

AGRONOMSKI GLASNIK 2/2019.
ISSN 0002-1954

Original scientific paper
Izvorni znanstveni članak

GENETIC VARIABILITY STUDIES FOR SELECTION OF ELITE GERMPLASM IN SESAME (*Sesamum indicum* L.)

ISTRAŽIVANJE GENETSKE VARIJABILNOSTI ZA SELEKCIJU
ELITNE GERMPLAZME U SEZAMU (*Sesamum indicum* L.)

Sabrin Sultana, Md Harun-Ur-Rashid, Firoz Mahmud, Md Abdur Rahim

ABSTRACT

Sesame (*Sesamum indicum* L.) is one of the oldest oilseed crops and important for high nutritional quality as well as medicinal value. Fifty diverse sesame genotypes were evaluated to study genetic variability. The results revealed that the genotypes were a significant variation in most of the studied characters. In all cases, the phenotypic variances were much higher than genotypic variances suggests a higher level of the environmental effect on the expression of these characters. The highest genotypic coefficient of variations (GCV) was observed in seed yield per plant while the highest heritability was exhibited by hundred seed weight followed by days to 80% maturity, pods per plant, number of branches per plant and seed yield per plant. The genotypic correlation with seed yield per plant showed a significantly strong positive with days to 50% flowering, plant height and number of pods per plant at both the genotypic and phenotypic level. The path coefficient analysis showed that pods per plant and seeds per pod were the most important contributing traits to seed yield. The 50 sesame genotypes were grouped into five clusters. The highest inter-cluster distance was observed between the cluster III and V while the lowest inter-cluster distance was observed between the cluster III and IV. Among 50 sesame genotypes G7, G36, G38 and G46 might be suggested for future hybridization program for the improvement of sesame yield.

Keywords: genetic variability, heritability, genetic diversity, yield, sesame, (*Sesamum indicum* L.)

SAŽETAK

Sezam (*Sesamum indicum* L.) je jedan od najstarijih usjeva uljarica i važan zbog visoke hranidbene kakvoće kao i medicinske vrijednosti. Procijenjeno je pedeset različitih genotipova sezama po genetskoj varijabilnosti. Rezultati su pokazali da su genotipovi značajna varijacija u većini proučavanih karakteristika. U svim slučajevima fenotipske varijance bile su mnogo više

nego genotipske varijance što upućuje na višu razinu djelovanja okoline na izražavanje tih karakteristika. Najviši genotipski koeficijent varijacija primijećen je za prinos sjemena po biljki dok je najviša heretabilnost u težini sto sjemenki zatim po danima do 80% zrelosti, mahuna po biljci, broju grančica po biljci i sjemena po biljci. Genotipska korelacija s prinosom sjemena po biljci bila je značajno vrlo pozitivna s danima do 50% cvjetanja, visinom biljke i brojem mahuna po biljci na genotipskoj i fenotipskoj razini. Prema analizi koeficijentata broj mahuna po biljci i prinos sjemena po mahuni bili su najvažniji doprinosi prinosu sjemena. Pedeset genotipova sezama svrstano je u pet klastera. Najveća udaljenost među klasterima primijećena je između klastera III i IV. Među 50 sezama genotipovi G7, G36, G38 i G46 mogu se predložiti za budući program hibridizacije za poboljšanje prinosa sezama.

Ključne riječi: genetska varijabilnost, heretabilnost, genetska raznolikost, prinos, sezam, (*Sesamum indicum* L.)

INTRODUCTION

Sesame (*Sesamum indicum* L.), a flowering plant of the genus *Sesamum* which is one of the ancient oilseed crops dating back to 3050-3500 B.C. (Tripathi et al. 2013). It ranked sixth in the world in respect of edible oil seed production (3,312,986 million tons) and twelve for vegetable oil (907,440 million tons) production (FAO, 2005). The climatic and edaphic conditions of Bangladesh are quite suitable for sesame cultivation. Traditionally, this crop is cultivated either as a pure stand or a mixed crop with *Aus* rice, jute, groundnut, millets and sugarcane. Sesame grows in both cropping seasons (summer and winter) and covers around two thirds of the total oil cropped area in Bangladesh (Sarker et al. 2007).

In 2012, in Bangladesh, 37000 ha of land were under sesame cultivation and the production was 34000 tons (FAOSTAT 2015). Sesame seeds containing 50% oil and 25% protein are used in baking, candy making, and some other food industries. Besides, it contains about 47% oleic and 39% linoleic acid. Oil from the sesame seeds is mainly used in cooking, salad and margarine. Moreover, it also provides important ingredients for pharmaceutical and cosmetic industries, and synergist for insecticides (Salunkhe and Desai 1986). Sesame oil is rich in antioxidant and fatty acids (oleic acid, 43%; linoleic acid, 35%; palmitic acid, 11%; stearic acid 7% (Tripathi et al. 2013). This oil has a long shelf life due to the presence of *sesamol* (an antioxidant). In addition, sesame oil has various health benefits such as helps to prevent diabetes, reduce

blood pressure and maintain lower blood cholesterol. It is also good for digestion, heart health, healthy skin, prevents cancer, helps in lessening anxiety, alleviates anemia, protects from radiation damage to DNA, good for respiratory health, good for oral health, good for bone health (www.care2.com/greenliving/20-health-benefits-of-sesame).

