

Assessment of genetic relationships within *Brassica rapa* subspecies based on polymorphism

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Genetic relationships of 10 subspecies of *B. rapa* was estimated using four isozyme systems. The interpreted genotypes were used to calculate genetic diversity measures (Mean number of alleles per locus (A), Proportion of polymorphic loci (P), observed and expected average heterozygosity, and F-statistics). Genetic distance matrix was used for clustering the collected subspecies. The UPGMA clustering based on Nei's genetic distance matrix separated *B. rapa* ssp. *Dichotoma* and *B. rapa* ssp. *oleifera ruvo-gruppe* in one main cluster. In the remaining subspecies, *B. rapa* ssp. *oleifera* and *B. rapa* *trilocularis* were grouped together in a subcluster supporting the suggestion based on RFLPs that *B. rapa* ssp. *Oleifera* had been derived from *B. rapa* ssp. *trilocularis*. The grouping of *B. rapa* ssp. *rapa*, *B. rapa* ssp. *chinensis* and *B. rapa* ssp. *pekinensis* also supports the hypothesis that Chinese cabbage *B. rapa*

ssp. pekinensis" originated from inter-specific hybridization between *B. rapa ssp. rapa* or *B. rapa ssp. oleifera* with *B. rapa ssp. chinensis*.

Key words: *Brassica rapa*; genetic diversity; isozymes; oilseed rape.