# Chromosome-level genome and methylome of vine tea suggest roles for tandem duplication and CHH hypomethylation in high dihydromyricetin accumulation

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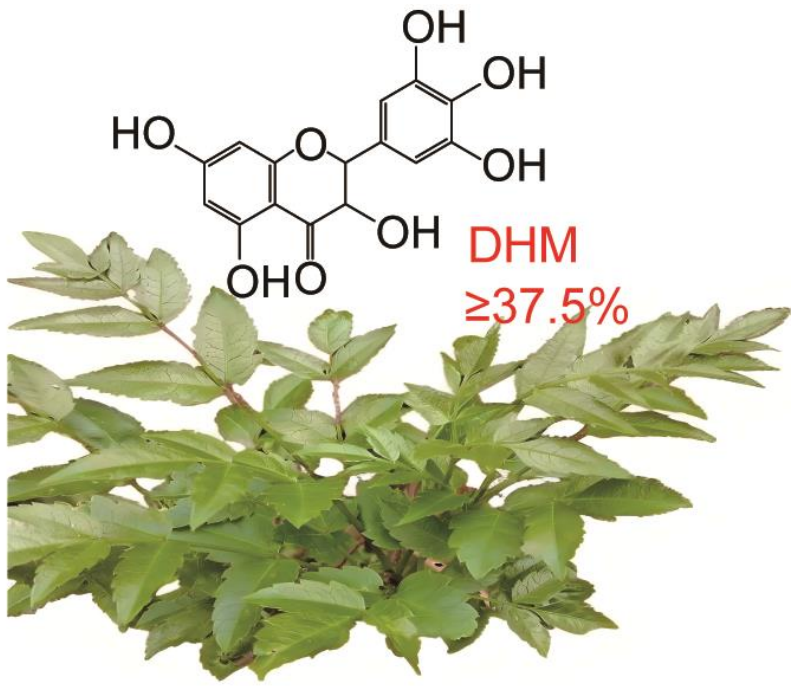
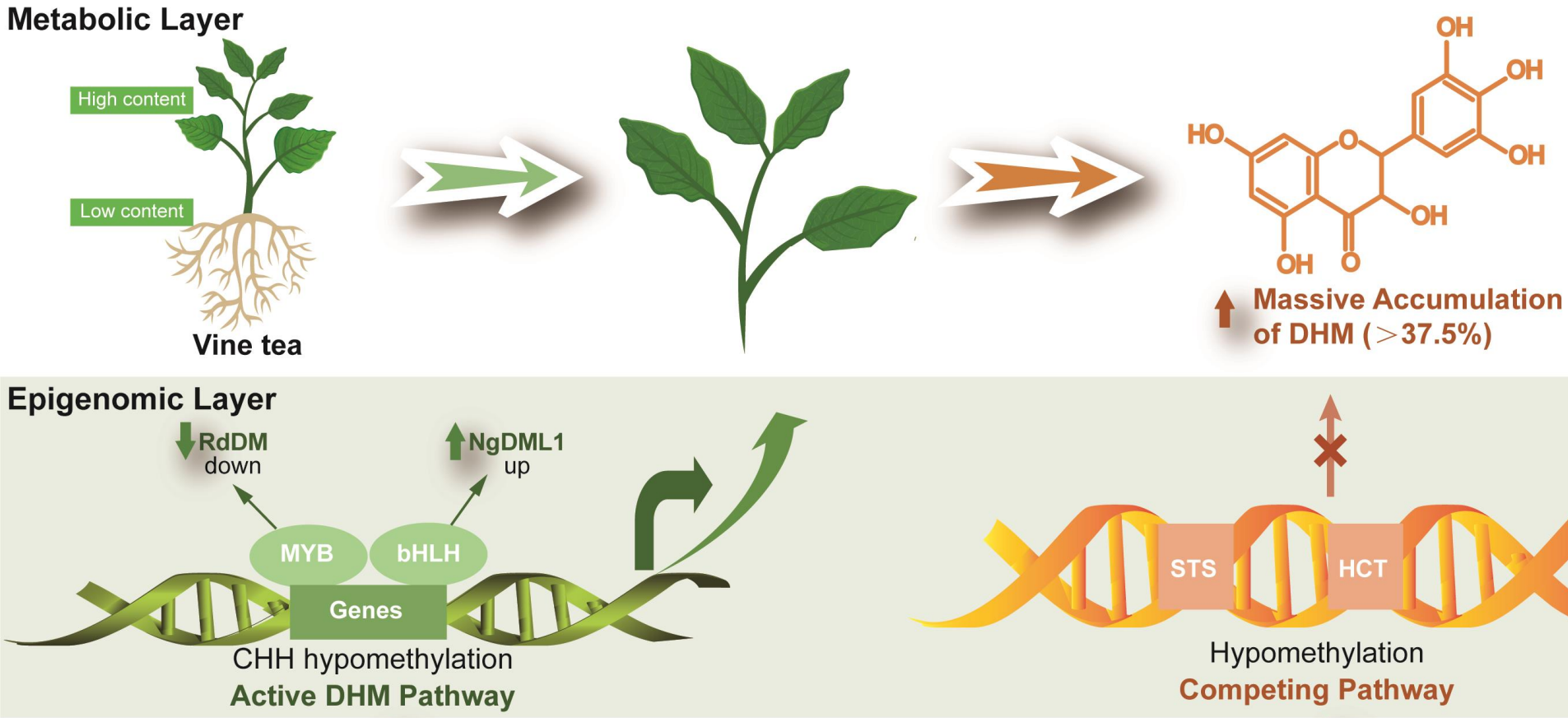
# Introduction

