Genetic variability, character association and path coefficient analysis in okra

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ABSTRACT

A study was conducted to investigate the genetic architecture of different okra assessions for fruit yield and its associated traits. Fourteen parents, consisting of twelve lines and two testers, were crossed using a Line × Tester mating design in the spring-summer season of 2019-20 at Vegetable Research Farm, CCSHAU, Hisar. The resulting twenty-four hybrids were cultivated in a randomized block design with three replications during the rainy season of 2020-21. Fruit yield/hectare showed a significant range from 87.86 to 150.18 quintals with an average of 117.73 quintals. The phenotypic coefficient of variation ranged from 3.91% (test weight) to 20.23% (No. of branches per plant), slightly surpassing the genotypic coefficient of variation, which ranged from 1.98% (test weight) to 12.15% (fruit yield) with high estimate of phenotypic coefficients of variation (PCV) for the number of branches per plant (20.23%) and a moderate estimate of both PCV and genotypic coefficients of variation (GCV) for fruit yield (14.67%, 12.15%), number of fruits per plant (14.34%, 12.06%), respectively. This suggests that the traits studied were more influenced by genetic factors than environmental factors. High heritability coupled with high genetic advance as percentage of mean for traits such as number of fruits/plant (70.74%, 20.89%) and fruit yield/hectare (68.65%, 20.74%) suggested that additive genes play a major role in determining these traits respectively. This indicates that it is possible to select high-yielding genotypes by selecting parents with desirable traits. Fruit yield/hectare displayed positive and significant associations with most of the traits like number of fruits per plant (0.95) and plant height (0.36) at phenotypic levels. The number of fruits per plant, 1000-seed test weight, fruit diameter, and number of branches per plant had the most significant positive effect on fruit yield. Ultimately, such analysis has the potential for deciding selection strategies aimed at enhancing fruit yield.

Key words: *Abelmoschus esculentus* (L.) Moench, correlation, GCV, path coefficient, PCV.

INTRODUCTION

The escalating global demand for highly nutritious and medicinal crops like okra has led to an increasing need for constant breeding programs aimed at producing new and improved varieties to satisfy both societal and economic requirements. Okra (*Abelmoschus esculentus* (L.) Moench) is a popular vegetable crop in India, belonging to the family Malvaceae. The fresh fruits of okra are a rich source of vitamins and minerals, including vitamin C, vitamin K, folate, potassium, and magnesium. A temperature range of 18 to 35°C, is ideal for growth and development of the crop. Its tender fruits are cooked, canned and dehydrated. India is the world's leading producer of okra, with an annual production of 6.87 mMT from an area of 0.55 mha, resulting in a productivity of 12.5 tonnes/ha (FAOSTAT, 6).

To meet the demands of the growing population, it is essential to enhance the production and productivity of crops like okra. However, plant breeders have encountered challenges in improving the crop due to the absence of suitable parents for recombinant breeding programmes. This will help in identification of transgressive segregates that can be used in further breeding programmes. Therefore, the identification of suitable genotypes becomes a pre-requisite for any successful breeding programme. The inefficiencies arise from a lack of adequate knowledge concerning the associations between yield and its component characters, which directly influence the complex quantitative trait of yield. Hence, successful breeding hinges on a comprehensive understanding of genetic diversity and gene interactions, enabling the selection of appropriate parental lines and the design of effective breeding schemes. Key genetic parameters, such as genotypic (GCV) and phenotypic (PCV) coefficients of variation, heritability, and genetic advance, play pivotal roles in facilitating the efficient selection and improvement of the breeding population (Das *et al.*, 3). Correlation and path analysis are useful tools for understanding the association between yield and its components, and their direct and indirect effects, thereby providing a clear understanding of their relationship with yield (Komolafe *et al.*, 8). The outcomes of this study are anticipated to offer valuable understandings on the selection of superior genotypes and the improvement of

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crop productivity in okra. This will be achieved by closing the knowledge divide between yield and its component traits. Consequently, it will facilitate the advancement of more efficient and effective breeding initiatives.

