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MORPHOMETRIC ANALYSIS OF *BRASSICA CARINATA* ELITE LINES REVEALS VARIATION FOR YIELD RELATED TRAITS

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Abstract

Brassica carinata is an important species that shows maximum agro-morphological based variations. The principal component analysis (PCA) is an effective method for the selection of best parent and further improvement of breeding program. In the present research work we evaluated the genetic variability among thirty eight elite genotypes of *B. carinata*. The data for fourteen agro-morphological quantitative traits were analyzed by PCA and correlation analysis. Our results show that maximum variability was found in the first six principal component (PC) groups that contributed 76.20% of overall variability. Among these PC groups the first PC group accounted for maximum variability (28.54%) as compared to other groups. Among different PC groups the days to flowering traits (from days to flower initiation to completion), pod length/width, height of plant etc. showed highest genetic variability. Some unique highly diverse genotypes were also screened through scatter plot including Chakwal raya, Bc-701, Bc-702, Bc-707, Bc-709, Bc-711, Bc-740, Bc-778, Bc-880 and Bc-881. All the flowering traits, pod length/width, pods/main raceme, thousand seed weight gave positive relation with yield trait. The elite screened genotypes can be useful for further improvement of this important *Brassica* species.

Key words: *B. carinata*, Correlation, Elite lines, Genetic variability, Principal component analysis

Introduction

Brassicaceae is one of the key plant families consisting about 350 genera and 3500 species, and is included among top ten most economically important plant families (Christopher *et al*., 2005). *Brassica carinata* (Ethiopian mustard) is useful to cultivate with other mustard and canola genotypes. It is highly useful for the area having low rain fall. This species shows maximum tolerance to both environmental and other biotic factors (Getinet *et al*., 1996). The presence of these positive properties this crop suffer several agronomic problems like longer time period, lower oil content, maximum height and poor harvesting index (Prakash &Hinata, 1980; Hirano *et al*., 2009). Therefore proper breeding methods like varietal hybridization and induced mutagenesis must be used for further improvement (Barro *et al*., 2003).

The success of crop improvement is possible through study of both the qualitative and quantitative traits of any plant species. The accurate measurement of genetic variability is useful for the collection of specific plant population and the selection of best parent for new cultivars development (Pervaiz *et al.,* 2010). However, the success of crop improvement is possible by using both morpho-biochemical and molecular methods (Shinwari *et al.,* 2014; Hussain *et al.,* 2016; Jan *et al.,* 2017[a,c]). Jan *et al.,* (2017)[b] reported the genetic variability found among three sub-species of *B. rapa*. Theses sub-species shows different response to yield and yield related important economic traits. Saleem *et al.,* (2017) evaluated *B. juncea* germplasm through principal component analysis and correlation methods. They recorded maximum diversity for economically important quantitative traits. The genetic divergence using PCA and cluster analysis have been also utilized by different researchers for important crops (Arif *et al.,* 2015; Qadir *et al.,* 2017). It is one of key statistical method to assess genetic variability. It is useful for the identification of diverse genotypes and other economically important traits. It is also useful for the proper planning and implementation of future molecular breeding methods (Venujayakanth *et al.,* 2017). Therefore, the present experiment was conducted to study the principal component and correlation analysis based variability among elite lines of *B. carinata*.

Materials and Methods

The fresh seeds of 37 elite lines of *Brassica carinata* with one check variety (Chakwal raya) were acquired from the gene-bank, of Bio-resources Conservation Institute (BCI), NARC, Islamabad, Pakistan. The elite germplasm information is given in Table 1. The experiment was designed during year 2016-2017 by following augmented deisign with replication of check after each ten genotypes. The row to row distance for seed sowing was 60 cm and the he row length of 2.5 meter was used. The sowing was performed after proper irrigation of field to maintain optimum moisture level for germination. The hand drill method was used for planting at depth of about 3-5 cm. After one week of germination all weeding was removed and all plants were checked for any pest attack. Some important quantitative morphological traits were recorded like days to flower initiation (DFI), days to fifty percent flowering (DF50%), days to flower completion (DFC), days to maturity (DM), plant height (PH), primary branches/plant (PB/P), main raceme length (MRL), stem thickness (ST), pods per main raceme (P/MR), pod length (PL), pod width (PW), seeds/pod (S/P), 1000-seed weight (1000-SW) and seed yield/plant (SY/P). All the data from five random plants were averaged and analyzed for principal component and correlation analysis by using Statistica version 7.0 software.