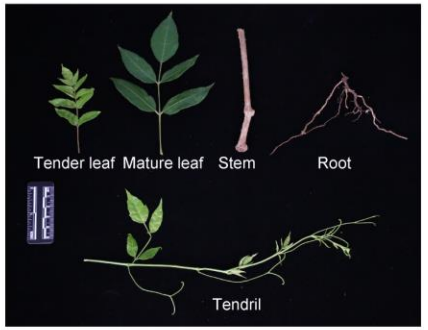

*Nekemias grossedentata* (Vine tea)

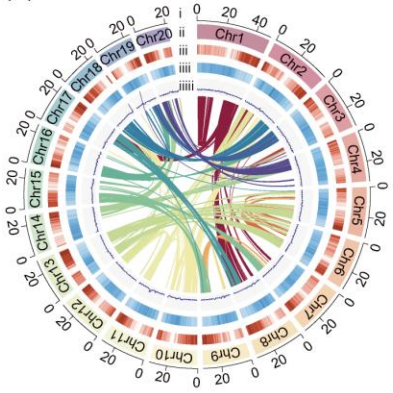
- **High medicinal value:** Young leaves contain up to 37.5% DHM and exhibit diverse bioactivities.
- **Strong research foundation:** Genome sequencing and biosynthetic gene variation analyses have been completed.
- **Key question:** The methylation and gene-duplication mechanisms underlying high DHM accumulation in young leaves remain unclear.

