International Journal of Ecology and Environmental Sciences
www.ecologyjournal.in
Online ISSN: 2664-7133; Print ISSN: 2664-7125; Impact Factor: RJIF 5.28
Received: 20-09-2020; Accepted: 05-10-2020; Published: 21-10-2020
Volume 2; Issue 4; 2020; Page No. 260-264

Assessment of genetic variability in advanced breeding lines of okra for identification of superior genotypes based on fruit yield and its attributing traits (*Abelmoschus esculentus* L. Moench)

Srinivasa Krishna[1*], Gangaprasad S[2], Dushyantha Kumar[3], Nagarajappa Adivappar[4], Mallikarjuna HB[5]
[1] M. Sc. Student, Department of Genetics and Plant Breeding, College of Agriculture, UAHS, Shivamogga, Karnataka, India
[2] Professor, Department of Genetics and Plant Breeding, College of Agriculture, UAHS, Shivamogga, Karnataka, India
[3] Professor, Department of Genetics and Plant Breeding, College of Agriculture, UAHS, Shivamogga, Karnataka, India
[4] Department of Horticulture, College of Agriculture, UAHS, Shivamogga, Karnataka, India
[5] Department of Agricultural Statistics, College of Agriculture, UAHS, Shivamogga, Karnataka, India

Abstract

The present study in okra [*Abelmoschus esculentus* (L.) Moench] was undertaken during *Kharif*, 2019 at ZAHRS, Navile, UAHS, Shivamogga, to study the extent of genetic variability and identification of superior lines among advanced breeding lines in respect to fruit yield and its attributing characters in F_5 lines of different crosses along with checks. The analysis of variance showed a significant amount of variability for all the traits studied in advanced breeding lines. Moderate PCV and GCV were observed for traits *viz.*, number of branches per plant, number of fruits per plant, and fruit weight. High heritability coupled with high genetic advance as per cent mean recorded for number of branches per plant, number of fruits per plant, fruit weight, and fruit diameter revealed that a very significant improvement is possible through selection for all these characters. On the basis of mean performance for fruit yield and its components three advanced breeding lines namely C_7F_5, 10-11-135 and Parbhani Kranthi, which exhibited higher fruit yield per plant, were identified in the crosses for advancing to the next generation.

Keywords: Okra, genetic variability, heritability, genetic advance

Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] is an economically most prominent vegetable crop grown in tropical and subtropical parts of the world. It is mainly grown for its tender fruits, cooked and consumed as vegetables. Okra is a popular vegetable and prominent source of energy**.** It contains vitamins and is a good source of proteins, dietary fiber, carbohydrates, minerals and iodine. The 100 grams of edible okra contains 89.60 g moisture, 0.70 g minerals, 1.90 g protein, 6.40 g carbohydrates, 0.20 g fat, 66 g calcium, 1.20 g fiber, 53 mg magnesium and 6.90 mg sodium (Hassan *et al.*, 2015) [12]. The stem is almost large with bark and fiber, suitable for spinning into the rope and paper and cardboard manufacturing (Chevalier, 1940) [6]. India ranks first in okra production in the world which is grown in 0.51 million ha area with an annual production of 6.09 metric tonnes and productivity of 11.97 tonnes ha^{-1} (INDIASTAT, 2018). But the increasing population of India demands more rate of productivity. Hence, there is an everlasting demand for a suitable variety with respect to yield and quality parameters.

For the improvement in the yield and other characters, knowledge about genetic variability is of great importance. Genetic variability present in a population is of primary importance for any successful selection in plant breeding programs. It is a prerequisite for the valid selection or screening of superior or elite genotypes. In a systematic breeding program, it is essential to identify superior parents for hybridization and crosses to expand the genetic variability to select superior genotypes (Inamullah *et al*., 2006) [13]. More significant variability in crop plants provides an opportunity for selecting desirable genotypes, which results in the development and release of a good number of okra varieties.

The relative values of phenotypic and genotypic coefficients of variation present in a population gives a more dependable idea about the magnitude of variability. Moreover, the estimates of heritability coupled with genetic advance will also serve the purpose. Keeping these things in view, the present investigation was undertaken to assess genetic variability with heritability and genetic advance so as to identify the superior genotypes for the further improvement in crop.

