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Research Article STUDY ON HERITABILITY AND GENETIC ADVANCE IN OKRA [ABELMOSCHUS ESCULENTUS (L.) MOENCH]

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Abstract: The experiment was conducted with 120 treatments (28 F1s, 28F2s, 28B1s and 28B2s populations) developed through diallel technique excluding reciprocals along with 8 parents viz., AB-2, AB-1, KS-312, BO-2, P-7, VRO-3, VRO-5 and PK in a randomized block design with three replications at the Research Farm of the Department of Vegetable Science, C.S. Azad University of Agriculture and Technology, Kalyanpur, Kanpur during *Kharif* 2006. The observations was recorded on 20 randomly selected plants for 10 quantitative traits viz; days to flowering, height of plant (cm), number of branches per plant, number of first fruiting node, number of nodes per plant, length of internode(cm), length of fruit (cm), width of fruit (cm), number of fruits per plant and yield per plant (g). Heritability estimate in narrow sense was high for number of branches per plant and moderate for other characters were found in both the generations. The studies based on genetic advance showed that an advancement of 8.9 g in fruit yield per plant was observed from single cycle of selection at K = 2.06. The probable genetic gain was high for number of branches per plant, length of inter node and number of first fruiting node.

Keywords: Okra, Heritability, Genetic advance

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Introduction

Okra [Abelmoschus esculantus (L.) Moench] is an important vegetable crop of Malvaceae family with having chromosome number of 2n=130 and grown in *Kharif* and Zaid season. Green edible fruits are consumed for table purpose. Okra is said to be very useful in curing diabetes, chronic dysentery and genitor urinary disorder. Ripe seeds are roasted grinded and used as substitute for coffee in turkey. The estimates of heritable and non-heritable variance are given an insight on the possible important for the characters under study [1]. To meet the ever-increasing demand for high production of fruit emphasis should be given the genetic improvement of the varieties.

Materials and Methods

The experiment was conducted with 120 treatments (28F₁s, 28F₂s, 28B₁s and 28 B₂s) developed through diallel technique excluding reciprocals along with 8 parents *viz.*, AB-2, AB-1, KS-312, BO-2, P-7, VRO-3, VRO-5 and PK in a randomized block design with three replications at the Research Farm of the Department of Vegetable Science, C.S. Azad University of Agriculture and Technology, Kalyanpur, Kanpur during *Kharif*-2006. Parents were sown in single row with ten plants and F₁s, F₂s, B₁s, B₂s grown in double with ten plants in each row. The plant to plant and row to row spacing were maintained at 45 cm apart. The observations were recorded for days to flowering, height of plant (cm), number of branches per plant, number of first fruiting node, number of nodes per plant, length of internode(cm), length of fruit (cm), width of fruit (cm), number of fruits per plant and yield per plant (g). The data obtained on all the parameters were subjected to the statistical analysis were worked out according to heritability and genetic advance in percent of mean.

Results and Discussion

Result of different parameters depicted in [Table-1]. The data were subjected to statistical and biometrical analysis. Any improvement of population depends on the magnitude and nature of variation present in particular population. The total variance is known as heritability. It is generally expressed in the percent. Thus, the heritability is a good index of spring. High heritability were observed for number of branches per plant in both the generations and length of internode only in F1 generation, which might be due to more contribution of additive genetic component responsible for the inheritance of these traits and these traits can be improve through mass selection or any other selection scheme aimed to exploiting fixable (additive) genetic variance resulting a widely adopted genotype / stains could be developed which might be passes good quality and productivity [2]. Other characters showed moderate heritability which involve both additive and nonadditive genetic components, it is obvious to not here that most of the characters showed higher estimates of heritability numerically in F₂ in comparison of F₁s except number of branches per plant, number of nodes per plant and length of internodes [3,4]. These higher estimates could be due to presence of additive x additive gene interaction in segregating, generation. Under such condition's intensive selection pressure during selection breeding programme might be given in early segregating generations and might be carried out in advancement of generations for direct effective selection. Heritability estimates alone could not be given the real picture of improvement which could be realized during selection. It is only steadfast when achievement of genetic advance under selection. In present study the genetic advance based on F1 and F2 generation presented in [Table-1] was estimated at K = 2.06 means 5% selection intensity. High genetic advance in the tune of 8.9 g for yield per plant and height of plant (5.26 cm) based on F₁ and 8.88 g and 6.66 cm for F₂ generation was observed for single cycle of selection at K = 2.06 [5,6].

Study on Heritability and Genetic Advance in Okra [Abelmoschus esculentus (L.) Moench]

| Characters | Population mean \overline{X} | | Heritability % (narrow sense) | | Genetic advance | | Genetic advance in percent of mean (narrow sense) | |
|-------------------------------|--------------------------------|--------|-------------------------------|----------------|-----------------|----------------|---|----------------|
| | F ₁ | F_2 | F ₁ | F ₂ | F ₁ | F ₂ | F ₁ | F ₂ |
| Days to flowering | 41.68 | 42.74 | 18.51 | 27.87 | 0.94 | 2.94 | 2.56 | 6.88 |
| Height of plant | 107.05 | 104.44 | 12.38 | 19.39 | 5.26 | 6.66 | 4.91 | 6.38 |
| Number of branches per plant | 3.24 | 3.61 | 51.03 | 34.02 | 1.21 | 0.81 | 37.35 | 22.44 |
| Number of first fruiting node | 6.67 | 7.19 | 25.99 | 26.06 | 0.99 | 1 | 14.84 | 13.91 |
| Number of nodes per plant | 20.82 | 19.87 | 21.34 | 20.19 | 1.84 | 1.77 | 8.84 | 8.91 |
| Length of internode | 11.35 | 11.43 | 30.52 | 20.05 | 1.79 | 1.38 | 15.77 | 12.07 |
| Length of fruit | 12.86 | 12.18 | 18.11 | 26.14 | 1.12 | 1.35 | 8.71 | 11.08 |
| Width of fruit | 1.91 | 1.99 | 15.54 | 16.75 | 0.13 | 0.11 | 6.81 | 5.53 |
| Number of fruits per plant | 17.04 | 16.22 | 15.57 | 18.49 | 1.33 | 1.43 | 7.81 | 8.52 |
| Yield per plant | 196.93 | 183.86 | 9.13 | 11.17 | 8.90 | 8.88 | 4.52 | 4.83 |

Table-1 Estimates of heritability and genetic advance in percent of mean for 10 characters in Okra

Other characters showed moderate to low genetic advance. The heritability estimates of these characters were moderate in nature indicating that these characters might under control of both additive and non-additive genetic effects [7]. Similarly, high genetic gain was observed in the tune of 37.35 percent in F_1 and 22.44 percent in F_2 for number of branches per plant followed by 15.77% in F_1 , 12.07% in F_2 for length of inter node and approximately 14.15% for number of first fruiting node was realized from single cycle of selection (8).

Conclusion

High heritability in narrow sense was observed for number of branches per plant in both generations and length of internode in F_1 generation only. Other characters showed moderate heritability in both generations. The probable genetic gains were high for number of branches per plant, length of internode and number of first fruiting node.

Application of research: Study of development of high yielding and disease resistant varieties of okra.

Research Category: Heritability and Genetics

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Author Contributions: All authors equally contributed

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Study area / Sample Collection: Vegetable Research Farm, Kanpur, 208002

Cultivar / Variety name: AB-1, AB-2, KS-312, BO-2, P-7, VRO-3 VRO-5 and PK.

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors. Ethical Committee Approval Number: Nil

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