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## Snapshot View of Expressed Sequences from *Brassica rapa*

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### Objectives

1. Provide a publicly available Brassica gene resource
2. Design and supply of a high-density cDNA chip for functional studies

### Materials and Methods

1. Plant Material : Chinese cabbage cultivar Chiifu (*Brassica rapa* ssp. *pekinensis*)
2. Web sites for EST analysis : NCBI, TIGR, TAIR, NIAB, etc.

### Results and Discussion

As a part of Korea Brassica Genome Project (KBGP), Brassica Genomics Team of NIAB has initiated Expressed Sequence Tags (EST) project of *B. rapa* with co-workers of BioGreen21 (BG21) program teams supported by RDA Korea. Since 2004, about 80,000 ESTs were analyzed from 14 cDNA libraries made from diverse tissues of leaf, seedling, silique, flower, callus, and root of Chinese cabbage cultivar Chiifu (*Brassica rapa* ssp. *pekinensis*). Using clustering tools, ESTs are assembled to makes contigs, over 25,000 non-redundant EST sequences were identified. These sequences of *B. rapa* were blasted against sequences of *A. tha*, *B. oleracea* and *B. napus* and analyzed in a comparative-view. For DNA chip printing, unique cDNA sequences will be selected and a plan for the 15k~20k cDNA chip is undergoing now. These EST analysis results ([www.brassica-rapa.org](http://www.brassica-rapa.org)) and details of a cDNA chip plans will be presented. This EST project and a high-density chip, with ongoing Korea Brassica Genome Project, will provide a high quality/quantity publicly available gene resource for a functional genomics research.