OC-02

Separation of Tocopherol and Tocotrienol Homologs by Using a Gas Chromatography

Kyoung-Shim Cho[1], and Young-Sang Lee[1*]

[1] Div. of Life Sciences, Soonchunhyang University, Asan 336-745. South Korea
* Corresponding Author Email: mariolee@sch.ac.kr

Vitamin E is a fat soluble vitamin having important functions in the body such as inhibiting cholesterol synthesis in the liver, lowering a serum cholesterol and acting as an antioxidant, etc. It consists of 8 homologs: alpha-, beta-, gamma-, delta- tocopherols and tocotrienols. For the quantification of all 8 vitamin E homologs by a GC, capillary columns of different polarities and various oven conditions were tested. Compared to HP-1, CP-SIL 5 CB and CP-SIL 19 CB columns, CP-SIL 8 CB (25 m × 0.25 mm, 0.4 um thickness) column was the best column and the optimal oven conditions were; from 230 C increased to 290 C at a increasing rate of 6 C/min, and after holing for 27 minutes at 290 C increased up to 310 C at a rate of 10 C/min. Injector and detector temperatures were 250 C and 310 C, respectively and the flow rate of He was 0.5 mL/min. Under this suggested method, all the 8 vitamin E homologs could be baseline-separated with good repeatability and 1 ug/mL of detection limit.

OD-01

Application of degenerate-primed PCR (DOP-PCR) method for SNP discovery in soybean

Agnieszka Janiak[1], Moon Young Kim[1,2], and Suk-Ha Lee[1*]

[1] Department of Plant Science, Seoul National University, Seoul 151-921, Korea
[2] Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul 151-921. Korea
* Corresponding Author Email: sukhalee@snu.ac.kr

Development of molecular markers has become one of the pivotal aims in the plant science of resent years. From among various types of available markers, SNPs represent the most common class of polymorphisms. As the initial cost of SNP markers development is relatively high, there is a need for finding cost-effective methods for this purpose. In the presented study, the degenerate-primed PCR (DOP-PCR) technique was used for development of new SNP markers in soybean. The PCR fragments were amplified from two cultivars Pureunkong and Jinpumkong 2, shotgun cloned and sequenced. The sequences of both varieties were then assembled and examined for occurrence of SNPs. The effectiveness of SNP discovery was much lower than expected, however. Over 1300 of analyzed sequences were grouped in 144 contigs, but only 51 putative SNP sites were found in 18 of them. The most significant limitation of the analysis was the presence of chloroplast DNA and multiple cloning of the same fragments, what reduced the effective number of data. The presence of putative SNPs is being to confirm and the mutations will be genotyped in Pureunkong x Jinpumkong 2 RIL mapping population. Thought initially promising, DOP-PCR technique was not efficient enough in SNP detection and other methods need to be apply for high-throughput SNP discovery.