Estimation of Correlation and Path Coefficient Analysis for Quantitative Characters in okra *(Abelmoschus esculentus* L. Moench) Genotypes

Abstract

The purpose of the present study was to evaluate the genetic variability and parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance, as well as perform correlation and path analyses on 20 different okra genotypes, including one check variety. The experiment was conducted during the kharif season of 2022 at the experimental farm of the Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology, and Sciences in Prayagraj, Uttar Pradesh. A randomized block design with three replications was employed for the study. Thirteen characteristics were observed and recorded, which includes: days to first flowering, days to 50% flowering, length of mature fruit (cm), diameter of fruit (cm), average fruit weight (gm), internodal length (cm), number of nodes on the main stem, number of primary branches, plant height (cm), number of fruits per plant, number of seeds per fruit, seed index (gm), and fruit yield per plant (gm). Azad Bhindi-1 exhibited the highest mean performance in terms of fruit yield per plant, followed by GO-3, among all the genotypes. The PCV values were consistently higher than the corresponding GCV values for all traits, indicating the influence of environmental factors on trait expression. Fruit yield per plant and number of primary branches displayed the highest GCV and PCV values. The number of primary branches exhibited both high heritability and genetic advance. The correlation analysis revealed a positive and significant association between number of fruits per plant and fruit yield per plant at both the genotypic and phenotypic levels. The traits with the highest positive direct effects on fruit yield per plant were observed for average fruit weight and plant height, as determined through genotypic and phenotypic path analysis. These identified traits can serve as effective selection criteria for strategizing an efficient breeding programme to enhance fruit yield in okra.

Keywords: okra, phenotypic, genotypic, correlation, heritability.

INTRODUCTION

Okra, scientifically named (*Abelmoschus esculentus* .L Moench) is a member of the Malvaceae family and is commonly referred to as Lady's finger or bhindi. It has a somatic chromosomal number of 2n=130. Okra is widely cultivated in various regions of the world, including temperate, subtropical, and tropical areas (Verma, L *et al.,* (2020) [16]. Okra is primarily a self-pollinated crop, but it has been observed that insect-mediated outcrossing occurs to some degree, ranging from 4 to 19 percent (Choudhury, B *et al* 1970) [5]. This outcrossing contributes to the emergence of significant genetic diversity in the crop. It is a day-neutral plant, cultivated as an annual crop throughout the year in various regions of the country, primarily for its delectable and tender pods (Balai *et al.,* 2015) [4]. The origins of okra are subject to debate, with proponents suggesting its roots in South Asia, Ethiopia, and Africa. However, it is believed that okra originated in the Ethiopian region (De Candolle, (1883) [6] & (Loskutov, (2020) [8].

India is the second largest producer of okra after china. Major crop growing states are Gujarat, Maharashtra, Uttar Pradesh, Andhra Pradesh, Karnataka, Tamil Nadu, Punjab etc. At national level during 2020-21, okra was grown in 531 ha area with 6466 tonnes of production with average productivity of 12.24qt/ha. In the state of Utter Pradesh, it was grown in 24.19 ha area with 325.59tonnes of production with average productivity of 11.30qt/ha **(Source: Agriculture Cooperation and Farmers Welfare (2020-2021)** [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, riboflavin, as well as minerals like calcium, phosphorus, iodine, iron, and potassium (Verma, V *et al* (2020) [16]. 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 (Saifullah, M *et al* (2009) [15]. 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) (Pal, B *et al.,* (1952) [11].

The correlation and path coefficient analyses are essential tools for selecting superior genotypes and improving various traits. In the field of plant breeding, correlation analysis plays a vital role by providing insights into the relationships among yield components. This information aids in the identification and selection of superior genotypes from diverse genetic populations.

Path coefficient analysis permits the separation of correlation coefficient into direct and indirect effects. It is basically a standardized partial regression analysis and deals with a closed system of variables that are linearly related. Such information provides a realistic basis for allocation of appropriate weightage to various yield components.

