pathway may involve the chloroplasts, mitochondria and cytosol in Arabidopsis. Interestingly, amino-terminal deletion in the presequence of PALE1, PALE1D(1-46), or replacement of the presequence with RBCS transit peptide, TP RBCS -PALE1D(1-46), was able to rescue the pale1 mutant. These results implicate that TMP can be steadily dephosphorylated to thiamin in the chloroplasts, mitochondria, and cytosol, if TMP phosphatase is present in these compartments.

Plant Central Metabolism

Concurrent Speaker - John Lunn

Abstract Title: TREHALOSE 6-PHOSPHATE – A SUGAR SIGNAL LINKING PLANT DEVELOPMENT TO METABOLISM

Primary Author(s) and Institution(s): JOHN LUNN Max Planck Institute of Molecular Plant Physiology, Potsdam-Golm, Germany; Max Planck Institute of Molecular Plant Physiology

Abstract

Trehalose 6-phosphate (Tre6P), the intermediate of trehalose biosynthesis, is an essential signal metabolite in plants that links developmental processes, such as flowering, shoot branching and embryogenesis, to the metabolic status of the plant. The sucrose-Tre6P nexus model postulates that Tre6P is both a signal and negative feedback regulator of sucrose levels in plant cells. The model envisages a role for Tre6P in sucrose homeostasis in plants that is analogous to the regulation of blood glucose levels by insulin in animals. In source leaves, Tre6P controls sucrose levels by regulating the partitioning of photoassimilates during the day and the turnover of transitory starch reserves at night. It appears to have a particularly important function in guard cells, affecting the sensitivity of stomata to abscisic acid. In sink organs, Tre6P regulates the import and utilization of sucrose for growth and the

accumulation of storage reserves. We are using forward and reverse genetics approaches to dissect the functions of Tre6P in specific source and sink tissues, to understand the molecular mechanisms that underlie the sucrose-Tre6P nexus and how Tre6P links plant growth and development to the availability of sucrose.

Plant Central Metabolism
Concurrent Speaker - Nicolas Rouhier

Abstract Title: ELUCIDATING THE FUNCTION OF THE CHLOROPLASTIC GLUTAREDOXIN S16 OF ARABIDOPSIS THALIANA

Primary Author(s) and Institution(s): Nicolas Rouhier 1 , Flavien Zannini 1 , Sowmya Subramanian 2 , Anna-Maria Moseler 3 , Andreas Meyer 3 , Michael K. Johnson 2 , Jérémy Couturier 1 1 Université de Lorraine, Inra, IAM, F-54000 Nancy, France. 2 Department of Chemistry, Centre for Metalloenzyme Studies, University of Georgia, Athens, Georgia 30602, USA. 3 INRES-Chemical Signalling, University of Bonn, Friedrich-Ebert-Allee 144, 53113, Bonn, Germany.; Université de Lorraine

Abstract

Glutaredoxins (GRXs) are oxidoreductases involved in diverse cellular processes through their capacity to reduce glutathionylated proteins and/or to coordinate iron-sulfur (Fe-S) clusters. The plant-specific, plastidial GRXS16 is a bimodular protein formed by an N-terminal endonuclease domain fused to a regular GRX domain. Deciphering its physiological role by reverse genetics may have been hampered so far by the existence of other plastidial GRXs. Here, we have deciphered the biochemical properties of the recombinant protein. It has the ability to bind several types of Fe-S clusters, a [2Fe-2S] cluster in a dimer or a [4Fe-4S] cluster in a tetramer. Both can be transferred to acceptor proteins, consistently with a role in the maturation of plastidial Fe-S proteins. Besides, it catalyzes the oxidation but not reduction of a redox-sensitive GFP2 (roGFP2) at the expense of glutathione. Accordingly, GRXS16 reacts efficiently with oxidized glutathione, leading to the formation of an intramolecular disulfide between the cysteines 158 and 215 that is not reduced by glutathione but by the light-dependent plastidial thioredoxin system. As GRXS16 reduction is key to Fe-S cluster binding or to catalyzing protein glutathionylation/deglutathionylation, the formation of this disulfide may constitute a redox switch in response to the dark or to oxidizing conditions.

Plant Virus Interaction
Concurrent Chair - Israel Pagán

Abstract Title: Disentagling the relationship between plant virus within-host fitness and seed transmission rate

Primary Author(s) and Institution(s): ISRAEL PAGÁN - Centro de Biotecnología y Genómica de Plantas (UPM-INIA). Campus de Montegancedo, Universidad Politécnica de Madrid, Pozuelo de Alarcón (Madrid), Spain.;

Abstract

Over 30% of plant viruses are seed transmitted. However, the genetic determinants of seed transmission are poorly understood. Viruses reach the seed by: (i) infection of ovules or pollen, and (ii)

embryo invasion before the programmed cell death of the embryonic suspensor. Hence, for seed transmission to occur the virus must reach plant reproductive organs before gametogenesis and/or while embryonic suspensor is still functional. Thus, virus genetic determinants of seed transmission would control virus multiplication and movement. We have analyzed whether the level of virus multiplication and the speed of within-host invasion determine seed transmission rate, using Cucumber mosaic virus (CMV) and its natural host Arabidopsis thaliana . We conducted a time course infection experiment, in which six arabidopsis accessions were challenged against CMV genotypes with high/low seed transmission rates. The level of virus multiplication in plant growth and reproductive structures was monitored every two days along the plant lifespan, and seed transmission rate was estimated. In parallel, we compared the genomic sequences of the utilized CMV genotypes. Results indicated that higher CMV multiplication leads to higher seed transmission, and that adaptation to this mode of transmission is linked to mutations in the 3´ UTR of the viral genome.

Plant Virus Interaction

Concurrent Speaker - Spela Baebler

Abstract Title: SPATIOTEMPORAL ANALYSIS OF POTATO HYPERSENSITIVE RESISTANCE RESPONSE TO POTATO VIRUS Y REVEALS THAT RBOHD IS REQUIRED FOR SUCCESSFUL VIRUS ARREST

Primary Author(s) and Institution(s): ŠPELA BAEBLER , Tjaša Lukan, Andrej Blejec, Maruša Pompe Novak, Aleš Kladnik, Magda Tušek Žnidarič, Maja Zagorščak, Kristina Gruden National Institute of Biology, Department of Biotechnology and systems biology, Ljubljana, Slovenia; National Institute of Biology

Abstract

Despite intensive ongoing research, mechanisms of viral arrest in hypersensitive resistance (HR) response have remained elusive We have recently shown that in potato – Potato virus Y HR interaction, as shown in some other plant-virus pathosystems, it is not the cell death or physical separation of the virus by callose deposition that prevents virus spread (Lukan et al., 2018). Additionally, no particular ultrastructural features were detected distinguishing HR in resistant cv. Rywal and its sensitive transgenic counterpart NahG-Rywal. Thus, we carried out a study of spatiotemporal transcriptional responses in small tissue sections surrounding the viral infection site. We have chosen 32 candidate genes for our analysis based on time-stamped whole leaf transcriptomic data. These included genes involved in ethylene, jasmonate and salicylate signalling , metabolism of reactive oxygen species, response to redox potential changes and a set of immune signalling actuator genes. Analysis showed that responses for almost all analysed genes are tightly spatiotemporally regulated. Interestingly, the response of redox state - related genes was showing a spatiotemporal response that differed between resistant and susceptible genotypes. In particular, responses of Respiratory burst oxidase homolog protein D (RBOHD) gene are focused on the border region of the lesion and correlate with the expression of thioredoxin H-type (TRX-H) gene known to be involved in regulation of SA signalling . Based on these results we hypothesized that RBOHD is essential for signalling leading to the successful arrest of the virus in HR response of potato. We have constructed transgenic lines with suppressed RBOHD gene activity, where the virus can spread systemically, breaking the HR response, thus validating our hypothesis.

Plant Virus Interaction

Concurrent Speaker - Daniel Hofius

Abstract Title: ANTIVIRAL SELECTIVE AUTOPHAGY AND ITS COUNTERACTION DURING PLANT VIRUS INFECTION

Primary Author(s) and Institution(s): DANIEL HOFIUS 1* , ANDERS HAFRÉN 1 , SUAYIB ÜSTÜN 1 , JEAN-LUC MACIA 2 , ANTON HOCHMUTH 1 , ANDREW J. LOVE 3 , STEINGRIM SVENNING 4 , JOEL J. MILNER 5 , TERJE JOHANSEN 4 , MARTIN DRUCKER 2 1 Department of Plant Biology, Uppsala BioCenter, Swedish University of Agricultural Sciences and Linnean Center for Plant Biology, Box 7080, 75007 Uppsala, Sweden; 2 National Institute for Agricultural Research (INRA), UMR 385 Biology and Genetics of Plant–Pathogen Interactions, Campus International de Baillarguet, 34398 Montpellier Cedex 5, France 3 Cell and Molecular Sciences, The James Hutton Institute, Dundee DD2 5DA, United Kingdom 4 Molecular Cancer Research Group, Institute of Medical Biology, University of Tromsø, 9037 Tromsø, Norway 5 Plant Science Group, School of Life Sciences, College of Medical Veterinary and Life Sciences, University of Glasgow, Glasgow G12 8QQ, United Kingdom *corresponding author: daniel.hofius@slu.se

Abstract

Autophagy plays a paramount role in mammalian antiviral immunity including selective degradation of viruses and their individual components. Many viruses have evolved measures to antagonize this “xenophagy” or even exploit autophagy mechanisms for the benefit of infection. In plants, however, the functions of autophagy in host immunity and viral pathogenesis have only recently started to emerge. By combining genetic, cell biological, and proteomic approaches, we found that the selective autophagy receptor NBR1 suppresses viral infection by targeting the viral capsid protein and particles of cauliflower mosaic virus (CaMV) as well as the RNA silencing suppressor HCpro of turnip mosaic virus (TuMV). Intriguingly, these unrelated DNA and RNA viruses have evolved distinct strategies to counteract autophagic degradation. While CaMV sequesters particles in autophagy-resistant viral inclusions, probably via the recruitment of host kinesin-like proteins, TuMV engages viral proteins to block NBR1 flux and HCpro degradation. Furthermore, we found that NBR1-independent autophagy prevents premature cell death during CaMV and TuMV infection and serves as proviral mechanism to extend the timespan for virus production. Together, our results provide evidence for the integration of selective autophagy into plant immunity against viruses and reveal viral strategies to escape, suppress, or adapt autophagic processes for successful pathogenesis.

Plant Virus Interaction

Concurrent Speaker - Paul Gouguet

Abstract Title: REMORINS: PM-ANCHORED PHOSPHOPROTEINS INVOLVED IN THE REGULATION OF PLASMODESMAL APERTURE AND VIRAL PROPAGATION

Primary Author(s) and Institution(s): PAUL GOUGUET 1,2 , ARTEMIS PERRAKI 1,2,4* , JULIEN GRONNIER 1,2*, ANTHONY LEGRAND 1,6 , MARIE BOUDSCOCQ 5 , ANNE-FLORE DEROUBAIX 1,2 , VINCENT SIMON 3 , SYLVIE GERMAN-RETANA 3 , CYRIL ZIPFEL 4 , BIRGIT HABENSTEIN 6 , EMMANUELLE BAYER 1,2 , SEBASTIEN MONGRAND 1,2 , VERONIQUE GERMAIN 1,2 1 CNRS, Laboratoire de Biogenèse Membranaire (LBM), UMR 5200, F-33000 Bordeaux, France 2 Univ. Bordeaux, Laboratoire de Biogenèse Membranaire (LBM), UMR 5200, F-33000 Bordeaux, France 3 Equipe de Virologie UMR BFP 1332 INRA, 33883

Villenave d'Ornon, France 4 The Sainsbury Laboratory, Norwich Research Park, Norwich, NR4 7UH, United Kingdom. 5 Institute of Plant Sciences Paris Saclay (IPS2), CNRS, INRA, Université Paris-Sud, Université d'Evry, Université Paris-Saclay, Université Paris-Diderot, Sorbonne Paris-Cité, Bâtiment 630, Plateau du Moulon, 91192 Gif sur Yvette, France. 6 , Institute of Chemistry; Biology of Membranes Nanoobjects (UMR5248 CBMN), IECB, CNRS, Universite Bordeaux, Institut Polytechnique Bordeaux, All. Geoffroy Saint-Hilaire, 33600 Pessac, France; Laboratoire de Biogenèse Membranaire UMR5200 CNRS/Université de Bordeaux

Abstract

Discovered in 1989 as being potentially involved in plant/pathogen interactions, the plant-specific Remorins (REMs) have since been shown to be directly implicated in these contexts and more precisely as regulators of intercellular connectivity via the regulation of Plasmodesmata (PD) aperture and to the cell-to-cell propagation of certain viruses. In order to decipher the true function of REMs, both its unconventional anchoring to PM nanodomains and its phospho-status(es) have been recently investigated, revealing a tight-link between these two processes as determinants of REM activity. Distinct residues of REM's C-terminal Anchor were shown to be essential for nanodomain segregation and dynamics at the PM as well as the phosphorylation of its N-terminal residues. After phosphorylation, REM is redistributed from PM to PD and trigger callose deposition at PD-pitfields. We performed a multiscale screen for REM interacting-proteins to reveal REMs' function at PD. Candidate proteins screened propose a potential implication of the actin cytoskeleton in the function of REM at PM nanodomains and PD aperture.

