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Genetic variability, heritability, and cluster analysis of yield-related traits in okra

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ABSTRACT

The present investigation was undertaken to assess genetic variability, heritability, genetic advance, and genetic divergence among twenty-two okra genotypes evaluated under field conditions during *kharif* 2024-25. The experiment was laid out in a randomized block design with three replications, and data were recorded for ten yield and yield-contributing traits. Analysis of variance revealed highly significant differences among genotypes for all characters, indicating the presence of ample genetic variability. Estimates of genotypic and phenotypic coefficients of variation were high for fruit yield, number of fruits, and number of branches per plant. High heritability coupled with high genetic advance as a percentage of mean was observed for fruit yield per plant, number of fruits per plant, and plant height, suggesting the predominance of additive gene action and effectiveness of direct selection. Multivariate analysis grouped the genotypes into four distinct clusters, with maximum inter-cluster distance observed between clusters III and IV, indicating substantial genetic divergence. Fruit yield per plant contributed the highest proportion to total genetic divergence. Correlation and regression analyses revealed strong positive associations of fruit yield with number of fruits per plant, fruit weight, and fruit length. The identified divergent and superior clusters may be effectively utilized in future hybridization programs to develop high-yielding okra cultivars.

Key words: Okra, genetic variability, heritability, genetic advance, cluster analysis.

INTRODUCTION

Okra (*Abelmoschus esculentus* L. Moench) is one of the most important vegetable crops cultivated extensively in tropical and subtropical regions due to its adaptability, nutritional value, and economic significance. The tender green fruits are rich in dietary fiber, vitamins, minerals, and bioactive compounds, making okra a valuable component of human diets (Kumari *et al.,* 8). India is the world's leading producer of okra, with an area of 0.557 million hectares, production of 7.806 million tonnes, and an average productivity of 14.01 t ha^{-1} during 2025–26 (First Advance Estimates, 5). Despite its importance, productivity levels remain sub-optimal in many regions, primarily due to narrow genetic base and limited exploitation of available variability. Genetic variability is the foundation of any crop improvement program, as it determines the potential for selection and genetic gain. Parameters such as genotypic and phenotypic coefficients of variation, heritability, and genetic advance provide insights into the nature and magnitude of genetic control governing important traits (Deshmukh *et al.*, 6; Nanditha *et al.*, 11). High heritability along with high genetic advance indicates additive gene action and greater effectiveness of phenotypic selection (Singh *et al.*, 17; Bambhaniya *et al.*, 3).

Yield in okra is a complex trait governed by several interrelated characters such as number of fruits per plant, fruit weight, fruit length, and plant height. Therefore, understanding the association and contribution of these traits to fruit yield is essential for formulating effective selection strategies (Reddy *et al.,* 16). Multivariate techniques such as cluster analysis and divergence studies further assist in identifying genetically diverse parents that can be exploited in hybridization programs to generate superior recombinants (Keerthana *et al.,* 7; Lal and Bahadur, 10). In this context, the present study was conducted to quantify the extent of genetic variability among okra genotypes, estimate heritability and genetic advance for yield and its components, examine associations among traits influencing fruit yield, and assess genetic divergence through multivariate analysis to identify promising parents for crop improvement.

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MATERIALS AND METHODS

The experimental material comprised twenty-two diverse okra genotypes collected from local farmers of Maharashtra and Telangana region, evaluated during the cropping season under field conditions during *kharif* 2024-25. The experiment was laid out in a randomized block design with three replications at School of Agriculture, SR University, Warangal Telangana India. Each genotype was grown following recommended agronomic practices to ensure uniform crop stand and minimize environmental variation. Observations were recorded on ten yield and yield-related traits, namely days to first picking (DTP), number of fruits per plant (NFPP), fruit weight (FW), fruit length (FL), fruit diameter (FD), number of nodes per plant (NNPP), plant height (PH), number of branches per plant (NBP), internodal length (IL), and fruit yield per plant (FYPP).

Analysis of variance (ANOVA) was performed to test the significance of differences among genotypes following standard statistical procedures. Genotypic and phenotypic variances, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense), genetic advance, and genetic advance as a percentage of mean were estimated as described by conventional biometrical methods (Kumari *et al.,* 8; Olayiwola *et al.,* 13). Multivariate analysis was carried out using cluster analysis based on Mahalanobis D^2 statistics to assess genetic divergence among genotypes. Inter- and intra-cluster distances were computed, and the relative contribution of individual traits toward total genetic divergence was estimated. Correlation, regression, and graphical analyses were employed to understand relationships among yield and its contributing traits. All the statistical analyses were performed using RStudio (v4.5.2) (Posit team, 14).

