

HIGHLIGHTS 2018-2019

Edito

This flyer gathers a selection of significant events that paved the activity of the Biochemistry and Plant Molecular Physiology (B_&PMP) institute during 2018-2019. These relate to the organization of conferences, the scientific production, the installation of new research groups, the training and public communication initiatives, and the advertisement of upcoming events in the coming years.

We hope you will enjoy the reading.

The B_&PMP staff

CONFERENCES



12TH CONGRESS OF THE INTERNATIONAL PLANT MOLECULAR BIOLOGY

5-10 AUGUST 2018 | MONTPELLIER FRANCE

The 12th International Plant Molecular Biology meeting (IPMB2018) took place from 5 to 10 August 2018 at « Le Corum » in Montpellier. This congress, which takes place every 3 years, brought together more than 900 researchers from all over the world working in all areas of plant sciences. The last edition took place at the Iguazu Falls (Brazil) in 2015 and the previous ones in Jeju (South Korea) in 2012 and Saint-Louis (USA) in 2009. After an introductory conference of Prof. Detlef Weigel (Germany) and a keynote by Prof. Pamela Ronald (USA), participants were able to benefit from 15 plenary sessions and 48 parallel sessions to see more than 250 oral presentations and 500 posters presenting the latest advances in the field of plant sciences.

Chair and member of B_&PMP in the scientific committee:



Chair
(CNRS, B_&PMP)



Member
(CNRS, B_&PMP)

The first iPSB2018 held in Roscoff (FR) gathered 100 attendees with a common interest in applying modeling techniques to problems in plant biology. Sharing of information on studies and discussing the data underlying findings allows researchers to verify, extend, and generalize findings. Healthy and vibrant scientific communities are beacons for attracting talent that can act as a positive feedback force on the community. Moreover, scientific communities can also help identify and articulate grand challenges that can only be undertaken by collaborative groups of researchers across the globe.

We hope this international community of scientists in the field of Systems Biology will continue to grow and thrive to resolve important outstanding questions in (Plant) Biology.

It is a symbol then that the first iPSB meeting was endorsed and funded to be a Jacques Monod Conference.

This meeting led to a publication in a special issue in *Molecular Plant*:

iPlant Systems Biology (iPSB): An International Network Hub in the Plant Community

12, 727–730, June 2019



1st international Plant Systems Biology meeting September 10-14, 2018 in Roscoff (FR)

Chair of the scientific committee:



(CNRS, B_&PMP)



Christophe Maurel (B&PMP, Aqua team), was grantee of the " ERC Advanced Grant in 2017 "

The starting date of the project was october 2018



European Research Council

HyArchi project

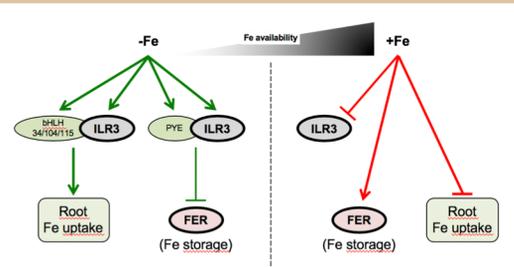
The European Research Council (ERC) is a prestigious European organism dedicated to exploratory research. The ERC advanced grant (2.5 M€ over 5 years) that was allocated to Christophe Maurel and his team provides a unique opportunity to develop an ambitious project with exciting application possibilities. The project named HyArchi will use maize as a model cereal to investigate how the architecture of the root system, its hydraulic properties and its environmental plasticity contribute to water uptake and to plant resistance to drought. Beyond a deep understanding of strategies used by plant roots to capture soil water, this project may allow to improve water management practices and introduce beneficial alleles into elite cultivars



