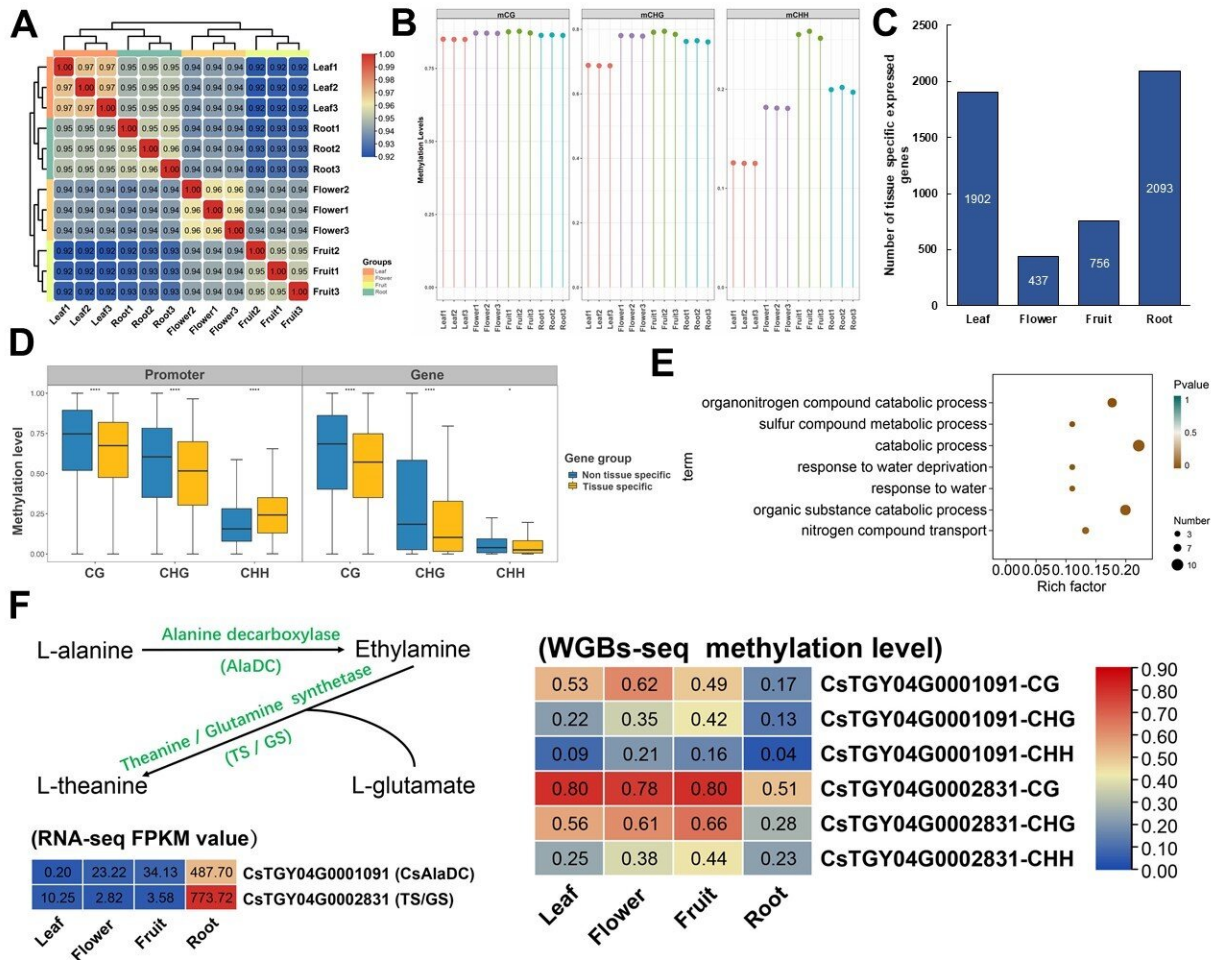


Using DNA to move flavors between different varieties of tea

August 29 2023



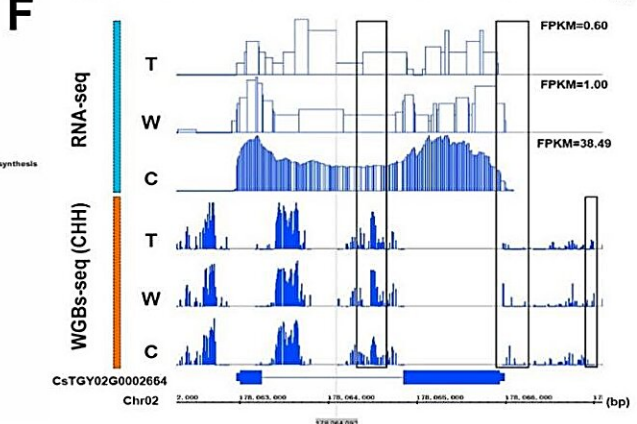
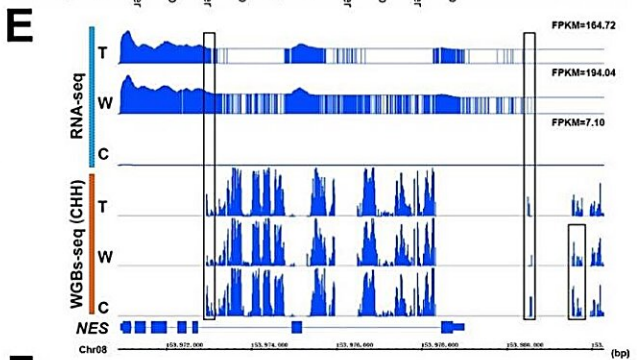
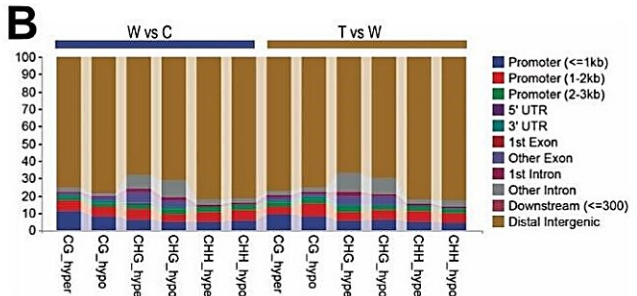
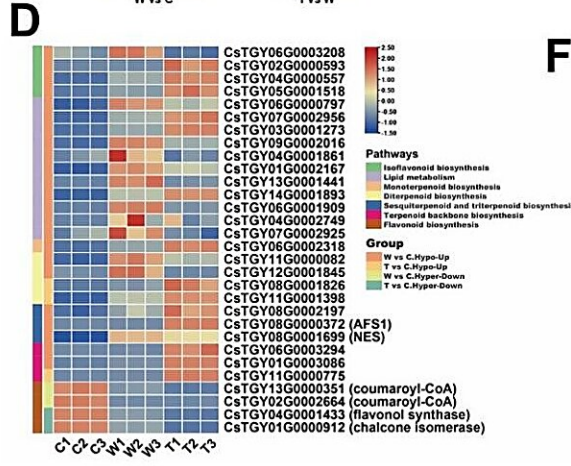
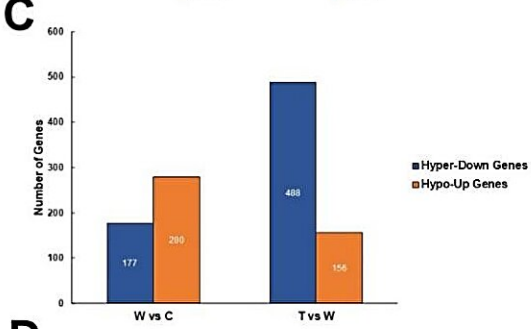
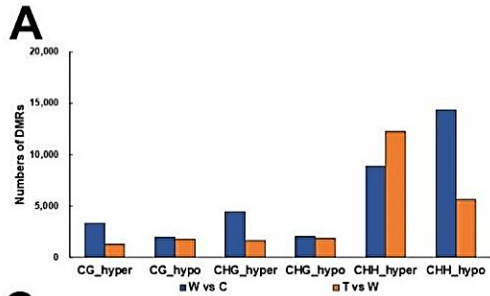
Differential methylation modification levels in different tissues and 5mC DNA-mediated theanine dominant synthesis in roots. Credit: *Horticulture Research*

In plants, 5mC DNA methylation is an important and conserved epistatic mark involving genomic stability, gene transcriptional regulation, developmental regulation, abiotic stress response, metabolite synthesis, etc. However, the roles of 5mC DNA methylation modification (5mC methylation) in tea plant growth and development (in pre-harvest) and flavor substance synthesis in pre- and post-harvest is unknown.

This article has been published in *Horticulture Research*.

In this study, we conducted a comprehensive methylation analysis of four key pre-harvest tissues (root, leaf, flower, and fruit) and two processed leaves during oolong tea postharvest processing. We found that differential 5mC methylation among four key tissues are closely related to tissue functional differentiation and that tissue-specific expressed [genes](#) responsible for tissue-specific functions maintain relatively low 5mC methylation levels relative to non-tissue-specific expressed genes.

