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Brassica-Arabidopsis genome browser: Overview of Brassica genome based on comparative genomics with Arabidopsis

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Objectives

Application of comparative genomics information for Brassica genome sequencing

Materials and Methods

BAC end sequence information of *B.rapa* BAC libraries (KBrB, KBrH, KBrS)

Results and Discussion

The genus *Brassica* is triplicated after divergence of *Arabidopsis* and *Brassica*. Comparative genome analyses of about 70 sequenced Brassica BAC clones revealed overall co-linearity with 82% sequence similarity with their counterpart regions of *Arabidopsis* genome. We have obtained 91,179 BAC end sequences (BES) from 46,848 BAC clones originated three BAC libraries (*HindIII*, *BamHI*, and *Sau3AI*). All BES were used for comparative genome analysis with the *Arabidopsis*. A total of 45,232 (45%) BES show significant hit (E-6) on a spot of *Arabidopsis* chromosomes. And a total of 4,317 BAC clones (9.5%) are allocated on *Arabidopsis* chromosomes by directional matches of both ends (8,634 BES), within 30-500 kb interval on *Arabidopsis* chromosome. These 4,317 clones span 92 Mb of *Arabidopsis* genome. We have selected a total of 629 BACs that are on the minimum tiling path of 86 Mb *Arabidopsis* genome. Sequencing and chromosomal allocation of the 629 minimum tiled path BACs will show the comparative overview of *Arabidopsis* and *Brassica* genome. All the comparative genome analysis of the BAC and BES are available from our Arabidopsis-Brassica Genome Browser (www.brassica-rapa.org) showing the positions of Brassica BAC clones on the counterpart Arabidopsis chromosomes. The genome browser will give great opportunity to the enlargement for understanding of the Brassica genome.

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