



Exploration Of Genetic Variations In Okra [*Abelmoschus Esculentus* (L.) Moench] Accessions Based On Quantitative Morphometric Traits

S. S. Keerthana^{1*}, J. L. Joshi^{2*}, Y. Anbuselvam³ and J. Sam Ruban⁴

^{1*}Ph. D Research Scholar, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalainagar-608002 (Tamil Nadu), India

^{2*}Assistant Professor, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalainagar-608002 (Tamil Nadu), India

³Professor, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalainagar-608002 (Tamil Nadu), India

⁴Associate Professor, Department of Horticulture, Faculty of Agriculture, Annamalai University, Annamalainagar-608002 (Tamil Nadu), India

***Corresponding Author:** S. Keerthana, J.L. Joshi

^{*}Ph. D Research Scholar, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalainagar-608002 (Tamil Nadu), India. Email: vidhyodh97@gmail.com

^{*}Assistant Professor, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalainagar-608002 (Tamil Nadu), India. Email: jeya.joshi@gmail.com

Article History	Abstract
Received: Revised: Accepted:	Within a species population, the amount of diversification is reflected by its genetic variability as it enumerates the genetical and environmental favour on that population. In terms of this, forty eight okra collections were field investigated in RCB design during 2022 as a summer crop. Significant difference among the collected okra accessions was statistically proven by ANOVA. <i>Per se</i> range for okra traits clarified the elaborate variation for fruit yield and others. As always, GCV was marked as lower than PCV which signalled the error regarding environment. Genetic advance along with heritability was noticed high for most of the traits especially yield and its related components that entrusted the selection of traits on phenotype for new trait based expectations perpetually in okra.
CC License CC-BY-NC-SA 4.0	Keywords: <i>Abelmoschus esculentus</i> , variation, yield traits, selection

Introduction

The vegetable that occupies prominent position in the weekly diet chart of people is the okra (*Abelmoschus esculentus* (L.) Moench), well known by its name Lady's finger. For plant species with various geographic origins, genetic variability serves as a reference point for genetic diversity (Tenam *et al.* 2020). Every crop breeding event works towards its own targeted path by effectively addressing crop diversity and variability. Effective morphometric description requires the field planting of number of plants in accordance with a predetermined layout (Kenaw *et al.* 2023).

Phenotypic descriptors can be utilized for evaluation to identify candidates with the best mean performance for a given set of complex traits (Hill, 2010). Genotypic variation is essential for addressing unanswered evolutionary questions related to the conservation of genetic diversity. Simultaneously, environmental variation is highly significant, as it reflects the cumulative interplay of external environmental influences on genetic factors, indicating the versatility of germplasm across diverse environments. Inherent allelic variation, which intrinsically represents gene sequence variation amid population groups, is morphologically visualized in the form of different phenotypes for various qualitative and quantitative traits (Sadia *et al.* 2020). Plant breeders deploy directional selection by manipulating the partner parameters in variability *viz.*, heritability in broad sense plus genetic advance to exploit the traits of target for efficient selection and expected genetic progress in selection phase (Pundir *et al.* 2022). These parameters are crucial for plant and animal breeders as they provide insights into the genetic makeup and potential for selection within a given population.

Great variation in germplasm aids in the efficient selection of high yielding, better adapted crop plants with possible uses of direct introduction as a variety or one of the parents in crossing scheme of breeders for variety development programs. From this context, okra accessions were explored to seek wider trait variations for phenological growth based and yield-based traits.

Materials and Methods

Forty-eight heterogeneous genotypes of okra were collected from different geographical regions of India and Africa that includes commercially released varieties, land races and accessions that were field experimented in research farm of Genetics and Plant Breeding Department, Faculty of Agriculture, Annamalai University, Chidambaram, India. During *kharif* season, the collected germplasm were sown in a layout design using randomized complete block design containing three replications. In every field plots, each genotype was allotted in random with ten plants per row at spacing of 60 x 30 cm. Cultural practices such as watering, hoeing, weeding, and earthing-up were consistently followed. Morphometrical data collection on quantitative characteristics was recorded according to the International Plant Genetic Resources Institute's (IPGRI, 1991) okra-specific descriptor list. Some of the major complex traits and genetic materials taken for research are listed in the table 1.

