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Discovery and Analysis of Vernalization-Related Genes Using A Chinese Cabbage cDNA Microarray

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Objectives

In many plants, flowering can be accelerated by exposure to a long period of cold. This phenomenon, termed *vernalization*, has been studied for decades at the physiological level but only recently at the molecular level. To accelerate the discovery of the molecular level mechanisms in Chinese cabbage, we adopted microarray technique. Here we report a fabrication of Chinese Cabbage cDNA microarray and microarray analyses results of vernalized seedling.

Materials and Methods

1. Materials-Genes: 6,233 ESTs from 5 different Chinese cabbage cDNA libraries.
-Plant: Cold-treated Chinese cabbage (*Brassica campestris* L. ssp. *pekinensis* cv. Jangwon)
2. Methods- Removing redundant ESTs by homology search, DNA amplification and purification, Printing, Hybridization, Data Analysis, Expression profiling.

Results and Discussion

Chinese cabbage cDNA microarrays containing 6,233 unique ESTs and 167 control elements were produced and used for profiling the vernalization-responding genes. Jangwon cultivar showed strong vernalization response by 4-week cold treatment, but not by 1-week cold treatment. From the analyses of the microarray hybridizations with probes derived from non-, 1- and 4-week cold treated seedlings, we found that

similar gene expression profiles were existed between 1- and 4-week seedlings, and the differently expressed genes were observed in small fractions. Major differences of the gene expression between 1- and 4-week treatments were observed in the functional categories of the cell growth, division and DNA synthesis, and these differently regulated genes could be classified into four clusters based on their expression behavior.

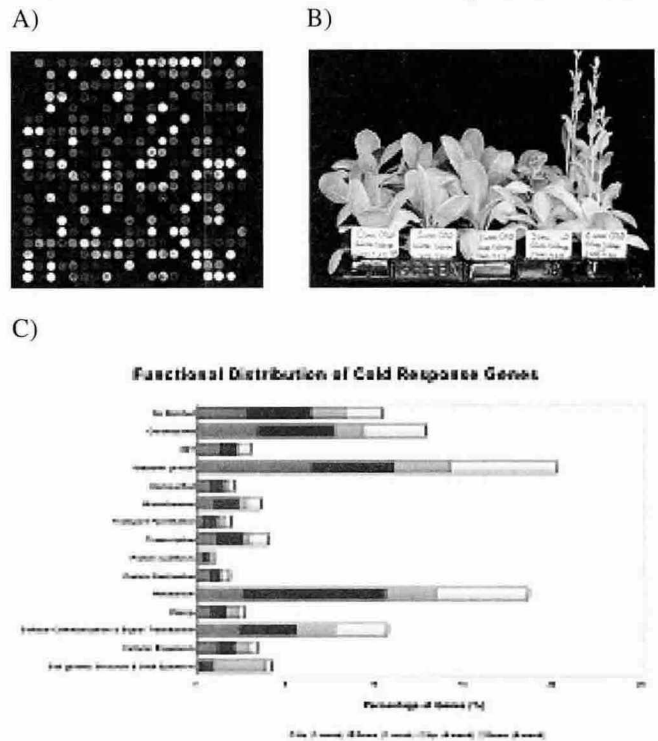


Figure 1. A) Phenotypes of untreated, non-cold and vernalized plants. B) Hybridization images of microarray. C) Comparison of functional distribution of vernalization-responding and cold-responding genes.