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Research Article

Exploring multivariate associations of yield and yield-associated traits in okra (*Abelmoschus esculentus* (L.) Moench) accessions in the Northwestern Region of India

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Abstract
Evaluating genetic diversity simplifies the identification of superior genotypes, facilitating the development of high-yielding, resilient to climatic conditions and promoting effective crop improvement. The present study aimed to examine the divergence, correlation and path analysis across 55 okra (*Abelmoschus esculentus* (L.) germplasms for 17 traits during the summer season (March- July) of 2022**.** The experiment utilized randomized complete block design with three replications conducted in Phagwara, Punjab. Analysis of variance suggested a sufficient amount of genetic variation was found among all genotypes. Using Mahalanobis D^2 analysis, the samples were classified into seven clusters, the largest being cluster I, composing 34 germplasm. Only one germplasm was found in Clusters II, IV, V, VI, and VII. The inter-cluster distance was highest between clusters II and VII, whereas the intra-cluster distance was greatest in Cluster III. The number of fruits per plant had the highest percent contribution to the divergence, accounting for 49.63%. At both phenotypic and genotypic levels, there was a strong positive correlation (+) observed between fruit yield and various characteristics, including plant height, fruit length, number of fruits per plant, number of marketable fruits per plant, average fruit weight, and the number of pickings. Genotypic path analysis revealed that characteristics such as the first flowering node, days to first flowering, days to 50% flowering, plant height, inter-nodal length, number of nodes per plant, number of fruits per plant, marketable fruits per plant, and average fruit weight exhibited a positive and direct effect on fruit yield. When selecting this trait to improve yield in okra through breeding, it is essential to focus on specific characteristics that directly contribute to higher production. This research will help resilient okra varieties understand yield-influencing factors in Punjab environmental conditions.

Keywords: Correlation, Diversity, D^2, Okra, Path Analysis, Variability

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. According to FAOSTAT (2022), India is the world's largest producer of okra, accounting for around 73.96% of the global okra area. Okra is often cross-pollinated, at a rate of 4–19% (Fufa, 2019) and, is cultivated on 555 thousand hectares in India, producing 6819 thousand MT with an average productivity of 12.07 tonnes per hectare (Agriculture Statistics at a Glance 2022). 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 (Sun *et al*., 2023). Correlation studies can help identify traits positively or negatively associated with fruit yield. This study helps breeders identify which traits are most strongly associated with fruit yield and, thus, which traits to select to improve the yield (Sunil *et al*., 2019). 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 (Vinod and Gabriyal, 2023). Therefore, the main goal of this study was to assess the genetic diversity, correlations, and direct and indirect influences of various component traits on okra (*Abelmoschus esculentus)* fruit production.

MATERIALS AND METHODS

Methodology

The study employed a complete randomized block design, incorporating 55 okra genotypes (Table 1). This study was conducted during the summer (March to July) of 2021-2022 at the School of Agriculture, Lovely Professional University, Punjab. Seeds were sown by dibbling 2-3 seeds per hole, spaced 45 x 30 cm. Each genotype was planted in three replications in Randomized Block Design (RBD) spaced at 60 x 30 cm.

A list created by the International Plant Genetic Resources Institute (IPGRI), especially for okra, was used for the study. Yield-contributing factors were seen in five plants per entry from all three replications, *viz*., first flowering node, first fruiting node, plant height, internodal length, number branches, number nodes per plant, fruit length (cm), fruit diameter (nm), number of ridges per fruit, marketable fruits plant^{-1}, number of fruits plant^{-1}, average fruit weight, number pickings plant^{-1}, and fruit yield per plant, traits such as days to first flowering, days to 50% flowering, and days to first fruit harvest, which were collected and observed per plot. *viz*., FFN: First flowering node, FFRN : First fruiting node, DFF: Days to first flowering, D50F: Days to 50% flowering, DFFH: Days to first fruit harvest, PH: Plant height, INL: internodal length, NB: number branches, NON: Number nodes per plant, FL: Fruit length (cm), FD: Fruit diameter (nm), NRG: Number of ridges per fruit, MFP: Marketable fruits plant^{-1}, NFP: Number of fruits plant^{-1}, AFW: Average fruit weight, NPS: Number pickings plant^{-1}, and FYP: Fruit yield per plant.

