



Genetic parameters and diversity studies of yield and yield contributing characters in *Brassica* genotypes

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ABSTRACT

The potential of a crop to favorably respond to breeding programs depends on its existing nature and magnitude of genetic variability, heritability and genetic advance. An experiment was conducted with eighteen *Brassica* genotypes following Randomized complete block design (RCBD) with three replications at the field of the department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh, Bangladesh to estimate genetic divergence, variability ranges and contribution of each trait towards genetic diversity. Analysis of variance showed significant variation among the genotypes for all the studied yield and yield contributing characters. The phenotypic coefficient of variation (PCV) was higher than the genotypic co-efficient of variation (GCV) for all the characters measured, indicated that the traits were influenced by environment. All traits showed high heritability (61.54% to 98.64%) which indicated possible improvement through selection. High heritability values (>60%) along with high genetic advance and genetic advance in percentage of mean indicated prevalence of additive gene action, which provides good scope for further improvement by selection. The genotypes were grouped into four clusters, most of the genotypes were grouped into Cluster I (8 genotypes), while cluster IV contained only one genotype. Considering the mean value, the cluster IV and Cluster II were ranked as the top groups in terms of yield and early maturity. High Heritability with high genetic advance in percentage of mean was observed for number of branches/plant, number of pod/plant, number of seeds/pod and yield/plant and selection focused on these traits could be useful for future breeding program of *Brassica*. The genotype BD-7114 was the best performer considering all the studied traits especially yield and days to maturity which could be used as an important breeding material for the improvement of *Brassica*.

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Introduction

Brassica is the world's third most important sources of edible vegetable oils after palm and soybean (FAO, 2017). It is an important genus of plant kingdom consisting of over 3200 species with high diverse morphology. *Brassica* belongs to the family Brassicaceae originated primarily from near Himalayan region and secondarily from European-Mediterranean area and Asia (Downey and Robelen1989). In Bangladesh various species of *Brassica* are grown. The genomic constitutions of the three diploid elemental species of *Brassica* are AA for *Brassica campestris*, BB for *Brassica nigra* and CC for *Brassica oleracea* having diploid chromosome

number of 20, 16 and 18, respectively. On the other hand, the species *Brassica juncea* (AABB), *Brassica carinata* (BBCC) and *Brassica napus* (AACC) are the natural amphidiploids having the chromosome 36, 34 and 38 respectively.

Rapeseed and mustard occupy the first position in respect to area and production among the oil crops grown in Bangladesh and contain 42% oil and 25% protein (Khaleque, 1985). They are the third highest source of edible oils supply in the world after palm and soybean with a worldwide production of 69.6 million tones (FAO, 2017). In Bangladesh, 787025 ha of land was under rapeseed and mustard cultivation which produced 361909

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tons in 2015-16 (BBS, 2016). Though, a range of *Brassica* oilseed are grown in the country, the local production of edible oil meets only fourth of the required quantity, the rest has to be imported by spending valuable foreign currency. Major cultivation of this crop is done with the traditional cultivars in the marginal lands. There is limited scope to increase yield of *Brassica* due to cultivation of existing low yielding varieties with low input and management and almost all cultivars are brown seeded and smaller in size (2-2.5 g/1000 seeds). Considering the dominancy of rice cultivation and space available between T. aman and Boro, there should be an attempt to develop short duration and high yielding varieties of mustard with more oil percentage in seed, tolerant to biotic and abiotic stress to fulfill the requirement of edible oils of the country by increasing the production.

The improvement of a crop is largely dependent on the nature and magnitude of available genetic variability, heritability and the transfer of desired characters into new varieties. The success of breeding programmes can be enhanced when variability within the existing germplasm is high, which allows the plant breeder to more rapidly produce new varieties or improve existing ones (Meena and Bahadur, 2013; Meena and Bahadur, 2014; Ranganatha *et al.* 2013; Yared and Misteru, 2016). Hence, knowledge on key genetic parameters is crucial for any crop improvement program, providing precise information for selection. Genetic parameters like the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (GA) are useful biometric tools for measuring genetic variability (Aditya *et al.*, 2013).

Multivariate analysis is a useful tool in quantifying the degree of divergence among biological populations at genotypic level and to assess relative contribution of different components to the total divergence both at intra- and inter-cluster levels (Murty and Arunchalam, 1966; Ram and Panwar, 1970). Considering the above aspects, the present study was undertaken to find out genetic diversity, variability ranges, heritability, genetic advance and the contribution of yield and yield contributing traits towards the genetic divergence among the 18 genotypes of *Brassica*.

