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Mean performance evaluation and path coefficient analysis with Mahalanobis D-square metrics in okra (*Abelmoschus esculentus* L.): A comprehensive multivariate approach

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Abstract
An experiment was conducted during the Monsoon season of 2020 to determine the relationship between grain yield and yield contributing traits in okra (*Abelmoschus esculentus* L. Moench). Twenty different genotypes were collected from Krishi Vigyan Kendra (KVK). Three replications of the experiment were carried out in Jawali, District Kangra, Himachal Pradesh, using a randomised complete block design. A wide variation among the genotypes for yield and contributing traits was manifested upon mean analysis. This variation indicated a great extent of genetic diversity among all the genotypes and provided opportunities for genetic improvement in okra. Path coefficient analysis indicates the direct and indirect causal relationships between multiple variables within a hypothesised model the genotypic and phenotypic path coefficients analysis revealed that the number of fruits (0.888), (0.948), respectively, had the highest direct positive effect on total yield per plant. Based on Mahalanobis D square analysis, all the genotypes were grouped into seven clusters and cluster I was the biggest accommodating 7 genotypes. The genotypes from clusters III, IV and VII can be used in the hybridisation programme because of presence of high variability.

Keywords: Genotypic path coefficient analysis, phenotypic path coefficient analysis, mahalanobis D^2 analysis, okra grain yield

Introduction

Okra (*Abelmoschus esculentus* L. Moench), also called Ladies' finger is the only significant vegetable crop of the Malvaceae family. It originated from North-Eastern African countries, Ethiopia and Sudan. Okra is considered one of the most popular vegetable crops in the tropics because of its ease of cultivation, consistent output, year-round export potential, high nutritional value, high tolerance to different moisture conditions and resistance to disease and pests. (Haq et al 2023, Ibitoye and Kolawole, 2022) [8, 9]. The plant is grown in tropical, sub-tropical and temperate regions all over the world (National Research Council, 2006) [15]. Okra can be grown on a wide range of soil, but it shows the best result when grown in well-drained soil (Akinyele *et al.*, 2007) [1].

Okra has nutritional as well as anti-oxidative value (Elkhalifa *et al.* 2021) [6]. Okra is a good source of proteins, carbohydrates, vitamins, calcium, potassium, enzymes and total minerals. The chemical composition of okra is 67.5% a-cellulose, 15.4% hemicellulose, 7.1% lignin, 3.4% pectin matter, 3.9% fatty and waxy matter and 2.7% aqueous extract (Kumar *et al.*, 2017). Its green tender pods are rich in oxalic acid, thiamine, riboflavin, and nicotinic acid as well as vitamins A, B and C. When compared with other crops, okra is a great source of calcium, which is about 66 mg per 100g (Yawalkar 1969) [24]. Rather than being rich in proteins, vitamins, and minerals, its high iodine content makes it helpful in playing a vital role in controlling goitre disease (Sindhumole *et al.*, 2014) [22]. Okra is not merely used for its nutritional and medicinal value but to our surprise, its ripened seeds are roasted, and grounded and are used as a substitute for coffee in some of the countries. Its greenish-yellow edible oil has a pleasant taste and odour and is high in monosaturated fatty acids (oleic) and palmitic acid (Martin and Rhodes, 1983) [12] and has a high level of lysine (Al-Wondawi, 1983).

Globally, from an area of 2.80 million hectares, okra production has reached 11.23 mil-lion hectares. This represents a hike of 5.90% in the production from the previous year and 13.40% when compared to the production of 10 years ago. India bags first position in okra pro-duction having an area of 509 thousand hectares with an annual production of 6094.9 thousand tonnes and productivity of 12 million tonnes per hectare (Moulana et al 2020) [13]. Moreover, okra is prone to several pests and diseases such as aphids, fruit borers, fusarium wilt and powdery mildew. Poor management of these issues can increase the risk of yield reduction by affecting both the quality and quantity of harvest. (Ranga *et al.*, 2024) [19].

The amount of genetic variability present in the germplasm is directly proportional to the improvement potential of a crop. (Singh *et al.* 2009) [21]. High variability provides the opportunity to elevate the quality as well as quantity of the crop yield. Thus, for selecting effective genotypes, understanding of mean performance of characters is crucial.

Path coefficient analysis is a statistical tool that was developed by Wright (1921). Using a path diagram derived from experimental data, it has been used to arrange and display the relationship between predictor and response variables. Path analysis has the benefit of allow-ing the correlation coefficients to be divided into their constituent parts. The path coefficient is one part that quantifies the direct impact of a predictor variable on its response variable, while the other part is the indirect impact of a predictor variable on the response variable via other predictor variables (Dewey and Lu, 1959) [26]. Path analysis is regarded as a significant and effective instrument that helps learn about the relationships between different characters by identifying the component qualities that can be used as the basis for selection to increase yield. This helps plant breeders to create high-yielding cultivars. The goal of the current study was to evaluate the mean performance of the genotypes and to determine the relationships between different traits and their direct and indirect effects.

Material and Methods

Location and Climatic Conditions: The experiment was conducted in the local fields of a town named Jawali, District Kangra of Himachal Pradesh during the monsoon season (May-August 2020). The geographic coordinates of the location are 32.15 N 76.01 E with an elevation of 625m (2051 ft.). The climate of the area represents sub-temperate conditions.

Experimental material and agronomic traits studied: Twenty okra genotypes were grown in three replications with a spacing of 60 cm X 45 cm in randomized block design (RBD). Table 1 represents the details of the genotypes used in the experiment. The germplasm was collected from Krishi Vigyan Kendra (KVK), Kangra, Himachal Pradesh, India and was evaluated at the Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Phagwara, Punjab, India. Five plants were selected randomly for the observation of different characteristics. The studied traits were DF: days to 50% flowering, DP; days to first picking, PH: plant height (cm), IL: inter-nodal length, PB: number of primary branches per plant, PL: pod length, PD: pod diameter, FP: number of fruits per plant, PW: average pod weight, FN: days to first flowering node, HD: harvest duration, SF: number of seeds per fruit, SW: 100 seed weight, DW: Tender pod dry weight, YP: Yield per plant.

Result and Discussion

Mean performance: For improving the genetic yield potential of any variety, the most important decision to be made is about the choice of parents for hybridization. The mean concerning yield and other desirable economic traits is considered for the selection of parents. The observed mean performance of twenty genotypes for fourteen quantitative traits has been presented in Table 2. The scrutiny of mean values of different genotypes showed wide variation in the performance for yield and its contributing traits. This indicated a great extent of genetic diversity among genotypes which would prove beneficial for the genetic improvement of okra.

