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Metabolic Engineering for Biosynthesis of Tocotrienol in Perilla frutescens (L.) Britton

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Tocotrienols, the lipid soluble vitamin E along with tocopherols are well-known for their strong antioxidant, anticancer, and cardiovascular disease-preventing health effects. They are plastid-localized molecules and are generally found in most monocot plant seeds but rarely in dicotyledons due to the lack of homogentisic acid geranylgeranyl transferase (HGGT). The cDNA encoding HGGT in Dongjinbyeo, a Japonica rice cultivar of Korea, was isolated and used for Agrobacterium tumefaciens-mediated transformation of leafy perilla, which does not produce tocotrienol. Southern and Northern analysis showed the expression of HGGT in transgenic plants, and the constitutive expression of the HGGT gene led to an leaf accumulation of tocotrienol, which was quantified and verified by GC-FID and GC-MSD, respectively. Apparently, this genetically modified perilla plants can be used for nutritionally improved leaf vegetables co-existing both tocopherol and tocotrienol forms of vitamin E.

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Genome sequence-based development of DNA markers and production of large scale EST sequence from ginseng

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The Korean ginseng (*Panax ginseng* C. A. Meyer) is the most important medicinal plants not only in Korea but also worldwide. Even though medicinal components and their functions were widely exploited, there were little information on genetics, breeding, and genomics in ginseng. Therefore we proposed to develop large scale sequence based-DNA markers and thus to apply them in ginseng breeding and to improve ginseng genetics and genomics. We collected all the sequence information of ginseng from public database and characterized repeat-oriented sequences and simple sequence repeat (SSR) motifs using RepeatMasker program. Among 22129 sequences, 2105 sequences have SSR motifs. For the primary research, we designed 62 primers from the flanking sequences of SSR motifs (SSR markers) using Primer3. We tried several PCR-based methods to identify large volume of DNA markers that can be used for authentication and protection of ginseng cultivars and genetic map construction. Furthermore, we proposed to obtain large scale expressed sequence tags (ESTs) and thus identify large amounts of gene-based markers and provide infra-structure for further genomics study.

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