Plant Response to Combinatorial Stress
Concurrent Chair - Jean-Benoît Morel

Abstract Title: Mechanisms Underlying the Increased Susceptibility to Blast Fungus of Rice and Wheat under High Nitrogen or Drought Stress

Primary Author(s) and Institution(s): JB Morel; INRA, UMR BGPI INRA/CIRAD/SupAgro, Campus International de Baillarguet

Abstract

Plants are often facing several stresses simultaneously that strongly modify their ways of reacting to pathogens. Understanding how plant react and the way pathogens adapt to such stresses imposed to plants is poorly documented. Here we developed several experimental systems mimicking field intermittent drought on rice or elevated nitrogen fertilization followed by inoculation by the pathogenic fungus Magnaporthe oryzae. Both abiotic perturbations induced susceptibility at the plant level and were respectively called DIS (drought-induced susceptibility) and NIS (nitrogen-induced susceptibility). These systems allowed us to analyze, in particular using RNASeq, how rice deploys immunity after abiotic stresses and how the blast fungus is behaving in drought-stressed or highly-fertilized plants compared to normal plants. The ways rice plants reacted to blast infection under DIS or NIS were strikingly different: while DIS almost completely abolished basal immunity and the functioning of some major resistance genes, NIS only slightly affected plants immunity and did not compromised resistance genes. On the fungus side, DIS and NIS also showed contrasting patterns. The transcription of pathogenicity genes, including putative effectors, was slightly increased under NIS. On the other hand,

during DIS the fungus is greatly modifying its virulence program: genes coding for small secreted proteins were massively repressed in droughted plants compared to unstressed ones whereas genes coding for enzymes involved in degradation of cell-wall were induced. These results suggest that the fungal virulence program can be greatly modified by abiotic stress imposed to plants before infection. We will also show data showing that some rice genes can be mutated to maintain reduced susceptibility even under high nitrogen fertilization. We will also present contrasting data on DIS in the case of wheat fungal pathogens.

Plant Response to Combinatorial Stress
Invited Speaker - Milos Tanurdzic

Abstract Title: Nitrate- and phosphate- triggered gene regulatory networks in wheat roots

Primary Author(s) and Institution(s): MILOS TANURDZIC , Indeewari Dissanayake School of Biological Science, The University of Queensland; The University of Queensland

Abstract

Levels of nitrate (N) and phosphate (P) available to the plant modulate the plant root system architecture (RSA), via signalling processes both locally within the root and systemically. Our knowledge of gene regulatory networks (GRN) that control RSA responses is largely limited to the eudicot Arabidopsis, whereas wheat, as do many other monocots, shows a different RSA response to N and P deficiency. We set out, therefore, to identify GRN underlying wheat root N and P responses using transcriptomics and systems biology approaches. Our results show that N supply in the absence of P triggered transcriptional changes for thousands of wheat genes during the first 24h. In contrast, P supply in the absence of N changes the expression levels of only 10 genes. However, concomitant supply of N and P shows a synergistic transcriptional response, often in a time-dependent manner, indicating that N and P signalling pathways in wheat are mutually dependent, in a manner that appears conserved between Arabidopsis, rice, and wheat. Using GO term enrichment analysis of N/P regulated genes identified several groups of wheat genes with functions in RSA modulation via presumptive local and systemic signalling cascades. Gene co-expression network analysis identified gene co-expression modules involved in wheat N/P homeostasis. I will present results of analyses that identify conserved and non-conserved N+P signaling modules, providing insights into gene regulatory mechanisms modulating root responses to nitrate and phosphate in wheat – a cereal crop with complex genetic structure.

Plant Response to Combinatorial Stress
Concurrent Speaker - Salma Balazadeh

Abstract Title: A Novel Control Module for Heat Stress Memory in Plants

Primary Author(s) and Institution(s): SALMA BALAZADEH 1 , MASTOUREH SEDAGHATMEHR 1 , VENKATESH THIRUMALAIKUMAR 1 , CELINE MASCLAUX-DAUBRESSE 3 , BERND MUELLER-ROEBER 2 1 Max Planck Institute of Molecular Plant Physiology, Am Mühlenberg 1, 14476 Potsdam-Golm, Germany 2 University of Potsdam, Institute of Biochemistry and Biology, Karl-Liebknecht-Straße 24-25, Haus 20, 14476 Potsdam-Golm, Germany 3 Unité Mixte de Recherche 1318, INRA, Institute Jean-Pierre Bourgin, 78026 Versailles Cedex, France; Max-Planck Institute of Molecular Plant Physiology

Abstract

Plants have the capacity to ' memorize ' stressful events and protect themselves from future stresses. Furthermore, they are able to 'reset ' or 'forget ' memories of certain stressful situations, which helps to maximize growth after returning to non-stress conditions. A delicate balance between the consolidation of stress memory and the degree of forgetfulness is critical for plant growth and productivity under changing environmental conditions. Here, we report a novel control module for heat stress memory (thermomemory) in plants. Recently, we identified chloroplast ic heat shock protein HSP21 as a crucial component of thermomemory. Variation in HSP21 protein level contributes to differential thermomemory performance of Arabidopsis accessions, revealing a strong positive correlation between HSP21 abundance and thermomemory capacity. Employing a pharmacological/genomics approach, we discovered plastid metalloprotease FtsH6 to be involved in the initial degradation of HSP21 during the memory phase in Col-0 [1]. We now show that autophagy contributes to the selective degradation of HSPs at later stages of the thermomemory phase. Our results thus reveal the presence of a novel HSP21 – plastidial protease – autophagy control module for thermomemory in plants; its further analysis holds great promise for understanding how plants grow and reproduce in highly dynamic environments with many predictable and unpredictable variables.

Plant Response to Combinatorial Stress
Concurrent Speaker - Huaming He

Abstract Title: THE ARABIDOPSIS MEDIATOR COMPLEX SUBUNIT 8 MODULATES OXIDATIVE STRESS RESPONSE

Primary Author(s) and Institution(s): Huaming He 1,2 , Jordi Denecker 1,2 , Katrien Van Der Kelen 1,2 , Patrick Williams 1,2 , Frank Van Breusegem 1,2 and Amna Mhamdi 1,2 1. Department of Plant Biotechnology and Bioinformatics, Ghent University, 9052 Gent, Belgium 2. Center for Plant Systems Biology, VIB, 9052 Gent, Belgium

Abstract

Plants have developed mechanisms using reactive oxygen species (ROS) as signaling molecules to adapt their development, growth and stress response. Current understanding of the network governing ROS sensing, transduction and eventually resulting in the transcriptional response in plants is still fragmentary. Our work reveals a new component of ROS signaling network and characterizes its function through a combined genetic, transcriptomic, and proteomic profiling approach. From a luciferase-based genetic screen for regulators of H 2 O 2 -responsive genes in Arabidopsis thaliana , we identified Mediator complex subunit 8 (MED8), which is involved in transcription initiation. Mutants lacking N-terminal domain of MED8 are embryonic lethal, suggesting its essential role in cell viability. However, mutants lacking C-terminal glutamate-rich domain (med8) display increased tolerance to methyl viologen, a potent oxidative stress-inducing herbicide. RNA-sequencing analysis showed that a variety of genes associated with the stress response display enhanced transcript abundance in med8 relative to Col-0. Protein-protein-interaction analysis demonstrated that the glutamate-rich domain of MED8 is required for interaction with the CDK8 module, which represses transcription. Analysis of H 2 O 2 -triggered lesion formation and gene expression in cat2med8 double mutants established the role of MED8 in mediating H 2 O 2 signaling. Our study thus reports a molecular link between mediator complex and ROS signaling.

Plant Response to Combinatorial Stress
Concurrent Speaker - Pascal Montoro

Abstract Title: MULTIPLE STRESS-INDUCED PHYSIOLOGICAL SYNDROME AFFECTING NATURAL RUBBER PRODUCTION INVOLVING ETHYLENE RESPONSE FACTORS IN HEVEA BRASILIENSIS

Primary Author(s) and Institution(s): MONTORO P. 1 , PUTRANTO R. 1, 2 , LESTARI R. 1,3 , LECLERCQ J. 1; CIRAD

Abstract

Hevea brasiliensis is the main source of natural rubber accounting for 42% of the worldwide rubber consumption. Latex-containing rubber particles is produced in laticifers, a specialized tissue differentiated in phloem. Latex is collected by tapping the soft bark of rubber trees. Ethephon, an ethylene releaser, is applied on bark to stimulate latex flow and regeneration between two tappings. Environmental and harvesting stresses are known to induce an oxidative stress triggering Tapping Panel Dryness (TPD). TPD is a physiological syndrome affecting latex production by promoting the agglutination of rubber particles. RNA sequencing analysis revealed an involvement of hormone

signalling pathways especially ethylene and jasmonate. Given the influence of ethephon, transcriptional and post-transcriptional regulation of ethylene response factors (ERF) were characterized in response to abiotic and harvesting stresses. Some members of ERF group IX are known to be essential integrators of ethylene and jasmonate signalling pathways. The functional analysis of HbERF-IXc5 was carried out. Its overexpression in transgenic rubber trees revealed its involvement in laticifer differentiation, a biological process known to be induced by wounding and jasmonate.

Rock around the clock
Concurrent Chair - Paloma Mas

Abstract Title: The circadian clock controls the rhythms of the cell cycle in Arabidopsis

Primary Author(s) and Institution(s): Jorge Fung-Uceda, Paloma Mas; Plant Development and Signal Transduction, Centre for Research in Agricultural Genomics (CRAG)

Abstract

The circadian clock function is essential for proper plant growth and development in synchronization with the environment. Plant growth and development is also regulated by the cell cycle. Broadly speaking, changes in the rate and duration of cell cycle progression determine the cell number and size that correlate with organ growth during development. In our studies, we found that a slow-running circadian clock decelerates the cell cycle and, conversely, a fast clock speeds it up. The clock component TOC1 safeguards the G1-to-S transition and controls the timing of the mitotic cycle at early stages of leaf development. TOC1 also regulates somatic ploidy at later stages of leaf development and in hypocotyl cells. The S-phase is shorter and delayed in TOC1 over-expressing plants (TOC1-ox), which correlates with the diurnal repression of the DNA replication licensing gene CDC6 through binding of TOC1 to the CDC6 promoter. The slow cell-cycle pace in TOC1-ox also results in delayed tumor progression in inflorescence stalks. Thus, TOC1 sets the time of the DNA pre-replicative machinery to control plant growth in resonance with the environment.

Rock around the clock
Invited Speaker - Tokitaka Oyama

Abstract Title: PROPERTIES OF CELLULAR CIRCADIAN RHYTHMS IN PLANTS

Primary Author(s) and Institution(s): TOKITAKA OYAMA , Kyoto University; Kyoto University, Graduate School of Science

Abstract

The circadian clock is the cell-autonomous system that oscillates with a period of “circa” 24 hours. In plants, individual cells carry photoreceptors that can function to reset the clock to day-night cycles. Thus, each cell has a complete set of clock components, however, circadian behavior of individual cells in the plant body remained unclear. To unravel the cellular circadian behavior, bioluminescence of a circadian reporter gene that was introduced into cells by a particle bombardment method was monitored. A duckweed plant, Lemna gibba , was used as the plant material since the small, flat, floating, soft body was suitable for the gene introduction and long-term monitoring. Bioluminescence rhythms of individual cells in a plant body were synchronous under 12-h light/12-h dark conditions.

Under continuous dark, cellular circadian rhythms severely dampened. Under continuous light, those rhythms were robustly sustained in an asynchronous state. The desynchronization resulted from instable and heterogeneous properties in the period lengths of cellular rhythms. The heterogeneity in the circadian behavior was masked under normal day-night cycles but became obvious under artificial light conditions such as continuous conditions and shorter day-night cycles. The cell-autonomy and the integration of circadian behavior in the plant body will be discussed.

Rock around the clock

Concurrent Speaker - Chin-Mei Lee

Abstract Title: The deubiquitinating enzymes UBP12/UBP13 stabilize ZEITLUPE-GIGANTEA complex in regulating plant circadian clock

Primary Author(s) and Institution(s): CHIN-MEI LEE , Department of Molecular Cellular and Developmental Biology, Yale University (Current Affiliation: Institute of Plant and Microbial Biology, Acedemia Sinica) MAN-WAH LI, Department of Molecular Cellular and Developmental Biology, Yale University ANN FEKE, Department of Molecular Cellular and Developmental Biology, Yale University JOSHUA GENDRON, Department of Molecular Cellular and Developmental Biology, Yale University; Academia Sinica/Yale University

Abstract

Circadian clock regulates approximately 24-hour rhythmicity of biological pathways to optimize their responses to the environment and thus increases fitness of plants. The central circadian oscillator is driven by transcription-translation feedback regulation, and protein stabilities and activities of central clock regulators are further regulated post-translationally. In plants, the F-box protein ZEITLUPE (ZTL) targets evening clock regulators, including TOC1, PRR5 and CHE, for dark-dependent ubiquitination and degradation. For the proper functions of ZTL, a co-chaperone protein GIGANTEA (GI) interacts with ZTL to facilitate ZTL protein folding and accumulation before dusk. However, the regulatory mechanism of the ZTL-GI complex is not fully resolved. In this study, we identified UBP12 and UBP13 deubiquitinating enzymes interact with ZTL-GI complex through immunoprecipitation-Mass spectrometry. The ubp12 and ubp13 mutants have short period phenotypes. Genetic analyses show that UBP12 and UBP13 function upstream of GI and ZTL to regulate circadian clock. We further demonstrate that UBP12 and UBP13 interact with GI to regulate its ubiquitination status and protein levels. This in turn affects rhythmic accumulation of ZTL protein and ZTL degradating targets. These results revealed a novel mechanism in which deubiquitination constitutes an additional layer of regulation in plant circadian clock.