Scientific highlights

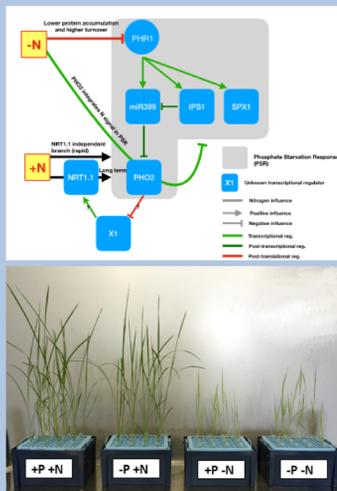
Tissot N, Robe K*, Gao F*, Grant-Grant S, Boucherez J, Bellegarde F, Maghiaoui A, Marcelin R, Izquierdo E, Benhamed M, Martin A, Vignols F, Roschttardt H, Gaymard F, Briat J-F, Dubos C (2019) [Transcriptional integration of the responses to iron availability in Arabidopsis by the bHLH factor ILR3](#). *New Phytol.*, 223(3):1433-1446

In this study, molecular, genetic and biochemical approaches were used to investigate transcriptional responses to both Fe deficiency and excess. A transcriptional activator of responses to Fe shortage in *Arabidopsis*, called bHLH105/ILR3, was found to also negatively regulate the expression of ferritin genes, which are markers of the plant's response to Fe excess. Further investigations revealed that ILR3 repressed the expression of several structural genes that function in the control of Fe homeostasis. ILR3 interacts directly with the promoter of its target genes, and repressive activity was conferred by its dimerisation with bHLH47/PYE. Last, this study highlighted that important facets of plant growth in response to Fe deficiency or excess rely on ILR3 activity. Altogether, the data presented herein support that ILR3 is at the centre of the transcriptional regulatory network that controls Fe homeostasis in *Arabidopsis*, in which it acts as both transcriptional activator and repressor.

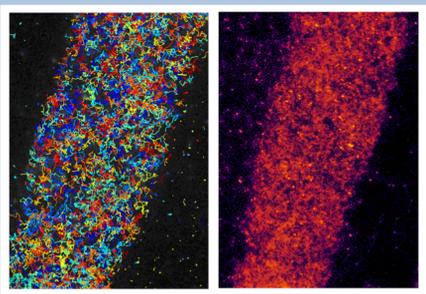


Medici A*, Szponarski W*, Dangeville P., Safi A, Dissanayake IM, Saenchai C., Emanuel A., Rubio V, Lacombe B., Ruffel S, Tanurdzic M, Rouached H, Krouk G (2019) [Identification of molecular integrators shows that nitrogen actively controls the phosphate starvation response in plants](#). *Plant Cell*, 31(5):1171-1184

Nitrogen (N) and phosphorus (P) are key macronutrients sustaining plant growth and crop yield. Understanding how plants perceive and interpret the combinatorial nature of these signals has important agricultural implications. Here we discovered an active control of the P Starvation Responses (PSR) by a combination of local and long-distance N signaling pathways in plants. We built a model for *A. thaliana* where N signal influence PSR in a framework with several molecular entry points: the nitrate transceptor (CHL1/NRT1.1), the master regulator of P sensing and signaling (PHR1), the ubiquitin conjugase PHO2. Furthermore we demonstrated that this phenomenon is conserved in rice (*Oryza sativa*) and wheat (*Triticum aestivum*) opening biotechnological perspectives in crop plants.



Platre MP, Bayle V, Armengot L, Bareille J, Marquès-Bueno MdM, Creff A, Maneta-Peyret L, Fiche J-B, Nollmann M, Miège C, Moreau P, Martinière A, Jaillais Y (2019) [Developmental control of plant Rho GTPase nano-organization by the lipid phosphatidylserine](#). *Science*, 364(6435):57-62



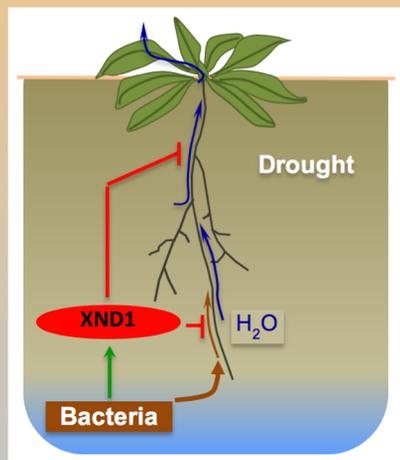
Some lipid variants that are rare in plasma membranes function as signaling components. Studying root tip cells of the model plant *Arabidopsis*, Platre *et al.* found that phosphatidylserine, which is relatively abundant in plasma membranes, also modulates signaling pathways. Phosphatidylserine is required for the clustering of ROP6, a small guanosine triphosphatase (GTPase), in membranes in response to signals from the plant hormone auxin. Changes in phosphatidylserine concentration altered the clustering of ROP6 and thus the auxin signaling response.

