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Studies on genetic variability, heritability and genetic advance in okra [*Abelmoschus esculentus* (L.) Moench]

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Abstract

The experiment was conducted to estimate the genetic variability in 40 okra genotypes. The variability parameters like range, coefficient of range, mean, genotypic coefficient of variation, phenotypic coefficient of variation, heritability in broad sense, genetic advance and genetic advance as percentage of mean were estimated for 13 different characters. The values of phenotypic coefficient of variation (PCV) were higher than the corresponding genotypic coefficient of variation (GCV) for all the 13 characters indicating less influence of environment in expression of traits. The high to moderate genotypic coefficient of variation and phenotypic coefficient of variation was observed for number of branches per plant, green fruit yield per plant, number of fruits per plant, internodal length, plant height, number of nodes on main stem per plant and fruit length, while high heritability (broad sense) values were observed for all the eleven characters except for the two characters days to first picking and days to first flowering. The genetic advance expressed as percentage of mean was found high for number of branches per plant followed by green fruit yield per plant, number of fruits per plant, internodal length, plant height, number of nodes on main stem per plant and fruit length. The analysis of variance for experimental design indicated highly significant differences among all the genotypes for all the thirteen traits studied suggesting the presence of considerable amount of variability in the experimental material, which can be exploited for improvement of fruit yield and yield attributes in okra.

Keywords: Genetic variability, heritability, GCV, PCV, genetic advance, okra

Introduction

Okra (*Abelmoschus esculentus* L.) is one of the most widely known and utilized species of the malvaceae family. An economically important vegetable crop originating in Tropical Africa, the subtropics and India. Okra is a tropical and subtropical plant that is primarily cultivated in warm tropical and subtropical climates around the world (Charrier, 1984)[6]. Okra is known by many local names in different parts of the world. It is called lady's finger in England, gumbo in United States of America, guino-gombo in Spanish, guibeiro in Portuguese and bhindi in India. Okra is also known as the “Queen of Vegetables”. Okra is a multipurpose crop due to its various uses of the fresh leaves, buds, flowers, pods, stems and seeds. Okra immature fruits, which are consumed as vegetables, can be used in salads, soups and stews, fresh or dried and fried or boiled. It offers mucilaginous consistency after cooking. Okra is a powerhouse of variable nutrients. It is cultivated for its green fleshy pods. It grows well with mulching practices (Vasava, *et al*. 2023) [27]. They are found to be an excellent source of iodine, which is effective in controlling goiter.

A logical way to start any breeding programme is to assess the variation existing in the available materials. It is said that genetic variability is the "sine quanon" of any such programme. Selection is said to be effective in a population having large heritable variability. The genetic variability and its components are the genetic fractions of observed variability that provides measures of transmissibility of the variation and response to selection. The knowledge of pattern of inheritance of various characters are important consideration while, determining the most approximate breeding procedures applicable to any particular crop. The breeder's choice of the material for any improvement work consequently depends on the amount of genetic variability present. For successful breeding programme, amount of genetic variability present in the experimental material is a basic requirement. Therefore, it is essential for the plant breeders to measure the variability with the help of parameters like phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance. Hence, these above said parameters provide the information regarding the availability of genetic variability for different characters in germplasm.

Materials and Methods

The present investigation was conducted to assess the genetic variability in okra [*Abelmoschus esculentus* (L.) Moench]. The study was carried out during late *kharif* 2023 at the Instructional farm, Jambuvadi, College of Horticulture, Junagadh Agricultural University, Junagadh. The climate of the area represents semi-arid and tropical. The weather during the growing season was favourable for normal growth and development of crop. The experimental material consisted of 40 genotypes and was evaluated in randomized block design with three replications during late *Kharif* 2023. The seeds of these genotypes were obtained from Vegetable Research Station, J.A.U., Junagadh. Each genotype was sown with a spacing of 60 × 30 cm. The genotypes were randomly allotted to the plots in each replication. The recommended agronomical practices and plant protection measures were followed for the successful raising of the crop. The observations were recorded on five randomly selected plants in each genotype from each replication. The observations were recorded for plant height (cm), number of branches per plant, number of nodes on main stem, internodal length (cm), days to first flowering, days to first picking, days to last picking, number of picking, number of fruits per plant, green fruits weight (g), green fruit yield per plant (g), fruit length (cm) and fruit width (cm).

The analysis of variance for randomized block design (RBD) was done for each character as per Panse and Sukhatme (1985) [17]. Genotypic co-efficient of variation and phenotypic co-efficient of variation were calculated as per the formula suggested by Burton and De Vane (1952) [5]. Heritability and genetic advance were estimated using the formula suggested by Allard (1960) [2].