Material and Methods

The experimental material of the present study consists of 16 advanced genotypes. The experiment was carried out at ZARHS, College of Agriculture, University of Agricultural and Horticultural Sciences, Shivamogga during *kharif* 2019. The genotypes were grown in a Randomized Complete Block Design (RCBD) with two replications with a spacing of 45 × 30 cm. All the agronomic recommended package of practices was taken up to raise a healthy crop. Data were recorded on randomly selected five plants from each genotype on days to first flowering, days to maturity, plant height at maturity (cm), number of branches per plant, number of internodes, number of fruits per plant, fruit weight (g), fruit diameter (mm), fruit length (cm), number of ridges per fruit, number of seeds per fruit and yield per plant (g). The mean values for all characters were analysed for their variance as per the standard statistical procedure (Cochran and Cox, 1957) [7]. Estimates of phenotypic and genotypic coefficients of variation were estimated as per the standard formulae suggested by Burton and De vane (1953) [5]. Broad sense heritability and genetic advance were calculated according to the formula suggested by Falconer (1981) [10] and Johnson *et al.* (1955) [15], respectively.

Results and Discussion

The analysis of variance revealed highly significant differences among 16 genotypes for 11 quantitative characters in okra out of 12, except number of ridges per fruit indicating sufficient amount of variability among the genotypes (Table 2). In other words, the performance of the genotypes was statistically different with respect to these traits, suggesting that there is an abundant scope for selection of different characters for the improvement in okra. This corroborates findings of Dakahe *et al*. (2007) [8] for number of internodes, Balai *et al.* (2014) [4] for plant height at maturity, number of seeds per fruit, fruit length, fruit weight and days to maturity, Prashanth *et al.* (2017) for number of branches per plant, fruit diameter, number of fruits per plant and fruit yield per plant.

The measures of variability like range of mean values, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2), genetic advance (GA) and genetic advance as per cent of mean (GAM) are depicted in Table 3. For all the characters studied, the ranges of mean values were showed sufficient variation. In the present study, the maximum range of variability was observed for yield per plant (146.64 to 343.52) followed by plant height at maturity (45.80 to 95.60), number of seeds per fruit (40.10 to 54.00) and fruit weight (9.03 to 19.13) indicating the presence of variability for these characters offers ample scope for selecting better genotypes.

Phenotypic coefficient of variation was found to be more than genotypic coefficient of variation for all significantly varied traits depicting the effect of environment on expression of the characters. These results were in accordance with that of Adiger *et al*. (2011) [1] and Kumar *et al*. (2014) [1]. The PCV estimates were relatively high for plant height at maturity and yield per plant. It indicates a higher magnitude of variability present in the experimental material included in the study. Similar findings of PCV was also reported by Reddy *et al*. (2012) [20], Sravanthi (2016) [22] and Kumar *et al*. (2019) [4]. High values of GCV were observed for yield per plant and moderate GCV for number of fruits per plant and fruit weight, which were similar with findings of Khajuria *et al.* (2015) [16].

Heritability is the only component to get transmitted to next generation and in the broad sense, it is also referred to as "degree of genetic determination". Heritability is the hereditary portion of phenotypic variance and is a useful index of transmission of characters from parents to offsprings (Falconer, 1981) [10]. In the advanced lines studied, high heritable characters found were days to first flowering, number of branches per plant, number of internodes, number of fruits per plant, fruit weight, fruit diameter, fruit length, number of ridges per fruit, number of seeds per fruit and yield per plant. The results of heritability were close to those of Reddy *et al*. (2012) [20], Jindal *et al.* (2010) [14], Koundinya *et al.* (2013) [17] and Shivaramegowda *et al*. (2016) [21]. Moderate heritability observed for plant height at maturity by Kumar *et al*. (2019) [16] and for days to maturity by Yonus *et al*. (2014) [23]. Hence, there is abundant scope for improving these traits with direct selection.

The heritability estimate provides knowledge about the magnitude of inheritance of quantitative characters. But it does not designate the extent of genetic gain obtained by selecting the best individuals from best population. And hence, heritability estimates more beneficial than the heritability alone when accompanied with genetic advance (Johnson *et al.*, 1955) [15]. High Genetic advance as per cent mean was observed for plant height at maturity, number of branches per plant, number of fruits per plant, fruit weight, fruit diameter and yield per plant, which were in close agreement with Reddy *et al*. (2012) [20]. These results helps to predict the extent of development that can be achieved by improving different characters. High heritability coupled with high genetic advance were recorded for number of fruits per plant, fruit weight, fruit diameter, number of seeds per fruits and yield per plant suggested the preponderance of additive genes. It also indicated a higher response for selecting high yielding genotypes as additive gene actions govern these traits and selection might be effective.