Scientific highlights

Ning Tang, Zaigham Shahzad, Fabien Lonjon, Olivier Loudet, Fabienne Vaillau, Christophe Maurel (Sep 2018)

[Natural variation at XND1 impacts root hydraulics and trade-off for stress responses in *Arabidopsis*.](#)

Nat. Commun. 9:3884

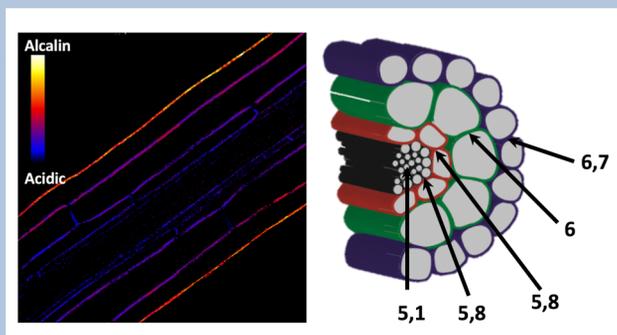


Soil water uptake by roots is a key component of plant performance and adaptation to adverse environments. Here, a genome-wide association analysis was used to identify the XYLEM NAC DOMAIN 1 (XND1) transcription factor as a negative regulator of *Arabidopsis* root hydraulic conductivity (L_p). Phenotyping of *xnd1* mutants and natural XND1 variants showed that XND1 modulates L_p through action on xylem formation and that it diminishes drought stress tolerance. XND1 also mediates the inhibition of xylem formation by the bacterial elicitor flagellin and counteracts plant infection by the root pathogen *Ralstonia solanacearum*. Thus, genetic variation at XND1, and xylem differentiation contribute to resolving the major trade-off between abiotic and biotic stress resistance in *Arabidopsis*.

Alexandre Martinière, Rémy Gibrat, Hervé Sentenac, Xavier Dumont, Isabelle Gaillard, Nadine Paris (Jun 2018)

[Uncovering pH at both sides of the root plasma membrane interface using noninvasive imaging.](#)

Proc. Natl. Acad. Sci. USA 115(25):6488-6493



The pH on both sides of the plant plasma membrane was accurately measured *in vivo* using ratiometric fluorescent sensors. This enabled noninvasive access to membrane-associated pH and transmembrane delta pH values from the surface of the root up to the deepest cell layers beyond the Casparian strip barrier. We demonstrate that despite direct contact with the soil, the apoplastic pH close to the plasma membrane was maintained at values ranging from 6.0 to 6.4 in mature root cells, whereas the overall pH in the apoplastic space is far more acidic. Furthermore, we found that the cell wall plays a role in proton homeostasis in mature root.

Mushtak Kisko, Nadia Bouain, Alaeddine Safi, Anna Medici, Robert C. Akkers, David Secco, Gilles Fouret, Gabriel Krouk, Mark G. M. Aarts, Wolfgang Busch, Hatem Rouached (Feb 2018)

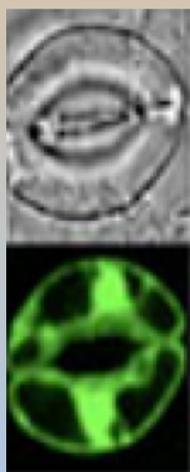
[LPCAT1 controls phosphate homeostasis in a zinc-dependent manner.](#)

