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Estimation of Path Coefficient Analysis and Genetic Diversity Studies in Okra (*Abelmoschus esculentus* L.)

Y. S. Yadav [a*], Harmanpreet Kaur [b] and S. R. Korake [b]

[a] *Department of Genetics and Plant Breeding, COAS Thane 421401, Dr. BSKKV, Dapoli, India.*
[b] *Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Phagwara-144411, Punjab, India.*

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The purpose of the present study was to evaluate the path analysis and D2 analysis on 20 different okra genotypes, including one check variety. The experiment was carried out during the Kharif season of 2023-2024 at Research Farm, College of Agriculture Saralgaon, Murbad, Thane. A randomized block design with three replications was employed for the study. The observations were recorded on thirteen traits viz., days to 50% flowering, plant height (cm), number of branches per plant, number of internodes, internodal length (cm), fruit length (cm), fruit diameter (cm), average fruit weight (gm), no. of fruits per plant, no. of seeds per fruit, seed index (%), and fruit yield per plant (g). The traits with the highest positive direct effect in phenotypic path coefficient analysis were observed for number of fruits per plant. The genotypic path coefficient analysis revealed

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**Corresponding author: E-mail: yashsingh240490@gmail.com;*

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highest positive direct effect on fruit yield per plant is days to 50% flowering. Thus, these characters need special attention during the time of selection strategy due to their contrasting direct effects. Based on D2 analysis, 20 genotypes were grouped into five clusters. The maximum inter-cluster distance was observed between cluster 5 and cluster 3 indicating that the genotypes falling in these clusters were highly divergent from each other implying a large amount of diversity within and between groups, which could be exploited in breeding programmes. The minimum Inter-cluster distance was found between cluster 5 and cluster 4 indicating that this cluster is less divergent. The cluster means for different characters showed considerable difference among the clusters for all the characters.

Keywords: Okra; path analysis; D2 analysis; clusters.

1. INTRODUCTION

"Okra (*Abelmoschus esculentus* (L.) Moench) (2n = 130) is a member of the Malvaceae family and a staple food in Indian cuisine. Okra, or Lady finger, is a plant that was created when *Abelmoschus tubercyulatus* (2n = 58) and *Abelmoschus ficulneus* (L.), a wild related species native to India with (2n = 72) chromosomes, mated. It is an amphidiploid (allotetraploid) plant. India is the world's largest producer of okra, accounting for around 73.96% of the global okra area" [1]. "Okra is often cross-pollinated, at a rate of 4–19%, and cultivated on 555 thousand hectares in India, producing 6819 thousand MT with an average productivity of 12.07 tonnes per hectare" [2,3].

"After being cooked, okra fruits are commonly utilized in curries and soups. These fruits are abundant in essential nutrients such as vitamin A and C, and riboflavin, as well as minerals like calcium, phosphorus, iodine, iron, and and potassium" [4]. "Fresh okra is highly nutritious, with a composition that includes 86.1 percent water, 0.2 percent fat, 9.7 percent carbohydrates, 2.2 percent protein, 1.0 percent fiber, and 0.8 percent ash" [5]. Additionally, it is a rich source of vitamin C (30 mg/100 g), calcium (90 mg/100 g), and iron (1.5 mg/100 g) [6].

"Plant genetic diversity is commonly assessed by examining morphological and quantitative traits. Mahalanobis' D^2 statistics serve as a valuable tool for identifying clustering patterns, establishing connections between genetic diversity and geographical variation, and exploring the influence of various quantitative traits in defining the maximum degree of divergence among plant populations or varieties" [7,8]. "Path analysis can be a useful tool in this process, as it allows breeders to decide the direct and indirect effects of each trait on yield and to identify which traits have the greatest potential for crop improvement" [9]. Therefore, the main goal of this study was to assess the genetic diversity, and direct and indirect influences of various component traits on okra (*Abelmoschus esculentus*) fruit production.

2. MATERIALS AND METHODS

The experiment was carried out during the *Kharif* season of 2023-2024 at Research Farm, College of Agriculture Saralgaon, Murbad, Thane. This place is situated at 19°16'53.9"N 73°29'41.3"E. This region has a humid subtropical climate with cool winters and long, hot summers. Summers last from April to June and winters from November to February. Temperatures in the summer vary from average highs of around 48 °C (118 °F) to average lows of around 25 °C (77 °F). Winter temperatures have highs of 19 °C to lows of 10°C. The climate is dry overall, except during the brief southwest monsoon season during July and August. The average annual rainfall is about 120 cm.

