

# An integrative analysis of DNA methylation and RNA-Seq data uncovers key genes involved in albino tea

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**Abstract:** Albino tea, a type of tea closely associated with the chlorophyll-deficient phenotype is of great interest due to its wide health benefits. To better understand potential mechanisms involved in albino tea, we performed DNA methylation and transcriptome analysis of the green and albino leaves in a special tea mutant Haishun2. A total of 385 candidate genes were identified by the integrative analysis. KEGG analysis revealed that these genes were mainly involved in biosynthesis of secondary metabolites, pantothenate and CoA biosynthesis and photosynthesis. Many candidate genes involved in catechin biosynthesis were down regulated in albino leaves, such as 4-coumarate-CoA ligase, flavonol synthase and leucoanthocyanidin reductase genes. CsMYB5 and CsGSTF11 were also down regulated in albino leaves, which might participate in regulating catechin accumulation. Furthermore, two NAC transcription factors were highly up regulated in the albino leaves and might function as controlling chlorophyll degradation. Overall, the identification of these candidate genes offers a global view of the potential mechanisms associated with albino phenotype, which will facilitate molecular breeding of albino tea cultivars.

**Keywords:** Albino tea; DNA methylation; Transcriptome analysis; Catechin biosynthesis; NAC transcription facto

Many thanks!

Best regards

Kang