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## Phenotyping of elite okra (*Abelmoschus esculentus*) germplasm accessions under Bastar plateau agroecological zone for yield and adaptability

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### Abstract

The research was conducted on Okra (*Abelmoschus esculentus* L. Moench) genotypes during the *Kharif* season of 2022 at the Instructional Cum Research Farm, S.G. College of Agriculture and Research Station, Kumhrawand, Jagdalpur, IGKV, Raipur (Chhattisgarh), in randomized block design. The research focused on studying the qualitative and quantitative traits of okra in order to characterize and evaluate the variability among 23 elite genotypes of okra. The analysis of variance showed highly significant differences among the 23 genotypes for each trait. The results showed that the okra genotypes had a wide variation in stem and fruit colour and quality factor like pod pubescence which is a determinant factor in consumer preference. Whereas, quantitative traits like plant height, days to flowering, days to 50% flowering, pedicel length, sepal length, petal length, flower circumference, fruit length, fruit diameter, number of fruits per plant, number of seeds per pod, seed weight per pod, weight of fruit, dry weight of fruit, 100 seed weight and fruit yield per plant were noticed to be more prevalent. The highest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values were recorded for Pod weight (66.87% and 67.05% respectively). High heritability coupled with high genetic advance as per cent of mean indicates the operation of additive gene action as in case of fruit yield per plant, 100 seed weight, pod weight, plant height and number of seeds per pod. Hence, the required improvement might be achieved through direct selection based on these qualities in genetically heterogeneous material.

**Keywords:** Characterization, analysis of variance and genetic variability

### Introduction

Okra, also known as bhindi or lady's finger, is a native of tropical Africa and a member of the Malvaceae family (*Abelmoschus esculentus* L. Moench). One of the most significant vegetable crops is grown for its summer and rainy-season fragile and delectable green fruits. The crop is thought to have its roots in the Hindustani region, specifically in India, Pakistan, and Burma. *A. esculentus*, *tuberculatus*, *angulosus*, *moschatus*, *ficulens*, *tetraphyllus*, *crinitus*, *manihot* and *callie* are the nine species that make up the genus *Abelmoschus*. It is a polyploid plant and has the chromosomal number  $2n = 8x = 72$  or  $144$ . Okra is an upright annual herb with a hibiscus-like flower that grows 3 to 8 feet tall, a tropical climate veggie that is directly seeded and grows for 90–100 days. India, Nigeria, Sudan, Pakistan, Ghana, Egypt, Benin, Saudi Arabia, Mexico, and Cameroon are the primary countries where okra is grown. India has the largest land area and highest production, followed by Nigeria. The total area and output of okra in India are estimated to be 519 thousand hectare and 6371 thousand metric tonnes, respectively, according to the 2nd advance estimate of NHB (2019) [14]. In addition to being used as veggies, it also has medicinal and ayurvedic benefits. A medicine to lessen inflammation is made from leaves. For the treatment of goitre, it is a great source of iodine. Additionally, it is advised that those who have kidney stones, or renal calculus, ingest it. Okra offers advantages in terms of nutrition, finances, and industry. Carbohydrate, protein, fat, iron, calcium, fibre, thiamine, nicotinamide, riboflavin, and ascorbic acid are among the nutrients found in okra. The dried seeds can be roasted and powdered and used as a coffee ingredient or substitute, or they can be used to make vegetable curds.

The degree of genetic variability in the population and the heritability of the desired traits are key factors in crop improvement success. For the crop's present and future genetic enhancement projects, characterising okra is crucial. To create varieties or to identify parental lines to employ in combination breeding, genetic diversity knowledge is a requirement.

The performance of plants can be permanently improved with proper crop diversity management, and breeders have a better chance of selecting directly for desired traits due to the high heritability of the traits. Information on genetic variability and the relationships between various features are needed to increase yield and other traits.