eLife 7:e32077

All living organisms require a variety of essential elements for their basic biological functions. While the homeostasis of nutrients is highly intertwined, the molecular and genetic mechanisms of these dependencies remain poorly understood. Here, we report a discovery of a molecular pathway that controls phosphate (Pi) accumulation in plants under Zn deficiency. Using genome-wide association studies, we first identified allelic variation of the *Lyso-PhosphatidylCholine (PC) AcylTransferase 1 (LPCAT1)* gene as the key determinant of shoot Pi accumulation under Zn deficiency. We then show that regulatory variation at the LPCAT1 locus contributes significantly to this natural variation and we further demonstrate that the regulation of LPCAT1 expression involves bZIP23 TF, for which we identified a new binding site sequence. Finally, we show that in Zn deficient conditions loss of function of LPCAT1 increases the phospholipid Lyso-PhosphatidylCholine/PhosphatidylCholine ratio, the expression of the Pi transporter PHT1;1, and that this leads to shoot Pi accumulation.



ATIP Avenir project 2018 “Intracellular ion flux coordination, a novel perspective on the mechanisms regulating ion transport in *A. thaliana* guard cells”



A new team was created in 2019 upon arrival of Alexis De Angeli (CNRS researcher) in january shortly after he obtained an ATIP

Abstract: Ion fluxes across cellular membranes are at the basis of fundamental biological functions. In plants, fluxes of ions across cellular membranes need to be coordinated to mediate biological responses to environmental stimuli. The control of the stomata aperture depends on the capacity of guard cells to absorb/release massive amounts of ions (K^+ , H^+ , Cl^- , NO_3^- , malate $^{2-}$) in a short time scale inducing a change in osmotic pressure and trigger opening/closure of the stomata.

Signaling pathways responding to drought, light or CO_2 control the absorption/release of ions in guard cells.

Guard cells present the typical cell architecture of mature plant cells: a central vacuole occupying up to 90% of the cell volume squeezing the cytosol against the plasma membrane and the cell wall.

The large majority of ions reside in the vacuole and consequently during stomata opening/closure cross the cytosol which is a crossroad at the interface of the extracellular space and intracellular compartments.

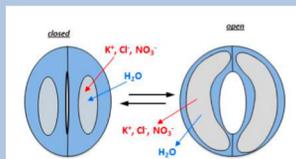
Notably, the cytosol is a minor fraction of the cell volume, thus the massive ion fluxes through the plasma and the vacuolar membranes are tightly controlled to avoid cytosolic “traffic jams”.

Despite the importance of ion flux coordination, we still have an extremely limited knowledge on the mechanisms involved in this process.

The aim of the present proposal is to decipher the mechanisms underlying the coordination of ion fluxes across the vacuolar and the plasma membranes using guard cells as a model system.

We plan to analyze the mechanisms operating for the coordination at different levels: i) the properties of ion transport systems mediating ion fluxes across the plasma and vacuolar membrane; ii) the *in vivo* dynamics of the ion concentrations in the cytosol of guard cells; iii) *in silico* modelling of ion fluxes.

We will use a combination of approaches (e.g. electrophysiology, imaging) to specifically address the different levels. We will analyze the functional specificities of a class of anion channels specific to plants being major actors of guard cell response, the ALMTs. We will use a method I developed to visualize the dynamics of anion concentration in the cytosol of guard cells with a biosensor, ClopHensor. We now have the unprecedented possibility to observe the fluctuation of ion concentrations *in vivo*. The combination of this technology with plants knockout in ion transporters will provide a mechanistic insight in ion flux coordination. The output of the project will give a completely novel perspective in the mechanisms regulating guard cell responses and more in general in (plant) cells.



