



E-ISSN: 2278-4136

P-ISSN: 2349-8234

JPP 2018; 7(5): 2132-2138

Received: 04-07-2018

Accepted: 06-08-2018

Suman Yadav

Department of Plant Breeding
and Genetics, Dr. Rajendra
Prasad Central Agricultural
University, Pusa, Samastipur,
Bihar, India

Anil Pandey

Department of Plant Breeding
and Genetics, Dr. Rajendra
Prasad Central Agricultural
University, Pusa, Samastipur,
Bihar, India

Multivariate analysis approach to select parents for hybridization aiming at yield improvement in Indian mustard (*Brassica juncea* L.) genotypes

Suman Yadav and Anil Pandey

Abstract

Indian mustard (*Brassica juncea* L.) germplasm consisting twenty accessions including one National and two zonal check cultivars were evaluated for quantitative traits. The present study was conducted to investigate genetic diversity and correlation among studied genotypes of *B. juncea* L. based on agro-morphological at research farm of TCA Dholi, Dr RPCAU, Pusa, Bihar (India). To investigate the genetic diversity based on morphological characters, data was recorded on eighteen quantitative traits. The calculated data was analyzed through two complementary methods, *i.e.* PCA (Principal Component Analysis) and cluster analysis. Among all the studied cultivars, significant diversity as well as analysis of dispersion was recorded for different agro-morphological characters. Among all the parameters, maximum variance was recorded for seed yield per plant, biological yield per plant, test weight, harvest index and siliqua on primary branches, secondary branches as well as on primary mother axis. Among all the characters, seed yield had significant and positive association with physiological maturity (1.12G & 0.43P), number of secondary branches (1.00G & 0.78P), siliqua on secondary branches (0.96G & 0.57P), number of primary branches (0.95G & 0.67) and biological yield per plant (0.90G & 0.81P), plant height (0.74G & 0.46P), siliqua on primary mother axis (0.73G & 0.49P), siliqua on primary branches (0.72G & 0.53P), length of primary mother axis (0.52G & 0.29P) at genotypic and phenotypic level. Using cluster analysis all the genotypes were divided into five major groups. It was observed that out of 8 of 18 principal components with an Eigen value of ≥ 1.0 calculated for 89.17% of the total diversity observed between twenty accessions of Indian mustard (*B. juncea* L.). The contribution of first three PCs in the total PCs was 31.94, 47.29 and 60.00 respectively. Among all the investigated clusters, cluster I and cluster IV showed great potential for plant height, number of primary branches, number of secondary branches, siliqua on primary branches, siliqua on secondary branches, siliqua on primary mother axis, biological yield/plant and seed yield/plant respectively, so these genotypes are recommended for future breeding programs for achieving promising results.

Keywords: Genetic diversity, GGRO-morphology, *Brassica juncea* L, PCA analysis

Introduction

The genus *Brassica* is an important member of the cruciferae family. It comprises of several economically important species which yield edible roots, stems, leaves, buds, flowers and seeds condiment. Most of the species are used as oilseed crop and some as forage. Indian mustard (*B. juncea* (Linn) (Czern and Coss) popularly known as rai, raya or laha is one of the most important oil seed crops of the country and it occupies considerably large acreage among the *Brassica* group of oil seed crops. India stands first both in acreage and production of rapeseed and mustard in Asia. The crops are cultivated in an area of 70 lakh ha with a production of 81 lakh tonnes and with an average yield of 1149 kg/ha (Anon., 2006). In India, mustard and rape seed are being grown largely in states like Uttar Pradesh, Rajasthan, Haryana, Assam, Gujarat, Punjab, West Bengal and Madhya Pradesh. Indian mustard (*B. juncea* L. Czern and Coss) have also major share in edible oil economy of Bihar, offering potential option for diversifying the predominant Rice-Wheat system (Khachatourians *et al.*, 2004) and grown mainly as rainfed / irrigated situations under early, timely and late sown agro-ecologies. The crop species is said to be one of the earliest domesticated species. *B. juncea* annually grows as wild and cultivated species over a large geographical range, across the Asia, Africa, Australia, America and Europe (Abbas *et al.*, 2009) [1]. So for the prosperity of the country, it is essential to increase the production of these crops and for maximum production, exploitation of genetic diversity of these crops is essential being an agricultural country but unfortunately it is deficient in the oilseed production.