Statistical analysis

The study computed the mean values from each replication and employed a randomized block design to assess the variance among germplasms (Panse and Sukhatme,1969). The analysis of variance (ANOVA) was conducted using the agricolae package in the R software environment (Mendiburu, 2021). To explore the relationships between various attributes, Pearson's

Table 1. List of fifty-five germplasm of okra taken in present study

Denotation	Germplasm	Denotation	Germplasm	Denotation	Germplasm	Denotation	Germplasm
O1	EC169450	O16	IC058235	O31	IC049972	O46	Salkeerthi
O2	EC169452	O17	IC058704	O32	IC049734	O47	Hisar Naveen
O3	EC169453	O18	IC058710	O33	IC049749	O48	Pusa sawani
O4	EC169455	O19	IC058712	O34	IC052298	O49	Arka Anamika
O5	EC169456	O20	IC058768	O35	IC052313	O50	Kashi Pragati
O6	EC169459	O21	IC086008	O36	IC052308	O51	Dhanvi66
O7	EC169461	O22	IC089712	O37	IC052320	O52	Hinarch
O8	IC052299	O23	IC089712	O38	IC052310	O53	GFS Gold
O9	IC052301	O24	IC045995	O39	P7	O54	Punjab 8
O10	IC052302	O25	IC050418	O40	Hari Kranti	O55	Somya
O11	IC052303	O26	IC046018	O41	Plamkomal		
O12	IC052312	O27	IC048281	O42	Anima		
O13	IC052321	O28	IC048948	O43	Pusa Makmali		
O14	IC052322	O29	IC045993	O44	VRO-4		
O15	IC057733	O30	IC045994	O45	Kasi Kranti		

correlation coefficients were calculated for pairs of variables using the metan (multi-environment trials analysis) package in R (Olivoto *et al*., 2020). To investigate path coefficient analysis, the method proposed by Wright (1921) and further expanded by Dewey and Lu (1959) was employed to estimate the direct and indirect effect of various traits on yield. The variability package in R was used (Popat *et al*., 2020) for calculations. Evaluation of the genetic diversity among 55 genotypes of okra (*Abelmoschus esculentus* (L.)) was calculated using Mahalanobis' D^2 statistics (Mahalanobis, 1936). Rao (1952) was the first to propose applying this method to assess plant genetic diversity. For clustering purposes, hierarchical clustering techniques were employed, as Ward (1963) suggested, using the 'dendextend' package in R (Galili, 2015).

RESULTS AND DISCUSSION

The ANOVA results on 55 okra genotypes, focusing on 17 characteristics, displayed that the mean sum of squares had significant variance at the 1% level, indicating considerable variability among the germplasm across all 17 traits. These results were compatible with previous studies on okra, as reported by Melaku *et al*. (2020) for 25 okra genotypes and Tudu *et al*. (2021) for 22 okra genotypes. The Mahalanobis D^2 analysis split 55 genotypes into seven distinct clusters, which were determined by Tocher's cut-off value, as presented in Table 2. This table provides insight into the distribution of genotypes and the clustering pattern within these different groups. A dendrogram representation of 55 different lady finger genotypes is shown in Fig. 1. Among the seven clusters, Cluster I contained a massive number of germplasms, with 34. Cluster III came next with 17 genotypes, whereas Clusters II, IV, V, VI, and VII each consisted of only one germplasm. Several researchers have previously documented genetic diversity in the okra, including Karthika and Uma Maheswari (2019), who observed seven Clusters among 98 okra (*A. esculentus* (L.) genotypes, in which Cluster VII (51 germplasms) was the largest Cluster, Melaku *et al*. (2022) observed seven Clusters among 25 okra (*A. esculentus* (L.) genotypes in which three clusters are solitary, Rai *et al*. (2022) observed 5 distinct Clusters among the 18 genotypes of okra (*Abelmoschus esculentus* (L.). This finding supports genotypes within the same Cluster demonstrating minimal genetic divergence, indicating high genetic similarity. In contrast, germplasms in different clusters displayed a broader spectrum of genetic variability.