### Materials and Methods

The experiment was carried out at Research cum Instructional Farm, SG College of Agriculture and Research Station, Jagdalpur, IGKV, Raipur, Chhattisgarh during *Kharif* 2022 – 23. The experiment was laid out in Randomized Block Design with three replications. Experimental material for the present investigation was collected from National Bureau of Plant Genetic Resources, New Delhi which comprised of 20 genotypes of *A. esculentus* belonging to different morphological and productive attributes and 3 genotypes belongs to local genotypes of Chhattisgarh. The spacing used was 45 × 30cm (rainy season crop). International Plant Genetic Resources Institutes descriptor list and guidelines published for the conduct of test for distinctiveness, uniformity and stability by PPV&FRA for okra species were used on qualitative traits. Data was recorded on the following 19 quantitative characters Plant height (cm), Days to flowering, Number of branches per plant, Number of nodes per plant, Internodal distance (cm), Days to 50 per cent flowering, Pedicel length, Sepal size, Petal size, Flower circumference, Fruit length (cm), Pod diameter (cm), Pod weight (g), Dry weight of pod, Number of pods per plant, Yield per plant (g/plant), Number of seeds per pod, 100 seed weight, Seed weight per pod. The average values were computed as treatment mean under each replication. Phenotypic and genotypic variability were calculated as per method proposed by Burton (1952) [2]. Heritability estimates in cultivated plants were as suggested by Robinson *et al.* (1966) [6]. Genetic advance was worked out by using the formula suggested by Johnson *et al.* (1955) [6].

### Results and Discussion

An assessment of the potential of the existing okra varieties is crucial since future progress is dependent on the genetic diversity of the original parental material. The observed variability is a measure of both environmental and genetic factors. The genetic makeup of the breeding material's heritable variability, and especially its genetic component, is obviously the most crucial factor since it directly affects how the breeding material responds to selection. However, a measure of heritability by itself cannot predict the projected gain in the following generation; it must be taken into account in conjunction with genetic progress. High yield can therefore be attained by choosing features with high heritability in conjunction with genetic advancement.

Only the genetic component of variation matters for crop development because it is the only one that is passed on to the following generation. The amount of genetic variance to the total variance, or phenotypic variance, for the characteristic in a population is typically stated as the ratio of genetic variance to total variance, or heritability. Heritability is calculated in two different ways: in a general sense as the "ratio of total genetic variance to phenotypic variance" and in a more specific sense as the "ratio of additive genetic variance to phenotypic variance."

### Qualitative traits

The qualitative traits that studied under this research were stem colour, pod colour and pod pubescence. A total of 23 genotypes, 10 genotypes (44%) showed green stem colour with red patches, while 6 genotypes (26%) were of green stem, however purple pigmented stem was observed in remaining 7 genotypes (30%). The current study reveals the presence of variation among tested genotypes for pod colour and pod pubescence. The fruit colour of 21 genotypes was green (30%), dark green (30%) and light green (31%) while 2 genotypes showed dark red purple fruit colour (9%). All genotypes were categorized into strong, medium, weak and absent fruit pubescence. Among all genotypes, 8 genotypes showed weak fruit pubescence (35%), 6 genotypes had medium pubescence (26%) while 3 genotypes had strong fruit pubescence (13%) which was an irritating character at harvest unless gloves were used during harvest. In the above result, 6 genotypes had absent fruit pubescence (26%). Tesfa and Yosef (2016) [27] reported that the fruit colour of okra had green 25.8%, 12.1% green with red, 3% dark green and 3% had dark red fruits. Temam *et al.* (2021) [26] revealed that 72.2% okra genotypes had green with a red patch stem colour, 19.4% had red or purple stem colour while 8.3% genotypes showed green stem colour. The results are also in accordance with findings of Tripathi *et al.* (2011) [29].