Days to 50% flowering: As early flowering plays a crucial role in selecting cultivars for different maturity groups and environments, it is considered an important trait in the crop improvement programme. The data presented in Table 2 showed that Days to 50% flowering for different genotypes ranged from 38.2 (Pusa Sawani) to 62.1 (Punjab Padmani) with a population mean of 47.21. Hisar Unnat, Palam Komal, Pusa Sawani AK0 107, Pusa Makhmali, Anmol, NRB-208 Super Green Research, Abhay, Arka Anamika, Meenakshi BS906, Research Soniya, Bhindi Shakti took fewer days to 50% flowering when compared with Prabhani, Chiranjeevi F1, Bhindi Preeti, P-8, Akola Bahar, VRO-4, Punjab Padmani and Durga.

Days to first flowering node: A smaller number of days to first flowering node is always desir-able as it will directly result in a higher yield and price. The data obtained from Table 2 depict-ed significant differences among the genotypes. Days to the first flowering node ranged from 4.18 (Meenakshi BS906) to 9.58 (Research Soniya). The average days to the first flowering node were calculated to be 7.43. Hisar Unnat, Pusa Sawani, Pusa Makhmali, Abhay, Meenakshi BS906, Bhindi Shakti, Akola Bahar, VRO-4 and Durga manifested lesser days to first flowering node when compared to the genotypes AKO 107, Anmol, Super Green Research, Prabhani Kranti, Arka Anamika, P-8, Bhindi Preeti, Chiranjeevi F1 and Punjab Padmani.

Plant height: As plant height and yield are directly proportional to each other, it is a crucial pa-rameter for breeders to consider. The data about plant height depicted in Table 2 revealed that plant height ranged from 131.2cm (Prabhani Kranti) to 154.2cm (Palam Komal). Data con-structed that NRB-208 Super Research, Prabhani, Abhay, Arka Anamika, Bhindi Shakti, Pun-jab Padmani, and Durga showed lesser height than Hisar Unnat, Palam Komal, Pusa Sawani, AKO 107, Pusa Makhmali, Anmol, Meenakshi, P-8, Research Soniya, Bhindi Preeti, Chiran-jeevi F1, Akola Bahar, VRO-4.

Internodal length: For optimal okra yield, plants with shorter internodal lengths are desired. The internodal length of okra varied significantly among the genotypes and ranged from 6.2 (Prabhani Kranti) to 12.9 (Palam Komal). The average internodal length was 8.84. Genotypes, Pusa Makhmali, Anmol, Super Green Research, Prabhani Kranti, Abhay, Arka Anamika, Meenakshi BS 906, Research Soniya, Bhindi Preeti, Chiranjeevi F1, Bhindi Shakti, Akola Ba-har had lesser internodal length as compared to Hisar Unnat, Palam Komal, Pusa Sawani, AKO 107, P-8, VRO-04, Punjab Padmani, Durga.

Pod length: As presented in the table, pod length varied significantly in the whole population ranging from 8.34 (Abhay) to 13.7 (Akola Bahar). The average pod length recorded was 10.32. Hisar Unnat, Pusa Makhmali, Anmol, Super Green Research, Prabhani Kranti, P-8, Akola Bahar, Punjab Padmani manifested greater pod length than Palam Komal, Pusa Sawani, AKO 107, Abhay, Research Soniya, Bhindi Preeti, Chiranjeevi F1, Bhindi Shakti, VRO-4 and Durga.

Pod diameter: The data about pod diameter showed significant variation among the genotypes. Pod diameter ranged from 1.70 (Prabhani Kranti) to 2.45 (Chiranjeevi F1). The mean pod diameter recorded was 2. AKO 107, Pusa Makhmali, Anmol, Super Green Research, Abhay, Ar-ka Anamika, Meenakshi BS 906, Research Soniya, Chiranjeevi F1, Akola Bahar and VRO-4 had higher diameters than Hisar Unnat, Palam Komal, Pusa Sawani, Anmol, Prabhani Kranti, P-8, Bhindi Shakti and Bhindi Preeti.

Number of fruits per plant: The number of fruits is in direct positive correlation with the yield. A higher number of fruits per plant is always desired for obvious reasons. Number of fruits per plant ranged from 6.4 (Bhindi Shakti) to 25.5 (Arka Anamika). Data constructed that Hisar Unnat, P-8, VRO-4, and Arka Anamika had the greatest number of fruits per plant. Among other 16 genotypes, Palam Komal, Pusa Sawani, Pusa Makhmali, Anmol, NRB-208 Super Green Research, Meenakshi BS-906, P-8, Chiranjeevi, Bhindi Shakti, Akola Bahar, VRO-4, Punjab Padmani had a greater number of fruits per plant than AKO 107, Prabhani, Abhay, Re-search Soniya, Bhindi Preeti, Durga.

Yield per plant: Higher yield is the prime objective of a farmer as well as a plant breeder. As per the data depicted in the table, the yield ranged from 97.63 (Durga) to 255.83 (Arka Ana-mika). The average yield recorded was 152.8. Pusa Makhmali, Anmol, Super Green Research, Abhay, Arka Anamika, Meenakshi BS906, P-8, Research Soniya, Chiranjeevi F1, Akola Ba-har, VRO-4, Punjab Padmani had higher yield per plant Hisar Unnat, Palam Komal, Pusa Sawani, Prabhani Kranti, Bhindi Preeti, Bhindi Shakti and Durga.

Days to first picking: Days to first picking ranged from 42.1 (Pusa Sawani) to 66.08 (Punjab Padmani). Palam Komal, Pusa Sawani, AKO 107, Pusa Makhmali, Anmol, NRB-208 Super Green Research, Abhay, Arka Anamika, Meenakshi BS-906, Research Soniya, Bhindi Shakti showed fewer days to first picking than the observed mean value, which was 13.26. While the other genotypes Prabhani Kranti, P-8, Bhindi Preeti 2, Chiranjeevi F1, Akola Bahar, VRO-4, Punjab Padmani, Durga had higher values than the mean value.

Harvest duration: The genotypes with fewer days to harvest are always desirable to avoid the pods becoming fibrous and inedible. The data showed high variation among the genotypes. Harvest duration ranged from 69.14 (Bhindi Shakti) to 98.86 (Arka Anamika). The mean har-vest duration was recorded to be 86.27. Hisar Unnat, Palam Komal, Pusa Sawani, AKO 107, Pusa Makhmali, Anmol, Super Green Research, Abhay, Arka Anamika, Meenakshi BS 906, Research Soniya, Bhindi Shakti manifested lesser days to harvest than Prabhani Kranti, Anmol, P-8, Bhindi Preeti, Chiranjeevi F1, Akola Bahar, VR0-4, Punjab Padmani and Durga.