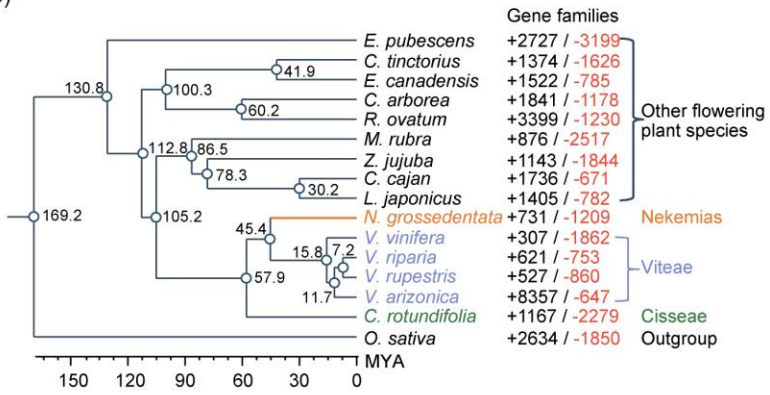
# Highlights

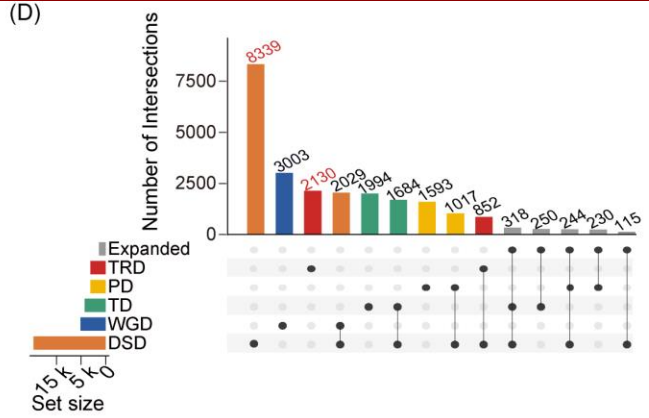

Metabolic Layer
High content
Low content
Vine tea
OH
OH
HO
O
OH
OH
OH
O
Massive Accumulation
of DHM (>37.5%)
Epigenomic Layer
RdDM
down
NgDML1
up
MYB
bHLH
Genes
CHH hypomethylation
Active DHM Pathway
STS
HCT
Hypomethylation
Competing Pathway
Genomic Layer
Tandem Duplications
NgCHS1
NgCHS2
NgCHS3
NgF3'5'H1
NgF3'5'H3
NgF3'5'H4

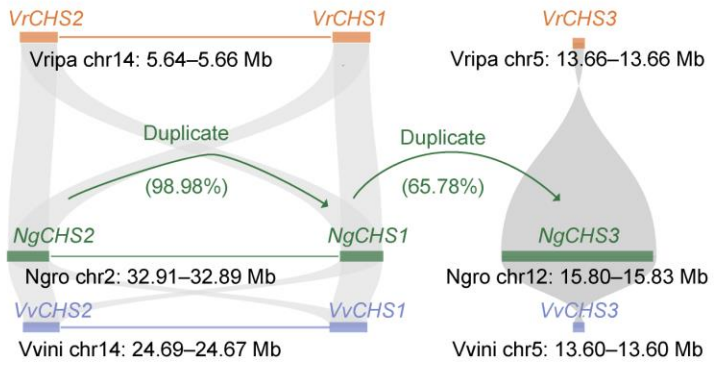
# Chromosome-level genome assembly reveals tandem duplication of DHM biosynthetic genes