The field drawn numerical data was subjected to analysis of variance (ANOVA). Using the least significant difference at the 5% probability level, the mean genotype performance was compared using the significance of mean squares (Panse & Sukhatme, 1954). Statistical software used was AGRISTAT for variability analysis. The PCV and GCV were calculated using Burton (1952) formulae and classified as Low (0–10%), Moderate (10–20%), and High (> 20%). According to Robinson (1966), broad sense heritability (bsh^2) values were determined, and the proportion was divided into Low (0–30%), Moderate (30–60%), and High (>60%) categories using Hanson *et al.* (1956) classification. Genetic advance was quantified by Johnson *et al.* (1955) as absolute values (GA) and as a percentage of the mean (GAM), which grouped into Low (0-10%), Moderate (10-20%), and High (> 20%).

Table 1. Materials taken for the experimental study

Quantitative traits observed		Name of the genotypes used					
PH	Plant height at 80% maturity (cm)	G1	EC329363	G17	IC45790	G33	Emerald
NoB	Number of branches per plant	G2	EC329365	G18	IC45796	G34	Arka anamika
NoI	Number of internodes	G3	EC329367	G19	IC45800	G35	Parbhani kranti
DFI	Days to first flower (days)	G4	EC329369	G20	IC45804	G36	Red long okra
FL	Fruit length (cm)	G5	EC329371	G21	IC45806	G37	Red short okra
FD	Fruit diameter (mm)	G6	EC329373	G22	IC45813	G38	Green okra
FW	Average fruit weight (gm)	G7	EC329377	G23	IC45817	G39	Green round okra
NoF/P	Number of fruits per plant	G8	EC329379	G24	IC45819	G40	Double color okra
NoS/F	Number of healthy seeds per fruit	G9	EC329381	G25	IC90174	G41	Pink okra
HSW	100 seed weight (gm)	G10	EC329383	G26	OKRA-26	G42	Cow horn okra
DFH	Days to first harvest (days)	G11	EC329386	G27	OKRA-27	G43	Elephant tusk okra
HD	Harvest duration (days)	G12	EC329396	G28	OKRA-28	G44	Tree okra
NoP	Total number of pickings	G13	IC44529	G29	OKRA-29	G45	Hill okra
PD	Plant duration at 80% maturity (days)	G14	IC45723	G30	Clemson spineless	G46	White velvet
FY/P	Fruit yield per plant (gm)	G15	IC45728	G31	African type	G47	White okra
		G16	IC45747	G32	Kasha kranti	G48	Multibranch okra

Results and discussion

I) ANOVA

The result of analysis of variance for all the studied characters is presented in table 2. All the analysed traits were shown high significance for both 0.05 and 0.01 significance level of probability. The highest positive significant value was secured by fruit yield per plant (155810.98**) and the lowest by 100 seed weight (2.96**). Reddy *et al.* 2022; Komolafe *et al.* 2023 and many researchers supported the present results.

In ANOVA table, replication showed no discernible variation in all the germplasm indicating the meagre accounting of environmental inaccuracies. The quantitative data used to determine ANOVA revealed the genotypes were significant genotype-to-genotype variance for all of the characters studied which represents the presence of appreciable genetic heterogeneity among the examined germplasm. This may help the breeders to put forward the accessions to additional analysis for examining its breeding behaviour and value in crop improvement programs.

Table 2. Analysis of variance for 15 quantitative traits in okra genotypes

Source of variation	Replication	Genotype	Error	SE	SEd	CD (5%)	CD (1%)	CV (%)
	df = 2	df = 47	df = 94					
PH	94.2183	5106.9139**	31.1339	3.22	4.56	9.02	11.98	4.48
NoB	2.4979	5.4456**	0.6648	0.47	0.67	1.32	1.75	17.86
NoI	21.7778	118.2055**	3.8345	1.13	1.60	3.17	4.21	7.69
DFP	3.4607	387.3937**	1.5453	0.72	1.02	2.01	2.67	2.05
FL	0.7319	26.2547**	0.4475	0.39	0.55	1.08	1.44	3.87
FD	22.3283	34.1691**	0.7784	0.51	0.72	1.43	1.89	3.82
FW	0.4130	68.6431**	1.6270	0.74	1.04	2.06	2.74	6.03
NoF/P	0.8587	122.3635**	1.7425	0.76	1.08	2.13	2.83	5.66
NoS/F	38.8557	493.7755**	10.0099	1.83	2.58	5.11	6.79	4.61
HSW	0.0196	2.9639**	0.0413	0.12	0.17	0.33	0.44	3.44
DFH	4.1120	377.6602**	1.8086	0.78	1.09	2.17	2.89	1.88
HD	10.5842	55.1462**	1.3216	0.66	0.94	1.86	2.47	2.31
NoP	0.9829	23.0617**	0.8605	0.54	0.76	1.50	1.99	7.72
PD	3.5473	281.6311**	2.3787	0.89	1.26	2.49	3.31	1.62
FY/P	2548.2963	155810.98**	490.5759	12.79	18.08	35.81	47.56	4.69

