

Gene Action for Yield and its Attributes by Generation Mean Analysis in Brinjal. (*Solanum melongena* L.)

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Abstract— Genetic studies assist the breeder in understanding the inheritance mechanism and enhance the efficiency of a breeding programme. Knowledge of gene action and their relative contribution in expression of character is of great importance. Eggplant yield depends on two components viz., fruit weight and number of fruits per plant. These traits are quantitative and therefore influenced by multiple genes. The objective of this study was to estimate the main gene effects (additive, dominance and digenic epistasis) and to determine the mode of inheritance for fruit Yield and its components. The generation mean analysis was employed in three crosses viz., Ac-2 x Annamalai, EP-45 x Annamalai and EP-89 X Annamalai to partition the genetic variance. Among the three crosses studied, the cross Ac-2 x Annamalai had complimentary type of epistasis along with significant additive gene effects and additive x additive interaction gene effects for all the three traits. Considering fruit yield per plant and its attributes, this cross was judged as the best cross for further selection programme.

Keywords— Brinjal, epistasis, five parameters, gene action, generation mean analysis, yield, yield attributes.

I. INTRODUCTION

Eggplant (*Solanum melongena* L., 2n=24), known as brinjal, originated from India and consumed extensively worldwide. In India, it is one of the most common and popular vegetable cultivated throughout the country except higher altitudes. In our country it is grown in an area of 6.63 lakh ha with production of 12.51 million tones and the productivity is 18868 kg/ha (Savaliya *et al.*, 2017). The major objective in most brinjal breeding programme is to improve the genetic potential for fruit yield.

Success of any crop improvement programme is mainly dependent upon the information regarding nature and magnitude of gene effects controlling economic

quantitative traits. The knowledge about nature and magnitude of fixable and non-fixable type of gene effects controlling quantitative yield traits is essential in order to achieve the genetic improvement in this crop. The information on the nature of the gene action could be helpful in predicting the effectiveness of selection in a segregating population. A distinct knowledge of the type of gene effect, its magnitude and composition of genetic variance are of fundamental important to a plant breeder. The efficient partitioning of genetic variance into its components viz., additive, dominance and epistasis helps in formulating an effective and sound breeding programme.

Though brinjal is a common crop but as compared to other solanaceous vegetable crops such as potato, tomato, capsicum etc., low breeding efforts have been carried out for developing potential hybrids and for genetic improvement by exploiting local germplasm. Considering this, an investigation was undertaken to evaluate the mode of gene action such as additive, dominance and their interactions (epistasis) for yield and its components by scaling test and estimation of some genetic parameter through generation mean analysis

II. MATERIAL AND METHODS

Crosses viz., Ac-2 x Annamalai (Cross I), EP-45 x Annamalai (Cross II) and EP-89 x Annamalai (Cross III) were made between four parents by manual emasculatation and pollen transfer. These crosses were further selfed and advanced to produce F2 and F3. Generations viz., P1, P2, F1, F2 and F3 were developed to study the genetic interactions. A total of three populations (3 crosses) and five generations of each cross were grown in Randomized Complete Block Design (RCBD) with four replications. Spacing adopted was 75 x 60 cm and the recommended cultural practices were followed throughout the cropping period. The experiment was conducted at APHC farm, Adhiparasakthi Horticultural College, G. B. Nagar,

Kalavai. Observations were recorded on three characters viz., number of fruits per plant (nos), individual fruit weight (g) and total fruit yield per plant (g).

III. STATISTICAL ANALYSIS

Action of the genes controlling quantitative characters can be described by the use of gene model. Mean of five generation viz., P₁, P₂, F₁, F₂ and F₃ were used to estimate genetic parameters following a perfect fit solution given by Cavalli (1952). The mid-parental effect (m) and the types of gene action viz., additive (d), dominance (h), additive x additive (i) and dominance x dominance (l) were determined using five parameter model of generation mean analysis. The adequacy of simple additive-dominance was detected by employing C and D scaling test suggested by Mather and Jinks (1971). The additive-dominance model was considered inadequate when any one of the two scales was found to deviate significantly from zero.

