

## **Methylation landscape in the genome of higher plants of agronomical interest**

In eukaryotic cells the methylation of cytosines in DNA is an essential mechanism which is implied in the dynamic organization of the genome structure, in relation to genes expression. Plant genomes contain a significant proportion and variable according to the species, of sequences which are likely to be methylated during the life of the plant. It is known that the establishment and the maintenance of methylation profiles in both genomic areas and specific sequences constitute a crucial mediator in the modulation of genes expression during development. Recent studies have evidenced the implication of epimutations in the adaptation of plants to their environment particularly in response to biotic and abiotic stresses. Recently, the complete mapping of methylation in the genomes of *Arabidopsis thaliana* and rice provided invaluable information on the distribution of methylation within genes in relation to their expression. The impact of changes in the methylation profiles on the characters of agronomic importance has not been intensively studied yet, whereas this question takes a considerable importance in the context of an increasing food demand and foreseen global climate changes. The METHYLANDSCAPE project proposes to isolate genomic DNA sequences on the basis of their degree of methylation and to connect the variation of their methylation profiles with, on the one hand, the expression of the corresponding genes and, on the other hand, with environmental or developmental processes. Thus, it should be possible to identify genes which expression is differentially controlled by methylation during development and/or in situation of stress, and likely to have an influence on the agronomic value of the plant. The METHYLANDSCAPE partners thus propose to bring signification advances in plant genomics on four original species, by integrating DNA methylation mapping and the relationship between epigenome and transcriptome, up to the generation of methylation-sensitive markers linked with characters of agronomic importance.

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