MATERIALS AND METHODS

The research was conducted at the Research Farm of the Department of Vegetable Science at CCS Haryana Agricultural University, Hisar. The experimental location was located at an altitude of 215.2 m above MSL, at 29.10 °N latitude and 75.46 °E longitude above mean sea level. The sea level was marked by extremely high and low temperatures, dryness, and little rainfall. It has a tropical dry climate and is located on the SW monsoon region's outskirts. In the study, 14 okra genotypes, including 12 lines and 2 testers (Table 1) were planted in the spring-summer 2019-20 at a spacing of 60 cm × 30 cm to produce 24 crosses. Seeds from the first season crop were harvested and planted in *kharif* 2020-21 along with a standard check okra hybrid HBH-142 in a Randomized Block Design (RBD) with three replications. Fruit yield and thirteen yield contributing characters were recorded, such as plant height at final harvest, number of primary branches per plant,

Table 1. List of parents and standard check included in the investigation.

Sl. No.	Parent	Source
Lines (Female)		
1.	HB-96-2	Deptt. of Veg. Science, CCS HAU, Hisar
2.	HB-98-1	Deptt. of Veg. Science, CCS HAU, Hisar
3.	HB-11-3-4	Deptt. of Veg. Science, CCS HAU, Hisar
4.	HB-76-2-4	Deptt. of Veg. Science, CCS HAU, Hisar
5.	HB-96-1	Deptt. of Veg. Science, CCS HAU, Hisar
6.	HB-20-3-4	Deptt. of Veg. Science, CCS HAU, Hisar
7.	HM-1	Deptt. of Veg. Science, CCS HAU, Hisar
8..	HM-3	Deptt. of Veg. Science, CCS HAU, Hisar
9.	HB-60-1	Deptt. of Veg. Science, CCS HAU, Hisar
10.	HB-10-2-5	Deptt. of Veg. Science, CCS HAU, Hisar
11.	HBMS-1	Deptt. of Veg. Science, CCS HAU, Hisar
12.	HBMS-2	Deptt. of Veg. Science, CCS HAU, Hisar
Testers (Male)		
1.	Hisar Naveen	Deptt. of Veg. Science, CCS HAU, Hisar
2.	Hisar Unnat	Deptt. of Veg. Science, CCS HAU, Hisar
Standard Check		
1.	HBH-142	Deptt. of Veg. Science, CCS HAU, Hisar

days to 50% flowering, first fruiting node, internodal length, petiole length, fruit length, fruit diameter, average fruit weight(g), number of fruits per plant, average number of seeds per pod, fruit yield (q/ha) and 1000-seed test weight (g). In each replication, five plants were taken at random and tagged, and data for all traits, except fruit yield (q/ha), were recorded from these plants. Fruit yield (q/ha) was determined by multiplying the average fruit weight per plant by the total number of plants per hectare based on the recommended spacing.

The analysis of variance (ANOVA) for each trait was estimated as per Panse and Sukhatme (10). Genetic variability parameters, such as genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV), were computed according to the method described by Burton and De Vane (2). Broad-sense heritability and genetic advance as percentage of mean (GAM) were determined as per Johnson *et al*. (7). Heritability values were categorized as per suggestion of Robinson (15) into low (<30%), moderate (30–60%) and high (>60%), while, GAM values were classified as low (<10%), moderate (10–20%), and high (>20%) as per suggestion of Johnson *et al*. (7). Coefficients of correlation were determined using the variance and covariance components suggested by Al-Jibouri *et al*. (1) to establish the degree of association of characters with yield and yield components. The path coefficient analysis was performed using the formula given by Wright (22) and adopted by Dewey and Lu (5). Data were analysed using R-Studio version 2023.06.2+561 and INDOSTAT.

