Original Research Article

Genetic Variability, Heritability, Character Association and Morphological Diversity in Okra (*Abelmoschus esculentus* L. Moench)

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ABSTRACT

Genetic variability, heritability, genetic advance, correlation coefficient analysis, path coefficient analysis and genetic divergence between yield and its contributing traits were studied in 28 okra genotypes. The phenotypic coefficient of variations was found slightly higher than the genotypic coefficient of variations for all characters studied, indicating that the apparent variation is not only genetic but also influenced by the growing environment in the expression of the traits. High genotypic and phenotypic coefficient of variation was observed primary branches (43.91 and 33.64) and fruit yield per plant (37.51 and 32.48). High heritability coupled with high genetic advance in percent of mean in number of plant height (97.32 and 29.98), no. of fruit per plant (88.55 and 50.44), fruit yield per plant (74.99 and 57.94), seed per fruit (73.02 and 34.00) and primary branches (58.70 and 53.10) suggested that these characters would be considered for varietal selection. The correlation studies revealed that fruit yield per plant showed significant positive correlation with no. of average fruit weight, number of fruit per, plant height and significantly negative correlation with seed per fruit at genotypic and phenotypic level which can be considered for selection of a good variety. Path analysis revealed days to 50% flowering, plant height, number of fruit per plant, average fruit weight had direct positive effect on pod yield per plant, indicating these traits are the main contributors to fruit yield per plant. The divergence value for cluster analysis showed the highest inter-cluster distance between clusters I and V which indicates that these genotypes may provide high heterosis in hybridization and expected to show wide variability in genetic architecture. The selection of high yielding genotypes should give emphasis to the days to flowering (earliness), number of fruits per plant, fruit yield per plant and less seeds per fruit.

Keywords: Heritability, Genetic advance, Path analysis, Correlation, Okra

1. INTRODUCTION

Okra [*Abelmoschus esculentus* (L.) Monech] is a polyploid, belonging to the family Malvaceae with 2n = 2x =72 or 144 chromosome. It is the only vegetable crop in the Malvaceae family (Santos, 2012). It is self-pollinated crop; occurrence of out crossing to an extent of 4 to 19% with the maximum of 42.2% is noticed with the insect assisted pollination

(Kumar, 2006). This self-pollinating crop is an example that requires a separation between varieties to maintain purity (Tripathi *et al.*, 2011). It is an important vegetable crop grown in the tropical and sub-tropical parts of the world (Raju *et al.*, 2008) and commonly known as “lady finger” (Anwar *et al.*, 2011). It is cultivated since ages, and extensively disseminated from Africa to Asia, Southern Europe and America and currently grown in many countries. It is extensively cultivated for its tender immature fruits, which are largely used as fresh vegetable. The fruits have various medicinal properties too. It is useful in fever, chronic dysentery, and irritable states of genitero. It is good for people suffering from renal colic, leucorrhoea, spermatorrhoea, chronic dysentery and general weakness. Now-a-days large number of commercial cultivars including F1 hybrids of okra is available in the market but all these are not adapted and suited to all the regions of the country. Further, no specific recommendation about the suitability of genotypes for a particular area is available. Farmers face problems in selecting genotypes/cultivars for commercial cultivation in a particular area. Considering the above mentioned facts, there is a need to compare some of the available genotypes/cultivars to select high yielding, better adaptable genotypes/cultivars for commercial cultivation in Bangladesh. Knowledge of genetic diversity among okra germplasm will play significant role in breeding program as it helps to develop varieties with desired traits. It is a prerequisite to develop high yielding okra varieties like in all other crop improvement. This is important for selecting parents in combination breeding and to obtain transgressive segregants (Prakash *et al*., 2011). The knowledge of pattern of inheritance of various characters are important consideration while, determining the most approximate breeding procedures applicable to any particular crop. The phenotype is often not true indicator of its genotype. The phenotypic variability is the result of the effect of environment and genotype interaction. Path coefficient analysis is also very useful in formulating breeding strategy to develop elite genotypes through selection in advanced generations. In that perspective, attempts need to be made to determine the magnitude of heritable and non-heritable components and genetic parameters such as genotypic and phenotypic coefficient of variation, heritability and genetic advance as percentage of mean in some of the quantitative characters of okra. Since the pattern of inheritance of quantitative characters is highly complex, therefore the present investigation was undertaken to determine the genetic divergence, genetic variability, heritability, genetic advance, character association in different okra genotypes and their direct and indirect contribution to fruit yield in okra with the ultimate goal of identifying the most diverse and high yielding genotypes for fruit yield.