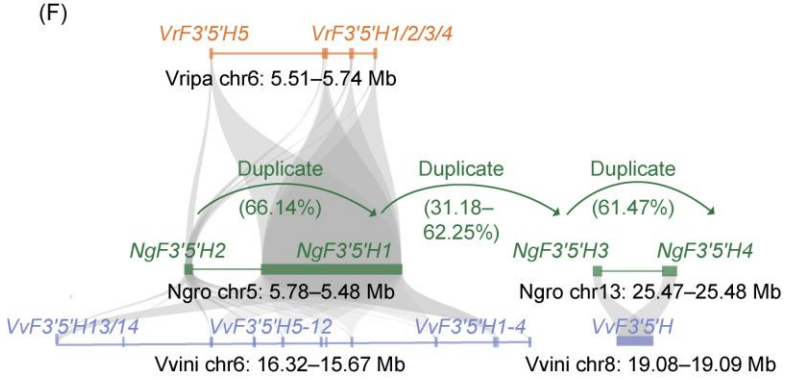


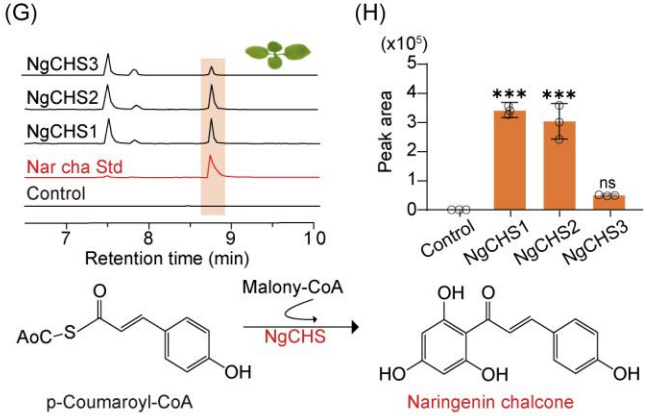



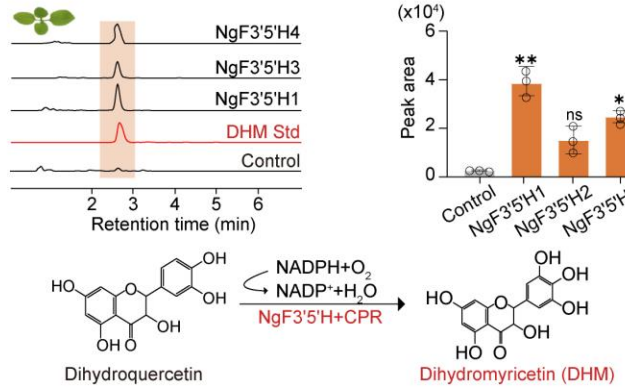


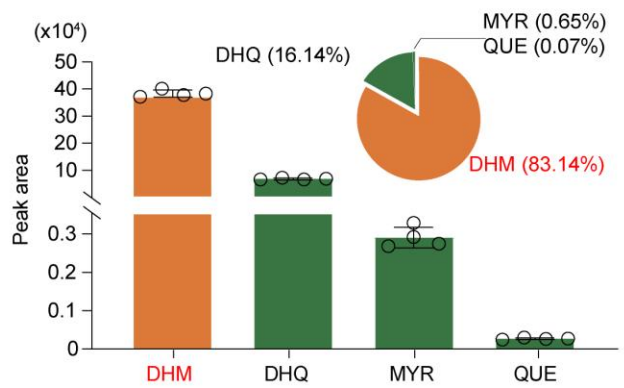



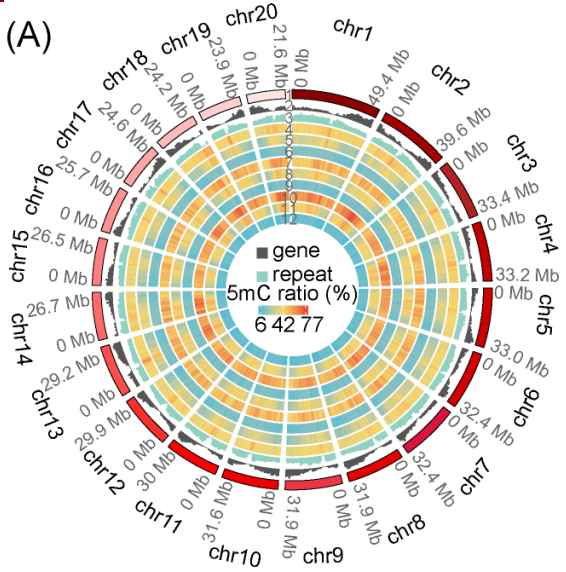



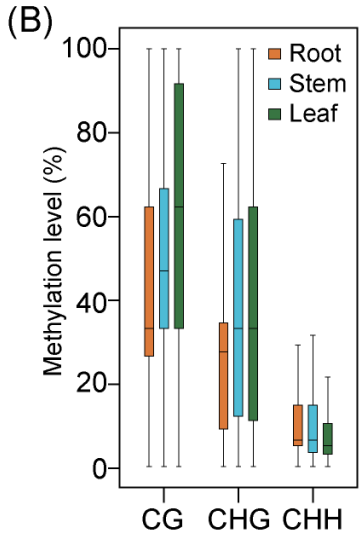


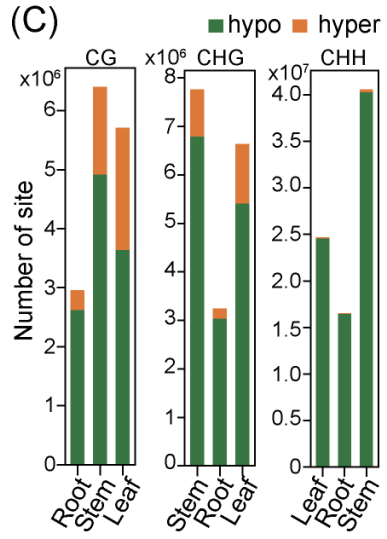


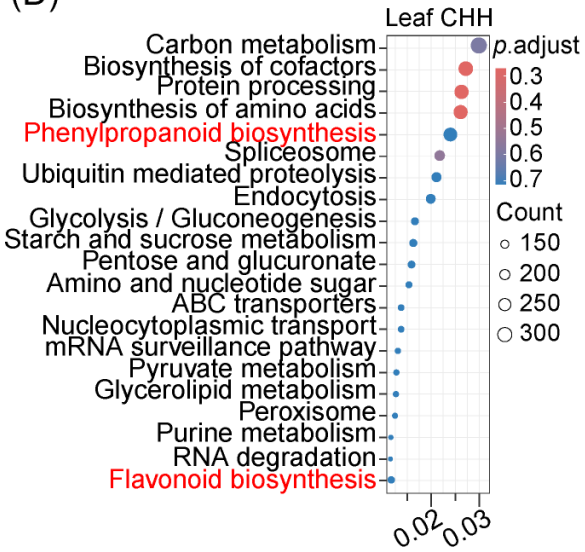