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1.1 Objectives

The current study aims to achieve the following objectives:

1. To assess genetic variability present in okra genotypes.

2. To estimates the correlation coefficient for fruit yield and its contributing traits.

3. To determine direct and indirect effect effects of yield contributing characters on fruit yield.

2. MATERIALS AND METHODS

The genetic materials used in this study consisted of 20 different genotypes of okra (*Abelmoschus esculentus* L. Moench). The experiment was conducted at the Experimental Farm of the Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology, and Sciences, located in Prayagraj, Uttar Pradesh. The genotypes were planted using a randomized block design with three replications. The row-to-row distance was maintained at 30cm, while the plant-to-plant distance was set at 20cm. Data were recorded on thirteen quantitative traits viz., days to first flowering, days to 50% flowering, length of mature fruit(cm), diameter of fruit(cm), average fruit weight(gm), internodal length(cm), number of nodes per plant, number of primary branches, plant height(cm), number of fruits per plant, number of seeds per fruit, seed index(g), fruit yield per plant(gm) (Table 1). The experimental materials used in the study were collected from the Indian Institute of Vegetable Research (IIVR) in Varanasi. The study was carried out during the *Kharif* season of 2022. It was conducted at the Department Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology, and Sciences in Prayagraj, Uttar Pradesh.The primary objective of the study was to estimate the correlation and path coefficient analysis for various quantitative characters in okra.

The Panse and Sukhatme (1967) method were used to analyse the variance in all of the recorded data for the characters under consideration. Additionally, the genetic parameters genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), Heritability in the broad sense, Genetic advance as percent of mean and correlation analysis was carried out by using the statistical methods. The additional components of variance include phenotypic variance, genotypic variance and Environmental Variance.

The Software called "R – Language" was used to perform the analysis mentioned above.

Table1. List of experimental material used in the present investigation.

The experimental materials for this research were obtained from the Indian Insitute of vegetable Research, Varanasi. The details of the experimental materials are mentioned below in table 1.

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SL.NO	NAMES OF GENOTYPES	SL.NO	NAME OF NAMES
01	Kashi Lalima	**11**	AZAD BHINDI-2
02	HRB-55	**12**	PUNJAB-8
03	VRO-4	**13**	GO-3
04	SB-6	**14**	HRB-231
05	EMS-8-1	**15**	KASHI PRAGATI
06	IIVR-11	**16**	PUNJAB-7
07	BO-13	**17**	UTTAKAL GAURAV
08	AZAD BHINDI-1	**18**	NO-55
09	ARKA ANAMIKA	**19**	PUNJAB SUHAVANI
10	ARKA ABHAY	**20**	KASHI CHAMAN(check)

Source: Indian Insitute of Vegetable Research, Varanasi, (IIVR).

Table 2. Analysis of Variance (ANOVA) Among 20 Okra Genotypes for 13 Quantitative Traits

Sl. No.	Source	Mean Sum of Squares (MSS)		
		Replication	**Treatment**	**Error**
	Degrees of freedom	**2**	**19**	**38**
1	Days to first flowering	2.62	20.56**	1.37
2	Days to 50% flowering	0.82	26.38**	1.55
3	Length of Mature fruit(cm)	1.94	4.44**	1.56
4	Diameter of fruit (cm)	0.02	0.05**	0.01
5	Inter nodal length (cm)	0.08	0.66**	0.21
6	Number of primary branches	0.02	0.41**	0.01
7	Average fruit weight (gm)	10.64	16.76**	5
8	Number of fruits per plant	1.49	8.53**	0.75
9	Number of nodes on main stem	1.99	10.04**	1.00
10	Plant height(cm)	78.63	482.75**	28.16
11	Number of seeds per fruit	48.64	72.49**	16.49
12	Seed index(gm)	0.001	0.44**	0.18
13	Fruit yield per plant (gm)	1191.84	6364.03**	1192.76

****1% level of Significance.**

3. RESULTS AND DISCUSSION

3.1 Analysis of varience

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Table 2 presents the mean sum of squares values for the 13 biometrical traits. The results indicate significant differences among the genotypes for all traits. Maximum mean sum of squares values was observed for fruit yield per plant and plant height at both 1% and 5% levels of significance. This suggests that there is a wide range of variation within the gene pool, providing ample scope for selecting promising lines with high yield and desirable component traits. Among the 20 okra genotypes evaluated, Azad Bhindi-1 (287.0), GO-3 (269.2), and Arka Anamika (237.3) exhibited the highest mean performance for fruit yield per plant.