Diversity can be determined by three different levels, first one is genetic diversity, in which the variation observed at gene and germplasm level, the second one is diversity of species, in which richness of species at a specific location and the third one is the Ecosystem diversity,

Correspondence

Suman Yadav

Department of Plant Breeding
and Genetics, Dr. Rajendra
Prasad Central Agricultural
University, Pusa, Samastipur,
Bihar, India

in which crop species interact with their environment. Diversity is potent for different crops to fulfill the gap between demand and production across the world (Amurrio *et al.*, 1995) [5]. Various morpho-biochemical and molecular methods are used to study genetic variability among local and exotic plant germplasm. The proper evaluation of important crop species helps in the identification and utilization of improved genotypes (Azadgoleh, E.M.A., Zamani, M *et al.*, 2009 and Hopkin *et al.*, 2007) [6, 11]. Therefore, the present study was performed to estimate and characterize the genetic variation and relationships among Indian mustard genotypes through agro-morphological traits to identify and select promising germplasm for traits of economic significance.

Materials and Methods

Plant material comprises of twenty germplasm including one national and two zonal check cultivars of *B. juncea* L. for estimation of agro-morphological variation. The germplasm were provided by All India Co-ordinated Research Project-Rapeseed and Mustard centres: DRMR, Bharatpur, Rajasthan, CCSHAU, Hisar, Haryana, BARC, Trombay, Maharashtra, GBPUAT, Pantnagar, Uttarakhand, CSAUAT, Kanpur, U. P, IARI, New Delhi, Sri Ganganagar, Rajasthan, DR. RPCAU, Dholi, Bihar, was laid out in Randomized Complete Block Design (RCBD) with three replications during Rabi season (2017-18) and was planted on 13th October 2017 at the research research farm of TCA Dholi, DRPCA, Pusa, Bihar (India) (25. 50 N, 85. 40E and 52. 12 m MSL) in Loam soil (8. 4 pH). The recommended package and practices were followed to raise good crop. The data was recorded on eighteen quantitative traits *viz*: plant height (cm), days to first flower open, days to 50 % flowering, number of primary branches, number of secondary branches, length of primary mother axis, days to physiological maturity, number of siliqua on primary branches, silique on secondary branches, silique on primary mother axis, number of seeds per siliqua, siliqua length (cm), 1000 seeds weight (g), total biological yield (g) per plant, harvest index (%) and seed yield per plant (g), vegetative phase duration and post-anthesis phase duration. The recorded morphological traits data were averaged and analyzed for simple statistics *i.e.* mean, variance, range, frequency distribution, coefficient of variance and standard deviation using computer software (MS-Excel 2007). Cluster and principal component analysis (PCA) was performed on the recorded data for quantitative traits. Before to cluster and PCA, mean of each parameter was standardized so that to avoiding scaling differences effects. For all the pairs of accessions Euclidean distance co-efficient were calculated. The Euclidean dis- similarity co-efficient matrices were utilized to estimate the association among the *B. juncea* germplasm with cluster analysis through complete linkage method (Windostat version 8. 5).

Results

Correlation Study Based on Agronomic and Morphological Traits

The association analysis revealed that, in general, the values of genotypic correlations were higher than their phenotypic correlations indicating the inherent association among the traits. Similar findings were also reported by Shah *et al.* (2002), Singh *et al.* (2003) and Joshi *et al.* (2009). Correlation coefficient analysis (Table-1) revealed that seed yield had significant and positive association with physiological maturity (1.12G & 0.43P), number of secondary branches (1.00G & 0.78P), silique on secondary branches (0.96G &

0.57P), number of primary branches (0.95G & 0.67) and biological yield per plant (0.90G & 0.81P), plant height (0.74G & 0.46P), silique on primary mother axis (0.73G & 0.49P), silique on primary branches (0.72G & 0.53P), length of primary mother axis (0.52G & 0.29P) at genotypic and phenotypic levels. Thus, these above said attributes can serve as marker characters for seed yield improvement in mustard. Such positive interrelationships between seed yield and these attributes have also been reported in mustard by Illmulwaret *et al.* (2003), Sirohi *et al.* (2004), Kardam and Singh (2005), Acharya (2006), Singh and Singh (2010) and Sekhar *et al.* (2012).

The significant and positive correlation coefficients were observed in primary branches per plant with secondary branches per plant (0.98G and 0.74P), plant height with days to physiological maturity (1.20G) and days to 50 % flowering with days to physiological maturity (0.51G and 0.22P) thereby establishing strong inherent relationship among themselves. These findings are in accordance with Shalini *et al.*, (2000), Choudhary *et al.*, (2003) and Singh and Singh (2010). The positive and significant association of harvest index and total biological yield with seed yield per plant made it possible to select genotypes having more biological yield with higher harvest index, a desirable combination must have resulted due to simultaneous selection of these characters.

