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Korea Brassica Genome Sequencing Project

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The haploid genome equivalent of *B. rapa* is about 550 Mb and closely related with *Arabidopsis* (125 Mb haploid genome equivalent), the completely sequenced model plant. Comparative genome analyses of about 200 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) and high-resolution fingerprints (SNaPshot) 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 47,748 (52%) BES hits significantly (E-6) on a spot of *Arabidopsis* pseudo chromosomes. And a total of 4,647 BAC clones (9.9%) are allocated on *Arabidopsis* chromosomes by directional matches of both ends within 30-500 kb interval on *Arabidopsis* chromosome. We selected a total of 629 BACs that are on the comparative minimum tiling path (comparative tile) of 86 Mb *Arabidopsis* genome. Up to now (AUG. 2006), a total of 620 BACs of the comparative tile are sequenced and published to GenBank. The sequence and chromosomal locations of the comparative-tile BACs will show the comparative syntenic 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). Based on in-depth comparative genome analyses, we propose a comparative genomics approach for conquering the Brassica genome. Sequence-based genetic mapping of 629 BAC clones, SNaPshot fingerprinting information, and BES data of more than 140,000 BAC clones will be used as step-stone for sequence extension and construction of physical map of all chromosomes. All information has been provided to multinational Brassica Genome Project (MBGP) members. And we have aiming to complete sequencing cytogenetic chromosome 1 and 2 by end of 2008.