

RESPONSE OF OKRA (*ABELMOSCHUS ESCULENTUS* L.) F_{5:6} POPULATION OF FOR EARLINESS AND YIELD TRAITS

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Abstract

Okra (*Abelmoschus esculentus* L. Moench) is a widely cultivated vegetable crop all over the world. It is a rich source of protein. The genetic diversity of okra germplasm can play a significant role in developing its high yielding varieties. Selection of best parents for okra hybridization program and subsequent selection of transgressive segregants is an important strategy in this regard. That's why the current study was conducted to investigate genetic variation among the okra (*Abelmoschus esculentus* L.) genotypes for yield and yield-related traits. The experimental material comprised fifteen F_{5:6} (SO1- SO15) okra cross combinations along with their 6 parents (Punjab Selection, Pusaswami, Arka Anamika, Super Green, Green Star and Subz Pari). Results showed that among okra parental populations, Punjab Selection took minimum days to 50% flowering (51.7 days), marketable fruit length (15.1 cm), marketable fruit girth (1.31 cm) and internode length (4.37 cm) while exhibited maximum, pods plant⁻¹ (22.9 pods), physiological mature pod length (16.8 cm), physiological mature pod girth (2.18 cm) and pod yield (6.18 kg), respectively. Maximum internodes plant⁻¹ (22.9 internodes) were observed for okra parental genotype Sabz Pari. Okra genotype SO8 and SO15 gave maximum pods plant⁻¹ (27.6 pods) internodes plant⁻¹ (19.5) and pod yield (7.10 kg), respectively. Based on excellent results okra parental genotypes, Punjab Selection and Sabz Pari along with F_{5:6} segregating populations SO8, SO12 and SO15 are recommended for future okra crossing programs.

Key words: Genetic advance, heritability, okra parents, GCV, PCV, segregating population.

Introduction

Okra (*Abelmoschus esculentus* L. Moench) is the most important vegetable crop grown widely all over the world. The place of origin of okra is Ethiopia but it is cultivated widely in hot and sub-tropical regions of the world. Okra plays pivotal role in the developing economy of a society. Worldwide India ranks first in terms of total area and production of okra while Pakistan ranks seventh. It is an annual herbaceous plant grown two times a year i.e., summer and spring seasons. Okra is mainly grown for its green immature nutritive fruits. Okra is a rich source of protein and is considered a low-fat food. It has unique nutrients and phytochemical profiles and is particularly rich in dietary fibers, minerals, vitamin C, folate, vitamins B1, B6, and K as well as bioactive components such as flavonoids (quercetin and phytosterols).

Okra is the best vegetable crop in Pakistan. During 2018 the okra total cultivated area in Pakistan was 15713 ha registering 120637 tons production (FAOSTATE, 2018). Okra is also grown in Khyber Pakhtunkhwa Province with an area of 16809 hectares with a production

of 2083 tons, respectively but the average pod yield of okra in the province is very low (<https://agrihunt.com>, 2018). Genetic diversity among okra germplasm plays a significant role in the breeding program as it helps to develop the best varieties with desired traits. It is a prerequisite to develop high yielding okra varieties to achieve high fruit yield per unit area. The selection of the best parents for the okra hybridization program and subsequent selection of transgressive segregants is a very important breeding strategy (Prakash *et al.*, 2011). Information about the inheritance of various characters and determining appropriate breeding procedures for a particular crop is important before the start of any breeding program. Fruit size, texture, color, fruit test, yield, adaptability to greenhouse/field condition and requirement of light/temperature are some of grower's specific choices for selection of any okra variety (Basiden, 1994). Genetic variation in okra genotypes can be estimated by observing the phenotypes of the plants and measuring the morphological characters. The morphological mode of characterization of the diverse genotypes is robust, reliable, and less costly.

Heritability is the percentage of genotypic variation to the total phenotypic change, which consist of both genetic and environmental variances. Heritability indicates only the effectiveness with which selection of a genotype can be based on phenotypic performance, but it fails to indicate the expected genetic progress in one cycle of selection. Heritable variation can be effectively used with a greater degree of accuracy when heritability is studied in conjunction with genetic advances (Ullangula, 2017). The heritability of a given trait shows the amount to which it is expected to be inherited to the coming generation and it's more useful when utilized in combination with the estimation of expected genetic gain/ genetic advance. While the genetic advance (GA) is an enhancement in mean phenotypic values of all chosen plants over the parental population. Genetic Advance (G A) is proof of the expected gain which we can get from the selection of higher individuals. Heritability, as well as genetic advance, is useful in calculating the expected gain under selection then heritability alone (Arshad Iqbal *et al.*, 2018).