Materials and Methods

The present study was conducted following Randomized Complete Block Design (RCBD) with three replications at the Experimental farm of the department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh during the Rabi season from November 2017 to December 2018 with 18 (eighteen) *Brassica* genotypes which are listed in the Table 1.

Different genotypes were matured at different times. Harvesting was done when 90% of the plant population

of each plot reached to maturity. Data were recorded on five randomly chosen plants of each genotype for each replication for different characters, such as days to first flowering, days to maturity, plant height, number of branches/plant, number of siliqua/plant, length of pod, number of seeds/pod, 1000-seed weight (g) and seed yield/plant (g).

Table 1. Name and sources of studied *Brassica* genotypes

Sl. no.	Genotype (code name)	Source
1	BARI Sarisa-8	BARI, BD
2	BARI Sarisa-16	BARI, BD
3	BD-7104	BARI, BD
4	Tori-7	BARI, BD
5	BARI Sarisa-10	BARI, BD
6	BARI Sarisa-11	BARI, BD
7	SAU-01	SAU, BD
8	BD-10111	BARI, BD
9	BD-6950	BARI, BD
10	BD-10115	BARI, BD
11	JUN-536	BARI, BD
12	Nap-0567	BARI, BD
13	Nap-0564	BARI, BD
14	BDJH-12	BARI, BD
15	BD-7114	BARI, BD
16	BD-7115	BARI, BD
17	BD-6957	BARI, BD
18	BD-6952	BARI, BD

BARI = Bangladesh Agricultural Research Institute, BD= Bangladesh, SAU= Sher-e- Bangla Agricultural University, Bangladesh, JUN = Juncea, Nap = Napa

The recorded data for different characters were analyzed using MSTAT-C. Estimation of genotypic and phenotypic variances, heritability in broad sense (h^2_b) as well as categorization of h^2_b and GA was done according to the formula given by Johnson *et al.* (1955). GA (%) was calculated by the formula of Comstock and Robinson (1952). GA (%) was categorized as low (0-10%), moderate (10-20%) and high ($\geq 20\%$) as given by Johnson *et al.* (1955) and Falconer and Mackay (1996). GCV and PCV values were estimated according to the formula given by Burton (1952) and Chaudhury and Singh (1985). GCV and PCV values were categorized as low (<10%), moderate (10-20%) and high (>20%) (Sivasubramanian and Madhavamenon, 1973). Genetic diversity as D^2 statistics were estimated by the techniques proposed by Mahalanobis (1936). Clustering was done by Tocher method (Rao, 1952). The genotypes were arranged in order to their relative distances from each other. Average intra and inter-cluster distances were calculated by the formula suggested by Rao (1952).

Results and Discussion

The analysis of variance showed (Table 2) significant differences among the genotypes for all the traits studied. This indicated that the genotypes possess inherent genetic variances among themselves with respect to the characters studied. Similar results were reported by (Bekele *et al.*, 2013). Rameeh (2013) also observed significant variation among different *Brassica* genotypes for morphological traits like plant height, days to flowering, days to maturity, number of pod/plant, pod length etc.

Estimation of genetic parameters for different morphological characters

Different genetic parameters *viz.*, genotypic variances, phenotypic variances, heritability, genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), genetic advance and genetic advance as percentage of mean, GA (%) of 18 *Brassica* genotypes for all the yield contributing traits were presented in (Table 3).

Table 2. Analysis of variance for different morphological characters of the *Brassica* genotypes

Source of variation	df	Mean square								
		Days to first flowering	Days to maturity	Plant height (cm)	No. of branches / plant	No. of pod/ plant	Pod length (cm)	No. of seeds/pod	1000-seed wt. (g)	Yield/ plant (g)
Replication	2	20.327	6.161	99.22	0.117	11.84	0.037	0.448	0.009	0.016
Genotypes	17	38.611**	205.567**	1401.04**	4.161**	2573.75**	1.715**	19.895**	0.337**	2.399**
Error	34	3.542	35.438	210.43	0.297	63.41	0.120	0.369	0.013	0.011

** = Significant at 1% level of probability

Table 3. Estimation of genetic parameter for morphological characters related to yield in *Brassica*

