

# Studies on generation mean analysis for yield and its associated traits in okra [*Abelmoschus esculentus* (L.) Moench]

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## SUMMARY

Generation mean analysis with six generations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$ ) was chosen to study the nature and magnitude of gene effects for yield and yield attributing traits. The studies were undertaken on Vegetable Research Farm, Department of Horticulture, Institute of Agricultural Sciences, Banaras Hindu University Varanasi, during rainy season of 2006 and 2007. Characters days to first flowering, first flowering node, plant height, number of branches per plant, number of fruits per plant, fruit length and fruit yield per plant. The analysis showed the presence of additive, dominance gene effects and epistatic interactions in almost all the cases indicating the importance of both additive and non-additive gene actions in the expression of the characters. For majority of characters, duplicate type of gene action was observed. Biparental mating which could exploit both additive and non-additive type of gene effects was suggested for the improvements of the traits in the cross studies.

**Key words :** Generation mean analysis, Gene action, Duplicate, Okra

Okra is one of the important vegetable crop grown during spring summer and rainy season. It has a prominent position among vegetables due to its wide adaptability, year round cultivation, export potential and high nutritive value. The knowledge of gene effects for different traits in okra is of prime importance before starting a breeding programme. Determination of the most important suitable method and selection strategy for improvement of a trait would depend on the knowledge of gene action operating in the breeding population. Generation mean analysis is an efficient tool to understand the nature of gene effects involved in the expression of the characters. Though, generation mean analysis has been extensively used to understand the gene effects in different crops, but very few reports are available on the use of this technique for understanding the gene effects in okra crop. In view of this, the present study has objective to estimate different kinds of gene effects in the inheritance of fruit yield and its important traits.

## MATERIALS AND METHODS

The experimental material consisted of four okra

crosses namely HRB-55 x P-7, HRB-55 x Pusa Sawani, BO-2 x P-7 and BO-2 x Pusa Sawani. Six generations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$ ) of each of the four crosses were raised in a randomized block design with three replications during rainy season of 2007 at Vegetable Research Farm, Department of Horticulture, Institute of Agricultural Sciences, Banaras Hindu University Varanasi (U.P.). In each replication one row of parents and  $F_1$ s, two rows of back crosses and four rows of  $F_2$ s were grown in 10 meter long rows following 60 cm distance between rows. An approximate distance of 45 cm between plants within the rows was maintained by thinning. Recommended agronomic practices were followed for raising a good crop. The data were recorded on 5 competitive plants in parents and  $F_1$ s, 15 plants in back crosses and 20 plants in  $F_2$ 's in each plot of each replications. The mean performance was used for the analysis. Observation were recorded on days to first flowering, first flowering node, plant height, number of branches per plant, number of fruits per plant and fruit yield per plant. In order to estimate additive, dominance and interaction (additive x additive, additive x dominance and dominance x dominance) parameters, generation mean analysis was carried out following Hayman, (1958) and Jinks and Jones (1958). This procedure led to estimate the genetic parameters which gave the relative magnitude of various gene effects in different traits.

## RESULTS AND DISCUSSION

All the four crosses were subjected to A, B, C and D scaling test Mather, (1949) to sort out interacting and non interacting crosses. The test indicated the presence

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of non-allelic interactions in almost all the cases except for days to first flowering in the cross HRB-55 x Pusa Sawani and BO-2 x P-7; first flowering node in cross HRB-55 x Pusa Sawani; plant height in the crosses BO-2 x P-7 and HRB-55 x Pusa Sawani; number of branches per plant, number of fruit per plant and fruit yield in the crosses HRB-55 x Pusa Sawani, BO-2 x Pusa Sawani and for fruit length in the cross BO-2 x Pusa Sawani. In all other cases, the additive dominance model found to be inadequate to explain gene action. The A and B scaling tests provided the evidence for the presence of 'i' (additive x additive), 'j' (additive x dominance) and 'l' (dominance x dominance) type of gene interactions. The C scaling tests provided for 'l' type of epistasis whereas 'D' scaling test gave information about 'i' type of gene interaction. The presence of epistatic interaction for most of the characters was also evident from the results of analysis of digenic epistatic model for four crosses.

