

PB-039

Genetic Diversity and Population Structure of Tea Gemplasms Conserved in Korea Genebank

Kyung Jun Lee^{1*}, Do Yoon Hyun¹, Gyu-Taek Cho¹

¹National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, Jeonju-Si 54874, Rep. Korea

[Introduction]

Tea (*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.

[Materials and Methods]

In this study, 462 tea accessions collected in National Agrobiodiversity Center at RDA were analyzed using 33 SSR markers.

[Results and Discussion]

A total of 428 alleles were detected in 33 SSR loci among 462 tea accessions. The Shannon-Wiener index and Nei's genetic diversity were estimated to be average of 1.78 and 0.77, respectively. Analysis of the SSR data using neighbor-joining method grouped the sampled accessions into three major clusters. In STRUCTURE analysis, 462 tea accessions were divided into two subpopulations ($\Delta K=2$). Using discriminant analysis of principal components, the four clusters were detected in 462 tea accessions. The result of AMOVA showed that most of the variation observed was within populations rather than among populations. Our results might contribute to provide data about genetic diversity for the conservation of tea germplasm and future breeding programs.

[Acknowledgement]

본 연구는 농촌진흥청 농업과학기술연구사업(사업번호: PJ013557)의 지원에 의해 이루어진 결과로 이에 감사드립니다.

*Corresponding author: Tel. +82-63-238-4861, E-mail. lkj5214@korea.kr