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Role of epigenetics in tree phenotypic plasticity

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Global climate changes in progress will impact forest productivity notably through reduced water availability and heat periods. One possibility to adapt is phenotypic plasticity for which epigenetic mechanisms are proposed to be a main source of flexibility. Our objective is to evaluate the potential of DNA methylation to significantly participate to phenotypic plasticity in trees, fixed and perennial organisms with major ecological roles. Over the 10 last years, using an integrative approach with eco physiological, biochemical, transcriptomics, epigenomics (MeDIP, WGBS, Mobilome) and reverse genetics (RNAi lines) tools, we were able to dissect the shoot apical meristem (center of the shoot morphogenesis) the response of trees to environmental variations. This work was assessed in distinct experimental set-ups from greenhouse to field plantations as well as during the stress or months post-stress. Our data (recently published and unpublished) showed that Differentially Methylated Regions (DMRs) are associated to active TE and differentially expressed genes with biological functions related to stress response and phyto hormone signaling. Altogether, our data proposed that DNA methylation is a source of flexibility associated to phenotypic plasticity in trees opening perspectives for tree breeding.

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