Rock around the clock
Concurrent Speaker - Eyal Fridman

Abstract Title: HER CLOCK, THEIR FITNESS: GROWTH AND CIRCADIAN CLOCK ROBUSTNESS IS CONTROLLED BY MATERNAL AND NUCLEAR INHERITANCE IN WILD BARLEY

Primary Author(s) and Institution(s): Eyal Fridman 1 , Eyal Bdolach 1,2 Manas Ranjan Prusty 1 , Adi Faigenboim-Doron 1 , Tanya Filichkin 3 , Laura Helgerson 3 , Karl Schmid 4 , Stephan Greiner 5 1 Plant Sciences Institute, Volcani Agricultural Research Organization (ARO), Bet Dagan, Israel ; 2 Department of Life Sciences, Ben-Gurion University, 84105, Beer-Sheva, Israel ; 3 Crop Soil Science Dept., Oregon State University, Corvallis, OR U.S.A. 4 Institute of Plant Breeding, Seed Science and Population Genetics, University of Hohenheim, Stuttgart, Germany ; 5 Max-Planck-Institut für Molekulare Pflanzenphysiologie, Am Mühlenberg 1, D-14476 Potsdam-Golm, Germany

Abstract

C haracteristics of the circadian clock have major influence on the growth of plants and synchronization with the diurnal cycle is considered a key adaptive trait. Although temperature compensation and entrainment are defining features of circadian clocks, recent studies suggest plasticity of the clock yet with poor understanding of the mechanism and evolutionary history underlying. In this study, we explore the genetic basis for the circadian clock modulation and plasticity against high temperature by utilizing a new doubled haploid population derived from two reciprocal hybrid Hordeum spontaneum genotypes. Phenotyping this population is conducted in the field and with a high-throughput platform (SensyPAM) under different temperature regimes. Notably, genetic analysis identified significant influence of the maternal organelle genomes, as well as cytonuclear interactions with nuclear quantitative trait loci (QTL), on clock phenotypes and days to flowering. Moreover, it indicates a differential contribution of these cytoplasmic genomes to buffering of the clock rhythm against high temperature. Resequencing of the parental plastid genomes suggest the presence of few candidate genes underlying this variation. The implications of these findings to the study of plant circadian clock and canalization against changing environments will be discussed.

Rock around the clock
Concurrent Speaker - Thiago Alexandre Moraes

Abstract Title: Response of the circadian clock and diel starch turnover to one day of low light or low CO2 in Arabidopsis

Primary Author(s) and Institution(s): THIAGO ALEXANDRE MORAES ; VIRGINIE MENGIN; MARIA GRAZIA ANNUNZIATA; BEATRICE ENCKE; NICOLE KROHN; MELANIE HÖHNE and MARK STITT Max Planck Institute of Molecular Plant Physiology; Max Planck Institute of Molecular Plant Physiology

Abstract

We investigated whether retrograde carbon-signalling to the clock regulates diel starch turnover in fluctuating light. Arabidopsis was shifted to three different reduced light levels or to low CO 2 for one light period, and returned to growth conditions. Widespread changes in clock transcript abundance were observed. Nevertheless, these effects were small compared to circadian oscillation, and mostly restricted to extreme treatments that led to carbon starvation. We observed repression of ELF4 , slower

decay of dusk components and a mild phase delay at the following dawn, possibly due to poor repressive Evening Complex function and higher expression of PHYTOCHROME INTERACTING FACTORs (PIFs) and REVEILLEs (RVEs). Starch was mobilized in a linear manner and paced to dawn both in moderate treatments that did not alter clock transcripts and in extreme treatments that caused severe carbon starvation. We concluded that pacing of starch mobilization to dawn does not require retrograde carbon-signalling to the transcriptional clock. On the following day, growth decreased, sugars rose and starch accumulation was stimulated compared to non-treated plants. Such adaptation occurred after moderate treatments and independently of changes in the transcriptional clock, and are possibly linked to low-C signalling and increased PIF and RVE expression in the preceding 24 h-cycle.

Molecular Breeding
Concurrent Chair - Ryohei Terauchi

Abstract Title: Next Generation Breeding of Crops by Whole Genome Approaches

Primary Author(s) and Institution(s): Ryohei Terauchi Laboratroy of Crop Evolution, Graduate School of Agriculture, Kyoto University;

Abstract

Owing to recent developments in DNA sequencing technologies, crop improvement by whole genome analysis has become routine. Here, I share our experiences on improvement of rice cultivars adapted to northern Japan. Generation of a large scale genetic resources combined with genome analyses using MutMap and QTL-seq allowed us to identify a gene for salt tolerance as well as those for blast disease resistance. Useful alleles are being used to generate rice cultivars. Whole genome analysis became applicable also to “orphan crops” that have been long neglected. We obtained a reference genome sequence of Guinea yam (Dioscorea rotundata), a dioecious tuber crop, by generating contigs by de novo assembly and anchoring the contigs on the linkage maps. This reference genome has subsequently served to identify a genomic region tightly linked to sex determination gene, which allowed us to develop a DNA marker useful for sex diagnosis.

Molecular Breeding
Invited Speaker - Sigrid Heuer

Abstract Title: PREPARING CROPS FOR THE FUTURE - USEFUL TRAITS AND GENES

Primary Author(s) and Institution(s): SIGRID HEUER , Rothamsted Research ALBERTO CASARTELLI, University of Adelaide, Australia MARK WILKINSON, Rothamsted Research, UK; Rothamsted Research

Abstract

Considerable efforts are undertaken globally to increase crop yields, however, yield losses due to biotic and abiotic stresses are significant and aggravated by extreme weather events due to climate change. Breeding programs now realize the value of landraces and wild relatives of modern crops to enhance genetic diversity and gain access to tolerance genes. This paper will provide an update on ongoing research programs in the UK and Australia to develop genetic populations for trait and gene discovery in wheat and, in this context, will review some lessons learned from tolerance genes identified in rice. Heat and drought stress are increasingly important problems globally affecting plants at different

developmental stages. Genetic diversity for heat tolerance at reproductive stages has now been identified in wheat, as well as in rice, and can potentially be exploited for breeding applications. The effect of heat stress on vegetative development in wheat is currently being investigated revealing large effects on tiller development. Based on a comparative drought study in rice, the metabolite allantoin (derived from purine catabolism) has been identified as a tolerant-specific metabolite and studies in wheat have confirmed the drought-responsiveness of this pathway and further suggest that allantoin is relevant under nitrogen starvation.

Molecular Breeding

Concurrent Speaker - Yuzuru Tozawa

Abstract Title: IDENTIFICATION OF A NOVEL MULTI-HERBICIDE RESISTANCE GENE FROM JAPONICA RICE VARIETY

Primary Author(s) and Institution(s): YUZURU TOZAWA 1 , HIDEO MAEDA 2 , KAZUMASA MURATA 3 , ATSUSHI IZUMI 4 , AKIHIKO YAMAZAKI 5 , NATSUKI TAKAMURA 1 , NOZOMI SAKUMA 1 , MOTOSHIGE KAWATA 2 , SAKIKO HIROSE 2 , MAKIO KAWAGISHI-KOBAYASHI 2 , HITOSHI YOSHIDA 2 , YOJIRO TANIGUCHI 2 , YUJI YAMADA 5 , KEISUKE SEKINO 5 , IKUO ANDO 2 , MAKOTO KUROKI 2 , MASAHIRO OHSHIMA 2 , HIROSHI KATO 2 1 Saitama University, Japan 2 National agriculture and food research organization, Japan. 3 Toyama Prefectural Agricultural, Forestry and Fisheries Research Center, Japan. 4 Kyoto University, Japan. 5 SDS Biotech K.K., Japan.; Saitama University

Abstract

Inhibitors of 4-hydroxyphenylpyruvate dioxygenase (HPPD) are widely used for weed control in crop production. For rice paddy fields benzobicyclon (BBC) had been developed and used, but, several new rice breeds were found to be BBC sensitive. As the BBC-sensitive phenotype causes a problem for further rice breeding, we attempted to identify the gene for BBC resistance. Map-based cloning identified a single locus gene, HIS1 (HPPD inhibitor sensitive 1), which encodes a novel Fe(II)/2-oxoglutarate dependent oxygenase, in the chromosome 2 of japonica varieties. On the other hand, some indica varieties had a 28-bp deletion in the 4th exon of HIS1 , showing a good agreement to their BBC-sensitive phenotype. We also confirmed that the expression of HIS1 confers herbicide resistance to rice by either conventional genetic cross or transgenic approach. The resistance was observed not only to BBC but also to other THs, such as mesotrione, sulcotrione, tembotrione and tefuryltrione. Cell-free synthesized HIS1 protein exhibited activity of Fe(II)/2-oxoglutarate dependent oxygenase, which mono-oxidizes the THs to their inactive forms and concomitantly converts 2-oxoglutarate to succinate. Moreover, Arabidopsis thaliana transformed with HIS1 also showed acquisition of resistance for these THs. HIS1 gene thus facilitates breeding of multi-herbicide-resistant crops as a useful genetic tool.

Molecular Breeding

Concurrent Speaker - Hélène Pidon

Abstract Title: INCREASING BARLEY'S ARSENAL AGAINST VIRUSES

Primary Author(s) and Institution(s): HELENE PIDON 1 ,Lisa Eichel 1 , Neele Wendler 2 , Antje Habekuss 3 , Klaus Oldach 2 , Ping Yang 4 , Eberhard Laubach 5 , Frank Ordon 3 , Viktor Korzun 2 , Nils Stein 1 1 Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben, 06466 Seeland 2 KWS LOCHOW GmbH, Ferdinand-von-Lochow-Straße 5, 29303 Bergen 3 Julius Kühn-Institute (JKI), Federal Research Institute for Cultivated Plants, Institute for Resistance Research and Stress Tolerance, 06484–Quedlinburg 4 CAAS Institute of Crop Science, Beijing, China 5 Nordsaat Saatzucht GmbH, Böhnshauser Straße 1, D-38895 Langenstein, Germany

Abstract

In Europe, Barley yellow dwarf virus (BYDV), transmitted by aphids, and soil-borne Barley yellow mosaic virus (BaYMV) and Barley mild mosaic virus (BaMMV), transmitted by Polymyxa graminis, are of prime importance in barley . We are investigating two resistance genes by forward genetics: rym7, a partial resistance locus to BaMMV, and Ryd4 Hb , a dominant resistance gene against BYDV. In previous studies, they were allocated to chromosomes 1H and 3H, respectively. After screening of 6000 F2 plants for recombination in the rym7 interval, 232 segmental recombinant inbred lines were selected, phenotyped, and genotyped by GBS . Linkage analysis revealed a 2 Mbp rym 7 interval in which seven high confidence genes are annotated . Ongoing work includes the exploitation of exome capture sequence data of both parents for an even finer mapping of rym7 and sequencing of the candidate genes in the RILs. Ryd4 Hb is a resistance gene derived from Hordeum bulbosum , a wild relative of barley. Recombination in crosses between H. vulgare and H. bulbosum are scarce: after screening around 16000 F2 plants, we were able to identify less than 120 recombinant plants in a 13.3 Mbp interval. Recombinants offspring are currently undergoing phenotyping and finer genotyping, with the aim to identify candidate genes.

Molecular Breeding

Concurrent Speaker - Jianlong Xu

Abstract Title: Genome-wide association mapping and BSA-seq analysis of Aluminum toxicity tolerance in rice

Primary Author(s) and Institution(s): YONGHONG TAO 1 , YANAN NIU 1 , JIAN ZHANG 2 , JIANLONG XU 1, 3* , ZHIKANG LI 1 1 Institute of Crop Sciences/National Key Facility for Crop Gene Resources and Genetic Improvement, Chinese Academy of Agricultural Sciences, Beijing, China; 2 Beijing Vegetable Research Center, Beijing Academy of Agricultural and Forestry Sciences, Beijing, China; 3 Shenzhen Institute of Breeding and Innovation, Chinese Academy of Agricultural Sciences, Shenzhen, China; Institute of Crop Sciences, Chinese Academy of Agricultural Sciences

Abstract

Aluminum (Al) stress is becoming the major limiting factor in crop production in acidic soils. We performed an association mapping of Al toxicity tolerance using a core collection of 211 indica rice accessions with 700 K high quality SNP data. A total of 21 putative QTL affecting shoot height, root

length, shoot fresh weight, shoot dry weight, root dry weight and shoot water content were identified at seedling stage. Total of 21 candidate genes for 7 important QTL regions associated with Al toxicity tolerance were identified based on combined haplotype analysis and functional annotation. BSA-seq and linkage analysis were further performed in the F 2 population derived from the cross of Al tolerant accession CC105 and super susceptible accession CC180 with opposite alleles at the major QTL on chromosome 2 detected by GWAS, revealing that Nrat1 (Os02g0131800) was responsible for Al toxicity tolerance of CC105. Haplotype analysis of Nrat1 using 327 3K RGP accessions indicated that minor allele variations in aus and indica subpopulations decreased Al toxicity tolerance in rice. Our research indicated that minor alleles are important for QTL mapping and its application in rice breeding when natural gene resources are used.

Programmed Cell Death
Concurrent Chair - Kazuyuki Kuchitsu

Abstract Title: CRITICAL ROLES OF AUTOPHAGY AND REACTIVE OXYGEN SPECIES IN REPRODUCTIVE DEVELOPMENT AND PROGRAMMED CELL DEATH

Primary Author(s) and Institution(s): KAZUYUKI KUCHITSU , SHIGERU HANAMATA, TAKAMITSU KURUSU Department of Applied Biological Science Imaging Frontier Center, Tokyo University of Science; Tokyo University of Science

Abstract

Reactive oxygen species (ROS) are highly toxic molecules generated during photosynthesis and aerobic respiration etc . However, tightly regulated ROS production by NADPH oxidases/Rbohs integrate multiple signal transduction network in plants. Rbohs are synergistically activated by Ca 2+ binding to the N-terminal EF-hand motifs and phosphorylation by several families of protein kinases. Spatiotemporal pattern of Rboh-mediated ROS production plays key roles in regulating a broad range of physiological processes including programmed cell death (PCD) and tip growth. In flowering plants, PCD of the tapetum, the innermost layer of the anther, is one of the most critical and sensitive steps for pollen maturation and fertility. It is severely affected by various environmental stresses, which cause serious problems in agriculture. We recently discovered that autophagy is induced at the uninucleate stage during pollen maturation and required for tapetal PCD, postmeiotic anther development and nutrient supply to the pollens in rice. Transcriptomic, metabolomic and microscopic analysis of the autophagy-deficient mutant suggested novel functions of autophagy in the regulation of reproductive development and lipid metabolism. Possible involvement of Rboh-mediated ROS production and transcriptional network in the regulation of autophagy and tapetal PCD during pollen maturation will be discussed.

