Gene Action Studies in Brinjal (*Solanum melongena*)

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Abstract: The study on genetic components of variation revealed that the importance of non-additive systems operating in inheritance of yield and its important components. Degree of dominance was in range of over dominance range for all the characters and close to complete dominance for plant height. The traits viz. plant height, plant spread, days to first flower, days to 50% flower, number of branches per plant, fruit length and yield exhibited significant environmental effect. For fruit diameter, chlorophyll content, days to 50% flower, number of fruits per plant, fruit weight and fruit length dominant genes were more frequently distributed in the parents.

Keywords: *Solanum melongena* · Growth · Yield parameter · Gene action · Studies

INTRODUCTION

Brinjal (*Solanum melongena* L.) is one of the important Solanaceous vegetable crops. It is widely cultivated in both temperate and tropical regions of the globe mainly for its immature fruits as vegetables. As India is the primary centre of origin of brinjal (Vavilov, 1931 [1] and Bhaduri, 1951) [2] it posses marked diversity. Most of the local varieties which are grown by the cultivators of India have not been fully utilized in any genetic improvement programme. The development of cultivars with improved fruit quality for better market value, through breeding has received relatively little attention in vegetables especially in eggplant. For the improvement in brinjal, one needs to elucidate the genetic nature and magnitude of quantitatively inherited traits and estimate prepotency of parents in combinations. The information generated in the process can be used to understand the magnitude of heterosis. However, genetic control of different yield related as well as agronomic traits has been studied extensively (Patil and Shinde, 1984; Sidhu and Chadha, 1985; Chadha *et al.,* 1990) [3] in eggplant. Direct selection for quality traits in eggplant, same as in all other crops, will not be successful due to interaction of many genes with environment.

Knowledge of the genetic controlling system of the character to be selected and genetic variation are the pre-requisite for viable breeding strategy. Therefore, the present study entitled Gene action studies in brinjal is undertaken to understand the nature of gene effects involved in the expression of a character in interacting and non-interacting crosses. An assessment of these genetic parameters will allow for the development of efficient breeding strategies for egg plant cultivar improvement.

MATERIALS AND METHODS

The experimental material for this study comprised of 9 genotypes viz. Local C-1, Asond long, Local -3, Selection -167 Local C -2, GADB –1, Local –2, AKL -11 and Asond Round which were selected based on their diversity for various traits and were crossed in all possible combinations excluding reciprocals to develop 36 F_1 using half diallel mating scheme. These 36 F_1 hybrids, 9 parents and two commercial hybrid checks (Pusa Hybrid-6 and Pusa Hybrid-9) comprised the material for gene action studies which were evaluated in randomized block design with three replications at the Main Garden, Department of Horticulture, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola during kharif season of 2011-12.

Observations were recorded on plant height, plant spread, days to first flower, days to 50 per cent flower, number of branches per plant, number of flowers per branch, number of fruits per plant, fruit length, fruit diameter, fruit weight, yield per plant, yield per plot, yield per hectare, infestation of shoot and fruit borer, chlorophyll content and protein content. The genetic

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components were derived from the mean values over replications. The data were analyzed as per the method given by Hayman (1954) [4, 5].

RESULTS

Estimation of genetic components of variation, their ratios and other relevant parameters for all the fourteen traits are presented in the table 1. The 't²' test carried out for ascertaining validity of assumptions indicated non-significant values for all traits except number of branches per plant and fruit length.

Plant Height: For plant height significant estimates of additive component (41.702) was accompanied by non-significant value of dominant component (37.287) and significant value of proportion of dominance variance due to positive and negative effects of genes (40.990) and net dominance variance expressed over all loci (45.272). The value of degree of dominance (0.946) was less than unity, pointing to partial dominance and estimate of heritability (0.381) was moderate.

Plant Spread: For plant spread estimates of additive component (30.112), dominance component (112.609), proportion of dominance variance due to positive and

Table 1: Genetic components of variation and their ratios for different traits.