Table 2. Showing Clustering arrangement of 55 different okra genotypes

Cluster No.	No. of genotypes	Germplasm
1	34	O45, O54,O46,O55,O42,O40, O41,O35,O26,O47,O49,O43, O39,O53, O36, O16, O52, O38, O30, O35, O32,027, O10, O8,O29,O44, O7,O14, O4,O12,O15,O13, O34,O48
2	1	O33
3	17	O21, O23, O51, O20,O24,O37, O50,O31,O11,O17,O28,O19, O9,O22, O2,O3,O3
4	1	O1
5	1	O18
6	1	O6
7	1	O5

The specific intra and inter-cluster distances are provided in Table 3. The intra-cluster distances, representing the genetic differences within the same Cluster, varied from 0.00 to 9.64. Cluster III exhibited the highest genetic divergence within its genotypes (9.64), followed by Cluster I with a value of 8.27. In contrast, Clusters II, IV, V, VI, and VIII displayed no genetic divergence within their respective genotypes, as indicated by zero intra-cluster distance. The inter-cluster distances, which estimate the variation across various clusters, varied between 7.89 and 20.22. The greatest distance between clusters was found between Clusters II and VII, recorded at 20.22, then Clusters III and V, which was recorded at 19.75, the distance between Clusters V and VII, measured 19.65, and the distance

Table 3. Showing Inter cluster and Intra (bold) distance of 55 okra germplasm

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
Cluster 1	**8.27**	9.98	15.61	9.96	10.4	12.51	17.22
Cluster 2		**0**	17.53	11.48	11.94	13.91	20.22
Cluster 3			**9.64**	11.83	19.75	14.42	11.9
Cluster 4				**0**	11.17	7.89	12.31
Cluster 5					**0**	12.27	19.65
Cluster 6						**0**	11.61
Cluster 7							**0**

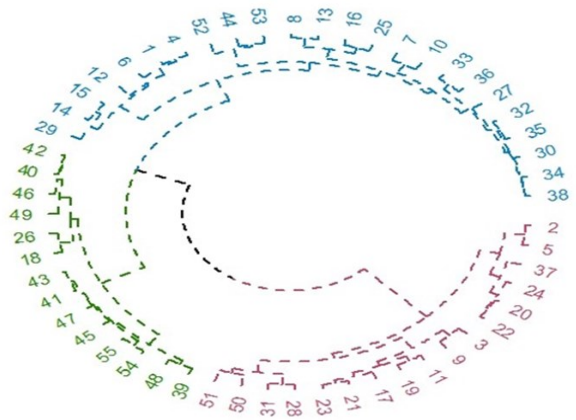

Fig. 1. *Dendrogram reprsenting the clustering of 55 okra genotypes*

between Clusters II and III, recorded was 17.53. On the other hand, the minimum inter-cluster distance was found between Cluster V and VI, which recorded 7.89, followed by Clusters IV and III, which recorded 9.98. A recent study by Saleem *et al*. (2023) found that the greatest inter-cluster distance was identified between Cluster I and Cluster II, with a value of 123.97, among a collection of twenty-four distinct okra (*Abelmoschus esculentus* (L.) germplasms, Munshi *et al*. (2023) found high inter-cluster distance between I and IX among 25 lady finger genotypes. This evidence supports that lower values of genetic distances suggest greater similarities among genotypes from different clusters. Selecting parents from genetically divergent clusters can be a strategic approach to harness the maximum amount of heterosis in breeding programs.