On the basis of mean performance for fruit yield per plant and its components three germplasms namely C_7F_5, 10-11-135 and Parbhani Kranthi were found to be horticulturally superior, which can be utilized for the development of open pollinated varieties or hybrids (Table 4). Through the study of various genetic resources available, several researchers have stressed about the potential of improvement in okra (Ariyo, 1990; Hamon, 1991) [3]. Dhankar and Mishra (2006) [9] directly released some exotic collections as primary introductions in India from USA namely Perkin's Long Green and Clemon's spineless. Based on mean performance for pod yield and its components and acceptable pod quality traits, ten germplasm lines namely IC282248, IC27826-A, IC29119-B, IC31398-A, IC45732, IC89819, IC89976, IC90107, IC99716 and IC111443 identified for making the selection to fix the desirable characters and to exploit for developing suitable parental materials (Reddy *et al*., 2012) [20].

The significant superior performance of advanced lines was due to the contribution of some component characters. The main contributor for increasing fruit yield per plant were found to be number of fruits per plant followed by fruit weight, number of branches per plant and fruit length (Table 5). It indicates that the parents possess divergent alleles and additive genes governing the respective characters. These genes inherited through further generations would be fixed and the superior advanced lines with the beneficial alleles were brought into a single genotype. Rigorous selection and evaluation of these lines for different characters and preference for yield are required to arrive at a desirable plant type.

The above findings suggested that the germplasm utilized in the present investigation possessed considerable genetic variations. The estimates of mean, range, coefficients of variation, heritability, genetic advance and genetic advance as per cent of mean for all characters showed an evidence of significant variations. The genetic variability of different characters in relation to fruit yield per plant will be worthwhile for future genetic improvement of okra and the traits showing high heritability with high genetic advance should be utilized in direct selection. On the basis of mean performance for fruit yield per plant and its component traits, three germplasms namely C_7F_5, 10-11-135 and Parbhani Kranthi could be advanced to next generation for isolating high yielding genotypes and the homozygous stable lines identified can be proposed for a multilocation trial.

Table 1: List of Advanced breeding lines (F_5) of okra (*Abelmoschus esculentus* (L.) Moench) utilized for genetic variability analysis.

Sl. No.	Advanced breeding lines		
1	Varsha Upahar × GOA (C_1F_5)	9	NOK-11-1008
2	Varsha Upahar × GOA (C_2F_5)	10	10-11-135
3	Pusa Makmali × K. K (C_3F_5)	11	OK-817-220-560118
4	Varsha Upahar × A. A. (C_4F_5)	12	Kashi Birathi
5	Abhay × Parbhani Kranthi (C_5F_5)	13	VROB-178
6	Varsha Upahar × VRU-109 (C_6F_5)	14	Pusa Makmali
7	NO-10-Bulk × Parbhani Kranthi (C_7F_5)	15	Kashi Sathodhata
8	NOK-11-1007	16	Parbhani Kranthi

Table 2: Analysis of variance for yield and its contributing characters in 16 F_5 advanced breeding lines of different crosses in okra

Source of variation	df	Days to first flowering	Days to maturity	Plant height at maturity (cm)	Number of branches per plant	Number of internodes	Number of fruits per plant	Fruit weight (g)	Fruit diameter (mm)	Fruit length (cm)	Number of ridges per fruit	Number of seeds per fruit	Yield per plant (g)
Replication	1	0.0100	3.5112	2.6449	0.1012	0.0112	0.0112	0.0001	0.0024	0.0153	0.0000	1.1249	420.7557
Genotype	15	6.8853**	5.9892**	322.9676**	0.5145**	0.7539**	9.7839**	14.3605**	0.1010**	1.8303**	0.0000	25.6770**	4928.0450**
Error	15	1.1146	1.8445	38.6183	0.0425	0.0312	0.2245	0.4020	0.0042	0.1686	0.0000	3.2876	432.7323
CD (5%)		2.2503	2.8948	13.2456	0.4398	0.3768	1.0101	1.3514	0.1384	0.8753	0.0000	3.8647	39.5200
CD (1%)		3.1111	4.0021	18.3121	0.6081	0.5209	1.3965	1.8684	0.1913	1.2101	0.0000	5.3430	53.9100
CV		2.10	2.45	7.33	5.52	2.05	2.79	4.57	4.19	3.46	0.00	3.73	8.39