RESULTS AND DISCUSSION

The analysis of variance and mean squares (*P < 0.01*) revealed significant differences among the genotypes for all thirteen traits of okra, indicating considerable genetic variability present in the experimental material (Table 2). This wide range of variation among genotypes provides plant breeders with ample scope for selection of superior genotypes for crop improvement. Significant variation among okra genotypes for different traits was also reported by Paul *et al*. (11) and Sujata *et al*. (20).

The average mean performance, range and estimates of genetic parameters, including genotypic (GCV) and phenotypic (PCV) coefficient of variation, heritability, and genetic advance as percentage of mean (GAM) were presented in Table 2. An ample amount of variability was observed for all the characters under study like PCV revealed relatively high values in comparison to the corresponding GCV for all the characters studied. However, the differences were narrow for almost all the traits,

Table 2. ANOVA and estimates of phenotypic and genotypic coefficients of variability, heritability and genetic advance as percentage of mean for different traits.

Character	Range		Mean	Coefficient of variability (%)		Broad sense heritability (%)	Genetic advance as % age of mean (GAM)	Mean sum of square		
	Min.	Max.		Phenotypic (PCV)	Genotypic (GCV)			Replication	Genotype	Error
Plant height (cm) at final harvest	74.33	117.6	85.62	10.04	9.83	95.97	19.84	0.07	216.19**	2.98
No. of branches/ plant	2.47	4.55	3.30	20.23	10.54	27.13	11.31	1.49*	0.69**	0.33
Days to 50% flowering	39.82	52.03	44.56	7.75	5.97	60.25	9.46	7.10	26.08**	4.86
First fruiting node	3.93	6.65	5.44	15.60	10.25	43.14	13.87	1.05	1.33**	0.41
Internodal length (cm)	2.85	4.60	3.73	12.63	9.00	50.81	13.22	4.90	21.04**	2.53
Petiole length (cm)	10.70	16.43	13.14	11.97	8.65	52.18	12.87	18.04**	5.07**	1.19
Fruit length (cm)	8.43	11.67	9.89	10.54	7.69	53.27	11.57	3.95**	2.24**	0.51
Fruit diameter (cm)	1.35	1.61	1.46	6.53	3.56	29.66	3.99	0.11**	0.02**	0.01
Average fruit weight (g)	8.07	9.01	8.59	4.05	2.17	28.66	2.39	0.28*	0.19**	0.09
No. of fruits / plant	15.00	25.33	20.83	14.34	12.06	70.74	20.89	4.27	21.43**	2.59
Average No. of seeds per pod	36.50	51.50	44.82	9.39	6.63	49.82	9.64	63.66**	35.25**	8.86
Fruit yield (q/ ha)	87.86	150.18	117.73	14.67	12.15	68.65	20.74	74.93	708.39**	93.59
Test weight (g)	55.33	62.00	59.54	3.91	1.98	25.78	2.08	77.71**	8.20**	4.01

which implied that there was little or no influence of environmental factors on phenotypic expression of these traits (Komolafe *et al*., 8). While some traits, *i.e.* number of branches per plant, first fruiting node and fruit diameter exhibited more difference between PCV and GCV indicating more influence of environment for governing of these traits. PCV ranged from 3.91 to 20.23%, reflecting the extent of phenotypic variability. GCV ranged from 1.98 to 12.15%, indicating presence of low to medium genetic variability. Values exceeding 20% of both PCV and GCV were categorized as high, while values falling within the range of 10-20% and below 10% were designated as medium and low, respectively (Deshmukh *et al*., 4; Sivasubramaniah and Meron, 19). Based on this categorization, a careful examination of the experimental outcomes revealed a high estimate of PCV for the number of branches per plant (20.23%) and a moderate estimate of both PCV and GCV, respectively for fruit yield (14.67%, 12.15%), number of fruits per plant (14.34%, 12.06%) and first fruiting node (15.60%, 10.25%). However, a moderate PCV was observed for plant height at final harvest (10.04%), internodal length (12.63%), petiole length (11.97%) and fruit length (10.54%), whereas the number of branches per plant showed moderate GCV with a value of 10.54%. Days to 50% flowering (7.75%, 5.97%), fruit diameter (6.53%, 3.56%), average fruit weight (4.05%, 2.17%), average number of seeds per pod (9.39%, 6.63%), and test weight (3.91%, 1.98%) displayed low values for both PCV and GCV, respectively. On the other hand, plant height at final harvest (9.83%), internodal length (9.00%), petiole length (8.65%), and fruit length (7.69%) exhibited low GCV values. In okra, Vani *et al.* (21) observed that the PCV ranged from 2.70 to 19.08%, slightly surpassing the GCV which ranged from 1.22 to 18.97%. These results were also consistent with previous findings by Shwetha *et al*. (18) and Setu (16) in okra.

