

Development of genic-SSR markers and genetic diversity of Indian lettuce (*Lactuca indica* L.) in South Korea

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[Introduction]

Indian lettuce (*Lactuca indica* L.) is an undomesticated wild plant with high economic potential. We know little about the plant's genome, such as its DNA markers, making genetic research using this plant difficult. Therefore, this study was performed to develop genic-SSR markers based on the transcribed sequences from *L. indica* leaf tissue, to investigate the transferability of SSR markers to related *Lactuca* species and the genetic diversity study in *L. indica* accessions collected from South Korea.

[Materials and methods]

Seventy-four *L. indica* accessions that cover 42 diverse collection sites in South Korea and two accessions of *L. serriola* and *Lactuca sativa* were used for the marker transferability test and genetic relationship analysis in *Lactuca* spp. Genic-simple sequence repeat (SSR) primers were synthesized from *L. indica* transcriptomic sequences using PRIMER 3 software. Genomic DNA was extracted using a GeneAll Exgene™ Plant SV kit and diluted to a working concentration of 30 ng/μL with Tris-EDTA buffer. The SSR genotyping was performed using Fragment Analyzer. Genetic diversity parameters and Nei's genetic distance were calculated using Popgene version 1.32. The resulting Nei's genetic distance matrix was used to construct an unweighted neighbor-joining (NJ) phylogenetic tree using Mega 6.0 program. Principal Coordinate Analysis (PCoA) and a hierarchical analysis of molecular variance (AMOVA) was performed using GenAlEx 6.5 software.

[Result and discussions]

Our genic-SSR markers were highly polymorphic with mean polymorphic information content of 0.61 and, on average, 10.89 alleles per locus. The average expected heterozygosity (0.76) was higher than the observed heterozygosity. An ANOVA test revealed that most of the total variance in our population is attributable to genetic variation among accessions, rather than among provinces and species. STRUCTURE, NJ trees, and PCoA analyses resulted in three clusters, where northern and central-southern *L. indica* accessions were grouped into two clusters with some admixture. Moreover, *L. serriola* and *L. sativa* accessions were clustered with *L. indica*, indicating the possibility of using *L. indica* as a lettuce gene pool. Therefore, our SSR markers will be useful in germplasm assessment and genetic studies of *L. indica* and other *Lactuca* species.

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