The yield of sesame is still lower compared to other oilseed crops in Bangladesh. Besides, it is treated as a less input intensive crop, therefore, genetic improvement via breeding has been considered as a promising approach (Ashri 1988). A potential higher yield has been achieved in Nigeria (Menzir 2012). Selection is an important part of any crop breeding program through which genotypes with higher yield are selected (Blessing et al. 2012). Nonetheless, the improvement of a complex trait like the yield is difficult due to its polygenic inheritance (Menzir 2012). Therefore, another suitable option for the yield improvement is indirect selection. Thus, the phenotypic and genotypic variability studies play an important role in the improvement of sesame crop. Besides, knowledge of the naturally occurring diversity in a population helps to identify diverse groups of genotypes that can be useful for the breeding program. Little is known about the genetic diversity and phenotypic variability of land race collections of sesame in Bangladesh. Therefore, the proposed research highlight on genetic variability, heritability and genetic advance and genetic diversity among different sesame germplasm.

MATERIAL AND METHODS

A total of 50 sesame genotypes was used in this experiment (Table 1). The seeds were collected from the Plant Genetic Resource Centre (PGRC) section of the Bangladesh Agriculture Research Institute (BARI), Jaydebpur, Gazipur, Bangladesh. This experimental work was conducted in the experimental field of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh. The 'Randomized Complete Block Design' (RCBD) with 3 replications was followed. The unit plot was 6 m with 6 rows and lines to line and plant to plant distances were 40 cm and 10 cm, respectively. The recommended rate of fertilized was applied for the healthy plant growth. The standard cultural practiced were done during the entire experiment. The harvest was done separately for each genotype when 80% of plants was mature. The data were recorded on fifteen selected plants for ten different traits including days to first flowering, days to 50% flowering, days to 80% maturity, plant height (cm), number of branches per plant, number of pods per plant, pod length (cm), number of seeds per pods, 1000-seed weight (g) and

seed yield per plant (g). The collected data were further subjected to statistical analysis. The phenotypic and genotypic variances were determined as per Johnson et al. (1955). Heritability and genetic advance were estimated according to Singh and Chaudhury (1985). Genotypic and phenotypic co-efficient of variation were calculated as per Burton (1952). The correlation coefficient was obtained using the formula suggested by Miller et al. (1958). Path coefficient analysis was done following the method outlined by Dewey and Lu (1995). Further, multivariate analysis, including principal component analysis (PCA), principal coordinate analysis (PCO), canonical variate analysis (CVA) and cluster analysis was performed by using a GENESTAT program (Digby et al. 1989).

Table 1 List of sesame genotypes used in this study.

Tablica 1. Popis genotipova sezama korištenih u ovom radu

Sl. no.	Accession	Sl. no.	Accession
G-1	BD-6960	G-26	BD-7000
G-2	BD-6961	G-27	BD-7001
G-3	BD-6970	G-28	BD-7003
G-4	BD-6972	G-29	BD-7004
G-5	BD-6974	G-30	BD-7005
G-6	BD-6978	G-31	BD-7006
G-7	BD-6979	G-32	BD-7007
G-8	BD-6980	G-33	BD-7008
G-9	BD-6981	G-34	BD-7009
G-10	BD-6982	G-35	BD-7011
G-11	BD-6983	G-36	BD-7012
G-12	BD-6984	G-37	BD-7013
G-13	BD-6985	G-38	BD-7014
G-14	BD-6986	G-39	BD-7015
G-15	BD-6988	G-40	BD-7016
G-16	BD-6989	G-41	BD-7017
G-17	BD-6990	G-42	BD-7018
G-18	BD-6991	G-43	BD-7019
G-19	BD-6992	G-44	BD-7020
G-20	BD-6993	G-45	BD-7021
G-21	BD-6994	G-46	BD-7022
G-22	BD-6995	G-47	BD-7023
G-23	BD-6996	G-48	BD-7024
G-24	BD-6997	G-49	BD-7026
G-25	BD-6999	G-50	BD-7029

RESULTS

Genetic variability among sesame genotypes

The analysis of variance (ANOVA) showed highly significant variations for all the studied traits among 50 sesame genotypes (Table 2 and 3). This considerable variability provides a great opportunity for improving traits for the genetic improvement of the sesame. The phenotypic variance (σ^2_p) and phenotypic coefficient of variation (PCV) was always higher than the genotypic variance (σ^2_g) and genotypic coefficient of variation (GCV) for all the traits reveals the predominance of environment for the expression of these traits. The higher σ^2_p , σ^2_g , PCV and GCV were observed for seed yield per plant, pods per plant, plant height and seeds per pod. The results suggest that the higher degree of genetic variability for these traits. A high heritability was found in 100-seed weight, days to 80% maturity, pods per plant, seed yield per plant, number of branches per plant and plant height. The high genetic advance was found in pods per plant and seed yield per plant while the number of branches per plant, number of pods per plant and seed yield per plant high showed high genetic advance in percentage of mean.