The genetic coefficient of variation (GCV) was not sufficient to measure the heritable portion of a genotype. Heritability estimates and genetic advance as percentage of mean (GAM) were more effective and reliable indicators of the improvement that could be achieved through selection (Johnson *et al*., 7). Heritability estimates indicated the extent to which the trait was influenced by genetics, while genetic advance as percentage of mean (GAM) estimated the expected improvement in the trait due to selection. Values of heritability and GAM varied from 25.78 to 95.97% and 2.075 to 20.89%, respectively (Table 2).

The data revealed high heritability estimates for plant height (95.97%) followed by number of fruits per plant (70.74%), fruit yield (68.65%) and days to 50% flowering (60.25%). Moderate estimates of heritability were recorded for fruit length (53.26%), petiole length (52.18%), internodal length (50.81%), average number of seeds per pod (49.82%) and first fruiting node (43.14%), which denotes high proportion of additive genetic components in the inheritance of these attributes. This means that selection for these traits based on phenotypic performance could have been more effective for improving okra. The highest estimate of GAM was observed for number of fruits per plant (20.89%) and fruit yield per hectare (20.74%). High heritability and GAM for these traits suggested their control by additive genes, indicating that selecting high-yielding genotypes would enhance these traits. In contrast, traits such as plant height had high heritability but low GAM, implying non-additive gene influence. Consequently, hybrid breeding will be rewarding for the improvement of these traits instead of simple selection. High heritability and high genetic advance

for different traits like number of fruits per plant and fruit yield were also reported by Reddy *et al.* (14), whereas Komolafe *et al.* (8) found similar results for the traits *viz.,* plant height and days to 50% flowering.

