Genetic Diversity and Population Structure of Tea (*Camellia sinensis* L.) Germplasm Using SSR Markers

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[Introduction]

The tea plant (*Camellia sinensis* L.) is an important commercial crop with remarkably high catechin concentrations. Tea germplasm, one of the valuable and fundamental materials for tea breeding and biotechnology, has a huge potential for the future of the whole tea industry. In this study, the genetic diversity and population structure of tea germplasm were analyzed using SSR markers.

[Materials and Methods]

Thirty-five tea germplasm conserved at the National Agrobiodiversity Center (NAC) (http://genebank.rda.go.kr) were selected for analyzing their genetic diversity and population structure. A total of 29 microsatellite markers were used for generating genotypic data.

[Results and Discussion]

A total of 145 alleles were amplified with an average of 4.93 per primer pair. The number of alleles ranged from 2 to 22 in different populations. Observed heterozigosity (Ho) and expected heterozigosity (He) ranged from 0.086 to 0.824 and 0.108 to 0.861, respectively. Effective number of alleles (Ae) ranged from 1.121 to 7.185 per locus for all populations. The average of polymorphism information content was 0.501 in all 35 tea accessions. AMOVA analysis showed that the percentage of molecular variance was 0.45%, 36.38%, and 63.17% among the populations, among individuals, and within individuals, respectively. Cluster analysis and principal coordinate analysis produced similar grouping patterns of all analyzed accessions. Population structure was best explained by K = 4 which revealed that only eleven accessions were highly assigned to a single cluster and the remaining 24 accessions could be considered as admixed. The differentiated genetic lineages found in this study could be useful information for tea improvement and conservation programs.

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