[** Significant at 1% probability level; SE- Standard error; SEd- Standard Error of difference; CD- Critical difference; CV- Coefficient of variation]

II) Mean performance of the genotypes

The genotypes performance on the basis of mean value is computed (Table 3a & 3b) and indicated the occurrence of many improvement traits with utmost importance. Days to first flower (43.52 days), first harvest (51.98 days) and plant duration (79.51) showed early average performance by the genotypes G27, G26 and G5 respectively. High positive phenological and growth traits plant height (215.51 cm) by G20, number of branches (8.73) by G39, and number of internodes (40.61) by G39 was recorded. For fruit yield based characters, the mean values reached high as such by the genotype G43 for fruit length (25.46 cm), G22 for fruit diameter (31.02 mm), G17 for average fruit weight (39.23 g), G29 for number of fruits per plant (40.28), G16 for harvest duration (61.05 days), G29 for both number of pickings (18.36) and fruit yield per plant (852.30 g). Some seed related traits also noted maximum for number of seeds per fruit (100.13 in G13), and 100 seed weight (8.17 gm in G36). The entire metric traits registered notable *per se* performance for particular genotypes, which could fulfill the maternal and paternal requirements of okra breeder's for their specific targets. Previous workers like Ranjit *et al.* 2016; Shivaramgowda *et al.* 2016; Kumar *et al.* 2019; Barman and Marboh, 2022; Setu, 2023 also remarked the importance of mean performance.

Table 3a. Mean performance of okra morphometric traits

Genotypes	PH	NoB	NoI	DFP	FL	FD	FW	NoF/P
G1	82.54	4.33	13.33	52.29	15.76	20.62	15.92	13.04
G2	147.33	3.67	25.00	57.18	17.14	19.54	18.07	14.45
G3	79.22	3.67	18.68	51.60	11.87	19.34	17.33	12.28
G4	64.19	2.68	18.06	54.25	13.35	21.46	18.32	16.43
G5	65.26	4.67	14.00	56.66	14.51	22.18	19.61	15.31
G6	94.77	5.68	21.00	59.58	13.64	22.17	19.20	17.43
G7	111.78	4.45	24.33	61.67	14.42	21.99	20.64	22.77
G8	141.81	5.23	26.56	61.78	13.93	24.25	16.74	20.60
G9	100.13	3.36	20.33	63.40	16.03	25.49	19.17	21.45
G10	67.71	3.67	21.36	53.95	13.82	26.02	21.14	17.31