### Quantitative traits

Under this study, 19 quantitative characters were evaluated among 23 genotypes of okra. The analysis of variance revealed highly significant differences among the genotypes for all the characters under study. The following discussion covers the findings for each character. The plant height ranged from 31.9 (IC-117078) to 156.1cm (Jdp local bhindi) with an overall mean performance of 54.3cm, among 23 genotypes, 22 genotypes recorded tall (96%) while only 1 genotype (4%) was short height. Days to flowering ranged from 49 (IC-117202) to 72 days (IC-117300 and IC-117078) with a mean of 65 days, meanwhile 11 genotypes flowered earlier than 12 genotypes which showed late flowering. Days to 50% flowering ranged between 57 (IC-117202 and IC-111478) to 72 (IC-117078, IC-282294 and IC-117300) days with a mean of 66 days, meanwhile all the 23 genotypes (100%) showed late flowering (>45 days). Number of nodes per plant ranged from 5.8 (IC-093734) to 10.8 (Jdp local bhindi) with an average of 7.8, among 23 genotypes, 14 genotypes (61%) showed less no. of nodes per plant, while 9 genotypes (39%) more no. of nodes were observed. Number of branches per plant ranged from 5.7 (IC-093734) to 11.3 (Jdp local bhindi) with 7.9 mean value for this character. Internodal length varied from 3.7 (Gujarati bhindi) to 10.1cm (IC-522273) with an overall mean performance of 7.1cm. There were 11 genotypes with short length (48% of the total) and 12 genotypes with long length (52%). Pedicel length ranged between 1.0 (IC-093734) to 2.1cm (IC-117238) with an overall mean performance of 1.5 cm, meanwhile all the 23 genotypes (100%) showed short pedicel length. The variation in sepal size ranged between 0.58 (Gujarati bhindi) to 1.10 cm<sup>2</sup> (Jdp Local Bhindi) with an overall mean performance of 0.82 cm<sup>2</sup>. The maximum (1.10 cm<sup>2</sup>) sepal size was recorded in genotypes Jdp Local Bhindi, while it was recorded minimum in genotype Gujarati Bhindi (0.58 cm<sup>2</sup>) where 12 (52%) genotypes had large sepal size while 11 genotypes (48%) had small size. The variation in petal size ranged between 0.67 (Bastar Local) to 1.49 cm<sup>2</sup> (IC-117238) with an

