Towards a role of DNA methylation in plant phenotypic plasticity

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Abstract

Global climate changes in progress will impact crops and forest productivity. Recently, epigenetic mechanisms such as DNA methylation have been shown to participate to the control of plant development and their adaptation to environment. Phenotypic plasticity defines as the different phenotypes for a given genotype in distinct environments is a key process for plant to adapt to their changing environment. We are developing an integrative approach to identify ecophysiological and molecular bases, particularly DNA methylation, involved in the phenotypic plasticity of complex traits such as growth, flowering and drought tolerance in plants. Contrary to animals, plants exhibit a continuous development and their germline arise from very specific somatic tissue: the shoot apical meristem. We focus our effort to the study the role of DNA methylation in shoot apical meristem using various epigenomic approaches (MeDIP-SEQ, MeDIP-CHIP, WGBS) in parallel to transcriptomics and phenotyping. The aim of our project is to identify Differentially Methylated Regions' (DMRs) among genotypes and in changing environments in order to establish the potential role of DNA methylation in controlling the expression of gene networks and to improve models used in plant breeding. Altogether, our results show the role of DNA methylation in memorizing environmental influence and identify first genes network in relation to phenotypic plasticity.

Keywords: Plant Phenotypic plasticity, DNA methylation, epigenomics

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