Results and Discussion

The estimates of mean sum of squares due to genotypes were highly significant for all characters indicating the presence of genetic diversity in the existing material among the studied genotypes for various traits as shown in Table 1.

The high magnitude of GCV and PCV was observed for number of branches per plant, green fruit yield per plant and number of fruits per plant. This is in relation with the earlier reports of Hallur *et al.* (2017) [9], Kumari *et al.* (2019) [14] for number of branches per plant, green fruit yield per plant and number of fruits per plant. Vani *et al.* (2021) [26] for number of branches per plant, Ranga *et al.* (2021) [22] for fruit yield per plant and number of fruits per plant.

The moderate magnitude of GCV and PCV was observed for internodal length, plant height, number of nodes on main stem per plant and fruit length. This is in accordance with the earlier reports of Prakash *et al.* (2022) [19] for internodal length, plant height, number of nodes on main stem and fruit length. Srivarsha *et al.* (2022) [25] for internodal length; Alam*et al.* (2020) [1] and Rana *et al.* (2020) [21] for plant height; Alam *et al.* (2020) [1] and Chetana *et al.* (2021) [7] for number of nodes on main stem and Duggi *et al*. (2013a) [8] for fruit length.

Heritability (h^2_{bs})

In the present study, high heritability estimates were observed for number of branches per plant, green fruit yield per plant, fruit length, number of fruits per plant, plant height, internodal length, number of nodes on main stem, fruit width, green fruits weight, number of picking and days to last picking. High heritability estimates indicated that the characters were least influenced by the environmental effects. This also suggested that the phenotypes were the true representative of their genotypes for these traits and selection based on phenotypic value could be more reliable.

Similar results of high heritability was reported by Komal *et al.* (2022) [12] and Nanditha *et al.* (2023) [16] for fruit yield per plant; Komal *et al.* (2022) [12] and Prakash *et al.* (2022) [19] for number of branches per plant; Kumar *et al.* (2020), Barman and Marboh (2022) [4], Komal *et al.* (2022) [12], Prakash *et al.* (2022) [19] and Reddy *et al.* (2022) [23] for plant height; Duggi *et al.* (2013a) [8] and Kerure *et al.* (2017) [11] for fruit length; Hamisu *et al.* (2021) [10] and Komal *et al.* (2022) [12] for number of fruits per plant; Chetana *et al.* (2021) [7], Komal *et al.* (2022) [12] and Prakash *et al.* (2022) [19] for internodal length; Chetana *et al.* (2021) [7] and Komal*et al.* (2022) [12] for number of nodes on main stem; Kumari *et al.* (2019) [14] for fruit width and Phani *et al.* (2015) [18] and Rambabu *et al.* (2019) [20] for number of picking.

Genetic advance (G_s)

The expected genetic advance value was high for characters green fruit yield per plant, plant height and green fruits weight. The result was in agreement with the findings of Chetana *et al.* (2021) [7] for green fruit yield per plant and plant height; Prakash *et al.* (2022) [19] for green fruit yield per plant and Ashraf *et al.* (2020) [3] for plant height.

Low genetic advance was observed for fruit width, number of branches per plant, days to first flowering, number of picking, days to first picking, fruit length, internodal length, number of nodes on main stem per plant, days to last picking and number of fruits per plant. The results are in agreement with the findings of Chetana *et al.* (2021) [7] for fruit width; Rambabu *et al.* (2019) [20] and Ashraf *et al.* (2020) [3] for number of branches per plant; Vinod and Gaibriyal (2023) [28] for days to first flowering; Rambabu *et al.* (2019) [20] for number of picking; Ashraf *et al.* (2020) [3] for days to first picking; Chetana *et al.* (2021) [7] for fruit length; Vinod and Gaibriyal (2023) [28] for internodal length; Rambabu *et al.* (2019) [20] for days to last picking; Chetana *et al.* (2021) [7] and Vinod and Gaibriyal (2023) [28] for number of nodes on main stem per plant and Chetana *et al.* (2021) [7] and Vinod and Gaibriyal (2023) [28] for number of fruits per plant.

