

## Karyotype Analysis of Subspecies of *Brassica campestris* by FISH

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### Objectives

FISH analysis was employed to analyze karyotype of *B. campestris* subspecies. 45S and 5S rDNA sequences were used as probe to localize NORs. A fine karyotype analysis was constructed by using molecular cytogenetic techniques.

### Materials and Methods

#### 1. Materials

*B. campestris* ssp. *rapa*, *B. campestris* ssp. *chinensis*, and *B. campestris* ssp. *pekinensis*

#### 2. Methods

Chromosome preparation, DNA probes preparation and FISH protocol was carried out according to Lim et al. (2001) with minor modifications.

### Results and Discussion

Since U (1935) confirmed the theory of genome synthesis between wild species known as U's triangle, *Brassica campestris* is considered as genome AA group. *B. campestris* (syn. *rapa*) is composed with about 10 subspecies. Phenotypically, for example, leaf shape, they could be divided into two or three groups with *pekinensis* type, *rapifera* type and intermediate of both types. The subspecies *rapifera*, *trilocularis* and *oleifera* are similar to *Raphanus* in leaf shape. And subspecies *chinensis* is similar to *pekinensis* type. DAPI band on the metaphase chromosomes showed condensed staining in the pericentromeric region indicating as heterochromatin and less condensed staining representing euchromatin region in the distal parts. Large amount of rDNA sequences were located on the heterochromatin region in interphase cell. However, the main domain of NOR was located on the satellite showing less condensation on chromosome 3. Differences of the rDNA hybridization pattern were observed between *pekinensis* and *chinensis*, while there were no differences between *rapifera* and *trilocularis*. The observation is discussed in terms of the phylogeny and variability of phenotype within the *B. campestris* species (genome AA).