

Summary and conclusions

The family *Brassicaceae* is considered one of the most ten important families. The genus *Brassica* is one of the most important genera of this family.

Brassica genus includes six types of crops; three of them are diploids *Brassica rapa*, *Brassica oleracea* and *Brassica nigra* while *Brassica napus*, *Brassica juncea* and *Brassica carinata* are amphidiploids originated from hyperdization between each pair of their diploid progenitors.

Brassica napus originated from natural hyperdization between *Brassica rapa* and *Brassica oleracea*, it is ranked as the third crop in oil production all over the world, but it is new crop it had been known from ~ 500 years ago and suffering from the narrowing of it's genetic diversity in comparison with it's progenitors.

In order to widening its genetic diversity the genetic diversity of *Brassica rapa* as one of the most closely related progenitors will studied.

The scientific importance of *Brassica rapa* is attributed to the close relationship between *Brassica* and the model plant *Arabidopsis* which aids in the study of its genome. The presence of amphidiploids and closely related species crops this aids in study of chromosomes evolution at different time-spans.

The economic importance of *Brassica rapa* due to its uses as vegetable, forage and oil source and it has great medical important also, due to its protective role against many diseases such as cancer, heart attack, Alzheimers and cataracts.

Genetic diversity is an important trait for survival of species and enables a population to adapt to new conditions brought by environmental change. During evolution of traditional farming systems, the transition from landraces to primitive then advanced cultivars had been achieved through successive selection for definite desired characters. This caused the narrowing of the genetic base and lack of genetic diversity in most crop plants.

The study of genetic diversity that can be present in the wild relatives and progenitors represent a strategic part of germplasm collection, so that for the improvement of *Brassica napus* as a valuable crop, it is necessary to broaden its genetic base therefore the aim of the present study is to characterize the genetic diversity and salt stress tolerance of *Brassica rapa* the direct progenitor of *Brassica napus*.

The objectives used to achieve such aim are: 1) Collection of plant material representative from the genus *Brassica rapa* this plant material was supplied by (IPK gene bank “Gaterselben Germany” and seed markets in EGYPT) 2) Characterization and evaluation of the genetic diversity measures, polymorphism and relationships among the sub-species with each other and populations with each other using isozymes. 3) The evaluation of the salt stress tolerance at early stages and germination in the collected samples. 4) Characterization of the genome of the selected salt tolerant and salt sensitive samples using RAPD as molecular marker (keeping in mind that the selected samples “tolerant and sensitive” are from the same sub-species to decrease the difference among them).The following aspects were concluded:

- 1- The UPGMA cluster analysis based on isozymes has shown that *B. rapa subsp chinensis*, *B. rapa subsp. pekinensis* and *B. rapa subsp rapa* were closely related and clustered with each other, the second cluster included the remaining sub-species where *B. rapa subsp. trilocularis* and *B. rapa subsp. oleifera* clustered with each other, *B. rapa subsp. oleifera biennis*, *B. rapa subsp. oleifera annua* and *B. rapa subsp silvestris* clustered with each other and *B. rapa subsp dichotoma* and *B. rapa subsp oleifera ruvo-gruppe* clustered in the same clusterapa
- 2- The highest values of genetic diversity measures were observed in sub-species *B. rapa subsp chinensis*, *B. rapa subsp. pekinensis*, *B. rapa subsp. trilocularis*, *B. rapa subsp. oleifera* and *B. rapa subsp dichotoma*, while the lowest values were recorded in sub-species *B. rapa subsp. rapa*, *B. rapa subsp. oleifera biennis*, *B. rapa subsp. oleifera annua*, *B. rapa subsp. oleifera ruvo-gruppe* and *B. rapa subsp. silvestris*
- 3- The UPGMA cluster analysis based on isozymes has shown that the majority of populations were clustered with each other according to their taxonomic classification not to their geographic distribution in other words the geographic isolation did not change the clustering of populations extremely, where the most of populations belonging to *B. rapa subsp. chinensis*, *B. rapa subsp. pekinensis* and *B. rapa subsp. rapa* clustered with each other and populations of the remaining subspecies have shown the same manner, the great exceptions were population 6 from KUP which was separated alone, population 19 from EGY which was characterized by the presence of Acp4 locus and population 17 which belongs to *B. rapa subsp. rapa*

and population 39 which belonging to *B. rapa subsp. trilocularis* they could be sharing common remote ancestor

- 4- The highest values of genetic diversity measures were observed in populations designated 4 from CHN which belongs to *B. rapa subsp. chinensis*, population designated 11 from KOR which belongs to *B. rapa subsp. pekinensis*, population designated 32 from CAN which belongs to *B. rapa subsp. dichotoma* and populations 38 from IND and 39 from UNG both belongs to *B. rapa subsp. trilocularis*.

The lowest values were observed in populations 5 from U.S.A which belonging to *B. rapa subsp. chinensis*, population 16 from U.S.A which belongs to *B. rapa subsp. pekinensis*, population 18 from TUN which belonging to *B. rapa subsp. rapa*, population 23 from SWE which belonging to *B. rapa subsp. oleifera annua* and population 26 from SUN which belongs to *B. rapa subsp. silvestris*.

- 5- The F_{IS} statistics in case of sub-species and populations F_{IS} was negative where $F_{IS} = -0.266$ and $F_{IS} = -0.724$ respectively. While F_{IT} has shown higher values than that expected for cross pollinating species where $F_{IT} = 0.640$ and $F_{IT} = 0.822$ respectively which could be attributed to the great geographic isolation among sub-species with each other and among populations with each other which decreasing the genetic flow where $Nm = 0.0995$ in case of sub-species and $Nm = 0.0287$ in case of populations. F_{ST} also has shown high values $F_{ST} = 0.715$ and $F_{ST} = 0.897$ respectively due to the same reasons.

- 6- Based on the results of germination percentage evaluation under salinity accessions designated 3 “BRA 1321/91” from UNG

belonging to *B. rapa subsp chinensis*, accession designated 25 “BRA78/84” from UNG belonging to *B. rapa subsp. pekinensis*, accession 41 “BRA 337/97” from UNG belongs to *B. rapa subsp. rapa*, accession 73 “CR 2596/87” from UNG belongs to *B. rapa subsp. oleifera ruvo-gruppe* and accession 85 “2232/88” from UNG belongs *B. rapa subsp. trilocularis* have shown the highest values (100%) they were considered the most salt tolerant.

The most salt sensitive accessions were accessions 19, 40, 43, 55, 61, 63, 64, 65, 66, 67, 68, 69, 70, 72, 74, 77, 80, 82 and 87 they have shown values varied from 10% to 30%.

7- The characterization of the selected accessions by RAPD has revealed great difference among salt tolerant and sensitive accessions this difference could be attributed to salt stress tolerance because in the UPGMA based on RAPD the most of salt tolerant accessions clustered together we suggest that the selection of new parents for salt stress progeny of *B. napus* should be from the most related tolerant accessions.