2. MATERIAL AND METHODS

2.1 Experimental Site

The experiment was conducted at the experimental field of Genetics and Plant Breeding Department of Sher-e-Bangla Agricultural University, Dhaka Bangladesh during March 2017 to July 2017. The experimental site was at 90022′ E longitude and 23041′N latitude at an altitude of 8.6 meters above the sea level. The experimental area was under the sub-tropical monsoon climate zone, which was characterized by heavy rainfall, high humidity, high temperature and relatively long day during the growing season. The soil was sandy loam in texture having pH 5.47-5.63. The mean temperature of the growing period was 26.43°C with average maximum and minimum being 36°C and 20.54°C, respectively.

2.2 Plant Materials

Twenty eight genotypes of okra were used in this study which was collected from Bangladesh Agricultural Research Institute (BARI), Gazipur and local market (Table 1).

2.3 Experimental Design

The experiment was conducted in randomized complete block design with three replications. In each block, each genotype was planted in one row of 8.4 m length and 1 m width, maintaining a plant to plant spacing of 0.6 m and accommodated 14 plants per plot.

2.4 Field Managements

All the fertilizers were applied as recommended dozes following appropriate application timing and method. The recommended dosage of Urea, TSP, MP was applied in field at the rate of 150, 100, 150 Kg/ha respectively. Irrigation was applied once a week at emergence and every two weeks at flowering and pod production. Chemical (Sevine, Marshal and deltanet) and cultural practices (hand picking and remove infected plant part) were applied to control insect pest (feel beetle, mealybug, aphid). Tender fruits were harvested two times per week to estimate fruit yield while mature fruits were harvested when fruits turned to loss green color and dry pods for seed yield parameter.

2.5 Data Collection and Analysis

Data for different plant parameters were recorded from 10 plants of each genotype. Mature fruit seed characteristics were measured from the two plants in each row. Genotypic and phenotypic variance was estimated by the formula used by Johnson et al. (1955). Heritability and genetic advance were measured using the formula given by Singh and Chaudhary (1985). Multivariate analysis viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA) were done by using GENSTAT 5.13 and Microsoft Excel 2007 software. Data of eleven characters were subjected to analysis of variance (ANOVA) using MSTATC software program to test the presence of significant differences among accessions for the traits measured. It was also measure of mean, range, CV, standard deviation by this software. Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (H^2) and expected genetic advance as percentage to mean (GAM) were computed. The phenotypic and genotypic correlation coefficients obtained from correlation study, were further partitioned into direct and indirect effects with the help of path coefficient analysis as suggested by Wright (1921) and applied in plant breeding by Dewey and Lu (1959).Diversity analysis was estimated from measured quantitative traits. Duncan's Multiple Range (DMRT) was employed to identify genotypes that are significantly different from each other. Descriptive statistic was used for qualitative traits data.

Table 1: Details of Experimental Materials

Genotypes	Name of Genotypes	Source
G1	BARI Dheros1	Bangladesh Agricultural Research Institute
G2	BARI Dheros2	Bangladesh Agricultural Research Institute
G3	BD-1928	Bangladesh Agricultural Research Institute
G4	BD-1929	Bangladesh Agricultural Research Institute
G5	BD-1930	Bangladesh Agricultural Research Institute

G6	BD-1931	Bangladesh Agricultural Research Institute
G7	BD-1932	Bangladesh Agricultural Research Institute
G8	BD-1933	Bangladesh Agricultural Research Institute
G9	BD-1934	Bangladesh Agricultural Research Institute
G10	BD-1935	Bangladesh Agricultural Research Institute
G11	BD-1936	Bangladesh Agricultural Research Institute
G12	BD-1937	Bangladesh Agricultural Research Institute
G13	BD-1938	Bangladesh Agricultural Research Institute
G14	BD-1939	Bangladesh Agricultural Research Institute
G15	BD-1940	Bangladesh Agricultural Research Institute
G16	BD-1941	Bangladesh Agricultural Research Institute
G17	BD-1942	Bangladesh Agricultural Research Institute
G18	Orka Onamika	Krishibid Seed Limited
G19	Ladies Finger	Krishibid Seed Limited
G20	Kohnur	Krishibid Seed Limited
G21	Mukta	Krishibid Seed Limited
G22	Soft Finger	Krishibid Seed Limited
G23	KS-3	Krishibid Seed Limited
G24	KS-1201	Krishibid Seed Limited
G25	Shruti-16	Local Market
G26	Preeti-72	Local Market
G27	NF-1003	Local Market
G28	SONIYA-86	Local Market

