

MULTIVARIATE ANALYSIS OF YIELD RELATED TRAITS IN *BRASSICA RAPA* GERMPLASM

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Abstract

Brassica rapa is one of the important oilseed crops and commonly grown all over the world for multiple purposes. In present study multivariate based variability among *B. rapa* genotypes collected from four different countries (Pakistan, Germany, Netherlands, and Sweden). The two years mean morphological data were recorded for 18 different economically important quantitative traits. The multivariate analysis recorded maximum variations at first 5 PCs group. A total of 66.34% variability was recorded in first five principal components (PCs) group. The contribution to first five PCs in overall PCs was 27.32%, 15.01%, 9.54%, 7.90%, and 6.58%, respectively. Among all characters the pod shattering stage IV and V gave maximum positive contribution in overall genetic variability in PC1 (0.58) and PC3 (0.66). The principal component analysis (PCA) further classified all 253 genotypes into different population groups on the basis of their geographic origin. Seven different geographic groups were recorded and all showed different evolutionary history. The population groups 1 and 2 predominantly included the Pakistani genotypes. The population group 5 and 6 mostly contained the European genotypes. The rest of the groups contained genotypes from all four countries (Pakistan, Germany, Netherlands and Sweden). The geographic information system (GIS) study further showed that Pakistani genotypes are highly diverged from the European genotypes and present in all seven PCs groups. All the groups are highly diverged from one another on the basis of traits and geographic origins. Our results may be used as a baseline for future *Brassica* species breeding programs in Pakistan.

Key words: *B. rapa*; Genetic variability; Geographic information system; Oilseeds; Principal component analysis.

Introduction

Brassica rapa is one of the important vegetable oils, bioenergy and fodder crops (Tahir *et al.*, 2012). The haploid chromosome number of *B. rapa* is 10 but with the passage of time increased variations within species and sub-species were observed (Qian *et al.*, 2006; Zhao *et al.*, 2009). The multivariate and cluster analysis studies are important to study many traits and large numbers of genotypes. It provides a clear picture on the classification of close or diverse genotypes. The dendrogram shows the phenetic relationship of genotypes with one another. The group number of a population increased, when genetic variability among genotypes is high (Choudhary & Joshi, 2001; Jan *et al.*, 2018).

Genetic diversity study is useful to identify promising genotypes (Nawaz *et al.*, 2015; Jan *et al.*, 2017; Shinwari *et al.*, 2018; Jan *et al.*, 2019; Sardar *et al.*, 2021). Ali *et al.*, (2015) studied morpho-biochemical based variability in 39 *Brassica juncea* genotypes. The principal component analysis data showed that PC1 contributed 22.21% variability followed by PC2 (14.65%) and PC3 (11.41%) respectively. The maximum variance (0.45) was noted for number of leaves per plant followed by silique/main raceme (0.43) in PC1 group. However lower variability was observed for glucosinolates, erucic acid, protein and oil contents in all PC groups in both years study. They recorded maximum variability based on morpho-biochemical characteristics of economically important Indian mustard germplasm collected from different regions of Pakistan. Neeru *et al.*, (2015) classified *Brassica juncea* genotypes on the basis of principal

component (PC) and cluster analysis. Eleven different PC groups were noted that contribute to overall 75% genetic variability. Khan *et al.*, (2014) reported intra-specific diversity among 211 diverse rapeseed germplasm through cluster and principal component analysis. Agromorphological study was recorded for 12 qualitative and 21 quantitative characters. Maximum variability was noted for important traits such as pod shatter resistance (394.4), plant height (200.7) and days to 50% flower completion (115.2). Among these PCs groups the PC1 group contributed 26.96% followed by PC2 group 10%. The genotypes 1697, 26068 and 24854 showed excellent yield/plant, yield/silique and 1000-seed weight.

B. rapa genotypes show considerable variations from one another for key quantitative characters. In order to screen best genotypes among these, it is important to screen unique genotypes for crop improvement and possibly to develop new high yield varieties. Therefore, the present study was designed to study multivariate based variability in diverse *B. rapa* genotypes with the aim to identify promising genotypes for further improvements of this important oilseed crop species.

Material and Methods

Plant material: The plant materials contained 253 local and exotic genotypes (251 new accessions with two check varieties) of *Brassica rapa*. The experimental seed materials were provided by Bio Resources Conservation Institute (BCI), National Agricultural Research Centre (NARC), Islamabad, Pakistan. The detailed information of *B. rapa* genotypes and its origin is given in (Table 1).

Table 1. Origins detail of *B. rapa* germplasm used.

Sr. No.	No of accessions	Origin
01	130	Pakistan
02	67	Germany
03	32	Netherlands
04	22	Sweden
05	02	Unknown
Total	253	

Table 2a. Principal components and their constituent traits contribution to overall variability among studied germplasm.