Based on the Cluster mean values presented in Table 4, regarding different genotypic characteristics, genotypes in Cluster I exhibited the highest number of nodes per plant, with an average of 17.17. Cluster II genotypes had favourable traits, including a minimal (desirable) trait day to 50% flowering (40.67 days) and maximum values for plant height (93.83), fruit length (14.5), fruit diameter (18.2), and the number of fruits per plant (26.7). Cluster III and VII did not exhibit the maximum value for any recorded characteristics. Genotypes in Cluster IV recorded the maximum number of branches per plant (5.27). Cluster V genotypes exhibited least mean value are desirable in these traits, such as the first flowering node (4.27), first fruiting node mean (4.87), days to first flowering (37 days) and days to 50% flowering (40.67 days), days to first fruit harvest (47 days) and high mean value desirable traits like number of ridges per fruit (5.53), marketable fruits per plant (26.47), number of pickings mean value (17.33), and fruit yield per plant (343.83).

Among all the clusters, genotypes in Cluster IV recorded the highest average fruit weight (13.07). Cluster VII showed the maximum value for internodal length (5.8). Similarly, Pattan *et al*. (2023) reported their study involved 48 genotypes of okra (*Abelmoschus esculentus* (L.) Moench), revealing that Cluster V exhibited low mean value for days to 50% flowering, Samiksha *et al*. (2020) reported their study involved 17 genotypes of okra (*Abelmoschus esculentus* (L.) Moench), revealed that Cluster III exhibited high mean value for fruit length and number of fruits per plant. These observations provide insights, high mean values, into the diverse characteristics and traits exhibited by the different clusters of genotypes, which can be valuable for breeding and selection purposes. But in situations where traits with lower cluster mean values, traits such as early flowering

Table 4. Cluster mean for different quantitative traits of 55 okra germplasms

	FFN	FFRN	DFF	D50F	DFFH	PH	INL	NB	NON
Cluster 1	4.57	5.10	38.21	41.13	47.57	88.15	5.65	5.12	17.17
Cluster 2	5.13	5.07	39.00	40.67	49.33	93.83	5.63	5.13	16.40
Cluster 3	4.53	5.05	38.42	41.67	47.69	84.49	5.41	5.16	16.72
Cluster 4	4.80	5.20	39.33	43.33	49.33	73.47	5.30	5.27	14.80
Cluster 5	4.27	4.87	37.00	40.67	47.00	72.47	5.57	4.93	15.13
Cluster 6	5.93	6.13	38.67	41.33	48.67	69.30	5.10	5.20	16.20
Cluster 7	5.13	5.80	39.67	44.00	49.33	72.37	5.80	5.07	17.60

	FL	FD	NRG	NFP	MFP	AFW	NPS	FYP
Cluster 1	13.79	15.7	5.2	25.01	23.11	12.71	15.01	317.75
Cluster 2	14.5	18.2	5.07	26.87	24.67	11.4	15.27	306.67
Cluster 3	12.39	16.01	5.24	16.37	14.86	12.31	11.93	200.27
Cluster 4	13.43	15.93	5.07	22.6	20.87	11.97	13.47	269.7
Cluster 5	14.5	16.07	5.53	27.93	26.47	12.33	17.33	343.83
Cluster 6	13.53	17.2	5.47	20.53	18.33	13.07	13.67	268.13
Cluster 7	13.97	15.1	5.47	15.87	13.6	11.13	11.27	176.13

Table 5. Contribution of different quantitative characters towards genetic divergence

S.No	Source	Contribution	S.No	Source	Contribution	S.No	Source	Contribution
1	NFP	49.63%	7	MFP	2.42%	13	D50F	0.34%
2	PH	16.03%	8	FD	2.29%	14	INL	0.34%
3	AFW	13.94%	9	NPS	2.22%	15	NB	0.34%
4	NON	3.64%	10	FFN	1.55%	16	NRG	0.34%
5	DFF	2.96%	11	FL	0.74%	17	FFRN	0.07%
6	FYP	2.49%	12	DFFH	0.67%			

and early fruit maturity, offer advantages, they can be effectively employed in stress breeding programs.