Sl no.	Characters	Phenotypic variance (δ^2p)	Genotypic variance (δ^2g)	PCV (%)	GCV (%)	Heritability (%)	GA	GA (% of mean)
1	Days to first flowering	15.23	11.69	13.75	12.04	76.75	6.17	21.73
2	Days to maturity	92.15	56.71	10.14	7.96	61.54	12.17	12.86
3	Plant height (cm)	607.30	396.87	22.42	18.12	65.35	33.18	30.18
4	No. of branches/ plant	1.59	1.29	24.50	22.09	81.26	2.11	41.02
5	No. of pod/plant	900.19	836.78	24.72	23.83	92.96	57.45	47.33
6	Pod length (cm)	0.652	0.532	15.85	14.32	81.59	1.36	26.64
7	No. of seeds/pod	6.88	6.51	19.81	19.27	94.63	5.11	38.62
8	1000-seed wt. (g)	0.121	0.108	11.48	10.85	89.26	0.64	21.11
9	Yield/plant (g)	0.807	0.796	31.60	31.39	98.64	1.83	64.22

Table 4. Clustering groups of *Brassica* genotypes

Cluster number	Number of genotypes	Percent	Name of genotypes
I	8	44.44	BARI Sarisha-8, BARI Sarisha-16, BD-7104, BARI Sarisha-10, BARI Sarisha-11, BD-6950, JUN-536 and BD-6952
II	7	38.89	Tori-7, SAU-01, BD-10111, Nap-0567, Nap-0.564, BD-7115 and BD-6957
III	2	11.11	BD-10115 and BDJH-12
IV	1	5.56	BD-7114

Genetic variability

The genotypes showed a wide range of variation which provides ample scope for selection of superior and desired genotypes by the plant breeder for further improvement. This suggested that there were inherent genetic differences among the genotypes. Significant genetic variation in various component traits exhibited by the genotypes indicated these traits might be effective for further breeding program. Phenotypic variance was higher than the genotypic variances for all the traits, thus indicated the influences of environmental factor on these traits. Phenotypic coefficient of variation (PCV) were higher than the genotypic coefficient of variation (GCV) for all the traits (Table 3) indicating that they all interacted with the environment to some extent. Similar

findings were earlier reported by Mekonnen *et al.* (2014) and Mahak *et al.* (2004). The high values of genotypic coefficient of variation (GCV) for these traits suggested the possibility of yield improvement through selection of these traits. So that these traits should be consider during parent selection for breeding program in *brassica*.

Heritability

The estimates of heritability act as predictive tool in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular trait.

Table 5. Intra and inter cluster distances among the *Brassica* genotypes

Cluster	I	II	III	IV
I	129.43 (11.38)	241.15 (15.53)	218.35 (14.78)	1407.94 (37.52)
II		260.85 (16.15)	319.21 (17.87)	1069.77 (32.71)
III			80.60 (8.98)	1241.14 (35.23)
IV				0.00

The bold figures are intra cluster distances

All the studied traits in the present investigation expressed high heritability estimates ranging from 61.54% to 98.64% (Table 3). High heritability values indicate that the traits under study are less influenced by environment in their expression and have greater possibility of genetic improvement through selection. Similar findings were earlier reported by Sikarwar *et al.* (2017). Hussain *et al.* (2016) and Mekonnen *et al.* (2014) also observed high heritability for days to 50% flowering, days to 80% maturity, number of primary branches/ plant, number of seeds/pod, pod length, number pod/plant, 1000- seed weight and yield/plant.

Genetic advance

The genetic advance is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population. Heritability in conjunction with genetic advance would give a more reliable index of selection value (Johnson *et al.* 1955). In the present study, high heritability along with high genetic advance in percentage of mean was noticed for the traits plant height, number of branches/plant, number of siliqua /plant, number of seeds/plant and yield/plant. Alam (2010) observed that high genetic advance and high genetic advance in percentage of mean were obtained for plant height, number of primary branches/ plant, number of secondary branches/plant, number of pod/ plant. Mahmud *et al.* (2008) found high genetic advance in percentage of mean for days to 50% flowering, number of secondary branches/plant, seed/ pod, and pod length. In general, the traits that showed high heritability with high genetic advance are controlled by additive gene action and can be improved through simple or progeny selection methods. Selection for the traits having high heritability coupled with high genetic advance is likely to accumulate more additive genes leading to further improvement of their performance.