Keeping in mind the importance of morphological characterization and variability, the present study was designed with the objectives to estimate genetic variation among the parental genotypes and segregating populations of okra and to identify the best performing segregating populations for yield and yield associated traits.

Materials and Methods

The present experiment was carried out to assess genetic variability among okra genotypes for morphological characteristics at Agricultural Research Station (ARS) Swabi during 2019. The experimental material comprised 15 F_{5,6} segregating populations and 6 parental genotypes which are listed in (Table 1). Randomized complete block design (RCBD) was used having three (03) replications. Every okra genotype was grown in 4 rows plot having a three-meter row length. The distance of 60.0 cm and 20.0 cm was kept respectively in row to row and plant to plant. All other

cultural practices were applied constantly to each experimental plot.

Days to first flower initiation, days to first pod development, days to 50% flowering, marketable pod length (cm), marketable pod girth (cm), physiological mature pod length (cm), physiological mature pod girth, plant height (cm), primary branches plant⁻¹, inter nod length (cm), inter nods plant⁻¹, stem diameter (cm), pods on primary branches, pods plant⁻¹, seed pod⁻¹ and yield plot⁻¹ (kg) were observed.

Statistical Analysis

The recorded data were analyzed by using the principle of Singh & Chaudhary (1985) for the F_{5,6} segregating populations along with okra parents (Table 2). The least significant difference test was estimated for means partition and appropriate association.

Heritability estimation: Heritability, as well as hereditary and natural fluctuation, was evaluated from the cruel square in ANOVA for each considered character concurring to Singh & Chaudhary (1979).

$$\text{Genotypic variance (Vg)} = \frac{\text{Genotypic mean square} - \text{Error mean square}}{\text{Number of replications}}$$

$$\text{Environmental variance (Ve)} = \text{Error mean square}$$

$$\text{Phenotypic variance (Vp)} = \text{Vg} + \text{Ve}$$

Broad sense heritability (h²_{bs}) assessed as:

$$h^2_{(bs)} = \frac{Vg}{Vp}$$

Vp → Phenotypic variance for a specific character

(h²_{bs}) → Broad sense heritability for a specific trait

Vg → Genetic difference

Table 1. Okra genotypes used in the study at Agricultural Research Station Swabi during 2019.

S. No.	Parents	S. No.	F ₅ Lines	Cross combination
1	Punjab Selection	1	SO1	Punjab Selection × Pusaswami
2	Pusaswami	2	SO2	Punjab Selection × Arka Anamika
3	Arka Anamika	3	SO3	Punjab Selection × Super Green
4	Super Green	4	SO4	Punjab Selection × Green Star
5	Green Star	5	SO5	Punjab Selection × Sabz Pari
6	Sabz Pari	6	SO6	Pusaswami × Arka Anamika
		7	SO7	Pusaswami × Super Green
		8	SO8	Pusaswami × Green Star
		9	SO9	Pusaswami × Sabz Pari
		10	SO10	Arka Anamika × Super Green
		11	SO11	Arka Anamika × Green Star
		12	SO12	Arka Anamika × Sabz Pari
		13	SO13	Super Green × Green Star
		14	SO14	Super Green × Sabz Pari
		15	SO15	Green Star × Sabz Pari

Table 2. Mean squares values of okra genotypes studied during 2019.

Trait	Replication	Genotypes	Parents	F _{5:6}	P Vs. F _{5:6}	Error
Degree of freedom	2	20	5	14	1	40
Days to 50% flowering	5.349**	11.18**	10.62**	1.984 ^{N.S}	142.8**	1.165
Marketable fruit length (cm)	1.269 ^{N.S}	2.193*	0.040 ^{N.S}	3.078**	0.561 ^{N.S}	1.031
Marketable fruit girth (cm)	0.0008 ^{N.S}	0.014*	0.0025 ^{N.S}	0.014*	0.066**	0.007
Pods plant ⁻¹	9.885**	13.57**	6.934**	6.616**	144.2**	0.625
Physiological mature pod length (cm)	11.96**	4.737**	2.820**	0.84 ^{N.S}	68.80**	0.807
Internode length (cm)	0.668*	0.868**	0.090 ^{N.S}	1.036**	2.395**	0.176
Internodes plant ⁻¹	1.710 ^{N.S}	18.94**	3.061*	6.906**	266.8**	1.202
Physiological mature Pod girth (cm)	0.144**	0.166**	0.153**	0.020*	2.279**	0.010
Pod yield (kg)	0.065 ^{N.S}	3.654**	3.093**	0.125**	55.86**	0.047

