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

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Abstract

The scope of improvement in any crop depends upon the magnitude of genetic variability present in the available germplasm. Therefore, fifty genotypes of okra collected from NBPGR, New Delhi and IIVR, Varanasi were evaluated during kharif 2016-17 to study the variability, heritability and genetic advance for different morphological and agronomic traits. The analysis of variance revealed significant differences among the genotypes for all the characters studied. The characters like number of branches per plant, fruit yield per plant, width of fruit, number of first fruiting node and length of internode showed high GCV and PCV estimates. The closeness of these parameters indicated the less influence of environment in the expression of characters. High heritability coupled with high genetic advance expressed as percent of mean were observed for yield per plant, width of fruit, number of first fruiting node indicating that they are governed by additive genes and could be effectively improved through selection.

Keywords: genetic variability, heritability, genetic advance, okra

Introduction

Okra, *Abelmoschus esculentus* (L.) Moench is predominantly a crop of tropics and subtropics. It is one of the important warm season fruit vegetables grown in summer as well as rainy seasons. Okra occupies fifth position, next to tomato, in area under vegetables in the country. Okra is mainly grown for tender fruits which are used as vegetable. Fruits are used in curry and soups after cooking. Fruits are rich in vitamin A and C, riboflavin, and minerals like calcium, phosphorus, iodine, iron and potassium (Gopalan *et al.*, 1991)^[3]. It is actually a potential export earner which provides high return to the growers. The dehydrated okra is processed product for preservation and export. Okra seeds form a nutritious ingredient of cattle-feed and are a source of vegetable oil. Among different vegetable crops, okra is most important both in terms of area and production. Okra grows successfully both in plains and hills. It is a crop of warm wet season in the northern India but is also taken as winter crop in the frost free areas Central and South India, particularly Gujarat and Maharashtra. Major growing states are Bihar and Andhra Pradesh. Okra is known by many local names in different parts of the world. In Indian subcontinent it is given different names in different regional languages (Chauhan, 1972)^[1].

Material and Methods

The experimental material of the present investigation comprising fifty genotypes of okra were evaluated in a randomized block design with three replications during *kharif* 2016-17 at Horticulture Research Centre, Sardar Vallabhbhai Patel University of Agriculture and technology, Meerut, U.P. Observations were recorded on five competitive plants for days to flowering, plant height (cm), number of branches per plant, length of first fruiting node (cm), number of first fruiting node, Length of internode (cm), length of fruit (cm), width of fruit (cm), number of fruits per plant, yield per plant (g). The analysis of variance was carried out as suggested by Panse and Sukhatme (1967)^[9]. The coefficients of variation, heritability in broad sense and expected genetic advance were estimated as suggested by Fisher (1950)^[2] and Johnson *et al.* (1955)^[5].

Results and Discussion

Analysis of variance showed that genotypes differed significantly among themselves for all the traits studied in the present investigation. The mean, genotypic and phenotypic coefficient of variations, heritability and genetic advance as percentage of mean for all traits are presented in table-1.

The range of mean values may present a rough estimate about the variation of magnitude of divergence present among different genotypes. But the estimates of genotypic and phenotypic coefficients are of greater use in determining the content of variability present within the material. Sufficient variability for all the ten characters *i.e.* days to flowering (42.46), plant height (108.52), number of branches per plant (2.80), length of first fruiting node (14.82), number of first fruiting node (5.54), Length of internode (5.92), length of fruit (13.80), width of fruit (1.65), number of fruits per plant (12.11) and yield per plant (138.93). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were high (more than 25%) showed table-1 for number of branches per plant (29.37, 23.37), yield per plant (21.34, 21.10), moderate (10 - 25%) for width of fruit (16.15, 15.79), number of first fruiting node (14.43, 14.10), length of internode (14.29, 13.88), length of first fruiting node (13.49, 13.10), number of fruits per plant (12.20, 11.86), and showed low (<10%) for length of fruit (9.47, 8.95), plant height (7.16, 6.25) days to flowering (6.49, 5.57). Similar variability for many of these traits has also been reported earlier by

Koundinya et al. (2013) ^[6], Shaikh et al. (2013) ^[10], Umrao et al. (2014) ^[12], Singh and Goswami (2016) ^[11]. High heritability estimates was observed (Table-1) for yield per plant (97.71), width of fruit (95.58), number of first fruiting node (95.47), number of fruits per plant (94.49), length of internode (94.35), length of first fruiting node (94.19), length of fruit (89.35), plant height (76.12), number of branches per plant (74.62) and days to flowering (73.80). Johnson et al. (1955) ^[5] suggested that character with high heritability coupled with high genetic advance would respond to selection better than those with high heritability and low genetic advance. Expected genetic advance (GA) as percentage of mean was observed maximum in number of branches per plant (45.15) followed by yield per plant (42.96), width of fruit (31.81), number of first fruiting node (28.38), length of internode (27.78), length of first fruiting node (26.18), number of fruits per plant (23.75), length of fruit (17.43) plant height (11.23) and days to flowering (9.86). Similar results have been reported by Shaikh et al. (2013)^[10], Mazid et al. (2013)^[8, 10], Kumar et al. (2012)^[7], Jagan et al. (2013)^[4].

Table 1: Estimation of variability (GCV & PCV), Heritability, Genetic Advance and Genetic Advance as percent of mean

Characters	Range	Mean	Heritability (%)	GA	GA as %	GCV (%)	PCV (%)
Days to 50% flowering	37.87 - 47.53	42.46	73.80	4.19	9.86	5.57	6.49
Plant height (cm)	95.32 - 125.81	108.52	76.12	12.19	11.23	6.25	7.16
Number of branches per plant	1.57 - 4.40	2.80	74.62	1.26	45.15	23.37	29.37
Length of first fruiting node (cm)	9.56 - 17.55	14.82	94.19	3.88	26.18	13.10	13.49
Number of first fruiting node	4.33 - 7.53	5.54	95.47	1.57	28.38	14.10	14.43
Length of internode (cm)	4.07 - 7.33	5.92	94.35	1.64	27.78	13.88	14.29
Length of fruit (cm)	10.18 - 15.83	13.80	89.35	2.41	17.43	8.95	9.47
Width of fruit (cm)	1.29 - 2.34	1.65	95.58	0.52	31.81	15.79	16.15
Number of fruits per plant	9.33 - 16.45	12.11	94.49	2.88	23.75	11.86	12.20
Yield per plant (g)	95.97 - 187.40	138.93	97.71	59.68	42.96	21.10	21.34

Conclusion

Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all traits. The estimates revealed that the days to flowering showed minimum phenotypic variation as well as genotypic variation, and number of branches per plant showed maximum phenotypic variation as well as genotypic variation. Estimates of heritability and genetic advance for different characters revealed that the highest heritability was found in Yield per plant and days to flowering shows minimum heritability among ten characters of okra. Expected genetic advance (GA) as percentage of mean was observed minimum in days to flowering and maximum in number of branches per plant. Genotypes which exhibited both high variability and high genetic advance for certain characters may be evaluated in multi-location trials and isolated as donors for these characters or used as parents in hybrid development programme.

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