The experimental material comprised of 20 Okra genotypes grown in randomized block design with three replications during, *Kharif* 2023. The material was planted 75 x 30cm on July 20, 2023. Data were recorded on five random and competitive plants of each genotype from each replication for various characters *viz*. days to first flowering, plant height (cm), number of branches per plant, number of internodes, internodal length (cm), fruit length (cm), fruit diameter (cm), average fruit weight (cm), number of fruits per plant, number of seeds per fruit, seed index (%), and fruit yield per plant (g) which were recorded. Dewey and Lu (1959) were "used to perform the path analysis for grain yield and its components keeping grain yield as the resultant variable and its components as causal variables" [10]. "The genetic divergence was estimated by Mahalanobis (1936) D^2 statistics and the grouping of the genotypes into clusters were done using the Tochers method" [7].

3. RESULTS AND DISCUSSION

3.1 Path Coefficient Analysis

The concept of path coefficient was developed by Wright S. (1921) and the technique was first used for plant selection by Dewey and Lu (1959). Path coefficient analysis can be defined as the ratio of the standard deviation of the effect due to a given cause to the total standard deviation of the effect, also called standard partial regression coefficients which splits the correlation coefficient into the measures of direct and indirect effects, *i.e.,* it measures the direct and indirect contribution of various independent characters on a dependent character. They are free from units, directional, and may be more or less than unity and therefore, enable easy interpretation. The basic assumption of path analysis is that the path diagram utilizes a complete representation of the causal factor involved in determining the product *i.e.*, fruit yield per plant per plant.

3.1.1 Phenotypic path coefficient analysis

The phenotypic path coefficient analysis indicated that several traits had a positive direct effect on fruit yield per plant. The traits with the highest positive direct effects were observed for number of fruits per plant (0.9237), number of internodes (0.3551), fruit length (0.1395), number of branches per plant (0.0924), fruit diameter (0.0377). On the other hand, days to 50% flowering (-0.5475), number of seeds per fruit (-0.4481), internodal length (-0.4194), seed index (-0.2328), plant height (-0.1756), and average fruit weight (-0.0431) exhibited negative direct effects on fruit yield per plant in (Table 1) [11,12,13].

3.1.2 Genotypic path coefficient analysis

The genotypic path coefficient analysis revealed positive direct effects on fruit yield per plant for several traits. Days to 50% flowering had the highest positive direct effect (2.2029), followed by number of fruits per plant (1.5721), seed index (1.4167), plant height (1.3289), average fruit weight (1.1366), number of branches per plant (0.8009), and internodal length (0.6034). On the other hand, the maximum negative direct effect on fruit yield per plant was number of internodes (-1.2314), followed by fruit length (-0.5017), number of seeds per fruit (-0.4087), and fruit diameter (-0.2704) in (Table 2) [14,15,16,17].

3.2 D^2 Analysis

"Genetic factors lead to genetic divergence, which is the foundation for improved heredity. Plant breeders have thus always been captivated by the wide variety of crops that may serve as the foundation for agricultural development initiatives. Accurate knowledge of genetic divergence is necessary for a breeding effort to be successful. It is commonly recognized that in culture media, genetically dissimilar parents result in a higher number of heterotic effects and, thus, attractive recombinants. As Mahalanobis (1936) showed, the D^2 statistic is a metric that quantitatively evaluates genetic diversity between a collection of genotypes in multivariate analysis" [7].

In the present study, 20 genotypes were grouped into 5 clusters by tocher method (Table 3). The maximum Intra-cluster (D^2) was registered for cluster 1 (7.94). The maximum inter-cluster distance was observed between cluster 5 and cluster 3 (15.98) followed by cluster 4 and cluster 3 (13.65), cluster 5 and cluster 1 (13.29), cluster 5 and cluster 2 (13.05), cluster 4 and cluster 1 (12.51), cluster 2 and cluster 1 (11.77), cluster 3 and cluster 2 (11.42), cluster 4 and cluster 2 (10.98), cluster 3 and cluster 1 (10.49) indicating that the genotypes falling in these clusters were highly divergent from each other implying large amount of diversity within and between groups, which could be exploited in breeding programmes. The minimum Inter-cluster distance was found between cluster 5 and cluster 4 (9.30) indicating that this cluster is less divergent (Table 4). The cluster means for different characters showed considerable difference among the clusters for all the characters (Table 5) [18,19,20].

