

OB1. BAC Library Construction and Approach to Genome Study using BAC-end Sequences of *Panax ginseng* C.A. Meyer

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Objectives

To understand the feature of Korean ginseng genome, *Hind*III BAC library were constructed, and BAC end sequences were analyzed.

Materials and Methods

- Materials : Korean ginseng cv. Chunpoong 4-years old leaf, pCUGIBacI
- Methods : (1) Construction of BAC library ; BAC vector isolation, preparation of partially digested DNA of Korean ginseng, ligation and transformation, and BAC insert size analysis
- (2) BAC end sequencing and sequence analysis using bioinformatics

Results and Discussion

We constructed *Hind*III BAC library of Korean ginseng containing 106,368 clones. The insert sizes of the Korean ginseng BAC library were distributed from 15 to 310 kb (Fig.1), and an average insert size was calculated 98.61 kb. The proportion of pseudo clones was estimated to about 2.7%. Korean ginseng BAC library estimated a total of 10,424 Mb of nuclear DNA. To understand the feature of Korean ginseng genome, 2,492 BAC end sequences were analyzed. The result of annotation of Korean ginseng BESs revealed 8.9% protein coding regions, 18.9% transposable elements (TEs), 5.8% microsatellites, and 66.4% unknown genomic sequences (Table 1). Korean ginseng genome seems to have more repetitive DNAs including various TEs and microsatellites than gene coding regions. These result may suggest that Korean ginseng genome have the significant possibility of evolution by transposition.

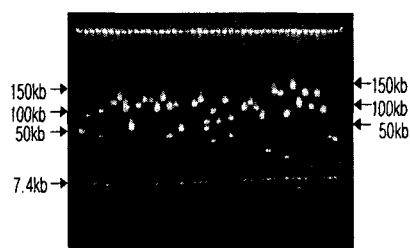


Table 1. Summary for BAC end sequencing of *Panax ginseng*

Contents	Total
No. of BAC clones used for end sequencing	2,167
No. of BAC end sequencing reactions	3,127
Sequencing success rate (%) ^a	79.7% (2,492 ^b)
Avg. of end read length (bp)	about 400
Total end read bases (Mb)	0.99
No. of protein coding regions	230 (9.2%)
No. of transposable elements	471 (18.9%)
No. of microsatellites	145 (5.8%)
No. of unknown genomic sequences	1,646 (66.1%)

Fig.1. Estimation of Korean ginseng BAC inserts.