Traits of interest	PC1	PC2	PC3	PC4	PC5
Eigenvalue	4.92	2.70	1.72	1.42	1.18
Cumulative eigenvalue	4.92	7.62	9.33	10.76	11.94
%cent of variance	27.32	15.01	9.54	7.90	6.58
Cumulative variance	27.32	42.32	51.86	59.76	66.34

Table 2b. Principal components and their constituent traits contribution to overall variability among studied germplasm.

Trait of interest	PC1	PC2	PC3	PC4	PC5
DFI (days)	-0.9	-0.15	0.02	-0.32	0.25
DF50% (days)	-0.90	-0.16	0.02	-0.30	0.23
DFC (days)	-0.89	-0.15	0.03	-0.31	0.23
DM (days)	-0.69	-0.07	-0.06	0.12	0.12
PS-4 (%)	0.58	-0.09	0.66	-0.39	0.01
PS-5 (%)	0.58	-0.03	0.66	-0.40	0.02
LL (cm)	-0.65	0.43	0.36	-0.05	-0.07
LW (cm)	-0.42	0.55	0.38	0.02	-0.27
PH (cm)	-0.27	0.50	0.22	0.28	-0.20
PB/P (No.)	0.03	0.48	0.10	-0.09	0.30
MRL (cm)	0.08	0.43	-0.35	-0.23	0.00
P/MR (No.)	-0.08	0.65	-0.29	-0.29	-0.16
ST (mm)	-0.59	0.26	0.34	0.29	-0.18
PL (cm)	0.15	-0.10	0.31	0.39	0.60
PW (mm)	0.34	0.38	-0.05	0.18	0.52
S/P (No.)	0.17	0.63	-0.05	-0.07	0.31
SY/P (g)	-0.22	0.16	0.19	0.52	0.04
TSW (g)	0.37	0.63	-0.21	-0.20	0.10

Agro-morphological characterization and crop management: Two years experiment was conducted in the experimental field of BCI, NARC, Islamabad, Pakistan. The inter-row to row distance of 60cm and inter-path distance of 30cm was maintained. The plot size was 2 rows of 5m length for each genotype. The field was irrigated in order to provide maximum moisture before one week of sowing and after the field was maintained under rain-fed condition by withholding water. The seeds were sown 2cm deep in soil with the help of a single row hand drill machine. After germination, thinning and weeding was carried out. Pesticides were sprayed across the field to control pest insects. The mean phenotypic data of five selected plants was used for data scoring. The two years mean morphological data were recorded for 18 different quantitative traits (Table 2b).

Data analysis: The taxonomic relationship between genotypes were studied for all agro-morphological

important traits using multivariate techniques of principal component analysis (PCA) through Statistica, version 7.0 software (Marques de Sa, 2007). Scatter plots of all principal components were made to determine the graphical depict of the pattern of genetic diversity among the *B. rapa* genotypes through Statistica, version 7.0 software (Marques de Sa, 2007). Environmental Systems Research Institute (ESRI) shape files were utilized to generate a diversity map on Arc GIS 10.2.2 software (Anon., 2015).

Results and Discussion

Agro-morphological based variation is important to screen best genotypes under field conditions. The agro-morphological based diverse genotypes are useful for further biochemical and molecular evaluation. The genetic diversity study is used for efficient utilization and for development of improved cultivar/varieties (Shinwari *et al.*, 2013; Anjum *et al.*, 2019). Morphological based screening of different crop species/sub-species is therefore so important for all plant breeders. Therefore, proper strategies and planning is needed to evaluate local and exotic germplasm and to select best genotypes against both qualitative and quantitative characters (Balkaya and Ergun, 2008). In the present study, morphological data of 18 quantitative traits recorded for 253 *Brassica rapa* accessions were subjected to multivariate procedure of Principal Component Analysis (PCA). The first five principal components (PCs) with eigen value unity or more (≥ 1) were considered important which accounted for 66.34% of overall phenotypic variation in population. The first principal component (PC1) has 4.92 eigen values and depicted 27.32% of variability among accessions. PC2 has eigen value 2.70 representing 15.01% of total variability. PC3 had 1.72 eigen value and showed 9.54% variation among accessions PC4, with eigen value 1.42 revealed 7.90% variability. Lastly, the PC5 was accounted for 6.58% of total variance in population with eigen value 1.18 (Table 2a). The contribution of all traits in 5 PCs groups are given in Table 2b.