The percentage contribution of 12 characters to total genetic diversity is presented in (Table 6). It was revealed that the main factor contributing to divergence accounting is seed index (48.90%) followed by internodal length (18.47%), Average fruit weight (8.12%), Number of branches per plant (5.04), Fruit diameter (3.93%) [21,22,23,24].

Table 1. Phenotypic direct and indirect effect of different characters on seed yield per plant in okra

S.N.	Characters	Days to first flowering	Plant height (cm)	Number of branches per plant	Number of internodes	Internodal length (cm)	Fruit length (cm)	Fruit diameter (cm)	Average fruit weight (cm)	Number of fruits per plant	Number of seeds per fruit	Seed index (%)	Fruit yield per plant (g)
1	Days to first flowering	**-0.5475**	0.0027	0.1314	-0.0643	0.4294	-0.0345	0.0646	0.0758	0.1702	-0.0098	0.2285	-0.5753
2	Plant height (cm)	0.1002	**-0.1756**	-0.0252	-0.0291	-0.0329	-0.0697	0.0939	0.1241	0.2285	0.0828	0.0781	0.0931
3	Number of branches per plant	-0.0333	0.0228	**0.0924**	0.0490	0.0335	-0.0313	-0.0183	0.0112	0.0117	0.0804	0.0211	0.1666
4	Number of internodes	0.0626	0.0482	0.2162	**0.3551**	-0.0281	-0.0823	-0.0360	-0.0291	-0.0953	0.0745	0.2442	0.0811
5	Internodal length (cm)	0.3116	-0.0399	-0.1367	0.0290	**-0.4194**	-0.0625	-0.1289	-0.0461	-0.2364	0.0744	-0.0749	0.5187
6	Fruit length (cm)	0.0112	0.0471	-0.0443	-0.0322	0.0722	**0.1395**	0.0193	0.0170	0.1239	-0.0285	-0.0377	0.2144
7	Fruit diameter (cm)	-0.0222	-0.0327	-0.0246	-0.0165	0.0386	0.0179	**0.0377**	0.0428	0.0296	-0.0531	0.0049	0.3993
8	Average fruit weight (cm)	0.0275	0.0196	-0.0162	0.0038	-0.0046	-0.0040	-0.0240	**-0.0431**	-0.0227	0.0456	-0.0078	0.2029
9	Number of fruits per plant	-0.3457	-0.1333	0.0196	-0.1965	0.5392	0.1334	0.1948	0.2902	**0.9237**	0.2440	0.2552	0.7883
10	Number of seeds per fruit	-0.0274	0.1793	-0.0621	-0.0751	0.0788	0.0684	0.1576	0.0275	-0.1180	**-0.4481**	0.0278	-0.1391
11	Seed index (%)	0.0783	0.1551	-0.0420	-0.0931	-0.0530	0.0614	-0.0664	-0.0204	-0.0719	0.0317	**-0.2328**	0.2786

R SQUARE = 0.9215 RESIDUAL EFFECT = 0.2802

Table 2. Genotypic direct and indirect effect of different characters on seed yield per plant in Okra

S.N.	Characters	Days to first flowering	Plant height (cm)	Number of branches per plant	Number of internodes	Internodal length (cm)	Fruit length (cm)	Fruit diameter (cm)	Average fruit weight (cm)	Number of fruits per plant	Number of seeds per fruit	Seed index (%)	Fruit yield per plant (g)
1	Days to first flowering	**2.2029**	0.0033	-0.6449	0.3537	-1.8312	-0.2169	-0.2830	-1.0052	-1.5410	0.4649	-0.6351	-0.7712
2	Plant height (cm)	0.0077	**1.3289**	0.2200	0.1302	0.1814	0.5015	-0.3438	-0.3086	-0.2868	-0.6817	-0.7618	0.0771
3	Number of branches per plant	-0.2333	0.1282	**0.8009**	0.5656	0.2606	-0.2830	-0.1102	0.0874	0.0034	0.1069	0.1026	0.1761
4	Number of internodes	-0.2037	-0.1302	-0.8725	**-1.2314**	0.0516	0.5069	0.0376	0.0084	0.4002	-0.2815	-0.5316	0.0147
5	Internodal length (cm)	-0.5020	0.0648	0.2007	-0.0204	**0.6034**	0.0673	0.1676	0.0333	0.3632	-0.1213	0.0116	0.5449
6	Fruit length (cm)	0.0419	-0.1779	0.1716	0.2000	-0.0432	**-0.5017**	-0.0325	-0.0283	-0.0876	0.1166	0.1004	0.2281
7	Fruit diameter (cm)	0.0262	0.0632	0.0306	0.0010	-0.0760	-0.0132	**-0.2704**	-0.0823	-0.0623	0.1507	-0.0206	0.3201
8	Average fruit weight (cm)	-0.5158	-0.2628	0.1282	-0.0189	0.0711	0.0785	0.3708	**1.1366**	0.3377	-0.0738	0.0701	0.4425
9	Number of fruits per plant	-1.1074	-0.3419	0.0077	-0.5130	1.0078	0.3089	0.4031	0.4700	**1.5721**	0.5722	0.3754	0.8104
10	Number of seeds per fruit	-0.0771	0.2008	-0.0486	-0.0855	0.0787	0.1028	0.2238	0.0203	-0.1409	**-0.4087**	0.0170	-0.2064
11	Seed index (%)	-0.4056	-0.8124	0.1714	0.6126	0.2267	-0.3018	0.1450	0.1001	0.3374	-0.0517	**1.4167**	0.2346