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among genotypes for all ten characters studied (Table 1), indicating the presence of substantial genetic variability in the experimental material. The existence of significant variation among genotypes suggests the availability of a broad genetic base that can be effectively utilized in crop improvement programmes through selection and hybridization (Vinay *et al.,* 19; Deshmukh *et al.,* 6; Singh *et al.,* 17). The presence of such variability is a prerequisite for achieving substantial genetic gain through selection.

Estimates of genetic variability parameters are presented in Table 2. The PCV values were marginally higher than the corresponding GCV values for all traits, suggesting a relatively low influence of environmental factors on trait expression and indicating that the observed variability was predominantly genetic in nature (Kumari *et al.,* 8; Bambhaniya *et al.,* 3; Behera, 4). High GCV and PCV were observed for fruit yield per plant, number of fruits per plant, and number of branches per plant, indicating the existence of wide genetic variability for these characters. The high magnitude of variation observed for these traits suggests greater scope for improvement through direct selection (Singh *et al.,* 17; Deshmukh *et al.,* 6; Laharika *et al.,* 9). The strip plot (Fig. 1) further

Table 1: Analysis of variance (ANOVA) for yield and yield-related traits in okra genotypes evaluated under field conditions.

Characteristics	Replication	Genotypes	Error	SE±	CD @ 5%	CD @ 1%
Df	2	21	42			
DTP	0.07	23.59**	1.55	0.72	2.05	2.74
NFPP	1.94	9.90**	1.02	0.58	1.67	2.23
FW	0.09	6.02**	0.43	0.38	1.08	1.45
FL	0.18	4.47**	0.52	0.42	1.19	1.60
FD	0.00	0.04*	0.00	0.03	0.09	0.12
NNPP	0.67	4.03**	0.44	0.38	1.10	1.47
PH	17.97	192.31**	19.76	2.57	7.33	9.79
NBP	0.03	0.46*	0.22	0.27	0.78	1.04
IL	0.14	0.89*	0.10	0.19	0.53	0.71
FYPP	203.90	5165.10**	293.80	9.90	28.24	37.76

*and ** significant at 5% and 1% level

[DTP: Days to first picking, NFPP: Number of fruits per plant, FW: Average fruit weight (g), FL: Fruit length (cm), FD: Fruit diameter (cm), NNPP: Number of nodes per plant, PH: Plant height at final harvest (cm), NBP: Number of branches per plant, IL: Internodal length (cm), FYPP: Fruit yield per plant (g)]

Table 2: Estimates of genetic variability parameters for yield and its contributing traits in okra.

Characters	Mean	Genotypic variance	Phenotypic variance	Genotypic coefficient of variance	Phenotypic coefficient of variance	Heritability (Broad bense)	Genetic advance	Genetic advance as percentage of mean
DTP	48.6	7.35	8.90	5.58	6.14	82.58	5.07	10.44
NFPP	13	2.96	3.98	13.36	15.50	74.28	3.05	23.71
FW	13.2	1.86	2.29	10.36	11.50	81.18	2.53	19.23
FL	12.6	1.31	1.84	9.07	10.73	71.48	2.00	15.80
FD	1.5	0.01	0.02	7.20	8.05	80.00	0.20	13.27
NNPP	12	1.19	1.64	8.97	10.51	72.90	1.92	15.79
PH	64.4	57.52	77.28	11.77	13.64	74.43	13.48	20.91
NBP	1	0.08	0.30	19.54	38.40	25.90	0.29	20.49
IL	6.6	0.26	0.36	7.78	9.18	71.78	0.89	13.58
FYPP	171.8	1623.79	1917.57	23.46	25.49	84.68	76.39	44.46

[DTP: Days to first picking, NFPP: Number of fruits per plant, FW: Average fruit weight (g), FL: Fruit length (cm), FD: Fruit diameter (cm), NNPP: Number of nodes per plant, PH: Plant height at final harvest (cm), NBP: Number of branches per plant, IL: Internodal length (cm), FYPP: Fruit yield per plant (g)]

demonstrates the wide distribution of genotypes for fruit yield and other important agronomic traits, confirming the presence of considerable variation among the evaluated genotypes.