Table 1. List of *B. carinata*elite lines used in the study.

Sr. No.	Accession	Source	Sr. No.	Accession	Source
1	Bc-701	NARC, Islamabad	20	Bc-775	NARC, Islamabad
2	Bc-702	NARC, Islamabad	21	Bc-776	NARC, Islamabad
3	Bc-703	NARC, Islamabad	22	Bc-777	NARC, Islamabad
4	Bc-704	NARC, Islamabad	23	Bc-778	NARC, Islamabad
5	Bc-705	NARC, Islamabad	24	Bc-779	NARC, Islamabad
6	Bc-706	NARC, Islamabad	25	Bc-742	NARC, Islamabad
7	Bc-707	NARC, Islamabad	26	Bc-743	NARC, Islamabad
8	Bc-708	NARC, Islamabad	27	Bc-751	NARC, Islamabad
9	Bc-709	NARC, Islamabad	28	Bc-752	NARC, Islamabad
10	Bc-710	NARC, Islamabad	29	Bc-770	NARC, Islamabad
11	Bc-711	NARC, Islamabad	30	Bc-771	NARC, Islamabad
12	Bc-734	NARC, Islamabad	31	Bc-772	NARC, Islamabad
13	Bc-735	NARC, Islamabad	32	Bc-773	NARC, Islamabad
14	Bc-736	NARC, Islamabad	33	Bc-774	NARC, Islamabad
15	Bc-737	NARC, Islamabad	34	Bc-780	NARC, Islamabad
16	Bc-738	NARC, Islamabad	35	Bc-881	NARC, Islamabad
17	Bc-739	NARC, Islamabad	36	Bc-891	NARC, Islamabad
18	Bc-740	NARC, Islamabad	37	Bc-892	NARC, Islamabad
19	Bc-741	NARC, Islamabad	38	Chakwal Raya	NARC, Islamabad

Results and Discussion

PCA Based Genetic Variability among elite *B. carinata* Germplasm: The data resulting from PCA showed that the first six principal component (PCs) groups having eigenvalue more than 1 contributed overall 76.20% variability. The PC1, PC2 and PC3 accounted for 28.54, 12.14 and 10.54% variability, respectively (Fig. 1). The response of different quantitative traits varied in all PC groups. In first PC group the DFI, DF50% and DFC account highest variability. In PC2 pod length, pod width and plant height showed maximum variability. In PC3 seeds/pod, pod length, stem thickness (Table 2, Fig. 2 a-c), In PC4 maximum positive variability was observed for pod length, pods/main raceme and seeds/pod. In PC5 the 1000-SW, pod length and stem thickness showed highest variability than other traits. In PC6 the stem thickness, Plant height and pods/main raceme traits were highest contributor in genetic variability (Table 2). The 2D diagram further characterized and identified the diverse genotypes. Among all the studied genotypes the Chakwal raya, Bc-701, Bc-702, Bc-707, Bc-709, Bc-711, Bc-740, Bc-778, Bc-880 and Bc-881 were highly diverged from the remaining accessions (Fig. 3a-c). Hussain *et al.*, (2017) characterized 28 sunflower hybrids through PCA methods and recorded 10 PCS groups having eigenvalue more than one. They recorded 73.7% overall variability in first ten PCs groups. Among these groups the first PC accountedfor maximum variability (59.7.7%) followed by PC2 (14%). as compared to other groups. Pankaj *et al.*, (2017) recorded nine PCs group having eigenvalue more than one and they contribute 77.17% of variability. Among these groups the PC1 explained maximum (16.65%) phenotypic variability than remaining PCs groups. Similar findings were also reported by Neeru *et al.*, (2015) in *B. juncea*. Our results show contradiction with the findings of Zada *et al.*, (2013) who found highest variability (17.79%) in first PC group by studying *B. carinata* genotypes. In addition they recorded different response of different traits in some PCs groups as compared to our results. These deviations from our findings might be due to genotypes difference or seasonal variations.