The percentage contribution of each character to the overall divergence is shown in Table 5. Notably, the number of fruits per plant was identified as the most significant contributor, accounting for (49.63%) of the observed divergence among the genotypes, followed by plant height contribution (16.03%), average fruit weight (13.49%), number of nodes per plant (3.64%), days to first flower (2.96%), fruit yield per plant (2.49%), number of marketable fruits per plant (2.42%), fruit diameter (2.29%), number of pickings per plant (2.22%), first flowering node (1.55%), fruit length (0.74%), days to first fruit harvest (0.67%), days to 50% flowering (0.34%), number of ridges per fruit (0.34%), number of branches per plant (0.34%), and internodal length (0.34%). To determine the percentage contribution of traits of ladyfinger (*Abelmoschus esculentus*) to the observed divergence as presented in (Fig. 2). Similar genetic divergence percent results were recorded for days of first fruit harvest by Pattan *et al*. (2023) among 48 genotypes of okra (*Abelmoschus esculentus*), Nanthakumar *et al*. (2021) observed 46 genotypes of okra (*Abelmoschus esculentus* (L.) reported that first fruiting node and days to 50% flowering exhibited comparable findings to the current study. As a result, it is crucial to prioritise features that contribute to divergence traits when selecting parental germplasms for hybridization and during the process of parental selection in segregating generations.

Correlation analysis

The genotypic and phenotypic correlation coefficients between seventeen traits are presented in Table 6. Plant height (r_G = 0.296, r_P = 0.275), fruit length (r_G = 0.723, r_P = 0.583), number of fruits per plant (r_G = 0.956, r_P = 0.935), number of marketable fruits per plant (r_G = 0.957, r_P = 0.934), average fruit weight (r_G = 0.453, r_P = 0.426), and the number of pickings per plant (r_G = 0.854, r_P = 0.759) demonstrated statistically significant positive relationships with fruit yield per plant. Corresponding results were observed previously by Aminu *et al*. (2016) observed 10 genotypes and Komolafe *et al*. (2021) study involved 40 genotypes of okra (*Abelmoschus esculentus* (L.) for plant height and Jadhav *et al*. (2022) observed 50 genotypes of okra (*Abelmoschus esculentus* (L.) for no. of pickings per plant. Understanding the connections between the factors affecting fruit production is crucial for developing a selection-based plant breeding program to boost yield. Yield, being a dependent trait, is influenced by numerous characteristics. Plant breeders can derive substantial advantages from positive associations among desirable traits. Positive correlations indi-