Principal Component Analysis Based on Agronomic and Morphological Traits

Principal component analysis (PCA) was carried out based on eighteen quantitative morphological characters. The 7 principal components account for 89.17% of the overall variability among the studied *B. juncea* L. accessions for the total phenotypic variations (Table 2, Figures 1-2). Among these seven principal components (PCs), the PCA-I was found to have 31.94% out of the total variability. Plant height (0.274), primary branches (0.367), number of secondary branches (0.277), length of primary mother axis (0.172), silique on primary branches (0.004), silique on primary mother axis (0.160), biological yield/plant (0.342), harvest index (0.341), physiological maturity (0.354) and seed yield per plant (0.374), days to 50% flowering (0.113) contributed positively to first principal component. In contrast, silique on secondary branches (-0.007), silique length (-0.224), seeds per silique (-0.097), days to first flower open (-0.012), vegetative phase duration (-0.191), post anthesis phase duration (-0.212) and test weight (-0.045) contributed negatively.

The contribution of PC-II in total differences was 15.34% and was positively associated with plant height (0.370), silique on primary branches (0.161), days to first flower (0.462), vegetative phase duration (0.174) and physiological maturity (0.002) whereas number of primary (-0.145) as well as secondary branches (-0.177), length of primary mother axis (-0.060), silique on secondary branches (-0.253), silique on primary mother axis (-0.230), silique length (-0.142), seeds per silique (-0.351), biological yield/plant (-0.149), harvest index (-0.017), seed yield /plant (-0.012), post anthesis phase duration (-0.399), days to 50% flowering (-0.148) and test weight (-0.265) were negatively associated with PC-II.

PC-III showed 11.24% of the total agro-morphological variation and positively associated with plant height (0.142), number of primary branches (0.068), siliqua length (0.045), seeds per siliqua (0.007), biological yield/plant (0.030), seed yield/plant (0.061), physiological maturity (0.115), post anthesis phase duration (0.261), and days to 50% flowering (0.273) while negatively associated with number of secondary

branches (-0.057), length of primary mother axis (-0.249), siliqua on primary branches (-0.446), siliqua on secondary branches (-0.446), siliqua on primary mother axis (-0.325), harvest index (-0.177), days to first flower open (-0.163), vegetative phase duration (-0.255) and test weight (-0.343).

The PC-IV contributed 10.29% in the total variability and were positively contributed to plant height (0.064), number of secondary branches (0.115), siliqua on primary branches (0.192), siliqua on secondary branches (0.296), siliqua length (0.081), seeds/siliqua (0.087), biological yield/plant (0.260), harvest index (0.190), vegetative phase duration (0.369), physiological maturity (0.250) and post anthesis phase duration (0.100). Similarly the traits *i.e.* number of primary branches (-0.055), length of primary mother axis (-0.365), siliqua on primary mother axis (-0.368), seed yield/plant (-0.037), days to first flower open (-0.294), days to 50% flowering (-0.287) and test weight (-0.295) contributed negatively.

In the total variability the contribution of PC-V was observed 7.32% and the parameter *i.e.* plant height (0.078), number of secondary branches (0.064), siliqua on secondary branches (0.172), seeds per siliqua (0.329), biological yield per plant (0.027), seed yield/plant (0.061), days to first flower open (0.298), vegetative phase duration (0.241), physiological maturity (0.134), days to 50% flowering (0.493) and 0.299) were positively contributed. Whereas the characters *i.e.* number of primary branches (-0.091), siliqua on primary branches (-0.039), length of primary mother axis (-0.429), siliqua on primary mother axis (-0.030), siliqua length (-0.344), harvest index (-0.170) and post anthesis phase duration (-0.069) contributed negatively.

The PC-VI depicted proportion of variability as 6.02% and were positively associated with plant height (0.096), number of primary branches (0.213), siliqua on primary branches (0.508), siliqua on secondary branches (0.244), siliqua on primary mother axis (0.006), siliqua length (0.177), biological yield/plant (0.229), seed yield/plant (0.099), days to first flower open (0.074), post anthesis phase duration (0.181) and days to 50% flowering (0.324). Similarly the traits *i.e.* number of secondary branches (-0.468), length of primary mother axis (-0.136), seeds per siliqua (-0.116), harvest index (-0.067), vegetative phase duration (-0.265), physiological maturity (-0.203) and -0.139) were negatively associated with PC-VI.

PC-VII accounted 5.52% of the total variation among agromorphological traits. Plant height (0.134), siliqua on primary branches (0.048), siliqua length (0.480), seeds/siliqua (0.616), harvest index (0.314), seed yield/plant (0.008), days to first flower open (0.204), physiological maturity (0.198), and test weight (0.085) were contributed positively to PC-VII. Whereas number of primary branches (-0.046), number of secondary branches (-0.162), length of primary mother axis (-0.021), siliqua on secondary branches (-0.119), siliqua on primary mother axis (-0.083), biological yield/plant (-0.135), vegetative phase duration (-0.245), post anthesis phase duration (-0.210) and days to 50% flowering (-0.088) depicted negative contribution.