Genetic advance (GA): The GA was calculated by using Panse and Sukhatme formula (1965).

$$GA = K \times \sqrt{\sigma^2 p} \times h^2$$

K ↔ 01.76 (10% intensity of selection)

$\sqrt{\sigma^2 p}$ ↔ PSD (Phenotypic standard deviation)

h² ↔ BSH (broad sense heritability) for a particular character.

$$GA \% = \frac{GA}{X} \times 100$$

In which

X ↔ mean of specific F_{5:6} okra population for particular character

Results

Days to 50% flowering: ANOVA exhibited significant ($p \leq 0.01$) differences amongst parents and interaction of parents Vs. F_{5:6} but non-significant differences were observed among F_{5:6} okra genotypes for days to 50% blooming (Table 2). Mean values among the parents for days to 50% flowering varied from 51.7 to 57.0 days. Punjab Selection took minimum (51.7 days) to 50% flowering following by Pusaswami, Arka Anamika, and Green Star with values of 53.5, 55.0 and 55.3 days, respectively. Maximum days to 50% flowering (57.0 days) were recorded for okra genotype Sabz Pari. Mean values of the F_{5:6} segregating populations varied from 50.3 to 53.3 days. Okra genotype SO9 showed minimum days to 50% flowering (50.3 days) followed by SO7, SO14 (50.7), SO2 and SO3 with minimum values of 51.0, 51.3 days, respectively (Table 3) while maximum days to 50% flowering (53.3 days) were recorded for okra genotype SO1 (Table 3). Among the okra genotypes, low PCV (6.60%), GCV (6.27%), high broad-sense heritability (90.25%) and low genetic advance (5.494%) were recorded for days to 50% flowering (Table 5).

Marketable fruit length (cm): The analysis of variance showed pronounced variations ($p \leq 0.01$) in F_{5:6} segregating

populations for marketable fruit length. Non-significant differences were manifested by parents and interaction of parents Vs. F_{5:6} segregating populations for this trait (Table 2). Among the okra parents, marketable fruit length varied from 15.1 to 15.4 cm. Punjab Selection manifested minimum fruit length (15.1 cm) followed by Pusaswami, Arka Anamika and Super Green with minimum values 15.2 and 15.3 cm respectively while maximum marketable fruit length (15.4 cm) was recorded for okra parent Green Star. Mean values for marketable fruit length among okra F_{5:6} segregating populations varied from 13.2 to 16.9 cm. Okra genotype SO12 observed minimum marketable fruit length (13.2 cm) followed by SO8, SO13, SO7 and SO15 with values of 14.1, 14.3, 14.4 and 14.6 cm, respectively. Maximum marketable fruit length (16.9 cm) was exhibited by okra genotype SO9 (Table 3). Among the okra genotypes moderate PCV (11.21%), low GCV (8.98%), high (64.20%) broad-sense heritability and low (1.917%) genetic advance was recorded for this trait (Table 5).

Marketable fruit girth (cm): Highly significant ($p \leq 0.01$) differences were shown by the parent's Vs. F_{5:6} segregating populations, substantial differences ($p \leq 0.05$) by the F_{5:6} segregating populations while parental genotypes exhibited non-significant differences for marketable fruit girth (Table 2). Among parents, mean values for marketable fruit girth ranged from 1.31 to 1.38 cm. Punjab Selection showed minimum marketable fruit girth (1.31 cm) followed by Pusaswami, Arka Anamika and Super Green with values 1.32, 1.33 and 1.36 cm, respectively. Maximum marketable fruit girth (1.38 cm) was observed for Sabz Pari. Among the F_{5:6} segregating populations, marketable fruit girth varied from 1.28 to 1.53 cm. Okra genotype SO5 manifested maximum marketable fruit girth (1.53 cm) while SO12 recorded minimum marketable fruit girth (1.28 cm) followed by SO14, SO7, SO6 and SO1 with marketable fruit girth values of 1.31, 1.36, 1.37 and 1.38 cm, respectively (Table 3). Among the okra genotypes low PCV, GCV (7.73%, 9.80%) and high heritability (62.37%) with low genetic advance 0.150% were observed for marketable fruit girth (Table 5).

Table 3. Mean values for days to 50% flowering, marketable pod length, marketable pod girth and pod plant⁻¹ of okra genotypes studied during 2019.