High heritability estimates were recorded for fruit yield per plant (84.68%), days to first picking (82.58%), fruit weight (81.18%), and fruit diameter (80.00%). High heritability indicates that these traits are largely governed by genetic factors and that their phenotypic expression is a reliable indicator of genotypic performance. Fruit yield per plant also exhibited high genetic advance as a percentage of mean (44.46%), suggesting the predominance of additive gene action and indicating that direct phenotypic selection would be effective for improving this trait (Bambhaniya *et al.,* 3; Lal and Bahadur, 10; Olayiwola *et al.,* 13). Number of fruits per plant and plant height also exhibited appreciable genetic advance, indicating their usefulness as selection criteria in breeding programmes aimed at yield enhancement.

The chord diagram (Fig. 2) revealed strong positive associations of fruit yield per plant with number of fruits per plant, fruit weight, and fruit length. These relationships indicate that improvement in these component traits is likely to contribute

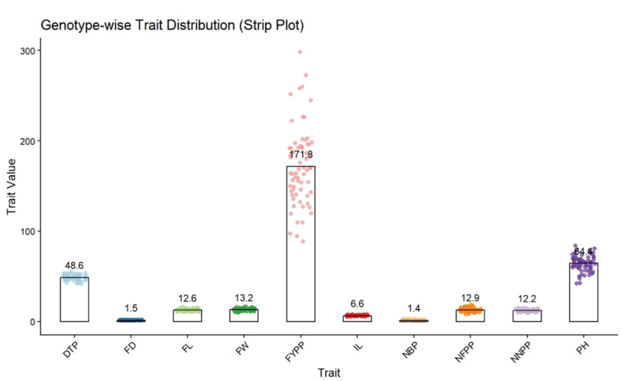

Fig. 1. Strip plot illustrating the distribution and variability of yield and yield-related traits among okra genotypes.

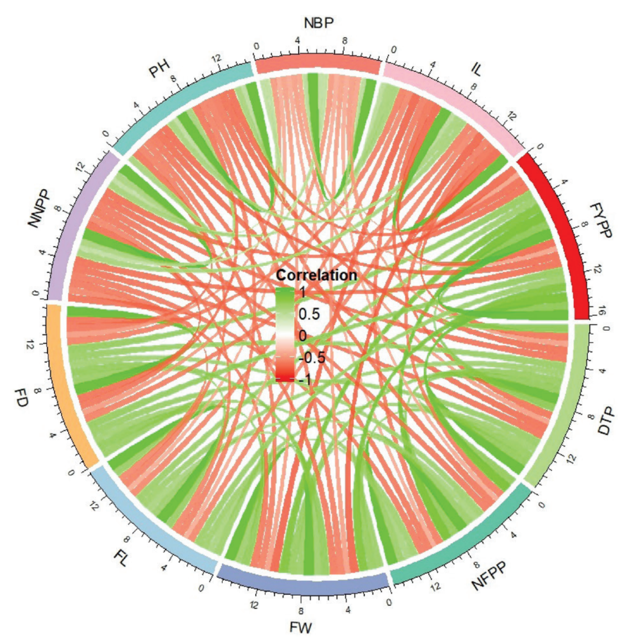

Fig. 2. Chord diagram depicting the relationships and associations among yield and yield-related traits in okra.

directly to enhanced fruit yield. Since yield is a complex quantitative trait governed by several interacting components, indirect selection through strongly associated characters can improve selection efficiency (Abhilash *et al.,* 1; Badiger and Yadav, 2; Kumari *et al.,* 8; Reddy *et al.,* 16). Regression analysis further confirmed the significant contribution of these characters to fruit yield (Fig. 3), suggesting that number of fruits per plant, fruit weight, and fruit length are major determinants of yield performance in okra. Therefore, these traits may be considered reliable selection indices for the development of high-yielding cultivars (Reddy *et al.,* 16).

Cluster analysis grouped the genotypes into four distinct clusters (Table 3; Fig. 5), indicating considerable genetic divergence among the studied material. The occurrence of genetically diverse clusters reflects the existence of substantial variability that can be exploited for broadening the genetic base of breeding populations. Similar clustering patterns and significant genetic divergence among okra genotypes have been reported earlier (Keerthana *et al.,* 7; Neeraja *et al.,* 12; Sravanthi *et al.,* 18). Cluster III recorded the highest mean values for fruit yield per plant and related traits, suggesting its potential as a source of high-yielding genotypes. Inter-cluster distance analysis revealed maximum divergence between clusters III and IV (Table 4), indicating that crosses between genotypes belonging to these clusters could produce superior recombinants. Greater inter-cluster distances generally reflect broader genetic diversity and are expected to enhance heterosis and generate wider variability in segregating generations (Lal and Bahadur, 10; Ranga and Darvhankar, 15; Keerthana *et al.,* 7). The relative contribution of individual traits toward total genetic divergence is depicted in Fig. 4, where fruit yield per plant contributed the maximum share, followed by fruit diameter and days to first picking. These findings are consistent with earlier studies highlighting the dominant role of yield components in genetic divergence of okra (Keerthana *et al.,* 7; Neeraja *et al.,* 12). The combined analysis of variability, association, and divergence suggests that simultaneous selection for fruit yield per plant along with number of fruits per plant, fruit weight, and fruit length would be effective for genetic improvement of okra. Furthermore, hybridization involving genetically divergent and