The first two principal components were depicted on a scatter plot to observe the relationship among all 253 accessions. The pattern was construed by distributing genotypes in 7 discrete groups and 25 outliers settling in none of the groups (Fig. 1). The contribution of different traits in different PCs groups are shown in Table 3. Group-I had 56 accessions of which 73% were from Pakistan. The second group was the largest group (59 accessions) including 39 from Pakistan and remaining 20 from Germany (8), Netherlands (7) and Sweden (5). Group-III had only 14 accessions from Pakistan (7), Netherland (4) and Germany (3). The fourth group comprised accessions from Pakistan, Germany and Netherland. Group-V had 19 least shattering genotypes of Dutch and German origin. The sixth group was second largest including 58 genotypes of all which predominantly included European accessions from Germany, Netherland and Sweden. The Group-VII had 10 accessions including eight from Pakistan and two from Sweden Out of these 25 genotypes showed some unique performances and they remained outlier (Fig. 1; Table 3).

Table 3. Description of 7 agro-morphologically diverse *B. rapa* populations revealed by PCA scatter plot.

Population	Characteristics	No. of accessions	Accessions Origin
Population 1	Early maturing, high pod shattering, minimum leaf length, leaf width, pod/main raceme and seed yield/plant	56	More than 70% from Pakistan, rest from other three countries (Netherlands, Germany and Sweden)
Population 2	Average performing genotypes for traits like plant height, primary branches/plant, leaf length and width, stem thickness and 1000 seed weight	59	More than 50% from Pakistan, rest from other three countries (Netherlands, Germany and Sweden)
Population 3	Earlier flowering initiation, days to 50% flowering, days to flowering completion and maximum 100-seed weight	14	Pakistan, Netherlands, Germany
Population 4	No pod shattering at later stages, shortest main raceme and minimum 1000 seed weight but highest seed yield/plant	12	Pakistan, Netherlands, Germany
Population 5	Late flowering and maturity, largest leaf length, minimum pod length, minimum number of branches/plant and seed/pod	19	Germany and Netherlands
Population 6	Maximum stem thickness and performed above average for most of the agronomic traits	58	Predominantly included European accessions from Germany, Netherland and Sweden
Population 7	Minimum days to flowering initiation, days to 50% flowering and days to flowering completion, Tallest plants with highest number of branches/ plants, longest main racemes, maximum leaf and pod width	10	Majority from Pakistan and Sweden

*25 Accessions were outlier at the edges of scatter plot due to distinctive traits. Most of these genotypes belonged to Germany and Pakistan

A diversity map was drawn on the basis of variability present among all 253 genotypes from four different countries (Pakistan, Netherlands, Sweden and Germany). All seven populations identified in PCA analysis were present in Pakistan having a maximum score of seven. The increased phenotypic variability in Pakistani populations resulted due to highest variance for various agro-morphological traits. The response of different quantitative traits varied with genotypes collected from different origins (Pakistan, Netherlands, Germany and Sweden) in all PCA groups (Fig. 2). Our results are not in agreement with the findings of Worekeneh *et al.*, (2016) as they reported that the first five groups contributed about 90% variability in 49 *B. carinata* genotypes as compared to other PCs groups. But their further findings strongly supported our results where the PC1 group contributed maximum (39.3%) in overall PC groups followed by PC2 (24.10%). According to them the plant height, primary branches/plant, plant height and 1000 seed weight had maximum variability as compared to other quantitative traits. Ilyas *et al.*, (2018) recorded maximum eigen values for first four PCs groups in a study on 329 *B. napus* accessions. Khan *et al.*, (2014) reported that the first three PCs groups accounted 45.94% variation in canola. According to them the first group contributed maximum followed by second one. These results are further confirmed by Yu *et al.*, (2007) who found similar types of results in European and Chinese *B. napus* genotypes. They also reported plant height, and number of siliquae/terminal raceme contributed maximum in PC1. Our results agree with Ali *et al.*, (2015) those reported that PC1 contributed 22.21% variability followed by PC2 (14.65%) and PC3 (11.41%) respectively. The maximum contribution in the first two groups was recorded in the number of leaves/plant and siliquae/main raceme. They also studied maximum variability was observed in Pakistani *B. juncea* genotypes in all PCs groups. Neeru *et al.*, (2015) also recorded similar results among *B. juncea* genotypes.

Conclusion

The local Pakistani genotypes showed a high degree of similarity with one another, but highly diverse from the European genotypes. However, some genotypes from Pakistan, Netherlands, Germany and Sweden showed similarity with one another. These important quantitative characters can be used in future to assess the genetic diversity in *B. rapa* and *B. napus* germplasm and widen the base for new varieties development. The GIS study showed that Pakistani genotypes are highly diverged from the European genotypes and present in all seven PCs groups. There is a need of multi-location experiments on diverse germplasm to check its performance in different climatic conditions. However further agro-morphological study between some more Asian's countries genotypes must be tested along with these tested genotypes to identify more elite genotypes.

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