Okra genotypes	Days to 50% flowering	Marketable pod length (cm)	Marketable pod girth (cm)	Pods plant ⁻¹
Punjab Selection	51.7	15.1	1.31	22.9
Pusaswami	53.7	15.2	1.32	22.7
Arka Anamika	55.0	15.3	1.33	20.9
Super Green	56.0	15.3	1.36	19.6
Green Star	55.3	15.4	1.37	19.8
Sabz Pari	57.0	15.4	1.38	19.7
SO1	53.3	15.0	1.38	24.1
SO2	51.0	16.1	1.49	23.7
SO3	51.3	14.9	1.41	23.9
SO4	52.3	16.5	1.47	26.5
SO5	51.3	16.1	1.53	24.3
SO6	51.0	15.5	1.37	23.3
SO7	50.7	14.4	1.36	22.4
SO8	52.0	14.1	1.49	27.6
SO9	50.3	16.9	1.43	25.9
SO10	51.3	15.7	1.48	25.5
SO11	51.3	14.3	1.40	22.8
SO12	52.7	13.2	1.28	23.0
SO13	51.0	14.3	1.44	23.6
SO14	50.7	14.7	1.31	24.7
SO15	51.3	14.6	1.39	23.0

Table 4. Mean values for physiological mature pod length, internode length, internodes plant⁻¹, physiological mature pod girth and pod yield of okra genotypes were studied during 2019.

Okra genotypes	Physiological mature pod length (cm)	Internode length (cm)	Internodes plant ⁻¹	Physiological mature pod girth (cm)	Pod yield (kg)
Punjab Selection	16.8	4.37	20.3	2.18	6.18
Pusaswami	16.0	4.46	20.7	1.97	5.43
Arka Anamika	15.6	4.55	21.7	1.90	4.23
Super Green	15.3	4.65	22.1	1.77	4.32
Green Star	14.6	4.68	22.4	1.63	3.97
Sabz Pari	14.1	4.85	22.9	1.57	3.43
SO1	18.1	4.33	15.9	2.11	6.58
SO2	17.6	4.30	18.0	2.31	6.66
SO3	17.6	3.89	16.9	2.31	6.48
SO4	17.4	3.96	17.3	2.33	6.84
SO5	18.5	4.37	17.3	2.19	6.76
SO6	17.6	3.93	17.9	2.33	6.23
SO7	18.3	3.78	19.1	2.19	6.42
SO8	17.5	3.59	19.5	2.39	6.54
SO9	18.5	4.00	17.3	2.27	6.74
SO10	17.7	3.81	17.3	2.29	6.73
SO11	16.4	5.59	17.1	2.31	6.82
SO12	17.9	4.04	13.9	2.11	6.76
SO13	17.5	5.26	14.2	2.26	6.75
SO14	17.4	3.33	18.1	2.19	6.74
SO15	18.1	4.26	17.0	2.25	7.10

Pods plant⁻¹: The difference amongst parents, F_{5,6} segregating populations and parents Vs. F_{5,6} for the pods plant⁻¹ were significant ($p \leq 0.01$), shown in Table 2. Among the okra parental genotypes mean values for pods plant⁻¹ varied from 19.6 to 22.9 pods. Punjab Selection exhibited a maximum (22.9 pods) pods plant⁻¹ followed by Pusaswami, Arka Anamika and Green Star with values of 22.7, 20.9 and 19.8 pods, respectively. Minimum pods (19.6 pods) were shown by okra parental genotype Super Green. Among the

F_{5,6} okra genotypes, pods plant⁻¹ varied from 22.4 to 27.6 pods. Okra genotype SO8 exhibited maximum pods plant⁻¹ (27.6 pods) followed by SO4, SO9, SO10 and SO14 with pods plant⁻¹ values of 26.5, 25.9, 25.5 and 24.7 pods, respectively. Minimum pods plant⁻¹ (22.4 pods) were shown by okra genotype SO7 (Table 3). Higher heritability (95.52%) and low genetic advance (6.289%), while moderate PCV (16.03%) and GCV (15.67%) values were manifested by okra genotypes for this trait (Table 5).

Table 5. Phenotypic variance, genotypic variance, environmental variance, phenotypic coefficient of variation, genotypic coefficient of variation and coefficient of variance, heritability and genetic advance studied during 2019.