IV. RESULTS AND DISCUSSION

Breeding method for any crop improvement programme is largely depends on the nature of gene action prevailed. Study of gene effects controlling different characters is therefore, a pre-requisite for launching a systematic and meaningful crop improvement programme. Quantitative characters which are of great interest, are governed by large number of genes having their own effects. These are too modified by several environmental factors (Johansen, 1926). Thus, analysis at the level of individual genes become impractical and whole genome analysis over the totality of the gene should be undertaken (Wright, 1956). The genetic variability, thus, should be partitioned into its broad components.

Most valuable genetic analysis of quantitative characters can be said to have initiated with the work of Fisher (1918). He showed that these character measure continuous variation and follow the Mendelian laws. He partitioned hereditary variance into three components, (i) an additive portion resulting from average effects of gene, (ii) a portion resulting from dominance effects (intra allelic interaction) of genes, and (iii) a portion resulting from epistatic effects (non-allelic interaction) of genes.

Hayman and Mather (1955) described the digenic interactions in continuous variation. Such partitioning of variation into its components requires growing a large number of related generations under an appropriate design. Hayman (1958) and Jink and Jones (1958) have developed independently the method of estimation of five genetic parameters using generation means. These model are based on certain assumptions such as (i) diploid inheritance, (ii) multiple allelism is absent, (iii) linkage is absent, (iv) absence of lethal genes, (v) constant variability for all genotypes and (vi) environmental effects are additive with the genotypic value.

In predominantly self-pollinated crops like brinjal only additive component of genetic variation can be utilized. Among the interaction effect additive x additive type of interaction effect are more useful for the breeders. Complementary epistasis can also be successful exploited in the selection programme.

The present study was planned to estimate the nature and magnitude of allelic and non-allelic interactions in brinjal. Four elite genotypes differing in many quantitative characters were chosen to generate variability in three cross combinations. The five generation of each of these crosses were grown and observation were recorded on three important characters. The discussions on the result obtained with regard to nature of gene action are reported here and character wise for all the three crosses

4.1 Number of fruits per plant

The result of scaling test either both or C and D alone revealed significant values indicates the additive-dominance model was not found adequate for all traits in the three crosses. The failure of additive-dominance model was attributed mainly due to the epistasis.

The cross II recorded negative and significant values for scale C and D, whereas cross III had negative and significant value for scale D alone. In all the crosses both additive and additive x additive gene effects were found significant for this trait. The 'h' and 'l' effects similar signs in cross I and III and opposite in II indicated that the type of epistasis were complimentary in cross I and III and duplicate in II.

Table.1: Scaling test and gene effects for number of fruits per plant in three brinjal crosses.

Components	Cross I	Cross II	Cross III
	Ac-2 x Annamalai	EP-45 x Annamalai	EP-89 x Annamalai
Scale			
C	-8.30 ±17.26*	-23.52±11.52*	-21.13±19.34
D	9.35±12.06	-24.52±11.07*	-24.95±12.52*
Gene effects			
(m) mean	19.15±4.00**	24.89±4.53**	27.28±4.47**

(d) additive	6±1.59**	5±1.74**	5.63±1.81**
(h) dominance	4.20±11.64	11.58±13.84	16.56±12.76
(i)additive x additive	19.85±10.02*	21.25±10.54*	20.15±10.02*
(l) dominance x dominance	8.80±36.15	-.72±39.74	5.76±40.55
Type of epistasis	Complementary	Duplicate	Complimentary

*Significant at 5 per cent level.

* Significant at 1 per cent level

4.2 Individual Fruit weight (g)

Significant values for scale C and D were recorded for this trait in all the crosses. Additive and Additive x Additive gene effects were significant in the cross I whereas the cross II exhibited significant value for

additive variance only. In the third cross the value for dominance x dominance gene effect was found significant. It had been observed that all the crosses had complimentary type of epistasis.

Table.2: Scaling test and gene effects for individual fruit weight per plant in three brinjal crosses.

