

Genetic Diversity and Selection for Salt Tolerant accessions of *Brassica rapa* populations

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Abstract: The present study was carried out to evaluate genetic diversity and genomic relationships of 14 populations of *B. rapa* with different centers of origins based on polymorphism of four isozyme systems. The selection of salt tolerant accessions was carried out by treatment with 150 mM NaCl and the molecular characterization was achieved using RAPD analysis. The studied populations were classified into three groups based on allele frequency confirming genetic divergence of the studied populations as a result of different breeding traditions in different parts of the world. The highest values of genetic diversity measures were observed for the populations of *B. rapa* ssp. *chinensis* with Chinese and unknown origin followed by the Chinese *B. rapa* ssp. *pekinensis*. The genetic relationships among the studied populations based on Nei' s genetic distance derived from

isozyme data coincide with their breeding history. The variation between the salt tolerant and salt sensitive accessions as observed from RAPD pattern was attributed to the genetic divergence among salt tolerant and sensitive accessions. The salt tolerant accessions can be selected as resources to improve the salt stress tolerance in *B. napus* by sequencing of characteristic RAPD bands in marker assisted selection.

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