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Title

Revealing Distinctions in Genetic Diversity and Adaptive Evolution Between Two Varieties of Camellia sinensis by Whole-Genome Resequencing

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Abstract

Camellia sinensis var. sinensis (CSS) and C. sinensis var. assamica (CSA) are the two most economically important tea varieties. They have different characteristics and geographical distribution. Their genetic diversity and differentiation are unclear. Here, we identified 18,903,625 single nucleotide polymorphisms (SNPs) and 7,314,133 insertion– deletion mutations (indels) by whole-genome resequencing of 30 cultivated and three wild related species. Population structure and phylogenetic tree analyses divided the cultivated accessions into CSS and CSA containing 6,440,419 and 6,176,510 unique variations, respectively. The CSS subgroup possessed higher genetic diversity and was enriched for rare alleles. The CSA subgroup had more non-synonymous mutations and might have experienced a greater degree of balancing selection. The evolution rate (dN/dS) and KEGG enrichment indicated that genes involved in the synthesis and metabolism of flavor substances were positively selected in both CSS and CSA subpopulations. However, there are extensive genome differentiation regions (2959 bins and approximately 148 M in size) between the two subgroups. Compared with CSA (141 selected regions containing 124 genes), the CSS subgroup (830 selected regions containing 687 genes) displayed more selection regions potentially related to environmental adaptability. Fifty-three pairs of polymorphic indel markers were developed. Some markers were located in hormone-related genes with distinct alleles in the two cultivated subgroups. These identified variations and selected regions provide clues for the differentiation and adaptive evolution of tea varieties. The newly developed indel markers will be valuable in further genetic research on tea plants.