F-O-1

Development of SSR markers for genetic mapping of Korean ginseng and authentication of Korean ginseng cultivars

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The Korean ginseng, *Panax ginseng* C. A. Meyer is a popular medicinal herb in Araliaceae. Genetic map in crops provides valuable information for breeding, genetic and genomic researches. However, little information is available for construction of genetic map in ginseng. Up to now, we have produced large amounts of expressed sequence tags (ESTs) from four ginseng cultivars (37Mb, 49Mb, 39Mb, 47Mb from Gopoong, Gumpoong, Chunpoong and Yunpoong respectively using pyrosequencing technique and 5Mb from normalized full-length cDNA library of Chunpoong) to obtain comprehensive information of gene expression, and constructed EST database including ESTs from public database. Till now, we designed 261 SSR primer sets using EST sequences and identified 106 intergenic polymorphic markers. And 44 of the 106 showed polymorphisms among *panax ginseng* cultivars. Among 44 markers, 27 SSR polymorphic markers were inspected to 51 F_2 population from Yunpoong x Chunpoong, which showed good at the fitness of Mendellian segregation ratio 1:2:1. To enrich the number of markers, and thus construct high resolution genetic map which can be used as frame map for further genome sequencing. we are planning to develop large scale EST-derived SNP markers which are available in the F_2 population. This study provides genetic information as well as foundation for ginseng researches such as genetics, genomics, breeding, and the final goal for whole genome sequencing. This study was supported by Technology Development Program for Agriculture and Forestry, Ministry for Food, Agriculture, Forestry and Fisheries, Republic of Korea (Grant No. 609001-051SB210).

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