Traits	V _p	V _g	V _e	PCV%	GCV%	h ² %	GA	CV
Days to 50% flowering	11.96	10.79	1.165	6.601	6.271	90.25	5.494	0.020
Marketable fruit length (cm)	2.880	1.849	1.031	11.21	8.982	64.20	1.917	0.067
Marketable fruit girth (cm)	0.018	0.011	0.007	7.740	9.800	62.37	0.150	0.060
Pods plant ⁻¹	13.99	13.36	0.625	16.03	15.67	95.52	6.289	0.033
Physiological mature pod length (cm)	5.275	4.468	0.807	13.46	12.39	84.69	3.433	0.052
Internode length (cm)	0.985	0.809	0.176	23.16	20.99	82.13	1.435	0.097
Internodes plant ⁻¹	1974	18.53	1.202	24.13	23.38	93.90	7.343	0.059
Physiological mature pod girth (cm)	0.173	0.163	0.010	19.52	18.91	93.84	0.688	0.0007
Pod yield (kg plot ⁻¹)	1.250	1.202	0.047	18.38	18.02	96.16	1.892	0.036

Physiological mature Pod length (cm): Pronounce differences ($p \leq 0.01$) were observed in okra parents and interaction of parents Vs. F_{5,6} segregating populations and non-significant differences were shown in okra F_{5,6} genotypes for physiological mature pod length (Table 2). Among okra parental genotypes, physiological mature pod length varied from 14.1 to 16.8 cm. Punjab Selection showed maximum physiological mature pod length (16.8 cm) followed by Pusaswami, Arka Anamika and Super Green with values of 16.0, 15.6 and 15.3 cm, respectively. Minimum physiological mature pod length (14.1 cm) was observed for Sabz Pari. Among F_{5,6} segregating populations, physiological mature pod length varied from 16.4 to 18.5 cm. Okra genotypes SO5 and SO9 exhibited maximum physiological mature pod length (18.5cm) followed by SO7, SO1 and SO12 with mean values of 18.3, 18.1 and 17.9 cm, respectively. Minimum physiological mature pod length (16.4 cm) was recorded for SO11 okra genotype (Table 4). High heritability (84.69%), low genetic advance (3.433%) and moderate PCV (13.46%), GCV (12.39%) were observed among okra genotypes for physiological mature pod length (Table 5).

Internode length (cm): Mean square values revealed visible differences ($p \leq 0.01$) in F_{5,6} segregating populations and parents Vs. F_{5,6} segregating populations for internode length while non-significant differences in parents were observed for this feature (Table 2). Among the parental genotypes, internode length varied from 4.37 to 4.85 cm. Punjab Selection manifested minimum internode length (4.37 cm) followed by Pusaswami, Arka Anamika and Super Green with minimum mean values 4.46, 4.55 and 4.65 cm, respectively. Maximum internode length (4.85 cm) was recorded for Sabz Pari. Among the okra F_{5,6} segregating generation, internode length varied from 3.33 to 5.59 cm. Okra genotype SO14 showed minimum internode length (3.33cm) followed by SO8, SO5, SO7 and SO3 with minimum mean values 3.59, 3.78, 3.81 and 3.89 cm whereas maximum internode length (5.59 cm) was observed for okra genotype SO11 (Table 4). For Internode length, high broad-sense heritability (82.13%), low genetic advance (1.435%), while high PCV and GCV (23.16%, 20.99%) values were displayed by okra genotypes (Table 5).

Internodes plant⁻¹: ANOVA displayed noticeable differences ($p \leq 0.01$) in F_{5,6} segregating populations and parents Vs. F_{5,6} populations for internodes plant⁻¹. Among

the parental genotypes, clear differences were observed for internodes plant⁻¹ (Table 2). Among the okra parental genotypes, internode plant⁻¹ varied from 20.3 to 22.9 internodes. Sabz Pari recorded maximum internodes plant⁻¹ (22.9 internodes) followed by Green Star, Arka Anamika and Super Green with maximum values 22.4, 21.7 and 21.1 internodes, respectively while minimum internodes plant⁻¹ (20.3 internodes) were exhibited by Punjab Selection. Among the okra F_{5,6} segregating populations, internode plant⁻¹ varied from 13.9 to 19.5 internodes. Okra genotype SO8 manifested maximum (19.5 internodes) internodes plant⁻¹ followed by SO7, SO14, SO2 and SO6 with maximum mean values 19.1, 18.1, 18.0 and 17.9 internodes, respectively. Minimum (13.9 internodes) internodes plant⁻¹ was observed by okra genotype SO12 (Table 4). Among the okra genotypes high PCV (24.13%), GCV (23.38%) and higher heritability (93.90%) with low genetic advance (7.343%) were observed for internodes plant⁻¹ (Table 5).