overall mean performance of 1.00 cm<sup>2</sup>. Ten genotypes (43%) exhibited small petal size whereas, thirteen genotypes (57%) showed large petal size. The variation in flower circumference ranged between 6.60 (IC-034190-A) to 20.43 cm (Jdp Local Bhindi) with an overall mean performance of 12.19 cm, where 12 (52%) genotypes had small perimeter while 11 genotypes (48%) had large circumference. Fruit length varied from 7.0 (IC-117078) to 14.8 cm (IC-117238) with a mean value of 10.9 cm. Among 23 genotypes, there were 16 genotypes with medium length (70% of the total) and 7 genotypes with short length (30%). Fruit diameter varied from 1.3 (IC-111478) to 2.7 cm (Jdp Local Bhindi) with a mean value of 1.9 cm. Among the genotypes, 12 genotypes (52%) were categorized into medium fruit diameter while 11 genotypes (48%) were categorized into large fruit diameter. Number of fruits per plant ranged from 3.5 (IC-111507) to 6.9 (IC-117238) with an average of 5.5, Among 23 genotypes assessed, 12 genotypes (52%) had a high number of fruits per plant and 11 genotypes (48%) had a low number of fruits per plant. Number of seeds per pod lied between 23.5 (EC-305616) to 88.4 (Jdp Local Bhindi), among all genotypes, 9 genotypes showed large number of seeds (39%) whereas 14 genotypes showed less no. of seeds (61%) while the mean was 42.5. Seed weight per pod lied between 1.5 (Gujarati Bhindi) to 4.3 g (IC-282294), with 2.8 g mean value, among the accessions investigated, 10 genotypes (43%) showed high seed weight while 13 had low seed weight (57%). Weight of fruit lied between 3.4 g (Gujarati Bhindi) to 26.9 g (Jdp Local Bhindi) with the mean value of 8.1 g. Out of the accessions studied, 7 genotypes recorded high pod weight and 16 genotypes showed low pod weight. Dry weight of fruit lied between 1.3 (IC-117300) to 6.2 g (Jdp Local Bhindi), while the mean value was 2.9 g. Among all the genotypes analyzed, 9 genotypes (52%) demonstrated high dry weight, whereas 14 genotypes (48%) showed low dry weight. 100 seed weight varies from 4.6 (Gujarati Bhindi) to 13.1 g (IC-282294), while the mean value was 8.1 g. Out of the accessions assessed, 13 genotypes (57%) displayed low seed weight, while 10 genotypes (43%) demonstrated high seed weight. Fruit yield per plant was ranged between 108.9 g (Pusa Sawani (C4)) and 344.5 g (Jdp Local Bhindi) and mean value of 157.0g. Low fruit yield was observed in 17 genotypes, accounting for 74% of the total, while high fruit yield was exhibited by 6 genotypes, representing 26% of the sample. These findings are in consonance with the findings of earlier research done by Kerure *et al.* (2017) [7]; Thulasiram *et al.* (2017) [28]; Makhdooni *et al.* (2018) [9]; Saleem *et al.* (2018) [22]; Ranpise *et al.* (2018) [20]; Kumari *et al.* (2019) [8] in different locations. For all the characters under study, phenotypic variances were higher than the corresponding genotypic variances showing the environmental factors influence the expression. The genotypic variance varies from 0.02 to 2824.34, while the phenotypic variance varies from 0.02 to 2941.03. The magnitude of genotypic variance and phenotypic variance was highest for fruit yield per plant (2824.34, 2941.03) followed by plant height (655.74, 663.59), number of seeds per pod (209.38, 215.15), pod weight (29.33, 29.49), days to flowering (26.91, 38.72) and days to 50% flowering (18.77, 29.45) respectively, while lowest value recorded for sepal size for both genotypic and phenotypic variance was 0.02. Both genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were highest for Pod weight (66.87% and 67.05% respectively), plant height (47.20% and 47.48% respectively), dry weight of pod (39.89% and 40.45%

respectively), fruit Yield per plant (33.86% and 34.55%), number of seeds per pod (34.07% and 34.53% respectively), 100 seed weight (26.51% and 27.21% respectively), seed weight per pod (26.44% and 27.04% respectively), petal size (26.24% and 26.77% respectively), internodal distance (25.23% and 25.47% respectively), flower circumference (21.97% and 22.28% respectively) and number of branches per plant (20.05% and 20.47% respectively). The high estimates of GCV and PCV for plant height, internodal distance, flower circumference, pod weight, dry weight of pod, number of seeds per pod, 100 seed weight, seed weight per pod and fruit yield per plant revealed that maximum variations exist among these traits and the genotypes respond to selection which can be a better tool for further improvement of these characters. The similar observations of high GCV and PCV values were observed by Kerure *et al.* 2017 [7]; Walling *et al.* 2020 [31]; Ranga *et al.* 2021 [19]; for number of seeds per pod; Nwangburuka *et al.* 2012; Kumar *et al.* 2019; Walling *et al.* 2020 for plant height; Ranga *et al.* 2021 [19] for 100 seed weight; Chandramouli *et al.* 2016; Shivaramgowda *et al.* 2016; Jadhav *et al.* 2016; Rambabu *et al.* 2019 (64.89% and 64.65% respectively) for fruit yield per plant; Sravanthi, 2017 (24.07% and 23.88% respectively); Rambabu *et al.* 2019 (29.88% and 28.83% respectively) for pod weight; Prakash *et al.* 2011; Vani *et al.* 2012 [30]; Mohammed *et al.* 2022 [11] (27.71% and 31.66% respectively) for internodal length. Traits with moderate estimates of GCV and PCV were sepal size (15.84% and 16.61% respectively), pedicel length (17.48% and 18.09% respectively), number of nodes per plant (18.62% and 19.25% respectively), number of pods per plant (14.93% and 15.44% respectively) and pod length (18.99% and 19.48% respectively), whereas the genotypic and phenotypic coefficients of variation were respectively moderate and high for fruit diameter (19.46% and 20.49% respectively). Similar observations for high PCV were noticed by Ranga *et al.* 2021 [19] (for pod width) and moderate GCV and PCV value was observed by Mehta *et al.* 2006 and Narkhede *et al.* 2015 for pod length; Nwangburuka *et al.* 2012 [15] (for number of pods per plant); Mohammed *et al.* 2022 [11] (for pod length (15.84% and 17.92% respectively) and no. of pods per plant (13.85% and 16.75% respectively)). Besides the former traits, days to flowering (8.03% and 9.63%) and days to 50% flowering (6.61% and 8.28%) showed a low value for GCV and PCV respectively. Likewise, Reddy *et al.* 2012 [21] reported low GCV and PCV for days to 50% flowering and Mohammed *et al.* 2022 conveyed low GCV and PCV for days to flowering (5.78% and 6.44% respectively). In general, the magnitude of phenotypic coefficient of variation was higher than the genotypic coefficient of variation.