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Table 3. Genetic parameters for 13 quantitative traits of 20 okra genotypes

Sl.No.	Characters	GCV	PCV	h^2 (Broad Sense)	Genetic Advance	Gen.Adv as % of Mean
1	Days to first flowering	6.114	6.328	93.3	5.033	12.167
2	Days to 50% flowering	6.543	6.745	94.1	5.749	13.076
3	Length of Mature fruit(cm)	7.563	9.397	64.8	1.623	12.54
4	Diameter of fruit (cm)	6.817	7.562	81.3	0.21	12.66
5	Inter nodal length (cm)	8.976	10.845	68.5	0.66	15.306
6	Number of primary branches	22.165	22.508	97	0.742	44.965
7	Average fruit weight (gm)	12.237	14.609	70.2	3.416	21.115
8	Number of fruits per plant	15.403	16.126	91.2	3.168	30.307
9	Number of nodes on main stem	10.887	11.472	90.1	3.394	21.284
10	Plant height(cm)	14.592	15.037	94.2	24.608	29.169
11	Number of seeds per fruit	8.479	9.647	77.3	7.823	15.353
12	Seed index(gm)	5.776	7.508	59.2	0.466	9.153
13	Fruit yield per plant (gm)	22.821	25.316	81.3	77.097	42.377

3.2 Genotypic and Phenotypic varience

The range for Phenotypic Coefficient of Variation (PCV) varies from (6.328%) in days to first flowering to (25.316 %) in case of fruit yield per plant. The PCV estimates in all the characters indicated that the phenotypic variability was low (<10%) for days to first flowering (6.328), days to 50% flowering (6.745), length of mature fruit (9.397), diameter of the fruit (7.562), number of seeds per fruit (9.647) and seed index (7.508). The phenotypic variability was moderate (10-20%) in case of internodal length (10.845), average fruit weight (14.609), number of fruits per plant (16.126), number of nodes on the main stem (11.472) and plant height (15.037). The phenotypic variability was high (>20%) in case of number of primary branches (22.508) and fruit yield per plant (25.316) from (Table 3) A similar declaration has been made by (Rana *et al.*, (2020) [12] and (Kumari *et al.*, (2017) [7].

Range for Genotypic Coefficient of Variation (GCV) varies from (5.776 %) in seed index to (22.821%) in case of fruit yield per plant. The GCV estimates in all the characters indicated that the genotypic variability was low (<10%) in days to first flowering (6.114), days to 50% flowering (6.543), length of mature fruit (7.563), diameter of the fruit (6.817), internodal length (8.976), number of seeds per fruit (8.479) and seed index (5.776). Genotypic variability was moderate (10-20%) in case of average fruit weight (12.237), number of fruits per plant (15.403), number of nodes on the main stem (10.887) and plant height (14.592). The genotypic variability was high (>20%) in number of primary branches per plant (22.165) and fruit yield per plant (22.821) from (Table 3) A similar identification was made by (Makhdoomi *et al.*, (2018) [9].

3.3 Heritability

The heritability for all 13 characters was estimated. The heritability in broad sense (h^2) ranged from (59.2%) in the case of seed index to 97% in case of number of primary branches. The magnitude of heritability was found to be moderate (30-60%) for seed index (59.2). High heritability (>60%) was found for days to first flowering (93.3), days to 50% flowering (94.1), length of mature fruit (64.8), diameter of the fruit (81.3), internodal length (68.5), number of Primary branches (97), average fruit weight (70.2), number of fruits per plant (91.2), number of nodes on the main stem (90.1), plant height (94.2), number of seeds per fruit (77.3) and fruit yield per plant (81.3) Such similar observations were reported by (Vani *et al.*, (2021) [17], (Alam *et al.*, (2020) [1].