G11	78.00	3.00	20.43	60.29	15.91	24.05	18.95	17.44
G12	74.34	3.16	23.67	65.28	16.64	27.27	21.86	22.73
G13	103.99	5.10	24.53	52.78	15.60	23.98	18.99	22.89
G14	146.59	3.33	27.00	59.41	17.99	26.38	17.07	26.29
G15	92.92	3.76	15.67	51.56	17.10	20.49	15.14	21.20
G16	80.31	4.16	16.68	62.88	14.85	23.57	19.83	26.20
G17	206.23	6.56	33.68	70.19	23.77	26.93	39.23	36.44
G18	122.82	3.25	24.66	61.61	17.21	25.86	17.17	23.81
G19	146.62	3.76	24.34	64.16	16.93	23.25	28.85	20.70
G20	215.51	5.48	36.75	92.58	18.32	29.91	24.89	19.39
G21	160.60	5.76	29.16	63.36	19.61	27.73	23.17	29.60
G22	106.03	6.53	28.76	67.46	20.45	31.02	27.58	33.11
G23	144.12	3.73	23.72	61.89	17.88	19.34	17.03	27.17
G24	129.33	3.72	21.32	59.10	15.36	18.06	15.85	25.25
G25	162.52	4.67	24.12	56.31	17.98	21.21	18.82	26.30
G26	125.95	4.86	25.36	43.52	20.56	23.08	21.64	31.81
G27	124.45	4.68	24.12	44.86	19.69	24.32	19.96	29.62
G28	94.93	4.66	23.13	46.68	14.87	21.54	23.45	34.36
G29	179.56	4.68	28.35	48.03	19.86	23.40	28.15	40.28
G30	125.71	3.44	29.22	53.01	14.79	21.35	18.61	26.79
G31	123.83	4.23	28.32	66.19	16.39	21.07	19.75	23.36
G32	128.83	6.10	32.11	50.20	14.66	21.04	21.76	28.03
G33	93.18	3.77	18.00	51.08	18.41	24.14	19.83	21.45
G34	92.95	3.57	23.43	54.62	17.81	19.10	21.96	28.19
G35	135.62	5.36	30.16	43.72	21.65	24.19	28.19	34.41
G36	190.56	6.86	32.42	74.40	22.58	23.01	30.12	32.07
G37	137.75	3.46	17.76	59.31	15.81	17.45	16.73	16.11
G38	127.52	2.67	16.86	55.51	18.21	20.07	16.50	15.04
G39	181.42	8.73	40.61	85.42	19.84	23.09	25.64	30.77
G40	128.20	5.45	29.70	71.16	18.15	28.27	25.51	20.73
G41	201.22	7.46	32.46	80.13	19.78	25.14	28.52	26.02
G42	201.74	6.62	33.76	85.04	21.10	30.42	31.29	22.26
G43	185.03	7.00	36.12	90.36	25.46	25.29	32.66	16.47
G44	111.45	3.11	30.67	59.95	14.82	25.78	17.93	20.72
G45	122.48	3.55	35.43	64.85	13.92	18.45	16.18	22.31
G46	87.35	4.11	24.12	52.45	21.51	19.09	16.96	16.20
G47	77.80	4.89	24.44	55.62	14.24	17.17	14.23	17.79
G48	71.49	6.67	31.30	60.29	16.13	21.02	19.35	20.79

Table 3b. Mean performance of okra morphometric traits

Genotypes	NoS/F	HSW	DFH	HD	NoP	PD	FY/P
G1	49.45	3.85	63.50	41.72	11.43	95.15	149.50
G2	71.55	4.43	57.82	40.80	10.35	92.97	184.81
G3	57.44	5.41	61.39	51.27	9.99	86.42	204.79
G4	63.42	5.39	65.48	45.29	10.79	81.07	253.83
G5	59.86	5.65	67.32	44.52	11.54	79.51	256.75
G6	61.02	6.10	69.34	47.74	11.12	86.74	283.65
G7	88.15	7.16	71.92	48.86	13.94	82.58	448.17
G8	78.32	4.44	73.09	49.49	12.21	85.99	244.61
G9	67.36	5.42	75.77	49.51	11.16	89.41	328.21
G10	57.88	5.43	65.51	51.59	8.28	90.14	296.95
G11	51.84	6.13	71.24	44.36	7.76	91.46	246.76
G12	66.01	5.02	75.55	48.63	13.70	94.78	323.41
G13	100.13	6.57	63.94	53.76	12.38	89.16	430.85
G14	51.18	5.55	71.25	50.45	12.94	96.81	411.99
G15	73.96	4.67	62.70	45.79	9.95	93.52	312.19
G16	70.32	5.61	73.88	61.05	13.51	99.05	432.67
G17	88.25	4.38	80.30	59.41	17.51	105.44	852.30
G18	69.21	7.37	72.93	50.89	10.95	91.56	408.87
G19	75.42	4.71	75.23	48.07	7.95	89.48	518.30
G20	65.04	5.56	101.02	46.64	7.62	122.06	525.92
G21	57.51	7.89	74.06	51.73	15.64	95.01	739.78
G22	82.70	5.36	76.66	49.23	15.39	99.83	759.44

