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Molecular differentiation of *Panax* species based upon the restriction fragment length polymorphism (RFLP) in the ribosomal ITS1-5.8S-ITS2 region

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Molecular authentication among three *Panax* species and within cultivars and accessions of *P. ginseng* were investigated using the DNA sequence in the ribosomal ITS1-5.8S-ITS2 region. Four single nucleotide polymorphisms (SNP) have been identified between *P. ginseng* and other *Panax* species. In the electrophoresis profile, digested with the enzyme TaqI, three fingerprinting patterns were obtained with cultivars and accessions of *Panax* species. Consequently, these authentication procedure based upon the restriction fragment length polymorphism (RFLP) in the ribosomal ITS1-5.8S-ITS2 region will be available to differentiate the concerned *Panax* species and major Korean cultivars such as Gopoong and Kumpoong from other cultivars and accessions in *Panax* species, at the DNA level.

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Fusion of ginseng farnesyl diphosphate synthase and Centella squalene synthase for improvement of triterpene saponin biosynthesis

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A clone encoding farnsesyl diphosphate synthase (FPS) and a cDNA clone encoding squalene synthase (SQS) was obtained by PCR from a root of Panax ginseng and leaves of Centella asiatica, respectively. To produce bifunctional enzymes, fusion of two genes encoding FPS and SQS was performed. Fusion and the two single cDNA clones were separately introduced into pET32 vector. After induction with IPTG for 4 hours, proteins were analyzed by SDS-PAGE. Not only two single proteins but also fused proteins were successfully over-expressed in Escherichia coli BL21 (DE3) pLysS. FPS and SQS activities of protein extracted from cells transformed with the vector including fused genes were higher than the empty vector. Our results showed that the fusion protein produced farnesyl diphosphate and squalene. These gene constructs will be introduced into a interest plant genome for improvement of triterpene production. The contribution of this fusion protein to triterpene saponin biosynthesis also will be investigated.

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