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IDENTIFICATION OF CYTOSINE-5 DNA METHYLTRANSFERASES AND DEMETHYLASES IN EGGPLANT AND THEIR EXPRESSION ANALYSIS DURING FRUIT RIPENING

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DNA methylation plays important roles in genome protection, regulation of gene expression and plant development. Cytosine DNA methylation, whose targets are CG, CHG and CHH (H is A, T, C) sequences, is catalyzed by three C5-MTase families: methyltransferase (MET), chromomethyltransferase (CMT) and domains rearranged methyltransferase (DRM).

MET and CMT are responsible for the maintenance of CpG and CpHpG methylation respectively, while DRM maintains CpHpH methylation and catalyses *de novo* methylation. Plants, like mammals, are also provided of DNA glycosylases which promote DNA demethylation

In the eggplant genome we identified six C5-MTases (1 MET, 3 CMTs and 2 DRMs) and one demethylase (DME1). The seven loci encode polypeptides ranging from 308 to 2001 amino-acids, that is consistent with homologue protein sizes in Arabidopsis and tomato.

The mRNA abundance of the seven genes was investigated at four ripening stages in four eggplant cultivars, and in all of them an increase of the expression of MET1, CMT2, CMT3, DRM1 and DRM2 was detected during the ripening process. In contrast, a reduction of transcript abundance of both CMT1 and DME1 was observed.

Our study reports the first identification of C5-MTases and demethylase in eggplant as well as a trend of their expression during fruit ripening. Further studies will investigate the relationship between global DNA methylation rates and gene expression trends.