



B&PMP presentation



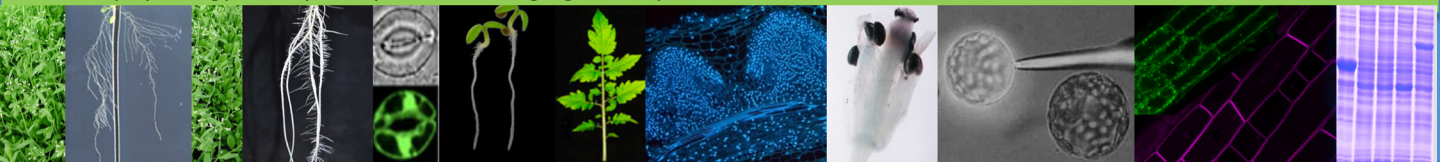
Director: Alain Gojon

Deputy director: Christophe Maurel

Administrative manager: Perrine Rudinger

B&PMP has predominantly a research activity, aiming at elucidating the molecular mechanisms involved in the water and mineral nutrition of plants, and at integrating these mechanisms into the whole plant. The focus is on (i) membrane and long-distance transport of water and mineral nutrients (nitrate, potassium, phosphate, iron, zinc, etc...), (ii) storage and metabolism of these nutrients, (iii) signaling pathways ensuring the regulation of these processes and (iv) developmental responses to changes in water or nutrient availability.

A main objective is to characterize the role of the above molecular mechanisms in the adaptive responses of the plants to abiotic stresses (drought, salinity, nutrient deficiency, metal toxicity). Most research projects are using model species (*Arabidopsis*, *Medicago*), but also involve work on crops (rice, wheat, grapevine, lupin, tomato, maize) and symbioses (mycorrhizae, legumes). The experimental strategies are those of the Integrative Biology approach, and mostly rely on genomics (transcriptomics, proteomics, gene network modeling) and on functional and developmental phenotyping (electrophysiology, isotopes, hydraulics, imaging, root system architecture).



Significant publications

B&PMP in brief

Staff in 2019 :

- 81 permanent staff, including 43 scientists and 38 engineers /technicians/administrative assistants.

- 98 non-permanent staff (post-docs, CDD, graduate and undergraduate students).

Publications : 38 in 2017, 33 in 2018 and 52 in 2019.

Funding 2052 (excluding salary of permanent staff and PhD students) :

1 762 k€, including 540 k€ of recurring State allocations and 1 222 k€ from competitive grants.

Demes E, Besse L, Cubero-Font P, Satiat-Jeunemaître B, Thomine S, De Angeli A (2020) [Dynamic measurement of cytosolic pH and \[NO₃⁻\] uncovers the role of the vacuolar transporter AtCLCa in cytosolic pH homeostasis](#). *P. Natl. Acad. Sci. USA*, 117(26):15343-15353

Bárbara Hufnagel, André Marques, Alexandre Soriano, Laurence Marquès, Fanchon Divol, Patrick Doumas, 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 (2020) [High-quality genome sequence of white lupin provides insight into soil exploration and seed quality](#). *Nat. Commun.*, 11(1):492

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

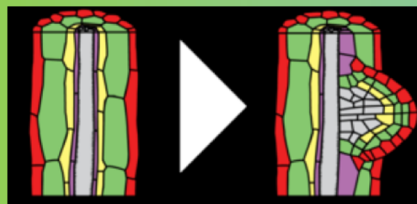
Medici A*, Szponarski W*, Dangeville P, Safi A, Dissanayake IM, Saenchai C, Emanuel A, Rubio V, Lacombe B, Ruffel S, Tanurdzic M, Rouached H, Krouk G (2019) [Identification of molecular integrators shows that nitrogen actively controls the phosphate starvation response in plants](#). *Plant Cell*, 31(5):1171-1184