Discussion

Maximum GCV and PCV was recorded for seed yield per plant (51.46 and 55.64) followed by biological yield per plant (48.98 and 52.27), harvest index (24.20 and 36.70), test weight (25.64 and 26.17) and siliqua on main primary mother axis (10.39 and 13.86). These results were well sported by similar findings by Kumar *et al.* (2006), Singh *et al.* (2011),

Shekhawat *et al.* (2012), Kumar *et al.* (2006) and Mondal & Khajuria (2000) reported high values for PCV and GCV for the biological yield per plant and seed yield per plant. These traits suggested the possibility of yield improvement through selection. Siliqua on primary branches as well as secondary branches and number of primary branches and secondary branches show moderate estimates of coefficient of variance respectively (13.54 and 18.28) and (20.25 and 32.74), (13.11 and 16.98) and (17.39 and 24.79).

Correlation coefficient analysis revealed that seed yield had significant and positive association with physiological maturity (1.12G & 0.43P), number of secondary branches (1.00G & 0.78P), silique on secondary branches (0.96G & 0.57P), number of primary branches (0.95G & 0.67) and biological yield per plant (0.90G & 0.81P), plant height (0.74G & 0.46P), silique on primary mother axis (0.73G & 0.49P), silique on primary branches (0.72G & 0.53P), length of primary mother axis (0.52G & 0.29P) at genotypic and phenotypic levels. Thus, these above said attributes can serve as marker characters for seed yield improvement in mustard. Such positive interrelationships between seed yield and these attributes have also been reported in mustard by Illmulwaret *et al.* (2003), Sirohi *et al.* (2004), Kardam and Singh (2005), Acharya (2006), Singh and Singh (2010) and Sekhar *et al.* (2012).

The significant and positive correlation coefficients were observed in primary branches per plant with secondary branches per plant (0.98G and 0.74P), plant height with days to physiological maturity (1.20G) and days to 50 % flowering with days to physiological maturity (0.51G and 0.22P) thereby establishing strong inherent relationship among themselves. These findings are in accordance with Shalini *et al.*, (2000), Choudhary *et al.*, (2003) and Singh and Singh (2010). The positive and significant association of harvest index and total biological yield with seed yield per plant made it possible to select genotypes having more biological yield with higher harvest index, a desirable combination must have resulted due to simultaneous selection of these characters.

Our results were strengthened by many earlier plant breeders and scientists. Numerous plant breeders and plant scientist in the earlier era had practiced and got remarkable results of diversity in agro-morphological parameters for various Brassica individuals through two complementary methods *i.e.* cluster analysis and principal component analysis (PCA). These techniques were successfully observed in Indian mustard (*Brassica juncea* L.) germplasm by Gupta *et al.*, (1991)^[10] and Shiva *et al.*, (1994)^[21]. In Ethiopian mustard by Alemayehu and Becker (2002)^[4] and in white head cabbage Balkaya *et al.* (2005)^[7]. All the above mentioned plant breeders and plant scientist's results gives support to our present investigation that these 2 techniques are very supportive in estimated associations among individuals in a more clear approach.. The classification of present studied *Brassica juncea* L. genotypes into five clusters on the basis of K Clustering method. Cluster I consists of four genotypes namely RGN-13, RAURD-14-18, RAURD-14-11, and BPR-541-4 having high cluster mean of following characters plant height, number of primary branches, number of secondary branches, siliqua on primary branches, siliqua on secondary branches, biological yield/plant, harvest index, seed yield per plant and minimum days to 50% flowering. Cluster II is oligo-genotypes namely TPM-1 and Pusa Mahak. Cluster III composed of four genotypes namely DRMR 4001, RAURD-212, RH0555, and Pusa mustard. Cluster IV is monogenic RAURD-78 showing highest cluster mean of following traits

plant height, number of primary branches, number of secondary branches, silique on primary branches, silique on secondary branches, biological yield/plant, harvest index, seed yield per plant. Cluster V having highest number of genotypes viz. DRMR 15-9, RGN-368, RAJENDRA SUFALAM, KMR (E) 16-1, PRE-2013-19, NPJ-197, NPJ-201, Varuna, and Urvashi. During the present investigation among different accessions of *Brassica juncea* L. considerable level of genetic differences was observed for different agronomic and morphological characters. These studied parameters can play significant and interesting role in *Brassica juncea* L. cultivars and varieties development programs in future. In present study the seven groups were recorded and PC1 showed highest level of variability. The same findings were also recorded by Dias *et al.* (1993) [8] in diverse germplasm of *Brassica oleracea* L. originated from Portugal.