Physiological mature pod girth (cm): For the physiological mature pod girth, the ANOVA table displayed substantial ($p \leq 0.01$) variations in parents and parents Vs. F_{5,6} segregating population while F_{5,6} okra genotypes displayed significant variations (Table 2). Among the parents, physiological mature pod girth varied from 1.57 to 2.18 cm. Okra parent Punjab Selection recorded maximum (2.18 cm) physiological mature pod girth followed by Pusaswami, Arka Anamika and Super Green with mean values of 1.79, 1.90 and 1.77 cm, respectively. Minimum physiological mature pod girth (1.57 cm) was shown by parental genotype Sabz Pari. Among the F_{5,6} segregating populations, physiological mature pod girth varied from 2.11 to 2.39 cm. Okra genotype SO8 displayed maximum (2.39 cm) physiological mature pod girth followed by SO4, SO6 (2.33 cm) and SO2, SO3 (2.31 cm), respectively. Minimum physiological mature pod girth (2.11 cm) was recorded for genotype SO1 (Table 4). Among the okra genotypes moderate PCV (19.52%), GCV (18.91%), higher heritability (93.84%) and low genetic advance (0.688%) were recorded for physiological mature pod girth (Table 5).

Pod yield (kg): Okra pod yield is the most important parameter, and every plant breeder is interested in evolving improved genotypes having high pods yield. Mean square data showed highly significant variation at

1% probability level among the okra parents, $F_{5:6}$ segregating populations and interaction of parents Vs. $F_{5:6}$ for pod yield (Table 2). Pod yield in okra parents ranged from 3.43-6.16 kg plot⁻¹. Okra parental genotype Sabz-pari gave minimum pod yield (3.43 kg) while maximum pod yield (6.18 kg) was observed for okra genotype Punjab Selection followed by Pusaswami, Super Green and Arka Anamika with pod yield values of 5.43, 4.32 and 4.23 kg plot⁻¹, respectively. Among okra $F_{5:6}$ segregating populations mean values for pod yield varied from 6.23 to 7.10 kg plot⁻¹. SO6 exhibited minimum pod yield (6.23 kg plot⁻¹) while maximum pod yield (7.10 kg plot⁻¹) was recorded for okra genotype SO15 followed by SO4 (6.84 kg plot⁻¹), SO11 (6.82 kg plot⁻¹), SO5 (6.76 kg plot⁻¹) and SO12 (6.76 kg plot⁻¹) (Table 4). Among the studied okra genotypes, moderate PCV (18.38%), GCV (18.02%), high broad-sense heritability (96.16%) and low genetic advance (1.892%) were observed among the okra genotypes for pod yield (Table 5).

Discussion

The results of the present investigation on genetic variability indicated the presence of adequate variability for all the characters. The analysis of variance indicated that differences among genotypes were found to be significant except following parameters days to 50% flowering of F_5 population, marketable fruit girth, and marketable fruit length of parental genotypes, physiological mature pod length and mean internode length of parents.

Days to 50 percent flowering showed appreciable variation. Early flowering genotypes were Punjab Selection, Pusaswami and Arka Anamika (Table 2). This earliness can be exploited either by using these lines in recombination breeding or through direct selection. Similar results were reported by Pravin *et al.*, (2016) and Abhilasha (2016) for the observation of days to 50% blooming and physiological mature pod length. Pods plant⁻¹ is one of the important yield contributing characters in okra. The fruit formation in okra takes place at the nodes. A short internode length with internode plant⁻¹ enhances the number of fruiting nodes thereby their increasing fruit yield per plant. Number of pods plant⁻¹ along with number of internode plant⁻¹ and internode length determines the geometry of okra plant. The wide variation in these characters provides an opportunity for selecting of superior genotypes.

The genotypes under study showed considerable variation in these characters. A good amount of variation for days to 50% flowering, internode length, number of internodes plant⁻¹ was reported by Pravin *et al.*, (2016), Tukaram *et al.*, (2019) and Hadiya *et al.*, (2018). The characters number of pods plant⁻¹, physiological mature pod length, physiological mature pod girth showed a considerable amount of variation. Thulasiram *et al.*, (2017) and Khishor *et al.*, (2016), Abhilasha (2016) observed similar results among okra genotypes. While marketable fruit girth and marketable fruit length showed a narrow range of variation. The same results were displayed by Hadiya *et al.*, (2018).

While evolving improved genotypes, plant breeders pay special attention to high pods yield. Punjab Selection, and Pusaswami registered noticeable pod yield, whereas Sabz-pari expressed low pod yield. A wide range of variation for this character was reported by Thulasiram *et al.*, (2017) and Olayiwola *et al.*, (2015) and also reported highly sizeable differences among okra genotypes for pod yield which is in line with our results. High phenotypic and genotypic coefficients of variation were recorded for internode length and internode plant⁻¹ suggesting that variability in these characters is due to genetic constitution. These results confirm the earlier finding of Abdullmanan *et al.*, (2018) and Mihreta *et al.*, (2014) these traits offer much scope for improvement by selection.