Number of seeds per fruit: The number of seeds ranged from 45.78 (Hisar Unnat) to 80.70 (Prabhani Kranti). The average number of seeds per fruit was 58.79. Genotypes, AKO 107, Pusa Makhmali, Super Green Research, Prabhani Kranti, Research Soniya, Bhindi Preeti, Chi-ranjeevi F1, and Akola Bahar had a greater number of seeds per plant than Hisar Unnat, Palam Komal, Pusa Sawani, Anmol, Abhay, Arka Anamika, Meenakshi BS 906, P-8, Bhindi Shakti, VRO-4, Punjab Padmani and Durga.

100 seed weight: As per the data presented in the table, 100 seed weight showed higher varia-tion among the genotypes and ranged from 3.38 (AKO 107) to 9.10 (Pusa Makhmali). The av-erage 100 seed weight recorded was 6.29. Hisar Unnat, Pusa Makhmali, Super Green Re-search, Abhay, Arka Anamika, Bhindi Preeti, Punjab Padmani, and Durga recorded greater 100 seed weight than other genotypes, Palam Komal, Pusa Sawani, Anmol, Prabhani Kranti, Meenakshi BS906. Research Soniya, Bhindi Preeti, Chiranjeevi F1, Bhindi Shakti, Akola Ba-har, VRO-4.

Average tender pod dry weight: Significant variation among genotypes for average tender pod dry weight was recorded. It ranged from 0.54 (Bhindi Preeti) to 1.4 (Meenakshi BS906). The average tender pod dry weight was recorded to be 0.97. Hisar Unnat, Pusa Sawani, Ako 107, Pusa Makhmali, Anmol, Super Green Research, Abhay, Akola Bahar, VRO-4, Punjab Pad-mani recorded higher tender dry pod weight than the other genotypes, Palam Komal, Pusa Sawani, Prabhani Kranti, Arka Anamika, P-8, Research Soniya, Bhindi Preeti, Chiranjeevi F1, Bhindi Shakti, Durga.

Path coefficient analysis

Each component has two path actions *viz*., direct and indirect effects on the yield through the components which are not revealed by correlation studies. Path analysis indicates the direct and indirect causal relationships between multiple variables within a hypothesized model. It gives an assertion for the selection of predominant genotypes from diverse populations (Komolafe *et al.*, 2021) [11].

Genotypic path coefficient analysis: The genotypic path analysis is presented in Table 3. The data revealed that number of fruits per plant (0.888) had the highest direct positive effect on total yield per plant. Traits like days to first picking (0.210), plant height (0.006), number of primary branches per plant (0.140), pod length (0.022), average pod weight (0.062), days to first flowering (0.006), tender pod dry weight (0.016) had positive direct effect on the yield per plant whereas other traits like days to 50% flowering (-0.203), internodal length (-0.010), pod diameter (-0.002), harvest duration (-0.031), number of seeds per plant (-0.026), 1000 seed weight (-0.003) had negative direct effect on yield per plant. The residual effect of 0.00004 indicated that a very small proportion of the variance in the dependent variable i.e. yield per plant is not explained by the included independent variables. These findings align consistently with similar studies conducted by Nbeaa et al (2023) and Mohammad et al (2022) [16, 14].

Phenotypic path coefficient analysis: The phenotypic path coefficient analysis is presented in Table 4. The data revealed that the number of fruits (0.948) had the highest direct effect on yield per plant. Other traits like days to 50% flowering (0.020), plant height (0.011), number of primary branches per plant (0.037), pod length (0.002), pod diameter (0.006), average pod weight (0.097), harvest duration (0.028), number of seeds per fruit (0.0003), tender pod dry weight (0.005) exhibited a positive direct effect on yield per plant. While the remaining traits such as internodal length (-0.008), days to 1st flowering (-0.002) and 100 seed weight (-0.003) had a negative direct effect on yield per plant. The residual effect of 0.0004 again indicated that a very small proportion of the variance in dependent variable i.e. yield per plant is not explained by the included independent variables. Similar results were observed by Ranga et al (2021), Dwivedi and Sharma (2017) and Hallur et al (2016) [5, 7, 18].

Mahalanobis D2 analysis

Clustering pattern of 20 genotypes of okra based on genetic diversity: Based on the clustering pattern obtained through Mahalanobis D2 analysis, all 20 genotypes were grouped in 7 clusters, indicating substantial genetic diversity among them. Among the 7 clusters, cluster I was the largest cluster accommodating 9 genotypes. The large number of genotypes in this cluster suggests a broad genetic base, possibly reflecting these genotypes may share similar genetic backgrounds or traits

(Table 5). The genotypes in cluster I are Hisar Unnat, AKO 107, Anmol, Meenakshi BS 906, P-8, Research Soniya, Chiranjeevi F1, Bhindi Preeti, Punjab Padmani. Cluster III was the second largest cluster among the seven clusters comprising four genotypes, namely, Palam Komal, Pusa Sawani, VRO-4 and Durga, followed by cluster II which consisted of three genotypes (Pusa Makhmali, NRB-208 Super Green Research and Arka Anamika. Clusters IV, V, VI and VII consisted of single genotypes Abhay, Akola Bahar, Bhindi Shakti and Prabhani Kranti respectively, which may indicate that these genotypes are genetically distinct from others.

Inter and Intra-cluster distance: Clusters are formed to get the intra and inter-cluster distanc-es. These distances are often used as an index for parents having diverse origins. The intra and inter-cluster values are means derived from D2 values of cluster elements. Table 5 represents the average D2 values of intra and inter-cluster distances of studied okra genotypes. Among the seven clusters formed from twenty okra genotypes, the uppermost. intra-cluster distance was recorded in cluster 1 (46.20), followed by cluster III (45.84) and cluster IV (37.52). The value ranged from 0 (cluster IV, V, VI, VII) to 46.20 (cluster I). Inter-cluster distances pro-vide insight into the genetic divergence between different clusters. The maximum inter-cluster distance value recorded was 169.15 between clusters III and VII followed by clusters IV and VII (150.35)., indicating a substantial genetic differentiation between these groups. The min-imum inter-cluster distance recorded was 56.25 between clusters V and VII, indicating relatively less genetic differentiation. (Table 5). Based on parameters in a breeding programme, the genotypes may be selected from clusters III, IV and VII. The genotypes from clusters III, IV and VII may be adopted in a hybridization programme which would show variability in segregating populations.