Table 2 Range, mean and CV (%) of 50 sesame genotypes.

Tablica 2. Raspon, sredina i CV (%) 50 genotipova sezama

Traits	Range		Mean	CV (%)
	Min	Max		
Days to first flowering	27.00	31.00	29.05	3.45
Days to 50% flowering	43.00	47.00	45.13	2.41
Days to 80% maturity	75.33	83.33	78.65	1.41
Plant height (cm)	88.07	136.02	104.16	6.80
Branch per plant	2.29	6.31	3.73	15.06
Pods per plant	42.56	142.15	71.31	19.33
Seeds per pod	59.92	75.82	68.10	5.57
Pod length (cm)	2.30	2.81	2.58	4.48
100 seed weight (g)	2.50	3.22	2.89	2.89
Seed yield per plant (g)	69.60	300.78	143.45	24.81

CV (%) = coefficient of variation.

Table 3 Estimation of genetic parameters for ten traits in 50 sesame genotypes.

Tablica 3. Procjena genetskih parametara za deset značajki u 50 genotipova sezama

Traits	Mean sum square	σ^2_p	σ^2_g	PCV	GCV	Heritability (%)	Genetic advance (5%)	Genetic advance (% mean)
DFE	3.202**	1.74	0.73	4.54	2.95	42.15	1.14	3.94
D50%F	2.776**	1.71	0.53	2.90	1.61	30.99	0.84	1.85
PH	10.625**	4.36	3.13	2.65	2.25	71.85	3.09	3.93
BPP	277.289**	125.84	75.73	10.77	8.35	60.18	13.91	13.35
PPP	2.053**	0.89	0.58	25.38	20.42	64.78	1.26	33.86
SPP	1357.935**	579.28	389.33	33.75	27.67	67.21	33.32	46.73
PL	33.833**	20.87	6.48	6.71	3.74	31.04	2.92	4.29
DM	0.036**	0.02	0.01	5.62	3.37	36.07	0.11	4.18
HSW	0.129**	0.05	0.04	7.59	7.01	85.29	0.38	13.33
SYP	8042.156**	3525.34	2258.42	41.39	33.13	64.06	78.36	54.62

** significant at 1% level of probability.

σ^2_p = Phenotypic variance, σ^2_g = Genotypic variance, PCV = Phenotypic coefficient of variation and GCV = Genotypic co-efficient of variation. DFE = days to first flowering, D50%F = days to 50% flowering, DM = days to 80% maturity, PH = plant height (cm), BPP = branch per plant, PPP = pods per plant, SPP = seeds per pod, PL = pod length (cm), HSW = 100-seed weight (g) and SYP = seed yield per plant.

Correlation coefficient analysis

Yield is a polygenic complex trait and influenced by various environmental factors. Therefore, phenotypic selection for genetic improvement based on only yield is not so effective. In such cases, association studies among yield contributing traits are very much helpful for plant breeding programs. It is possible to improve some other characters along with yield via correlation coefficient. The results of the correlation analysis are presented in Table 4, Table 5 and Fig. 1. Seed yield had a highly significant positive correlation with days to 50% flowering, plant height, number of pods per plant at both genotypic and phenotypic level while with seeds per pod, pod length and 100-seed weight only at genotypic level.

Table 4 Genotypic correlation coefficients among different pairs of yield and yield contributing traits for different genotype of sesame.

Tablica 4. Koeficijenti genotipske korelacije među raznim parovima prinosa i značajki koje doprinose prinosu za različite genotipove sezama

3	DFF	D50%F	PH	BPP	PPP	SPP	PL	DM	HSW	SYP
DFF	1									
D50%F	-0.156	1								
PH	-0.881**	0.712**	1							
BPP	0.805**	-0.908**	-0.128	1						
PPP	-0.717**	0.705**	0.510**	-0.825**	1					
SPP	0.130	-0.868**	0.986**	0.039	0.881**	1				
PL	0.530**	-0.773**	0.956**	-0.832**	-0.857**	0.893**	1			
DM	0.706**	0.373**	-0.873**	0.943**	-0.087	-0.868**	0.991**	1		
HSW	0.899**	-0.739**	-0.716**	0.826**	0.350**	-0.705**	-0.715**	0.802**	1	
SYP	-0.852**	0.736**	0.932**	-0.725**	0.891**	0.997**	0.391**	-0.765**	0.481**	1

*, ** = Significant at 5% and 1% level of significance, respectively.

DFF = days to first flowering, D50%F = days to 50% flowering, DM = days to 80% maturity, PH = plant height (cm), BPP = branch per plant, PPP = pods per plant, SPP = seeds per pod, PL = pod length (cm), HSW = 100-seed weight (g) and SYP = seed yield per plant (g).

Table 5 Phenotypic correlation coefficients among different pairs of yield and yield contributing traits for different genotype of sesame.

