

Genome Research of Korean Ginseng (*Panax ginseng* C. A. Meyer)

Yong Pyo Lim

Department of Horticulture, and Genome Research Center, Chungnam National

University, Daejeon 305-764, Korea

To study the genome of Korean ginseng (*Panax ginseng* C.A. Meyer cv. Chonpung, Araliaceae), a world-wide used medicinal herb, we estimated the genome size, constructed a *HindIII* BAC library and performed BAC-end sequencing. The genome size of Korean ginseng was estimated to about 3.12 X 1,000 Mbp. Approximately 97.3% BAC clones in the *HindIII* BAC library consisted of 106,368 clones containing nuclear DNA inserts with an average of 98.6 kbp, and this library is expected to cover 3.34 genome equivalents. Partial genome-survey sequences of about 1 Mb were acquired from 2,492 BAC end sequences (BES) with the average length of 400 bases. BES analysis using BLAST and motif searches revealed that 9.3%, 18.9%, and 3.8% of the BES contained protein-coding regions, transposable elements (TEs) and microsatellites, respectively. The known gene products of the protein-coding regions (127 of the 231 protein-coding regions) were categorized by gene ontology annotation as the ones involved in biological process (22.2%), cellular component (11.8%), molecular function (61.5%) or unclassified (5.8%). Most of the TE-coding regions (83.4%) were retrotransposons comprising 353 *gypsy*-like and 63 *copia*-like elements. In the case of the microsatellites, 87 were simple, whereas 16 were compound. Based on 1 Mb BES analysis, the Korean ginseng genome appears to contain higher levels of TEs than the protein-coding regions. The results suggest that this genome might have been subjected to a considerable rearrangement due to the transposition of the retrotransposons.