Press Releases



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White lupin: the genome of this legume has finally been sequenced

January 24, 2020

BIOLOGY ENVIRONMENT



White lupin is a particularly abstemious crop, requiring very little fertiliser and producing high-protein seeds of great nutritive quality. The plant has just yielded the secrets of its genome thanks to the collaboration of eleven French and foreign laboratories coordinated by Benjamin Péret, a CNRS researcher at B&PMP (CNRS/Inrae/Université de Montpellier/Montpellier SupAgro). Lupin has the distinctive feature of possessing “proteoid” or cluster roots, which enable it to solubilise phosphate and extract it efficiently. However, similar to petroleum, stocks of this vital component are limited and currently being depleted. Knowing the plant’s genome could accelerate programmes for lupin selection and help make this legume a major asset in future plant-based protein production. The results of this project financed by an ERC Starting Grant were published on 24 January 2020 in the journal *Nature Communications*:

[High-quality genome sequence of white lupin provides insight into soil exploration and seed quality.](#) [Bárbara Hufnagle](#), [André Marques](#), [Alexandre Soriano](#), [Laurence Marquès](#), [Fanchon Divol](#), [Patrick Doulmas](#), [Erika Sallet](#), [Davide Mancinotti](#), [Sébastien Carrere](#), [William Marande](#), [Sandrine Arribat](#), [Jean Keller](#), [Cécile Huneau](#), [Thomas Blein](#), [Delphine Aimé](#), [Malika Laguerre](#), [Jemma Taylor](#), [Veit Schubert](#), [Matthew Nelson](#), [Fernando Geu-Flores](#), [Martin Crespi](#), [Karine Gallardo](#), [Pierre-Marc Delaux](#), [Jérôme Salse](#), [Hélène Bergès](#), [Romain Guyot](#), [Jérôme Gouzy](#) and [Benjamin Péret](#). *Nature Communications*, January 24 2020.



White lupin has a root system that is highly adapted for poor soils thanks to its proteoid or cluster roots, which allow it to extract phosphate from the soil very effectively. The mapping of its genome represents a major step toward understanding this mechanism.

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New funded research projects

Results of the 2019 call for proposal of The French research funding (ANR)

The results of the ANR generic call for projects have been published. The balance sheet is exceptionally positive for B_&PMP with 6 accepted projects.

PHLOWZ: System Level Understanding of Zinc and Phosphate Signaling Crosstalk

ABSTRACT: Phosphate (Pi), a major cell component, is a strategically important plant resource due to the impending shortage of high-quality sources of this element. Diminishing the use of Pi in crop production requires a better understanding of the factors that stimulate Pi uptake. It has been widely observed that plants exposed to Pi and Zinc (Zn) deficiencies accumulate more Pi than when they are in more Zn-rich soils. Current data suggest that a specific signaling pathway is involved in the crosstalk between Pi and Zn homeostasis. Although some regulators have been identified recently, most of the early players involved in this pathway remain unknown. The PHLOWZ project aims to clarify the early events involved in this crosstalk, using live imaging of changes in Zn and Pi homeostasis and transcriptomics. PHLOWZ will combine these results with the power of GWAS studies and reverse genetics to identify new early players and regulatory nodes of the Zn/Pi pathway. The discovery of these regulators will have great significance for basic research and agronomical applications. Hélène Javot and **Hatem Rouached** (Research Associate INRA, B_&PMP)

CellOsmo: Cell membrane nanodomains: a role in plant osmotic stress signalling

ABSTRACT: Climate change, world population growth and decrease in agricultural lands impose strong constraints on ecosystems, as is the case of water bio-availability. In the coming decades, it will be mandatory to adapt food production in a more thrifty way, as agriculture is the first user of fresh water stocks. Acquiring fundamental knowledge on plant water usage is consequently becoming a challenge.

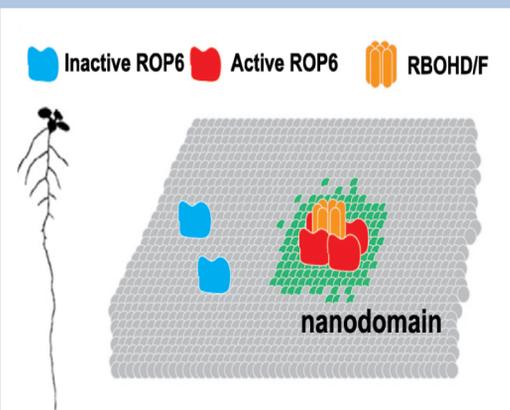
Whereas phenotypic plasticity of plant (growth and organogenesis) in response to water scarcity is well study, very little is known about the cell signaling events that lead to perception and transduction of the hydric signal.