Conclusion

Among all the characters, valuable genetic diversity was observed through different agro-morphological traits *i.e.*, plant height (cm), days to first flower open, days to 50 %

flowering, number of primary branches, number of secondary branches, length of primary mother axis, days to physiological maturity, number of silique on primary branches, silique on secondary branches, silique on primary mother axis, number of seeds per siliquae, siliquae length (cm), 1000 seeds weight (g), total biological yield (g) per plant, harvest index (%) and seed yield per plant (g), vegetative phase duration and post-anthesis phase duration. Most of the traits contributed highly significant association for the said trait during the present investigation. These genotypes show that there is great potential in the studied accessions, which can be used in future breeding program as a productive genotypes.

Acknowledgements

Authors are thankful to different All India Coordinated Research Project-Rapeseed and Mustard centres namely, DRMR, Bharatpur, Rajasthan, CCSHAU, Hisar, Haryana, BARC, Trombay, Maharastra, GBPUAT, Pantnagar, Uttarakhand, CSAUAT, Kanpur, U. P, IARI, New Delhi, ARS, RAU, Sri Ganganagar, Rajasthan for providing genotypes of rapeseed and mustard.

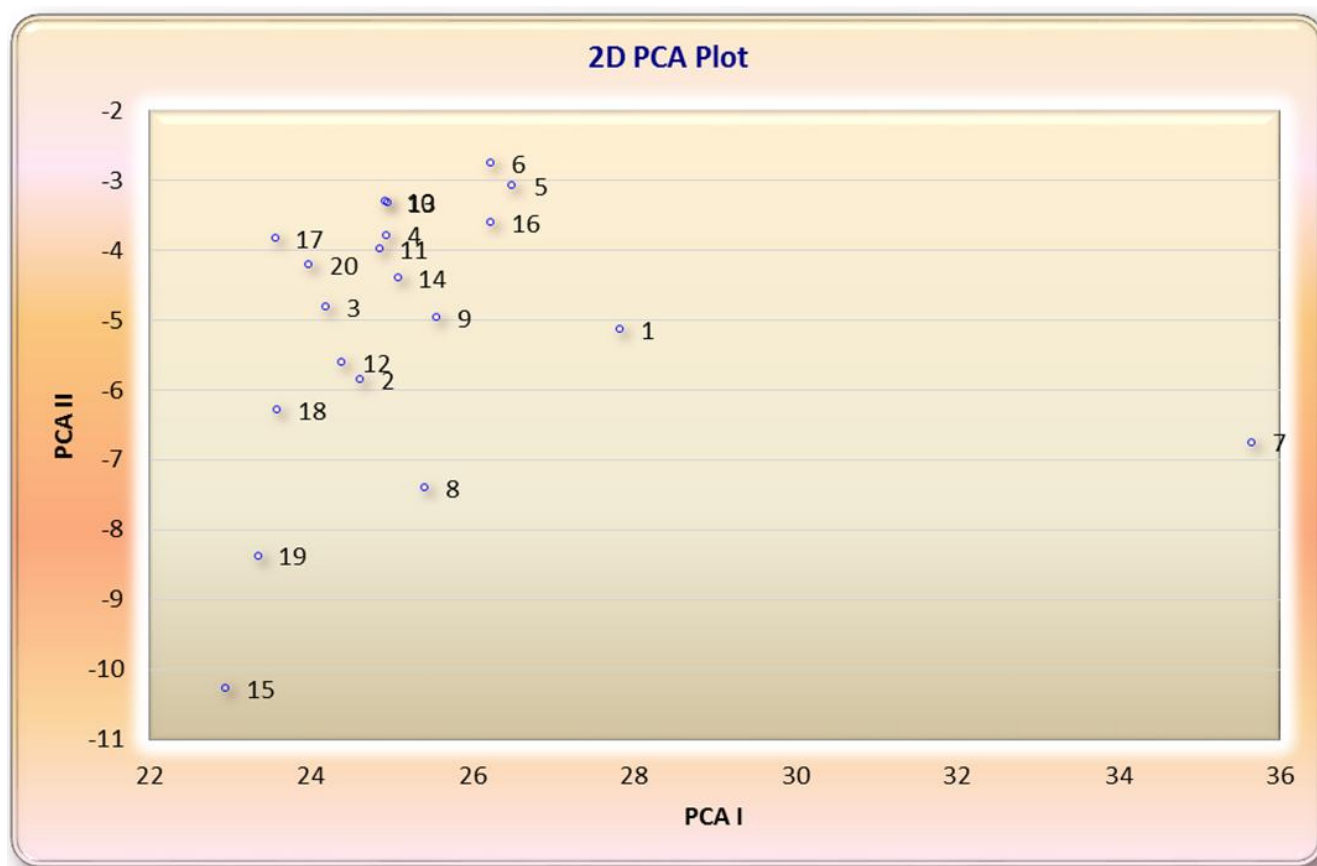


Fig 1: Scatter diagram of PC I and PC II for agro-morphological traits

Table 1: Genotypic (r_g) and phenotypic (r_p) correlations coefficients among 18 characters of mustard

