

## **Genetic Diversity and Population Structure of Ginseng (*Panax ginseng* Meyer) Germplasm Using SSR Markers**

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### **[Introduction]**

Ginseng (*Panax ginseng* Meyer), a rare perennial plant belonging to the *Araliaceae* family, has been used in Korea and China as herbal medicine for decades. In this study, the genetic diversity and population structure of ginseng germplasm were analyzed using SSR markers to provide data for ginseng genetic resources preservation and breeding.

### **[Materials and Methods]**

Forty-six ginseng germplasm were conserved at the National Agro-biodiversity Center (NAS) of the Rural Development Administration (RDA), Republic of Korea (<http://genebank.rda.go.kr>). These were investigated using 35 microsatellite (SSR) markers.

### **[Results and Discussion]**

Among the 35 SSR markers, 20 SSRs did not show polymorphism. In 15 polymorphic SSRs, a total of 39 alleles were amplified with an average of 2.6 per primer pair. The number of alleles varied from 2 to 5 in different populations. Effective number of alleles ( $N_e$ ) ranged from 1.09 to 2.09 per locus for all population. The average of polymorphism information content was 0.321 for all 46 ginseng accessions. AMOVA analysis showed only the percentage of molecular variance within individuals which was 100%. Cluster analysis and principal coordinate analysis produced similar grouping patterns of all analyzed accessions. Population structure was best explained by  $K = 3$  revealing that 28 accessions were highly assigned to a single cluster while 18 accessions could be considered as admixed. Findings of the study could provide basic data for future studies on ginseng genetic diversity and ginseng cultivars breeding.

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