G23	69.65	6.43	73.18	45.79	11.60	87.95	359.25
G24	65.57	5.59	69.47	45.50	10.37	84.24	341.99
G25	71.48	7.56	68.62	49.41	11.42	95.10	428.28
G26	74.95	6.51	51.98	50.12	15.04	93.25	716.14
G27	69.86	5.95	52.43	49.15	15.22	93.47	712.71
G28	63.99	5.72	59.25	47.41	14.38	92.50	789.07
G29	89.33	7.43	59.43	51.12	18.36	100.46	844.95
G30	79.26	5.46	64.40	43.95	11.19	87.68	604.21
G31	67.79	6.42	76.77	46.49	11.39	90.86	463.16
G32	67.00	6.15	62.61	47.77	15.24	85.49	695.91
G33	58.17	6.10	64.93	50.87	15.47	100.58	471.12
G34	64.47	5.03	64.59	47.71	14.50	91.43	734.21
G35	93.40	7.30	53.34	54.47	16.85	100.82	824.02
G36	93.09	8.17	84.95	57.42	16.43	109.87	283.34
G37	57.90	5.43	70.58	45.09	6.80	83.67	236.87
G38	55.70	5.60	66.62	47.63	8.02	83.24	229.36
G39	65.41	6.34	96.25	53.16	13.07	114.92	818.79
G40	75.54	4.72	81.92	55.62	10.95	100.96	548.87
G41	76.32	4.95	90.74	58.70	12.92	109.36	665.96
G42	85.59	7.32	94.75	51.62	11.05	115.95	815.53
G43	79.01	7.84	97.47	49.04	9.60	115.69	752.55
G44	51.59	5.62	75.12	55.35	9.49	103.45	324.74
G45	46.28	5.27	79.05	58.40	10.33	99.13	257.61
G46	62.38	5.88	67.30	55.73	10.82	95.51	190.85
G47	49.50	5.02	63.83	48.09	9.26	88.88	157.66
G48	56.68	5.83	71.32	51.42	11.05	95.79	259.03

III) Variability estimates:

In common, the most accessible parameters of variability studies are phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (bs), and genetic advance in both absolute and as percent of mean are evaluated and tabulated in table 4. for fifteen okra traits.

Table 4. Variability estimates for fifteen quantitative traits

Characters	Grand mean	Range	CV (%)		bs h ² (%)	GA	GAM (%)
			PCV	GCV			
Plant height at 80% maturity (cm)	124.51	64.19 - 215.51	33.34	33.04	98.19	83.97	67.44
Number of branches per plant	4.56	2.67 - 8.73	32.92	27.66	70.56	2.18	47.86
Number of internodes	25.45	13.33 - 40.61	25.45	24.26	90.86	12.12	47.64
Days to first flower (days)	60.78	43.52 - 92.58	18.77	18.66	98.81	23.22	28.21
Fruit length (cm)	17.30	11.87 - 23.77	17.39	16.96	95.05	5.89	34.05
Fruit diameter (mm)	23.12	17.17 - 31.02	14.93	14.43	93.46	6.64	28.74
Average fruit weight (gm)	21.16	14.23 - 39.23	23.14	22.34	93.21	9.62	44.43
Number of fruits per plant	23.33	12.28 - 40.28	27.76	27.18	95.85	12.79	54.82
Number of seeds per fruit	68.66	46.28 - 100.13	19.06	18.49	94.16	25.38	36.97
100 seed weight (gm)	5.91	3.85 - 8.17	17.06	16.71	95.93	1.99	33.71
Days to first harvest (days)	71.47	51.98 - 101.02	15.77	15.66	98.58	22.89	32.03
Harvest duration (days)	49.72	40.80 - 61.05	8.83	8.52	93.14	8.42	16.94
Total number of pickings	12.02	6.80 - 18.36	23.92	22.64	89.58	5.31	44.14
Duration at 80% maturity (days)	94.97	79.51 - 122.06	10.29	10.16	97.51	19.63	20.67
Fruit yield per plant (gm)	472.46	149.50 - 852.30	48.39	48.16	99.06	466.51	98.74

a) Genotypic and phenotypic coefficient of variation

PCV is the measurable total variation in the experiment of which GCV accommodates the inherent genetic part. Statistical error variants in the research can be evaluated by elucidating the values of PCV and GCV. Some unavoidable error sources in the field experiments among equally treated plots may be due to field heterogeneity, competition effects, mechanical errors and other unmanageable factors. The experimental results conveyed GCV was lower than the PCV for each characters listed. This show the occurred variability results are because of appropriate environmental influence over the genotypes along with its genetic influence. Same variability influence was experienced by Pattnaik *et al.* (2023); Reddy *et al.* (2022); Kumar and Chakraborti (2023) in okra.