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3.4 Genetic advance and Genetic advance as percent of Mean

The expected genetic advance for different characters ranged from (0.21) in the case of diameter of fruit to (77.097) in case of fruit yield per plant. Lowest to moderate values of expected genetic advance (<20) were found in the days to first flowering (5.033), days to 50% flowering (5.749), number of primary branches (0.742), length of mature fruit (1.623), diameter of the fruit (0.21), inter nodal length (0.66), average fruit weight (3.416), number of fruits per plant (3.168), number of nodes on the main stem (3.394), number of seeds per fruit (7.823) and seed index (0.466). More than 20 values were obtained for plant height (24.608) and fruit yield per plant (77.097) similar findings were observed in (Kumari *et al*., (2017) [7].

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The expected genetic advance as percent of mean for different characters ranged from (9.153%) in the case of seed index to (44.965 %) as in the case of number of primary branches. The values were lowest (<50%) for all the characters; days to first flowering (12.67), days to 50% flowering (13.076), length of mature fruit (12.54), diameter of the fruit (12.66), inter nodal length (15.306), average fruit weight (21.115), number of fruits per plant (30.307), number of nodes on the main stem (21.284), number of seeds per fruit (15.353), seed index (9.153), plant height (29.169) and fruit yield per plant (42.377).

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Table 4: Estimation of correlation and coefficient for phenotypic (PC) and genotypic (GC) levels among different characters in okra genotypes.

Traits		DFF	DTFPF	LMF	DOF	INL	NOPB	AFW	NFPP	NNMS	PH	NSPF	SI	FYPP
DFF	PC	1.00	0.9523**	-0.2187	-0.1862	-0.179	0.0389	0.0908	0.0296	0.3002**	-0.027	0.3442**	0.2727*	0.0818
	GC	1.00	0.9816**	-0.2805*	-0.2068*	-0.2212*	0.0448	0.0684	0.0407	0.3388**	-0.0217	0.3642**	0.4449**	0.0998
DTFPF	PC		1.000	-0.1968	-0.0444	-0.077	-0.0713	0.2232*	-0.0314	0.318**	0.083	0.4617**	0.3664**	0.1817
	GC		1.000	-0.2331*	-0.0838	-0.0721	-0.0718	0.2384*	-0.0478	0.3403**	0.0886	0.5145**	0.5446**	0.2111*
LMF	PC			1.000	0.2036*	0.1753	-0.3015**	0.2952**	0.644**	0.3119**	0.3735**	-0.209*	-0.3192**	0.651**
	GC			1.000	0.228*	0.286*	-0.4071**	0.3127**	0.8787**	0.4464**	0.4641**	-0.3652**	-0.6808**	0.7994**
DOF	PC				1.000	0.1078	-0.3138**	0.4894**	-0.0657	0.067	0.2722*	0.1174	0.3618**	0.2092*
	GC				1.000	0.1163	-0.3313**	0.5664**	-0.1296	0.0828	0.284*	0.1628	0.5656**	0.1814
INL	PC					1.000	-0.5733**	-0.025	-0.3495**	-0.0922	0.6962**	0.3457**	-0.0681	0.0051
	GC					1.000	-0.669**	-0.018	-0.4514**	-0.1654	0.7827**	0.5306**	-0.0066	-0.0711
NOPB	PC						1.000	-0.0779	0.1079	0.1507	-0.3167**	-0.1389	-0.0202	-0.0042
	GC						1.000	-0.087	0.1165	0.1557	-0.3289**	-0.1706	-0.0779	0.0117
AFW	PC							1.000	0.2619*	0.1235	0.1719	0.142	0.4637**	0.6709**
	GC							1.000	0.3321**	0.1678	0.2038*	0.1945	0.8573**	0.7944**
NFPP	PC								1.000	0.2999*	-0.1322	-0.414**	-0.2943*	0.728**
	GC								1.000	0.3236**	-0.1488	-0.4743**	-0.367**	0.7878**
NNMS	PC									1.000	0.3803**	0.3681**	-0.1804	0.3487**
	GC									1.000	0.3776**	0.4505**	-0.2462*	0.4113**
PH	PC										1.000	0.4653**	0.0092	0.3131**
	GC										1.000	0.5382**	0.0122	0.3228**
NSPF	PC											1.000	0.2506*	-0.1039
	GC											1.000	0.4113**	-0.0877
SI	PC												1.000	-0.0013
	GC												1.000	-0.0189
FYPP	PC													1.000
	GC													1.000