- Constructed a chromosome-level genome assembly of vine tea.
- Identified key genes involved in DHM biosynthesis.
- Revealed that tandem duplication contributes to high DHM accumulation.

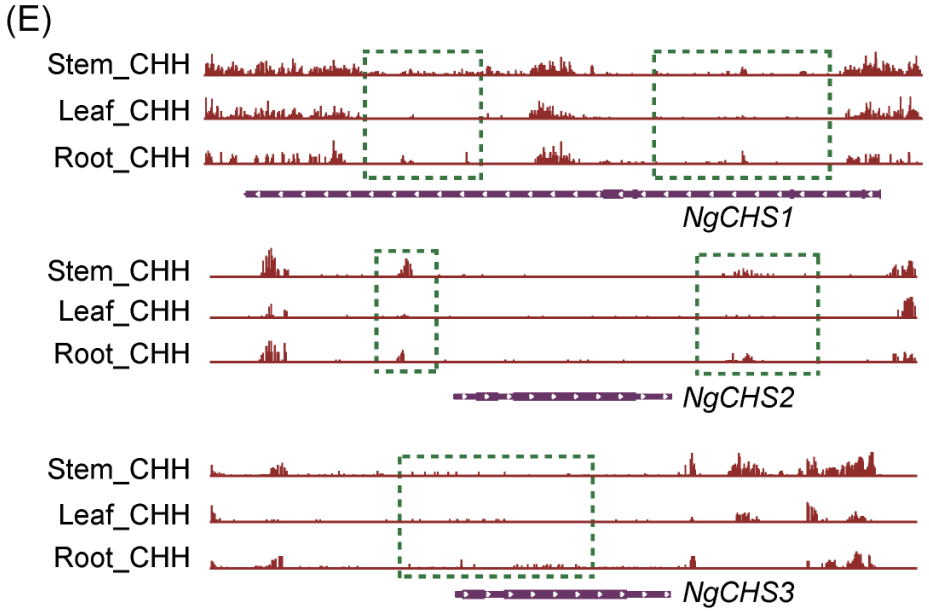
# Tissue-specific CHH hypomethylation is associated with the activation of DHM pathway genes