The traits plant height, number of branches, number of internodes, fruit weight, number of pickings and fruit yield estimated for higher (above 20%) PCV and GCV values suggested the broad genetic base of these traits

and there is scope for its improvement *via* simple selection. The narrow difference between phenotypic and genotypic coefficient of variation indicates that characters were less affected by environment. Moderate (10% - 20%) values of both estimates was registered for days to first flower, fruit length, fruit diameter, fruit weight, number of seeds, 100 seed weight, days to first harvest, and plant duration. The presence of moderate variability signifies that either enhances the base population or introduces stress conditions during selection in order to uncover latent genetic potential. Low (<10%) estimates of PCV and GCV was found in the trait harvest duration (8.83 and 8.52). Low variability suggests that the base population has to be improved. Trait based high, low values of CV were moreover in line with earlier studies of Yıldız *et al.* 2016; Bhardwaj *et al.* 2021; Srivarsha *et al.* 2022; Setu *et al.* 2023 and so.

b) Heritability and genetic advance

The percent trait transfer from parent to progeny can be better indexed by the heritability as it mentions the inherent part of variation. It establishes reliable phenotypic and appreciable genotypic proof for trait expression in order to predict breeding value (Mohammad *et al.* 2022). The result table showed the range of 70.56 (number of branches) to 99.06 (fruit yield per plant) for broad sense heritability. For all the fifteen traits, high heritability (>60%) was noticed. Pair results of genetic advance and heritability aids in better conclusion for selection advancement of plant characters than their single picture. Higher GAM was registered for fourteen traits out of fifteen which ranges 20.67 (plant duration) to 98.74 (fruit yield). Moderate GAM was secured by the trait harvest duration (16.94) while none of the traits exhibited low GAM values in this work which are in coincidence with Idehen and Ola (2021); Pundir *et al.* (2022); Komolafe *et al.* (2023); Munshi *et al.* (2023) and Pattnaik *et al.* (2023).

High estimated values of heritability and GAM was observed for plant height, number of branches per plant, number of internodes, days to first flower, fruit length, fruit diameter, average fruit weight, number of fruits per plant, number of seeds per fruit, hundred seed weight, days to first harvest, number of pickings, plant duration and fruit yield per plant. Result for these traits would recommend for further improvement in advance generation as it have maximum influence by additive effects of gene action (Aswathi *et al.* 2022; Pundir *et al.* 2022). Hence direct phenotypic selection could be useful with respect to these traits. High heritability with moderate GAM was observed for harvest duration trait suggesting both additive and non-additive genes acting in that attribute alongside there may be favorable influence of environment in the expression which circumlocutorily limiting the potential for selective improvement of that trait (Tenam *et al.* 2020; Rai *et al.* 2022)

Conclusion

Significant genotype mean sum of square and wider range of trait performance emphasizes broader genotypic variability among examined genetic materials. Out of twenty traits, 100 seed weight marked for narrowest variation while fruit yield per plant recognized for ample variation. Some control of environment was noted for each and every trait on view of subpar of GCV than PCV. The traits recorded high for all variability estimates (PCV, GCV, $bs h^2$, GAM) are plant height, number of branches, number of internodes, fruit weight, number of pickings and fruit yield per plant. These characters on selection could stand effective over generations as because of additive effects. In consonance with breeding intention, the genotypes with short span flowering and harvest would be selected to improve earliness traits, genotypes having high fruiting behaviour, number and yield would be considered for commercial high yielder. Also, the need to breed for specific environments is crucial because the response of most characters to environment was non-linear.

References

1. Awasthi, S., Singh, D. P., Lal, B., Singh, P., Upadhyay, A., Singh, P. K., ... & Kumar, A. (2022). Assessment of Genetic Variability, Heritability and Genetic Advance of Okra Genotypes (*Abelmoschus esculentus* L. Moench). *AMA*, 53(04), 7501- 7512.
2. Barman, A., & Marboh, R. (2022). Genetic variability and correlation analysis in indigenous germplasm of okra (*Ablemoschus esculentus* L. Moench). *Annals of Plant and Soil Research*, 24(3), 452-457.
3. Hanson, C. H., Robinson, H. F., & Comstock, R. E. (1956). Biometrical studies of yield in segregating populations of Korean lespedeza. *Agronomy journal*, 48(6), 268-272.
4. Hill, W. G. (2010). Understanding and using quantitative genetic variation. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 365(1537), 73-85.