Cluster means for different traits among 20 genotypes of okra: The cluster analysis of 20 genotypes of okra reveals considerable variation across multiple traits, demonstrating the genetic diversity present within and between the seven clusters. (Table 6). The importance of the contribution of yield components towards divergence can be judged by the group means of 20 characters. Cluster II recorded desirable low mean values for days to 50% flowering (43.47) and days to first picking (47.57). The desirable lowest mean value for days to the first flowering node (5.39) and harvest duration (69.14) were recorded in cluster VI. The highest mean values were recorded for Cluster I for average pod weight (10.42), cluster II for maximum number of branches per plant (2.27), number of fruits per plant (21.55) and yield per plant (218.5), cluster III for plant height (148.3), cluster IV for 100 seed weight (8.90) and tender pod dry weight (1.35), cluster V for pod diameter (2.23), cluster VII for pod length (14.11) and number of seeds per fruit (80.7). The genetic diversity present across clusters provides the opportunity to select diverse parent genotypes to meet specific breeding objectives.

Table 1: List of okra genotypes used for evaluation

Sr. No.	Genotypes
1.	Hisar Unnat
2.	Palam Komal
3.	Pusa Sawani
4.	AKO 107
5.	Pusa Makhmali
6.	Anmol
7.	NRB-208 Super Green Research
8.	Prabhani Kranti
9.	Abhay
10.	Arka Anamika
11.	Meenakshi BS 906
12.	Punjab-8
13.	Research Soniya
14.	Bhindi Preeti 21
15.	Chiranjeevi F1
16.	Bhindi Shakti
17.	Akola Bahar
18.	VRO-4
19.	Punjab Padmani
20.	Durga

Table 2: Mean performance analysis of twenty genotypes for fourteen quantitative traits in okra.

Genotypes	DF	FN	PH	IL	PB	PL	PD	FP	YP	DP	HD	SF	SW	DW
Hisar Unnat	40.4	6.3	148.0	11.4	1.5	10.5	1.9	14.2	152.8	44.4	86.1	45.7	7.4	1.0
Palam Komal	46.0	8.5	154.2	12.8	1.1	8.4	1.9	11.6	114.3	49.9	78.3	51.4	6.1	0.7
Pusa Sawani	38.2	6.4	144.2	10.8	1.0	8.9	1.7	10.0	105.2	42.1	75.2	56.5	5.6	0.8
AKO 107	41.9	7.7	145.7	9.6	1.8	9.5	2.0	19.4	191.0	45.8	83.9	60.3	3.3	1.3
Pusa Makhmali	46.2	5.7	145.7	8.0	2.1	11.5	2.0	20.4	206.4	49.9	93.5	59.9	9.1	1.3
Anmol	43.2	9.4	142.3	7.2	1.9	11.0	1.9	18.3	185.9	47.1	87.9	56.9	5.7	1.1
NRB208	42.1	8.6	136.9	6.7	1.9	11.4	2.0	18.6	193.3	46.3	89.1	67.8	6.6	0.9
Prabhani Kranti	53.2	9.5	131.2	6.1	1.0	14.1	1.7	10.3	106.4	57.2	76.8	80.7	4.1	0.8
Abhay	45.5	6.4	138.5	6.7	2.2	8.3	2.0	20.4	205.1	49.5	92.1	56.9	8.9	1.3
Arka Anamika	42.1	8.6	136.7	6.2	2.6	10.3	2.1	25.5	255.8	46.4	98.8	57.2	6.9	0.7
Meenakshi BS906	47.1	4.1	144.5	8.3	2.2	10.2	2.1	21.4	222.8	51.1	96.3	54.3	5.1	1.4
Punjab-8	47.3	7.7	149.2	10.0	1.7	10.9	1.9	15.2	162.9	51.8	87.1	52.2	4.9	0.7

Research Soniya	46.2	9.5	146.6	8.6	1.7	9.6	2.1	14.8	160.7	52.1	87.5	60.7	5.7	0.7
Bhindi Preeti	48.4	8.6	144.5	7.8	1.5	9.7	1.7	13.7	147.2	53.0	84.5	62.2	6.8	0.5
Chiranjeevi F1	54.6	9.3	144.3	7.6	1.6	9.6	2.4	16.1	167.1	60.0	86.2	61.6	6.0	0.7
Bhindi Shakti	45.7	5.3	138.1	6.6	0.6	9.1	1.7	6.4	165.4	50.1	69.1	58.5	6.1	0.5
Akola Bahar	51.0	6.4	143.9	8.6	1.9	13.7	2.2	18.5	188.9	55.9	88.6	72.5	5.4	1.1
VRO-4	49.8	5.8	144.6	10.5	2.0	8.4	2.0	19.8	200.7	55.6	94.8	50.0	5.8	1.2
Punjab Padmani	62.1	9.3	137.8	9.3	2.0	10.9	2.1	19.6	198.1	66.0	93.9	55.1	6.8	1.3
Durga	52.3	4.4	150.3	12.0	0.9	9.7	1.7	9.6	97.6	57.2	74.8	54.6	8.6	0.6
Range	38.2-62.1	4.4-9.5	131.2-154.2	6.1-12.8	0.6-2.6	8.3-14.1	1.7-2.2	6.4-25.	97.6-255.8	42.1-66.0	69.1-98.8	45.7-80.7	3.3-9.1	0.5-1.4
Mean	47.2	7.43	143.4	8.8	1.7	10.3	2.0	16.2	152.8	51.6	86.2	58.7	6.2	0.97
SE (m)	0.57	0.18	0.64	0.05	0.05	0.03	0.02	0.42	2.63	0.66	0.89	0.86	0.08	0.02
CD	1.64	0.51	1.84	0.14	0.13	0.09	0.06	1.2	7.53	1.89	2.55	2.46	0.22	0.06

Table 3. Path using genotypic correlation coefficient

	DF	DP	PH	IL	PB	PL	PD	FP	PW	DFN	HD	SF	SW	DW	CYP
DF	-0.203	0.209	-0.001	0.000	-0.004	0.006	-0.000	-0.019	-0.006	0.001	-0.002	-0.005	-0.000	0.000	-0.027^{NS}
DP	-0.202	0.210	-0.000	0.000	-0.004	0.005	-0.000	-0.022	-0.003	0.001	-0.002	-0.005	-0.000	-0.000	-0.026^{NS}
PH	0.031	-0.027	0.006	-0.008	-0.024	-0.009	-0.000	-0.159	0.008	-0.001	0.003	0.015	-0.000	-0.001	-0.167^{NS}
IL	0.004	-0.003	0.005	-0.010	-0.046	-0.008	0.000	-0.269	0.000	-0.001	0.007	0.015	-0.000	-0.000	-0.306*
PB	0.006	-0.006	-0.001	0.003	0.140	0.002	-0.001	0.881	-0.009	0.000	-0.030	0.002	-0.000	0.009	0.997**
PL	-0.055	0.051	-0.002	0.003	0.012	0.022	-0.000	0.070	0.009	0.001	-0.002	-0.018	0.000	0.001	0.095^{NS}
PD	-0.047	0.057	0.000	0.001	0.088	0.000	-0.002	0.567	-0.002	0.001	-0.020	0.001	0.000	0.005	0.650**
FP	0.004	-0.005	-0.001	0.003	0.139	0.001	-0.001	0.888	-0.016	0.000	-0.029	0.002	-0.000	0.010	0.997**
PW	0.020	-0.012	0.000	-0.000	-0.022	0.003	0.000	-0.228	0.062	0.000	0.000	0.000	0.000	-0.007	-0.179^{NS}
FN	-0.034	0.034	-0.001	0.003	0.012	0.004	-0.000	0.077	0.006	0.006	-0.002	-0.009	0.001	-0.004	0.095^{NS}
HD	-0.016	0.019	-0.000	0.002	0.137	0.001	-0.001	0.846	-0.001	0.000	-0.031	0.004	-0.000	0.009	0.969**
SF	-0.045	0.046	-0.003	0.006	-0.012	0.015	0.000	-0.075	-0.000	0.002	0.005	-0.026	0.001	-0.002	-0.090^{NS}
SW	-0.007	0.006	0.000	-0.000	0.019	-0.004	0.000	0.079	-0.002	-0.001	-0.005	0.008	-0.003	0.000	0.088^{NS}
DW	-0.002	-0.006	-0.000	0.000	0.083	0.001	-0.000	0.562	-0.026	-0.001	-0.018	0.003	-0.000	0.0168	0.612**

