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Comparative analysis of expressed sequence tags of *Brassica rapa*

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Objectives

The primary goal of this research is an analysis of 100,000 ESTs of *B. rapa*. Ultimately, we'd like to make a D/B of EST and to serve as a public source of genes of *Brassica* plant.

Materials and Methods

1. Material

Plant - *Brassica rapa* (ssp. *peckinensis*) cv. Chiifu

Results and Discussion

A set of 100,000 EST sequences was analyzed from 20 different cDNA libraries of *B. rapa* (ssp. *peckinensis*) cv. Chiifu in co-operation with BioGreen21 project teams. These ESTs were clustered and assembled using megablast-Cap3 and produced a set of 25,000 unigene sequences that have an un-biased collection of 50~60% of *Brassica* genes (ca. 45,000 genes) and covers 75% of *Arabidopsis* genes. About 90% and 82% fractions of *Brassica* unigenes were matched to the *Arabidopsis* and rice, respectively, from the blastx(E-30) analysis. *In-silico* localization of *Brassica* unigenes onto the *Arabidopsis* chromosomes resulted in 23.3%, 13.1%, 18.4%, 13.9%, and 20.1% of localized genes onto the chr1, 2, 3, 4, and 5 of *Arabidopsis*, respectively. When ESTs from five different tissues were localized onto the chromosome #1 of *Arabidopsis*, there was no clear evidence of tissue-specific regions or islands on the chromosome in an overall view. However, in a detailed (50kb scale) view, there were numbers of regions that shows high-level expression of genes from specific tissue(s) though this should be confirmed by experiment. Details will be discussed in this poster.

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