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단순 내부 반복 서열에 의한 한국과 중국산 도라지의 유전적 다양성과 동정

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Genetic Diversity and Identification of Korean and Chinese *Platycodon grandiflorum* Using ISSR Markers

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Objectives

Platycodon grandiflorum (Campanulaceae) is a very important traditional medicinal plant and called Doragi in Korea. It is indispensably important issue to establish the distribution system on the basis of discrimination of the herbal medicines and quality control. The domestic Doragi is currently being sold at a price 10 times higher than the Chinese one. Although these two accessions can be identified by root morphology, it is impossible to distinguish between the two accessions when the roots are sliced. Moreover, in herbal markets the Chinese Doragi is illegally sold either without the correct label or by mixing with domestic Doragi. Therefore, finding a rapid means to discriminate between the two accessions when they were dried and sliced is very important in Korea. This study was carried out to develop a method that could be used to discriminate between Korean and Chinese *P. grandiflorum* based on molecular markers.

Materials and Methods

○ Materials

All of the four accessions of *P. grandiflorum* were collected from populations in Korea and China. Wild and domestic accessions of *P. grandiflorum* were collected from Mt. Giri and Andong Province in Korea, respectively. The imported cultivated accession of *P. grandiflorum* from China was purchased from market and Chinese wild *P. grandiflorum* was gifted from National Crop Experiment Station, Suwon, Gyonggi Province.

○ Methods

The genomic DNA of the 270 samples including outgroup was extracted from fresh roots using the plant DNA Zol Kit according to the manufacturer's protocol. Eleven arbitrarily chosen primers of Bioneer Technoligies were used. All the reactions were repeated twice and only reproducible bands were scored for analyses. The following genetic parameters were calculated using a POPGENE computer program: the percentage of polymorphic loci (Pp), mean numbers of alleles per locus (A), effective number of alleles per locus (Ae) and gene diversity (H).

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Results

In a simple measure of intraspecies variability by the percentage of polymorphic bands, the Chinese cultivated exhibited the lowest variation (16.7%). The Korean wild accession showed the highest (40.5%) (Table 2). Mean number of alleles per locus (A) ranged from 1.167 to 1.405 with a mean of 1.292. The effective number of alleles per locus (Ae) ranged from 1.099 to 1.298. ISSR01-02 locus can be recognized as unique locus of Korean groups (wild and cultivated accessions) (Fig. 2). Thus the locus can be used distinguish Korean accessions from Chinese accessions. While ISSR04-06 locus was found specific to Chinese groups (wild and cultivated accessions) and did not shown in Korean accessions.

The phenetic tree showed the distinct groups Korean and Chinese accessions were well separated each other. The tree also shows genetic differentiation between wild and cultivated accessions for Korean species.

Table 1. Measurements of genetic variation for accessions of Doragi (Platycodon grandiflorum)

Accession	Np	Pp	A	AE	H	I
Korean wild	17	40.5	1.405	1.298	0.164	0.239
Korean cultivated	9	21.4	1.214	1.138	0.079	0.117
Chinese wild	7	16.7	1.167	1.099	0.059	0.088
Chinese cultivated	16	38.1	1.381	1.285	0.157	0.228

The number of polymorphic loci (Np), percentage of polymorphism (Pp), mean number of alleles per locus (A), effective number of alleles per locus (AE), gene diversity (H), and Shannon's information index (I).

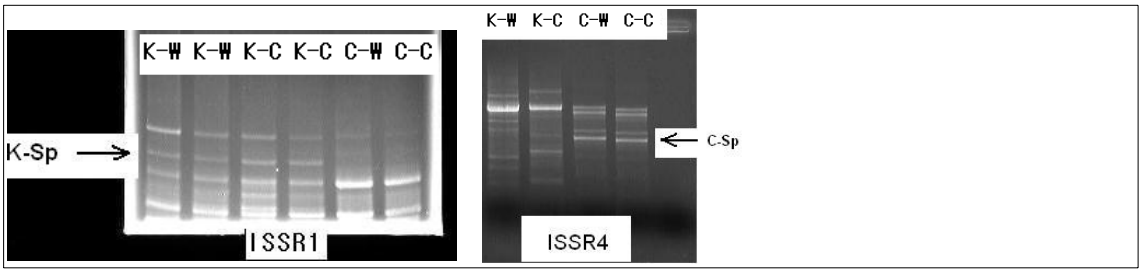

Fig. 1. A portion of ISSR patterns in four accessions of Platycodon grandiflorum using primer ISSR01 and ISSR04. K-W: Korean wild, K-C: Korean cultivated, C-W: Chinese wild, and C-C: Chinese cultivated. K-Sp: Specific band to Korean group. C-Sp: Specific band to Chinese group.