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UNDERSTANDING THE ROLE OF 5-METHYL CYTOSINE DNA DEMETHYLASES IN CONTROLLING WINTER DORMANCY OF WOODY PLANTS

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Winter dormancy is the mechanism used by perennial plants to survive the harsh conditions of winter in temperate and cold regions and determines the geographical distribution of tree species (Chuine and Beaubien 2001; Horvath et al. 2003; Allona et al. 2008). Epigenetic control of winter dormancy in woody plants is barely known. Among the important epigenetic marks, 5-methyl cytosine (5mC) regulates gene expression in animals and plants. Global changes in 5mC DNA methylation have been shown in the transition of developmental stages in plants such as chestnut bud set and burst, flowering in azalea, aging in pine trees among other. However, the mechanism and the enzymes involved in the modification of the methylome and its control over those development processes remain to be identified. Our previous results showed higher DNA methylation and less acetylated Lys 8 of histone H4 global levels in poplar stem during winter dormancy compared to active growing season (Conde et al. 2013). Analysis of the 5-methyl cytosine levels by the application of the immunofluorescence-based method set up in our lab showed that DNA methylation levels fall suddenly when trees are near to restore the growing season coming from the dormant state. We have identified two poplar homologs to Arabidopsis DME gene: *PtaDML8/PtaDML10*. DME protein promotes global DNA demethylation along the genome during the endosperm development. Our RT-PCR analyses indicate that the expression of *PtaDML8/PtaDML10* genes increases significantly when trees are near to restart growing after winter dormancy. The phenological assays showed that *PtaDML8/PtaDML10* knockdown plants have a delayed in resuming of growth after dormancy.

Taken together, we hypothesize that an active control of the 5mC DNA methylation might play a key role in winter dormancy and that 5mC demethylases would be crucial in this process.

References

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