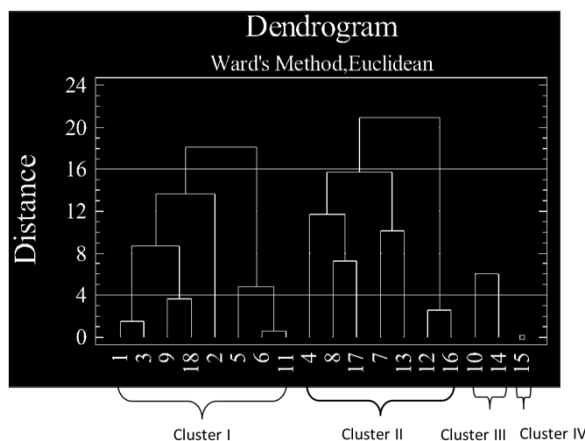


Fig. 1 Dendrogram based on summarized data on differentiation among the *Brassica* genotypes according to Ward's method

Divergence study among the *Brassica* genotypes

Depending on the range of diversity, eighteen *Brassica* genotypes were grouped into four clusters (Table 4, Figure 1). The inter-cluster distances in all the cases were greater than the intra-cluster distances suggesting wider

diversity among the genotypes of the distant groups (Table 5). The range of intra-cluster values indicated generally heterogeneous nature of the genotypes within the clusters. The intra-cluster degree of diversity was maximum in cluster I (44.44) and minimum in cluster IV (5.56), indicating that the genotypes in cluster I might be heterogeneous compared to those in cluster IV. Sandhu et al. (2017) revealed that 38 genotypes of *Brassica napus* L. including four checks were grouped into 3 clusters using Ward's method. Cluster I contained three genotypes, cluster II contained three genotypes, cluster III contained 16 genotypes. Khan et al. (2013) also reported that 32 genotypes of *Brassica rapa* L. were grouped into 6 clusters on the basis of D² analysis.

Table 6. Cluster mean for nine yield and yield attributing characters of 18 genotypes of *Brassica*

Characters	Cluster I	Cluster II	Cluster III	Cluster IV
Days to first flowering	29.53	26.07	34.87	22.60
Days to maturity	99.57	88.72	104.50	76.93
Plant height (cm)	118.98	96.00	142.00	70.60
No. of branches/ plant	4.24	5.80	6.31	5.40
No. of pod/plant	110.32	118.52	164.59	143.53
Pod length (cm)	4.74	5.68	4.28	5.47
No. of seeds/pod	12.12	14.50	10.47	18.93
1000-seed wt. (g)	3.00	2.97	3.06	3.62
Yield/plant (g)	2.51	2.82	2.94	5.51

Table 7. Contribution of individual characters towards the divergence

SL no.	Characters	% Distribution of toward divergence
1	Days to first flowering	13.07
2	Days to maturity	3.27
3	Plant height (cm)	2.61
4	No. of branches/ plant	4.58
5	No. of pod/plant	7.19
6	Pod length (cm)	4.58
7	No. of seeds/pod	16.34
8	1000-seed wt. (g)	16.34
9	Yield/plant (g)	32.03

Mean performances of different clusters for the characters studied reflected that all the high yielding genotypes were grouped into cluster IV followed by Cluster II, cluster III

and Cluster I having long duration and lower yield indicating maximum contribution towards divergence between Cluster I and cluster IV (Table 6). A wide range of variation for several characters among the multi genotypic cluster was observed. However, the difference was clear for days to maturity, plant height (cm), number of branches/plant, number of pods/plant, pod length, number of seeds/pod, 1000-seed weight (g) and yield/plant (g), which has contributed largely to the divergence (Table 7). Hence, for the improvement of different characters like days to maturity, number of branches/plant, number of siliqua/plant, number of seeds/plant and yield/plant, genotypes from cluster IV and Cluster II could be used as the promising materials.

Conclusion

The present study revealed the genetic divergence, variability ranges, heritability, genetic advance and contribution of each trait towards divergence in eighteen genotypes of *Brassica*. From the analysis of variance (ANOVA), significant variations were observed for all the characters among the genotypes. Significant variation among genotypes indicated existence of wide genetic diversity that would provide better scope of selection. The PCV was higher than the GCV for all the characters studied, which indicated that there was environmental influence on the expression of the characters. High Heritability with high genetic advance in percentage of mean was observed for number of branches/plant, number of siliqua /plant, number of seeds/pod and yield/plant. Future breeding program focused on these traits could be a milestone for the improvement of *Brassica*. Eighteen (18) genotypes were grouped into four clusters. This clustering suggested that early maturity with high yielding genotypes included into cluster IV followed by cluster II and cluster III. Therefore, the present study revealed that the adequate genetic diversity was present among 18 *Brassica* genotypes which would be a source of useful breeding materials for future breeding program in *Brassica*.

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