

## GENETIC DIVERSITY IN *Brassica* SPECIES AND *Eruca sativa* FOR YIELD ASSOCIATED PARAMETERS

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Kanwal Mahwish, Farhatullah, M. Ashiq Rabbani, S. Iqbal, L. Fayyaz and M. Afzal (2014): *Genetic diversity in Brassica species and Eruca sativa for yield associated parameters*- Genetika, vol., No.46, No.2, 537-543.

Brassica species are vulnerable to narrow genetic base due to the ignorance of their wild relatives which possess many superior characters. This study was aimed to explore the genetic diversity in five Brassica species from U triangle as well as in their wild relative *Eruca sativa*. For the complete insight of genetic diversity, four accessions, each from five species of genus Brassica along with one species of *Eruca* collected from different geographical locations (exotic and indigenous) were selected. Six yield associated parameters viz., primary branches plant<sup>-1</sup>, plant height, main raceme length, silique length, silique width and silique main raceme<sup>-1</sup> were studied. Highly significant variations among all species were observed. Mean performance showed that wild relative *E. sativa* was superior for primary branches plant<sup>-1</sup> and plant height, which are the main yield associated traits. In case of Brassica species, *B. campestris* gave the lengthiest main racemes, *B. nigra* produced more silique main raceme<sup>-1</sup> and *B. carinata* produced the longest and widest silique.

*Key words: Brassica, genetic divergence, E. sativa, wild relatives*

### INTRODUCTION

Genetic diversity, the level of biodiversity refers to the differences in the genetic makeup of species. It can be better estimated by analyzing the quantity of genetic variation within and among populations of species of particular crop (LAPEGENE *et al.*, 1997). The knowledge of genetic diversity plays significant role and is indispensable in the development of commercial hybrids (RIAZ *et al.*, 2014). Since the advent of agriculture, people have been

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exploring the genetic diversity within crop species by studying relationship between pollen and the fertilization of flowers for formation of grains and fruit (RIAZ *et al.*, 2013), to meet the food requirements. The distribution of plant genetic diversity within and among populations is a function of rate of gene flow between them. Estimation of quantity and distribution of genetic variation within and among populations of species of particular crop can facilitate the understanding the reasons for genetic diversity and also helps in providing the important basic information for better utilization in future breeding programs (LAPEGENE *et al.*, 1997). Genetic diversity particularly refers to the collection of germplasm of plants, animals and other organisms with varying characters contributing in genetic variation between and within populations (CROMWELL *et al.*, 1999). In fact, variability is a tool which provides the extent of genetic variation and hence enables species to adapt themselves in fluctuating environments. If these species could survive in fluctuating environments, they provide an insurance to meet the unfavorable conditions, thereby contributing to stability in world-wide farming system. The members of Brassicaceae family are vulnerable to limited genetic base due to the ignorance of their wild relative for improvement of crop production. By keeping in view this fact, the said study was conducted for the estimation of genetic diversity among Brassica genotypes and *E. sativa* at morphological level for certain yield related traits.

#### MATERIALS AND METHODS

The said experiment was conducted in New Developmental Farm, Department of Plant Breeding and Genetics, The University of agricultural, Peshawar; Pakistan during the main cropping season of 2010-2011. Plant material comprised of five brassica species (*B. campestris*, *B. nigra*, *B. napus*, *B. juncea* and *B. carinata*) and a wild relative (*Eruca sativa*). For the complete insight of genetic diversity four accessions from each species were selected from different geographical areas (Table 1). Altogether, a set of 24 accessions (four from each brassica species and *E. sativa*) were evaluated in Randomized Complete Block Design with three replications under natural field conditions. Data were recorded on six yield associated parameters viz, primary branches plant<sup>-1</sup>, plant height (cm), main raceme length (cm), silique main raceme<sup>-1</sup>, silique length (cm) and silique width (mm).

#### RESULTS AND DISCUSSION

Among Brassica species and *E. sativa*, highly significant ( $P \leq 0.01$ ) variations for all parameters were observed (Table 2). Significant variations were also observed within species for primary branches plant<sup>-1</sup> and plant height. Plant height and primary branches plant<sup>-1</sup> are very important traits which form the stature of a plant and also contribute to the yield. Tall plants with more primary and secondary branches will produce more silique with many seeds. In case of silique width, highly significant variation was observed in *B. carinata* only. *B. napus*, *B. juncea*, *B. campestris* and *Eruca sativa* exhibited highly significant variations for silique length. In case of silique main raceme<sup>-1</sup>, significant variations were observed in all lines within brassica species. Silique is fruit of brassicaceae family. The lengthiest and the widest silique will accommodate more seeds. Our results for significant variation in yield associated parameters are in correspondence to the previous findings by (KHAN *et al.* 2008).

