A13 RAPD와 SSR을 이용한 서로 다른 지역에서 수집된 같은 형태적 형질을 가진 대두 유전자원에서의 유전적 다형성 탐색

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Identification of Genetic Polymorphism using RAPD and SSR in the Soybean Germplasms Collected from Different Areas with Same Morphological Traits

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Objectives

Molecular marker has been widely used to detect the genetic difference in cereal crops with a little same morphological traits. The objective of this study was to identify the genetic difference among soybean germplasms collected from different areas with six same morphological traits using RAPD and SSR marker.

Materials and Methods

- **Soybean materials** : Eight soybean germplasms collected from different growing areas in 1999.
- **DNA extraction** : Genome DNA was isolated from young leaf grown in green-house using CTAB method.
- **Molecular marker** : RAPD and SSR markers were detected in eight soybean germplasms. Twenty Operon(OPAA01-OPAA20), two SSR primers (Satt002 and Satt231) were used (Table 1).
- **Morphological traits** : Flower, pubescence, seed, hilum and mature cotyledon color and plant leaf type traits were checked.

Results and Discussion

Collection areas and morphological traits of eight soybean germplasms used are shown in table 2. Eight soybean germplasms have the same morphological traits. Primer sequences used are shown in table 1. RAPD and SSR banding pattern produced on the eight soybean genomic DNA was the absolutely same (Fig. 1). This result indicates that these eight soybean germplasms would be from the one same genotype although they have been grown in different areas. Therefore, when collecting Korea-native soybean germplasms, genetic similarity of the strains with many same morphological traits should be checked before using.

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Table 1. Primer sequence used to produce molecular marker.

Primer	Sequence (5′ to 3′)	Primer	Sequence (5′ to 3′)
OPAA01	CAGGCCCTTC	OPAA02	TGCCGAGCTG
OPAA03	AGTCAGCCAC	OPAA04	AATCGGGCTG
OPAA05	AGGGGTCTTG	OPAA06	GGTCCCTGAC
OPAA07	GAAACGGGTG	OPAA08	GTGACGTAGG
OPAA09	GGGTAACGCC	OPAA10	GTGATCGCAG
OPAA11	CAATCGCCGT	OPAA12	TCGGCGATAG
OPAA13	CAGCACCCAC	OPAA14	TCTGTGCTGG
OPAA15	TTCCGAACCC	OPAA16	AGCCAGCGAA
OPAA17	GACCGCTTGT	OPAA18	AGGTGACCGT
OPAA19	CAAACGTCGG	OPAA20	GTTGCGATCC
Satt002	Foward	TGT GGG TAA AAT AGA TAA AAA T	
	Reverse	TCA TTT TGA ATC GTT GAA	
Satt231	Foward	GCGTGTGCAAAATGTTCATCATCT	
	Reverse	GGCACGAATCAACATCAAAACTTC	

Table 2. Collection area and morphological traits of eight soybean germplasms used.

Strain	Collection area	Morphological traits					
		flower color	pube-scence color	leaf type	seed coat color	hilum color	seed cotyledon color
M06	Kyongnam Sanchong	purple	white	normal	black	black	green
M15	Kyongnam Sanchong	purple	white	normal	black	black	green
M17	Kyongnam Hapcheon	purple	white	normal	black	black	green
M18	Kyongnam Hapcheon	purple	white	normal	black	black	green
M91	Chonnam Tamyang	purple	white	normal	black	black	green
M111	Chonnam Changsung	purple	white	normal	black	black	green
M112	Chonnam Kurye	purple	white	normal	black	black	green
M117	Chonnam Kurye	purple	white	normal	black	black	green

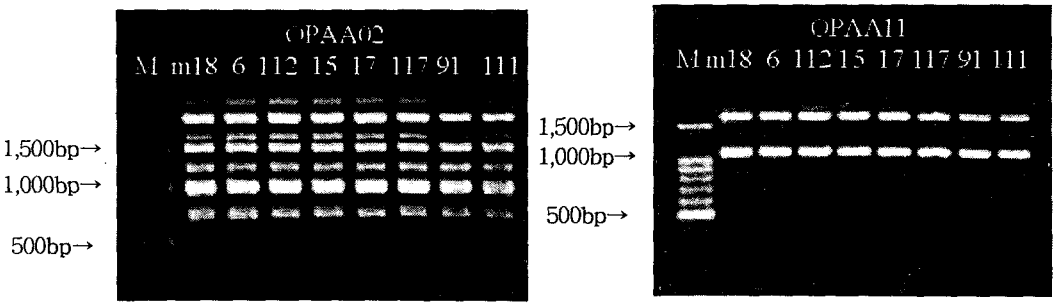

Fig.1. DNA amplification patterns obtained with RAPD primers OPAA02 and OPAA11. M is molecular marker. PCR products were separated on a 1.2% agarose gel followed by staining with ethidium bromide.

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