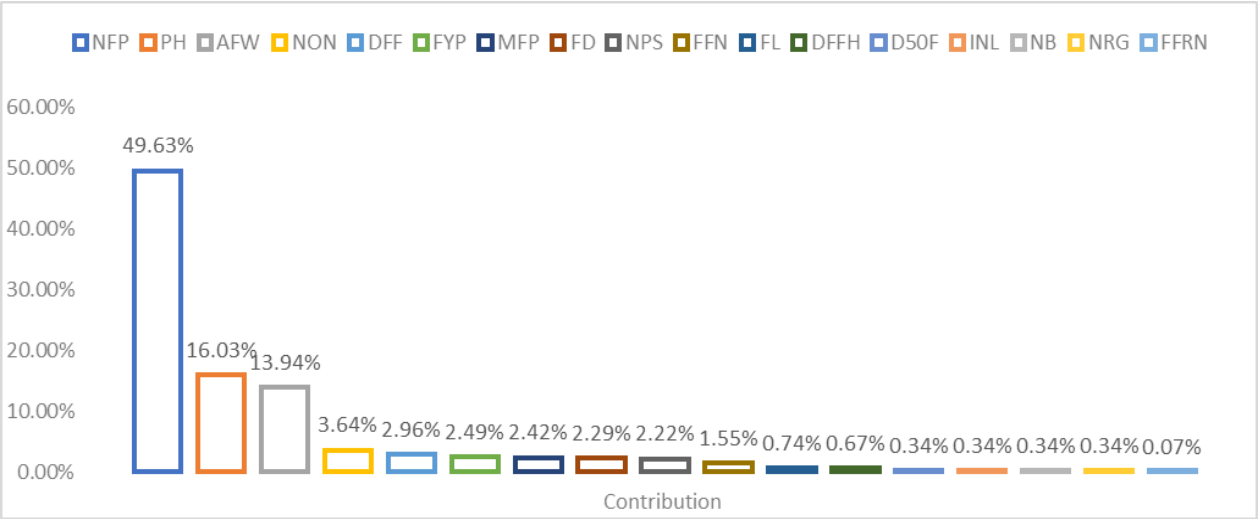

Fig. 2. *Contribution of various characters towards genetic diversity*

Table 6. Association between fruit yield and its component traits at genotypic and phenotypic level

Traits	FFN	FFRN	DFF	D50F	DFFH	PH	INL	NB	NON	FL	FD	NRG	NFP	MFP	AFW	NPS	FYP
FFN	1	-0.218**	-0.185*	-0.212**	-0.373**	-0.229**	**0.296****	0.176*	-0.210**	0.138	0.723**	-0.086	-0.148	0.956**	0.957**	0.453**	0.854**
FFRN	-0.174*	1	0.918**	0.204**	0.272**	0.243**	-0.147	0.227**	-0.202**	-0.035	0.005	0.034	0.133	-0.116	-0.166*	-0.356**	-0.096
DFF	-0.09	0.721**	1	0.068	0.169*	0.102	-0.259**	0.165*	-0.453**	-0.064	-0.045	0.002	0.132	-0.13	-0.182*	-0.237**	-0.018
D50F	-0.174*	0.138	0.038	1	0.909**	0.691**	-0.163*	0.124	0.052	-0.133	-0.111	0.119	-0.239**	-0.182*	-0.215**	-0.168*	-0.144
DFFH	-0.304**	0.187*	0.103	0.857**	1	0.729**	-0.395**	0.209**	-0.109	-0.238**	-0.277**	0.071	-0.203**	-0.336**	-0.378**	-0.267**	-0.318**
PH	-0.15	0.054	-0.014	0.483**	0.462**	1	-0.439**	0.036	-0.116	-0.445**	-0.107	0.387**	0.055	-0.151	-0.148	-0.268**	-0.079
INL	0.275**	-0.092	-0.125	-0.095	-0.301**	-0.222**	1	0.254**	-0.05	0.692**	0.304**	-0.337**	-0.248**	0.327**	0.352**	0.025	0.350**
NB	0.081	0.138	0.028	0.051	0.095	-0.076	0.13	1	0.097	0.379**	0.160*	-0.229**	0.235**	0.224**	0.191*	-0.091	0.240**
NON	-0.113	-0.07	-0.109	0.089	-0.029	-0.036	-0.031	0.056	1	0.073	0.05	-0.336**	-0.014	-0.160*	-0.179*	-0.161*	-0.285**
FL	0.105	0.03	0.026	-0.069	-0.163*	-0.177*	0.639**	0.193*	-0.001	1	0.220**	-0.529**	-0.078	0.118	0.13	0.081	0.075
FD	0.583**	-0.024	-0.051	-0.057	-0.143	-0.036	0.224**	0.084	0.066	0.098	1	-0.284**	0.081	0.742**	0.725**	0.204**	0.663**
NRG	-0.04	0.001	0.046	0.041	0.024	0.102	-0.224**	-0.144	-0.057	-0.181*	-0.169*	1	0.147	-0.062	-0.056	-0.068	-0.005
NFP	-0.084	0.004	0.041	-0.116	-0.142	0.046	-0.104	0.085	-0.07	-0.031	-0.071	-0.042	1	-0.147	-0.097	-0.025	0.107
MFP	0.935**	-0.098	-0.068	-0.147	-0.265**	-0.105	0.302**	0.094	-0.103	0.09	0.566**	-0.042	-0.116	1	0.994**	0.180*	0.896**
AFW	0.934**	-0.127	-0.095	-0.180*	-0.305**	-0.101	0.327**	0.081	-0.121	0.102	0.564**	-0.06	-0.08	0.986**	1	0.206**	0.896**
NPS	0.426**	-0.229**	-0.086	-0.123	-0.209**	-0.137	0.025	-0.017	-0.023	0.05	0.217**	0.013	0.068	0.087	0.122	1	0.199*
FYP	0.759**	-0.079	-0.035	-0.069	-0.199*	-0.052	0.304**	0.154*	-0.091	0.054	0.468**	-0.012	-0.084	0.804**	0.798**	0.126	1