Tablica 5. Koeficijenti fenotipske korelacije među raznim parovima doprinosa za različite genotipove sezama

	DFF	D50%F	PH	BPP	PPP	SPP	PL	DM	HSW	SYP
DFF	1									
D50%F	-0.600**	1								
PH	-0.363**	-0.193*	1							
BPP	0.423**	-0.051	-0.641**	1						
PPP	-0.319**	0.436**	-0.106	-0.206*	1					
SPP	-0.210**	-0.077	0.609**	-0.111	-0.594**	1				
PL	-0.140	-0.207*	0.261**	0.230**	-0.338**	0.425**	1			
DM	0.577**	-0.103	-0.261**	0.161*	-0.171*	-0.156	-0.634**	1		
HSW	0.253**	0.197*	-0.406**	0.257**	-0.140	-0.171*	-0.344**	0.394**	1	
SYP	-0.238**	0.269**	0.253**	-0.420**	0.629**	-0.124	-0.214**	-0.035	-0.583**	1

*, ** = Significant at 5% and 1% level of significance, respectively.

DFF = days to first flowering, D50%F = days to 50% flowering, DM = days to 80% maturity, PH = plant height (cm), BPP = branch per plant, PPP = pods per plant, SPP = seeds per pod, PL = pod length (cm), HSW = 100-seed weight (g) and SYP = seed yield per plant.

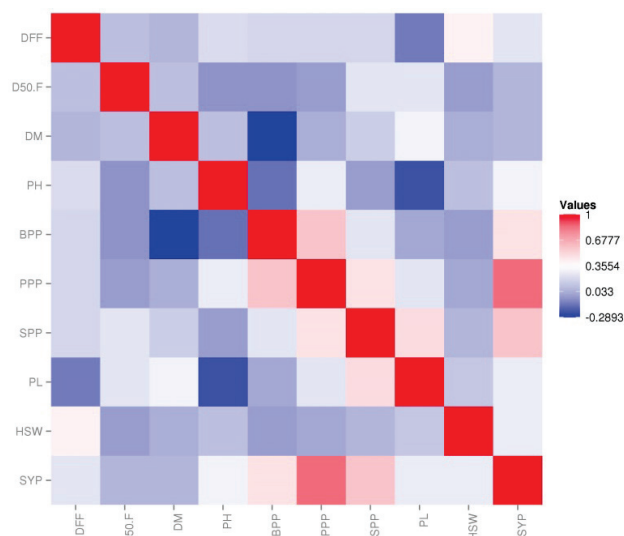


Fig. 1 Correlation matrix represents correlation between different characters of 50 Sesame genotypes.

Slika 1. Matrica kerelacije predstavlja korelaciju između različitih karakteristika 50 genotipova sezama

DFE = days to first flowering, D50%F = days to 50% flowering, DM = days to 80% maturity, PH = plant height, BPP = branch per plant, PPP = pods per plant, SPP = seeds per pod, PL = pod length, HSW = 100-seed weight, SYP = seed yield per plant.

Path coefficient analysis

By using path co-efficient analysis, various direct and indirect effects of yield on various yield contributing characters can be measured. Estimation of direct and indirect effect of path coefficient analysis is presented in Table 6. The results revealed that number of pods per plant had a high direct effect followed by the number of seeds per pod on seed yield per plant. Number of pods per plant showed a positive indirect effect via days 50% flowering, number of branches per plant, number of seeds per pod and pod length and finally contributed to the positive correlation with seed yield. Likewise, the number of seeds per pod had a positive indirect effect via days 50% flowering number of pods per plant and 100-seed weight, and it also made positive correlation with seed yield. The residual effect was 0.124 which revealed that the influence of component trait was 87.6%. The remaining 12.4% was the influence of other factors.

Table 6 Partitioning of genotypic correlations into direct (bold) and indirect effects of ten important traits by path analysis of sesame.

Tablica 6. Dijeljenje genotipskih korelacija u direktno i indirektno djelovanje deset važnih značajki analizom sezama

	Effect via									r _g
	DFE	D50%F	PH	BPP	PPP	SPP	PL	DM	HSW	
DFE	-0.451	0.174	1.607	-0.449	-3.175	0.129	-0.011	0.810	-0.090	-0.852**
D50%F	0.070	-1.115	-0.969	0.405	6.040	-2.245	0.050	0.180	0.020	0.736**
PH	0.533	-0.794	-1.361	0.017	1.230	2.501	-0.054	-1.220	0.090	0.932**
BPP	-1.536	3.421	0.174	-0.132	-5.847	0.039	0.028	2.730	-0.110	-0.725**
PPP	0.594	-2.793	-0.694	0.320	2.411	1.466	0.039	-0.040	-0.010	0.891**
SPP	-0.059	2.529	-3.438	-0.005	3.571	0.990	-0.111	-1.650	0.170	0.997**
PL	-0.239	2.646	-3.490	0.173	-4.477	5.240	-0.021	0.470	0.090	0.391**
DM	-0.770	-0.420	3.500	-0.760	-0.210	-3.430	-0.020	0.480	-0.130	-0.765**
HSW	-1.220	0.820	3.700	-0.440	0.840	-5.250	0.060	2.000	-0.030	0.481**

Residual effect: 0.124

** significant at 1% level of probability.

σ^2_p = Phenotypic variance, σ^2_g = Genotypic variance, PCV = Phenotypic coefficient of variation and GCV = Genotypic co-efficient of variation. DFE = days to first flowering, D50%F = days to 50% flowering, DM = days to 80% maturity, PH = plant height (cm), BPP = branch per plant, PPP = pods per plant, SPP = seeds per pod, PL = pod length (cm), HSW = 100-seed weight (g), SYP = seed yield per plant and r_g = genotypic correlation with yield.