3. RESULTS AND DISCUSSION

Variance Components and Coefficient of Variation

Estimated variability components viz. phenotypic and genotypic variance, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability in broad sense and genetic advance as percent of means (GA%) for 11 characters are presented in Table 2.The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters studied. The highest phenotypic variances were calculated for fruit yield per plant (12212.49) followed by plant height (263.24) and seed per fruit (99.90) while the lowest value was recorded for fruit diameter (0.03) followed by primary branches per plant (1.25) and fruit length (3.28). The genotypic variance ranged from 0.01 (fruit diameter) to 9158.14 (fruit yield per plant). Consistence result was reported by Mehta *et al.* (2006); Pradip *et al.* (2010) for fruit yield per plant, plant height, number of seeds per fruit and number of tender fruit per plants. This result is in agreement with Ehab *et al.* (2013) who reported that phenotypic variances were higher than the corresponding genotypic variances indicating predominance of environmental effects on the expression of these studied characters. The phenotypic coefficient of variation (PCV) ranged between 6.50% (days to 50% flowering) to 43.91% (primary branches per plant) while genotypic coefficient of variation (GCV) ranged between 5.10 (days to 50% flowering) to 33.64% (number of primary branches per plant) (Table 2). Similar results were reported by Ehab *et al.* (2013), Mihretu *et al.* (2014) for okra. According to Sivasubramaniah and Meron (1973) PCV and GCV values greater than 20% are regarded as high, values between 10% and 20% to be medium whereas values less than 10% are considered to be low. Based on this delineation PCV and GCV recorded in this study, days to first flowering (7.23% and 5.62%), days to 50% flowering (6.50% and 5.10%) had low values (<10%) for both phenotypic and genotypic coefficient of variations and it was low in case of genotypic level for fruit length (7.36%) and fruit diameter (8.91%). Sibsankar *et al.* (2012) reported that low PCV and GCV values for days to first flowering. The low PCV and GCV value of traits suggests the higher influence of environment on these traits thus; selection on the phenotypic basis would not be effective for the genetic improvement (Das *et al.* 2012; Thirupathi *et al.* 2012; and Ehab *et al.* 2013).

Moderate GCV and PCV were found in germination% (9.375 and 10.10%), plant height (14.75% and 14.96%) and average fruit weight (16.25% and 20.89%) (Table 2). Medium PCV and GCV value suggests that these characters are controlled more of by the genetic factors. Hence, these characters amenable to selection for further improvement. Among all characters exhibiting high degree of genotypic and phenotypic coefficients of variation were in number of primary branches per plant (33.64% and 43.91%), number of fruits per plant (26.02% and 27.65%), seed per fruit (19.32% and 22.61%) and fruit yield per plant (32.48% and 37.51%), respectively. The closer magnitude of genotypic and phenotypic coefficients of variation indicated that a greater role was played by genotypes rather than environment. The results of the present investigation are consistent with Hazra and Basu (2000), Dhall *et al.* (2001), Gandhi *et al*. (2001), Ravindra *et al.* (2004) and Singh and Singh (2006). The results of this study suggests that traits with high PCV and GCV are amenable for selection whereas hardly possible to improve traits contrarily to those traits with low phenotypic and genotypic coefficient of variations.

