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Clarifying the role of DNA methylation in tree phenotypic plasticity

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In a context of global climate change, trees as sessile and long lifespan organisms need to develop mechanisms enabling them to adapt and to survive. These last years, epigenetic mechanisms such as DNA methylation have been proposed as a valuable resource since they can be triggered by the environmental conditions in a reversible-way. However, evidences for their role in tree phenotypic plasticity are still lacking (Bräutigam *et al.*, 2013; Plomion *et al.*, 2016). In this context, we develop different complementary approaches:

- i) A correlative approach with simultaneous analysis of methylome and transcriptome dynamics in the shoot apical meristem (center of shoot morphogenesis) of poplar in various environments (Gourcilleau *et al.*, 2010; Lafon-Placette *et al.*, 2013; Bastien *et al.*, 2015; Le Gac, 2017; Lafon-Placette *et al.*, 2017).
- ii) A reverse genetic approach, using RNAi clones of *Populus tremula x alba* (Zhu *et al.*, 2013; Condé *et al.*, 2017; Le Gac *et al.*, in prep) hypo or hypermethylated and grown under environmental constraints.
- iii) A population approach, using natural populations from diverse geographic origins to explore microevolutive adaptation to local environment and phenotypic plasticity (Project 'EPITREE' ANR 2018-2021, S. Maury). Our previous data highlight a relationship between DNA methylation in the shoot apical meristem biomass productivity and a possible connection with phytohormone signaling in response to abiotic stress. New data will be also presented concerning the stability of the epigenetic modifications and their genetic diversity in populations. Altogether, our data provide new insights into how trees modulate their epigenomes to ensure developmental plasticity and adaptation in a changing environment.