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Analysis of EST clones during seed development of Chinese cabbage (*Brassica rapa* L. ssp. *pekinensis* inbred line, Chiifu)

Jeongyeo Lee, Jeongah Han, Hayoung Song, Yong-Pyo Lim, and Yoonkang Hur*

Genome Research Center, Chungnam National University, Kung-dong 220, Yousong-ku, Daejeon 305-764, Korea

Objectives

EST data base has to be established as a part of Chinese cabbage genome project. This data can be able to use both genetic mapping and cloning of new genes. First of all, we have carried out EST experiment using cDNA library constructed by seed development mRNAs and study expression of several unique genes.

Materials and Methods

1. Plant material

Brassica rapa L. ssp. *pekinensis* Inbred line Chiifu

2. Methods

mRNA isolation → cDNA library construction → sequencing → data analysis → gene selection → expression study

Results and Discussion

A cDNA library for EST experiment was constructed using a mixture of RNA extracted from different developmental stages of Chinese cabbage seeds. This work was a part of *Brassica rapa* Genome Project. The result of 3,287 EST analysis showed that 60% and 40% genes are single and multiple copy, respectively. Therefore, we obtained 2,086 unique genes from the cDNA library, which uncovers 63.4% of 3,287 ESTs. Most genes, 65%, intracellular proteins and 24% are membrane bound proteins. With regarding to biological function, 48% genes are involved in metabolism and 45% for cellular physiological process. We found 67 hypothetical protein genes, 41 expressed protein genes and 386 unknown protein genes. We select 97 clones for further study that are abundantly expressed in Chinese cabbage and that include seed tetraubiquitin, pentameric polyubiquitin, lipid transfer protein, ribulose bisphosphate carboxylase, putative calcium-binding protein, metallothionein-like protein type2, transmembrane channel protein, and pherophorin-dz1 protein. We will discuss more informations obtained from EST analysis in the poster.

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* Corresponding author : Yoonkang Hur, TEL: 042-821-6279, E-mail: ykhour@cnu.ac.kr