In case of days to first flowering, all the crosses exhibited significant additive x additive and additive x dominance and dominance x dominance type of gene effects, except the interaction of additive x additive in the cross BO-2 x Pusa Sawani (Table 1). All the genetic components were also important in the entire cross. Dominance gene action for days to first flowering was reported by many workers Kulkarni *et al.* (1976) and Rao and Sathyavathi (1977). The epistasis for days to first flowering was found to be duplicate type in all the cases except in the cross HRB-55 x Pusa Sawani confirming the complex nature of inheritance of yield.

For first flowering node, additive and dominance gene effects were found to be important for all cross except in the cross BO-2 x Pusa Sawani. All the epistasis interaction except 'j' were found to be significant for all the crosses. The additive and additive x dominance type of interaction were found to be important. Additive x additive was significant in the entire cross except HRB-55 x P-7 whereas additive x dominance was found to be significant in all the crosses except BO-2 x Pusa Sawani. Dominance x dominance type of gene interaction was exhibited by all the crosses. Duplicate type of epistasis was observed for first flowering node for all the crosses except BO-2 x Pusa Sawani. Importance of both additive and non-additive gene effects for this character was reported by Singh and Singh (1978) and Elangovan *et al.* (1981).

For plant height, all crosses exhibited additive and dominance type of gene effects. Whereas, epistasis type of gene interaction such as additive x additive, additive x dominance and dominance x dominance found to be significant except the additive x dominance type of gene interaction in the cross HRB-55 x P-7 for this character.

Duplicate type of gene interaction were exhibited in all the crosses, in this regard importance of non-additive gene action was reported by Kulkarni *et al.* (1976), Rao and Ramu (1977), Elangovan *et al.* (1981) and Panda and Singh (2003). Additive and dominance gene effect was found to be relatively more important in the entire cross for number of branches per plant. All type of gene interaction (additive x additive, additive x dominance and dominance x dominance) were exhibited significant in all the crosses. Duplicate type of epistasis was observed for this trait in all the crosses. Importance of epistatic interaction in control of this character was also reported by Korla and Sharma (1987).

For number of fruits per plant additive gene effects were found to be relatively more important because of higher values of additive than those of dominance component in all the crosses except in BO-2 x Pusa Sawani, whereas the cross BO-2 x P-7 and BO-2 x Pusa Sawani exhibited significant for additive x additive type of gene effects. Its results are also in conformity with the Arumugam and Muthukrisnan (1979). Among epistasis, additive x additive, additive x dominance and dominance x dominance exhibited significant in all the crosses except HRB-55 x Pusa Sawani and BO-2 x P-7 for dominance x dominance type of gene effect this trait. Duplicate type of epistasis was observed for this trait only in the cross BO-2 x Pusa Sawani. Importance of epistasis interaction in control of this character was reported by Arora (1990).

For fruit length the additive gene effects were found to be relatively more important in the cross, HRB-55 x Pusa Sawani, BO-2 x P-7 and BO-2 x Pusa Sawani. Dominance and additive x additive type were found to be significant in the cross HRB-55 x P-7. Additive x dominance type of gene interaction were significantly exhibited in all cross except HRB-55 x P-7 for this trait whereas, dominance x dominance type of gene interaction were exhibited by only the cross BO-2 x Pusa Sawani and HRB-55 x P-7. Importance of additive and non-additive gene action for this character was reported by Pratap and Dhankar (1980). Duplicate type of gene interaction was significantly exhibited only in the cross, HRB-55 x P-7.

In case of fruit yield per plant, additive gene effect was found to be significant in all crosses whereas dominance gene effect were exhibited all the crosses for this trait except the cross HRB-55 x P-7. Among non allelic interactions additive x additive, additive x dominance and dominance x dominance of gene effects were exhibited by the entire cross for fruit yield per plant. Duplicate type of epistasis was observed in all crosses except HRB-55 x P-7. Importance of non-additive gene



effects for this trait was observed by Chaudhary *et al.* (1993) and Aher *et al.* (2003).

The estimation of different type of gene effects provide a test for gene action and were useful for analyzing genetic architecture of a crop so as to further improve it for desired traits. The estimates obtained from each cross may be unique in varying degrees and may not be applicable to the parental population Sprague, (1966).

Dominant genetic variance formed the major part of genetic variance for the important yield components. The use of intermating of selects followed by visual selection in early segregating generations which would simultaneously exploit gene effects has been suggested. Further, this approach is likely to break some undesirable linkage resulting in the establishment of rare and useful recombinants.

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