Programmed Cell Death
Invited Speaker - Noni Franklin-Tong

Abstract Title: POST-TRANSLATIONAL MODIFICATIONS TRIGGERED DURING EARLY SELF-INCOMPATIBILITY RESPONSES IN PAPAVER POLLEN ARE LIKELY TO INDUCE PCD

Primary Author(s) and Institution(s): VERNONICA E. FRANKLIN-TONG , TAMANNA HAQUE 1 , DEBORAH J. EAVES, HELEN J COOPER, MAURICE BOSCH 2 School of Biosciences, College of Life and Environmental

Sciences, School of Biosciences, University of Birmingham, Edgbaston, Birmingham, B15 2TT, UK. 1 Current address : Department of Horticulture, Bangladesh Agricultural University, Mymensingh-2202, Bangladesh 2 Institute of Biological, Environmental Rural Sciences (IBERS), Aberystwyth University,Gogerddan, Aberystwyth, SY23 3EB, UK; University of Birmingham

Abstract

Self-incompatibility (SI) is used by many angiosperms to prevent self-fertilization and inbreeding. In Papaver rhoeas (poppy) interaction of cognate pollen and pistil S-determinants, PrsS and PrpS, triggers programmed cell death (PCD) and rejection of incompatible pollen. SI triggers several intracellular events in incompatible pollen, including increases in Ca 2+ , ROS, NO and acidification. Post translational modifications (PTMs) to proteins regulate numerous important cellular processes. We used liquid chromatography tandem mass spectrometry (LC-MS/MS) to map oxidative post-translational modifications (oxPTMs) triggered by SI in incompatible pollen. I will present the first analysis of the protein targets of ROS triggered by SI in incompatible pollen. Notably, we identified 200 irreversible oxidative modifications to different amino acids in SI-induced pollen; in contrast, untreated pollen only had 13. Analysis of H 2 O 2 -treated pollen revealed a similar pattern to SI-induced pollen. The type of oxPTM is important, as protein function is inhibited by irreversible oxidation. Our data show that during SI many pollen proteins are oxidatively damaged; this damage is likely to lead to PCD.

Programmed Cell Death

Concurrent Speaker - Volodymyr Radchuk

Abstract Title: PROGRAMMED CELL DEATH IN MATERNAL SEED TISSUES CONTROLS ENDOSPERM DEVELOPMENT AND FILLING OF CEREAL GRAINS

Primary Author(s) and Institution(s): Volodymyr Radchuk , Van Tran, Joerg Fuchs, Goetz Hensel, Eberhard Munz, Hardy Rolletschek and Ljudmilla Borisjuk Leibniz-Institute of Plant genetics and crop plant research (IPK), gatersleben, germany; Institute of Plant genetics and Crop Plant Research (IPK)

Abstract

In angiosperms, the embryo and endosperm develop being covered by diverse maternal seed tissues which ensure supply of water and nutrients to the embryo and endosperm but restrict their expansion. Using barley grains as a model, we elucidated the role of programmed cell death (PCD) on endosperm development and seed filling in cereal grains. The distributions of TUNEL-positive nuclei, expression of PCD-related genes and cascades of caspase-like activities have revealed that each seed tissue follows an individual PCD pattern. We compromised PCD in distinct maternal grain tissues by down-regulation of tissues-specific genes of vacuolar processing enzymes (VPE). The VPE proteins exhibited caspase-1 properties. The repression of the pericarp-specific VPE4 as well as the nucellar-specific VPE2a-VPE2d genes resulted in PCD delay in targeted tissues, lower caspase-like activities and smaller grains at maturity which accumulated less starch. Using transcriptional and metabolic profiling, flow cytometry, 13 C-feeding experiments, histology and nuclear magnetic imaging of grains we demonstrated that PCD in pericarp is required to provide space for the expanding endosperm and embryo while PCD in the nucellar projection mainly contributes to nutrient flow towards endosperm. These results prove the role of PCD in maternal control of endosperm development and seed size in cereals.

Programmed Cell Death

Concurrent Speaker - Elizabeth Fontes

Abstract Title: A PLANT-SPECIFIC CELL DEATH SIGNALING FROM THE ENDOPLASMIC RETICULUM

Primary Author(s) and Institution(s): ELIZABETH P. B. FONTES , LUIZ FERNADO CAMARGO; PEDRO A.B. REIS Department of Biochemistry and Molecular Biology, Universidade Federal de Vicosa, 36570000, Vicosa, MG, Brazil

Abstract

Prolonged endoplasmic reticulum (ER) and osmotic stress synergistically activate the stress-induced N-rich protein (NRP)-mediated signaling that transduces a cell death signal by inducing the GmNAC81/ GmNAC30?VPE module. GmNAC30 and GmNAC81 interact in the nucleus of plant cells to coordinately regulate common target promoters, which harbor the cis-element TGTG[TGC]. Consistent with a role in programmed cell death, GmNAC81 and GmNAC30 bind in vivo to and transactivate the caspase-1-like vacuolar processing enzyme (VPE) gene, which is involved in programmed cell death in plants. GmNAC81 and GmNAC30 fully transactivates the VPE gene in soybean protoplasts, which is associated with an increase in caspase-1-like activity. We propose that the stress-induced GmNAC30 cooperates with GmNAC81 to activate PCD through the induction of the cell death executioner VPE. We also show that the ER molecular chaperone BiP functions as a negative regulator of the ER stress cell death signaling leading to a delay in drought-induced senescence and conferring tolerance to drought. We will also present and discuss recent data, which indicate that the cell death signal derived from ER stress is connected to the NRP-mediated transduction pathway through the ER stress transducer GB1, an ER membrane-associated β subunit of the trimeric G protein.

Programmed Cell Death

Concurrent Speaker - Inès Beaugelin

Abstract Title: Antagonistic regulators of high light-induced cell death in Arabidopsis

Primary Author(s) and Institution(s): INES BEAUGELIN 1 , ANNE CHEVALIER 1 , FABIEN MONNET 1,2 , MICHEL HAVAUX 1 1 CEA/Cadarache, DRF, BIAM, UMR7265, Aix Marseille Université, 13108 Saint-Paul-les-Durance, France 2 Université d'Avignon et des Pays du Vaucluse, 84000 Avignon, France; CEA

Abstract

Under high light (HL) stress, reactive oxygen species, including singlet oxygen (1 O 2), are produced in chloroplasts. 1 O 2 is toxic and is able to oxidize cellular macromolecules. However, 1 O 2 also acts as a signal molecule that can lead through mediators either to acclimation or to programmed cell death (PCD). Transcriptomic analyses performed on the 1 O 2 -overproducing Arabidopsis mutant chlorina1 led to the identification of 1 O 2 signaling candidates. In particular, the OXI1 kinase was identified as a positive regulator of 1 O 2 -induced PCD through activation of the jasmonate pathway. Using OXI1 overexpression* in Arabidopsis thaliana , we confirmed the link between OXI1, jasmonate and HL-induced PCD, and we showed the concomitant involvement of salicylate in this pathway. We also identified a negative regulator of HL-induced PCD which was found to be able to down-regulate OXI1 expression, leading to an inhibition of jasmonate and salicylate accumulation under HL stress. Orientation of the response of plants to HL towards cell death or acclimation thus appears to be the

result of a complex interplay between the antagonistic actions of cell death regulators which modulate phytohormone levels. A model of functional interactions between those new PCD regulators will be presented. *Collaboration H. Hirt, KAUST.

The Algal Revolution from the ocean to the agricultural field
Concurrent Chair - Philippe Potin

Abstract Title: RECENT ADVANCES IN BROWN ALGAL GENOMICS AND GENETICS : AN HIGHLIGHT ON THE PHENOLIC METABOLISM

Primary Author(s) and Institution(s): PHILIPPE POTIN 1 , , EMELINE CREIS 1 , LUDOVIC DELAGE 1 , LAURENCE MESLET-CLADIERE 1 , SOPHIE GOULITQUER 1 , ERWAN AR GALL 2 , VALERIE STIGER-POUVREAU 2 , J. MARK COCK 1 , CATHERINE LEBLANC 1 , 1 Centre National de la Recherche Scientifique, Université Pierre et Marie Curie, Paris 6, Unité Mixte de Recherche 8227, Laboratory of Integrative Biology of Marine Models, Station Biologique de Roscoff, CS 90074, 29688 Roscoff Cedex, Brittany, France (potin@sb-roscoff.fr) 2 Université de Bretagne Occidentale, Laboratoire des Sciences de l'Environnement Marin, Unité Mixte de Recherche 6539, Institut Universitaire Européen de la Mer-IUEM, 29280 Plouzané, Brittany, France

Abstract

Brown algae are multicellular photosynthetic organisms belonging to the stramenopile lineage, which encompasses also unicellular diatoms and oomycetes. They are foundation species of marine rocky shore ecosystems worldwide and are economically significant for different markets including as crop biostimulants in agriculture. The genus Ectocarpus , and especially strain Ec32, has been established as a genetic and genomic model for brown algae. Genome mining in Ectocarpus has allowed to confirm the first step in the biosynthetic pathway of phlorotannins, i.e. the synthesis of phloroglucinol monomers using malonyl-CoA. Brown algal phlorotannins are structural analogues of terrestrial plant condensed tannins and similar to plant phenols they carry numerous bioactive functions. A predicted type III polyketide synthase in the Ectocarpus genome, EsiPKS1, was structurally characterized and shown to function as a phloroglucinol synthase. However, phlorotannins are formed by the condensation of phloroglucinol units, following a biosynthetic route that is still non elucidated. New candidate genes were expressed and characterized, such as a CHalcone Isomerase Like (CHIL) protein, several Phenol Sulfotransferases and a Vanadium-dependent Bromoperoxidase and their studies led to some new functions and hypotheses. Novel genetic approaches and the availability of 40 new genomes from most orders of brown algae (Phaeoexplorer) are shining a new light on the understanding of this biosynthetic pathway as well as on many other biological processes that have evolved specifically in multicellular brown algae.

The Algal Revolution from the ocean to the agricultural field
Invited Speaker - Maria Immacolata Immacolata Ferrante

Abstract Title: GENETICS AND GENOMICS IN PLANKTONIC DIATOMS

Primary Author(s) and Institution(s): MARIA IMMACOLATA FERRANTE Stazione Zoologica Anton Dohrn, Villa Comunale, 80121, Naples, Italy.; Stazione Zoologica Anton Dohrn

Abstract

Diatoms, an important and very diverse group of microalgae, carry out 1/5 of the photosynthesis on Earth and are essential to aquatic ecosystems, being primary producers at the base of the ocean food web. They are phylogenetically close to brown algae, and share metabolic pathways with plants as well as animals. Genomic data and genetic resources, initially available for only two model species out of the 100,000 estimated, are steadily increasing, enabling advanced functional studies and providing new opportunities for biotechnological exploitation. We focus on two model species, Phaeodactylum tricornutum , for which many resources are available, and Pseudo-nitzschia multistriata , an ecologically relevant planktonic diatom with a controllable life cycle, suitable for genetic studies. We sequenced the P. multistriata genome, defining gene gains and losses, events of retrotransposition, and gene acquisitions via horizontal gene transfer. This study coupled with transcriptomics allowed us to define the gene set involved in diatom sexual reproduction, and to elucidate the genetic program that defines mating types identity. Loss of function approaches and genetic engineering, including the CRISPR/Cas9 technology, are being used with the aim to characterize the role of diatom genes with unknown function, as well as to produce strains with improved properties.

The Algal Revolution from the ocean to the agricultural field
Concurrent Speaker - Patrice Salomé

Abstract Title: CO-EXPRESSION ANALYSIS IN THE ALGA CHLAMYDOMONAS REINHARDTII IDENTIFIES KNOWN AND NOVEL CONNECTIONS BETWEEN GENES

Primary Author(s) and Institution(s): PATRICE A SALOME , SABEEHA S MERCHANT UCLA, Department of Chemistry and Biochemistry, 607 Charles E Young Drive East, Los Angeles CA 90095, USA; UCLA, Department of Chemistry and Biochemistry

Abstract

The unicellular green alga Chlamydomonas reinhardtii is a choice model organism for the study of photosynthesis, flagellar assembly and function, lipid and starch metabolism and metal homeostasis. Aim: Despite decades of research, the function of many genes remains unknown, and new approaches are needed to categorically assign genes to cellular pathways. Growing collections of transcriptome and proteome data allows a systematic approach based on co-expression analysis. Methods: We are using a dataset comprising 518 RNAseq samples derived from 60 independent experiments to identify potential co-expression relationships between genes encoding proteins that perform similar function and/or belong to the same protein complex. Results: We found that ribosome protein genes cluster according to their final localization, and this pattern appears conserved in Arabidopsis and Physcomitrella. Genes with roles in cell cycle control, photosynthesis, respiration and flagella biology are similarly co-expressed within, but not between groups, highlighting pathway-specific gene expression programs. In particular, gene products identified in the cilium proteome and belonging to the CiliaCut (associated with flagella and basal body functions) are fully co-expressed. We are now extending gene expression networks from these known pathways and complexes assigning function to unknown genes.

The Algal Revolution from the ocean to the agricultural field
Concurrent Speaker - Robert Doczi

Abstract Title: THE ROLE OF MITOGEN-ACTIVATED PROTEIN KINASE SIGNALING IN OXIDATIVE STRESS IN THE MODEL UNICELLULAR MICROALGA, CHLAMYDOMONAS REINHARDTII

Primary Author(s) and Institution(s): RÓBERT DÓCZI 1 , TÍMEA V. NÁDAI 1,2 , BALÁZS KALAPOS 1 , GÁBOR GALIBA 1,2 , KATERINA BISOVA 3 1 Department of Plant Molecular Biology, Institute of Agriculture, Centre for Agricultural Research, Hungarian Academy of Sciences, Brunszvik u. 2., Martonvásár, H-2462, Hungary 2 Festetics Doctoral School, Georgikon Faculty, University of Pannonia, 8360 Keszthely, Hungary 3 Centre Algatech, Institute of Microbiology Academy of Scences of the Czech Republic, Opatovicky mlyn, CZ 379 81, Trebon, Czech Republic

Abstract

Biotechnological use of microalgae by exploiting the rich repertoire of algal metabolites as high-value products is a rapidly developing field, often involving shifts in culturing conditions to induce reprogramming of gene expression. Moreover, a unicellular plant model offers an efficient experimental system and an evolutionary framework to study cellular processes in the plant kingdom. The photosynthetic microalga, Chlamydomonas reinhardtii is a suitable laboratory model species, and has been utilised to study photosynthesis or lipid biosynthesis, yet our knowledge on environmental signalling in algae is very limited. The mitogen-activated protein kinase (MAPK) pathways play key roles in regulating stress responses in plants. Oxidative stress is commonly experienced by all types of eukaryotic cells, while reactive oxidative species (ROS) also act as secondary messengers and are well-known MAPK activators in mammals, fungi and plants. Therefore we set out to study MAPK signalling in photosynthetic microalgae. For functional analysis we have cloned selected Chlamydomonas MAPK signalling genes and generated various overexpression constructs. Transgenic Chlamydomonas lines along with insertion mutants are characterised in terms of stress responses. Our results reveal a unique involvement of MAPK in modulating ROS response and the expression of ROS metabolic enzymes in Chlamydomonas . (Funding: OTKANN 114511)

Symbiosis
Concurrent Chair - Uta Paszkowski

Abstract Title: Molecular genetics of arbuscular mycorrhizal symbiosis in cereals.