Table 1: Analysis of variance showing mean squares of 13 characters in 40 genotypes of okra

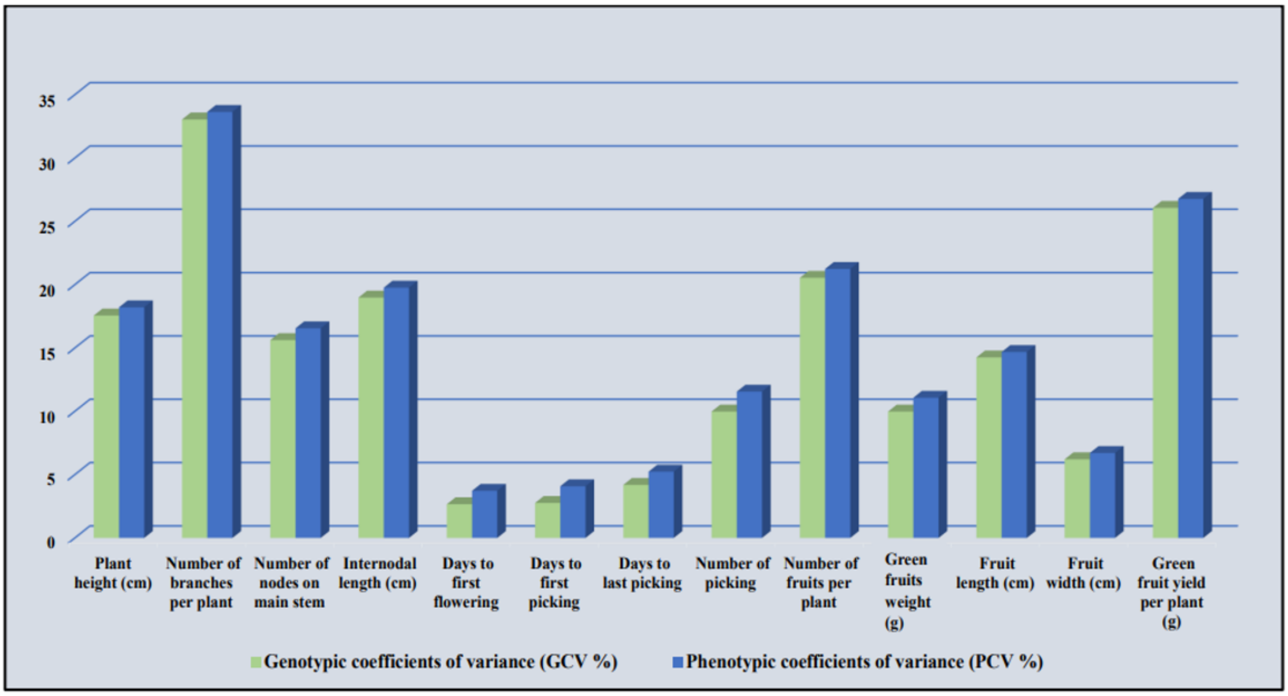
Source	d.f.	No. of picking	No. of fruits per plant	Fruit length	Fruit width	Green fruits weight	Green fruit yield per plant
Replications	2	0.23	1.19	0.18	0.0041	1.35	0.62
Genotypes	39	4.19	38.49	6.62	0.03	633.48	10682.60
Error	78	1.06	2.51	0.38	0.0040	119.17	559.80

Source	d.f.	Days to first flowering	Days to first picking	Plant height	No. of branches per plant	No. of nodes on main stem	Internodal length	Days to last picking
Replications	2	0.92	2.66	146.90	0.02	1.44	1.12	3.78
Genotypes	39	8.18**	12.85*	3608.41**	1.15**	13.62**	8.40**	55.81**
Error	78	4.00	6.97	254.51	0.04	1.49	0.65	19.89

