

Expressed Sequence Tags of Chinese Cabbage Flowering-related Tissue cDNAs

Soo In Lee, Myung Chul Lee, Ki-Byung Lim, Jin A Kim, Soo Jin Kwon, Jung Sun Kim, Beom-Suk Park, Ho-II Kim, Dong-Hern Kim, Yong Moon Jin*

Genomics Division, National Institute of Agricultural Biotechnology (NIAB) RDA, Suwon, 441-707, Korea

Objectives

In order to study gene expression in reproductive organ, we constructed four cDNA libraries from flower buds (lower and higher 2 mm in size), flowering and pollen in Chinese cabbage (*Brassica campestris* L. ssp. *pekinensis*) and characterized expressed sequence tags (ESTs).

Material and Methods

1. Materials : flower buds (lower and higher 2 mm in size), flowering and pollen from Chinese cabbage (*Brassica campestris* L. ssp. *pekinensis*)
2. Methods
 - cDNA synthesis : ZAP-cDNA Gigapack III Gold cloning Kit (Stratagene)

Results and Discussion

Non-redundant expressed sequence tags (ESTs) were generated from four libraries of Chinese cabbage (*Brassica campestris* L. ssp. *pekinensis*) made from flower buds (lower and higher 2 mm in size), flowering and pollen. From BLAST and FASTA search analyses of protein and DNA databases, 1,853 ESTs matched with proteins of identified biological function, 1,677 with hypothetical proteins or non-annotated *Arabidopsis* genome sequences, and 186 with other ESTs. About 85% of the top-scored matching sequences were from *Arabidopsis* or Brassica, but overall 1,482 (80%) ESTs matched with *Arabidopsis* ESTs at the nucleotide sequence level. Ten known flower-specific genes were identified: the anther-specific proline-rich protein, the beta-ketoacyl-CoA synthase (FIDDLEHEAD), the MADS-box protein SEP1-a, anther-specific protein BNA237, the beta-expansin pollen allergen protein, the anther-specific protein Bcp1, the self-incompatibility locus glycoprotein SLG29, the anther-specific proline-rich protein APG precursor, the Ole e I (main olive allergen)-like protein, and the allergen. Our extensive EST analysis of genes expressed in floral organs not only contributes to the understanding of the dynamics of genome expression patterns in floral organs but also adds data to the repertoire of all genomic genes.