

Single Nucleotide Polymorphisms(SNPs) of *rpoC1* gene for origin identification between Korean and Chinese cultivars in *Liriope* & *Ophiopogon* Genus

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맥문동속 한국산과 중국산 품종 사이의 기원정립을 위한 *rpoC1* 유전자의 단일염기다양성(Single Nucleotide Polymorphisms)

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Objectives

The purpose of our study was to develop SNP markers for origin identification of Korean and Chinese cultivar in *Liriope* and *Ophiopogon* collected from Seoul, Daegu, Geumsan herb marketplace and Cheongyang using *rpoC1* in DNA barcode region.

Materials and Methods

- Materials
 - We used 14 Selected Korean and Chinese *Liriope* and *Ophiopogon* cultivars collected from Seoul(Yangnyeongsi marketplace), Daegu(Yangyeongsi marketplace), Geumsan(Geumsan ginseng marketplace).
- Methods
 - Sequencing : DNA of 14 collected *Liriope* and *Ophiopogon* samples were amplified using *rpoC1* primer. Amplified (PCR) product were cloned and three recombinant colonies were randomly picked up from the primary transformation plates containing ampicillin, X-gal, and IPTG. Plasmid DNAs were sequenced using an ABI 3730xl DNA sequencer with a BigDye terminator kit (Applied Biosystems).
 - The resulted sequences were assembled and aligned using SeqMan software program. UPGMA dandrogram was drawn using sequence data of 3 colonies for each of 6 samples and two colonies for KULP006 and KULP008 with Mega4 program .
 - SNP marker development : SNP markers were designed using the Primer 3 free release internet program.

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Results

Among 14 collected cultivars, 6 cultivars (KULP001, KULP003, KULP004, KULP005, KULP009 and KULP010) did not shown clear sequence result when aligned. So, only the rest 8 cultivars were used for cluster analysis. In UPGMA dendrogram, the genetic relationship of 8 *Liriope* and *Ophiopogon* could be seen clearly as two groups. Group 1 as a Korea cultivars and composed of cultivar 2, 11, 12, 13 and 14 and group 2 as a China cultivar and composed of cultivar 6, 7 and 8 respectively (fig. 1).

Table 1. shown the alignment result showing SNP position of the two cultivars (Korea and China).

Table 1. SNPs(Single Nucleotide Polymorphisms) between Korean and Chinese cultivars found from the genic region of *rpoCl* in *Liriope* and *Ophiopogon* genus.

Origin	sample	1	4	16	25	37	55	70	97	103	115	139	144	153	167	177	183	198	207	224	231	241	249
Korea	KULP002	G	A	A	T	A	A	C	G	T	T	T	G	G	A	A	A	G	A	G	C	A	T
	KULP011	G	A	A	T	A	A	C	G	T	T	T	G	G	A	A	A	G	A	G	C	A	T
	KULP012	G	A	A	T	A	A	C	G	T	T	T	G	G	A	A	A	G	A	G	C	A	T
	KULP013	G	A	A	T	A	A	C	G	T	T	T	G	G	A	A	A	G	A	G	C	A	T
	KULP014	G	A	A	T	A	A	C	G	T	T	T	G	G	A	A	A	G	A	G	C	A	T
China	KULP006	A	C	G	C	G	G	T	A	C	C	C	A	A	G	G	C	A	G	A	T	C	G
	KULP007	A	C	G	C	G	G	T	A	C	C	C	A	A	G	G	C	A	G	A	T	C	G
	KULP008	A	C	G	C	G	G	T	A	C	C	C	A	A	G	G	C	A	G	A	T	C	G

Origin	sample	252	258	259	264	267	297	312	339	340	376	382	388	391	398	407	413	416	419	449	452	461	473	
Korea	KULP002	C	G	A	A	A	A	A	G	T	G	A	G	C	A	G	A	T	G	C	T	C	C	
	KULP011	C	G	A	A	A	A	A	G	T	G	A	G	C	A	G	A	T	G	C	T	C	C	
	KULP012	C	G	A	A	A	A	A	G	T	G	A	G	C	A	G	A	T	G	C	T	C	C	
	KULP013	C	G	A	A	A	A	A	G	T	G	A	G	C	A	G	A	T	G	C	T	C	C	
China	KULP006	T	A	G	T	G	G	G	A	C	A	T	A	T	G	A	G	C	T	A	C	T	T	
	KULP007	T	A	G	T	G	G	G	A	C	A	T	A	T	G	A	G	C	T	A	C	T	T	
	KULP008	KULP008-1	T	A	G	T	G	G	G	A	C	A	T	A	T	G	A	G	C	T	A	C	T	T
		KULP008-2	T	A	G	T	G	G	G	A	C	A	T	A	T	G	A	G	C	T	A	C	T	T



Fig. 1 UPGMA dendrogram showing genetic relationships among the 8 genotypes collected from various parts of hub marketplace. The colored solid squares next to each genotype indicate the place of origin where the individuals were collected.