

P018

Development and validation of SSR markers in *Eleutherococcus senticosus*

Kyung Jun Lee¹⁾*, Yong-Jin An²⁾, Jin-Kwan Ham²⁾, Kyung-Ho Ma¹⁾, Jung-Ro Lee¹⁾,
Yang-Hee Cho¹⁾, Gi-An Lee¹⁾

¹⁾ National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, 370 Nonsaengmyeong-Ro, Wansan-Gu, Jeonju-Si, Jeollabuk-Do, 54874, Republic of Korea

²⁾ Ginseng & Medicinal Herb Experiment Station, Gangwon Provincial ARES, 83, Chungyeol-ro, Chuncheon-si, Gangwon-do, 24226, Republic of Korea

Abstract

Eleutherococcus senticosus (Siberian ginseng) is an important medicinal tree found in Russian taiga, and northern regions of Korea, Japan, and China. In this study, we analyzed the genome-wide distribution of microsatellites in *E. senticosus* using developed SSR markers. A total of 711 clones from an SSR-enriched genomic DNA library were sequenced, of which 47 clones (6.6%) were redundant. Of the 664 independent clones, only 12 polymorphic SSR markers were obtained, which also revealed successful amplicons in *E. senticosus* accessions. Using the developed SSR markers, we estimated genetic diversity and population structure among 131 *E. senticosus* accessions in Korea and China. The number of alleles ranged from 2 to 11, with an average of 7.4 alleles. The mean values of observed heterozygosity (H_O) and expected heterozygosity (H_E) were 0.59 and 0.56, respectively. The average polymorphism information content (PIC) was 0.51 in all 131 *E. senticosus* accessions. *E. senticosus* accessions in Korea and China showed a close genetic similarity. Significantly low pairwise genetic divergence was observed between the two regions, suggesting a relatively narrow level of genetic basis among *E. senticosus* accessions. Our results not only provide molecular tools for genetic studies in *E. senticosus* but are also helpful for conservation and *E. senticosus* breeding programs.

Keywords: *Eleutherococcus senticosus*, SSR, Genetic diversity, Population structure

Corresponding author*

Kyung Jun Lee

Address: National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, 370 Nonsaengmyeong-Ro, Wansan-Gu, Jeonju-Si, Jeollabuk-Do, 54874, Republic of Korea

Tel and Fax: +82-63-238-4861/+82-63-238-4859

E-mail: lkj5214@korea.kr