The sink-source relationship in cucumber (*Cucumis sativus* L.) is modulated by DNA methylation

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Abstract

Optimization of sink-source relationship is important to increase vegetable yield. DNA methylation is one of the most important epigenetic modifications in plants, and its role in sink-source regulation of sucrose-translocating plants have been widely reported. Cucumber is a worldwide important vegetable, raffinose family oligosaccharides (RFOs) (mainly stachyose and raffinose) are the major sugars transported between "source" and "sink" organs in cucumber. To date, the effect of DNA methylation on the sink-source relationship has not been reported in RFOs-translocating species. In this study, whole-genome bisulfite sequencing (WGBS-seq) were used to compare none fruiting-node leaves (NFNL) and leaves at the same node of fruit setting (FNL) in the cucumber plant. The results showed that 6531 differentially methylated regions (DMRs) were identified in CG/CHG/CHH sites, many differentially methylated genes were enriched in photosynthesis and carbohydrate metabolic process. To further analyze the network of sink-source relationship, data of transcriptome sequencing of FNL and NFNL were also employed. Many differentially expressed genes (DEGs) with DMRs involved in RFOs synthesis pathway, sucrose metabolism, plant hormone and signal transduction related to sink-source regulation. It is worth noting that the relative expression of galactitol synthase (CsGolS1), raffinose synthase (CsRS) and CsSTS responsible for cucumber assimilate loading was elevated in FNL, and CsRS was hypermethylated in FNL, indicating that DNA methylation may affect assimilate loading in cucumber. Furthermore, application of the DNA methylation inhibitor 5-aza-dC-2'-deoxycytidine (5Aza-dC) promoted fruit growth. We further showed that 5Aza-dC upregulated the relative expression of CsGolS1, CsRS and CsSTS, enzyme activity of CsSTS and stachyose content involved in leaf assimilate loading, suggesting an essential role of 5Aza-dC in sink-source regulation. This study sheds light on the important role of DNA methylation in sink-source relationships and provides a possibility of improving cucumber yield by altering DNA methylation.

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