Importantly, hypomethylation modifications of CsAlaDC and TS/GS genes in roots provided the [molecular basis](#) for the dominant synthesis of theanine in roots.



Differential methylation modification-mediated gene expression differences associated with the synthesis of key flavor substances during oolong tea processing. Credit: Horticulture Research

In addition, integrating of 5mC DNA methylationomics, metabolomics, and transcriptomics of postharvest leaf revealed that content changes in flavor metabolites during oolong tea processing were closely associated with transcription level changes in corresponding metabolite synthesis

genes, and changes in transcript levels of these important synthesis genes were strictly regulated by 5mC methylation.

We further reported that some key genes during processing are regulated by 5mC methylation, which can effectively explain the content changes of important aroma metabolites, including α -farnesene, nerolidol, lipids, and taste substances such as catechins.

In total, our results not only highlight the key roles of 5mC methylation in important flavor substance synthesis in pre- and post-harvest, but also provide epimutation-related gene targets for future improvement of tea quality or breeding of whole-tissue high theanine varieties.

More information: Weilong Kong et al, 5mC DNA methylation modification-mediated regulation in tissue functional differentiation and important flavor substance synthesis of tea plant (*Camellia sinensis* L.), *Horticulture Research* (2023). [DOI: 10.1093/hr/uhad126](https://doi.org/10.1093/hr/uhad126)

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