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Role of epigenetic in tree phenotypic plasticity in a context of climate changes

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Global climate changes in progress will impact forest productivity notably through reduced water availability and heat Gperiods. 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 perennials organisms with major ecological roles. Over the 10 last years, using an integrative approach with ecophysiological, biochemical, transcriptomics, epigenomics (MeDIP, WGBS, Mobilome) and reverse genetics (RNAi lines) tools, we were able to dissect in 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 Our data (recently published and unpublished) showed that differentially methylated regions (DMRs) are associated to active TE and differentially expressed genes with biological functions related to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 phytohormone signaling. Altogether, our data proposed that DNA methylation is a source of flexibility associated to phenotypic plasticity in trees opening perspectives for tree breeding. The role of epigenetic mechanisms in tree adaptation and microevolution will be also presented through the results obtained in the frame of the national project EPITREE.