Moderate phenotypic and genotypic coefficients of variation were observed for pod plant⁻¹, physiological mature pod length, physiological pod girth and pod yield. Similar results were reported by Rambabu *et al.*, (2019), Khajura *et al.*, (2015), Nwangburaka *et al.*, (2012) and Thulasiram *et al.*, (2017). The phenotypic and genotypic coefficient of variation was low for the trait's days to 50% flowering, marketable fruit length and marketable fruit girth. Earlier, similar findings by Chandra *et al.*, (2014), Phanikrishna *et al.*, (2015) and Jagan *et al.*, (2013) in okra were observed.

The characters showing prominent estimates of coefficient of variation shown more genetic variability in genotypes for these attributes, making an effective selection. Whereas low estimates indicated that genotypes in the present study possessed less genetic variability for these traits. Estimation of variability in population is an effective tool for the breeder to design the selection procedures more accurately for identifying superior genotypes. According to Rambabu *et al.*, (2015), lowest differences in phenotypic and genotypic coefficients of variation indicate lowest environmental influence, however high differences indicate that environmental variation contributes major role in trait expression.

In the current study, high heritability coupled with low genetic advance as percent of mean was observed for all studied traits *viz* days to 50% flowering, marketable fruit length, marketable fruit girth, pod plant⁻¹, physiological mature pod length, internode length, internode plant⁻¹, physiological mature pod girth and pod yield. Similar observation was recorded in okra by phanikrishna *et al.*, (2015), Khajuria *et al.*, (2015), Jagan *et al.*, (2013), Rambabu *et al.*, (2019), Abdulmanan *et al.*, (2018), Mihreti *et al.*, (2014), Nwangburaka *et al.*, (2012) and Thulasiram *et al.*, (2017).

Conclusions and Recommendations: It is concluded from the results of the experiment that among all okra parental genotypes evaluated for different traits, Punjab Selection exceeded in performance for days to 50% flowering, marketable fruit length, marketable fruit girth, pods plant⁻¹, physiological mature pod length, internode length, internode plant⁻¹, physiological mature pod girth and pod yield. Among okra $F_{5:6}$ segregating generations, Okra genotype SO8 observed maximum values for pods plant⁻¹, internodes plant⁻¹ while SO12

produced minimum marketable fruit length and girth, respectively. Maximum yield was recorded for okra segregating population SO15. Based on the results of the experiment, it is recommended that:

1. The okra parental genotype Punjab Selection excelled in yield and yield-related parameters having great potential in okra crossing programs to develop segregating generations for identification and selection of improved okra lines.
2. The F_{5:6} segregating populations, SO8, SO12 and SO15 could be further advanced to the next generation and desirable single plant selections should be carried out for the development of improved variety (s) of okra.