Heritability and Genetic Advance

Heritability values are effective in predicting the expected enhancement to be achieved through the process of selection; high heritability in accordance with high genetic advance is an indicator of obtaining high output from the selection (Singh and Rai, 1981).In the present study, estimate of heritability in broad sense ranged from 27.58% for fruit length to 88.55% for fruits per plant (Table 2). According to Robinson *et al.* (1955) heritability is categorized as low (0-30%), moderate (31-60%) and high > 60%. Accordingly, heritability estimate in broad sense was high (>60%) for germination% (85.95%), days to 50% flowering (61.66%), plant height (97.32%), number of fruits per plant (88.55%), seed per fruit (73.02%) and fruit yield per plant (74.99%). This result is in strong agreement with Mihretu *et al.*2014,Pradip *et al*. (2010); Hazem *et al.* 2013 ;Simon *et al.* 2013 . Moderate heritability values (31- 60%) were registered for days to first flowering (60.55%), average fruit weight (60.51%), primary branches per plant (58.70%), fruit diameter (42.23%). On the other hand, low broad sense heritability value was recorded for fruit length (27.58%). If heritability of a character is very high around 80% or more, selection for such character is fairly easy. On the other hand Very low heritability reveals the ineffectiveness of direct selection for the improvement of the traits while moderate heritability suggests improvement through selection. Genetic advance as percent mean was categorized as high (≥20%), moderate (10-20%) and low (0-10%) (Johnson *et al.,*1955). As per this suggestion, the highest (≥20%) genetic advance was observed for number of branches, number of fruit per plant, plant height, average fruit weight, seed per fruit and fruit yield per plant. Consistence result was reported by Hazem *et al.* (2013). Johnson *et al.* (1955) suggested that heritability estimates along with genetic advance were more useful in predicting the effect of selecting the best individual. High heritability along with high genetic advance as percent of the mean was obtained for plant height (97.32% and 29.98%), fruits per plant (88.55% and 50.44%), seeds per fruit (73.02% and 34.00%), average fruit weight (60.51% and 26.04%) and fruit yield per plant (74.99% and 57.94%). Consistent result was reported by Ikram *et al*. (2010). However, the result from the combination of heritability and genetic advance indicated that the variation is attributable to a high degree of additive effect. Therefore, the character can be improved by selection.

Table 2. Estimation of variance parameters for eleven characters in okra genotypes

Parameters	Range	Mean	CV	σ^2p	σ^2g	σ^2 e	PCV	GCV	ECV	h^2_b (%)	GA	GAM
Germination (%)	60.67- 88.00	75.40	3.79	58.06	49.90	8.16	10.10	9.37	3.79	85.95	13.49	17.89
Days to 1st flowering	29.67- 36.00	32.74	4.54	5.60	3.39	2.21	7.23	5.62	4.54	60.55	2.95	9.02
Days to 50% flowering	36.00- 43.00	39.27	4.02	6.51	4.02	2.50	6.50	5.10	4.02	61.66	3.24	8.25
Plant Height (cm)	79.83- 152.67	108.48	2.45	263.24	256.19	7.05	14.96	14.75	2.45	97.32	32.53	29.98
Primary branches (cm)	1.50- 6.00	2.54	28.22	1.25	0.73	0.51	43.91	33.64	28.22	58.70	1.35	53.10
No. of fruit per plant	10.33- 26.33	17.10	9.36	22.35	19.79	2.56	27.65	26.02	9.36	88.55	8.62	50.44
Fruit length (cm)	10.21- 16.46	12.92	11.93	3.28	0.90	2.37	14.02	7.36	11.93	27.58	1.03	7.96
Fruit diameter (cm)	1.07- 1.60	1.35	10.42	0.03	0.01	0.02	13.71	8.91	10.42	42.23	0.16	11.93
Average Fruit weight(g)	10.67- 25.33	17.07	13.12	12.71	7.69	5.02	20.89	16.25	13.12	60.51	4.44	26.04
Seed per fruit	24.00- 58.67	44.21	11.74	99.90	72.94	26.96	22.61	19.32	11.74	73.02	15.03	34.00
Fruit yield per plant (g)	124.0-535.33	294.65	18.76	12212.49	9158.14	3054.35	37.51	32.48	18.76	74.99	170.72	57.94

σ^2p: Phenotypic variance, PCV: Phenotypic coefficient of variation, σ^2g: Genotypic variance, GCV: Genotypic coefficient of variation, σ^2e: Environmental variance, ECV: Environmental coefficient of variation

Association among Characters

Mutual association of characters is often expressed in phenotypic and genotypic with direction and magnitude of correlation coefficients among yield and yield related traits which are presented in Table 3. Plant breeders always look for genetic variation among characters to select the desirable types which are highly correlated among themselves and with yield and the analysis of the relationship among these characters are vital for selection criteria. Magnitude of genotypic coefficients of correlation was higher compared to their corresponding phenotypic coefficient values indicating that there was an inherent association among various traits studied (Table 3). Fruit yield has shown positive and significant phenotypic and genotypic correlations with plant height (0.699 and 0.618), number of fruits per plant (0.879 and