5. Idehen, E. O., & Ola, O. E. (2021). Performance and character contributions to variability in okra (*Abelmoschus esculentus* L. Moench) genotypes, *Acta hort regiotec*, 24(2): 127–133.
6. International Plant Genetic Resource Institute (IPGRI). (1991). Okra Descriptor, Diversity for Development, International Plant Genetic Resource Institute, Rome, Italy.
7. Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy journal*, 47(7), 314-318.
8. Kenaw, W., Mohammed, W., & Woldetsadik, K. (2023). Morpho-agronomic variability of okra [*Abelmoschus esculentus* (L.) Moench] genotypes in Dire Dawa, eastern Ethiopia. *Plos one*, 18(7), e0288534.
9. Komolafe, R. J., Ariyo, O. J., Alake, C. O., & Oduwaye, O. A. (2023). Genetic variability, heritability, genetic advance, association between fruit yield and yield components of okra (*Abelmoschus esculentus* L. Moench) accessions grown in two different years. *Israel Journal of Plant Sciences*, 1(aop), 1-13.
10. Kumar, A., Kumar, M., Sharma, V. R., Singh, M. K., Singh, B., & Chand, P. (2019). Genetic variability, heritability and genetic advance studies in genotypes of okra [(*Abelmoschus esculentus* (L.) Moench)]. *Journal of Pharmacognosy and Phytochemistry*, 8(1), 1285-1290.
11. Mohammed, J., Mohammed, W., & Shiferaw, E. (2022). Performance and genetic variability of okra (*Abelmoschus esculentus* (L.) Moench) genotypes in Ethiopia for agromorphology and biochemical traits. *Advances in Agriculture*, 1-8. <https://doi.org/10.1155/2022/5521151>
12. Panse, V. G., & Sukhatme, P. V. (1954). Statistical methods for agricultural workers, ICAR, New Delhi.
13. Pattnaik, P., Singh, A. K., Singh, B. K., & Pal, A. K. (2023). Statistical estimation of genetic parameters to study variability in okra (*Abelmoschus esculentus* (L.) Moench) for enhancement in economic and quality attributes. *The Pharma Innovation Journal*, 12(8), 1505-1508.
14. Rai, M., Singh, R. K., Sharma, V., & Mishra, A. C. (2022). Studies on genetic parameters in okra [*Abelmoschus esculentus* (L.) Moench]. *Electronic Journal of Plant Breeding*, 13(2), 590-596.
15. Reddy, J. P., Anbanandan, V., & Kumar, B. S. (2022). Genotypic, phenotypic variability and evaluation of okra [*Abelmoschus esculentus* (L.) Moench] genotypes for yield components. *Journal of applied and natural science*, 14(1), 180-187.
16. Robinson, H. F. (1966). Quantitative genetics in relation to breeding on centennial of Mendelism. *Indian Journal of Genetics and Plant Breeding*, 26, 171– 187.
17. Sadia, B., Awan, F. S., Saleem, F., Altaf, J., Umar, A. B., Nadeem, M., ... & Nasir, M. (2021). Exploring plant genetic variations with morphometric and molecular markers. *In genetic variation. IntechOpen*, 101-126.
18. Setu, H. (2023). Genetic Variability Analysis for Traits in Okra (*Abelmoschus esculentus* L. Moench) Genotypes. *International Journal of Food Science and Agriculture*, 7(1), 95-104.
19. Shivaramgowda, K. D., Krishnan, A., Jayaramu, Y. K., Kumar, V., & Koh, H. J. (2016). Genotypic variation among okra (*Abelmoschus esculentus* (L.) Moench) germplasm in South India. *Plant breeding and biotechnology*, 4(2), 234-241.
20. Srivarsha, J., Dalvi, V. V., Bhave, S. G., Desai, S. S., Joshi, M. S., Mane, A. V., & Sawardekar, S. V. (2022). Genetic variability studies in the indigenous and exotic accessions of okra (*Abelmoschus* sp.) under Konkan conditions. *The Pharma Innovation Journal*, 11(4), 1876-1880.
21. Temam, N., Mohamed, W., & Aklilu, S. (2020). Agro morphological characterization and evaluation of okra [*Abelmoschus esculentus* (L.) Moench] genotypes for yield and other variability components at Melkassa, Central Ethiopia, *MOJ Ecology & Environmental Sciences*, 5(2), 80-87.
22. Yıldız, M., Ekbiç, E., Düzyaman, E., Serçe, S., & Abak, K. (2016). Genetic and phenotypic variation of Turkish Okra (*Abelmoschus esculentus* L. Moench) accessions and their possible relationship with American, Indian and African germplasm. *Journal of Plant Biochemistry and Biotechnology*, 25, 234-244