



كلية العلوم



جامعة الفيوم

Karam, M.A., Morsi, Y.S., Sammour, R.H. and Ali, R.M., 2014. Assessment of genetic relationships within *Brassica rapa* subspecies based on polymorphism. *International Journal Current Microbiology and Applied Science*, 3(3), pp.1-10.

Abstract

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*.