**1% level of significance **5% level of significance

DFF: Days to first flowering**, DTFPF:** Days to 50% flowering**, LMF:** Length of mature Fruit(cm)**), DOF:** Diameter of fruit(cm), **INL:** Internodal length (CM), **NOPB:** Number of primary branches, **AFW:** Average fruit weight(gm)**), NFPP:** Number of fruits per plant, **NNMS:** Number of nodes on main stem**, PH:** Plant height, **NSPF:** Number of seeds per fruits**, SI:** Seed index, **FYPP:** Yield per plant (gm).

4. Correlation coefficient

By assessing the relationship between different traits, a study of correlation coefficients facilitates the identification of certain traits in plants that could potentially be focused on for genetic yield improvement. In order to increase yield, it is important to look into the existence of these features to understand how they are connected. The correlation coefficient reveals the degree to which two attributes are related to one another as well as if it is possible to simultaneously improve both traits.

4.1 Phenotypic Correlation Coefficient

Phenotypic Correlation coefficient analysis revealed that fruit yield per plant exhibited positive and significant correlation with length of mature fruit (0.651**), average fruit weight (0.6709**), number of fruits per plant (0.728**), number of nodes on main stem (0.3487**), plant height (0.3131**) (Similar with Rana *et al.,* 2020) [12] and diameter of fruit (0.2092*). Fruit yield per plant exhibited positive and non-significant correlation with days to first flowering (0.0818), days to 50% flowering (0.1817). Fruit yield per plant exhibited negative and non- significant correlation with number of seeds per fruit (-0.1039) and seed index (-0.0013) from (Table 5) such similar observations have been made by (Rai *et al.,* (2022) [14], (Neeraja *et al.,* (2022) [10].

4.2 Genotypic Correlation Coefficient

Genotypic Correlation coefficient analysis revealed that fruit yield per plant exhibited positive and significant correlation with length of mature fruit (0.7994**), average fruit weight (0.7994**), number of fruits per plant (0.7878**), number of nodes on main stem (0.4113**) and plant height (0.3228**). Fruit yield per plant exhibited positive and non-significant correlation with days to first flowering (0.0998), diameter of fruit (0.1814) and number of primary branches (0.0117). Fruit yield per plant exhibited negative and non-significant correlation with number of seeds per fruit (-0.0877), internodal length (-0.0711) and seed index (-0.0189) from (Table 5) such similar observations have been made by (Ahraf *et al.,* (2020) [2] and (Rathava *et al.,* (2019) [13].

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Table 5: Direct and Indirect Effect of Twelve Characters with Fruit Yield per Plant at Phenotypic (PC) and Genotypic (GC) levels in okra genotypes.

