

Identification of *Panax* species and *Panax ginseng* cultivars using SNP markersYurry Um^{*}, Eunjung Cho, Chan-Moon Chung, Yi Lee[†]Department of Industrial Plant Science & Technology,
Chungbuk National University Cheongju, Korea**Objectives**

The single nucleotide polymorphism (SNP) has been widely used for species or variety identification from many crops. Direct sequencing of DNA fragments amplified by PCR from several individuals is one of direct way to identify single nucleotide polymorphisms. In this experiment, we carried out SNP discovery by direct sequencing of PCR fragments for identification of *Panax* species and *Panax ginseng* cultivars.

Materials and Methods

We used 2,549 genome survey sequence (GSS) of *P. ginseng* for design of 96 random PCR primer sets to amplify 500~700 bp fragments. DNA was extracted from leaf tissue of five *Panax* cultivars, Chunpoong, Yunpoong, Jakyungjong, *Panax quinquefolius* L., and *Panax notoginseng* Wall, and used for PCR amplification. The PCR products were directly sequenced with one of each primer set. SNPs were discovered from the sequence data with CodonCode Aligner software. We tested the reproducibility of the SNP markers using *Panax* cultivars.

Results

Sequence data of five *Panax* cultivars were obtained from the fragments amplified using 96 random PCR primer sets. We identified 251 SNPs or INDELs by aligning of the sequences using CodonCode Aligner program. Most of the SNPs showed polymorphism from different *Panax* species, but, only 6 SNPs showed polymorphism from *Panax ginseng* cultivars. We tested the reproducibility of the 6 SNPs using multiple samples of each *Panax ginseng* cultivars. Among the 6 SNPs, 944 showed reproducibility and differentiate Yunpoong from other *Panax ginseng* cultivars, Chunpoong and Jakyungjong. The other SNP positions were not reproducible.

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Table 1. Primer sets for SNP marker discovery in *Panax ginseng* cultivars

Marker #	GenBank #	Primer sequence(5'→3')	Tm(°C)
903	BZ958992	Forward : TAATTCCTTGGGCACGTAGTAT Reverse : TGATCCGTAAAGATCTCCACTT	56
910	BZ958926	Forward : CGCCCCTAAAATAGGTATACAA Reverse : AGGGATAAAAATATTGATGATGGA	56
937	BZ958782	Forward : GGAAAGTTATTTTTCAACAAATGC Reverse : AATTTTCAGTATCTTCCATCTCTGAA	56
944	BZ958754	Forward : GAAGTAAGAGAACGTCTGAATGC Reverse : CGTTTTGAAGAAAAGAAGTGC	56
951	BZ958717	Forward : GCATCGAGAACATCTCTGTAAAA Reverse : TTATGACATGTTACTGTTGCGA	56
955	BZ958711	Forward : TTTATTTCTCCTACTTGCGCTC Reverse : ACAAATTCAACTTCACGCTCT	56

Table 2. Haplotypes of *Panax* cultivars

Marker #	<i>Panax ginseng</i> C. A. Meyer			<i>Panax</i>	<i>Panax</i>	Reproducibility
	Chunpoong	Yunpoong	Jakyungjong	<i>quinquefolius</i> L.	<i>notoginseng</i> Wall	
903	G	A or G	G	A or G	A	NR
910	T	T	C	T	C	NR
910	A	G	G	A	A	NR
937	G	T	G	T	G	NR
944	A	G	A	G	G	R
951	A	-	A	-	A	NR
955	G	A	G	A	G	NR

R : Reproducible, NR : Not Reproducible