Primary Author(s) and Institution(s): Uta Paszkowski;

Abstract

The arbuscular mycorrhizal (AM) symbiosis is a fascinating mutualistic interaction between roots of most land plants and fungi of the phylum of the Glomeromycota. The development of this life-long alliance starts with reciprocal recognition in the rhizosphere, reprogramming both symbionts for the anticipated association. The interaction proceeds towards extensive root colonization which culminates in the formation of fungal feeding structures, the arbuscules, inside root cortex cells. As the arbuscule develops, the plant cell dramatically increases membrane biogenesis to envelope the growing hyphal structure. Thereby a hugely enlarged intracellular surface area is created between the two organisms, appearing ideally adapted for the exchange of signals and nutrients. The nature and complexity of the

establishment of AM symbioses must be the result of a well-orchestrated exchange of molecular signals between the plant and the fungus. The nature of some of the signals has been discovered in recent years, providing a first insight into the type of chemical language spoken between the two symbiotic partners. My laboratory has taken genetics and lately advanced imaging approaches to elucidate the molecular mechanisms underpinning this apparently harmonious symbiosis. I will introduce some of our recent observations which have led us to propose fundamentally new communication mechanisms operating during this intimate plant-fungal partnership.

Symbiosis

Invited Speaker - Jens Stougaard

Abstract Title: SIGNALS AND RECEPTORS INVOLVED IN LEGUME-MICROBE INTERACTIONS

Primary Author(s) and Institution(s): JENS STOUGAARD Department of Molecular Biology and Genetics, Aarhus University, Denmark; Aarhus University

Abstract

Legumes form endosymbioses with rhizobia and arbuscular mycorrhizal fungi, host endophytes, support a rhizosphere community and like other plants they are attacked by pathogens. One of the features enabling legumes to distinguish between these very different microbes appears to be a large family of LysM receptor kinases monitoring microbial signals. LysM receptor kinases have been shown to play a crucial role for perception of rhizobial Nod factors while others have not been studied. The function of some of these receptors in perception of signal molecules including lipochito-oligosaccharides, exopolysaccharides and chitin derived signal molecules and in plant-microbe interaction will be presented together with the genetic and biochemical methods used for functional studies. Biochemical approaches for detailed characterization of ligand – LysM receptor interactions will be presented and a model for legume recognition of rhizobial bacteria and pathogens will be discussed.

Symbiosis

Concurrent Speaker - Man-Yuan Guo

Abstract Title: BUILDING A FUNCTIONAL REPERTOIRE OF ION CHANNELS ACTIVE AT THE PLASMA MEMBRANE OF APICAL REGIONS OF MEDICAGO TRUNCATULA LEGUME ROOT HAIRS

Primary Author(s) and Institution(s): GUO MAN-YUAN * , WANG LIMIN*, SENTENAC HERVE, VERY ANNE-ALIENOR BPMP, University Montpellier-CNRS-INRA-SupAgro, Montpellier, France BPMP, University Montpellier-CNRS-INRA-SupAgro

Abstract

Root hairs are elongated epidermal cells essential for the acquisition of mineral nutrients by the plant. In legumes, they are also the seat of initiation of symbiotic interactions with N2-fixing rhizobia. In these plants, early ionic signals initiated at the root hair plasma membrane, involving changes in H + , Ca 2+ , anions and K + ion fluxes and resulting in transient depolarization of the cell membrane, are triggered as initial responses to perception of the signaling Nod factors secreted by the rhizobial partners present in the rhizosphere. Here, we aimed at building a repertoire of ion channel activities present at root hair plasma membrane of the model legume M. truncatula , which could be implicated in these early

signaling events leading to symbiosis establishment. Apical spheroplasts of plasma membrane of young growing root hairs, recovered through cell-wall laser ablation, were used in patch-clamp experiments. Six ionic conductances selective for Ca 2+ , K + or anions, involved in ion influx and/or effluxes, were identified and their sensitivity to NF checked. This provides a first sketch of the set of transport systems involved in the Nod-factor-triggered electrical signals, paving the way to future confirmation through reverse genetics on corresponding candidate genes in this sequenced model legume.

Symbiosis

Concurrent Speaker - Sona Pandey

Abstract Title: Regulation of nodule formation in soybean by interaction between G-protein components and multiple receptors

Primary Author(s) and Institution(s): SONA PANDEY, SWARUP ROY CHOUDHURY Donald Danforth Plant Science Center, St. Louis, Mo, 63132, USA; Donald Danforth Plant Science Center

Abstract

Heterotrimeric G-proteins and their regulatory RGS proteins regulate a wide array of signaling pathways in all eukaryotes. We have recently provided the first genetic evidence that the specific G protein subunits of soybean are involved in regulation of nodule formation. We established the role of nod factor receptor (NFR1) mediated phosphorylation in regulation of G-protein cycle during nodule formation. Our data suggested a model where the Gα subunit of the G-protein trimer acts as a negative regulator, as overexpression of individual Gα genes results in lower nodule numbers per root. We also showed that during nodulation the G-protein cycle is regulated by the activity of RGS proteins. Lower or higher expression of RGS proteins due to the RNAi-mediated suppression, or overexpression resulted in fewer or more nodules, respectively. The RGS proteins interact with NFR1 proteins and are phosphorylated by them. Phosphorylated RGS maintains Gα proteins in their inactive, trimeric conformation, leading to nodule development. We now present data to show that the Gα proteins' activity is directly affected by their interaction with specific co-receptors of nodulation. Our current model suggests both direct and indirect regulation of the G-protein cycle during nodule formation by the activity of multiple receptors and co-receptors.

Symbiosis

Concurrent Speaker - Ronelle Roth

Abstract Title: A PERI-ARBUSCULAR MEMBRANE SER/THR RECEPTOR-LIKE KINASE, ARK1, IS REQUIRED TO MAINTAIN ARBUSCULAR MYCORRHIZAL SYMBIOSIS IN RICE

Primary Author(s) and Institution(s): RONELLE ROTH 1 , MARCO CHIAPELLO 2 , HECTOR MONTERO 1 , DENISE HARTKEN 3 , FERGUS WALTERS 1 , RUAIRIDH SAWERS 4 , UTA PASZKOWSKI 1 1 Department of Plant Sciences, University of Cambridge, UK; 2 Cambridge Centre for Proteomics, University of Cambridge, UK; 3 Department for Plant Biochemistry, Albrecht-von-Haller-Institute for Plant Sciences, Georg-August-University of Goettingen, Germany; 4 Langebio Cinvestav, Guanajuato, México

Abstract

Land plants and beneficial arbuscular mycorrhizal (AM) fungi form life-long associations that dependent on the reciprocal trade of essential soil minerals such as inorganic phosphate (Pi) in exchange for host photosynthates. As obligate biotrophs, AM fungi rely on plants for fatty acids, needed to form highly branched ephemeral intracellular feeding structures called arbuscules, and essential for completion of the fungal life cycle. Transient invasion of arbuscules into root cortical cells results in membrane surfaces becoming greatly expanded to provide a large symbiotic interface for symbiotic exchange. Although such synchronized intimacy between the two partners must be the consequence of a precisely tuned exchange of signals, to date, plant signalling components operating at the plant-derived peri-arbuscular membrane (PAM) surrounding arbuscules have not been reported. Here, by applying innovative proteomics, we identified a PAM-specific Ser/Thr receptor-like kinase that while not required for arbuscule establishment is indispensable for completion of the fungal life-cycle. We, thereby, define for the first time that the stage post-arbuscule development is critical for maintaining AM symbiosis.

Life at the Interface: Membrane Delimited Signaling and Transport

Concurrent Chair - Dirk Becker

Abstract Title: Wounding induced stomatal closure requires Jasmonate-dependent activation of the guard cell K+ channel GORK via Ca2+ sensor-kinase CBL1-CIPK5 complexes

Primary Author(s) and Institution(s): Dirk Becker; University of Wuerzburg

Abstract

Guard cells integrate various hormone signals and environmental cues to balance plant gas exchange and transpiration. The wounding-associated hormone jasmonic acid (JA) and the drought hormone abscisic acid (ABA) both trigger stomatal closure. In contrast to ABA however, the molecular mechanisms of JA-induced stomatal closure have remained largely elusive. Here, we identify a fast-signaling pathway for JA action targeting the K+ efflux channel GORK. Wounding triggers stomatal closure, both locally and systemically. Wounding induced activation of the JA signaling cascade in guard cells stimulates GORK phosphorylation and activation by Ca2+-activated CBL1-CIPK5 Ca2+ sensor-kinase complexes. GORK activation strictly depends on plasma membrane targeting and Ca2+ binding of CBL1-CIPK5 complexes. Accordingly, in gork, cbl1 and cipk5 mutants, JA-induced stomatal closure is specifically abolished. The ABA-coreceptor ABI2 counteracts CBL1-CIPK5 dependent GORK activation. In

this way, JA-induced Ca2+ signaling in response to biotic stress converges with the ABA mediated drought stress pathway to facilitate GORK-mediated stomatal closure upon wounding.

Life at the Interface: Membrane Delimited Signaling and Transport
Invited Speaker - Gabriele Monshausen

Abstract Title: FERONIA-dependent Ca2+ signaling in response to RALF1 and mechanical stimulation

Primary Author(s) and Institution(s): Gabriele Monshausen, Cassidy Cornblatt, Aditi Bhat and Han-Wei Shih; Biology Department, Pennsylvania State University, University Park, Pa, USA

Abstract

The receptor-like kinase FERONIA is an important regulator of a broad array of developmental and stress responses. FER activity is modulated by its ligand, the secreted signaling peptide RAPID ALKALINIZATION FACTOR1, which triggers an immediate FER-dependent cytosolic Ca2+ increase and subsequent extracellular alkalinization. We have previously shown that FER is also required for normal mechanically induced Ca2+ transients, suggesting that RALF1 may play a role in FER-dependent mechanical signal transduction. Here we show that RALF1 pretreatment rapidly desensitizes Arabidopsis roots to mechanical stimulation. Both RALF1 treatment and mechanical wounding also trigger a loss of FER-GFP from the plasma membrane; in both cases the process is Ca2+-dependent and requires a functional FER kinase domain as well as the presence of the FER-interacting protein LLG1. However, notwithstanding these similarities, FER degradation in response to RALF1 and wounding treatments appears to follow different pathways; only RALF1-induced FER-GFP degradation seems to involve endocytosis and late endosomal trafficking. This suggests that while FER-dependent mechanical and RALF1 signal transduction can intersect, RALF1 is unlikely to be an integral component of mechanical signaling. This conclusion is further supported by our finding that mechanically and RALF1-induced ion signaling are mediated by distinct ion channels. Given the well-supported role of FER as a RALF1 receptor, this raises the interesting question of whether FER is a dual function receptor, directly but differentially activated by RALF1 and mechanical stimulation, or whether FER modulates the activity of an as yet unidentified mechanosensor in a RALF1-dependent manner.

Life at the Interface: Membrane Delimited Signaling and Transport
Concurrent Speaker - Brian Rutter

Abstract Title: ARABIDOPSIS EXTRACELLULAR VESICLES MEDIATE THE INTERCELLULAR TRANSPORT OF PROTEINS AND RNA

Primary Author(s) and Institution(s): BRIAN D. RUTTER (Indiana University) PATRICIA BALDRICH (Dondald Danforth Plant Science Center) RAM PODICHETI (Indiana University) HANA ZANDKARIMI (Indiana University) BLAKE MEYERS (Dondald Danforth Plant Science Center) ROGER W. INNES (Indiana University); Indiana University

Abstract

Arabidopsis cells secrete extracellular vesicles (EVs) under sites of pathogen attack. These small, external organelles contribute to the formation of defensive barriers and are thought to facilitate intercellular signaling through the transfer of proteins and RNA. In order to better understand the defensive and

signaling roles of plant EVs, our lab developed methods for isolating and purifying EVs from Arabidopsis leaves. We found that Arabidopsis secretes EVs that are highly enriched for defense-related proteins, including the syntaxin PENETRATION1/SYP121 and the ABC transporter PEN3. In line with this finding, EV secretion was enhanced in response to the stress hormone salicylic acid (SA). Next-generation sequencing of Arabidopsis EVs identified several small RNAs enriched in EVs compared to total leaf RNA or RNA isolated from EV-depleted supernatant. Interestingly, EVs were enriched for 10-15 nt long RNAs that map back to miRNA and siRNA precursors. Finally, our lab developed transgenic plants expressing the EV marker protein PEN3 fused to GUS. These plants were used to show long-distance EV trafficking in grafted plants, as well as uptake by pathogenic fungi. Our findings suggest that Arabidopsis EVs play an important role in plant immunity, intercellular signaling and interkingdom communication.