ns p>=0.05*, p<0.05**, p<0.01, and ***p<0.001

Table 7. Showing genotypic path matrix (diagonal and bold are direct effects) for fruit yield per plant in okra, direct and indirect effects of Analysis

Traits	FFN	FFRN	DFF	D50F	DFFH	PH	INL	NB	NND	FL	FD	NRG	NFP	MFP	AFW	NPS
FFN	**-0.018**	0.008	0.000	0.002	-0.001	0.001	0.001	0.001	0.000	0.002	0.000	0.000	-0.089	-0.003	-0.079	0.002
FFRN	-0.013	**0.011**	0.000	0.001	0.000	0.002	0.003	0.001	0.000	0.000	0.001	0.001	-0.062	-0.002	-0.030	0.001
DFF	-0.003	0.000	**0.002**	0.011	-0.006	0.003	0.000	-0.001	-0.001	0.000	0.000	0.000	-0.134	-0.005	-0.043	0.002
D50F	-0.003	0.001	0.002	**0.013**	-0.005	-0.012	0.000	0.000	-0.002	0.001	0.000	0.001	-0.241	-0.008	-0.072	0.006
DFFH	-0.001	0.000	0.001	0.006	**-0.012**	0.004	0.000	0.000	-0.002	0.000	-0.001	0.000	-0.096	-0.003	-0.048	0.002
PH	0.002	-0.001	0.000	-0.004	0.003	**-0.016**	0.001	0.000	0.008	-0.001	0.002	-0.002	0.274	0.008	0.009	-0.009
INL	-0.003	0.000	0.000	0.001	0.001	-0.002	**0.004**	-0.001	0.003	0.000	0.001	0.000	0.085	0.002	-0.006	-0.005
NB	0.001	-0.001	0.001	0.000	0.000	0.001	0.000	-0.013	0.000	0.000	0.000	0.002	-0.093	-0.003	-0.008	0.003
NON	-0.001	0.000	0.000	-0.002	0.002	-0.010	0.001	0.000	**0.013**	0.000	0.001	0.000	0.082	0.003	0.018	-0.002
FL	0.001	-0.001	0.001	-0.002	0.000	-0.004	0.000	-0.001	0.001	**-0.004**	0.001	0.000	0.514	0.014	0.076	-0.015
FD	-0.002	0.001	0.000	0.000	-0.001	0.004	-0.001	0.001	-0.002	0.001	**-0.008**	0.000	-0.038	-0.002	0.005	0.000
NRG	0.000	0.000	0.000	-0.002	-0.001	0.002	0.000	0.001	0.000	0.000	0.000	**-0.004**	-0.105	-0.002	0.024	0.003
NFP	0.002	-0.001	-0.002	-0.003	0.001	-0.005	0.001	0.001	0.001	-0.002	-0.001	0.000	**0.909**	0.025	0.030	-0.025
NMF	0.002	-0.001	0.000	-0.004	0.001	-0.005	0.000	0.002	0.001	-0.002	0.000	0.000	0.896	**0.026**	0.042	-0.025
AFW	0.004	-0.001	0.002	-0.003	0.002	0.000	0.000	0.000	0.001	-0.001	0.000	-0.002	0.079	0.003	**0.347**	-0.004
NPS	0.001	0.000	0.000	-0.003	0.001	-0.005	0.001	0.001	0.001	-0.002	0.002	0.000	0.731	0.020	0.044	**-0.030**