Character		Plant height	Number of primary branches	Number of secondary branches	Length of primary mother axis	Siliqua on primary branches	Siliqua on secondary branches	Siliqua on primary mother axis	Siliqua length	Number of seeds/siliqua	Biological yield/plant	Harvest index	Days to first flower open	Vegetative Phase duration	Physiological maturity	Post Anthesis phase duration	Days to 50% flowering	Test weight	Seed yield per plant
Plant height	rg	1.00	0.56**	0.69**	0.45**	0.56*	0.49**	0.34**	-0.23	-0.62	0.61**	0.18	0.56**	0.21	1.20**	-0.69	0.60**	-0.36	0.74**
	rp	1.00	0.33**	0.47**	0.45**	0.34**	0.41**	0.41**	-0.04	-0.13	0.52**	-0.07	0.27*	0.21	0.18	-0.28*	0.20	-0.23	0.46**
No. of primary branches	rg		1.00	0.98**	0.62**	0.66**	0.86**	0.80**	-0.30*	-0.26	0.96**	-0.08	0.06	-0.26*	0.90**	-0.29*	0.46**	-0.02	0.95**
	rp		1.00	0.74**	0.33*	0.59**	0.57**	0.56**	-0.02	-0.08	0.75**	-0.11	-0.009	-0.09	0.34**	-0.11	0.28*	-0.01	0.67**
No. of secondary branches	rg			1.00	0.66**	0.62**	0.87**	0.86**	-0.45**	-0.26*	1.01**	-0.04	0.02	-0.14	1.27	-0.29*	0.48**	0.00	1.00**
	rp			1.00	0.32*	0.62**	0.73**	0.66**	-0.06	-0.21*	0.79**	-0.03	0.02	0.05	0.35**	-0.11	0.23*	0.002	0.78**
Length of primary mother axis	rg				1.00	0.53**	0.48**	0.66**	-0.31*	-0.43**	0.53**	-0.07	0.36**	0.12	0.52**	-0.50**	0.32*	0.19	0.52**
	rp				1.00	0.25*	0.26*	0.39**	-0.20*	-0.005	0.47**	-0.25*	0.15	0.13	0.11	-0.20*	0.17	0.15	0.29*
Siliqua on primary	rg					1.00	1.00**	0.78**	-0.35**	-0.39**	0.82**	-0.12	0.44**	0.34**	0.85**	-0.60**	0.63**	0.05	0.72**
	rp					1.00	0.70**	0.58**	-0.04	-0.23*	0.65**	-0.12	0.28*	0.34**	0.45**	-0.34**	0.38**	0.03	0.53**
Siliqua on secondary branches	rg						1.00	0.90**	-0.43**	-0.28*	1.07**	-0.06	0.28*	0.18	1.36**	-0.53**	0.74**	0.18	0.96**
	rp						1.00	0.66**	-0.18	-0.18	0.76**	-0.23*	0.24*	0.29*	0.31*	-0.30*	0.26*	0.08	0.57**
Siliqua on primary mother axis	rg							1.00	-0.42**	-0.30*	0.77**	-0.23*	0.37**	0.24*	0.92**	-0.60**	0.70**	0.29*	0.73**
	rp							1.00	-0.14	-0.13	0.65**	-0.31*	0.31*	0.33*	0.29*	-0.39**	0.29*	0.23*	0.49**
Siliqua length	rg								1.00	0.71**	-0.28*	0.42**	-0.45**	-0.45**	-0.34**	0.48**	-0.46**	-0.45**	-0.18*
	rp								1.00	0.33*	-0.12	0.36**	-0.14	-0.03	-0.03	0.20	-0.003	-0.25*	0.02
No. of seeds/siliqua	rg									1.00	-0.32*	0.63***	-0.33**	-0.47**	0.01	0.41**	-0.34**	0.32*	-0.11
	rp									1.00	-0.16	0.22*	-0.22*	-0.21*	-0.16	0.19	-0.27*	0.17	-0.09
Biological yield/plant	rg										1.00	-0.13	0.11	-0.05	1.02**	-0.32*	0.58**	-0.04	0.90**
	rp										1.00	-0.19	0.14	0.01	0.41**	-0.28*	0.34**	-0.03	0.81**
Harvest index	rg											1.00	-0.50**	-0.10	0.44**	0.51**	-0.96**	-0.12	0.21*
	rp											1.00	-0.41**	-0.16	0.07	0.43**	-0.30*	-0.11	0.31*
Days to first flower open	rg												1.00	0.77**	0.32*	-1.00**	1.06**	0.16	-0.09
	rp												1.00	0.65**	0.21*	-0.95**	0.53**	0.12	-0.08
Vegetative phase duration	rg													1.00	0.41**	-0.77**	0.59**	0.21	-0.07
	rp													1.00	0.19	-0.57**	0.43**	0.14	-0.03
Physiological maturity	rg														1.00	-0.53**	0.51**	-0.28	1.12**
	rp														1.00	-0.25*	0.22*	-0.09	0.43**
Post anthesis phase duration	rg															1.00	-1.16**	-0.18	-0.11
	rp															1.00	-0.53**	-0.15	-0.05
Days to 50% flowering	rg																1.00	0.02	0.21*
	rp																1.00	-0.02	0.15
Test weight	rg																	1.00	-0.06
	rp																	1.00	-0.07