Table 1. List of different accessions of Brassica species and *E. sativa* used during present study

S. No	Species	Codes	Source	Locations
1	<i>B. nigra</i>	N-157	PC	Ethiopia
2		N-1191		Ethiopia
3		N-1187		India
4		N-1186		India
1	<i>B. juncea</i>	J-2720	PC	Vihary-Punjab Pakistan
2		J-24000		Bannu-KP Pakistan
3		J-2757		South Korea
4		J-2738		France
1	<i>B. campestris</i>	C-2000	PC	Kohat-KP Pakistan
2		C-1500		Chitral, Pakistan
3		C-908		Poland
4		C-119		France
1	<i>B. napus</i>	N-2762	PC	Pakistan
2		N-2717		Hari Banda KP Pakistan
3		N-2752		France
4		N-2760		Poland
1	<i>B. carinata</i>	Ca-024997	PARC/PGRI	Islamabad, Pakistan
2		Ca-025000	PARC/PGRI	Islamabad, Pakistan
3		Ca-026196	IPK, Germany	Germany
4		Ca-025944	CGN, Netherland	Netherland
1	<i>E. sativa</i>	E3-7		Peshawar-KP, Pakistan
2		E4-15		Peshawar-KP, Pakistan
3		E1-15		Saudi Arabia
4		E2-7		Saudi Arabia

\*PC. Principal coordinator: HEC funded project "Development of Desi Sarsoon (*Brassica campestris*. L) through conventional and modern techniques"

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Although the accessions were of the same species, yet they exhibited significant variation as they were collected from different sites of locations. It has been reported that the similar morphotypes from different origins are different due to their distinct breeding and domestication (ZHOU *et al.*2005). Mean values revealed that *E. sativa* being a wild relative of family Brassicaceae possessed more primary branches (23) on the tallest plants (200.22cm). On the other hand, *B. napus* was poor in bearing primary branches (5) on the shortest plants (140.83cm) as compared to other species. Main raceme in *B. campestris* was the lengthiest as compared to the rest of species, while the shortest racemes were produced by *B. carinata*. In case of siliques length (8.99cm) and siliques width (0.53mm), *B. carinata* was the superior whereas *B. nigra* was the inferior and produced the smallest (1.38 cm) and thin (0.22 mm) siliques (Table 3). Mean values of accessions within each species is given in (Table 3). Significant variations for all these traits within each species will help in facilitating the selection of superior genotypes for future breeding programs. The variations in these traits for different species are very effective to broaden the genetic base of brassica species by incorporating the superior characters from one brassica species to another through interspecific hybridization and with *E. sativa* through intergeneric hybridization. The comparison of Brassica species with their wild relative was supported by the previous findings of COURTNEY *et al.*, 2002 MURTY and QUADRI., 1996, MEHROTRA, 1983, AMJAD *et al.*, 2000). The variations in studied traits would increase the yield and nutritional value of *E. sativa* that could be a useful tool for increasing the quality of brassica species.

Table 2. Mean sum of squares for studied parameters in brassica species and *E. sativa*

SOV	df	Primary branches plant <sup>-1</sup>	Plant height	Main raceme length	Siliques length	Siliques width	Siliques main raceme <sup>-1</sup>
Replications	2	0.01	57.35	194.29	0.09	0.01	26.12
Genotypes	23	198.22**	2515.12**	526.28**	20.16**	7.54**	1172.18**
Species	5	2211.16**	26424.58**	5019.38**	355.73**	137.72**	17110.32**
<i>B. napus</i>	3	4.67**	598.58**	850.73**	1.06**	0.001 <sup>ns</sup>	205.82**
<i>B. juncea</i>	3	7.56**	1357.87**	89.16 <sup>ns</sup>	2.11**	0.018 <sup>ns</sup>	231.83**
<i>B. campestris</i>	3	12.78**	4233.53**	219.92 <sup>ns</sup>	1.58**	0.01 <sup>ns</sup>	708.51**
<i>B. nigra</i>	3	46.56**	1354.75**	587.95**	0.11 <sup>ns</sup>	0.003 <sup>ns</sup>	512.11**
<i>B. carinata</i>	3	13.42**	503.57**	59.80 <sup>ns</sup>	0.57 <sup>ns</sup>	0.37**	148.29**
<i>E. sativa</i>	3	513.42**	224.06*	135.86 <sup>ns</sup>	0.94**	0.009 <sup>ns</sup>	50.82 <sup>ns</sup>
Error	46	0.65	79.24	87.79	0.24	0.02	20.71
CV (%)		6.5	5.4	15.2	10.8	12.8	15.2

Df, degree of freedom.\* significant at 5% level of probability,\*\* highly significant at 1% level of probability, CV(%)=coefficient of variation.

