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Development of CAPS markers using mitochondrial consensus primers for molecular authentication of Korean ginseng cultivars

미토콘드리아의 consensus 프라이머를 활용한 고려인삼 품종의 분자적 입증을 위한 CAPS 마커 개발

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Objectives

Ginseng (*Panax ginseng* C.A Mayer) has been used as a tonic, a stimulant, and a fatigue-resistance medicine for over 2000 years in Oriental countries. New Korean ginseng cultivars with superior agricultural traits have been developed such as Chunpoong, Yunpoong, Gopoong, Kumpoong, Sunpoong, and Sunwon for last several decades. However, discrimination of these ginseng cultivars is very difficult owing to their extremely similar external morphology. This difficulty can cause various problems in seed purity management, cultivar protection, registration, and quality control of ginseng products. Therefore, in this study, multiple consensus primer sets, which were previously developed on the basis of conserved regions of mitochondrial genome, were tested to detect genetic polymorphism discriminating Korean ginseng cultivars as well as them from foreign *Panax* species, and then their PCR products were applied to CAPS marker system in order to detect secondary polymorphism which may exist within amplified PCR products.

Materials and Methods

1. Korean ginseng cultivars : Chunpoong, Yunpoong, Gopoong, Kumpoong, Sunpoong, and Sunwon
2. Foreign ginseng : American ginseng (*P. quinquefolius*)
   Chinese ginseng (*P. notoginseng*)
3. PCR primers : 34 mitochondrial consensus primers (Dumolin-Lapegue et al. 1997; Demesure et al. 1995; Duminil et al. 2002)
4. Restriction enzymes for CAPS analysis : *Alu* I, *Hae* III, *Hinf* I, *Rsa* I, *Taq* I and *Tsp509* I

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Results

In the PCR amplification results, four primers generated co-dominant polymorphic banding patterns discriminating the Korean ginseng cultivars from *P. quinquefolius and P. notoginseng.* In the CAPS analysis results, the majority of the cleaved PCR products also yielded additional latent polymorphisms between the Korean ginseng cultivars and two foreign Panax species. Specific latent CAPS polymorphisms for cultivar Gopoong and Chunpoong were detected from internal region amplified with mt9 primer by treating *Hinf* I and *Tsp509* I endonucleases, respectively.

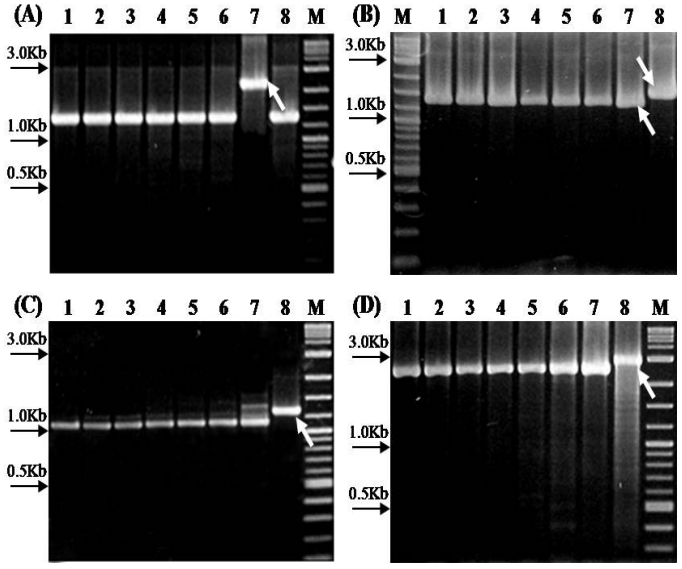

Fig. 1 Length polymorphism by PCR amplification using the consensus primer sets of mtDNA among six Korean ginseng cultivars, *P. quinquefolius*, and *P. notoginseng* lane 1, Chunpoong; lane 2, Yunpoong; lane 3, Gopoong; lane 4, Kumpoong; lane 5, Sunpoong; lane 6, Sunwon; lane 7, *P. quinquefolius;* lane 8, *P. notoginseng.*

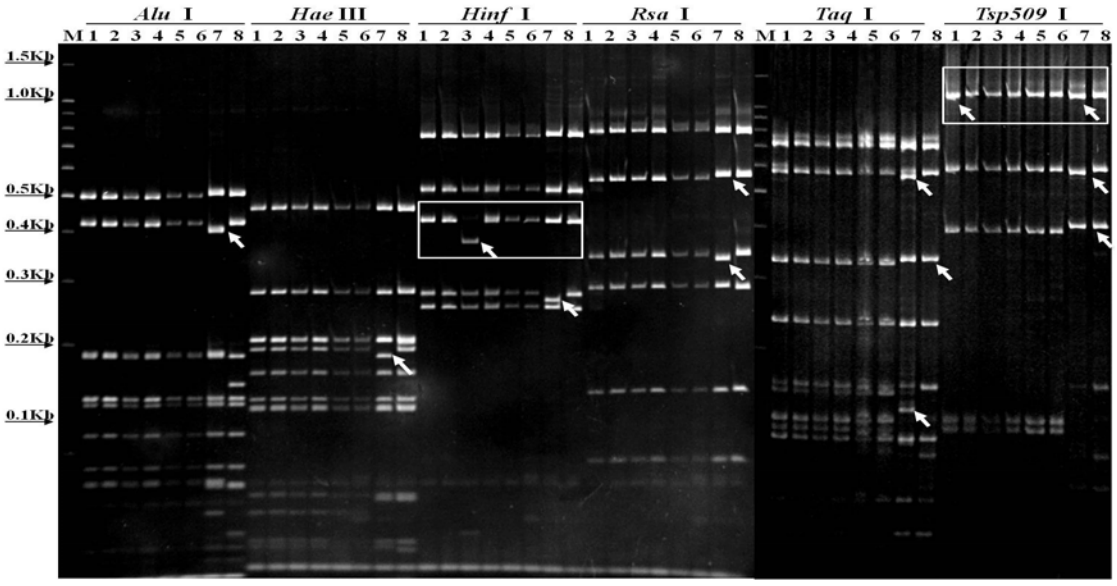

Fig. 2 CAPS markers for Korean ginseng (cv.) Chunpoong and Gopoong. lane 1, Chunpoong; lane 2, Yunpoong; lane 3, Gopoong; lane 4, Kumpoong; lane 5, Sunpoong; lane 6, Sunwon; lane 7, *P. quinquefolius;* lane 8, *P. notoginseng.* Lane 'M': 100bp DNA ladder (Promega).