Correlation and path analysis ascertain the degree of connection between yield and its constituent factors, revealing both the direct and indirect impacts and highlighting their relative significance. Consequently, this analytical approach provides clear insights into the relationship with grain yield. Ultimately, such analysis can assist breeders in formulating effective selection strategies aimed at enhancing grain yield. Fruit yield, a complex poly-genetically controlled trait and as a dependent variable is influenced by various yield contributing traits, resulting in significant alterations in its magnitude and direction. An increase in number of fruits per plant ultimately increased the fruit yield (q/ha). From results it was visible that number of fruits per plant (0.95) and plant height (0.36) displayed positive and significant associations with the fruit yield at phenotypic levels (Fig. 1). Additionally, plant height exhibited positive associations with petiole length (0.51), internodal
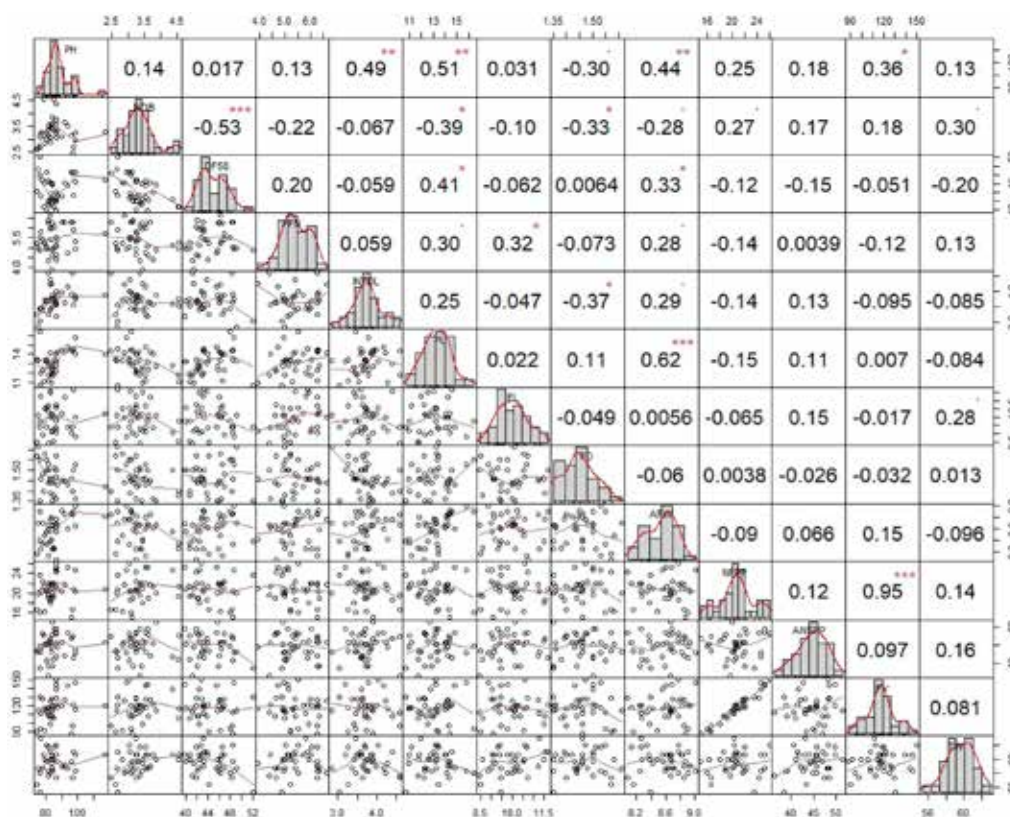
Fig. 1. Phenotypic correlation coefficients among different characters in okra.

[PH: Plant height at final harvest (cm), NOB: No. of branches per plant, DF50%: Days to 50% flowering, FFN: First fruiting node, INTDL: Internodal length (cm), PL: Petiole length (cm), FL: Fruit length (cm), FD: Fruit diameter (cm), FW: Av. fruit weight (g), NFPP: No. of fruits per plant, ANSPP: Av. No. of seeds per pod, TW: Test weight (g)]

length (0.49), and average fruit weight (0.44). The days to 50% flowering were positively associated with petiole length (0.41) and average fruit weight (0.33) at the phenotypic level. The petiole length showed a highly significant positive correlation with average fruit weight (0.62) at the phenotypic level. The characters which had non-significant correlations suggest that they are independent of each other. The findings collaborated with previous studies of Raval *et al*. (13) and Shinde *et al*. (17), who also observed positive associations between most traits and fruit yield, suggesting that selecting these traits could substantially enhance fruit yield.

A path coefficient analysis of the twelve characters was conducted to determine their direct effects on fruit yield (Table 3). Five characters had a positive direct effect on fruit yield, while seven characters had a negative direct effect. Notably, the number of fruits per plant had the highest positive direct effect (0.981), followed by test weight (0.051), fruit diameter (0.020), and number of branches per plant (0.005). On the other hand, days to 50% flowering (-0.008), first fruiting node (-0.014), internodal length (-0.007), petiole length (-0.076), fruit length (-0.005), average fruit weight (-0.096), and average number of seeds per plant (-0.019) exhibited negative direct effects on fruit yield. Komolafe *et al*. (9) reported that the number of pods per plant had the highest positive direct effect (0.96) on pod yield per plant. Earlier, Rana *et al*. (12) also reported similar results in okra.