Traits		DFF	DTFPF	LMF	DOF	INL	NOPB	AFW	NFPP	NNMS	PH	NSPF	SI	FYPP
DFF	**PC**	**-0.6191**	-0.5896	0.1354	0.1153	0.1108	-0.0241	-0.0562	-0.0183	-0.1859	0.0168	-0.2131	-0.1689	0.0818
	GC	**0.1068**	0.1048	-0.03	-0.0221	-0.0236	0.0048	0.0073	0.0043	0.0362	-0.0023	0.0389	0.0475	0.0998
DTFPF	**PC**	0.7312	**0.7678**	-0.1511	-0.0341	-0.0591	-0.0547	0.1714	-0.0241	0.2442	0.0637	0.3545	0.2813	0.1817
	GC	-0.1619	**-0.165**	0.0384	0.0138	0.0119	0.0118	-0.0393	0.0079	-0.0561	-0.0146	-0.0849	-0.0898	0.2111*
LMF	**PC**	-0.0015	-0.0014	**0.007**	0.0014	0.0012	-0.0021	0.0021	0.0045	0.0022	0.0026	-0.0015	-0.0022	0.651**
	GC	-0.0207	-0.0172	**0.0739**	0.0168	0.0211	-0.0301	0.0231	0.0649	0.033	0.0343	-0.027	-0.0503	0.7994**
DOF	**PC**	0.0146	0.0035	-0.016	**-0.0784**	-0.0085	0.0246	-0.0384	0.0052	-0.0053	-0.0213	-0.0092	-0.0284	0.2092*
	GC	0.1182	0.0479	-0.1303	**-0.5714**	-0.0665	0.1893	-0.3236	0.0741	-0.0473	-0.1623	-0.093	-0.3232	0.1814
INL	**PC**	-0.0215	-0.0092	0.0211	0.013	**0.1201**	-0.0688	-0.003	-0.042	-0.0111	0.0836	0.0415	-0.0082	0.0051
	GC	0.1109	0.0362	-0.1434	-0.0583	**-0.5014**	0.3355	0.009	0.2264	0.083	-0.3925	-0.2661	0.0033	-0.0711
NOPB	**PC**	0.0088	-0.0162	-0.0685	-0.0713	-0.1303	**0.2273**	-0.0177	0.0245	0.0343	-0.072	-0.0316	-0.0046	-0.0042
	GC	-0.0053	0.0086	0.0485	0.0395	0.0797	**-0.1192**	0.0104	-0.0139	-0.0186	0.0392	0.0203	0.0093	0.0117
AFW	**PC**	0.0183	0.045	0.0596	0.0988	-0.005	-0.0157	**0.2018**	0.0528	0.0249	0.0347	0.0287	0.0936	0.6709**
	GC	0.0365	0.1272	0.1669	0.3022	-0.0096	-0.0464	**0.5336**	0.1772	0.0895	0.1088	0.1038	0.4575	0.7944**
NFPP	**PC**	0.0125	-0.0133	0.2723	-0.0278	-0.1478	0.0456	0.1107	**0.4228**	0.1268	-0.0559	-0.175	-0.1244	0.728**
	GC	-0.018	0.0211	-0.3874	0.0571	0.199	-0.0514	-0.1464	**-0.4409**	-0.1427	0.0656	0.2091	0.1618	0.7878**
NNMS	**PC**	-0.0048	-0.0051	-0.005	-0.0011	0.0015	-0.0024	-0.002	-0.0048	**-0.0159**	-0.0061	-0.0059	0.0029	0.3487**
	GC	0.0456	0.0458	0.0601	0.0111	-0.0223	0.021	0.0226	0.0436	**0.1346**	0.0508	0.0606	-0.0331	0.4113**
PH	**PC**	-0.0079	0.0243	0.1093	0.0797	0.2038	-0.0927	0.0503	-0.0387	0.1113	**0.2927**	0.1362	0.0027	0.3131**
	GC	-0.0145	0.0592	0.3105	0.19	0.5236	-0.2201	0.1363	-0.0996	0.2526	**0.669**	0.36	0.0082	0.3228**
NSPF	**PC**	-0.0769	-0.1031	0.0467	-0.0262	-0.0772	0.031	-0.0317	0.0925	-0.0822	-0.104	**-0.2234**	-0.056	-0.1039
	GC	-0.1547	-0.2185	0.1551	-0.0691	-0.2254	0.0725	-0.0826	0.2015	-0.1914	-0.2286	**-0.4248**	-0.1747	-0.0877
SI	**PC**	-0.0002	-0.0003	0.0003	-0.0003	0.0001	0.00001	-0.0004	0.0003	0.0002	0.00001	-0.0002	**-0.0009**	-0.0013
	GC	-0.0192	-0.0235	0.0293	-0.0244	0.0003	0.0034	-0.0369	0.0158	0.0106	-0.0005	-0.0177	**-0.0431**	-0.0189