Genetic diversity analysis

The ANOVA revealed that there were significant differences among the studied traits indicted presence of the considerable genetic variability among 50 sesame genotypes. The computed Eigen values for the 10 variables subjected to principal component analysis together with the subsequent proportion and corresponding explained variance are given in Table 7. First three Eigen values of three principal coordination axes of genotypes accounted for 60.95% variation. According to the principal axes I and II, a two dimensional chart (Z1 – Z2) of the genotypes using component score 1 and 2, in X axis and Y axis. The scatter diagram showed that there were five visible clusters. The genotypes were distantly located from each other (Fig. 2). The genotypes of cluster III were more diverse than those of cluster V (Fig. 3). Fifty sesame genotypes were grouped into 5 clusters through non-hierarchical clustering the (Table 8). The maximum number of genotypes was grouped in cluster II (14), followed by cluster III (13) respectively. Ten genotypes were grouped into each cluster I and cluster IV while

cluster V contains only 3 genotypes (Table 8). The genotypes from cluster V earned the highest cluster mean value for plant height (111.8), branch per plant (4.83), days to first flowering (29.89), pods per plant (124.4), seeds per pod (74.18), pod length (2.68), hundred seed weight (3.01), seed yield per plant (276.9) (Fig. 4). This indicates that genotype of this cluster could be used as parent in the future hybridization program for higher yield. On the other hand, cluster I exhibited the highest mean value for days to 50% flowering. The cluster II produces highest days to 80% maturity. This means that for developing late maturing variety we have to select the genotypes of cluster II. In cluster III, the lowest mean for plant height (95.95), days to first flowering (28.59), pods per plant (51.63), seeds per pod (65.83), pod length (2.54), days to 80% maturity (78.31), hundred seed weight (2.84), seed yield per plant (91.73) were found. It indicates the genotype of this cluster could be used for future hybridization program for developing dwarf plant for improving early maturing plant. In cluster IV had the lowest means for branch/ plant (3.37) and days to 50% flowering. Canonical Variate Analysis (CVA) was done to compute the inter-cluster distances. The intra and inter-cluster distance (D^2) values were shown in Table 9 and the nearest and farthest cluster from each cluster based on D^2 value is given in Table 10. In this experiment, the inter-cluster distances were higher than the intra-cluster distances thus indicating broader genetic diversity among the genotypes of different groups. The intra cluster D^2 values were given in Table 10. The intra cluster distance was observed in the clusters. The intra cluster distance was higher in cluster I (2.40) and lowest in cluster IV (0.73) (Table 10). The intra cluster distances in all the five clusters were lower than the inter cluster distances and which indicated that genotypes within the same cluster were closely related. The inter cluster distances were larger than the intra cluster distances which indicated wider genetic diversity among the genotypes of different groups. The latent vectors (Z_1 and Z_2) collected from principal component analysis (PCA) (Table 11). The significant characters which responsible for genetic divergence in the axis of differentiation in vector I (Z_1) were days to 50% flowering (0.0417) and hundred seed weight (0.6124). In vector II (Z_2), first flowering (0.4553), plant height (0.1128), number of branch per plant (0.3436), seeds per pod (0.0939), pod length (6.4232) (Table 11).

Table 7 Eigen values and yield percent contribution of ten traits of 50 genotype.

Tablica 7. Vrijednosti i postotak prinosa deset značajki 50 genotipova

Principal component axes	Eigen values	Percent variation	Cumulative % of variation
I	2.966	29.66	29.66
II	1.663	16.63	46.29
III	1.466	14.66	60.95
IV	1.128	11.28	72.23
V	0.921	9.21	81.44
VI	0.668	6.68	88.12
VII	0.509	5.09	93.21
VIII	0.368	3.68	96.89
IX	0.234	2.34	99.23
X	0.077	0.77	100

