Epigenomics in poplar: the methylome of non-condensed chromatin

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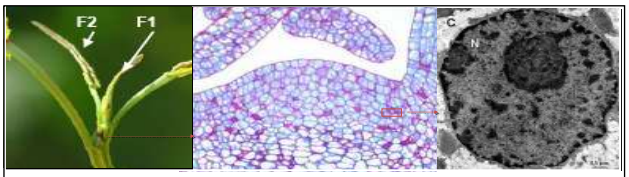
Context and objectives

Poplars are among the fastest growing trees under temperate latitudes with strong genotypic variability and plasticity facing environmental changes such as a water deficit. In the context of global climatic changes, **our general objective is to improve the knowledge on the processes involved in the plasticity of poplar towards drought.**

Epigenetic mechanisms such as DNA methylation have now been clearly identified as key processes to control animal and plant development as well as their responses to environmental changes. Epigenetic variations have been recently reported between *P. euramericana* hybrids and in response to a water deficit (Gourcilleau *et al.*, 2010). Our hypothesis is that DNA methylation in the shoot apical meristematic cells (center of morphogenesis) participates to the control of gene expression and consequently to the control of morphogenesis (Figure 1). **Our first specific objective is to identify methylated genomic loci in poplar.**



Active apical bud | Shoot apical meristem (SAM) | Nucleus with different chromatin compactions

Variations of chromatin compaction (DNA methylation) in SAM

↓ Gene expression

↓ Shoot morphogenesis

↓ Biomass production

Figure 1 : hypothesis of epigenetic mechanisms controlling shoot morphogenesis

Strategy and Results

Our strategy consisted to focus the methylome analysis on the non-condensed DNA methylated chromatin fraction that should be enriched in gene and depleted in repeated sequences. This chromatin fraction was obtained using DNase I, **Me**thyl **D**NA **I**mmino**P**recipitation (5-methycytosine antibodies) and Illumina **Seq**uencing (MeDIP-Seq) as described Figure 2.

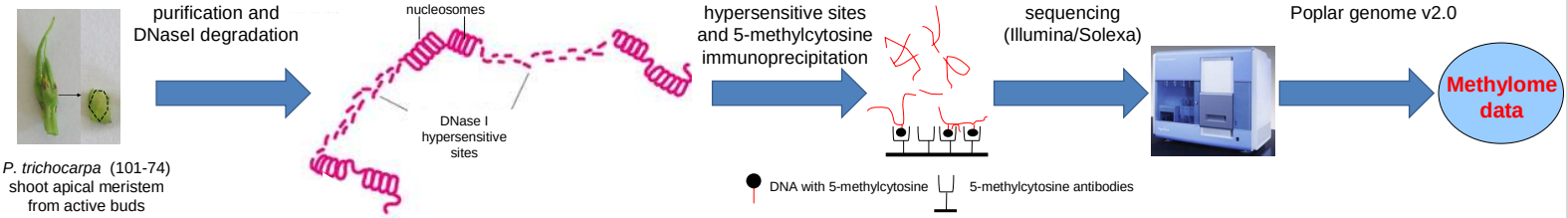


Figure 2 : DNase I / MeDIP-Seq applied on poplar shoot apical meristem

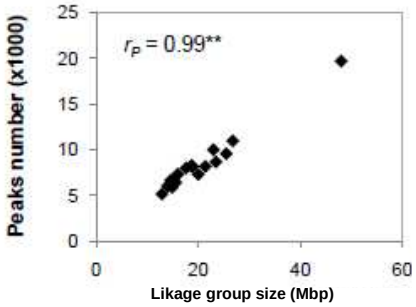


Figure 3 : Correlation between the number of solexa reads mapped on the 19 poplar linkage groups and the linkage group size in Mbp.

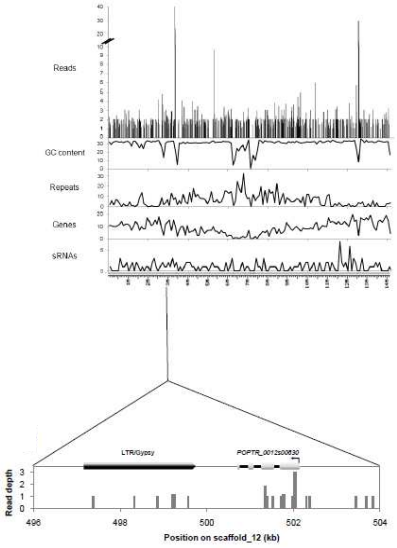


Figure 4 : Mapping of solexa reads, GC content, repeats density, gene density and sRNA desnsity for the linkage group XII.

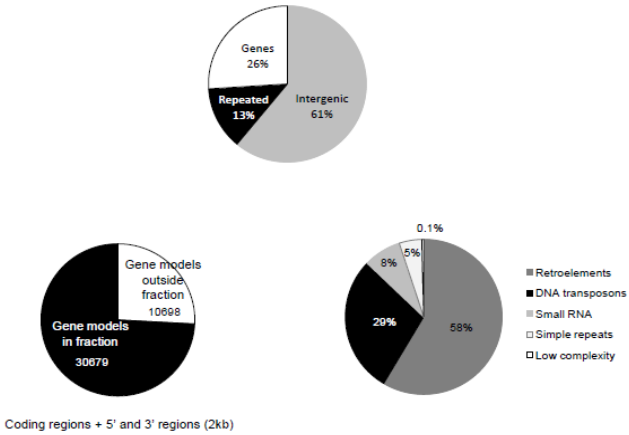


Figure 5 : Analysis of the sequences mapped by solexa reads.

Conclusions and Perspectives

1. Methylation was distributed throughout all linkage groups in positive correlation to their sizes but the distribution along a linkage group is not uniform.
2. Methylation mapping is influenced by the GC content but did not scale with the repeat, gene and sRNA densities.
3. Genes (particularly exons) and TEs showed intense mapping of methylated reads.
4. More than 75% of the poplar model genes were found in the methylated DNase I fraction.

To conclude, DNase I / MeDIP-seq is a simplified and representative approach for methylome analysis.

Further bioinformatics analyses and bisulfite sequencing verifications have been done on our methylome (Lafon Placette et al. *in prep*) to conclude about the specificities of poplar methylation. Further investigations are also actually done to characterize the variations of methylome during a drought.

Gourcilleau D, Bogeat-Triboulot MB, Le Thiec D, Lafon-Placette C, Delaunay A, El-Soud WA, Brignolas F, Maury S. (2010) DNA methylation and histone acetylation: genetic variations in hybrid poplars, impact of water deficit and relationships with productivity. Ann. For. Sci. *67*, 208(1-10)

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