References

- Abdul M.S., A. Muhammad, Z. Khurram and T.S. Shahbaz. 2018. Characterization of Okra (*Abelmoschus esculentus*) Genotypes for Fruit Firmness, other Horticultural Traits and Heritability Studies. *Int. J. Agric. Biol.*, 20: 345-352.
- Abhilasha, K. 2016. Evaluation of advance lines of okra for productivity and quality traits. MSc. Thesis, *Uni. Hort. Sci. Bagalkot*.
- Ahamed, K.U., B. Akter, N. Ara, M. F. Hossain and M. Moniruzzaman. 2015. Heritability, correlation and path coefficient analysis in fifty seven okra genotypes. *Int. J. Appl. Sci. Biotechnol.*, 3(1): 127-133.
- Anonymous. 2018. FAOSTAT database. Food and Agriculture organization of the united nation, Rome, Italy. <http://faostat.fao.org>.
- Arihant. 2018. Available at <https://agrihunt.com>, 2018 (accessed on 16th February, 2019.)
- Arshad I., M.A.S. Syed, R. Hidayat, A. Faiza and R. Aziz. 2018. Genetic Variability, Heritability and Genetic Advance for Morphological Traits in F_{5:6} Rice Lines. *Sarhad J. Agri.*, 34(4): 888-895.
- Baisden, G. 1994. Franken food, bioengineered bonanza of the future, or your worst night more come true. *The Growing Edge*, 5(4): 34-42.
- FAO. 2018. Food and Agricultural Organization, Statistics Division, <http://www.fao.org>
- Hadiya, D.N., S.C. Mali, V.K. Baraiya and A.I. Patel. 2018. Studies on assessment of heterosis for fruit yield and attributing characters in okra [*Abelmoschus esculentus* (L.) Moench]. *IJCS.*, 6(5): 1919-1923.
- Jagan K., K.R. Ravinder, M. Sujatha, V. Sravanthi and S.R. Madhusudhan. 2013. Studies on genetic variability, heritability and genetic advance in okra (*Abelmoschus esculentus* (L.) Moench). *J. Agri. and Vet. Sci.*, 5(1): 2319-2372.
- Khajuria, R.K., J.P. Sharma, R.K. Samnotra, S. Kumar and K. Ranjit. 2015. Variability studies in Okra (*Abelmoschus esculentus* L. Moench). *Elect. J. Plant Breed.*, 7(2): 226-234
- Kishor, D.S., K. Arya, K.J. Yogeesh, K. Vinod, Yashoda and K. Hee-Jong. 2016. Genotypic Variation among Okra (*Abelmoschus esculentus* (L.) Moench) Germplasms in South India. *Plant Breed. Biotech.*, 4(2): 234-241.
- Mihretu, Y., G. Wryessa and D. Adugna. 2014. Variability and association of quantitative characters among okra (*Abelmoschus esculentus* L. Moench) in south western Ethiopia. *J. Biol. Sci.*, 14(5): 336-342.
- Nwangburuka, C.C., O.A. Denton, O.B. Kehinde, D.K. Ojo and A.R. Popoola. 2012. Genetic variability and heritability in cultivated okra [*Abelmoschus esculentus* (L.) Moench]. *Spanish J. Agri. Res.*, 10(1): 123-129.
- Olayiwola, M.O., O.A. Dabo and O.J. Ariyo. 2015. Assessment of morphological variation among Okra (*Abelmoschus esculentus* L. Moench) accessions to aid selection of ideal parents. *Elect. J. Plant Breed.*, 6(3): 663-667.
- Panase, V.G. and P.V. Sukhatme. 1965. Statistical methods for agriculture workers. *Indian Council of Agric. Res.*, New Delhi: 381.
- PhaniKrishna, M., B. Hameedunnisa, A.R. Manohar and N.K. Sunil. 2015. Estimation of heritability and genetic advance in okra [*Abelmoschus esculentus* (L.) Moench.]. *Plant Arch.*, 15(1): 489-491.
- Prakash, K., M. Pitchaimuthu and K.V. Ravishankar. 2011. Assessment of genetic relatedness among okra genotypes [*Abelmoschus esculentus* (L.) Moench] using rapd markers. *Elect. J. Plant Breed.*, 2(1): 80-86.
- Pravin, K.S., D.P. Mishra and P. Amit. 2016. Genetic variability studies for yield and it contributing trait in okra (*Abelmoschus esculentus* (L.) Moench). *J. Appl. & Nat. Sci.*, 8(3): 1634-1637.
- Rambabu, B., D.P. Waskar and V.S. Khandare. 2019. Genetic variability, heritability and genetic advance in okra. *Int. J. Pure App. Biosci.*, 7(1): 374-382.
- Singh, R.K. and B.D. Chaudhary. 1985. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, N. Delhi, India.
- Sudip, C., M.L. Bhardwaj, K. Ramesh, K. Dharminder, K. Sandeep, G. Nidhish, D. Balbir and S. Subhash. 2014. Estimation of parameters of variability for different quantitative traits in okra, *Abelmoschus esculentus* (L.) Moench. *Intern. J. Farm Sci.*, 4(3): 33-41.
- Thulasiram, L.B., S.R. Bhople, S. Mekala and B.N. Ravi. 2017. Genetic variability and heritability studies in okra (*Abelmoschus esculentus* (L.) Moench). *Plant Arch.*, 17(2): 907-910.
- Tukaram, A., P.B. Chavan¹, B.R. Wadikar, Chavan and G.H. Naik. 2019 Genetic Variability Study in Segregating Generations of Okra (*Abelmoschus esculentus* L.). *Int. J. Curr. Microbiol. App. Sci.*, 8(9): 2270-2275.
- Ullangula, S. 2017. Studies on variability, heritability and genetic advance in okra [*Abelmoschus esculentus* (L.) Moench.]. *Int. J. Curr. Microbiol. App. Sci.*, 6(10): 1834-1838.
- Vrunda, R., I.P. Akshay, R. Snehal, S. Zinzala, J.M. Vashi and B.N. Chaudhari. 2018. Genetic variability, heritability and genetic advance studies in genotypes of okra (*Abelmoschus esculentus* (L.) Moench). *I.J.C.S.*, 6(3): 3319-3321.

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