Ning Tang, Zaigham Shahzad, Fabien Lonjon, Olivier Loudet, Fabienne Vailleau, Christophe Maurel (2018) [Natural variation at XND1 impacts root hydraulics and trade-off for stress responses in Arabidopsis](#). *Nat. Commun.* 9:3884

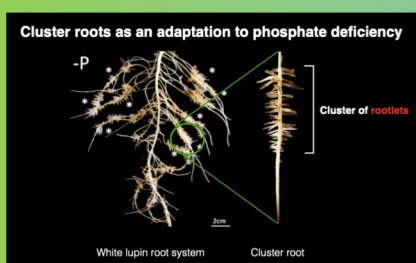
Alexandre Martinière, Rémy Gibrat, Hervé Sentenac, Xavier Dumont, Isabelle Gaillard, Nadine Paris (2018) [Uncovering pH at both sides of the root plasma membrane interface using noninvasive imaging](#). *P. Natl. Acad. Sci. USA* 115(25):6488-6493

« Development and Plasticity of the Root System (*Placticity*) »

Group Leader: Benjamin Peret - benjamin.perret@cnr.fr



Plants show a strong level of developmental plasticity that is controlled by a complex combination of perception, integration and response. Root system is a fantastic tool to study this plasticity since the number and position of lateral roots is deeply altered by the environment. The « Development and Plasticity of the Root System » team studies the fundamental mechanisms of root development and its plasticity, focussing on two plant models, *Arabidopsis thaliana* and white lupin (*Lupinus albus*). White lupin is a Legume pulse, that has the ability to produce cluster roots. These structures are developmental adaptations to low phosphate. Recent work has generated numerous tools in white lupin (high quality genome sequence and assembly, root mutants from a mutagenized population, detailed transcriptomics datasets...). Funding sources are european (ERC, Post-doctoral grants), national (ANR) and local (Labex Agro, Doctoral grants).



« Electrophysiology of plant nutrition and root symbioses (*Elsa*) »

Group Leader: Hervé Sentenac - herve.sentenac@inra.fr

Our group is interested in the role of ion channels and ion transporters in mineral nutrition and interactions of the plant with symbiotic microorganisms (ectomycorrhizae, nitrogen-fixing rhizobia, plant growth promoting rhizobacteria). The model organisms are the ectomycorrhizal fungus *Hebeloma cylindrosporum* in interaction with the pine *Pinus pinaster*, the legume *Medicago truncatula* in interaction with nitrogen-fixing rhizobia *Sinorhizobium meliloti*, and the model plant *Arabidopsis thaliana* in interaction with plant growth promoting rhizobacteria.

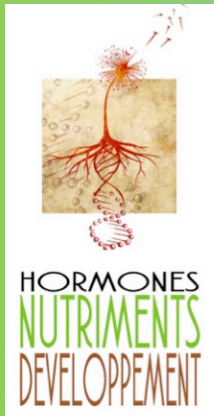
The developed strategies include molecular and cell biology, reverse genetics, electrophysiology and whole plant biology.

The objective is to describe physiological functions and roles of the involved transport systems and to get an integrative view of their contribution to the plant mineral nutrition, root symbioses and adaptation to environmental conditions.



« Hormones, Nutriments Développement (HoNuDe) »

Responsable : Benoît Lacombe - benoit.lacombe@supagro.fr



We develop complementary approaches to understand the molecular basis of development regulated by the hormone-nutrient interactions. We focus on interactions during root development with different approaches taking advantage of our skills in biophysics, molecular and cellular biology, physiology and systems biology. The project uses an approach at the interface between biology and modeling to reveal the molecular mechanisms involved in the interaction between nutritional and hormonal signals in plants. Our goal is to identify the mechanisms through which plants perceive their mineral environment and modify their development to adapt to nutritional constraints by using complementary approaches: targeted approaches on different nitrate, auxin, ABA and cytokinins transporters, and approaches without preconceptions using systems biology.