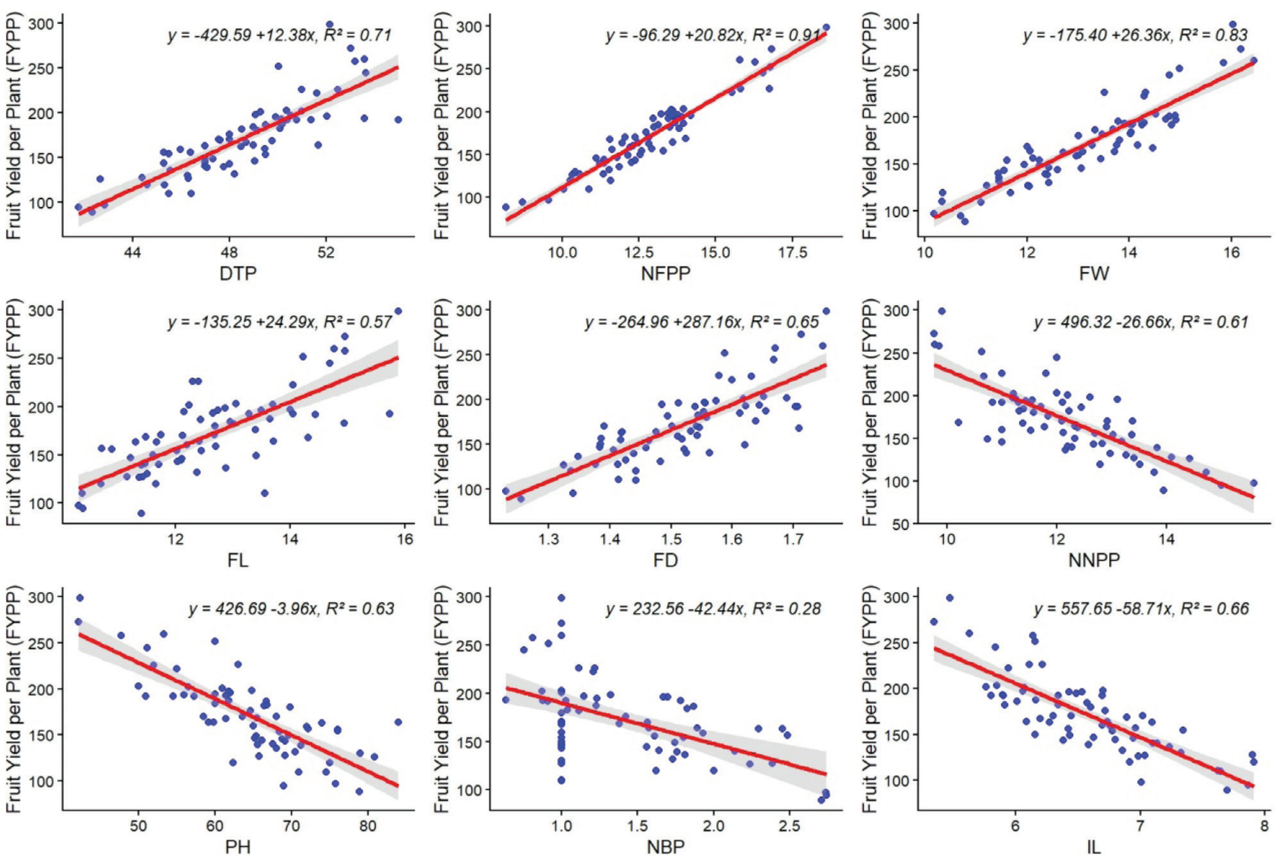

Fig. 3. Regression plot showing the relationship between fruit yield per plant and its contributing traits in okra genotypes.

Table 3: Cluster mean values for yield and yield-related traits among okra genotypes grouped using multivariate cluster analysis.

