

Estimation of genetic diversity on wild and cultivated *Panax ginseng* populations using SSR (simple sequence repeat) markers

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[Introduction]

Korean ginseng (*Panax ginseng* C. A. Meyer) is one of the most famous medicinal plant in the world. But there is a lack of genetic and genomic researches because of the characteristics of a complex allotetraploid genome structure and a huge genome size of 3.6Gbp. The genetic diversity study on ginseng wild collections and cultivated accessions will be fundamental to further assist breeding researches.

[Materials and Methods]

Using the Microsatellite identification tool (MISA) and Primer3 programs, simple sequence repeat (SSR) markers were developed based on whole genome sequence data. The genotypes of ginseng wild collections and cultivated accessions were identified using polyacrylamide gel electrophoresis (PAGE). As statistical analysis with the genotype information, major allele frequency (MAF), gene diversity (GD), polymorphic information content (PIC) value, the proportion of heterozygosity and Nei's genetic distance of each microsatellite locus were calculated using the PowerMarker program. Phylogenetic relationships among the ginseng populations was performed based on Nei's genetic distance and the unweighted pair group method with arithmetic mean (UPGMA) as implemented in MEGA 7.0

[Results and Discussions]

At the SSR markers called gws218, gws450, gws454, gws936, and gws1070, there were 20 alleles in total. The MAFs were calculated in the range of 43.5% to 87.8%, with an average of 62.4%. The GDs were broadly ranged from 0.218 to 0.734 with an average of 0.508. The proportions of heterozygosity were ranged from 0.199 to 0.701, with an average of 0.454. Although we found that there were no significant differences in genetic diversity between wild collections and cultivated accessions, ginseng populations showed a relatively high genetic diversity indicating that cultivated accessions contained enough diversity. Consequently we elucidated phylogenetic relationships of 147 populations based on the genotypes of five SSR markers. The phylogenetic information will support genetic and genomic studies and breeding of elite cultivars.

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