

## Genetic diversity analysis of tea (*Camellia sinensis* (L.) O. Kuntze) germplasm in Korea genebank

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### ABSTRACT

Tea plant (*Camellia sinensis* (L.) O. Kuntze) has been cultivated widely in many developing Asian, African, and South American countries, where it is the most widely consumed beverage in the world next to water. It has critical importance to understand the genetic diversity and population structure for effective collection, conservation, and utilization of tea germplasm. In this study, 410 tea accessions collected from South Korea were analyzed using 21 SSR markers. Among 410 tea accessions, 85.4% (310 accessions) accessions were collected from Jeollanam-do. A total of 286 alleles were observed, and the genetic diversity and evenness were estimated to be averagely 0.79 and 0.61, respectively, across all the tested samples. Using discriminant analysis of principal components, the four clusters were detected in 410 tea accessions. Among them, cluster 1 showed higher frequency of rare alleles (less than 1%) than other clusters. Using calculation of the index of association and  $r_{baD}$  value, each cluster showed a clonal mode of reproduction. The result of AMOVA showed that most of the variation observed was within populations (99%) rather than among populations (1%). Our results might contribute to provide data about genetic diversity for the conservation of tea germplasm and for future breeding programs.

**Keywords:** *Camellia sinensis* L., Genetic diversity, Plant germplasm, SSR marker, Tea

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\*\* (Acknowledgement) 본 연구는 농촌진흥청 농업과학기반기술연구사업(사업번호: PJ013557)의 지원에 의해 이루어진 결과로 이에 감사드립니다