Table 3. Genotypic (G) and phenotypic (P) correlations among different pairs of traits for different genotype of okra

Traits		DFF	D50%F	PH	PB	NFP	FL	FD	AFW	SPF	FYP
G (%)	G	-0.339*	-0.001	0.169	0.062	0.101	0.350*	-0.299	0.292	0.037	0.137
	P	-0.302	-0.059	0.169	0.025	0.084	0.171	-0.147	0.196	0.027	0.101
DFF	G		0.536**	0.260	0.055	0.337*	-0.331*	-0.151	-0.392*	0.110	0.104
	P		0.607**	0.191	0.029	0.204	-0.200	-0.048	-0.219	0.088	0.047
D50%F	G			0.164	0.003	0.084	0.094	0.145	-0.040	0.095	0.056
	P			0.114	-0.033	0.055	0.056	0.045	-0.070	0.113	-0.002
PH	G				-0.319*	0.809**	-0.256	-0.361*	0.069	0.055	0.699**
	P				-0.252	0.761**	-0.115	-0.236	0.066	0.045	0.618**
PB	G					-0.307	0.044	0.351*	0.322*	-0.235	-0.109
	P					-0.251	-0.069	0.167	0.219	-0.147	-0.098
NFP	G						-0.271	-0.319*	0.130	-0.128	0.879**
	P						-0.132	-0.211	0.083	-0.134	0.796**
FL	G							-0.112	0.163	0.056	-0.198
	P							-0.278	0.162	-0.043	-0.030
FD	G								0.123	-0.571**	-0.169
	P								-0.001	-0.284	-0.162
AFW	G									0.150	0.569**
	P									0.047	0.629**
SPF	G										-0.021
	P										-0.065

G (%): Germination (%), DFF: Days to 1st flowering, D50%F: Days to 50% flowering, PH: Plant height (cm), PB: Primary branches, NFP: No. of fruit per plant, FL: Fruit length (cm), FD: Fruit diameter (cm), AFW: Average fruit weight (gm), SPF: Seed per fruit and FYP: Fruit yield per plant (g).

0.796), and average fruit weight (0.569 and 0.629), respectively. Fruit yield per plant has also shown negatively and insignificantly correlated with number of seeds per pod (-0.021 and -0.065), fruit length (-0.198 and -0.030), fruit diameter (-0.169 and -0.162) and also only negative phenotypic correlation with days to 50% flowering (-0.002). The findings of positive correlation are also confirmatory with Dhall *et al*. (2001), Dhankhar and Dhankhar (2002), Nimbalkar *et al.* (2002), Niranjan and Mishra (2003), Chhatrola and Monpara (2005), Alam and Hossain (2006), Mehta *et al.(*2006) and Pal *et al*.(2008 and 2010). Analysis revealed that fruit yield per plant had positive and significant phenotypic and genotypic correlation coefficient with plant height (0.699 and 0.618), number of fruits per plant (0.879 and 0.796) and average fruit weight (0.569 and 0.629) (Table 2). On other hand, fruit yield showed positive and non-significant genotypic and phenotypic correlation with germination% (0.137 and 0.101), days to first flowering (0.104 and 0.047), but fruit yield per plant exhibited negative and non-significant correlation coefficient with primary branches per plant (-0.109 and -0.098), fruit length (-0.198 and -0.030) and fruit diameter (-0.169 and -0.162).This result is in consistent with Dhankhar (2002).

Path Coefficient Analysis

The mutual relationship of component characters might vary both in magnitude and direction and the simple correlation coefficient may not provide the exact relationship between yield and yield attributes. Therefore, it is necessary to conduct path coefficient analysis which permits a critical examination of specific direct and indirect effects of characters and measures their relative intensity in determining the ultimate goal yield. The path coefficient analysis (Table 4) showed that the number of fruits per plant (0.756) had highest positive direct effects on fruit yield per plant followed by fruit weight (0.538) and plant height (0.037). The indirect positive effects were recorded of number of fruits per plant via plant height (0.0293), fruit weight (0.0597), and primary branches per plant (0.0062) and fruit length (0.0046). The direct positive effect of number of fruits per plant on yield in okra was also observed by Dhankhar and Dhankhar (2002), Jaiprakashnarayan and Ravindra (2004), Bali *et al.* (2005). Hence, direct selection for average number of fruits per plant was suggested to improve yield.

