

DNA METHYLATION VARIATION IN OXFORD POPLAR CLONE UNDER OZONE STRESS

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The potential role of DNA methylation as an epigenetic mechanism involved in local adaptation of trees is of interest for its implications for understanding short-term responses to environmental change. Gene body CG methylation variations are correlated strongly with latitude and climate variables and therefore could be associated with local adaptation by natural selection. DNA methylation in response to climate variation is of particular interest in long-lived trees because their long generation time limits the ability of populations to respond to rapid environmental changes through genetic mechanisms. Among tree species, poplar has been paid particular attention because it is widely used for wood production and as a model system in plant biology. However, the knowledge of O₃ dose-response relationships for poplar is still limited. Oxford poplar clone (*Populus maximoviczii* Henry x *Populus berolinensis* Dippel) under ozone stress were studied in order to: i) describe the patterns of methylation composition and distribution across the genome, ii) identify which climate variables are most associated with methylation variation under ozone stress. Ozone treatments were applied at three levels: ambient air concentration (AA), 1.5 x AA and 2.0 x AA, from 1st May to 1st October, 2016, 24 h per day, in a free air controlled exposure (FACE) system located in Sesto Fiorentino (FI). Total DNA was extracted from leaves of control and stressed trees in triplicated and analyzed to identify single-methylation variants polymorphism (SMVs). SMVs identification was carried out by reduced-representation bisulphite sequencing (RRBS) libraries on NGS torrent platform, and data analysed by TABSAT software. The analyses are in progress. This first study will be useful to identify the SMVs associated to climate variations and ozone response to be used in screening natural populations for the evaluation of the effects of short and medium to long-term climate change forest resistance and resilience, and to give information useful for assisted migration and to breeders to develop future provenance trials for tree selection.