

Plant roots: major scientific challenges – key areas of research of relevance to the French public-private research community

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A one-day workshop on “Plant Roots” was organised by the GIS BV and the AllEnvi Alliance in Montpellier on February 27th 2012. It brought together 45 scientists and laboratory representatives from the French public and private research community. The workshop demonstrated the strength of the French research community, originating from various research organisations and areas of expertise, in this internationally competitive research field. The position paper reflects the presentations and discussions of the “Plant Roots” workshop and summarizes the areas of research to which the French public and private research community would be particularly fit to contribute, through trans-disciplinary and translational projects. This position paper is endorsed by the Governing Council of the GIS BV and by the working group “Plant Biology and Biotechnologies” of the AllEnvi Alliance.

1

The continuously developing root system of plants adapts to endogenous and environmental cues to optimize water and nutrient uptake. This adaptation is made possible through the plasticity of root development (root growth and branching) and physiology, and through root interactions with beneficial soil microorganisms. In the context of climate change, of increasing soil degradation and of water and mineral resources scarcity, breeding crops with more efficient root systems is a highly desirable target. A number of French research groups working on root system development, adaptation to the environment, and root-rhizosphere interactions, may contribute to this internationally important challenge.

Root system architecture: regulation and plasticity

A lot of information about root developmental plasticity has been gathered from numerous studies on model plant species. Today, an

urgent effort is needed to extend this knowledge about root architecture regulation as a whole (systems biology) and to explore it in crop species and in field conditions. To this end, efforts should focus on the following key research areas:

Deciphering the genetic bases of root system architecture (RSA)

The root increases in length through the activity of the root apical meristem which generates most of the different root cell types. Later, other processes can modify root tissue characteristics or generate new root meristems leading to branching. Although these mechanisms are crucial for the adaptation of the root system to environmental constraints (e.g. ground tissue adaptation to submergence, branching and growth modulations in response to local biotic or abiotic signals), our knowledge about their genetic regulation is still scarce. Three novel approaches need to be developed to tackle

this issue: i) analyses of the gene networks involved in root development regulation, ii) quantitative (QTL) analyses of RSA in crop species, iii) integrative and dynamic approaches through mathematical modelling (systems biology).

Understanding the molecular bases of root plasticity

The ability of the root system to adapt to various endogenous and environmental cues is a key aspect of its efficiency. One of the actual frontier researches is to unravel the cellular and molecular mechanisms modulating root development in response to environmental signals such as nutrient or water deficiency. Many regulatory factors have been shown to be involved in this modulation, especially hormones and transcription factors. Understanding how these factors transduce local biotic or abiotic cues to modify root development is a key goal for the future. In addition, recent genomic approaches have unravelled the role of other molecules in modifying gene network activities: miRNAs, siRNAs, and other diverse non-protein-coding transcripts (or npcRNAs) have been shown to be involved in the control of root architecture and its adaptation to the environment. These factors could be a major driving force in RSA evolution. Yet, very little is known about their impact on RSA regulation.

Fastening translational genomics from model plants to crop species

Identifying conserved and original RSA regulation processes in crop species, as well as modelling corresponding gene networks are needed to strengthen our ability to select new crops with higher root system efficiency.

Unlocking root phenomics

A major bottleneck for this research field remains the development of high-throughput, non-invasive and multi-scale root phenotyping systems in agronomically relevant substrates.

Interactions between the plant root and rhizosphere microorganisms

The root system of plants interacts with numerous and diverse microorganisms in a soil volume called the rhizosphere. Some of these microorganisms are detrimental to plant growth (pathogens), while others establish beneficial mutualistic interactions with the plant (symbioses, see below). Many other microorganisms positively influence plant growth by increasing nutrient availability, stimulating plant development, or eliciting protective responses against pathogens. Understanding these plant-microorganism relationships in the rhizosphere is of great agronomical and ecological importance, especially in the context of climate change and soil degradation, which impair crop yields. A key aspect is to understand the co-selection of microorganisms and plants in the rhizosphere, which leads to beneficial interactions. Two approaches need to be developed to that aim:

-Analysing some known functional traits of commensal microorganisms

A wealth of data has been generated about plant-pathogen interactions and microorganism features eliciting plant defence responses have been identified. Plants that recognize these features display higher resistance to these pathogens, thus reducing the need for pesticide treatments. In addition, some commensal bacteria are also able to elicit plant immunity responses, yielding higher resistance of the plant to pest diseases. The study of this property needs to be strengthened.