Life at the Interface: Membrane Delimited Signaling and Transport

Concurrent Speaker - Jung-Youn Lee

Abstract Title: INTEGRATIVE SYMPLASMIC SIGNALING UNDER BIOTIC AND ABIOTIC STRESS

Primary Author(s) and Institution(s): JUNG-YOUN LEE and WEIER CUI Department of Plant and Soil Sciences, Delaware Biotechnology Institute, University of Delaware, Newark, DE 19711, U. S. A.; University of Delaware

Abstract

Plasmodesmata (PD) are intercellular bridges that facilitate molecular movement between cells. They are essential for normal developmental progression and survival of the plant against various environmental challenges. Many signals and stressors are known to influence PD function; however, it is not well understood how different signals bring about changes in symplasmic movement. Previously, we have shown that it is vital for innate immunity to integrate the salicylic acid (SA)-mediated signaling pathway with a callose-dependent PD-regulating mechanism governed by the PD-located protein PDLP5. PDLP5 induces local and systemic PD closure by stimulating CalS1, a callose synthase . Yet, PDLP5-CalS1 pathway is not required for reactive oxygen species (ROS)-induced PD closure. Genetic mutant analysis combined with cellular techniques led us to identify another callose synthase CalS8 to be responsible for ROS-dependent PD closure. Strikingly, the kinetics of PD callose accumulation are quite dissimilar between these two enzymes; one is slow and sustained while the other is instantaneous and transient. A model will be discussed that illustrate how symplasmic movement is regulated by recruiting different molecular players to PD in response to diverse stressors with speculations on what advantages of having such mechanisms might be to the fitness of the plants.

Life at the Interface: Membrane Delimited Signaling and Transport
Concurrent Speaker - Nadine Paris

Abstract Title: Non invasive imaging use to shed light on pH at both sides of the plasma membrane interface in living root.

Primary Author(s) and Institution(s): NADINE PARIS , Alexandre Martinière, Rémy Gibrat, Hervé Sentenac, Xavier Dumont and Isabelle Gaillard. BPMP, CNRS, INRA, Montpellier SupAgro, Univ Montpellier, Montpellier, France.

Abstract

The proton gradient across a biological membrane is a matter of great importance for plant development and nutrition. To gain a better understanding of proton distribution in the plant root apoplast as well as across the plasma membrane, we generated Arabidopsis plants expressing stable membrane-anchored ratiometric fluorescent sensors based on pHluorin. These sensors enabled non-invasive and specific pH measurements in mature root cells from the medium-epidermis interface up to the inner cell layers that lie beyond the Casparian strip. We found that the membrane-associated apoplastic pH was much more alkaline than in the overall apoplastic space. In apparent contradiction with the direct connection between root intercellular space and the external medium, proton concentration associated with the plasma membrane was very stable, even when the growth medium pH was altered. The plasma membrane-associated pH in the stele was the most preserved, and displayed the lowest apoplastic pH (6.0 to 6.1) and the highest transmembrane delta pH (1.5 to 2.2). Both pH values also correlated well with optimal activities of channels and transporters involved in ion uptake and redistribution from the root to the aerial part. In growth medium where ionic content is minimized, the root plasma membrane-associated pH was more affected by environmental proton changes, especially for the most external cell layers. Calcium concentration appears to play a major role in apoplastic pH under these restrictive conditions, supporting a role for the cell wall in pH homeostasis of the unstirred surface layer of plasma membrane in mature roots. Alexandre Martinière, Rémy Gibrat, Hervé Sentenac, Xavier Dumont, Isabelle Gaillard and Nadine Paris. Shedding light on pH at both sides of the root plasma membrane interface using non-invasive imaging. PNAS, in press under embargo.

Gene and Metabolic Regulatory Network
Concurrent Chair - Siobhan Brady

Abstract Title: Transcriptional regulation of nitrogen and nitrogen-related metabolism in Arabidopsis thaliana

Primary Author(s) and Institution(s): Allison Gaudinier 1 , Joel Rodriguez-Medina 1 , Lifang Zhang 2 , Andrew Olson 2 , Christophe Liseron-Monfils 2 , Anne-Maarit Bågman 1 , Jessica Foret 1 , Shane Abbitt 3 , Michelle Tang 1 , Baohua Li 4 , Daniel E. Runcie 4 , Daniel J. Kliebenstein 4 , Bo Shen3, Mary J. Frank 3 , Doreen Ware 2,5 , Siobhan M. Brady 1; UC Davis

Abstract

Nitrogen is essential for plant growth. Insufficient nitrogen leads to decreased agricultural yield while nitrogen application from fertilizers results in increased plant productivity but can have a negative impact on the environment. Changes in nitrogen availability are perceived by dual function nitrate

transporters in the root resulting in a signaling cascade and subsequent changes in gene expression. Despite the importance of transcriptional regulation in this adaptive response, a minimal number of nitrogen metabolic transcriptional regulators have been identified. Here we present a transcriptional regulatory network and twenty-three novel transcription factors that regulate root and shoot system architecture upon changes in nitrogen availability. Genetic perturbation of a subset of these transcription factors revealed coordinate transcriptional regulation of nitrogen metabolic enzymes. Feedback is a common form of metabolic regulation. Transcriptional regulators in the network are transcriptionally modified by feedback via genetic perturbation of nitrogen metabolism.

Gene and Metabolic Regulatory Network
Invited Speaker - Alisdair Fernie

Abstract Title: Investigating regulatory networks underpining tomato metabolism and growth

Primary Author(s) and Institution(s): Alisdair Fernie , Max-Planck-Institute of Molecular Plant Physiology, Potsdam-Golm, Germany; MPI-MP

Abstract

Incomplete knowledge of biochemical pathways renders the holistic description of plant metabolism a non-trivial undertaking. Sensitive analytical platforms, which are capable of accurately quantifying the levels of the various molecular entities of the cell, can assist in tackling this task as can the use of advanced breeding populations. That said, the ever-increasing amount of high-throughput data, often from multiple technologies, requires significant computational efforts for integrative analysis. In my lecture I intend to discuss the advantage of using natural diversity in the frame of introgression and backcross inbred lines to study the complex networks linking whole plant metabolism with that of the fruit in tomato. I also will describe recent insights gained into tomato ripening and source-sink interactions following this approach and finallly will described how the relationship between structural and biological roles of network components can be evaluated and employed to aid metabolic engineering.

Gene and Metabolic Regulatory Network
Concurrent Speaker - Wolfgang Dröge-Laser

Abstract Title: THE C/S1 BZIP TRANSCRIPTION FACTOR NETWORK: A REGULATORY HUB ORCHESTRATING PLANT ENERGY HOMEOSTASIS

Primary Author(s) and Institution(s): Wolfgang Dröge-Laser , Lorenzo Pedrotti, Christoph Weiste, Julius-von-Sachs-Institut, Pharmazeutische Biologie, Julius-Maximilians-Universität Würzburg, Julius-von-Sachs-Platz 2, D-97082 Würzburg; Uni Würzburg, Julius-von-Sachs-Institue

Abstract

Sustaining energy homeostasis is crucial to every living being. To balance energy supply and demand, plants make use of an evolutionarily conserved managing system consisting of two counteracting kinases: TOR (TARGET OF RAPAMYCIN) supports anabolic, energy-consuming metabolism, whereas SnRK1 (SNF1-RELATED PROTEIN KINASE1) activates catabolic, energy-preserving responses. The nine Arabidopsis bZIP (basic leucine zipper) transcription factors of the groups C and S 1 preferentially

heterodimerize and perform as downstream mediators of SnRK1 signalling in a partially redundant manner 1 . Here, we propose a mechanistic model how SnRK1 phosphorylates group C bZIP63, which triggers the formation of C/S 1 -heterodimers 2 and thus, the recruitment of SnRK1 directly to target promoters 3 . A transiently formed ternary C/S 1 -bZIP-SnRK1 complex interacts with the histone acetylation machinery to remodel chromatin to facilitate transcription 3,4 . The C/S 1 -bZIP network is involved in SnRK1-dependent and -independent signalling such as metabolic reprogramming in response to carbon or nitrogen limiting conditions, pathogen infection or abiotic stress. Moreover, it coordinates root growth and seed development 1 . As transcription factor heterodimerization provides a mechanism to integrate information, we propose that the C/S 1 -bZIP transcription factor network functions as a major hub orchestrating plant energy homeostasis, development and stress response. 1 Dröge-Laser and Weiste (2018) TIPS (in press) 2 Mair et al. (2015) eLife 4: e05828 3 Pedrotti et al. (2018) Plant Cell 2: 495-509 4 Weiste and Dröge-Laser (2014) Nature com. 5:3883.

Gene and Metabolic Regulatory Network
Concurrent Speaker - Pengcheng Wang

Abstract Title: A GLOBAL SURVEY OF ALTERNATIVE SPLICING IN ALLOPOLYPLOID COTTON: LANDSCAPE, COMPLEXITY AND REGULATION

Primary Author(s) and Institution(s): MAOJUN WANG # PENGCHENG WANG # , FAN LIANG, ZHENGXIU YE, JIANYING LI, CHAO SHEN, LIULING PEI, FENG WANG, JIANG HU, LILI TU, KEITH LINDSEY, DAOHUA HE, XIANLONG ZHANG; Huazhong Agricultural University

Abstract

Alternative splicing (AS) is a crucial regulatory mechanism in eukaryotes, which increases transcriptome diversity. The extent and complexity of AS has been revealed in model plants using high-throughput next-generation sequencing. However, this technique is less effective to accurately identify transcript isoforms in polyploid species because of high sequence similarity between coexisting subgenomes. Here we characterized AS in the polyploid species cotton. Using Pacific Biosciences single-molecule long-read isoform sequencing (Iso-Seq), we developed an integrated pipeline for Iso-Seq transcriptome data analysis. A total of 176,849 full-length transcript isoforms from 44,968 gene models were identified. These data helped us to identify 15,102 fibre-specific AS events. About 51.4% of homoeologous genes produced divergent isoforms in each subgenome. The small RNA sequencing revealed that AS allows differential regulation of the same gene by miRNAs at the isoform level. Furthermore, MNase-seq showed that nucleosome occupancy might play a role in defining exons at the chromatin level. DNA methylation might be another mark for exon definition and the 3’ UTR processing, which increased transcript isoform diversity. To summarize, the methodology of Iso-Seq and epigenetic analysis provides new insights into the complexity and regulation of AS in cotton. It will enhance our understanding of AS in polyploid species.

Gene and Metabolic Regulatory Network
Concurrent Speaker - Arthur Korte

Abstract Title: Natural Variation of Gene Regulatory Networks in Arabidopsis thaliana

Primary Author(s) and Institution(s): ARTHUR KORTE , AMMARAH ANWAR, JAN FREUDENTHAL and WILLIAM LOPEZ

Abstract

Understanding the causal relationship between genotype and phenotype is a major objective in biology . The main interest is in understanding trait architecture and identifying loci contributing to the respective traits. Genome-wide association mapping (GWAS) is one tool to elucidate these relationships and has been successfully used in many different species. However, most studies concentrate on marginal marker effects and ignore epistatic and gene-environment interactions. These interactions are problematic to account for, but are likely to make major contributions to many phenotypes that are not regulated by independent genetic effects, but by more sophisticated gene-regulatory networks. A further complication arises from the fact that these networks vary in different natural accessions. However, u nderstanding the differences of gene regulatory networks and gene-gene interactions is crucial to conceive trait architecture and predict phenotypes. I will present d ata on statistical aproaches to tackle these challenges and present examples - using data from the Arabidopsis 1001 Genomes Project – of gene regukatory networks that have been realized differntly in different natural accessions.

Natural Variation and Adaptation
Concurrent Chair - Kirsten Bomblies

Abstract Title: The evolution of meiosis and meiotic recombination in polyploid Arabidopsis arenosa

Primary Author(s) and Institution(s): KIRSTEN BOMBLIES; John Innes Centre

Abstract

Meiosis is essential for fertility of sexual eukaryotes. Its core structures and progression are strongly conserved across kingdoms. Meiosis efficiently separates pairs of homologous chromosomes, but in polyploids, the presence of more than two copies of every chromosome presents a challenge. In newly formed polyploids, the multiple available chromosomes can pair and recombine to form multivalents, which can cause chromosome segregation problems and reduced fertility. Evolved polyploids rarely make multivalents showing that solutions to this problem can evolve. We are interested in discovering those mechanisms. In a genome scan for adaptation to whole genome duplication in Arabidopsis arenosa , we found that eight interacting meiotic proteins were under strong selection in the polyploid. Using genetics coupled with cytology, we found that alternate alleles of at least three of these have effects on meiosis that parallel differences between diploids and tetraploids. Modifications of these proteins, all of which are structural proteins essential for pairing and recombination, appear to stabilize polyploid meiosis by altering crossover number and/or the strength of crossover interference, leading to fewer multivalent associations among the available chromosome copies. Our work provides insights not only into polyploid stabilization, but also more generally how modified recombination rates can evolve.

Natural Variation and Adaptation

Invited Speaker - Angela Hancock

Abstract Title: ARABIDOPSIS THALIANA'S AFRICAN ROOTS

Primary Author(s) and Institution(s): ANGELA M HANCOCK; Max Planck Institute for Plant Breeding, Germany

Abstract

A. thaliana has typically been considered a weed associated primarily with human-mediated environments, including agricultural fields, urban sites and railways. However, it was recently shown that it is native also in remote natural areas, including high altitude locations in Eurasia and Africa, from the Atlas Mountains in Morocco and the Afro-alpine regions in Eastern and South Africa to Yunnan in China, the Himalayas and the Tibetan Plateau. I will describe our ongoing work to unravel evolutionary history in Africa and to integrate this with findings from other studies focused on European and Asian populations of Arabidopsis thaliana.