R SQUARE = 1.0175 RESIDUAL EFFECT =SQRT (1- 1.0175)

Table 3. Clustering pattern of 20 Okra genotypes & based on Mahalanobis's D^2 statistic

Cluster No.	No. of Genotypes	Genotypes
Cluster 1	13	IC-27879, IC-27898, EC-169355, EC-112112, IC-27831, EC-169481, IC-27878, EC-112241, EC-169468, EC-169364, IC-23594, IC-27874, IC-27877
Cluster 2	4	IC-22285, IC-27881, EC-169499, IC-28359
Cluster 3	1	IC-27875
Cluster 4	1	IC-29117
Cluster 5	1	IC-22283

Table 4. Estimates of average intra and inter-cluster distances for the five clusters in okra

Clusters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	**7.30**	11.77	10.49	12.51	13.29
Cluster 2		**8.06**	11.42	10.98	13.05
Cluster 3			**0.00**	13.65	15.98
Cluster 4				**0.00**	9.30
Cluster 5					**0.00**

Bold figures indicate intra-cluster D^2 value

Table 5. Cluster means for different characters in okra

Cluster No.	Days to 50% Flowering	Days to Maturity	Plant height (cm)	Inflorescence Length (cm)	Branches/ Plant	Biological Yield/ Plant	Harvest Index (%)	Seed Volume Weight (g/10ml)	Protein Content (%)	Seed Yield/ Plant (g)
Cluster 1	40.62	66.93	4.13	9.25	6.16	14.36	5.10	11.14	9.20	46.11
Cluster 2	45.93	71.42	4.14	9.56	5.21	14.52	5.86	11.02	7.58	46.94
Cluster 3	44.00	71.27	4.91	9.91	5.13	14.20	4.23	13.30	7.18	46.18
Cluster 4	40.00	84.67	4.81	8.12	6.13	17.96	5.10	13.10	10.09	44.82
Cluster 5	41.67	95.97	5.77	9.19	6.13	17.79	5.23	10.00	7.12	44.17

Table 6. Contribution of 12 traits of Okra towards divergence

Sr. No.	Source	Times Ranked 1st	Contribution %
1	**Days to first flowering**	3	1.18 %
2	**Plant height (cm)**	9	3.43 %
3	**Number of branches per plant**	13	5.04 %
4	**Number of internodes**	3	1.47 %
5	**Internodal length (cm)**	48	18.47 %
6	**Fruit length (cm)**	6	2.78 %
7	**Fruit diameter (cm)**	10	3.93 %
8	**Average fruit weight (cm)**	22	8.12 %
9	**Number of fruits per plant**	7	2.89 %
10	**Number of seeds per fruit**	0	0.00 %
11	**Seed index (%)**	122	48.90 %
12	**Fruit yield per plant (g)**	9	3.48%

4. CONCLUSION

The traits with the highest positive direct effect in phenotypic path coefficient analysis were observed for number of fruits per plant. The genotypic path coefficient analysis revealed highest positive direct effect on fruit yield per plant is days to 50% flowering. Thus, these characters need special attention during the time of selection strategy due to their contrasting direct effects. The genotypes found in these clusters were substantially varied from one another, suggesting a great deal of variation both within and across groups that might be utilized in breeding programs. The largest inter-cluster distance was found between clusters 5 and 3. Cluster 5 and cluster 4 have the smallest inter-cluster distance, suggesting that this cluster is less divergent. The means of the clusters for the various characters revealed a significant variation between each cluster for every character.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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