Components	Cross I	Cross II	Cross III
	Ac-2 x Annamalai	EP-45 x Annamalai	EP-89 x Annamalai
Scale			
C	-83.86 ±26.47**	-45.86±21.68**	-77.34±21.12**
D	-80.84±21.04**	-29.52±20.83	-19.78±12.52
Gene effects			
(m) mean	56.72±6.16**	46.76±4.95**	38.79±4.95**
(d) additive	19.50±3.28**	5.50±2.00**	-12.00±2.01**
(h) dominance	29.27±16.36	12.49±15.72	13.55±17.96
(i)additive x additive	78.92±17.32**	1.04±14.63	-23.70±14.83
(l) dominance x dominance	4.03±53.63	21.79±46.03	76.75±38.25*
Type of epistasis	Complementary	Complimentary	Complimentary

*Significant at 5 per cent level.

* Significant at 1 per cent level

4.3 Total fruit yield per plant (g)

The values of scaling test C and D were highly significant indicated the presence of epistasis in all the three crosses for this trait. In all the crosses both additive and additive x additive gene effects were found significant. The type of epistasis were complimentary in

the cross I and duplicate in the crosses II and III. three crosses with complementary type of epistasis in the cross I and duplicate type of epistasis in the other two crosses viz., Cross II and Cross III.

Table.3: Scaling test and gene effects for total fruit yield per plant in three brinjal crosses

Components	Cross I	Cross II	Cross III
	Ac-2 x Annamalai	EP-45 x Annamalai	EP-89 x Annamalai
Scale			
C	-1229.86± 123.66**	-957.91±136.72**	-1057.33±122.51**
D	-1097.28±113.61**	-1590.97±107.73**	-1087.31±125.45**
Gene effects			
(m) mean	1025.54±27.06**	1130.51±30.04**	1030.63±27.21**
(d) additive	36.65±17.18*	137.53±14.10**	37.03±16.31*
(h) dominance	764.35±84.30**	1011.02±84.82**	709.56±91.65**
(i)additive x additive	599.84±86.68**	1176.05±91.23**	622.64±86.93**
(l) dominance x dominance	176.77±261.12	-844.08±297.46**	-39.84±256.99
Type of epistasis	Complementary	Duplicate	Duplicate

*Significant at 5 per cent level

* Significant at 1 per cent level

Present findings revealed the digenic control of all the characters under study. Similar result has also been reported by ChintanMistry *et al.*, (2016). Fruit yield per plant being a complex character showed its genetic control under additive, dominance and epistasis in all the fruits per plant, individual fruit weight and total fruit yield per plant showed significant additive and additive x additive gene effect. This is in accordance with the findings of Kathiria *et al.*, (1998). The positive and significant dominance and dominance x dominance gene effects were also observed for the traits number of fruits per plant, individual fruit weight and total fruit weight per plant. Similar results were obtained by Singh *et al.* (2002). Additive and Additive x Additive genetic variance is a pre-requisite for genetic gain under selection, because this is the only genetic variance which responds to selection and it can be fixed in homozygous cultivars in crops like brinjal while the variation due to dominance effects and their interactions cannot be exploited effectively.

The phenomenon of duplicate epistasis is unfavourable from the breeder's point of view because of its decreasing effect on the analysed trait (Zdravkovic *et al.*, 2000). The presence of duplicate epistasis would be detrimental for rapid progress, making it difficult to fix genotypes with increased level of character manifestation because the positive effects of one parameter would be cancelled out by the negative effect of another whereas complementary type of epistasis is favourable effect in breeding programme.

V. CONCLUSION

The characters governed by additive gene effects and additive x additive gene interaction effects are fixable. Also, the crosses which are governed by complementary epistasis where sign of dominance gene effects and dominance x dominance gene interaction effects are similar are also worth for exploitation. Such crosses have the potentiality to produce transgressive segregants on the positive side. Pedigree method of breeding followed by simple selection in later segregating generations will be a meaningful breeding strategy to be followed in such crosses for the improvement of the characters under consideration. On the other hand in case of duplicate type of epistasis, selection in the early segregating generations may not yield desirable recombinants. This may possible be overcome by delaying the selection to later generations otherwise, one or two cycle of intermating of segregating population may be useful to improve the characters. Considering all the three crosses, the cross Ac-2 x Annamalai had complimentary type of epistasis for all the three traits including total yield per plant and this cross was judged as the best cross for further selection.

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