The study found that there was a high degree of variability among the okra genotypes for most of the traits studied. The trend of phenotypic coefficient of variation (PCV) was almost similar to the genotypic coefficient of variation (GCV), with the PCV being slightly higher for most traits, indicating that most of the traits studied were more influenced by genetic factors than the environmental factors. Some traits like number of fruits per plant and fruit yield per hectare exhibited high heritability coupled with high genetic advance as a percentage of mean (GAM). This showed that the traits were under the predominant control of additive genes, and there was a great scope for selection for these traits. However, days to 50% flowering exhibited high heritability but low GAM, whereas, internodal length (cm), first fruiting node, petiole length (cm), and fruit length (cm) exhibited medium heritability and GAM implying non-additive gene influence. Consequently, simple selection procedures may not be effective for improvement of these traits, but hybrid breeding could improve them. Phenotypic correlation coefficients between fruit yield and most of the traits were found significant. The number of fruits per plant, test weight, fruit diameter, and number of branches per plant had the most significant positive effect on fruit yield. This indicates that it is possible to select high-yielding genotypes by selecting parents with desirable traits. Therefore, the present study suggested that plant height, number of branches per plant, number of fruits per plant and average fruit weight, which are the main components of the fruit yield of these genotypes should be given high priority in selection for future breeding programs.

Table 3. Path coefficient for different traits in different okra genotypes.

Trait	PH	NOB	DF50%	FFN	INTDL	PL	FL	FD	AFW	NFPP	ANSPP	TW
PH	0.002	-0.002	-0.001	-0.003	-0.003	-0.040	-0.001	-0.007	-0.061	0.128	-0.003	0.010
NOB	-0.001	0.005	0.007	0.007	-0.003	0.047	0.002	-0.009	0.050	0.336	-0.003	0.034
DF50%	0.003	-0.004	-0.009	-0.003	0.001	-0.029	0.004	0.001	-0.034	-0.182	0.003	-0.025
FFN	0.004	-0.002	-0.002	-0.014	-0.001	-0.019	-0.003	-0.001	-0.017	-0.297	0.001	0.016
INTDL	0.008	0.002	0.002	-0.001	-0.007	-0.019	0.000	-0.012	-0.041	-0.099	-0.001	0.003
PL	0.001	-0.003	-0.003	-0.003	-0.002	-0.076	-0.001	0.003	-0.091	-0.216	-0.003	-0.006
FL	0.004	-0.002	0.001	-0.008	0.000	-0.014	-0.005	-0.004	-0.015	0.015	-0.002	0.024
FD	-0.006	-0.002	-0.001	0.000	0.004	-0.012	0.001	0.020	0.028	-0.060	0.001	-0.005
AFW	0.002	-0.002	-0.003	-0.002	-0.003	-0.071	-0.001	-0.006	-0.096	-0.081	-0.002	-0.006
NFPP	0.002	0.002	0.002	0.004	0.001	0.017	-0.008	-0.001	0.008	0.981	-0.001	0.012
ANSPP	0.003	0.001	0.001	0.001	-0.004	-0.014	-0.001	-0.001	-0.009	0.077	-0.019	0.016
TW	0.001	0.003	0.004	-0.004	-0.004	0.009	-0.002	-0.002	0.010	0.232	-0.006	0.051

*and ** significant at 5% and 1% level
[PH: Plant height at final harvest (cm), NOB: Number of branches per plant, DF50%: Days to 50% flowering, FFN: First fruiting node, INTDL: Internodal length (cm), PL: Petiole length (cm), FL: Fruit length (cm), FD: Fruit diameter (cm), FW: Av. fruit weight (g), NFPP: Number of fruits per plant, ANSPP: Average number of seeds per pod, TW: Test weight (g)]

AUTHORS' CONTRIBUTION

Conceptualization of research (SKD); Designing of the experiments (SKD and KY); Contribution of experimental materials (SKD and KY); Execution of field/lab experiments and data collection (KY); Analysis of data and interpretation (A, KY and US); Preparation of the manuscript (KY and DS).

DECLARATION

The authors declare that there is no conflict of interest.

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