* Level of significance at 5 % ** Level of significance at 1%

Table 3: Genetic variability parameters for yield and its attributing traits in F_5 advanced breeding lines of different crosses in okra

Sl. No.	Characters	Range		Co efficient of variation		h^2 (bs) (%)	GA	GAM (%)
		Max	Min	PCV (%)	GCV (%)			
1	Days to first flowering	45.00	51.90	4.10	3.53	73.90	3.01	6.25
2	Days to maturity	53.50	59.50	3.53	2.54	51.90	2.11	3.77
3	Plant height at maturity (cm)	45.80	95.60	20.99	15.78	56.50	18.08	24.43
4	Number of branches per plant	2.80	2.70	17.76	16.88	90.30	1.09	33.05
5	Number of internodes	8.45	8.10	7.65	7.37	92.80	1.18	14.64
6	Number of fruits per plant	16.20	13.10	14.12	13.84	96.10	4.47	27.95
7	Fruit weight (g)	9.03	12.68	19.47	18.92	94.50	5.27	37.90
8	Fruit diameter (mm)	16.20	13.30	14.37	13.74	91.50	0.42	27.09
9	Fruit length (cm)	12.20	11.20	8.54	7.80	83.40	1.67	14.68
10	Number of seeds per fruit	52.90	49.10	8.76	7.93	81.90	6.93	14.78
11	Yield per plant (g)	146.64	166.16	24.73	23.26	88.50	101.78	45.08

Where,
PCV = Phenotypic coefficient of variation
GCV = Genotypic coefficient of variation
h^2 (bs) = Broad sense heritability
GA = Genetic advance
GAM = Genetic advance as per cent of mean

Table 4: Superior lines identified for fruit yield per plant in the F_5 advanced breeding lines of different crosses in okra in comparison with check

Sl. No.	Advanced breeding lines	Fruit yield per plant	Increase in yield over Abhay (g / plant)	Per cent of increase over Abhay
1	Varsha Upahar × GOA (C_1F_5)	190.13	-	
2	Varsha Upahar × GOA (C_2F_5)	195.30	-	
3	Pusa Makmali × K. K (C_3F_5)	241.94	-	
4	Varsha Upahar × A. A. (C_4F_5)	194.48	-	

5	Abhay × Parbhani Kranthi (C_5F_5)	246.37	-	
6	Varsha Upahar × VRU-109 (C_6F_5)	199.13	-	
7	NO-10-Bulk × Parbhani Kranthi (C_7F_5)	343.53	133.64	63.67
8	NOK-11-1007	197.52	-	
9	NOK-11-1008	197.88	-	
10	10-11-135	319.16	109.27	52.06
11	OK-817-220-560118	208.86	-	
12	Kashi Birathi	154.65	-	
13	VROB-178	243.06	-	
14	Pusa Makmali	248.74	-	
15	Kashi Sathodhata	187.71	-	
16	Parbhani Kranthi	250.39	40.50	19.29
Mean yield of Check Abhay			209.88	

Table 5: Superior advanced breeding lines of okra with yield attributing characters on fruit yield per plant

Sl. No.	Advanced breeding lines	Number of fruits per plant	Fruit weight (g)	Number of branches	Fruit length (cm)	Fruit yield per plant (g)
1	NO-10-Bulk × Parbhani Kranthi (C_7F_5)	19.80	17.35	4.30	13.10	343.53
2	10-11-135	18.00	17.72	3.90	12.80	319.16
3	Parbhani Kranthi	15.30	16.36	4.30	11.00	250.39
Mean		16.00	13.91	3.30	11.37	225.77
CD @ 5%		1.01	1.35	0.43	0.87	39.52
CV		2.79	4.57	5.52	3.46	8.39