Natural Variation and Adaptation
Concurrent Speaker - Julia Bally

Abstract Title: THE MODEL PLANT NICOTIANA BENTHAMIANA : A PLANT FOR ALL REASONS

Primary Author(s) and Institution(s): JULIA BALLY 1,2 , KENLEE NAKASUGI 2 , FANGZHI JIA 2 , ROGER HELLENS 1 , MEI WONG 2 HYUNGTAEK JUNG 1 , AURELIANO BOMBARELY 3 , MICHAEL M. GOODIN 4 and PETER M. WATERHOUSE 1,2 1 Centre for Tropical Crops and Biocommodities, QUT, Brisbane, QLD, Australia 2 School of Molecular Biology, the University of Sydney, Sydney, NSW 2006, Australia 3 Department of Horticulture, Virginia Tech, Blacksburg, USA 4 Department of Plant Pathology, University of Kentucky, Lexington 40546, U.S.A; CTCB, QUT

Abstract

Nicotiana benthamiana , is a member of the Solanaceace family which includes many of the world's agricultural crops (e.g. potato, tomato, tobacco…), and more than 3000 wild species. One isolate of N. benthamiana , collected from arid habitat of central Australia, is used in ever-increasing numbers as a model plant in laboratories worldwide. It has been instrumental in making revolutionary discoveries about RNA interference, plant–pathogen interactions and metabolic pathway engineering. The plant is peerless in its susceptibility to a vast range of viruses. However, the proposed mechanism(s) behind this hypersusceptibility and the evolutionary implications of this property, have been controversial, as they are based solely on analysis of a single, poorly provenanced, laboratory isolate. We have collected accessions from the extremities of the species natural distribution and analysed them, alongside laboratory isolates, at genome, transcriptome, pathogen-response, morphological and phylogenetic levels. Our study shows that the commonly used N. benthamiana line originates from a defence-deficient mutant population that has survived for about 800,000 years in the extreme habitat of central Australia. For its adaptation to harsh conditions the plant has divested itself of non-essential genes and pathways and has traded its defence capacity for early vigour and survival in a hostile environment.

Natural Variation and Adaptation
Concurrent Speaker - Karla Azucena Juárez Núñez

Abstract Title: THE ROLE OF PHOSPHOLIPID BALANCE IN MAIZE HIGHLAND ADAPTATION

Primary Author(s) and Institution(s): KARLA JUÁREZ-NÚÑEZ 1 , JUAN ESTÉVEZ-PALMAS 1 , LI WANG 2 , MATTHEW HUFFORD 2 ,JEFFREY ROSS-IBARRA 3 , OLIVER FIEHN 4, RUAIRIDH JH SAWERS 1 , RUBÉN RELLÁN-ÁLVAREZ 1 1. Laboratorio Nacional de Genómica para la Biodiversidad (LANGEBIO) 2. Department of Ecology, Evolution and Organismal Biology, Iowa State University 3. Department of Plant Sciences, University of California Davis 4. NIH West Coast Metabolomics Center, Genome Center, University of California Davis LANGEBIO

Abstract

Aim To investigate the role of phospholipid balance in maize highland adaptation. Methods We utilized a 120 landraces diversity panel and 100 recombinant inbred lines (RILs). Diversity panel consists of 60 Mesoamerican and 60 South American landraces, each subcontinental group with 30 highland and 30 lowland landraces. RILs were generated by crossing lowland parent B73 to mexican highland landrace palomero toluqueño (PT). Populations were grown in highland and lowland fields where leaves were sampled for lipid profiling using UHPLC-QTOFMS. A quantitative trait locus (QTL) analysis was performed using RILs biochemical phenotype and genotypic data. Results We identified a major environment-independent QTL peak, in chromosome 3. At QTL region lays a putative phospholipase A1, which can hydrolyze phospholipids into lysophospholipids and free fatty acids. At the marker at the QTL peak, PT allele leads to significant higher phosphatidylcholine(PC)/lysophosphatidylcholine(LPC) ratio than B73 allele, suggesting that conversion PC to LPC is not properly occuring in PT. Diversity panel data shows that highland landraces, particularly Mesoamerican, have higher PC/LPC ratio than lowland ones, suggesting that this biochemical phenotype was selected in highlands. Using highland and lowland whole genome sequences we showed that several genes involved in PC-LPC transition were selected in highland maize.

Natural Variation and Adaptation
Concurrent Speaker - Katelyn Sageman-Furnas

Abstract Title: Genetic and molecular mechanisms of F1 hybrid incompatibility of A. thaliana accessions Shahdara and Lagodechi

Primary Author(s) and Institution(s): KATELYN SAGEMAN-FURNAS MARKUS NURMI BJOERN PLOETNER LISA SMITH ROOSA LAITINEN

Abstract

Hybrid incompatibility is a phenomenon in which hybrids show reduced fitness in comparison to their parents; this can result in reproductive isolation and eventually speciation. While hybrid necrosis is the most studied form of hybrid incompatibility in A. thaliana , much is still unknown about other traits and how they relate to adaptation. We have found that the F1 hybrid between Shahdara and Lagodechi 2-2 shows altered shoot architecture in comparison to its parents. We demonstrate that a single allelic interaction in outgrowth associated kinase (OAK) leads to uncontrolled rosette branching and aberrant growths on the leaf. We now aim to further characterize the function of OAK in shoot branching and outgrowth formation. So far, expression analysis revealed that mechanical stress genes are upregulated in the outgrowths of the hybrids. This analysis also indicated an upregulation of hormone expression markers, which will be studied further. Mechanical stress and wind experiments showed that the outgrowth phenotype is mitigated by mechanical stress and further data on OAK ’s role in mechanical stress and in the hybrid phenotype will be presented. In addition, sequence comparisons and crosses of 13 different Lagodechi accessions to Shahdara revealed functionally different OAK alleles found in Lagodechi area.

Cell and Organ Size
Concurrent Chair - Hirokazu Tsukaya

Abstract Title: Reexamination of the impact of endoreduplication on cell size in leaves

Primary Author(s) and Institution(s): HIROKAZU TSUKAYA Graduate School of Science, The University of Tokyo, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan Bio-Next project, Exploratory Research Center on Life and Living Systems, NINS, Okazaki 444-8787, Japan; The University of Tokyo

Abstract

It has been revealed that endoreduplication-dependent increase of the nuclear ploidy level is often associated with increased cell volume, and the increase in cell volume is frequently discussed as a result of enhanced endoreduplication. However, our recent studies revealed that the relationship between ploidy levels and cell size is not that simple (Katagiri et al. , 2016; Kawade and Tsukaya, 2017). In the present study, I carried out metadata analyses to desipher the relationship between observed cell size and endoreduplication profile based on previous publications. The results showed that the observed cell size phenotypes are far stronger than expected from changes in the ploidy profile. This inconsistency is quite large and cannot be overlooked, and thus urges us to reconsider the contribution of the endoreduplication-dependent ploidy increase on cell size changes. In this symposium, one plausible explanation to this discrepancy will be discussed. References: Katagiri et al. (2016) Development 143 :

1120-1125. doi:10.1242/dev.130021 Kawade and Tsukaya (2017) PLOS ONE 12 : 9, 10.1371/journal.pone.0185050

Cell and Organ Size

Invited Speaker - Hilde Nelissen

Abstract Title: The dynamics of molecular and cellular processes in the maize leaf growth zone

Primary Author(s) and Institution(s): HILDE NELISSEN , NIENKE BESBRUGGE, JELLE VAN LEENE, MICHIEL BONTINCK, TOM VAN HAUTEGEM, KIRIN DEMUYNCK, JOLIEN DE BLOCK, GEERT DE JAEGER, DIRK INZE; VIB / UGent

Abstract

One of the most fascinating open questions in biology is how organ and organism size is controlled. The maize leaf offers an excellent experimental system to study leaf growth, due to the linear organization of cell division and expansion along its longitudinal axis: active cell divisions occur at the base of the leaf, and as the distance from the base increases cells will cease division and start expanding until they reach their mature cell size. The aim of our research is to map the dynamics of cellular and molecular processes during the transition between cell division and cell expansion with high resolution throughout the growing maize leaf. We identified some key players that increase organ growth when ectopically expressed and we introduced interactomics tools, such as tandem affinity purification and chromatin immunoprecipitation, in maize to study the changes in protein complex composition and protein-DNA interactions in the growth zone.

Cell and Organ Size

Concurrent Speaker - Hirotomo Takatsuka

Abstract Title: ATRICHOBLAST EPIDERMAL CELLS ELONGATE WITH POLARITY IN ARABIDOPSIS ROOTS

Primary Author(s) and Institution(s): Authors: HIROTOMO TAKATSUKA 1 and Masaaki Umeda 1 Affiliations: 1 Nara Institute of Science and Technology, JAPAN Nara Institute of Science and Technology

Abstract

Indeterminate root growth is controlled by continuous cell division and cell elongation, the latter of which is also involved in the rapid response to environmental changes, as represented by gravitropism. Roots of Arabidopsis are composed of a variety of cell types, such as epidermis, cortex, endodermis and so on. Epidermis is further divided into atricoblast and trichoblast. Recently, we found that atrichoblast cells possess the ability to grow more rapidly than other types of root cells, suggesting that atrichoblast cells deploy an unraveled mechanism that enables rapid cell elongation. To clarify this, we developed a photobleaching-based live-imaging system for monitoring cell elongation. In general, cell elongation is classified into two modes, diffuse growth and tip growth, and it is believed that most cells in plants undergo diffuse growth, except for specialized cells, such as root hairs and pollen tubes. Surprisingly, however, our data indicates that the atrichoblast cells grow with polarity during rapid cell elongation, reminiscent of tip growth. Moreover, we found that RHO-OF-PLANT (ROP)-mediated non-uniform distribution of actin in an atrichoblast cell is a cause of polar cell elongation. We shall also discuss a requirement of polar elongation for optimal root growth in response to environmental conditions.

Cell and Organ Size

Concurrent Speaker - Constance Musseau

Abstract Title: FUNCTIONAL CHARACTERIZATION OF A NEW PLANT DYNAMIN PROTEIN INVOLVED IN CYTOSKELETON ORGANIZATION AND CELL SHAPE

Primary Author(s) and Institution(s): MUSSEAU, Constance. 1 , JORLY, Joana. 2 , MÜLLER, Sabine. 3 , HERRMANN, Arvid. 3 , SORENZEN, Iben. 4 , ROSE, Jocelyn. 4 , CHEVALIER, Christian. 2 , ROTHAN, Christophe. 2 , GEVAUDANT, Frédéric. 1 and FERNANDEZ, Lucie. 2 1 University of Bordeaux, UMR1332 Biologie du Fruit et Pathologie, INRA Bordeaux Aquitaine, Villenave d'Ornon cedex, France 2 INRA, UMR1332 Biologie du Fruit et Pathologie, INRA Bordeaux Aquitaine, Villenave d'Ornon cedex,France 3 University of Tübingen, Center for Plant Molecular Biology, ZMBP, Developmental Genetics, Tübingen, Germany 4 Plant Biology Section, School of Integrative Plant Science, Cornell University, Ithaca, USA; University of Bordeaux

Abstract

A forward genetic strategy, combining tomato EMS mutant variability and mapping-by-sequencing (Garcia et al., 2016; Musseau et al., 2017) allowed the identification of a DYNAMIN protein, as a key regulator of tomato fruit tissue morphology. DYNAMINs (DYNs) are large GTPase that can interact with cytoskeleton-associating proteins. In animals, DYNs are reported to be involved in cytokinesis, membrane trafficking, cytoskeletal dynamics and pathogen resistance (Konopka et al., 2006; Praefcke Mcmahon, 2004) . Plants present homologs for most dynamins found in animals, with some proven to be functional redundant. However, the role and molecular mechanisms of this particular dynamin have never been described in plants so far. In order to investigate its role in plants, experiments were conducted in both tomato and Arabidopsis thaliana models. dyn mutants share common aberrant cell size and shape, affecting pericarp cells in tomato and trichomes in Arabidopsis . Aberrant Arabidopsis trichome morphology is strikingly similar to the well described Arabidopsis mutants affected in the WAVE and ARP2/3 pathways, that are involved in actin filament nucleation (Isner et al., 2017; Sambade et al., 2014; Zimmermann et al., 2004) . Our data suggest a role of this plant dynamin in actin cytoskeleton remodeling, supporting rapid cell elongation. References Catherine A. Konopka, Justin B. Schleede, A. R. S. and S. Y. B. (2006). Dynamin and Cytokinesis. Traffic , 7 (3), 239–247. http://doi.org/10.1111/j.1600-0854.2006.00385.x.Dynamin Garcia, V., Bres, C., Just, D., Fernandez, L., Wong, F., Tai, J., … Evry, F.-. (2016). Rapid identification of causal mutations in tomato EMS populations via mapping-by-sequencing. Nature Protocols . Isner, J. C., Xu, Z., Costa, J. M., Monnet, F., Batstone, T., Ou, X., … Hetherington, A. M. (2017). Actin filament reorganisation controlled by the SCAR/WAVE complex mediates stomatal response to darkness. New Phytologist , 215 (3), 1059–1067. http://doi.org/10.1111/nph.14655 Musseau, C., Just, D., Jorly, J., Gévaudant, F., Moing, A., Chevalier, C., … Fernandez, L. (2017). Identification of Two New Mechanisms That Regulate Fruit Growth by Cell Expansion in Tomato. Frontiers in Plant Science , 8 (June), 1–15. http://doi.org/10.3389/fpls.2017.00988 Praefcke, G. J. K., Mcmahon, H. T. (2004). THE DYNAMIN SUPERFAMILY : UNIVERSAL MEMBRANE TUBULATION AND FISSION MOLECULES ? Nature Reviews , 5 (February). http://doi.org/10.1038/nrm1313 Sambade, A., Findlay, K., Schaffner, A. R., Lloyd, C. W., Buschmann, H. (2014). Actin-Dependent and -Independent Functions of Cortical Microtubules in the Differentiation of Arabidopsis Leaf Trichomes. The Plant Cell , 26 (4), 1629–1644. http://doi.org/10.1105/tpc.113.118273 Zimmermann, I., Saedler, R., Mutondo, M., Hulskamp, M. (2004). The Arabidopsis GNARLED gene

encodes the NAP125 homolog and controls several actin-based cell shape changes. Molecular Genetics and Genomics , 272 (3), 290–296. http://doi.org/10.1007/s00438-004-1052-2

Cell and Organ Size

Concurrent Speaker - Natalia Wozniak

Abstract Title: MOLECULAR BASIS OF THE CONVERGENT EVOLUTION OF FLOWER MORPHOLOGY AFTER THE TRANSITION TO SELFING IN THE GENUS CAPSELLA

Primary Author(s) and Institution(s): NATALIA WOZNIAK 1 , ANAHID POWELL 1 , USHIO FUJIKURA 1 , CHRISTIAN KAPPEL 1 , MICHAEL LENHARD 1 and ADRIEN SICARD 1,2 1 Institute for Biochemistry and Biology, Universität Potsdam, 14476 Potsdam-Golm, Germany 2- Present address: Department of Plant Biology, Uppsala BioCenter, Swedish University of Agricultural Sciences, PO-Box 7080, SE-75007 Uppsala, Sweden

Abstract

A common event in the higher-plant evolution is the transition from outcrossing to selfing. In many cases this switch in mating system was followed by similar changes in flower morphology and function termed “the selfing syndrome”. One of the main features of this syndrome is a dramatic reduction of flower size. We are using the genus Capsella to study the molecular basis of the convergent evolution of flower size after the transition to selfing. In this genus, the self-incompatibility system has broken down twice independently, leading to the emergence of two selfing species Capsella rubella and C. orientalis from the outcrossing ancestor C. grandiflora . Despite evolving independently both selfing lineages have very similar flower size and shape. The reduction in the petal size has occurred in both cases through the same developmental process - a decrease in cell proliferation. This suggested a common genetic basis to the independent evolution of flower morphology after the transition to selfing. We tested this using comparative transcriptomics and QTL mapping approaches, which allowed us to identify several loci involved in the reduction of flower size in both selfing species. Here, I will present the characterisation and positional cloning of one of the common QTL.

