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## Comparative Analysis of the Genomes *Brassica oleracea* and *B. campestris* That are Homeologous to Sequenced Regions of Chromosomes 4 and 5 of *Arabidopsis thaliana*

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### Objectives

Due to their relatedness to *Arabidopsis thaliana*, the cultivated *Brassica* species represent the first group of crops that can be applied to the comparative genomic approaches for understanding the biological processes and manipulating the agricultural important traits. Using the *Arabidopsis* genome sequence and clones from the BAC library of *B. campestris*, we have analyzed the aspects of gene conservation and microsynteny among a 222kb region of the genome of *Arabidopsis* and homeologous segments of the genome of *B. oleracea* and *B. campestris*.

### Materials and Methods

1. Material: Chinese cabbage *HindIII* BAC library

2. Method: Southern hybridization, Physical mapping, FISH

### Result and Discussion

Total 19 predicted genes were hybridized with the BAC library, and the result indicated that a high level of gene conservation existed in *B. campestris* genome. Using the identified BAC clones, physical mapping was performed to construct clone contig maps and analysis is processing about the gene content and organization in the set of paralogous segments identified in the genome of *B. campestris* using shotgun sequencing and BAC FISH.