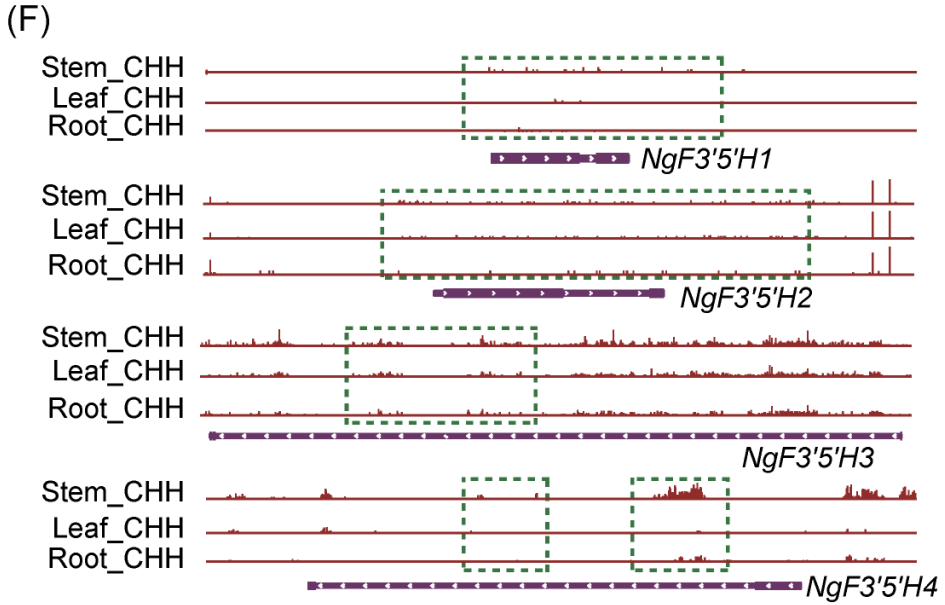


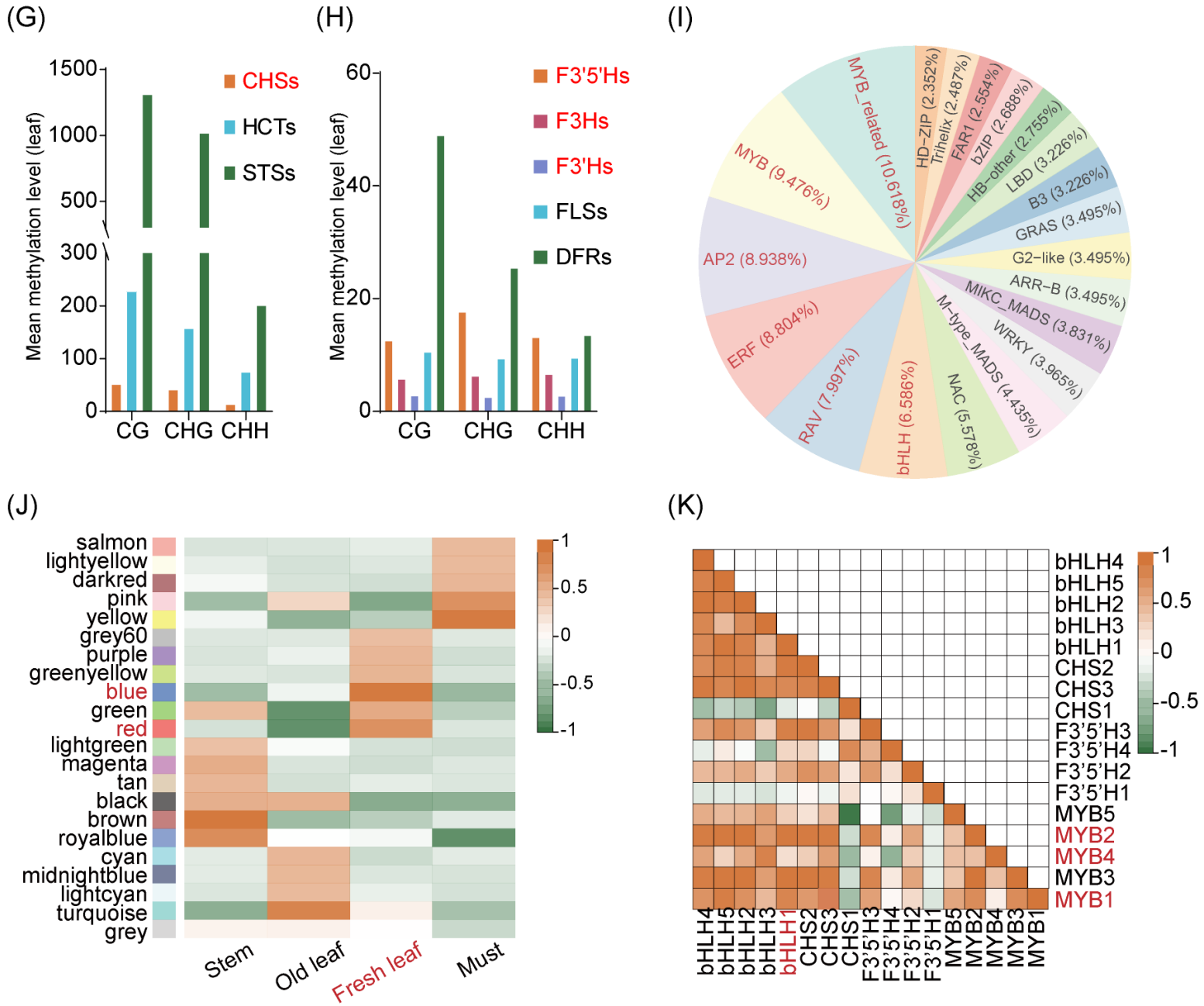




- Young leaves show reduced CHH methylation.
- CHH hypomethylation activates DHM biosynthetic genes.

# Tissue-specific CHH hypomethylation is associated with the activation of DHM pathway genes




- CHH hypomethylation activates DHM biosynthetic genes.
- Gene duplication and MYB/bHLH promote DHM accumulation.

# Summary

- Genetic basis: Tandem duplication of CHS and F3’5’H supports high DHM biosynthesis.
