Nature of gene action in okra through diallel analysis

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To find the nature of gene action in okra, experiment was carried out with 10 x 10 half-diallel mating design and found 45 F_1 cross combinations. The present study indicated that both additive and non-additive gene action present in three traits *i.e.*, days to 50 per cent flowering, fruit weight and number of nodes per plant and dominant gene action with asymmetrical distribution of genes and over dominance was found for all the characters. The positive and non-significant estimate of 'F' for all other characters except fruit weight suggests that the dominant genes are preponderant. In the present study the significance of t^2 value suggested the failure of the one or more assumption of diallel analysis for all the characters except days to 50 per cent flowering, fruit girth, plant height and number of nodes per plant.

Key words : Okra, Half-diallel cross, Gene action

Okra [*Abelmoschus esculentus* (L.) Moench] is an annual vegetable crop grown throughout the tropics and warmer parts of the temperate regions. It is an important vegetable crop for nutritional as well as economic point of view. Okra is special valued for its tender and delicious fruits all over the country. A knowledge of gene action helps to set an appropriate breeding strategy to accumulate fixable genes through selection. Keeping this in view, the experiment was designed to study the genetical aspects in okra through diallel mating.

The varieties DOV-1, Pusa Sawani, 1089, IC6924B-1, Barka, Sel-7, Sel-10, Arka Anamika, Pusa A-4 and Sel-4 were chosen in this study to represent substantial amount of genetic diversity for different quantitative traits. These ten genotypes were involved in 10×10 half diallel combinations to develop 45 straight crosses. During 2010, these 45 F_1s and ten parents were evaluated in RCBD with two replications. Each entry was sown in 3 m row and from this row; five random plants were tagged and used for recording observations on yield and other important quantitative traits.

Components of genetic variance were estimated from the data obtained on the diallel crosses by the method given by Hayman (1954).

In the present study the significance of t^2 value suggested the failure of the one or more assumption of diallel analysis for all the characters except days to 50 per cent flowering, fruit girth, plant height and number of nodes per plant (Table 1).

Additive genetic variance was predominant for the expression of fruit weight and days to fifty per cent flowering. While, dominance genetic variation was predominant for the expression of fruit yield per plant, plant height and fruit weight. Dominance genetic variance is being non-fixable, so success of developing homozygous lines through any selection scheme is limited. Heterosis breeding in general is likely to be most effective for the improvement of fruit yield and its contributing characters.

The positive and non-significant estimate of 'F' for all other characters except fruit weight suggests that the dominant genes are preponderant. These results are in conformity with those reported by Das *et al.* (1996), Kumar *et al.* (2004) and Rajani and Manju (1999).

Ratio $\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F}$ which indicates the proportion of dominant and recessive genes in the parents was more than unity suggesting an excess of dominant alleles controlling all the traits. These results are in consonance with those reported by Rajani and Manju (1999) and Vachhani and Shekhat (2008).

The estimates of narrow sense heritability were relatively high for number of nodes per plant (0.32), fruit girth (0.28) and