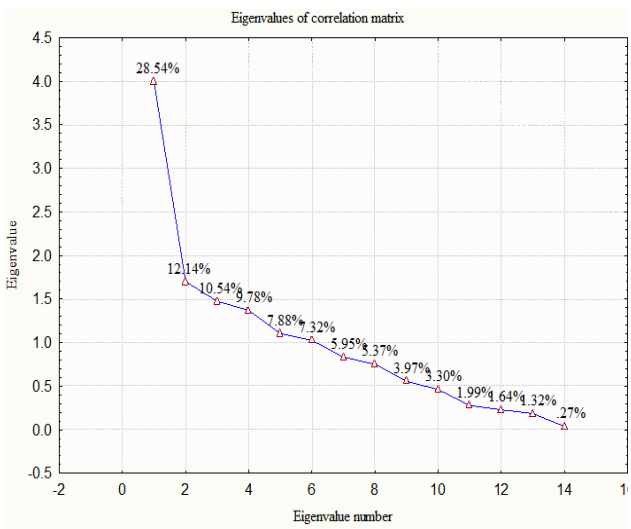

Fig. 1. Scree plot of elite *B. carinata* lines between eigen values and number of PCs.

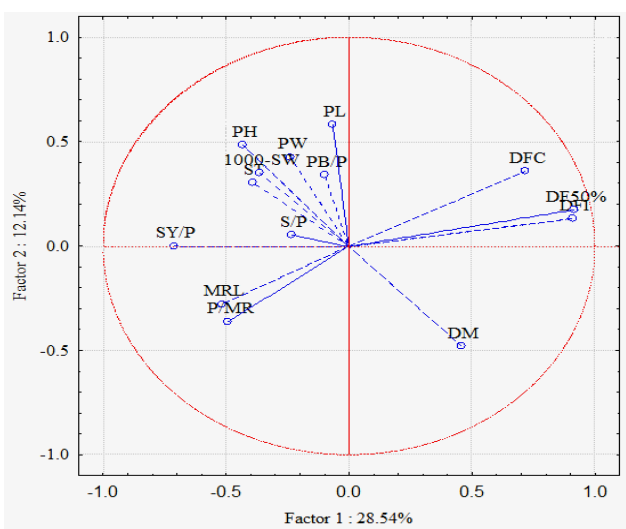

Fig. 2a. Contribution of different agro-morphological traits in first two PC groups.

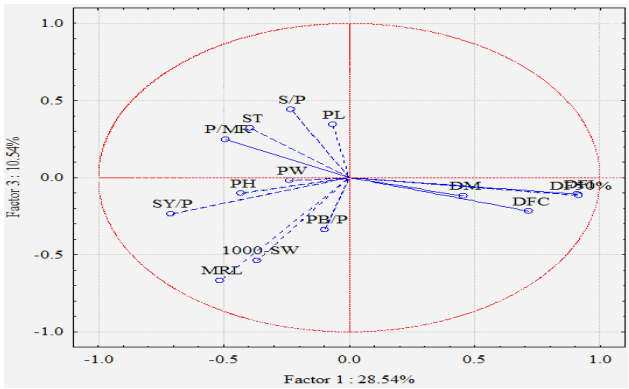

Fig. 2b. Contribution of different agro-morphological traits in first and third PC groups.

