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Sequence based genetic mapping of Brassica BAC clones which compose comparative tiling path on the Arabidopsis chromosomes

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Objectives

To identify actual location of 503 *Brassica* BAC clones that compose comparative tiling path on *Arabidopsis* chromosome, we have tried to genetic mapping of BAC clones using SSR in its sequence. These BAC clones will be provided as starting point for selection of seed_BAC clones to sequence fully genome of *Brassica rapa.*

Materials and Methods

1. Materials
- 55 Hind III & BamHI &Sau3AI BAC sequences of *B. rapa* var. Chiifu in phase 2
- Mapping progenies : Jangwon F3 pooled population 134 lines

2. Methods
- Program for repeat search and analysis & primer designing
  - Tandem Repeat Finder (http://tandem.bu.edu/trf/trf.html)
  - Fgenesh(http://www.softberry.com/berry.phtml?topic=fgenes_plus&group=programs&subgroup=gfs)
  - Primer3 (http://frodo.wi.mit.edu/)
- Polymorphism check : 1% Agarose gel or 5% Polyacrylamide gel
- Linkage analysis : JoinMap 3.0

Results and Discussion

The genome of *Arabidopsis* and *Brassica* is syntenic and co-linear. Based on comparative sequence analysis of 91,179 BAC end sequences (BES), we have allocated a total of 4,317 BAC clones (9.5%) on the counterpart region of *Arabidopsis* chromosomes that span 92 Mb of unique sequence of *Arabidopsis* chromosome. Furthermore, we have selected 629 *Brassica* BAC clones that compose comparative tiling path on *Arabidopsis* chromosome (http://www.brassica-rapa.org). The comparative tiled BACs evenly distributed in the Brassica genome will be sequenced in this year. The actual location of each BAC clone can be identified by FISH or sequence based genetic mapping. Up to date, we have tried to map a total of 55 sequenced BAC clones through development of SSR markers in each BAC. A total of 697 SSRs have been identified from 32 BAC sequences and of these, 176(3 to 4 every BAC clones) SSRs primer pairs were designed. Among 176 SSR primers, 48(27.8%) had shown polymorphism between parental lines of two mapping populations (Jangwon F_3-pooled and Chiifu X Kenshin). SSRs derived from intron and 5'UTR region revealed higher polymorphism than SSRs derived from exon and intergenic regions suggesting that non-coding would be good target regions to develop polymorphic SSR markers. Using these SSR markers, 29 (52.7 %) BAC clones were mapped to linkage groups and in detail results will be shown in the presentation. Sequnce based and genome widely well distributed DNA markers can be introduced by the end of 2005. These may be a valuable resource to provide unlimited information for breeding as well as genome sequencing of the genus Brassica.

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