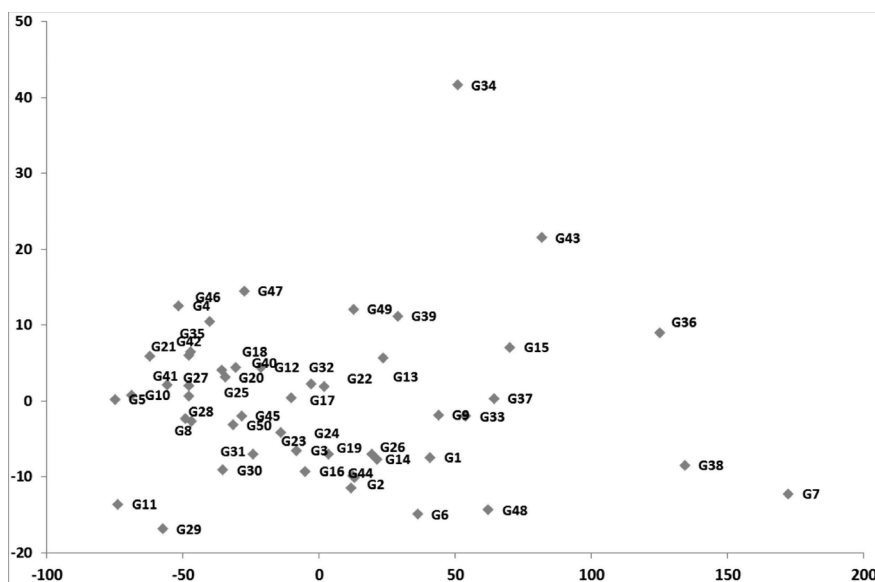


Fig. 2 Scatter diagram of sesame genotypes based on their principal component scores.

Slika 2. Dijagram genotipova sezama na osnovi rezultata glavnih komponenata

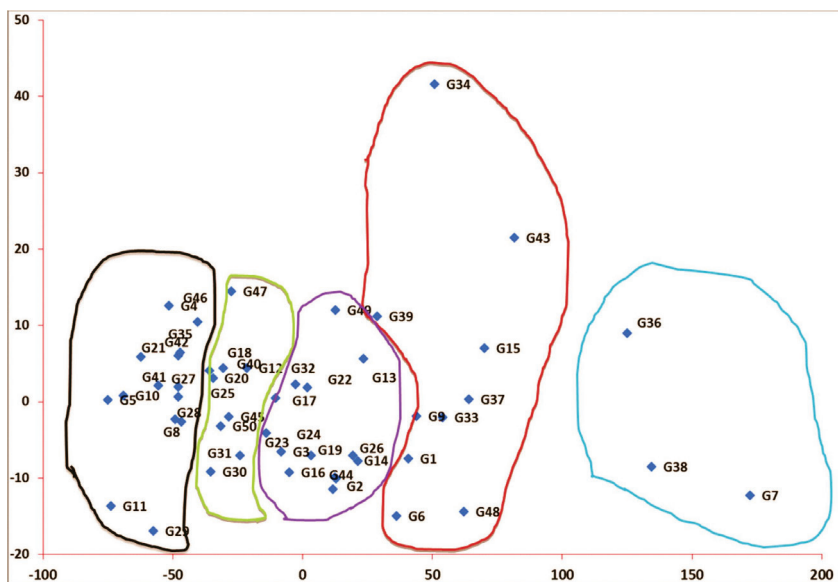


Fig. 3 Cluster diagram showing average intra and inter cluster distances of 50 sesame genotypes.

Slika 3. Klaster dijagram koji prikazuje prosječne udaljenosti unutar i unutar klastera od 50 sezamovih genotipova

Table 8 Distribution of fifty sesame genotypes in different clusters.

Tablica 8. Raspodjela pedeset genotipova sezama u raznim klasterima

Cluster no.	Genotypes	No. of genotypes
I	G1, G6, G9, G15, G33, G34, G37, G39, G43, G48	10
II	G2, G3, G13, G14, G16, G17, G19, G22, G23, G24, G26, G32, G44, G49	14
III	G4, G5, G8, G10, G11, G21, G27, G28, G29, G35, G41, G42, G46	13
IV	G12, G18, G20, G25, G30, G31, G40, G45, G47, G50	10
V	G7, G36, G38	3
Total		50

Traits	I	II	III	IV	V
Days to first flowering	29.17	29.05	28.59	29.30	29.89
Days to 50% flowering	45.27	45.21	45.26	44.70	45.22
Days to 80% maturity	78.90	78.95	78.31	78.40	78.78
Plant height (cm)	107.50	102.90	96.95	109.70	111.80
Branch per plant	3.92	3.94	3.38	3.37	4.83
Pods per plant	85.64	76.75	51.63	59.01	124.40
Seeds per pod	69.16	69.11	65.83	66.76	74.18
Pod length (cm)	2.56	2.62	2.54	2.55	2.68
100 seed weight (g)	2.92	2.89	2.84	2.87	3.01
Seed yield per plant (g)	194.70	147.50	91.73	113.80	276.90

Fig. 4 Heat map representation of cluster mean for ten yield and yield related traits among 50 sesame genotypes. The red and blue color codes represent highest and lowest values.

Slika 4. Prikaz toplinske karte nakupine srednje vrijednosti za deset osobina prinosa i prinosa između 50 sezamovih genotipova. Kodovi crvene i plave boje predstavljaju najviše i najniže vrijednosti

Table 9 Intra (Bold) and inter cluster distances (D^2) for 50 genotypes.

Tablica 9. Udaljenosti unutar i između klastera (D^2) za 50 genotipova

Cluster	I	II	III	IV	V
I	2.40	4.212	9.409	7.145	8.093
II		1.34	5.564	3.404	11.877
III			0.87	3.068	17.361
IV				0.73	14.953
V					1.23

Table 10 The nearest and farthest clusters from each cluster between (D^2) values in sesame.