Estimating GCV alone is insufficient to assess the degree of heritable variation. Therefore, when heredity is researched in conjunction with genetic advancement, heritable variation can be determined with a higher degree of accuracy. High heritability coupled with high genetic advance as per cent of mean indicates the operation of additive gene action as in case of fruit yield per plant (96.03%; 68.35%), 100 seed weight (94.90%; 53.20%), pod weight (99.46%; 137.38%), plant height (98.82%; 96.66%) and number of seeds per pod (97.32%; 69.23%). Hence, the required improvement might be achieved through direct selection based on these qualities in genetically heterogeneous material. These results are in close conformity with the findings of Chandramouli, 2016; Walling *et al.* 2020 and Bhardwaj *et al.* 2021.

**Table 1:** Analysis of variance for 19 characters in okra genotypes

Characters	Replication mean sum of squares	Genotype mean sum of squares	Error mean sum of squares	SE(d)	C.D.	C.V.
DF	2	22	44			
Plant height (cm)	1.04	1975.08	7.85	2.29	4.63	5.16
Days to 1 <sup>st</sup> flowering	0.33	92.54	11.82	2.81	5.68	5.32
Days to 50% flowering	10.74	67.00	10.68	2.67	5.40	4.99
Pedicle length (cm)	0	0.224	0.005	0.06	0.12	4.65
Sepal size (cm <sup>2</sup> )	0.001	0.053	0.002	0.03	0.07	5.03
Petal size (cm <sup>2</sup> )	0.001	0.211	0.003	0.04	0.09	5.31
Flower circumference	0.12	21.47	0.32	0.46	0.93	4.64
Number of nodes	0.002	6.502	0.148	0.31	0.63	4.92
Number of branches	0.025	7.607	0.107	0.27	0.54	4.16
Internodal distance	0.6	9.68	0.06	0.20	0.40	3.44
Number of pods	0.702	2.08	0.05	0.18	0.36	3.93
Pod length (cm)	2.11	13.12	0.23	0.39	0.79	4.35
Pod weight (g)	1.01	88.14	0.16	0.33	0.66	4.94
Number of seeds per pod	6.21	633.92	5.77	1.96	3.97	5.66
Seed weight/pod (g)	0.108	1.685	0.025	0.13	0.26	5.63
Dry weight of pod (g)	0.199	3.982	0.038	0.16	0.32	6.75
Fruit diameter (cm)	0.068	0.420	0.015	0.10	0.20	6.44
100 seed weight (g)	0.094	15.47	0.27	0.43	0.86	6.15
Yield (g/plant)	39.72	8589.71	116.68	8.82	17.84	6.88