References

1. Adiger SG, Shanthkumar PI, Gangashetty, Salimath PM. Association studies in okra [*Abelmoschus esculentus* (L.) Moench]. Electronic J. Plant Breed. 2011; 2(4):568-573.
2. Anonymous. Indiastat, India Statistics-Statistical Analysis, Data information and facts. New Delhi, 2018.
3. Ariyo OJ. Effectiveness and relative discriminatory abilities of techniques measuring genotype × environment interaction and stability in okra (Abelmoschus esculentus (L.) Moench). Euphytica, 1990; 47:99-105.
4. Balai TC, Maurya IB, Verma S, Kumar N. Correlation and path analysis in genotypes of okra [Abelmoschus esculentus (L.) Mench]. The Bioscan (Supplement on Genetics and Plant Breeding). 2014; 9(2):799-802.
5. Burton GW, DE Vane EH. Estimating heritability in tall Fescue (Festuca aurundinacea) from replicated clonal material. Agron. J. 1953; 45:478-481.
6. Chevalier A. L'origin, la culture et les usage de cinq Hibiscus de la section Abelmoschus. Rev. Bot. Appl. Agric. Trop. 1940; 20:319-328.
7. Cochran WG, Cox GM. Experimental designs, 1957, 127-131.
8. Dakahe K, Patil HE, Patil SD. Genetic variability and correlation studies in Okra [Abelmoschus esculentus (L.)]. The Asian J. Horticulture. 2007; 2(1):201-203.
9. Dhankar BS, Mishra JP. Tropical and sub-tropical vegetables: plant introduction, achievements and opportunities in South Asia. Indian Journal of Plant Genetic Resources. 2006; 19(3):388-396.
10. Falconer DS. Introduction to Quantitative Genetics, 2nd edition, Longman Group Limited, Longman Burnt Mills, Harlow, Essex, England, 1981.
11. Hamon S, Charrier A, Koechlin J, Sloten DH Van, Sloten VDH. Potential improvement of okra (Abelmoschus spp.) through the study of its resources. Plant Genetic Resources, 1991; 86:9-15.
12. Hassan MA, ALI HM. The nutritional composition of three cultivars of okra [Abelmoschus esculentus (L.) Moench] seeds flour. World J Dairy Food Sci. 2015; 10(2):122-131.
13. Inamullah Ahmed H, Muhammad F, Sirajuddin Hassan G, GUL R. Evaluation of heterotic and heterobeltiotic potential of wheat genotype for improved yield. Pakistan J Bot. 2006; 38(4):1159-1168.
14. Jindal SK, Arora D, Ghai TR. Variability studies for yield and its contributing traits in okra [Abelmoschus esculentus (L.) Monech]. Electronic J Plant Breed. 2010; 1(6):1495-1499.
15. Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlations in Soybean and their application in selection. Agron. J. 1955; 47:477-483.
16. Khajuria RK, Sharma JP, Samnotr RK, Kumar S, Ranjit K. Variability studies in okra [Abelmoschus esculentus (L.) Moench]. Electronic J. Plant Breed. 2015; 7(2):226-234.
17. Koundinya AVV, Dhankhar SK, Yadav AC. Genetic variability and divergence in okra [Abelmoschus esculentus (L.) Moench]. Indian J Agri. Sci. 2013; 83(6):685-688.
18. Kumar A, Kumar M, Sharma VR, Singh MK, Singh B, Chand P, *et al*. Genetic variability, heritability and genetic advance studies in genotypes of okra [Abelmoschus esculentus (L.) Moench]. J Pharm. Phyto. 2019; 8(1):1285-1290.
19. Prasath G, Reddy KR, Saidaiah P. Correlation and Path Coefficient Analysis of Fruits Yield and Yield Attributes in Okra [Abelmoschus esculentus (L.) Moench]. Int. J Curr. Microbiol. App. Sci. 2017; 6(3):463-472.
20. Reddy TM, Babu HK, Ganesh M, Reddy CK, Begum H, Reddy PB, *et al*. Genetic variability analysis for the selection of elite genotypes based on pod yield and quality from the germplasm of okra [Abelmoschus esculentus (L.) Moench]. J Agric. Techno. 2012; 8(2):639-655.
21. Shivaramegowda KD, Krishnan A, Jayaramu YK, Kumar V, Yashoda, Hee-Jong K, *et al*. Genotypic variation among okra

[Abelmoschus esculentus (L.) Moench]. Germplasms in South India. Plant Breed. Biotech. 2016; 4(2):234-241.

22. Sravanthi U. Studies on variability, heritability and genetic advance in okra [Abelmoschus esculentus (L.) Moench]. J. Agric. Eng. Food Technol. 2016; 3(4):281-284.
23. Yonus M, Garedew W, Debela A. Variability and association of quantitative characters among okra [Abelmoschus esculentus (L.) Moench] collection in southwestern Ethiopia. J Biol. Sci. 2014; 14(5):336-342.