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Feasibility of 5S rRNA spacer and atpB-rbcL intergenic spacer region to the identification of ginseng cultivars

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Objectives

Ginseng (panax ginseng) is one of the most important medicinal plants in the Orient, in which almost every species of the genus has been employed as a source of medicine. It has been used as a tonic, a stimulant and an agent for more than 2000 years both in China and Korea. There are 5 cultivars have been found in Korea, making the identification of them necessary for both consumers and agriculture. Therefore, it is necessary to develop a time-saving technology to clearly and precisely differentiate ginseng cultivars. 5S rRNA spacer and atpB-rbcL intergenic region of chloroplast DNA can be used as molecular markers for cultivar identification, but the feasibility to the identification of ginseng cultivars need to be further studied. In our research, 5S rRNA spacer and atpB-rbcL intergenic spacer region of chloroplast DNA were amplified by polymerase chain reaction (PCR) from the isolated genomic DNA. The amplified spacer regions of different cultivars of ginseng were sequenced and compared to investigate the utility of 5S rRNA spacer and atpB-rbcL intergenic region in discriminating ginseng cultivars.

Material and methods

① DNA extraction of panax ginseng cultivars.

② PCR of 5S rRNA spacer and atpB-rbcL intergenic region.

3 Purification and sequencing.

④ Comparison of 5S rRNA spacer and atpB-rbcL intergenic region of different cultivars.

Results and discussions

Although the 5S rRNA spacer and *atpB-rbcL* intergenic region evolve rapidly, 5 cultivars of *panax ginseng* exhibited complete homology. We concluded that the two regions mentioned above can't be used for the identification of ginseng cultivars. As for closely related cultivars, determination of single gene is far not enough because the gene may be not where the difference located. In order to discriminate of 5 *ginseng* cultivars, DNA sequences of other genes need to be studied.

are of 5 guilleting cultivates, 21111 sequences of outer genes need to be studied.

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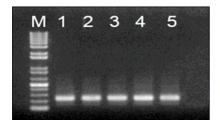


Fig.1 PCR products by 5S rRNA primers 5SP1 and 5SP2. Lane M: 100bp DNA ladder; lane 1: yunpoong; lane 2: gopoong; lane 3: sunpoong; lane 4: gumpoong; lane 5: chunpoong.

yunpoong	GGATTCGTGCTTGGGCGAGAGTAGTACTAGGATGGGTGACCCCCTGGGAAGTCCTCGTGT	60
gopoong	GGATTCGTGCTTGGGCGAGAGTAGTACTAGGATGGGTGACCCCCTGGGAAGTCCTCGTGT	60
sunpoong	GGATTCGTGCTTGGGCGAGAGTAGTACTAGGATGGGTGACCCCCTGGGAAGTCCTCGTGT	60
chunpoong	GGATTCGTGCTTGGGCGAGAGTAGTACTAGGATGGGTGACCCCCTGGGAAGTCCTCGTGT	60
gumpoong	GGATTCGTGCTTGGGCGAGAGTAGTACTAGGATGGGTGACCCCCTGGGAAGTCCTCGTGT	60

	5SP1	
yunpoong	TGCACCCCTTTTTATTTTTTTTTGCGATGTTCGGTGAAGAAGAGCGTACTAGTGAA	120
gopoong	TGCACCCCTTTTTATTTTTTTTTGCGATGTTCGGTGAAGAAGAGCGTACTAGTGAA	120
sunpoong	TGCACCCCTTTTTATTTTTTTTTTGCGATGTTCGGTGAAGAAGAGCGTACTAGTGAA	120
chunpoong	TGCACCCCTTTTTATTTTTTTTTGCGATGTTCGGTGAAGAAGAGCGTACTAGTGAA	120
gumpoong	TGCACCCCTTTTTATTTTTTTTTTGCGATGTTCGGTGAAGAAGAGCGTACTAGTGAA	120

yunpoong	CGTGTCTTGGTAAACTCGCATGCACGACGTAAGCGTCACTGCGTTCCACCCATATGTGGG	180
gopoong	CGTGTCTTGGTAAACTCGCATGCACGACGTAAGCGTCACTGCGTTCCACCCATATGTGGG	180
sunpoong	CGTGTCTTGGTAAACTCGCATGCACGACGTAAGCGTCACTGCGTTCCACCCATATGTGGG	180
chunpoong	CGTGTCTTGGTAAACTCGCATGCACGACGTAAGCGTCACTGCGTTCCACCCATATGTGGG	180
gumpoong	CGTGTCTTGGTAAACTCGCATGCACGACGTAAGCGTCACTGCGTTCCACCCATATGTGGG	180

yunpoong	AATATAGGAATAAAAATGGAGAATCCTAACGGGTGCGATCATACCAGCACTAAGGATCC 2	239
gopoong	AATATAGGAATAAAAATGGAGAATCCTAACGGGTGCGATCATACCAGCACTAAGGATCC 2	239
sunpoong	AATATAGGAATAAAAATGGAGAATCCTAACGGGTGCGATCATACCAGCACTAAGGATCC 2	239
chunpoong	AATATAGGAATAAAAATGGAGAATCCTAACGGGTGCGATCATACCAGCACTAAGGATCC	239
gumpoong	AATATAGGAATAAAAATGGAGAATCCTAACGGGTGCGATCATACCAGCACTAAGGATCC 2	239

	5SP2	

Fig.2 Comparison of 5S rRNA spacer sequences of 5 ginseng cultivars