Table 2: Principal components (PCs) of agronomic traits among *B. juncea* L. genotypes.

	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Eigen value	5.749	2.76	2.28	1.85	1.31	1.08	0.99
Percent Variance	31.94	15.34	12.71	10.29	7.32	6.02	5.52
Cumulative Variance	31.9	47.29	60.00	70.30	77.62	83.65	89.17
Traits		Eigen vectors					
Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Plant height	0.274	0.370	0.143	0.064	0.078	0.096	0.048
Primary branches	0.367	-0.145	0.069	-0.056	-0.091	0.214	-0.104
Secondary branches	0.278	-0.178	-0.058	0.116	0.064	-0.469	0.359
Length of primary mother axis	0.173	-0.060	-0.250	-0.365	-0.430	-0.136	-0.022
Silique on primary branches	0.005	0.161	-0.446	0.192	-0.039	0.509	-0.001
Silique on secondary branches	-0.007	-0.254	-0.447	0.296	0.173	0.245	0.050
Silique on primary mother axis	0.160	-0.231	-0.326	-0.368	-0.031	0.006	0.437
Silique length	-0.225	-0.143	0.045	0.081	-0.345	0.177	0.478
Seeds per silique	-0.097	-0.352	0.007	0.088	0.330	-0.116	-0.036
Biological yield/plant	0.343	-0.149	0.031	0.261	0.028	0.230	0.024
Harvest index	0.341	-0.017	-0.177	0.191	-0.170	-0.068	-0.190
Seed yield per plant	0.375	-0.012	0.062	-0.038	0.061	0.100	-0.151
Days to first flower open	-0.012	0.462	-0.164	-0.295	0.299	0.075	0.038
Vegetative phase duration	-0.192	0.174	-0.255	0.369	0.241	-0.266	0.188
Physiological maturity	0.354	0.002	0.116	0.250	0.134	-0.204	0.032
Post anthesis phase duration	-0.212	-0.399	0.261	0.100	-0.070	0.181	-0.208
Days to 50% flowering	0.114	-0.149	0.274	-0.288	0.494	0.325	0.333
Test weight	-0.046	-0.266	-0.343	-0.295	0.299	-0.139	-0.428

