

## BAC sequencing and comparative analysis between Arabidopsis and Chinese cabbage (*Brassica campestris* cv Chibu)

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### Object

We have tried to micro-collinearity between Arabidopsis and Chinese cabbage by BAC sequencing of specific region.

### Material and Method

#### 1. Material

- Hind III BAC library of Chinese cabbage

#### 2. Method

- Sequencing of BAC shotgun library
- Phred/Phrep Assembling
- Gene prediction and comparative analysis between Arabidopsis and Chinese cabbage.

### Abstract

The Brassica contains many economically important crop species, but their genomes are not well characterized, and comparative genetic mapping lags well behind that of other families. A bacterial artificial chromosome (BAC) of Chinese cabbage (*Brassica campestris* cv Chibu) was sequenced and compared with Arabidopsis genome to facilitate genome comparisons and gene discovery in the Brassica. Three 150 kb BAC clones of Chinese cabbage were isolated using FLC (Flowing Locus C) cDNA clone and it was divided three groups. The gene density of sequenced BAC clones was revealed each 5.4kb that was expected by Genescan, GeneMark program using Arabidopsis algorithm and directly compared with Arabidopsis genome by BLASTX and N. In compare of Arabidopsis genome, gene arrange was very similar with Arabidopsis, but numerous small rearrangements, insertion/deletions duplications, inversion and translocation have been detected. The sequenced BAC revealed region of different Arabidopsis chromosome 5. In general, coding region of gene was very similar with Arabidopsis, but non coding region was not shown collinearity. About 50 % of genes were shown the same order of specific region of Arabidopsis and these genes has highly homologous at DNA sequence or deduced amino acid level. The remained 50% genes of sequenced region has similar with scatter region of Arabidopsis.