Trafficking

Concurrent Chair - Federica Brandizzi

Abstract Title: ROLE OF MEMBRANE INTERACTION SITES IN TRAFFIC

Primary Author(s) and Institution(s): FEDERICA BRANDIZZI MSU-DOE Plant Research Lab and Plant Biology Department, Michigan State University, East Lansing, MI 48824, USA. Email: fb@msu.edu; MSU DOE-Plant Research Laboratory

Abstract

The plant secretory pathway is critical to the life of the cell and of the entire organism because it synthesizes essential proteins, lipids and carbohydrates. At the core of the secretory pathway lies the endoplasmic reticulum (ER). Protein synthesis and glycosylation as well as lipid synthesis initiate at the ER. Notwithstanding the importance of the biosynthetic ability of the ER to the life of the cell, this organelle assumes a unique structure of interconnected tubules and cisternae, which are continuously remodeled. Disruption of the morphological integrity of the ER hampers the ability of this organelle to respond to proteotoxic stress and negatively affects plant growth. Homeostasis of the ER morphology is therefore critical to sustain life and growth. Despite the incessant remodeling of the membranes of the ER, this organelle is attached to the membrane of other organelles that execute distinct functions from

those of the ER. In this talk, we will illustrate novel findings on the identity of the machinery that bridges the ER with heterologous membranes and on the function of this machinery in membrane traffic.

Trafficking

Invited Speaker - Karin Schumacher

Abstract Title: Vacuoles – Pumping up the plant volume

Primary Author(s) and Institution(s): Karin Schumacher; Centre for Organismal Studies (COS), Heidelberg University

Abstract

The presence of a large central vacuole that fulfills multiple functions in storage, detoxification and cell growth is one of the hallmarks of a prototypical plant cell. Vacuolar transport is channeled by a battery of transport proteins that are all assumed to be energized by the combined activity of two proton-pumps, the vacuolar H+-pyrophosphatase (V-PPase) and the vacuolar H+-adenosinetriphosphatase (V-ATPase). In my presentation, I will discuss the physiological roles of the two proton-pumps, their trafficking routes to the tonoplast as well as the process of vacuole biogenesis.

Trafficking

Concurrent Speaker - Marta Garcia Leon

Abstract Title: ALIX, A NOVEL REGULATOR IN THE ENDOSOMAL TRAFFICKING AND DEGRADATION OF THE ABSCISIC ACID RECEPTORS

Primary Author(s) and Institution(s): MARTA GARCIA-LEON; LAURA CUYÀS, DIAA ABD EL-MONEIM 2 , LESIA RODRIGUEZ3, BORJA BELDA-PALAZÓN; YOLANDA FERNÁNDEZ &, BRICE ROUX, ANGEL MARÍA ZAMARREÑO, JOSÉ MARÍA GARCÍA-MINA, LAURENT NUSSAUME, PEDRO L. RODRIGUEZ, JAVIER PAZ-ARES, NATHALIE LEONHARDT, VICENTE RUBIO -Centro Nacional de Biotecnología (CNB-CSIC) Darwin, 3. 28049 Madrid, Spain (M.G.-;L.; D.A.E.-M.; Y.F.; J.P.-A.; V.R.) -Department of Plant Production, Arish University, North Sinai, Egypt (D.A.E.-M.) -Instituto de Biología Molecular y Celular de Plantas (CSIC-UPV), Avda. de los Naranjos. Edificio CPI, 8E, 46022, Valencia, Spain (L.R.; B.B.-P.; P.L.R.) -Department of Environmental Biology, Agricultural Chemistry and Biology Group-CMI Roullier, Faculty of Sciences, University of Navarra, Irunlarrea 1, 31008 Pamplona, Spain. (A.M.Z.; J.M.G.-M.) -Laboratoire de Biologie du Développement des Plantes, Institut de Biosciences et Biotechnology Aix-Marseille, Commissariat à l'Energie Atomique et aux énergies alternatives, Saint-Paul-Lez-Durance 13108, France. (L.C.; B.R.; L.N.; N.L.) -Centre National de la Recherche Scientifique, UMR 7265 Biol. Végét. and Microbiol. Environ., Saint-Paul-Lez-Durance, France. (L.C.; B.R.; L.N.; N.L.) -Aix-Marseille Université, UMR 7265, Marseille, France. (L.C.; B.R.; L.N.; N.L.); CNB (Spanish National Centre of Biotechnology)-CSIC

Abstract

The plant endosomal trafficking pathway controls abundance of membrane-associated soluble proteins, as shown for abscisic acid (ABA) receptors. ABA receptor targeting for vacuolar degradation occurs through the late endosome route and depends on FYVE1 and VPS23A, components of ESCRT-I complexes. FYVE1 and VPS23A interact with ALIX, an ESCRT-III-associated protein, although the functional relevance of such interactions and their consequences in cargo sorting are unknown. Using

biochemical techniques and confocal microscopy we demonstrate that ALIX directly binds to ABA receptors at endosomes, promoting their degradation. Impaired ALIX function alters endosomal location and ABA receptor abundance. In line with this, partial loss of function alix-1 mutants display ABA

hypersensitivity during growth and stomatal closure, unveiling a role for the ESCRT machinery in the control of water loss through stomata. Interestingly, ALIX interaction with FYVE1, VPS23A and ABA receptors was disrupted when the ALIX-1 mutated version was used, highlighting the relevance of ALIX in the stabilization of ESCRT-cargo complexes, and providing a molecular basis for ABA hypersensitivity in alix-1 mutants. Collectively, our data support a role for ALIX as a bridge between ESCRT-I and -III complexes during cargo trafficking and emphasize the importance of the endosomal pathway in the modulation of ABA signaling.

Trafficking

Concurrent Speaker - Ying Fu

Abstract Title: ARABIDOPSIS RAB GTPASE-MEDIATED TRAFFICKING OF CELLULOSE SYNTHASE IS ESSENTIAL FOR HYPOCOTYL GROWTH

Primary Author(s) and Institution(s): YING FU , MING HE, MIAO LAN; LEI ZHU; MING YUAN, State Key Laboratory of Plant Physiology and Biochemistry, College of Biological Sciences, China Agricultural University, Beijing 100193, China; China Agricultural University

Abstract

In plant cells, cellulose is synthesized by cellulose synthase (CESA) complexes (CSCs) in the plasma membrane (PM). Trafficking of CSCs between endomembrane compartments and the PM is vital for cellulose biosynthesis. However, the mechanism for this process is not well understood. In this study, we revealed that Rab-H1b, a Golgi–localized small GTPase, mediates the membrane trafficking that important for distribution and function of CSCs in the PM. Loss of Rab-H1b function resulted in short, fragile etiolated hypocotyls, and rab-h1b mutant cells exhibited altered distribution and moving motility of CESA6 in the PM and reduced cellulose content. Further investigation showed that exocytosis of CESA6 was impaired in rab-h1b cells, and endocytosis from PM was retarded as well. We observed accumulation of vesicles around an abnormal Golgi apparatus with an increased number of cisternae in rab-h1b cells, indicating a defect in cisternal homeostasis caused by the loss function of Rab-H1b. Our study links Rab GTPases to cellulose biosynthesis during hypocotyl growth, and demonstrates that Rab-H1b is crucial for modulating the trafficking of CESAs between Golgi and the PM. Our finding also suggests that the role of Rab-H1b in maintaining Golgi organization and morphology is closely related to CSCs trafficking.

Trafficking

Concurrent Speaker - Jean-Marc Neuhaus

Abstract Title: FUNCTIONS OF RMR PROTEINS IN THE MOSS SECRETORY PATHWAY: SORTING RECEPTORS AND UBIQUITIN LIGASES ?

Primary Author(s) and Institution(s): NOEMIE FAHR, CARLA COPPOLA, SOPHIE MARC-MARTIN, DIDIER SCHAEFER, JEAN-MARC NEUHAUS , UNIVERSITY OF NEUCHATEL, SWITZERLAND

Abstract

The role of VSR receptors in protein targeting to vacuoles has been extensively studied in flowering plants. Another family of putative vacuolar receptors, the RMRs (Receptor Membrane RING-H2) has been identified. Their functions and mechanism are still unclear. We study them in the moss Physcomitrella patens . P. patens has five RMR genes. RMR knock-out mutants were produced but even quintuple knock-outs had no obvious phenotype. Many fluorescent reporters with sequences addressing proteins to various compartments of the secretory pathway of flowering plants were tested. A single vacuolar marker was clearly dependent on RMRs: a reporter with a VSD from cardosin A (cardoon). Its vacuolar targeting was disrupted in all mutant lines (5KO, 3KO and even 1KO). Inhibitors of the secretory pathway (BFA and Wortmaninn) inhibited vacuolar targeting of all vacuolar markers. RMR proteins belong to the PA-TM-RING family of transmembrane proteins, which in animals have been identified as E3 ubiquitin ligases (e.g. GRAIL in mammals). Ubiquitylation could play a role in protein trafficking to plant vacuoles. An in vitro assay confirmed that a moss RMR is indeed a ubiquitin ligase. A GST pull-down assay and a 2-hybrid library screen identified potential interaction partners for this moss RMR.

Friday, August 10th

Epigenetic and Genome Function
Concurrent Chair - Xiaofeng Cao

Abstract Title: MOLECULAR MECHANISMS OF HISTONE DEMETHYLASES IN SUBSTRATE SPECIFICITY AND GENOME-WIDE TARGETING IN ARABIDOPSIS

Primary Author(s) and Institution(s): State Key Laboratory of Plant Genomics and National Center for Plant Gene Research, CAS Center for Excellence in Molecular Plant Sciences, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing 100101, China;

Abstract

Transcription activity of chromatin is regulated by covalent modifications on nucleosomes and DNA. Recent efforts have identified a lot of chromatin modifiers, which play important roles in various aspects of biological processes. These chromatin modifiers normally bind a subset of specific genomic loci. Discovering the mechanisms of recruiting these modifiers is essential for understanding the biological function of them. We previously identified Arabidopsis JMJ14 and JMJ12/REF6 as H3K4 and H3K27-specific histone demethylases. Further study shows both of them bind to their target genes in DNA sequence specific ways, but use distinct mechanisms. The C-terminal FYR domain of JMJ14 interacts with a pair of NAC domain containing transcription factors, which bring JMJ14 to their common target genes; whereas REF6 recognizes its target loci by direct recognizing specific DNA sequence through its tandem C2H2-Zinc finger domains. We also solved the crystal structure of JMJ14 catalytic domain demonstrating the sequence specific recognition of the H3K4me3 substrate, indicating a conserved mechanism of substrate specificity of KDM5 subfamily both in plants and animals. In this talk, I will illustrate how DNA sequence and other chromatin features fine-tune REF6 genome-wide targeting in Arabidopsis.

Mechanisms of Biotic Interactions
Plenary Speaker - Jian-Min Zhou

Abstract Title: RLCKS AS CENTRAL COMPONENTS IN IMMUNE RECEPTOR KINASE SIGNALING AND DISEASE RESISTANCE

Primary Author(s) and Institution(s): Xiangxiu liang, Miaomiao Ma, jinlong wang, guozhi bi, zhaoyang zhou, meijuan hu, chulei gao, weibing wang, xiuming li, wei wang, jiayu wang, Jian-Min Zhou; State Key Laboratory of Plant Genomics, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing 100101, China; Institute of Genetics and Developmental Biology, Chinese Academy of Sciences

Abstract

Receptor kinases (RKs) govern transmembrane signaling that regulates plant reproduction, growth and development, and interactions with diverse microbes. Receptor-like cytoplasmic kinases (RLCKs), which lack extracellular ligand-binding domains, have emerged as a major class of signaling proteins acting directly downstream of various RKs. We have been using immune RKs as a model to understand role of RLCKs in transmembrane signaling and underlying mechanisms. We have shown that several bacterial

virulence proteins target various members of RLCK VII subfamily, such as BIK1 and PBL1, to suppress host immune signaling and promote pathogenesis, highlighting the importance of RLCKs in plant immunity. In addition, these RLCKs are rate-limiting and are dynamically controlled at levels of phosphorylation and stability. RLCKs are a point of bifurcation in immune RK signaling and regulate an array of downstream responses. The aforementioned RLCKs phosphorylate downstream signaling components to directly regulate oxidative burst, MAP kinase cascades, G protein signaling, and ion channels, culminating in coordinated defenses against pathogenic microbes. We will discuss how these findings have helped advance our understanding of RK-mediated transmembrane signaling and execution of specific cellular responses.