Residual effect: 0.00004: DF: days to 50% flowering, DP: days to first picking, PH: plant height, IL: internodal length, PB: number of primary branches per plant, PL: pod length, PD: pod diameter, FP: number of fruits per plant, PW: average pod weight, FN: days to first flowering node, HD: harvest duration, SF: number of seeds per fruit, SW: 100 seed weight, DW: average tender pod dry weight, YP: yield per plant.

Table 4: Path using phenotypic correlations

	DF	FP	PH	IL	BP	PL	PD	FP	PW	FN	HD	SF	SW	DW	CYP
DF	0.020	-0.020	-0.001	0.000	-0.001	0.000	0.001	-0.020	-0.008	-0.000	0.002	0.000	-0.000	0.000	-0.028^{NS}
FP	0.020	-0.020	-0.001	0.000	-0.001	0.000	0.001	-0.025	-0.005	-0.000	0.002	0.000	-0.000	-0.000	-0.028^{NS}
PH	-0.003	0.002	0.011	-0.007	-0.006	-0.000	0.000	-0.171	0.0110	0.000	-0.003	-0.000	-0.000	-0.000	-0.167^{NS}
IL	-0.000	0.000	0.009	-0.008	-0.012	-0.000	-0.000	-0.285	0.001	0.000	-0.006	-0.000	-0.000	-0.000	-0.304*
BP	-0.000	0.000	-0.001	0.002	0.037	0.000	0.003	0.932	-0.014	-0.000	0.027	-0.000	-0.000	0.003	0.990**
PL	0.005	-0.004	-0.004	0.003	0.003	0.002	0.000	0.074	0.011	-0.000	0.002	0.0002	0.000	0.000	0.094^{NS}
PD	0.004	-0.005	0.000	0.001	0.023	0.000	0.006	0.588	-0.000	-0.000	0.0180	-0.000	0.000	0.001	0.639**
FP	-0.000	0.000	-0.002	0.002	0.037	0.000	0.003	0.948	-0.026	-0.000	0.026	-0.000	-0.000	0.003	0.994**
PW	-0.001	0.001	0.001	-0.000	-0.005	0.000	-0.000	-0.259	0.097	-0.000	-0.001	-0.000	0.000	-0.001	-0.171^{NS}
FN	0.003	-0.003	-0.003	0.002	0.003	0.000	0.001	0.077	0.008	-0.002	0.002	0.000	0.001	-0.001	0.089^{NS}
HD	0.001	-0.001	-0.001	0.002	0.036	0.000	0.004	0.893	-0.006	-0.000	0.028	-0.000	-0.000	0.003	0.959**
SF	0.0045	-0.004	-0.006	0.005	-0.003	0.001	-0.000	-0.076	-0.001	-0.000	-0.004	0.0003	0.001	-0.000	-0.086^{NS}
SW	0.000	-0.000	0.000	-0.000	0.004	-0.000	-0.000	0.080	-0.003	0.000	0.004	-0.000	-0.003	0.000	0.085^{NS}
DW	0.0003	0.000	-0.000	0.000	0.021	0.000	0.002	0.584	-0.029	0.000	0.016	-0.000	-0.000	0.005	0.602**

Residual effect 0.00044: DF: days to 50% flowering, DP: days to first picking, PH: plant height, IL: internodal length, PB: number of primary branches per plant, PL: pod length, PD: pod diameter, FP: number of fruits per plant, PW: average pod weight, FN: days to first flowering node, HD: harvest duration, SF: number of seeds per fruit, SW: 100 seed weight, DW: average tender pod dry weight, YP: yield per plant

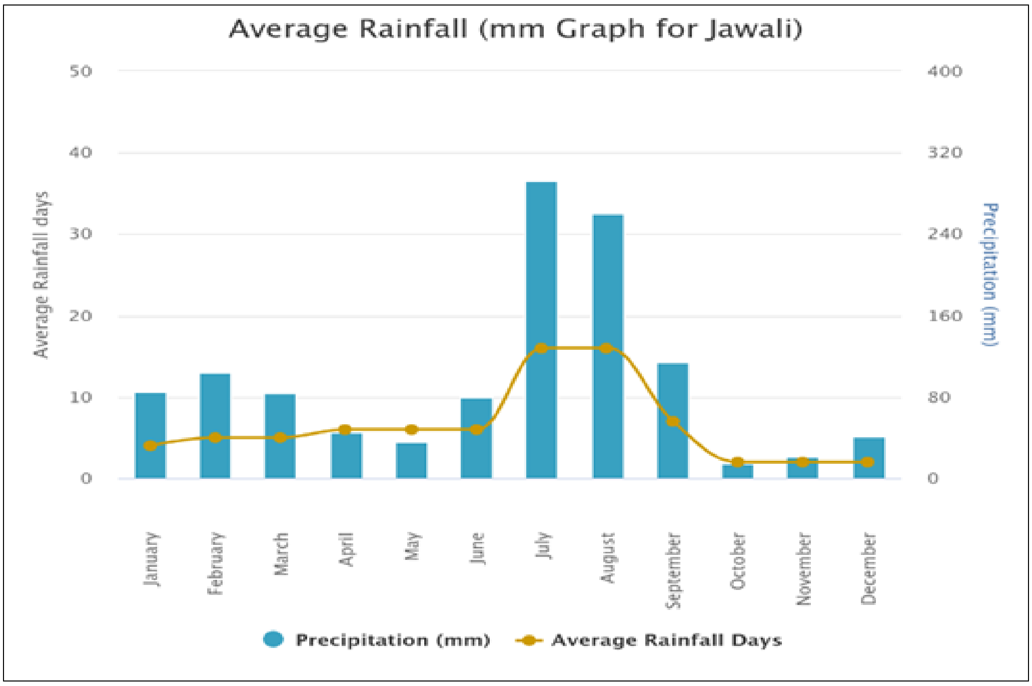
Table 5: Clustering pattern and average intra and inter-cluster distance (D^2) of 20 genotypes of okra based on genetic variability.