**Table 2:** Genetic variability parameters

Characters	Mean	Min	Max	var (g)	var (p)	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)
Plant height (cm)	54.25	31.87	156.12	655.74	663.59	98.82	52.44	96.66	47.20	47.48
Days to 1 <sup>st</sup> flowering	64.59	48.60	71.87	26.91	38.72	69.49	8.91	13.79	8.03	9.63
Days to 50% flowering	65.55	56.67	72.33	18.77	29.45	63.74	7.13	10.87	6.61	8.28
Pedicle length (cm)	1.54	1.05	2.10	0.07	0.08	93.38	0.54	34.79	17.48	18.09
Sepal size	0.82	0.58	1.10	0.02	0.02	90.88	0.26	31.10	15.84	16.61
Petal size	1.00	0.67	1.49	0.07	0.07	96.07	0.53	52.98	26.24	26.77
Flower circumference	12.19	6.60	20.43	7.05	7.37	95.67	5.35	43.90	21.79	22.28
Number of nodes	7.82	5.80	10.80	2.12	2.27	93.48	2.90	37.08	18.62	19.25
Number of branches	7.89	5.67	11.33	2.50	2.61	95.88	3.19	40.43	20.05	20.47
Internodal distance	7.10	3.67	10.07	3.21	3.27	98.18	3.66	51.50	25.23	25.47
Number of pods	5.51	3.53	6.87	0.68	0.72	93.51	1.64	29.75	14.93	15.44
Pod length (cm)	10.92	6.97	14.77	4.30	4.53	95.01	4.16	38.12	18.99	19.48
Pod weight (g)	8.10	3.38	26.90	29.33	29.49	99.46	11.13	137.38	66.87	67.05
Number of seeds per pod	42.48	23.53	88.40	209.38	215.15	97.32	29.41	69.23	34.07	34.53
Seed weight/pod (g)	2.81	1.50	4.33	0.55	0.58	95.66	1.50	53.28	26.44	27.04
Dry weight of pod	2.87	1.30	6.20	1.31	1.35	97.22	2.33	81.02	39.89	40.45
Fruit diameter (cm)	1.89	1.33	2.70	0.14	0.15	90.13	0.72	38.05	19.46	20.49
100 seed weight (g)	8.49	4.60	13.07	5.06	5.34	94.90	4.52	53.20	26.51	27.21
Yield (g/plant)	156.97	108.90	344.47	2824.34	2941.03	96.03	107.28	68.35	33.86	34.55

**Table 3:** Variability of fruit colour in okra genotypes

Light green	Green	Dark green	Dark red purple
IC-111478	IC-111507	IC-117235	
EC-550848	IC-111206	IC-034190-A	
IC-117202	IC-522273	IC-039137	IC-282294
Parbhani kranti	IC-093734	IC-117300	EC-305616
Pusa sawani(C4)	IC-117078	IC-117021	
Arka anamika	IC-117238	Gujarati bhindi	
Jdp local bhindi	Bastar local	Durg local bhindi	

**Table 4:** Variability of stem colour in okra genotypes

Green	Green with red patches	Purple
IC-117021	IC-111507	IC-111206
IC-117078	IC-111478	IC-039137
IC-117235	IC-117238	IC-282294
IC-093734	IC-522273	IC-117202
EC-550848	EC-550848	IC-117300
Jdp local Bhindi	IC-034190-A	Bastar local
	Arka Anamika	Durg local Bhindi
	Gujarati bhindi	
	Parbhani kranti	
	Pusa sawani (C4)	

**Table 5:** Variability of pod pubescence in okra genotypes

Absent	Weak	Medium	Strong
IC-117021	IC-111507	IC-034190-A	
IC-117078	IC-111478	IC-039137	
IC-093734	IC-117238	IC-111206	Durg local bhindi
EC-550848	IC-117300	IC-117202	Jdp local bhindi
Gujarati bhindi	IC-522273	IC-117235	IC-282294
Arka Anamika	EC-550848	Bastar local	
	Parbhani kranti		
	Pusa sawani(C4)		

### Conclusion

According to the findings of the experiment, it is indicated that future genetic improvements in okra will benefit from the genetic variability documented for various features in relation to pod yield and the characters showing high heritability with high genetic advance *viz.*, plant height, pod weight and pod yield should be utilized in direct selection.

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