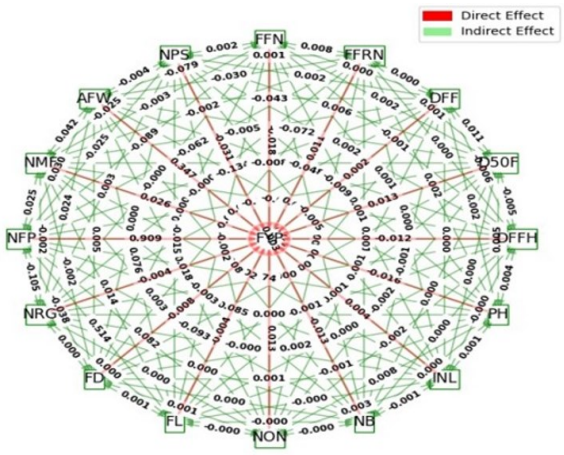

Fig. 3. *Genotypic path diagram of direct & indirect effect on okra fruit yield*

cate that enhancing one specific trait often leads to the simultaneous improvement of related characteristics.

Path analysis

The breeder primarily aims to minimize production potential while having specific defects. Some of them are significant components that directly impact yield, while others have an indirect effect through the development and behavior of other traits. Therefore, it is better to understand how other factors, directly and indirectly, affect yield. Path analysis has been used to identify each feature's relative value and limit the total number of characteristics used in selection programs. Path analysis at the genotypic level can reveal how plant parts work together to produce yield by studying both the direct and indirect effects of genotypic features on yield. The estimates for the path coefficient matrix, are tabulated in Table 7 and represented in Fig. 3.

The positive direct impact on yield was achieved by the first flowering node (0.011), days to taken first flowering (0.002), days to 50% flowering (0.013), internodal length (0.004), no. of nodes (0,013), number of fruits per plant (0.909), number of marketable fruits per plant (0.026), and average fruit weight (0.347). Similarly, Nayak *et al*. (2023) conducted genotypic path analysis, revealed that characteristics such as the first flowering node, days to first flowering, number of nodes, average fruit weight, and the number of fruits per plant exhibited positive direct impact on yield among 46 genotypes of okra (*Abelmoschus esculentus* (L.) Moench), Sujata *et al*. (2019) found that internodal length had a positive direct impact on yield among 33 genotypes of okra (*Abelmoschus esculentus* (L.). Direct selection in plant breeding involves choosing plants for further breeding based on their performance regarding the desired traits so plant breeders can establish a clear link between the selected traits and the desired outcome, such as improved yield in okra.

Conclusion

The present study assessed the genetic diversity of 55 okra (*Abelmoschus esculentus* (L.) Moench) germplasms by examining 17 distinct traits. Cluster III had the highest intra-cluster distance, indicating that the germplasms within this Cluster possess the most diversity. The Clusters II and VII had the highest inter-cluster distance. These two clusters were more diverse, and crossing programs would be effective between the genotypes within these clusters. Number of fruits per plant, plant height and average fruit weight contributed more divergence. This attribute of parents is good for hybridization and segregation generations. The traits like plant height, number of fruits per plant, marketable fruits per plant, and average fruit weight affected yield in both correlation and path analysis; thus, selection for these traits would help increase the fruit yield.

Conflict of interest

The authors declare that they have no conflict of interest.

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