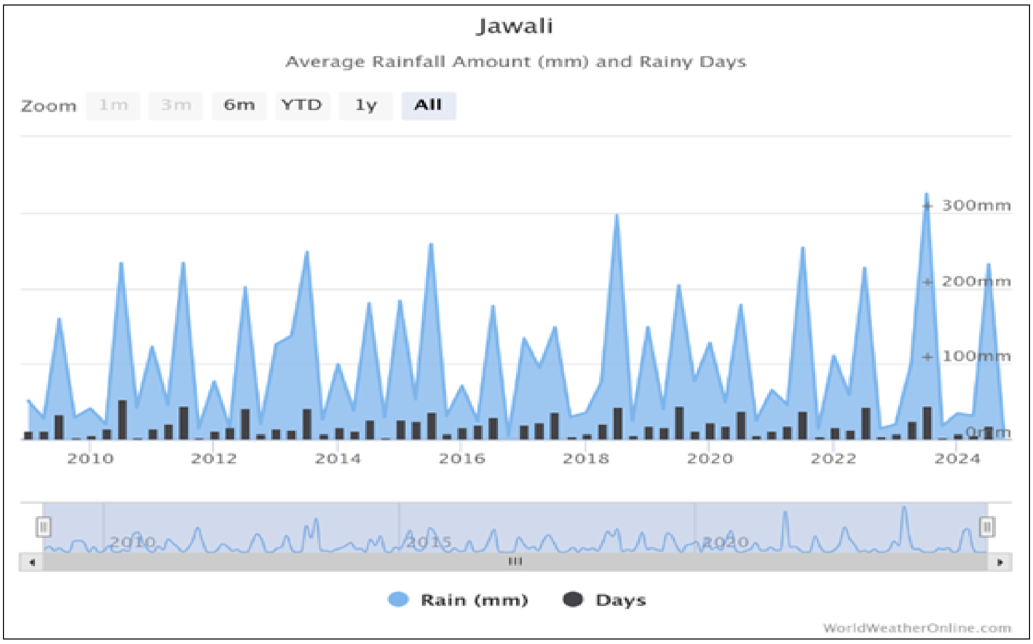
Clusters	I	II	III	IV	V	VI	VII	Number of genotypes in a cluster	Genotypes
I	46.20							9	Hisar Unnat, AKO 107, Anmol, Meenakshi BS 906, Punjab-8, Research Soniya, Chiranjeevi F1, Bhindi Preeti, Punjab Padmani
II	61.92	37.52						3	Pusa Makhmali, NRB-208 Super Green Research, Arka Anamika
III	71.61	110.03	45.84					4	Palam Komal, Pusa Sawani, VRO-4, Durga
IV	65.14	65.63	88.52	0				1	Abhay
V	87.84	68.65	134.42	120.97	0			1	Akola Bahar
VI	75.26	87.08	92.71	72.97	113.37	0		1	Bhindi Shakti
VII	122.74	101.85	169.15	150.35	56.25	122.61	0	1	Prabhani Kranti

Table 6: Cluster means for different characters among 20 genotypes of okra

Characters	Clusters						
	I	II	III	IV	V	VI	VII
Days to 50% flowering	47.97	43.47	46.62	45.50	50.99	45.78	53.27
Days to first picking	52.41	47.57	51.24	49.54	55.99	50.12	57.23
Plant height	144.81	139.81	148.37	138.51	143.91	138.19	131.20
Internodal length	8.94	7.04	11.59	6.78	8.67	6.68	6.18
Number of primary branches per plant	1.79	2.27	1.30	2.23	1.92	0.63	1.07
Pod length	10.25	11.09	8.91	8.34	13.70	9.16	14.11
Pod diameter	2.06	2.06	1.88	2.00	2.23	1.77	1.70
Number of fruits per plant	17.01	21.55	12.81	20.49	18.56	6.44	10.33
Average pod weight	10.42	10.17	10.13	10.02	10.19	10.16	10.31
Days to first flowering node	8.05	7.68	6.32	6.41	6.45	5.39	9.55
Harvest duration	88.19	93.85	80.82	92.17	88.60	69.14	76.89
Number of seeds per fruit	56.60	61.68	53.17	56.91	72.54	58.56	80.70
100 seed weight	5.80	7.56	6.58	8.90	5.45	6.13	4.18
Average tender pod dry weight	1.00	1.00	0.87	1.35	1.10	0.58	0.83
Yield per plant	176.52	218.54	129.51	205.17	188.98	65.48	106.44

Average precipitation





Conclusion
Based on the mean performance of different genotypes, it can be concluded that genotype Arka Anamika (255.17g) had the highest yield per plant followed by Meenakshi BS 906 (221.87g) and Pusa Makhmali (203.72g). Path coefficient analysis indicated that the number of fruits had the highest direct positive effect on yield per plant in both, genotypic and phenotypic path coefficient analysis. Based on Mahalabonis D square analysis, all 20 genotypes were grouped in 7 clusters. Among those 7 clusters, clusters III, IV and VII showed the highest variation and thus these clusters can be further used in hybridization programmes for crop improvement.

Discussion
Mean Performance
The selection of hybridization parents is the most crucial choice for enhancing the genetic yield potential of any variety. When choosing parents, the average yield and other desirable economic characteristics are considered. Examining the average values of various genotypes revealed significant variance in yield performance and the factors that contribute to it. This suggested a high level of genetic variation across genotypes, which would be advantageous for okra's genetic advancement. Different genotypes can be considered for different breeding objectives. For instance, Pusa Sawani (38.2), (42.1) recorded lowest days to 50% flowering and days to first picking, respectively, followed by Hisar Unnat (40.4) and (44.4), respective-ly. Bhindi Shakti (69.1) recorded lowest harvest duration followed by Pusa Sawani (75.2). All the genotypes can be considered as good parental lines in case of hybridization for developing early maturing varieties. On the other hand, Arka Anamika recorded highest number of fruits per plant (25.5) and yield per plant (255.8) followed by Meenakshi BS906 (21.4) and (222.8), respectively. For developing varieties with high yield, Arka Anamika and Meenakshi BS906 can be proven as promising parents. For other characteristics, such as nutritional enhancement, genotypes Pusa Makhmali (9.1) and Durga (8.6) can be considered as good parents for creating varieties with high nutritional values.