Days to first flowering showed negative direct effect on fruit yield (-0.011) whereas Days to 50% flowering showed positive direct effect on fruit yield (0.007). It was positive indirect effect through germination (0.0021), plant height (0.0053) and number of fruits per plant (0.0537). Plant height had positive direct phenotypic and genotypic effects on pod yield (0.037). The indirect positive effects of plant height on pod yield were recorded via days to 50% flowering (0.001), primary branches (0.0064), number of fruits per plant (0.5988), fruit length (0.0043), and fruit diameter (0.0024) and fruit weight (0.036). Fruit length showed negatively direct effects on fruit yield (-0.024). Its indirect effects through fruit weight (0.0861), fruit diameter (0.0017), days to first flowering (0.0028) and days to 50% flowering (0.0005) were positive. The findings of the present study are also in accordance with the results as reported by Niranjan and Mishra (2003), Jaiprakashnarayan and Ravindra (2004), Bali *et al.* (2005), Alam and Hossain (2006).

Diversity Analysis

The clustering pattern of all genotypes has been presented in (Table 5). All 28 genotypes grouped into five clusters on the basis of yield components studied. The cluster I comprised two genotypes including G1 and G18. Cluster II contained six genotypes namely, G6, G10, G15, G17, G20 and G25. Cluster III consisted of five genotypes viz., G2, G3, G4, G7 and G11. Cluster IV comprised five genotypes viz., G5, G9, G12, G13 and G21. Cluster V includes highest ten genotypes namely G8, G14, G16, G19, G22, G23, G24, G26, G28 and G30. Clustering of genotypes on the basis of genetic diversity would help the breeder for selecting diverse plants for using in hybridization under further breeding program. Clustering pattern was not influenced by geographical distribution of genotypes. Patro and Ravisankar (2004) studied cluster analysis and revealed considerable variation among forty one genotypes of okra, which were grouped into eight clusters.

Table 4. Partitioning of genotypes into direct (bold) and indirect effects of eleven traits by path analysis of okra

Traits	G (%)	DFF	D50%F	PH	PB	NFP	FL	FD	AFW	SPF
G (%)	-0.0890	0.0036	-0.0002	0.0063	-0.0010	0.0718	-0.0060	0.0018	0.1356	-0.0001
DFF	0.0287	-0.0110	0.0040	0.0085	-0.0009	0.2124	0.0061	0.0008	-0.1689	-0.0003
D50%F	0.0021	-0.0062	0.0070	0.0053	0.0003	0.0537	-0.0017	-0.0007	-0.0285	-0.0003
PH	-0.0150	-0.0025	0.0010	0.0370	0.0064	0.5988	0.0043	0.0024	0.0360	-0.0002
PB	-0.0042	-0.0005	-0.0001	-0.0107	-0.0220	-0.2139	0.0005	-0.0020	0.1474	0.0006
NFP	-0.0085	-0.0031	0.0005	0.0293	0.0062	0.7560	0.0046	0.0022	0.0597	0.0004
FL	-0.0221	0.0028	0.0005	-0.0066	0.0004	-0.1459	-0.0240	0.0017	0.0861	0.0000
FD	0.0198	0.0012	0.0006	-0.0111	-0.0056	-0.2034	0.0050	-0.0080	0.0312	0.0013
AFW	-0.0224	0.0035	-0.0004	0.0025	-0.0060	0.0839	-0.0038	-0.0005	0.5380	-0.0003
SPF	-0.0029	-0.0011	0.0007	0.0019	0.0043	-0.0983	-0.0001	0.0035	0.0565	-0.0030

Residual effect: 0.144** = Significant at 1%. * = Significant at 5%.

G (%): Germination (%), DFF: Days to 1st flowering, D50%F: Days to 50% flowering, PH: Plant height (cm), PB: Primary branches, NFP: No. of fruit per plant, FL: Fruit length (cm), FD: Fruit diameter (cm), AFW: Average Fruit weight (g), SPF: Seed per fruit and FYP: Fruit yield per plant (g).