References

1. Abbas SJ, Farhatullah MKB, Khan IA, Munir I. Molecular Analysis of Genetic Diversity in Brassica Species. *Pakistan Journal of Botany*. 2009; 41:167-176.
2. Abideen SN, Nadeem F, Abideen SA. Genetic Variability and Correlation Studies in Brassica napus L. Genotypes. *International Journal of Innovation and Applied Studies*. 2013; 2:574-581.
3. Ahmad M, Naeem M, Khan IA. Relative Abundance of Aphids Population on Different Brassica Genotypes. *Sarhad Journal of Agriculture*. 2013; 29:133-138.
4. Alemayehu N, Becker H. Genotypic Diversity and Patterns of Variation in a Germplasm Material of Ethiopian mustard (*Brassica carinata* A. Braun). *Genetic Resources and Crop Evolution*. 2002; 49:573-582.
5. Amurrio JM, De Ron AA, Zeven AC. Numerical Taxonomy of Iberian Pea Landraces Based on Quantitative and Qualitative Characters. *Euphytica*. 1995; 82:195-205.
6. Azadgoleh EMA, Zamani M, Esmaeil Y. Agronomical Important Traits Correlation in Rapeseed (*Brassica napus* L.) Genotypes. *Research Journal of Agriculture & Biological Sciences*. 2009; 5:798-802.
7. Balkaya A, Yanmaz R, Kar AA. Morphological Characterization of White Head Cabbage (*Brassica oleracea* var. capitata subvar. Alba) Genotypes in Turkey. *New Zealand Journal of Crop and Horticultural Science*. 2005; 33:333-341.
8. Dias JS, Monteiro AA, Lima MB. Numerical Taxonomy of Portuguese-tronchuda Cabbage and Galega Kale Landraces Using Morphological Characters. *Euphytica*. 1993; 69:51-68. <https://doi.org/10.1007/BF00021725>
9. González-Rubio C, Rodríguez-Estrella R, Lozano-Garza OA, García-De-León FJ. Genetic Diversity of the Endemic Xantus' Hummingbird Using 16 Novel Polymorphic Microsatellite Loci, and Their Cross Amplification between Six Related Species. *Open Journal of Genetics*. 2016; 6:19-27.
10. Gupta VP, Sekhon MS, Satija DR. Studies on Genetic Diversity, Heterosis and Combining Ability in Indian Mustard (*Brassica juncea* (L.) Czern. & Coss). *Indian Journal of Genetics*. 1991; 51:448-453.
11. Hopkins CJ, Cogan NOI, Hand M, Jewell E, Kaur J, Li X, et al. Sixteen New Simple Sequence Repeat Markers from *Brassica juncea* Expressed in Sequences and Their Cross-Species Amplification. *Molecular Ecology Notes*. 2007; 7:697-700.
12. Jan SA, Shinwari ZK, Rabbani MA. Agro-Morphological and Physiological Responses of Brassica rapa Ecotypes to Salt Stress. *Pakistan Journal of Botany*. 2016; 48:1379-1384.
13. Jan SA, Shinwari ZK, Rabbani MA. Determining Genetic Divergence among Brassica rapa Ecotypes through Electrophoretic Mobility of Total Seed Proteins. *Journal of Animal and Plant Sciences*. 2016; 26:1758-1764.
14. Jan SA, Shinwari ZK, Rabbani MA. Morpho-Biochemical Evaluation of Brassica rapa Sub-Species for Salt Tolerance. *Genetika*. 2016; 8:323-338.
15. Jan SA, Shinwari ZK, Rabbani MA, Shah SH, Ibrahim MI, Ilyas M. Optimization of an Efficient SDS-PAGE Protocol for Rapid Protein Analysis of Brassica rapa. *Journal of Biodiversity and Environmental Sciences*. 2016; 9:17-24.
16. Khan Q, Khan AS, Khurshid H, Jan SA, Ahmad N, Khan SA, et al. Exploring Durable Genetic Resistance against Leaf Rust through Phenotypic Characterization and LR34 Linked STS Marker in Wheat Germplasm. *Bioscience Journal*. 2016; 32:986-998.
17. Khan SA, Iqbal J, Khurshid H, Saleem N, Rabbani MA, Zia M, et al. The Extent of Intra-Specific Genetic Divergence in Brassica napus L. Population Estimated through Various Agro-Morphological Traits. *European Academic Research*. 2014; 2:2254-2275.
18. Nasim A, Ferhatullah IS, Shah S, Azam SM. Genetic Variability and Correlation Studies for Morpho-Physiological Traits in Brassica napus L. *Pakistan Journal of Botany*. 2013; 45:1229-1234.

19. Rabbani MA, Iwabuchi A, Murakami Y, Suzuki T, Takayanagi K. Phenotypic Variation and the Relationships among Mustard (*Brassica juncea*) Germplasm from Pakistan. *Euphytica*. 1998; 101:357-366.
20. Rabbani MA, Iwabuchi A, Murakami Y, Suzuki T, Takayanagi K. Collection, Evaluation and Utilization of Oilseed Mustard (*Brassica juncea* L.) in Pakistan. *Pakistan Journal of Biological Sciences*. 1999; 2:88-94.
21. Shiva V. Agriculture and Food Production. UNESCO/Environment Education Dossiers. 1994; 9:2-3.
22. Vinu V, Singh N, Vasudev S, Kumar D, Kumar YS, Naresh S, *et al.* Assessment of Genetic Diversity in *Brassica juncea* (Brassicaceae) Genotypes Using Phenotypic Differences and SSR Markers. *Revista de Biología Tropical*. 2013; 61:1919-1934.
23. Yasir A, Farhatullah RH, Nasim A, Azam SM, Khan A. Heritability and Correlation Analysis for Morphological and Biochemical Traits in *Brassica carinata*. *Sarhad Journal of Agriculture*. 2013; 29:359-370.
24. Zare M. Interrelationship between Grain Yield and Related Traits in Rape seed (*Brassica napus* L.). *African Journal of Agriculture Research*. 2011; 6:6684-6689.