

in the formation of green-leaf volatiles, while terpene synthases (TPS) regulate the accumulation of floral and fruity compounds such as linalool and geraniol. Transcription factors, including MYB, bHLH, ERF, and MYC, play central regulatory roles in these pathways. For example, CsMYB1, CsERF2, and bHLH13 form regulatory networks that influence bitterness and temperature adaptability by modulating flavonoid synthesis and carbon allocation (Shen et al., 2024). In addition, pan-genome studies have shown that LTR transposon expansion can lead to gene copy number variation, resulting in functional diversity affecting leaf color, sprouting time, and flavor metabolism. This indicates that quality differences in Longjing tea arise not only from gene expression regulation but also from structural genetic variation.

7.2 Application of multi-omics technologies in quality research

Multi-omics technologies—including genomics, transcriptomics, metabolomics, and proteomics—have become essential tools for elucidating the mechanisms of Longjing tea quality formation, enabling systematic analysis from genes to metabolites to phenotypes. At the genomic level, the LJ43 reference genome and population resequencing have revealed the evolutionary history of tea plants and selection signals in quality-related genes. Pan-genome studies further integrate structural variation information across multiple cultivars, allowing the detection of presence/absence variation (PAV) and copy number variation (CNV), which can then be associated with flavor and leaf color traits (Chen et al., 2023).

In integrated transcriptomic and metabolomic analyses, thousands of differentially expressed genes have been identified among cultivars, mainly enriched in pathways such as amino acid metabolism, flavonoid biosynthesis, lipid metabolism, and carbon metabolism. The expression patterns of these genes can directly explain differences in catechin, theanine, and caffeine contents (Wen et al., 2023). Through weighted gene co-expression network analysis (WGCNA), key hub gene modules regulating flavonoid and aroma biosynthesis can be identified, enabling the pinpointing of core regulatory nodes of quality traits (Yu et al., 2025). At the metabolomic level, analytical techniques such as LC-MS, GC-MS, and NMR are widely used to compare metabolic differences among cultivars, production regions, and processing methods, and to identify quality markers. For example, the dynamic changes of polyphenols and amino acids during processing can be tracked to elucidate the regulatory pathways of quality formation.

Notably, multi-omics research has evolved from single-layer analysis to multi-scale integration, including genome×transcriptome×metabolome integration, as well as epigenetics × environmental factors × quality phenotypes. These integrative analyses reveal that environmental factors such as shading and temperature influence quality formation in a cultivar-dependent manner by regulating gene expression and metabolic networks (Shen et al., 2024; Wu et al., 2025). Therefore, multi-omics approaches not only deepen the understanding of quality formation mechanisms but also provide molecular targets for precision breeding.

7.3 Marker-assisted breeding and development of new cultivars

With the advancement of molecular technologies, the breeding of cultivars suitable for Longjing tea processing is shifting from traditional empirical selection to molecular design breeding. Molecular marker-assisted selection (MAS), QTL mapping, and genome-wide association studies (GWAS) have provided powerful tools for the precise improvement of quality traits. For example, in QTL mapping studies based on a genetic population derived from Longjing 43 and albino cultivars, high-density SNP maps (average spacing of 0.69 cM) have successfully identified multiple QTLs controlling free amino acids such as theanine and glutamic acid, explaining approximately 11.8%-23.7% of phenotypic variation (Chen et al., 2023). These findings provide clear genetic targets for breeding high-umami Longjing tea cultivars. At the genome-wide level, GWAS has identified multiple loci associated with catechins, caffeine, leaf color, and stress resistance (Gao et al., 2023a). Meanwhile, SNP resources based on the LJ43 reference genome facilitate the development of molecular markers, enabling early-stage prediction and selection of quality traits.

In terms of marker types, ILP (intron length polymorphism) markers, due to their high polymorphism and cross-species applicability, are widely used in cultivar identification and genetic analysis (Liu, 2024). In addition, graph-based pan-genome technologies allow structural variations to be incorporated into breeding systems,