CellOsmo aims at (i) identifying new genetic factors that are involved in this perception pathway, but also (ii) finding allelic variants from natural population by association genetic.

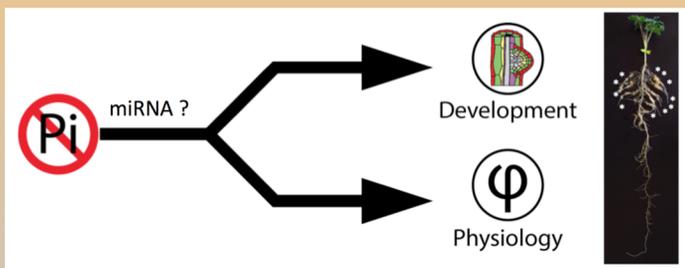
However, one of the major short-term impacts of this work is our future ability to question the relation between stress perception and plant phenotypic plasticity.

Especially, (i) how does osmotic perception influence plant fitness and (ii) do allelic variations in genes involved in osmotic perception impact plant adaptation to their environment? Answering these two questions is a prerequisite to further determine if the molecular players involved in osmosensing may be ultimately used in crop selection

Alexandre Martinière (Research Associate CNRS, B_&PMP)



MicroLUP: Deciphering how miRNAs control cluster root development in white lupin



ABSTRACT: White lupin can form cluster roots as an adaptation to low phosphate, allowing an efficient acquisition of this fundamental nutrient for plant growth. Transferring this ability to other crops would help sparing the limited stocks of phosphorus. Indeed, experts predict that massive use of fertilizers will lead to an exhaustion of rock phosphorus stocks in the coming decades. In order to better understand the molecular mechanisms controlling cluster root formation, the MicroLUP project will study the role of microRNAs during the development of this organ.

The project gathers a consortium of 3 partners including the team of Benjamin Péret (Scientific coordinator – root development specialist – B&PMP unit), Martin Crespi (miRNA specialist – IPS2 unit) and Adnane Boualem (TILLING platform – IPS2). Based on preliminary data and analysis, we have identified potential miRNAs targeting known genes, including transcription factors from the GRAS family. The MicroLUP project will analyse and create gene/miRNA networks supported by the study of organ-deregulated mutants (identified by Partner 1) to help selecting regulatory miRNA candidates involved in cluster root formation (Partner 2). Functional analysis of these candidates will be performed in planta using transient transformation, expression studies and mutant production (Partner 1). In parallel, the generation of a TILLING population using EMS-mutagenized seeds produced by Partner 1 will be amplified and screened to find additional white lupin mutants (Partner 3). This project will combine the development of gene regulatory networks involving miRNAs and their target genes and the generation of genetic resources through TILLING that can be used to improve our understanding of cluster root development as well as for field applications. We predict that MICROLUP will open wide perspectives to improve other crop root systems through translational biology in the future. **Benjamin Péret** (Senior Scientist CNRS, B&PMP)

SCOOP: Selecting for cooperative crops to develop sustainable agriculture

ABSTRACT: Agriculture is nowadays challenged by the need to ensure crop production while limiting environmental costs. Breeding for cooperative phenotypes that do not invest resources in competitive interactions at high planting density could help sparing natural land from conversion to agriculture. In SCOOP, we use durum wheat as model plant and take an integrative approach linking evolutionary biology and functional ecology. We will address three main questions: (1) Which phenotypes and alleles are cooperative at high planting density? (2) Has cooperation evolved during domestication and breeding? (3) Which breeding schemes can select for cooperation? . **Hélène FREVILLE** (**Jean-Benoît Peltier** Research Associate INRA, B&PMP)



DEFIMAN: Molecular bases of plant adaptation to manganese deficiency

ABSTRACT: Manganese (Mn) is a precious nutrient for plants, which use it as an enzymatic cofactor. Low availability of Mn occurs frequently in soils and represents a challenge to plants. In addition, the amount of Mn contained in the seed has proven crucial for seedling vigor.