-Looking for new traits selected by the plant-microorganism interaction

Selected traits can be identified through non-biased analyses of multiple plant-microorganism couples, taking advantage of high-throughput genome sequencing technologies. Recent data showed that various traits related to mineral nutrition, detoxification, or signalling could have been selected during evolution of different plant-microorganism partnerships. This knowledge is important to understand the recruitment of commensal microorganisms by the plant in order to optimize plant-microorganism interactions in agricultural practices.

Concerning mutualistic interactions, the *Rhizobium*-legume (RL), the actinorhizal (AR), and the arbuscular mycorrhizal (AM) root endosymbioses are of great agronomic and ecological importance through improving plant nutrition. Recent research has shown that these symbioses share a common evolutionary origin based on symbiotic signalling. The selection of several plant-microsymbiont model systems, underpinned by genome sequencing and bioinformatics tools, has led to progress in deciphering the molecular and cellular processes leading to effective symbioses. With the aim of moving towards more sustainable agricultural systems, there is increasing interest in exploiting endosymbioses to improve plant growth in low input or stress conditions. Studies on model systems coupled with translation to crop species would help attain this aim. French groups are already involved and could make important contributions to the following future challenges:

-Establishing nitrogen fixing endosymbioses with cereals: advances in the knowledge of symbiotic signalling have evoked new strategies to transfer nitrogen-fixing symbiosis ability to cereals. French groups working on the diversity and evolution of AM, RL, and AR symbioses, as well as cereal and microorganism physiology, could decisively contribute to this goal.

-Improving the Rhizobium-legume symbiosis: integrated studies, involving model as well as crop species and taking advantage of natural variation, need to be performed to optimise bacteria/plant couples which maximise nitrogen-fixation in different agronomical conditions.

-Improving the arbuscular mycorrhizal symbiosis: there is increasing interest both in academic laboratories and industrial partners in the use of this symbiosis to improve growth of various crop species, including cereals. Breeding for plant responsiveness to AM fungi, studies on beneficial effects of the AM symbiosis in agronomical conditions and optimisation of plant-fungal partnerships would help attain this goal.

-Exploiting symbiotic signals: lipochito-oligosaccharides are microbial effectors, produced by *Rhizobium* bacteria and AM fungi, which influence root architecture and plant-microorganism interactions. More work is needed to explore the use of these, and potentially other, symbiotic signals in agriculture, particularly for non-legume crops such as cereals.

Position of industrial partners from the GIS BV

Selecting crops with higher root system efficiency is a critical goal for the next coming years. Improving root system properties of crops will help to maintain yields in a context of climate change and soil and water resource degradation, while decreasing the need for high nutrient, water, or pesticides inputs and thus leading to more sustainable agricultural practices. Despite the wealth of scientific approaches using model plants and important data generated by French public research laboratories about the regulation of root system architecture, root adaptation to environmental stresses and its interactions with rhizosphere microorganisms, they are still poorly known and exploited. A major bottleneck for industrial laboratories remains the technical difficulties of high-throughput analyses on crop root systems in field conditions. Yet, major advances are under way, to which the industrial partners attending the workshop were willing to contribute:

-Developing high-throughput and ideally non-destructive phenotyping technologies for root systems to select crops with desirable root traits. A particular effort should be done on imaging systems and associated informatics tools (including data storage to image analysis).

-Deciphering the genetic basis of root system development and of its adaptation to environmental stresses will provide molecular factors that could be targeted by the breeding programs. This knowledge, generated mostly from model plants (*Arabidopsis*, Rice, etc...),

should be evaluated in crops using the expertise of the public and private sectors in common projects. In particular, the interaction between the physiology of the root development and the soil composition or type should be more studied.

-Understanding plant-microorganisms interactions will allow the optimised use of plant-microorganism pairs in field conditions, for the higher benefit to plant growth. In that area, the interaction with academic partners to work towards the transfer of nitrogen-fixing symbiosis ability to cereals is a major challenge for industrial partners, in order to tackle the need for increased crop yields while reducing nutrient inputs.

The GIS BV and the AllEnvi Alliance strongly support the need expressed by the dynamic French scientific community present at the “Plant Roots” workshop to develop and integrate the knowledge generated in this research area in the public laboratories, using complementary strategies. Strengthening the interactions between public and private partners, through regular meetings on the topics described in this position paper will allow the identification and the development of industrial applications of the discoveries. Availability of public and/or private funding dedicated to this topic, from national or international funders (such as the Bill & Melinda Gates Foundation) is necessary to sustain the leadership and/or fulfil the potential of the French research community in this area of research