« Integration of Nutrient Signaling (Integration) »

Group Leader: Alain Gojon - alain.gojon@inra.fr



Our group investigates the mechanisms governing the uptake of nitrate by plant roots, focusing on two main components controlling root nitrate acquisition: the membrane transport systems for nitrate and the root system architecture. The main aim is to identify molecular mechanisms allowing the plants to modulate root nitrate uptake in response to changes in external nitrate availability or in their own nutritional status (N starvation or satiety, fluctuations of photosynthesis, CO₂ elevation). We mostly work on *Arabidopsis thaliana*, using molecular physiology, functional genomics and systems biology approaches: transcriptomics, gene networks modeling, proteomics, reverse genetics, functional phenotyping, root architecture analysis, imaging, isotope labeling.

« Iron Transport and Adaptation to Environment in Cereals (*Elsa*) »

Group Leader: Anne-Aliénor Véry – anne-alienor.very@supagro.fr



The team investigates the role of transporters and ion channels in the mineral nutrition of the plant and its adaptation to abiotic stresses: K^+ deficiency, salt or water stress or soil contamination with toxic monovalent cations like Cs^{+137} in relation with Fukushima accident (collaboration with Japanese teams and CEA).

The plants studied are mainly cereals (rice , barley, wheat), rice being selected as a model species.

Targeted transport systems mainly belong to the family of K^+ and / or Na^+ HKT transporters, and families of K^+ carriers or channels (KUP / HAK and Shaker).

« Ion Flux Coordination and signaling in plant cells (*Influx*) »

Group Leader: Alexis De Angeli- alexis.de-angeli@supagro.fr



The group's objective is to understand the molecular mechanisms involved in the regulation and coordination of ion flows through plant cell membranes, using guard cells of *A. thaliana* stomata as a model.

The opening and closing of the stomata depend on the ability of cells to generate and control massive flows of ions (e.g. Cl^- , NO_3^- , malate $^{2-}$, K^+ , Ca^{2+} and H^+) through the plasma and vacuolar membrane. Guard cells are an ideal paradigm for the study of ion flow coordination and, in addition, are important for the adaptation of plants to the environment. We use different experimental approaches:

(i) Electrophysiology (TEVC patch-clamp) for the study of the biophysical properties of plasma and vacuolar membrane ion transporters with specific interest in the ALMT (Aluminum Activated Malate Transporters) anion channels.

(ii) Cell imaging coupled with genetically coded fluorescent probes to visualize the dynamics of intracellular ion concentrations (e.g. NO_3^- , Cl^- and H^+) and transporter activity *in vivo*.

(iii) Genetics and physiology.

(iv) Mathematical models.

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

« KaliPHruit »

Group Leader: Isabelle Gaillard - isabelle.gaillard@inra.fr

The aim of the KaliPHruit team is to characterize the molecular and functional gene combination involved in the control of grape berry acidity in relation with the potassium (K^+) accumulation in the context of the climate change. Potassium (K^+) ions accumulate during berry ripening and are involved in the neutralization of organic acids. However, K^+ content of grape berries has been steadily increasing over the last decades, in part due to warmer climate, resulting in berries with a low acidity level at harvest and consequently unbalanced wines with poor organoleptic quality. The team combines multidisciplinary approaches extending from molecular biology, modern transcriptomic methods, biochemical studies, electrophysiology and plant physiology, with a continuum of scales from gene to whole plant. We are working on K^+ transport systems and their regulators, in relation with H^+ distribution in berry at the subcellular scale obtained with live cell imaging and fluorescent pH sensors. In addition, a part of our program also looks at molecular mechanisms involved in nutritional benefits of the mycorrhizal symbiosis in grapevine and in a better adaptation of the host plant towards abiotic stress.

« Metal mobility (Memo)»

Group Leader: Cathy Curie – catherine.curie@cnr.fr

Our team studies iron (Fe) and manganese (Mn) homeostasis in the flower plant *Arabidopsis thaliana* and the moss *Physcomitrella patens*. Our objective is to understand the mechanisms by which plants cope with Fe or Mn scarcity in soils. To that aim, we focus on membrane transporters and their regulators, which we study through a combination of approaches including biochemistry, cell biology, analytical chemistry, physiology and molecular biology.

