

P 38

## Physical Mapping Using BAC Clone of Chinese cabbage and Contig Assembly

Gene Woo Jeon, Chang Pyo Hong, Jee Young Park, Sang Hoon Lee, Yong Pyo Lim\*

Department of Horticulture, and Genome Research Center, Chungnam National University, Daejeon, 305-764, Korea

### Objectives

A physical mapping for making it possible to select clones for sequencing that would ensure comprehensive coverage of Chinese cabbage genome.

### Materials and Methods

1. Materials: Chinese cabbage *Hind*III BAC library
2. Methods
  - BAC DNA preparation using the alkaline lysis method
  - BAC fingerprinting
    - Restriction digestion
    - Electrophoresis
  - Fingerprinting analysis and contig assembly.
    - Determination of the number and positions of DNA fragments of each of BAC clone through band calling and marker locking by the IMAGE program
    - Contig assembly by FPC(fingerprinted contigs) program

### Results and Discussion

A total of 17,616 BAC clones of Chinese cabbage were fingerprinted successfully, and assembled into contigs with tolerance value of 7 and cut-off value of  $10^{-12}$  on FPC. As the results, The 1,204 contigs, which was composed of 3,714 clones, were built, and the size of these was evaluated 132.1 Mb covering 24% of Chinese cabbage genome. The remaining 13,902 clones were classified into the singleton group. The longest contig on size was ctg715 and evaluated the size of 192 kb. The number of clones in average contig is about 3 and the number of average bands in each clone is about 27.

For the contig assembly of whole genome, we are conducting BAC fingerprinting for 56,592 clones (*Hind*III BAC library) and constructing *Bam*HI BAC library for complete contig assembly now.

### Acknowledgement

This research is supported by Biogreen.

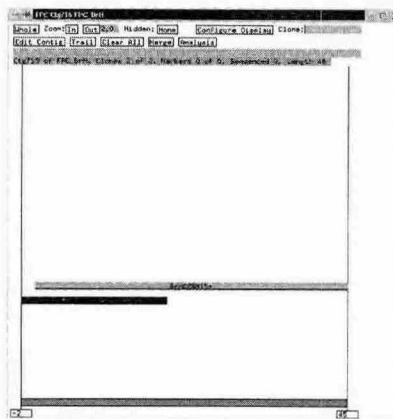


Figure 1. Contig assembly data (ctg.715)