Cluster	DTP	NFPP	FW	FL	FD	NNPP	PH	NBP	IL	FYPP
1	46.5	12	12.1	11.7	1.4	13	70.7	2	7.0	141.9
2	50.4	14	14.0	13.3	1.6	12	60.1	1	6.3	193.9
3	52.9	17	16.2	15.2	1.7	10	46.0	1	5.5	276.9
4	42.3	9	10.6	10.7	1.3	15	74.5	3	7.5	93.4

[DTP: Days to first picking, NFPP: Number of fruits per plant, FW: Average fruit weight (g), FL: Fruit length (cm), FD: Fruit diameter (cm), NNPP: Number of nodes per plant, PH: Plant height at final harvest (cm), NBP: Number of branches per plant, IL: Internodal length (cm), FYPP: Fruit yield per plant (g)]

Table 4: Inter- and intra-cluster distances among clusters of okra genotypes based on multivariate divergence analysis.

	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Cluster 1	27.73			
Cluster 2	71.48	10.14		
Cluster 3	135.17	297.40	0.00	
Cluster 4	180.18	83.30	381.13	0.00

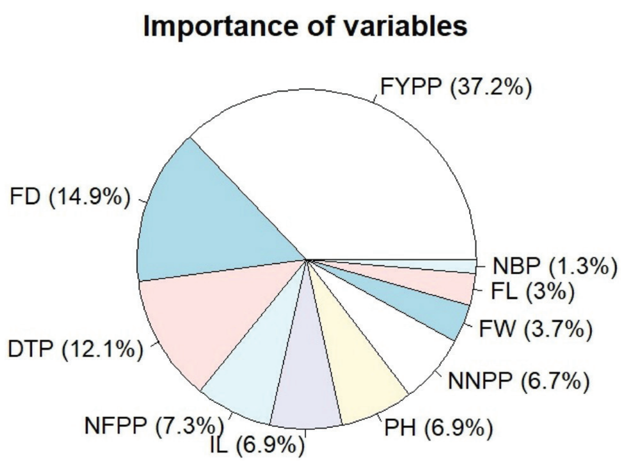

Fig. 4. Percentage contributions of individual traits to total genetic divergence among okra genotypes

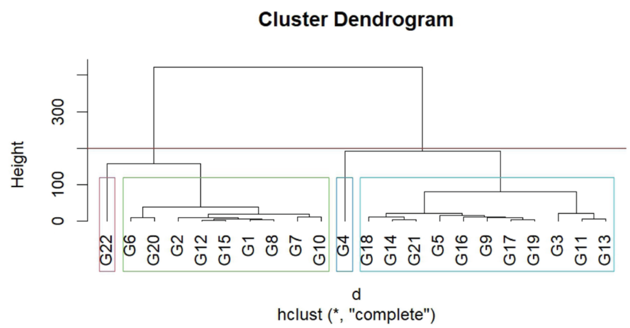

Fig. 5. Cluster dendrogram showing genetic divergence among okra genotypes based on yield and yield-related traits using hierarchical clustering

high-performing genotypes from clusters III and IV may facilitate the development of superior cultivars with enhanced yield potential and wider adaptability.

Overall, the results demonstrated the existence of substantial genetic variability among the evaluated okra genotypes for yield and yield-related traits. High heritability coupled with high genetic advance for fruit yield per plant indicated the effectiveness of direct selection, whereas correlation and regression analyses identified number of fruits per plant, fruit weight, and fruit length as important yield determinants. The considerable genetic divergence observed among clusters, particularly between clusters III and IV, highlights the potential of these genotypes for utilization in future hybridization programmes aimed at developing high-yielding and genetically diverse okra cultivars.

The present investigation demonstrated the existence of substantial genetic variability and divergence among okra genotypes. Fruit yield per plant, number of fruits per plant, fruit weight, and fruit length were identified as important traits for selection and yield improvement. Genotypes belonging to genetically divergent clusters may serve as valuable parental lines for future breeding programmes aimed at developing superior okra cultivars.

AUTHOR'S CONTRIBUTION

Conceptualization of research (K. A. and N. G. W.); Designing of the experiments (K. A., N. G. W., and G. P.); Contribution of experimental materials (K. A., H. V. K., D. S. S. and N. G. W.); Execution of field experiments and data collection (K. A., S. G. S., and H. V. K.); Analysis of data and interpretation (K. A., N. G. W., and K. S. B.); Preparation of the manuscript (K. A. and N. G. W.). All authors reviewed and approved the final manuscript.

DECLARATION

The authors declare that there is no conflict of interest.

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