« Metal phytotoxicity »

Co-responsible : Françoise Gosti – francoise.gosti@inra.fr et Claude Nespoulous - claud.nespoulous@inra.fr

The Metal phytotoxicity team study plant adaptation to heavy metals taking advantage of extremophile species, which can tolerate and hyperaccumulate metals without sign of toxic symptoms. We use molecular genetic approaches to decipher gene expression modification and genomic organisation occurring in *A. halleri* extremophile as compared to the closely related model *A. thaliana*. In parallel, we perform biochemical analysis to understand protein mode of action.

Following this rationale we could study 2 major actors of plant transport and storage, the *Heavy Metal ATPase type 4* and the *Metal Tolerance protein 1* and discovered that, beside their role in response to pathogens, plant defensins are part of the arsenal developed by plants to withstand zinc toxicity. We are presently studying their role *in planta* and their mode of action.

« Mineral Nutrition and Oxidative Stress (*FeRos*) »

Group Leader: Christian Dubos – christian.dubos@inra.fr



Iron is an essential micronutrient for plant growth and development as it is an essential cofactor in many biological processes involving electron transfers such as photosynthesis or respiration.

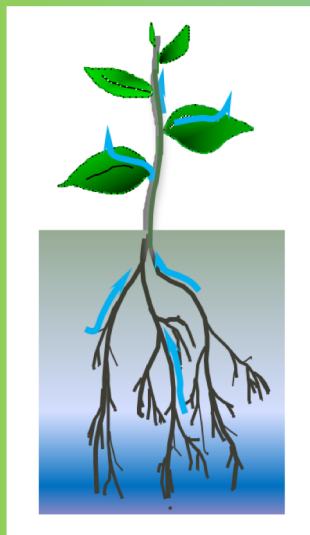
The availability of this micronutrient in the soil has a direct influence on the productivity of crop species, as well as on the quality of their derived products, particularly for human nutrition and health.

In order to avoid any deficit or excess that could be detrimental their metabolism, plants have evolved molecular mechanisms to finely tune iron uptake, assimilation and storage.

In this context, our research aims at (i) characterizing the molecular mechanisms involved in the control of iron homeostasis in plants, (ii) studying the dynamics of coumarin secretion in the soil by plants to improve iron nutrition and (iii) characterizing the assembly machinery of Fe-S clusters in chloroplasts and mitochondria, a key step in iron assimilation.

« Water, signaling and hydraulic architecture (*Aqua*) »

Group Leader: Christophe Maurel - christophe.maurel@cnrs.fr



The *Aqua* team studies the different modes of water transport in plant tissues. The main objective is to understand how these processes are regulated and linked to plant growth and responses to environmental stresses. Supported by national (ANR) and European (ERC) funding, the team combines studies on the model plant *Arabidopsis thaliana* and maize.

A first axis concerns cell signalling processes. The early mechanisms of plant response to water stress are investigated through molecular (interactomics, proteomics) and high-resolution microscopy approaches, with a particular focus on the role of reactive oxygen species and protein phosphorylation. A second axis concerns the hydraulic architecture of roots. Quantitative genetics, root phenotyping and mathematical modelling are combined to describe the dynamics of root growth and hydraulics. The aim is to understand how they adapt to environmental constraints and water stress in particular, by integrating local and systemic signalling processes.

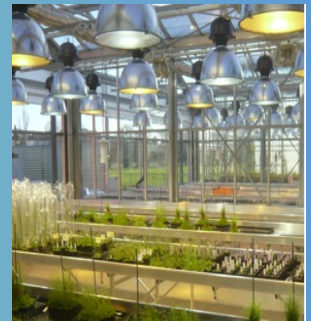
B&PMP and training

B&PMP is strongly involved in higher education training with University of Montpellier and SupAgro engineering school, particularly at master level and the doctoral school GAIA. Since many years, B&PMP annually organise thematic schools for french and foreign students training.