Table 3. Mean performance in five brassica species and *E. sativa* along with their accessions for studied parameters

Species	Codes	Primary branches plant-1	Plant height (cm)	Main raceme length (cm)	Siliques length (cm)	Siliques width (cm)	Siliques main raceme-1
<i>B. napus</i>	N- 2762	4	143.53	39.67	5.15	0.52	31.9
	N- 2717	4	135.63	79.23	6.41	0.56	44.2
	N- 2752	3	125.33	62.7	6.42	0.51	35.93
	N- 2760	6	158.83	69.55	5.97	0.54	50.37
	Mean	4	140.83	62.79	5.99	0.53	40.6
<i>B. juncea</i>	J- 2738	5	178.43	60.48	3.75	0.43	31.93
	J- 2757	5	184.5	70.12	2.65	0.31	43.6
	J- 2400	6	217.3	57.87	4.5	0.33	36.17
	J- 2720	8	218.8	60.03	4.34	0.41	51.93
	Mean	6	199.76	62.13	3.81	0.37	40.91
<i>B. campestris</i>	C- 2000	12	177.33	86.09	3.48	0.35	70.63
	C- 1500	8	95.5	65.67	4.47	0.46	43.5
	C- 908	10	162.23	72.1	4.21	0.42	67.1
	C- 119	8	169.27	73.03	5.24	0.36	79.5
	Mean	9.48	151.08	74.23	4.35	0.39	65.18
<i>B. nigra</i>	N- 157	15	158.83	69.15	1.38	0.23	68.67
	N- 1191	19	201.53	61.81	1.17	0.17	61.03
	N- 1187	18	155.6	49.6	1.33	0.25	64.1
	N- 1186	10	164.67	83.07	1.63	0.22	89.97
	Mean	15	170.16	65.91	1.38	0.22	70.94
<i>B. carinata</i>	Ca- 24997	10	183.17	47.27	9.1	0.62	23.53
	Ca- 25000	13	189.17	45.1	8.84	0.12	22.83
	Ca- 26196	14	190.3	36.9	8.51	0.43	16.57
	Ca- 25944	15	162.4	43.03	9.54	0.95	33.57
	Mean	13	181.26	43.08	8.99	0.53	24.13
<i>E. sativa</i>	E1-15	5	149.93	54.5	2.21	0.37	32.73
	E2-7	37	375.8	66.37	2.05	0.5	33.6
	E3-7	23	130.6	68.63	2.13	0.4	28.13
	E4-15	25	144.53	57.92	3.24	0.43	24.8
	Mean	23	200.22	61.86	2.41	0.43	29.82
Grand mean		11.87	173.88	61.66	4.49	1.08	45.26
LSD 0.05		1.26	125.03	15.4	0.8	0.23	7.48

### CONCLUSION

The present study inferred that the variations for yield associated traits in brassica species can be utilized in future breeding crops for the development of high yielding brassica lines. Particularly *E. sativa* is worth mentioning as it showed outstanding performance for plant

height and primary branches, which are very important traits contributing to high yield. Hence, incorporation of these characters in other brassica species may result in high yielding varieties. In addition, the utilization of wild relatives in hybridization with brassica species may broaden the genetic base of brassicaceae family.

Received January 16<sup>th</sup>, 2014

Accepted May 28<sup>th</sup>, 2014

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**GENETIČKA DIVERGENTNOST VRSTA *Brassica* I *Eruca sativa*  
ZA PARAMETRE PRINOSA**

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Izvod

*Brassica* vrste su osjetljive u uskoj genetičkoj osnovi zbog ignorancije od divljih srodnika koji poseduju veliki broj superiornih osobina. Vršena su istraživanja kolekcije pet grupa od kojih je svaka bila sastavljena od pet vrsta roda *Brassica* i i jedne vrste *Eruca* kolekcionisanih iz različitih geografskih lokaliteta (egzotičnih i lokalnih). Vršena su ispitivanja šest parametara vezanih za prinos i utvrđene su statistički značajne razlike varijabilnosti između ispitivanih vrsta. Utvrđena je superiornost divljeg srodnika *E. sativaje* kod razgranatosti biljaka i visine biljaka koje su glavne osobine vezane za prinos. Za *B. Nigra*, *B. Campestris* i *B. carinata* su utvrđene statistički značajne razlike kod ispitivanih osobina.

Primljeno 16. I. 2014.

Odobreno 28. V. 2014.