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Development of Analytic and Comparative EST and BAC_end information Browsing System for the *Brassica rapa* Genome project.

Kwanghee Lee[1], Myungho Lim[2], Daesang Lee[1], Hyeweon Nam[1], Kiejung Park[1]
[1]Information Technology Institute, SmallSoft Co., Ltd., Daejeon, [2]National Institute of Agricultural Biotechnology, Suwon, South Korea

Objectives

We have developed *Brassica rapa* EST and BAC-end comparative information browsing system, *Br*ESBAS, which handles all data produced from the *Brassica rapa* genome project. It also provides comparison and analysis information between *Brassica rapa* and *Arabidopsis thaliana* through the user-friendly graphical web interface.

Materials and Methods

1. Methods:

The MySQL used as DB engine for constructing Brassica EST Contig and BAC-end databases. The information retrieval and viewers are mainly programmed by Perl.

Results and Discussion

The *Br*ESBAS mainly consists of EST analysis and BAC-end information part. The EST analysis part shows the contigs data produced form the clustered and assembled *Brassica rapa's* ESTs as well as their distributional information on the *Arabidopsis thaliana* genome resulted from the comparative inter-species sequence analysis. Through its major browsers (ESTView, ESTInfoView, and ContigView), user can access and retrieve the detail information of the contigs and the relationship between two species by graphic interface. Especially, the ContigView shows the ESTs expression rate, which shows where hot-spots are and what kinds of contigs are expressed more than others. BAC-end information part treats BAC_end comparative data with *Arabidopsis* and composed of ScatterView and ComparaView. The ScatterView provides the clue that which BAC clones are adjacent when determining the BAC's location and orientation on the chromosome. The synteny information between two genomes is easily accessed by ComparaView that displays comparativeness of single vs. multiple chromosomes and multiple vs. multiple chromosomes. Based on the *Br*ESBAS, we hope that *Brassica* genome project could be accelerated and finished earlier as expected.

**Corresponding author :* Kiejung Park, Tel : 042-864-2524, E-mail : kjpark@smallsoft.co.kr