To cope with Mn shortage, plants produce the NRAMP1 high affinity Mn transporter at the root surface and adapt to fluctuations of Mn by tightly controlling its membrane trafficking.

In addition to NRAMP1, a complex set of transporters, most of which still uncharacterized, achieve Mn distribution to the main plant organs and target cell compartments.

The objective of the DEFIMAN project is to combine the complementary expertise of 2 partners and use the knowledge generated to unravel the molecular bases of plant adaptation to Mn availability. We propose to address the following 3 specific aims:

1) **To understand how root Mn uptake adapts to variation of Mn in the soil**, we propose to decipher the mechanism of post-translational regulation of NRAMP1, more specifically the phosphorylation and ubiquitination events.

Since Mn triggers transient calcium release in roots, part of the work will target Ca²⁺-activated kinases (CIPKs, CPKs).

2) **We wish to enlarge the inventory of genes involved in the overall process of Mn accumulation in seeds to help design biofortification strategies.**

To identify new actors, we will study the natural variation of the complex trait of the efficiency of Mn allocation to the seeds by classical QTL analysis and through GWAS study.

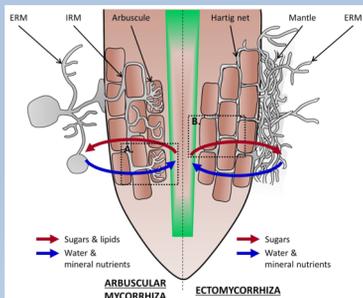
3) To study these genes, **we sought to equip the community of Mn scientists with tools to image Mn in cells.** This consortium brings the necessary skills to achieve elemental mapping of Mn in seeds by synchrotron μ XRF; Moreover we will attempt to implement chemical probes and genetically-encoded sensors with specificity for Mn.

A better knowledge of the regulatory processes of the Mn transporters involved will provide a toolbox to efficiently manipulate Mn concentration in plants. (Catherine Curie Research Director CNRS, B&PMP)

MYCOTRANS: Role of mycorrhiza-induced fungal transporters in ectomycorrhizal symbiosis



ABSTRACT: MYCOTRANS aims at producing basic knowledge on the functioning of symbiotic exchange between plant roots and fungal symbiont, a beneficial interaction crucial for plant nutrition and adaptation. Transcriptional studies have revealed mycorrhiza-induced fungal membrane transport systems that need to be analyzed with respect to their molecular function, cellular and subcellular localization, regulation and physiological role in the mycorrhiza. So far, we have studied transport of macronutrients as potassium and phosphate. MYCOTRANS will focus on the most mycorrhiza-induced transporter putatively involved in micronutrient transport within the ectomycorrhizal model *Hebeloma cylindrosporum* – *Pinus pinaster*. To dissect the physiological role of candidate genes, the gene editing approach CRISPR/Cas will be developed. Analyses of the mycorrhizal proteome will give further clues on the regulation of fungal membrane proteins by the symbiotic regulation of the host plant. **Sabine Zimmermann** (Research Associate CNRS, B&PMP)



Guerrero-Galán et al., 2018, [The Role of Plant Transporters in Mycorrhizal Symbioses](#). ABR 87, 303-342. Chapter10 in "Membrane Transport in Plants", Elsevier.

Results for The iSITE project MUSE (Montpellier University of Excellence) 2019



Winner of the I-Site MUSE's 2018 Call for Proposals for Research Support, the "eCO₂THREATS" project focuses on an aspect of global change that is still unknown and misunderstood: the negative effect of rising atmospheric CO₂ on the mineral status of plants and the threat it poses to the nutritional quality of the food of the future.

The iSITE project MUSE (Montpellier University of Excellence) to which B_&PMP contributes was launched in 2017. Its main objective is to structure the Life Sciences community of Montpellier. MUSE gathers 120 research units and focusses on scientific questions related to three main research communities that are strongly represented in the Montpellier area: (i) Animal and Medical sciences, (ii) Ecology and Environment, and (iii) Plant Sciences and Agronomy. Despite its recent creation (2017), MUSE already funded around 70 competitive research projects, among which 10 major ones in 2018. **One of the major projects (360 k€) is coordinated by B_&PMP**, highlighting our visibility in the iSITE.

