
OLIVIER LOUDET

CV

PARTICIPANT AT:

EVOLUTION OF PLANT PHENOTYPES FROM GENOMES TO TRAITS

**March, 17th-18th, 2015, Barcelona****Olivier Loudet**, Group Leader at INRA - IJPB Versailles, Versailles, France

Olivier Loudet is a group leader at INRA in Versailles, in the department IJPB which gathers 25 research groups dedicated to plant biology and genetics. Research approaches in the lab are essentially devoted to better understanding the genetic architecture of complex traits, and especially Arabidopsis response to environmental constraints, using different model traits from very integrative growth parameters down to transcript accumulation. We hope to contribute a more general picture as to how -and where in the pathways- adaptation is shaping natural variation. Olivier is funded essentially by the ERC and the French ANR.

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ABSTRACT

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EVOLUTION OF PLANT PHENOTYPES FROM GENOMES TO TRAITS

**March, 17th-18th, 2015, Barcelona****Olivier Loudet**, Group Leader at INRA - IJPB Versailles, Versailles, France**Decoding the Complexity of Quantitative Natural Variation and Response to the Environment in *Arabidopsis thaliana***

Following a long history of quantitative genetics in crop plants, it is now relatively popular as well to use naturally-occurring variation contained in *Arabidopsis thaliana* accessions as the source of quantitative genomics approaches, designed to map QTLs and try and resolve them at the gene level. Apart from being able to exploit –in multiple genetic backgrounds– allelic variation that cannot be easily retrieved from classical mutagenesis, the (relatively few) success of the QTL studies has often been because of the use of quantitative phenotyping, as opposed to the qualitative scales often used in typical mutant screens. The objective of our work is to apply genome-wide quantitative molecular genetics to both, a very integrative and classical quantitative trait (shoot growth) and a molecular trait a priori more directly linked to the source of variation (gene expression under cis-regulation), in both cases studied in interaction with the abiotic environment (especially drought stress). We are using a combination of our unique high-throughput phenotyping robot (the Phenoscope), RNA-seq, fine-mapping, complementation approaches and association genetics to pinpoint a significant number of QTLs and eQTLs to the gene level and identify causative polymorphisms and the molecular variation controlling natural diversity. Exploiting these strategies at an unprecedented scale thanks to the Phenoscope should allow to resolve enough quantitative loci to start drawing a more general picture as to how and where in the pathways adaptation is shaping natural variation. I will present recent results obtained when trying to decipher the genetic architecture of growth response to the environment, to illustrate our strategies and research.

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