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Characterization of *Flowering locus C (FLC)* in *Brassica campestris*

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Objectives

The analysis of chromosomal location of replicated flowering time gene *FLC* and characterization with their sequences

Materials and Methods

1. Materials:
'Jangwon' genetic map, HindIII BAC library (CHNU), FLC gene homolog of *B. campestris* to *A. thaliana*

2. Methods : BAC colony hybridization by Kim (2002), BAC preparation of alkaline lysis

Results and Discussion

Replication of genes, as chromosomal blocks, or by whole genome polyploidization, is thought to be a major mechanism for new genetic and phenotypic diversity. Functional genetic redundancy is widespread in plants and could have an important impact on phenotypic diversity if the multiple gene copies act in an additive or dosage-dependent manner. *FLCs* also act in a dosage-dependent manner to delay flowering. By colony hybridization, we have cloned five type BAC clones, which are containing *FLC* gene. The homolog of *Brassica napus FLC1* was located on Chr 10 of *Brassica campestris*, and the homologs of *B. napus FLC3* were located at two adjacent loci (5cM) of Chr 2 of *B. campestris*. Five *FLC* genes showed the high similarity with nucleotide and protein level.

Brassica species contain a wide range of morphological variations that have been selected for use as vegetables, oilseeds, and condiments. The expression of these variations may be due, in part, to allelic variation at redundant copies of key regulatory genes controlling developmental process. So, these five *FLC* genes of *B. campestris* would be good materials for genetic study of duplicated genes. Expression and functional analysis of each *FLC* gene will be further discussed.

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