ABSTRACT: As a main driver of climate change, rising atmospheric CO₂ concentration poses a major environmental threat to the future of human civilizations. Indeed, increasing evidence show that eCO₂ will have a strong negative impact on the mineral nutrition of most crops, thereby lowering their nutritional value and raising concern about human nutrition and health. eCO₂THREATS is a fully integrated and multidisciplinary project funded by MUSE, addressing scientific questions associated with the consequences of rising atmospheric CO₂ on crop productivity and crop quality for human nutrition. The main objective is to acquire knowledge on key fundamental issues associated with unresolved questions on how plants adapt to elevated CO₂, and propose solutions to maintain and improve crop yield and nutritional value under future climate.

Alain Gojon (Research Director INRA, B_&PMP)



Interactions with the public

fête de la Science **JEUDI 12 OCTOBRE de 9h00 à 17h30**
LES PLANTES : DE LA MOLECULE A L'ENVIRONNEMENT

B_gPMP is participating every year in the 'Fête de la Science' national event. The aim is to open the doors of the research institutions to welcome the public interested in learning more about research in France. Together with another research unit (UMR LEPSE), B_gPMP welcomes during one day about 50 pre-graduate students to explain them the objectives and activities associated to our scientific projects. We show them how a set of complementary technologies is used into a coherent approach to clone a gene, discover the function of the protein it encodes, locate its expression in the plant, determine the conditions of this expression, and finally characterize the resulting physiological function and phenotype for the plant. On this occasion the students participate in seven workshops presented by the scientists and technicians of both B_gPMP and LEPSE.

Training

Mistral Montpellier Bienvenue

July 2 - 13, 2018

Mistral Montpellier

Montpellier International School on ion and water TRANSPORT in Plants

In higher plants, autotrophy and biomass production involve assimilation of CO₂ from the atmosphere, as well as uptake and transport of mineral nutrients and water from the soil. Gaining fundamental knowledge on the uptake and transport functions is becoming of crucial importance.

The biology of ion and water transport in plants involves specific concepts and methods that are generally not acquired during classical Master and PhD studies. The MISTRAL summer school on ion and water transport in plants puts emphasis on such concepts and methods.

More information on the 2018 session website:

<https://workshop.inra.fr/mistral>



Coming in 2020....

Arrival of two new research scientists

Enric Zelazny, CNRS Research scientist (Aqua team)



Enric moves from the Institute for Integrative Biology of the Cell (CNRS, Gif-sur-Yvette, France)

to B&PMP, to develop a novel research program on membrane microdomains, with special emphasis on the role of HIR proteins. The cellular dynamics of these proteins and their putative role in regulation of aquaporins or NADPH oxidases within membrane microdomains will be investigated.

Sandra Cortijo, CNRS Research scientist (Integration team)



Sandra comes from the Sainsbury Laboratory of Cambridge University in England

She was post-doc in the group of James Locke, studying inter-individual gene expression variability in *Arabidopsis thaliana*. Inter-individual gene expression variability has been proposed to be beneficial for populations when environmental conditions are unpredictable and potentially challenging. The project of Sandra at B&PMP will focus on the regulation and consequences of gene expression variability for N nutrition in *Arabidopsis*. To answer this question, she will use a combination of genetic, genomic and cellular approaches.

Coming in 2021....

iPSB 2021

The 2nd international Plant Systems Biology meeting will be held in Venice, Italy, from 21-25 Sept 2020

NEW DATES

Second **iPSB** INTERNATIONAL PLANT SYSTEMS BIOLOGY - 2021
 EMBO Workshop 26-30 April 2021, Venice (Italy)

Joe Ecker
Keynote Speaker

Pamela Ronald
Keynote Speaker

#iPSB2021 Board

S. Brady, G. Coruzzi, G. Krouk, K. Denby

M. Gifford, P. Falter-Braun, R. Gutierrez, S. Rhee

See you in the Spring!

Contact: ipsb2021embo@gmail.com
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