Path coefficient analysis
Wright S. (1921) created the idea of the route coefficient, and Dewey and Lu (1959) [26] applied the method for the first time in plant selection. Path coefficient analysis, also known as stand-ard partial regression coefficients, divides the correlation coefficient into measures of direct and indirect effects, i.e., the direct and indirect contribution of various independent characters on a dependent character. It is defined as the ratio of the standard deviation of the effect due to a given cause to the total standard deviation of the effect. They provide for easy inter-pretation because they are directional, unit-free, and may be greater or less than unity. The fundamental premise of route analysis is that the path diagram makes use of a comprehensive depiction of the causal factor that determines the result, namely the fruit yield per plant.

Genotypic path coefficient analysis: A thorough grasp of the direct effects of different features on yield per plant is provided by the genotypic path coefficient analysis, which also identifies important parameters that favourably influence okra yield potential. Characteristics that have a direct positive influence on the yield per plant are number of fruits per plant, days to first picking, plant height, number of major branches per plant, pod length, average pod weight, days to first flowering, and average tender pod dry weight. These traits demonstrate a strong correlation with increased yield. According to this association, production is directly increased by high number of fruits and branches per plant, early flowering, ideal plant height, and a proper pod length and weight; hence, these traits are desirable targets for selection in breeding programs that aim to maximize output. Finding characteristics that directly reduce yield per plant draws attention to possible trade-offs that breeding programs may need to carefully monitor. For example, features that negatively affect yield can still be useful for other qualities like disease resistance or adaptability; therefore, it's critical to balance these with traits that increase yield. Breeders can use multi-trait selection to balance the effects of some yield-detracting traits or select against them by having a thorough understanding of these intricate interactions. According to the genotypic path coefficient study, okra breeding efforts that aim to maximize both yield and nutritional value could greatly benefit from concentrating on features that directly increase pod yield per plant while carefully controlling traits that have adverse impacts.

Phenotypic path coefficient analysis
According to phenotypic path coefficient analysis, number of fruits per plant is the prime trait which can be selected for enhancing the overall yield per plant, followed by other traits like days to 50% flowering, plant height, number of primary branches per plant, pod length, pod diameter, average pod weight, harvest duration, number of seeds per fruit, tender pod dry weight. Direct positive effect of these traits on the yield per plant indicates true relationship and can be considered for selection for further crop improvement programs. On the other hand, traits like internodal length, days to 1st flowering and 100 seed weight are not in direct positive association with yield per plant. Thus, these traits are not promising for increasing the overall yield per plant and can be avoided for further selection. A very low residual effect indicates that most of the variance in dependent variable (yield per plant) can be explained by the included independent variables (other traits) in the model.

Mahalanobis D2 analysis
Clustering pattern of 20 genotypes of okra based on genetic diversity: Informed selection in breeding programs is supported by the clustering pattern obtained from Mahalanobis D2 analysis, which offers important insights into the genetic linkages and diversity among the 20-okra genotype. Cluster I, which is the largest cluster, accommodating 9 genotypes, indicates a wider genetic base. This broad variability suggests that Cluster I could serve as a diverse pool for selecting genotypes with a range of traits, offering flexibility for breeding objectives focused on both stability and adaptability. Clusters with fewer genotypes, like Cluster II and III, show close genetic relationships, suggesting potential for stabilizing specific traits. For example, the genetic similarities between Pusa Makhmali, NRB-208 Super Green Research, Arka Anamika in cluster II and Palam Komal, Pusa Sawani, VRO-4 and Durga in Cluster III could facilitate the development of uniform lines with specific desired characteristics inherit-ed from these closely related genotypes. The unusual genetic profile of this genotype is high-lighted by the unique single-genotype Cluster IV, V, VI and VII, which only contains single genotype, Abhay, Akola Bahar, Bhindi Shakti and Prabhani Kranti respectively. This suggests that when these genotypes are crossed with other genotypes, it may contribute novel features. Breeding strategies aimed at increasing genetic diversity or introducing novel

features might provide preference to these genotypes. All things considered, the clustering pattern shows a balance between similarity and variation across the genotypes, providing breeding programs with tactical alternatives. While genotypes from genetically similar clusters may be employed to create stable, trait-specific lines, from genetically similar clusters may be employed to create stable, trait-specific lines, those from high genetic diversity clusters, such as cluster are appropriate for expanding the genetic base and establishing heterosis. All things considered, the clustering pattern shows a balance between genetic similarity and variation across the genotypes, providing breeding programs with tactical alternatives. While genotypes from genetically similar clusters may be employed to create stable, trait-specific lines and those from high genetic diversity clusters for expanding the genetic base and expanding heterosis. This variety offers a solid basis for creating enhanced okra cultivars suited to different breeding goals.

Inter and Intra-cluster distance

The genetic structure inside and between the okra genotypes is high lightened by the examination of intra- and inter-cluster distances, providing important information for breeding tactics. Greater genetic homogeneity is seen in clusters with short intra-cluster distances, like Cluster IV, suggesting that the genotypes inside these clusters have comparable genetic histories. Since the genetic similarities within these clusters may improve the prediction of features in subsequent generations, this homogeneity may be beneficial for creating stable lines.

On the other hand, Clusters I and III are useful repositories for introducing a variety of phenotypes due to their increased intra-cluster distances, which suggest significant genetic variability. With an intra-cluster distance of zero, the distinct genotype in Cluster IV, V, VI and VII reflects a unique genetic identity that might be carefully crossed with clusters that are genetically varied to produce hybrids with novel combinations of traits. Significant genetic difference is highlighted by the noticeable inter-cluster distances, especially between Clusters III and VII, which raises the possibility that these clusters could be attractive parent sources for hybridization. Breeders can take advantage of heterosis by crossing genotypes from highly divergent clusters, possibly producing hybrids with better vigor and phenotypic performance. On the other hand, Clusters V and VII have comparatively shorter inter-cluster distances, which indicates closer genetic ties and makes them appropriate for backcrossing initiatives or the creation of lines with comparable genetic backgrounds intended to preserve desired features. Overall, the results indicate that while the more genetically similar clusters present chances for stabilizing desired traits, choosing genotypes from genetically remote cluster may improve the genetic basis in breeding operations. Breeders may be able to create more diversified cultivars that are suited to different market or environmental requirements in addition to high-yielding, homogeneous types with this balanced strategy.

Cluster means for different traits among 20 genotypes of okra: Clusters I, which have high average pod weight and Cluster II which have high number of fruits per plant and overall yield per plant, indicate strong potential for breeding programs aimed at increasing okra productivity; high-yielding traits in these clusters align with productivity-focused objectives and could be used as parental lines to develop high-yielding varieties. The notable diversity observed among clusters offers valuable opportunities for targeted breeding.