Tablica 10. Najbliži i najudaljeniji klasteri od svakog klastera između (D^2) vrijednosti u sezamu

Sl No.	Cluster	Nearest cluster (D^2 values)	Farthest cluster (D^2 values)
1	I	II (4.212)	III (9.409)
2	II	IV (3.404)	V (11.877)
3	III	IV (3.068)	V (17.361)
4	IV	III (3.068)	V (14.953)
5	V	I (8.093)	III (17.361)

Table 11 Relative contributions of the ten traits of 50 varieties to the total divergence.

Tablica 11. Relativni doprinos deset značajki 50 vrsta do potpune različitosti

Characters	Principal Component	
	Vector-1	Vector-2
Days to first flowering	-0.1561	0.4553
Days to 50% flowering	0.0417	-0.6079
Days to 80% maturity	-0.0731	-0.1109
Plant height (cm)	-0.0258	0.1128
Branch per plant	0.2077	0.3436
Pods per plant	-0.0459	-0.0123
Seeds per pod	-0.1214	0.0939
Pod length (cm)	1.2054	6.4232
100 seed weight (g)	0.6124	-0.7875
Seed yield per plant (g)	-0.0698	-0.0135

DISCUSSION

There were significant variations present in the studied traits among 50 sesame genotypes. The number of pods per plant seed yield and per plant showed high heritability with high genetic advance and high genetic advance in percentage of mean indicating these traits are under control of additive genetic effect. Therefore, genetic improvement of these traits might be effective via phenotypic selection. It has been reported that heritability estimates coupled with genetic advance were more valuable for selecting the elite genotype (Jonson et al. 1955). Kanak and Rajani (2017) reported the similar results for seed yield per plant in sesame. Gupta and Chopra (1984) reported high heritability with high genetic advance for branches per plant in sesame. Rahim et al. (2010) reported for high heritability with genetic advance for number of pods per plant and seed yield per plant in mungbean.

The significantly strong correlation at genotypic and phenotypic level indicates the high of association of these traits. Sumathi et al. (2007) reported that plant height and number of capsules per plant had significant positive correlations with seed yield per plant at both genotypic and phenotypic levels in sesame. Hakim (2008) mentioned that yield had a significant positive correlation with number of pods per plant in mungbean.

The result of correlation and path analyses showed that number of pods per plant as the important yield contributor and phenotypic selection might be effective for trait. Similar result was also reported by Rahim et al. (2010) in mungbean. Sumathi et al. (2007) reported highest direct positive correlation for number of capsules per plant on seed yield per plant in sesame.

In hybridization program during the selection of parents the characters contributing the most to the divergence are given greater importance. In this study, 50 sesame genotypes were grouped into five diverse clusters which suggest the presence of genetic variations among the studied genotypes. Swain and Dikshit (1997) grouped 40 genotypes of sesame into 14 different clusters. A wide range of genetic diversity was observed in 50 genotypes of *Sesamum indicum* which were grouped into V clusters. The highest inter-cluster distance was observed between the cluster III and V. The cluster V and cluster III showed maximum and minimum cluster means for most of the traits for 50 sesame genotypes indicates the genotypes of these clusters are more diverse (Fig. 5.) and hybridization between these two clusters might produce high level of heterosis and could be used as parents for future hybridization program to develop new improved sesame variety. The role of branch per plant and pod length in both the vectors are important components for genetic divergence in these materials. Roshan et al. (1998) and Rahim et al. (2010) reported similar results for number of pods per plant.

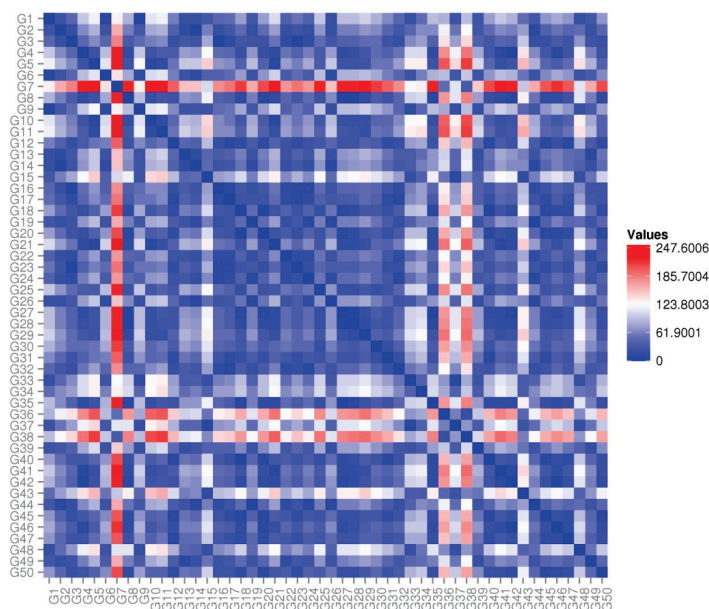


Fig. 5 Distance matrix denotes the pairwise comparisons between sesame genotypes in respect of 10 characters.

