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Genetic Diversity and Population Structure of Ginseng Germplasm Conserved in Korea Genebank

Do Yoon Hyun^{1*}, Kyung Jun Lee¹, Gyu-Taek Cho¹

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

[Introduction]

Ginseng (*Panax ginseng* C.A. Meyer), commonly known as Korean or Asian ginseng, is a perennial herb native to Korea and China. There has been limited research effort to analyze the genetic diversity and population structure of ginseng germplasm because of its growth habits. In the present study, genetic diversity and population structure of ginseng germplasm conserved in the National Agrobiodiversity Center (NAC) of South Korea were analyzed to provide basic data for future preservation and breeding of ginseng genetic resources.

[Materials and Methods]

In this study, 451 Korean ginseng accessions conserved at NAC were genotyped using 33 SSR markers to reveal the genetic diversity and population structure in the ginseng germplasm.

[Results and Discussion]

Total 451 ginseng accessions used in this study were collected from 22 cities at six provinces in South Korea. Among 451 ginseng accessions, 390 (86.5%) and 61 (13.5%) ginseng accessions were landraces and breeding lines, respectively. A total of 226 alleles were detected in 33 SSR loci among the 451 ginseng accessions. The result of STRUCTURE analysis of ginseng landraces and breeding lines showed the best grouping number (K=2) based on the delta K. Using the discriminant analysis of principal components, only three sub-populations have been identified within 61 ginseng breeding lines while 11 sub-populations were detected in 390 landraces. The result of AMOVA showed that most of the variation observed was within populations rather than among populations. The quantitative analysis of the genetic diversity and population structure in this study could be useful for genetic and genomic analysis and utilization of the genetic variation in ginseng breeding program.

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*Corresponding author: Tel. +82-63-238-4912, E-mail. dyhyun@korea.kr