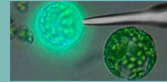
Plant culture facilities



B&PMP hosts state-of-the-art facilities that allow researchers to grow various plant species under controlled conditions. These facilities can be grouped into 2 categories: controlled conditions greenhouses that comply with S2-level of confinement for transgenic plants production, and artificial conditions devices (17 growth chambers and 7 phytotronic cabinets). In addition to providing a precise control of aerial environmental conditions, phytotrons and growth chambers are extensively used for growing plants in hydroponics as it allows easy access to the roots and enables a fine monitoring of the mineral nutrition.



Heterologous Expression and Electrophysiology Platform



Molecular analysis of membrane transport of water and mineral ions in plants requires the identification of proteins responsible for these different transports. A plant has several hundreds of different proteins performing this function, often specific (e.g., for potassium, nitrate, iron, water, etc ...). Therefore, one must be able to isolate them and study them separately.

The heterologous expression and electrophysiology platform of B&PMP is a unique device in France dedicated to this type of work for plant proteins. It allows in particular characterizing in detail the activity of membrane transport proteins by measuring the electrical signature of their activity, due to the fact that most nutrients are transported in an ionic form. This platform is largely open to outside users.



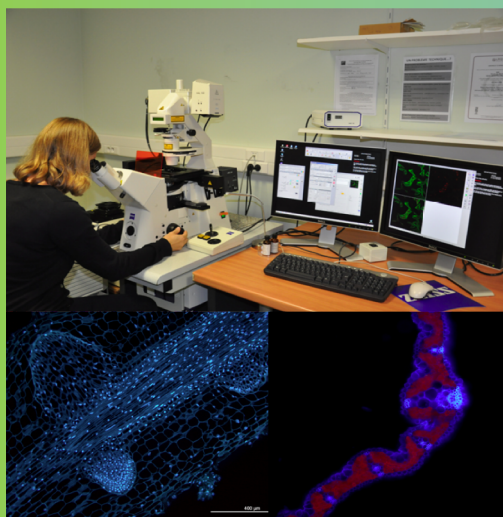
Stable Isotope Analytical Platform (AIS)



The AIS is a platform fulfilling a national analytical service for INRAE, but it is also open to other French and foreign users.

The AIS is devoted to the analysis of stable isotopes of nitrogen and carbon (^{15}N and ^{13}C) in plant samples (mostly). As such, it is strictly necessary for supporting research projects aiming at investigating transport of nitrogen (nitrate, ammonium, amino acids) or carbon (sugars, carboxylic acids) compounds. It makes it possible to perform tracer experiments for quantifying fluxes of these compounds between the external medium and the plant, and between the various plant organs.

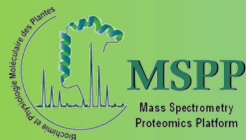




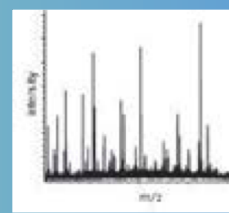
Understanding the integrated function of genes and proteins in the whole plant requires the determination of their expression sites. This is made possible with various imaging techniques that enable visualizing gene activation and protein localization in each plant cell.

To run these techniques, B_&PMP has developed a histocytology and plant cell imaging platform (PHIV), together with the AGAP laboratory. This platform is located on two different sites: SupAgro-INRA campus (PHIV – La Gaillarde) for B_&PMP, and CIRAD campus (PHIV-Lavalette) for AGAP. PHIV is part of the large regional MRI platform (www.mri.cnrs.fr, ISO9001 and NFX 50-900 certification), and gathers a team of technicians, engineers and researchers making available a large palette of plant imaging skills and facilities to research groups (plant anatomy, histocytology, *in situ* hybridization, immunofluorescence, live cell imaging microscopy, spectral imaging, fluorescent and luminescent probes, biosensors).