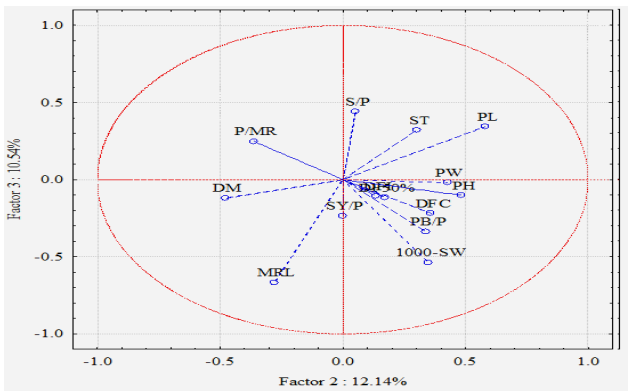

Fig. 2c. Contribution of different agro-morphological traits in second and third PC groups.

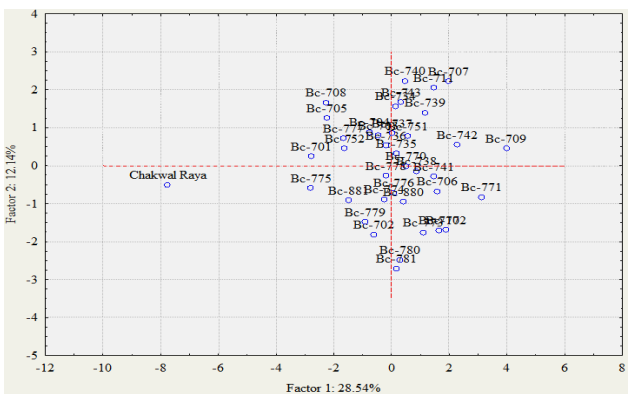

Fig. 3a. 2D ordination of 38 elite lines of *B. carinata* in first two PC groups for the year 2016-17.

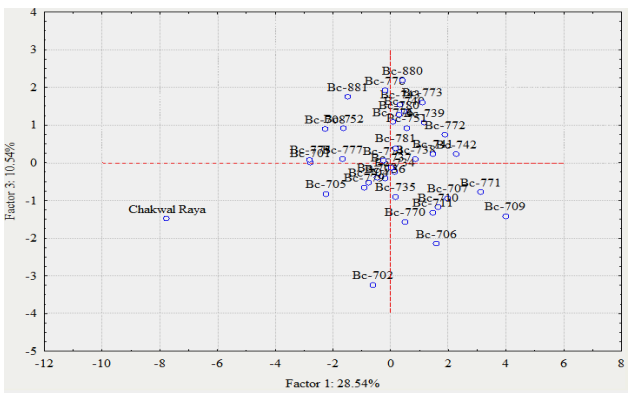

Fig. 3b. 2D ordination of 38 elite lines of *B. carinata* in first and third PC groups for the year 2016-17.

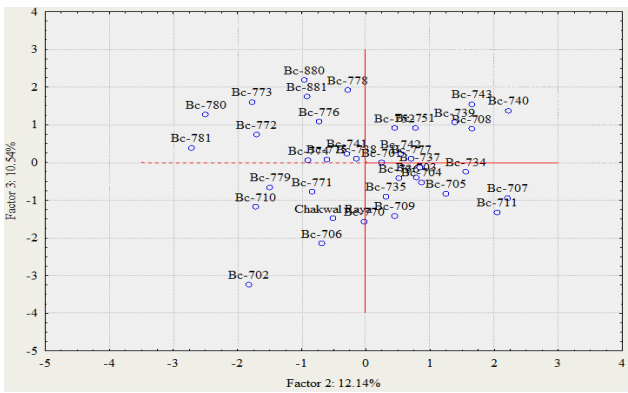

Fig. 3c. 2D ordinations of 38 elite lines of *B. carinata* in second and third PC groups for the year 2016-17.