On the other hand, Cluster II with lesser days to 50% flowering and Cluster VI for lesser days to first flowering node and early harvest duration may be a useful resource for breeding early maturing cultivars due to its early flowering and maturity. Furthermore, certain characteristics, like heavier seed weight in Cluster IV, indicate the possibility of specialized breeding objectives, such as nutritional enhancements. The genetic diversity found in each cluster not only supports a range of selection opportunities for parental genotypes but also serves as a basis for expanding the genetic base in breeding programs, which in turn promotes the development of improved okra cultivars for a variety of agronomic and consumer demands.

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Conflict of interest

All the authors declare that they do not have any conflict of interest and agree on all the parameters.

References

1. Allard RW. Principles of plant breeding. New York: John Wiley & Sons, Inc.; 1960.
2. Akinyele BO, Temikotan T. Effect of variation in soil texture on the vegetative and pod characteristics of okra (*Abelmoschus esculentus* (L.) Moench). Int J Agric Res. 2007;2(2):165-169. https://doi.org/10.3923/ijar.2007.165.169
3. Al-Wandawi H. Chemical composition of seeds of two okra cultivars. J Agric Food Chem. 1983;31(6):1355-1358. https://doi.org/10.1021/jf00120a051
4. Chanchal DK, Alok S, Kumar M, Bijauliya RK, Rashi S, Gupta S. A brief review on *Abelmoschus esculentus*. Int J Pharm Sci Res. 2017;7:58-66.
5. Dwivedi M, Sharma DP. Correlation and path analysis studies in okra [*Abelmoschus esculentus* L. Moench] under Jabalpur condition. Int J Agric Sci. 2017;9(34):4504-4509.
6. Elkhalifa AEO, Alshammari E, Adnan M, Alcantara JC, Awadelkareem AM, Eltoum NE, *et al*. Okra (*Abelmoschus esculentus*) as a potential dietary medicine with nutraceutical importance for sustainable health applications. Molecules. 2021;26(3):696. https://doi.org/10.3390/molecules26030696
7. Hallur R, Shantappa T, Koppad SB, Jagadeesha RC. Correlation and path coefficient analysis of yield attributes in okra (*Abelmoschus esculentus* (L.) Moench.). Indian J Ecol. 2016;43(1):188-191.
8. Haq I, Azam N, Ashraf M, Javaid MM, Murtaza G, Ahmed Z, *et al.* Improving the genetic potential of okra (*Abelmoschus esculentus* L.) germplasm to tolerate salinity stress. Sci Rep. 2023;13(1). https://doi.org/10.1038/s41598-023-48370-48374
9. Ibitoye DO, Kolawole AO. Farmers' appraisal on okra [*Abelmoschus esculentus* (L.)] production and phenotypic characterization: A synergistic approach for improvement. Front Plant Sci. 2022;13. https://doi.org/10.3389/fpls.2022.787577
10. Joshi BK, Mudwari A, Bhatta MR, Ferrara GO. Genetic diversity in Nepalese wheat cultivars based on agro-morphological traits and coefficients of parentage. Nepal

Agric Res J. 2004;5:7-18.
11. Komolafe RJ, Ariyo OJ, Alake CO. Correlation and path coefficient analysis of fruit yield attributes in forty genotypes of okra (*Abelmoschus esculentus*). Agric Res. 2022;11(1):15-23. https://doi.org/10.1007/s40003-021-00549-9
12. Martin FW, Rhodes AM. Seed characteristics of okra and related Abelmoschus species. Qual Plant Foods Hum Nutr. 1983;33(1):41-49. https://doi.org/10.1007/bf01093736
13. Moulana S, Prasad V, Kumar P. Economic importance and production technology of okra. 2020.
14. Mohammed J, Mohammed W, Shiferaw E. Performance and genetic variability of okra [*Abelmoschus esculentus* (L.) Moench] genotypes in Ethiopia for agromorphology and biochemical traits. Adv Agric. 2022;Article ID 5521151.
15. National Research Council. Okra. In: Lost Crops of Africa: Volume II: Vegetables. Washington (DC): National Academies Press; 2006.
16. Nbeaa RA, Abo-Trabi AE. Phenotypic correlation and path coefficient and relative importance studies in okra (*Abelmoschus esculentus* L. Moench). Basrah J Agric Sci. 2023;36(1):50-59.
17. Ranga A, Kumar S, Darvhankar M. Variability parameters in okra (*Abelmoschus esculentus* L.)-A review. Agric Rev. 2019;40(1):75-78. https://doi.org/10.18805/ag.r-1852
18. Ranga AD, Kumar S, Darvhankar MS. Variability among different yield and yield contributing traits of Okra (*Abelmoschus esculentus* L. Moench) genotypes. Electron J Plant Breed. 2021;12(1):74-81. https://doi.org/10.37992/2021.1201.011
19. Ranga AD, Vikram A, Kumar R, Dogra RK, Sharma R, Sharma HR. Exploitation of heterosis and combining ability potential for improvement in okra (*Abelmoschus esculentus* L.). Sci Rep. 2024;14(1). https://doi.org/10.1038/s41598-024-75764-75769
20. Ranga AD, Vikram A, Kumar R, Dogra RK, Sharma R, Bairwa MK. Genetic assessment and potence ratio of various traits of okra (*Abelmoschus esculentus*) in mid hills of Himachal Pradesh. Indian J Agric Sci. 2024;94(1):26-32. https://doi.org/10.56093/ijas.v94i1.139435
21. Singh Y, Sharma M, Sharma A. Genetic variation, association of characters, and their direct and indirect contributions for improvement in chilli peppers. Int J Veg Sci. 2009;15(4):340-368. https://doi.org/10.1080/19315260903004158
22. Sindhumole P, Manju PR. Evaluation of Okra [*Abelmoschus esculentus* (L.) Moench] germplasm for yield and quality of fruits. Indian J Plant Genet Resour. 2014;27:28-35.
23. Thirupathi Reddy M, Hari Babu K, Ganesh M, Chandrasekhar Reddy K, Begum H, Purushothama Reddy B. Genetic variability analysis for the selection of elite genotypes based on pod yield and quality from the germplasm of okra (*Abelmoschus esculentus* L. Moench). J Agric Technol. 2012;8(2):639-655.
24. Yawalkar KS. Vegetable crops in India. Nagpur: Agri-Horticultural Publishing House; 1969. p.158.
25. Al-Wandawi H. Chemical composition of seeds of two okra cultivars. J Agric Food Chem. 1983;31(6):1355-1358. https://doi.org/10.1021/jf00120a051
26. Dewey DR, Lu KH. A correlation and path-coefficient analysis of components of crested wheatgrass seed production. Agron J. 1959;51(9):515-518.