

양한 식물유전자원을 수집하여 본 기술에 대한 적합성을 검토 중에 있으며, 식물종자 뿐 아니라 미생물이나 동물조직에도 적용시키고 있다. 본 발표에서는 지금까지의 추진경과 및 금후방향에 대하여 소개하고자 한다.

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## Overview of Brassica Genome Structure based on Comparative Genomics with Arabidopsis:

### Sequencing 629 comparative-tile BACs and their utility for physical mapping of *B. rapa* genome

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The genus Brassica is triplicated after divergence of Arabidopsis and Brassica. Comparative genome analyses of about 600 sequenced Brassica BAC clones revealed overall co-linearity with 82% sequence similarity with their counterpart regions of Arabidopsis genome. We have obtained 91,511 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 show significant hit (E-6) on a spot of Arabidopsis chromosomes. And a total of 4,647 BAC clones (10%) are mapped on Arabidopsis chromosomes by directional matches of both ends (9,294 BES) within 30-500 kb interval on Arabidopsis chromosome. These 4,647 clones span 92 Mb of Arabidopsis genome. We have selected a total of 629 BACs that are on the comparative minimum tiling path (comparative-tile) of 86 Mb Arabidopsis genome. Up to now (May 2006), about 600 BACs of the comparative-tile are sequenced. The other BACs will be sequenced soon. Sequence-based genetic mapping of each BAC and their FPC information will be used as step-stone for walking and construction of physical map of all chromosomes. All information will be provided to multinational Brassica Genome Project (MBGP) members, soon. Collectively, combined sequence 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](http://www.brassica-rapa.org)).

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