The correlation study was performed to study low moderate or high level of both positive and negative correlation among fourteen quantitative traits. The high strong positive correlation (0.94) was recorded among DFI and DF50% followed by 0.73 between DFI and DFC (Table 3). The yield, one of economically important quantitative traits showed low to moderate positive correlation with main raceme length, 1000-seed weight, pod width and pods/ main raceme. However, the highest negative correlation values (-0.54 and -0.53) was observed among seed yield/plant and DFI and DF50%, respectively. Similarly the pods/main raceme trait also showed negative correlation with DFI and DF50% (Table 3). According to Sharafi *et al.,* (2015) the seeds pods/plant and weight of 1000 seed have significant positive relationship with yield trait in *B. napus*. Lodhi *et al.,* (2017) also found positive relationship of yield trait with height of plant, number of grains/plant, thousand weights of grains, length of spike and weight of spike in wheat crop. Bibi *et al.,* (2017) found strong positive interaction of plant maturity with plant height and flowering related traits and negative correlation with seeds/pod and pod length in *B. juncea* genotypes.

Table 2. Contribution of different quantitative traits in different PCs groups.

Traits	PC1	PC2	PC 3	PC4	PC5	PC6
DF1	0.910	0.133	-0.108	0.066	-0.110	0.055
DF50%	0.914	0.173	-0.116	0.147	0.012	0.042
DFC	0.716	0.359	-0.219	0.094	-0.167	0.068
DM	0.456	-0.480	-0.119	-0.202	0.104	-0.197
PH	-0.431	0.483	-0.102	0.011	-0.055	0.342
PB/P	-0.098	0.340	-0.338	-0.659	-0.159	0.004
MRL	-0.516	-0.279	-0.667	-0.032	-0.062	0.090
P/MR	-0.491	-0.361	0.248	0.402	-0.215	0.317
ST	-0.393	0.302	0.321	-0.502	0.168	0.422
PL	-0.066	0.580	0.344	0.428	0.353	-0.118
PW	-0.237	0.426	-0.019	0.146	-0.749	-0.228
S/P	-0.234	0.052	0.440	-0.357	-0.058	-0.621
SY/P	-0.711	0.000	-0.235	0.302	-0.092	-0.237
1000-SW	-0.365	0.350	-0.536	0.143	0.499	-0.256

Table 3. Correlation among different quantitative traits (p=0.05).

Variable	DFI	DF50%	DFC	DM	PH	PB/P	MRL	P/MR	ST	PL	PW	S/P	Y/P	1000SW
DF1	1.00													
DF50%	0.94	1.00												
DFC	0.69	0.73	1.00											
DM	0.32	0.27	0.22	1.00										
PH	-0.25	-0.30	-0.01	-0.31	1.00									
PB/P	-0.05	-0.06	0.00	-0.03	0.09	1.00								
MRL	-0.35	-0.37	-0.28	-0.04	0.23	0.17	1.00							
P/MR	-0.44	-0.43	-0.40	-0.08	0.15	-0.22	0.24	1.00						
ST	-0.34	-0.37	-0.21	-0.27	0.31	0.25	0.00	0.04	1.00					
PL	-0.02	0.09	0.02	-0.23	0.16	-0.08	-0.32	0.09	0.10	1.00				
PW	-0.11	-0.18	0.05	-0.28	0.20	0.19	-0.01	0.10	-0.04	0.10	1.00			
S/P	-0.23	-0.27	-0.20	0.02	0.08	0.04	-0.09	-0.06	0.16	0.07	0.09	1.00		
SY/P	-0.54	-0.53	-0.35	-0.35	0.20	-0.07	0.52	0.30	0.07	0.08	0.25	0.14	1.00	
1000-SW	-0.31	-0.22	-0.11	-0.15	0.26	0.15	0.31	-0.15	-0.01	0.26	0.03	-0.08	0.34	1.00

Conclusion

The evaluation of any crop species for yield and yield related traits have prime importance in genetic diversity study. In present study high degree of genetic variability was observed among traits and elite *B. carinata* genotypes through PCA and correlation analysis. Many important traits that account maxium genetic variabilitywere screened. The unique elite screened lines can be useful for the average and potential yield improvement of this important crop in different areas of the world. In addition these elite screened genotypes can be useful for further advanced and adaptability yield trials.

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