Mass Spectrometry Proteomics Platform (MSPP)



Changes in the abundance and/or activity of key proteins play a major role in the response of plants to adverse environmental conditions. The objective of MSPP (Mass Spectrometry Proteomics Platform of B_&PMP) is to develop skills and expertise in the fields of protein identification, molecular characterization of their post-translational states and protein quantification by mass spectrometry. MSPP is one of the two mass spectrometry sites of the Pôle Proteome of Montpellier (PPM). PPM is certified ISO 9001, and has national (GIS IBISA) and regional (Large Equipment for Technological Evolution and Scientific Initiation) labels.



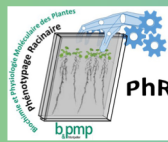
Technology Platform GeneAtlas® System

B_&PMP is equipped with the GeneAtlas System from Affymetrix Company, which allows fast acquisition of genome-wide transcriptome data by hybridization of microarrays. To date, the system provides access to gene expression in several species such as *Arabidopsis thaliana*, *Medicago truncatula*, soybean and rice. For example, Arabidopsis microarrays provide expression data for more than 28,000 genes, including precursors of miRNAs.



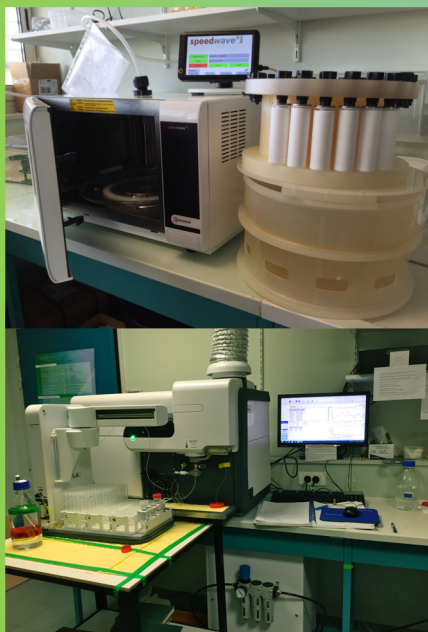
This facility is a key tool for developing Systems Biology approaches, involving systematic and iterative strategies in which each transcriptomic analysis feeds the elaboration of models of gene regulatory networks that control nutrient homeostasis in plants.

Root phenotyping Platform



The Root Phenotyping facility is dedicated to kinetic and non-destructive analysis of seedling root system architecture of many species including *Arabidopsis*, rice, tomato, rapeseed, and *Medicago*.... grown *in vitro*. Its main objective is to develop approaches, tools and methods to characterize the effect of different stresses, nutrient deficiency or excess, or biotic interactions alone or in combination providing the basis for further genetic and molecular physiology approaches. The phenotyping facility includes a self-contained imaging unit that can handle up to 200 plates at 12µm resolution with high contrast. Images are analyzed through semi-automated or fully automated pipelines integrated in the OpenAleaLab suite (<https://team.inria.fr/virtualplants/software/>).

Technological platforms



Multi-Elemental Analyses Platform (SAME)



The Multi-Elemental Analyses Service (SAME), created in July 2016, is devoted to the atomic quantification from plant samples (roots, leaves, fruits, seeds, cellular fluids...) as well as from soil materials. Basically, the samples (dry material) are digested by acidic hydrolysis that disrupts molecular structures to release their atomic content (phosphorus, calcium, magnesium, sodium, iron, zinc...). After this hydrolysis step, the chosen elements are quantified by atomic emission spectrometry. The service proposed by the platform includes the hydrolysis of the samples, the choice of elements and the quantification by spectrometry. The equipment is composed of a microwave with 2x24 reactors for the acidic digestions and a microwave-plasma atomic emission spectrometer (MP-AES, Agilent) equipped with an autosampler.

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