Phenotypic path correlation (1 level of significance, *5 level of significance, Residual effect= 0.1722). Genotypic path correlation **1% level of significance, *5% level of significance, Residual effect = SQRT (1- 1.2853).**

DFF: Days to first flowering**, DTFPF:** Days to 50% flowering**, LMF:** Length of mature Fruit(cm**), DOF:** Diameter of fruit(cm), **INL:** Internodal length (CM), NOPB**:** Number of primary branches, **AFW:** Average fruit weight(gm**), NFPP:** Number of fruits per plant, **NNMS:** Number of nodes on main stem**, PH:** Plant height, **NSPF:** Number of seeds per fruits**, SI:** Seed index, **FYPP:** Yield per plant (gm).

5. Path coefficient Analysis

Through path-coefficient analysis, the phenotypic and genotypic correlation coefficients of all the individual parameters assessed with fruit yield have been separated into direct and indirect effects. Fruit yield is directly or indirectly affected by numerous factors at the genotypic and phenotypic levels. The findings indicate the direct as well as indirect effects of numerous variables on plant fruit yield. Path coefficient analyses revealed that direct and indirect impacts at the genotypic level were somewhat greater than direct and indirect effects at the phenotypic level.

5.1 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 days to 50% flowering (0.7678), number of fruits per plant (0.4228), plant height (0.2927), number of primary branches (0.2273), average fruit weight (0.2018), internodal length (0.1201), and length of mature fruit (0.007). On the other hand, days to first flowering (0.6191), number of seeds per fruit (-0.2234), diameter of fruit (-0.0784), number of nodes on the main stem (-0.0159), and seed index (-0.009) exhibited negative direct effects on fruit yield per plant in (Table 5) similar findings were obsereved in (Kumari et al., (2017) [7], (Makhdoomi et al., (2018) [9].

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5.2 Genotypic Path Coefficient Analysis

The genotypic path coefficient analysis revealed positive direct effects on fruit yield per plant for several traits. Plant height had the highest positive direct effect (0.669), followed by average fruit weight (0.5336), number of nodes on the main stem (0.1346), days to first flowering (0.1068), and length of mature fruit (0.0739). On the other hand, the maximum negative direct effect on fruit yield per plant was observed from diameter of fruit (-0.5714), followed by internodal length (-0.5014), number of fruits per plant (-0.4409), number of seeds per fruit (0.4248), seed index (-0.0431), days to 50% flowering (-0.165), and number of primary branches (-0.4409) similar findings were observed in (Neeraja *et al.*, (2022) [10]

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4. CONCLUSION

Genotypes namely, Azad bhindi-1, GO-3, BO-13 had high fruit yield. These genotypes could be used further breeding programmes or recommended to farmers for profitable okra cultivation. The results for coefficients of variability for different characters suggested that the experimental material utilized had a significant amount of variability. Genetic analysis revealed that estimates of phenotypic coefficients of variability (PCV) were higher than genotypic coefficients of variability (GCV) which indicated the consequence of environmental impact on the phenotypic expressions of the characters. The maximum values were obtained for fruit yield per plant and number of primary branches. High heritability together with high genetic gain was obtained for number of primary branches. Hence, selection of these characters for improvement could be more effective and efficient. Fruit yield had a strong, positive and significant association with the number of fruits per plant, average fruit weight, length of mature fruit, number of nodes on main stem and plant height. Therefore, improvement of okra can be practiced with direct selection of these characters. Plant height and average fruit yield had a positive direct effect on fruit yield at both levels, showing their suitability for direct selection.

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Comment [d36]: Add volume/ page number

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