Slika 5. Matrica udaljenosti označava parne usporedbe sezamovih genotipova u odnosu na 10 znakova

CONCLUSION

Considering the extent of genetic distance, contribution of character towards divergence, extent of cluster means and agronomic performance the genotypes G7 for higher seed yield per plant, pods per plant, pod length and G48 for short duration and early maturity. These elite genotypes might produce high level of heterosis and could use future hybridization program for the improvement of sesame yield as well as early harvest.

ACKNOWLEDGEMENTS

We thank SAURES, Shere-Bangla Agricultural University, Dhaka-1207, Bangladesh for providing experimental field and other supports for successful completion of the research. We also thank Bangladesh Agricultural Research Institute (BARI) for providing sesame germplasm.

REFERENCES

1. Ashri A. (1998.): Sesame breeding. Plant breeding reviews. 16: 179-228.
2. Blessing CA, Michael IU, Benedict CO. (2012.): Genetic variability and interrelationship among some Nigerian pumpkin accessions (*Cucurbita spp.*). Int. J. Plant Breed. 6: 34-41.
3. Burton GW. (1952.): Quantitative inheritance in grass pea. Proc. of the 6th Int. Grassland Cong. Pennsylvania, USA. pp. 277-283.
4. Dewey DR, Lu K. (1959.): A correlation and path-coefficient analysis of components of crested wheatgrass seed production. Agron. J. 51: 515-518.
5. Digby P, Galway M, Lane P. (1989.): GENSTAT5. A second course. Oxford Science Publications, Oxford. pp. 103-108.
6. FAOSTAT. 2015. FAO Statistics Division. Accessed on 04 July (2015.): Rome, Italy. <http://faostat.fao.org>.
7. FAO (Food and Agriculture Organization). (2005.): FAO, Rome, Italy. <http://faostat.fao.org>.
8. Gupta BS, Chopra DP. (1984.): Genetic variability, correlation and path coefficient analysis in sesame. Indian J. Agril. Sci. 54: 1030-1033.
9. Hakim L. (2008.): Variability and correlation of agronomic characters of mungbean germplasm and their utilization for variety improvement program. Indonesian J. Agril. Sci. 9: 24-28.
10. Johnson HW, Robinson HF, Comstock R. (1955.): Estimates of genetic and environmental variability in soybeans. Agron. J. 47: 314-318.
11. Kanak S, Rajani B. (2017.): Genetic variability, correlation and path analysis studies for yield and yield component traits in sesame (*Sesamum indicum* L.). Int. J. Agril. Sci. 8: 3487-3489.
12. Menzir A. (2012.): Phenotypic variability, divergence analysis and heritability of characters in sesame (*Sesamum indicum* L.) genotypes. Nature and Science. 10: 117-126.
13. Miller PA, Williams JC, Robinson HF, Comstock RE. (1958.): Estimates of genotypic and environmental variances and covariances in upland cotton and their implications in selection. Agron. J. 50: 126-131.
14. Rahim MA, Mia AA, Mahmud F, Zeba N, Afrin KS. (2010.): Genetic Variability, Character Association and Genetic Divergence in Mungbean (*Vigna radiate* L. Wilczek). Plant Omics. 3: 1-6.

15. Roshan L, Charanjit S, Satija DR, Gupta VP, Lal R, Singh, C. (1998.): Morphological and biochemical genetic divergence in Mungbean (*Vigna radiata* L. Wilczek). Crop Improvement. 25: 172-176.
16. Salunkhe DK, Desai BB. (1986.): Postharvest biotechnology of oilseeds. CRC press. Boca Raton, Florida. pp. 105-117.
17. Sarkar MA, Salim M, Islam N, Rahman MM. (2007.): Effect of sowing date and time of harvesting on the yield and yield contributing characters of sesame (*Sesamum indicum* L.) seed. Int. J. Sust. Crop Prod. 2: 31-35.
18. Singh RK, Chaudhary BD. (1985.): Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi, India. p. 56.
19. Sumathi P, Muralidharan V, Manivannan N. (2007.): Trait association and path coefficient analysis for yield and yield attributing traits in sesame (*Sesamum indicum* L.). Madras Agric. J. 94: 174-178.
20. Swain D, Dikshit UN. (1997.): Genetic divergence in rabi sesame (*Sesamum indicum* L.). Indian J. Genet. Plant Breed. 57: 296-300.
21. Tripathi ANJAY, Bisen RAJANI, Ahirwal RP, Paroha SEEMA, Sahu ROSHNI, Ranganatha ARG. (2013.): Study on genetic divergence in sesame (*Sesamum indicum* L.) germplasm based on morphological and quality traits. Bioscan. 8: 1387-1391.

Author's address - Adresa autora:

Sabrin Sultana,
Md Harun-Ur-Rashid,
Firoz Mahmud,
Md Abdur Rahim, correspondence author: rahimgpb@sau.edu.bd
Department of Genetics and Plant Breeding,
Faculty of Agriculture, Sher-e-Bangla Agricultural University,
Dhaka-1207, Bangladesh

Received - Primiĵeno

21.02.2019.