- Key tissue: Young leaves show the strongest DHM biosynthetic activity.
- Epigenetic regulation: CHH hypomethylation may activate DHM pathway genes.
- Duplication-associated activation: Gene duplication, CHH hypomethylation, and MYB/bHLH factors jointly promote DHM accumulation.

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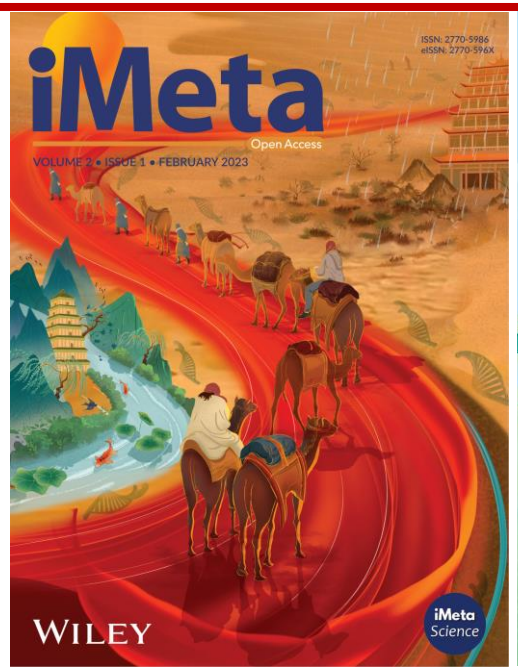


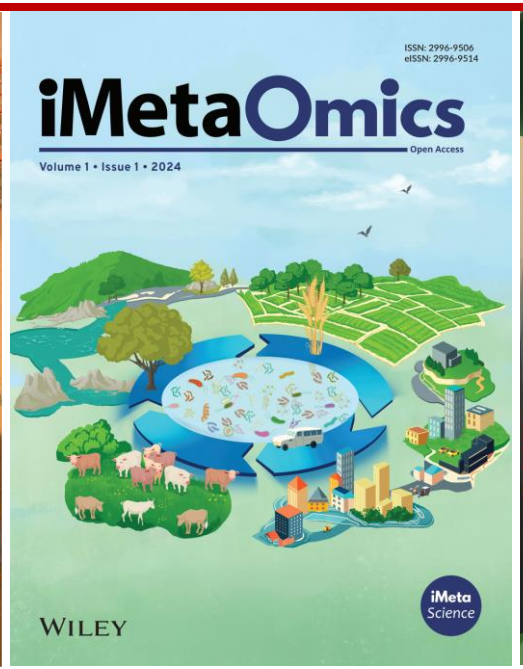





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