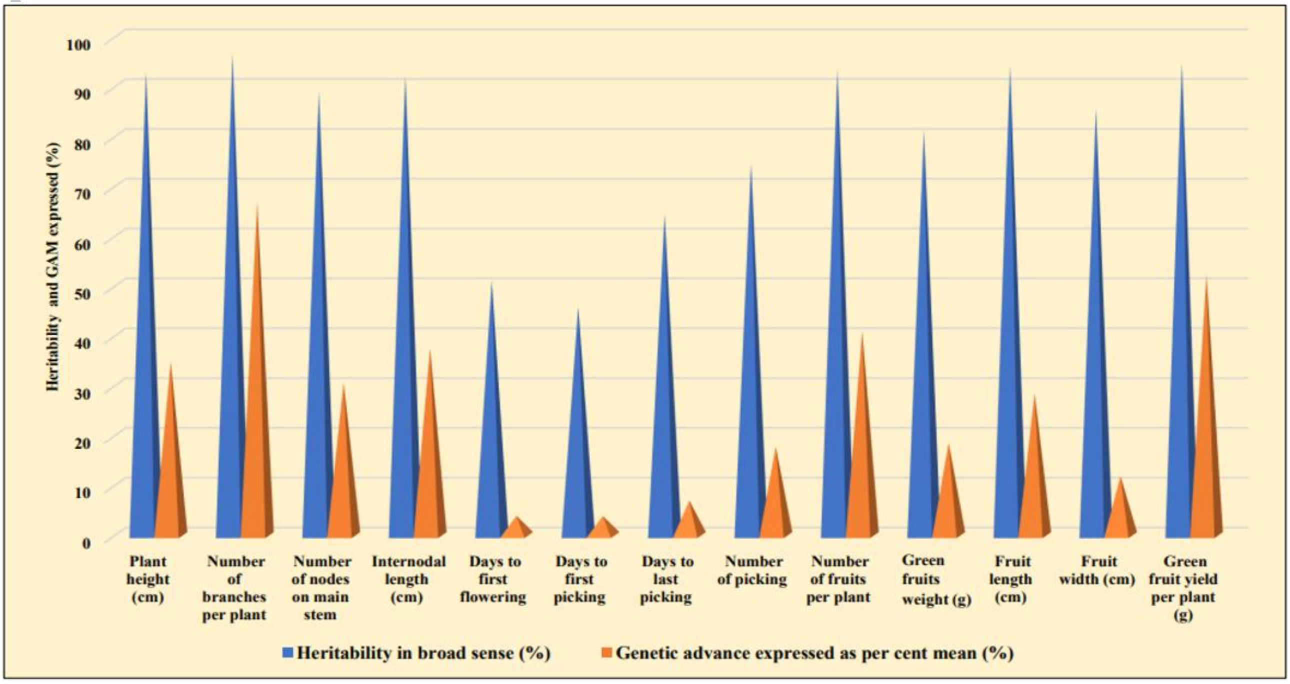
*, ** Significant at 5 % and 1 % levels, respectively

Table 2: Range, Coefficient of range (%), Mean, GCV (%), PCV (%), Heritability, GA and GA expressed as % of mean for various characters in okra

Sr. No	Characters	Range	Coefficient of range (%)	Mean	(GCV %)	(PCV %)	Heritability in broad sense h^2_{bs} (%)	Genetic Advance (GA)	Genetic advance as % of mean (GAM %)
1.	Plant height	114.37 – 252.12	37.59	190.44	17.56	18.21	92.95	66.40	34.87
2.	No. of branches per plant	0.87 – 3.40	59.25	1.85	33.04	33.64	96.48	1.23	66.85
3.	No. of nodes on main stem	8.13 – 17.47	36.48	12.88	15.62	16.55	89.05	3.91	30.58
4.	Internodal length	6.10 – 12.30	33.70	8.48	18.98	19.76	92.28	3.18	37.56
5.	Days to first flowering	40.87 – 49.2	9.25	44.38	2.66	3.72	51.04	1.74	3.91
6.	Days to first picking	45.53 – 55.73	10.07	50.69	2.76	4.08	45.80	1.95	3.85
7.	Days to last picking	75.2 – 92.47	10.30	82.51	4.19	5.23	64.35	5.72	6.93
8.	No. of picking	8.07 – 12.67	22.18	10.23	9.98	11.55	74.61	1.82	17.76
9.	No. of fruits per plant	11.20 – 23.87	36.13	16.86	20.54	21.24	93.48	6.90	40.90
10.	Green fruits weight	103.66 – 157.95	20.75	131.21	9.98	11.07	81.19	24.30	18.52
11.	Fruit length	7.14 – 15.42	36.70	10.12	14.25	14.68	94.24	2.88	28.49
12.	Fruit width	1.31 – 1.74	14.10	1.44	6.21	6.71	85.60	0.17	11.84
13.	Green fruit yield per plant	132.92 – 369.91	47.13	222.92	26.06	26.77	94.76	116.48	52.25



Genotypic Coefficient of Variation and Phenotypic Coefficient of Variation of thirteen characters in okra



Heritability and Genetic advance expressed as per cent of mean for thirteen characters in okra

Conclusion

The analysis of variance revealed that mean square due to genotypes was found significant for all the thirteen characters studied which indicated the presence of sufficient variability for all the characters studied. The magnitude of phenotypic coefficient of variation was slightly higher than that of genotypic coefficient of variation for all the characters studied. The high to moderate genotypic coefficient of variation and phenotypic coefficient of variation was observed for number of branches per plant, green fruit yield per plant, number of fruits per plant, internodal length, plant height, number of nodes on main stem per plant and fruit length, while high heritability (broad sense) values were observed for all the eleven characters except for the two characters days to first picking and days to first flowering. The genetic advance expressed as percentage of mean was found high for number of branches per plant followed by green fruit yield per plant, number of fruits per plant, internodal length, plant height, number of nodes on main stem per plant and fruit length.

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