The intra cluster and inter cluster divergence (average D^2 values) of all clusters have been presented in Table 6. Intra cluster average D^2 values ranged from 0.00 to 1.34. It recorded maximum (1.34) in cluster II with six genotypes followed by 1.23 in cluster V with ten genotypes. Inter cluster average D^2 values were higher (20.07) between cluster I and cluster V followed by 14.94 between cluster I and cluster II. The minimum inter cluster value for all the characters were as 5.34 between cluster II and cluster IV. Singh and Jain (2007) also found highest intra cluster distance (22.46) in cluster-IV and inter cluster distance (101.93) between cluster-XIV and XVII in the germplasm they studied.

Table 5. Distribution of 28 genotypes in different clusters

Cluster no.	Genotypes	No. of populations
I	G1, G18	2
II	G6, G10, G15, G17, G20, G25	6
III	G2, G3, G4, G7, G11	5
IV	G5, G9, G12, G13, G21	5
V	G8, G14, G16, G19, G22, G23, G24, G26, G27, G28	10
	Total	28

Table 6. Intra (Bold) and inter cluster distances (D^2) for 28 genotypes

Cluster	I	II	III	IV	V
I	0.00	14.91	7.23	10.97	20.07
II		1.34	8.93	5.34	5.84
III			0.87	5.43	14.54
IV				0.73	10.46
V					1.23

The characters which contributed most toward the D^2 matrix are presented in the Table 7. A close perusal of these cluster mean for different characters indicated considerable genetic differences among the clusters for all the characters. Cluster I showed highest mean values for plant height (137.12 cm), number of fruits per plant (23.00), fruit weight (22.00 g), seeds per fruit (49.17) and fruit yield per plant (508.17) among all the clusters. Apart from observing high cluster mean, low mean values were also envisage for its important in getting early that was recorded in cluster I for the characters viz., days to first flowering (31.33) and days to 50% flowering (38.33). Cluster II had none of highest mean values but lowest value for fruit weight (16.09 g) and seed per fruit (38.78). Cluster III had shown the high mean values days to first flowering (33.80). Among all the clusters, the lowest mean values for germination% (72.40) and primary branches per plant (2.17) was recorded in cluster III. Cluster IV had shown high mean values for germination% (83.67) and days to 50% flowering (39.93). Among all clusters, cluster V had highest mean values for primary branches per plant (2.87) followed by fruit length (13.21 cm). A substantial variation in cluster mean observed for various characters in okra was also reported by Hazra *et al.* (2002), Bendale *et al.* (2003), Ghai *et al.* (2004) and Singh and Jain (2006).

Table 7. Cluster mean for 11 yield and yield related characters in 28 okra genotypes

Characters	I	II	III	IV	V
Germination (%)	75.33	72.50	72.40*	83.67**	74.53
Days to 1st flowering	31.33*	32.83	33.80**	33.20	32.20
Days to 50% flowering	38.33*	38.94	39.73	39.93**	39.10
Plant Height (cm)	137.12**	106.90	113.72	117.83	96.41*
Primary branches (cm)	2.66	2.54	2.17*	2.22	2.87**
No. of fruit per plant	23.00**	17.00	21.73	20.27	12.07*
Fruit length (cm)	12.43*	12.68	13.17	12.56	13.21**
Fruit diameter (cm)	1.30	1.36	1.36	1.23*	1.40**
Average Fruit weight (g)	22.00**	16.09*	18.40	16.50	16.30
Seed per fruit	49.17**	38.78*	40.33	48.53	46.27
Fruit yield per plant (g)	508.17**	271.20	402.20	329.67	194.73*

* Lower value, ** Higher value

4. CONCLUSION

Genetic advancement in okra is possible through varietal selection exercised for the plant height, number of fruits per plant, fruit yield per plant, seeds per fruit and primary branches which showed high heritability coupled with high genetic advance. Moderate to high positive or negative direct effects also exerted by these characters on fruit yield. Therefore, proper emphasis should be given to these characters in okra breeding program for fruit yield improvement. Considering diversity, variability and all agronomic traits the genotypes G1 and G18 could be selected from cluster I for earliness and high fruit yield of okra while G6 and G 20 could be selected for less seeds per fruit from cluster II.

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