Components	Plant Height (cm)	Plant spread(cm)	Days to first flower	Days to 50% Flower	No. Branches per plant	No. Flower Per branch	No. fruits Per plant	Fruit length (cm)	Fruit Dia. (cm)	Fruit Weight (g)	Yield /plant. (kg)	Yield Per plot (kg)	Yield per ha. (q)	Chlorophyll (%)
D	41.702** (±9.217)	30.112* (±13.092)	24.408** (±2.994)	50.754** (±16.461)	0.131 (±0.145)	2.153 (±4.411)	10.616 (±6.204)	0.229 (±0.408)	2.271** (±0.432)	1384.164 (±770.660)	0.076** (±0.014)	24.886** (±4.397)	5925.876** (±1046.869)	4.160* (±1.610)
F	-8.127 (±21.501)	-4.647 (±30.541)	-43.005 (±6.986)	39.333 (±38.402)	-0.781 (±0.339)	-1.023 (±10.289)	8.902 (±14.474)	0.043 (±0.953)	3.037** (±1.008)	251.539 (±1797.799)	-0.028 (±0.032)	-8.813 (±10.258)	-2101.984 (±2442.141)	7.874* (±3.755)
H_1	37.287 (±20.343)	112.609** (±28.897)	-41.750 (±6.610)	104.670** (±36.333)	-1.857 (±0.321)	36.531** (±9.73482)	46.207** (±13.695)	4.069** (±0.901)	4.043** (±0.954)	7788.996** (±1700.979)	0.271** (±0.030)	87.423** (±9.705)	20823.960** (±2310.620)	21.607** (±3.553)
H_2	40.990* (±17.488)	120.040** (±24.841)	-23.110 (±5.682)	86.858** (±31.233)	-1.219 (±0.276)	34.318** (±8.368)	34.859** (±11.773)	3.664** (±0.775)	2.844** (±0.820)	6933.599** (±1462.225)	0.277** (±0.026)	89.304** (±8.343)	21272.040** (±1986.295)	17.033** (±3.054)
h^2 (Dominance Effect)	45.272** (±11.715)	276.154** (±16.641)	-9.932 (±3.806)	17.031 (±20.923)	2.188** (±0.185)	11.585* (±5.606)	-0.878 (±7.886)	3.292** (±0.519)	3.884** (±0.549)	8811.545** (±979.560)	1.575** (±0.017)	509.066** (±5.589)	121228.300** (±1330.640)	-0.067 (±2.046)
Degree of Dominance	0.946	1.934	1.308	1.436	3.762	4.119	2.086	4.212	1.334	2.372	1.882	1.874	1.875	2.279
h^2/H_2 (No. of Gene groups)	1.104	2.301	0.430	0.196	-1.795	0.338	-0.025	0.898	1.365	1.271	5.692	5.700	5.699	-0.004
$H_2/4H_1$ (Proportion of positive and negative alleles among the parents)	0.275	0.266	0.138	0.207	0.164	0.232	0.189	0.225	0.176	0.223	0.256	0.255	0.255	0.197
KD/KR (Proportion of dominant and recessive genes in the parents)	0.813	0.923	0.195	1.739	0.117	0.891	1.503	1.045	3.009	1.080	0.821	0.827	0.827	2.420
h^2 (Heritability in Narrow sense)	0.381	0.185	0.547	0.238	0.128	0.206	0.357	0.179	0.186	0.355	0.293	0.293	0.993	0.080
E(Environ. Component)	27.170** (±2.914)	30.166** (±4.140)	26.009** (±0.947)	25.038** (±5.205)	1.242** (±0.04597)	1.815 (±1.39474)	3.055 (±1.96208)	0.446** (±0.129)	0.236 (±0.137)	72.167 (±243.704)	0.050** (±0.004)	16.066** (±1.390)	3826.337** (±331.049)	0.652 (±0.509)
t^2	0.019	0.049	0.004	0.101	0.351	3.758	0.002	6.993	0.157	0.526	1.832	1.860	1.860	0.960
H:b=0	-4.520	-2.081	-4.837	-0.281	-3.246	1.577	0.085	-1.077	-1.016	-0.957	-6.931	-6.948	-6.950	-1.368
H:b=1	0.858	1.070	0.613	0.281	1.576	7.154	2.683	5.460	1.450	2.674	1.964	1.975	1.975	2.747

D- Additive genetic variance,

F- Measures of covariance between additive and dominance effects,

H_1, H_2 and h^2– Dominance components of variance,

Figures in parenthesis indicate standard errors

* Significance at 5 percent.

** Significance at 1 percent [12].

negative effects of genes (120.040), net dominance variance expressed over all loci (276.154) and estimates of environmental effects (30.166) were statistically significant. The value of degree of dominance (1.934) was greater than unity, pointing to dominance and estimate of heritability (0.185) was low.

Day's to First Flower: The value of degree of dominance (1.308) was greater than unity, pointing to dominance and estimate of heritability (0.547) was moderate. The value of ratio of proportion of dominant and recessive genes in the parents (0.195) was less than unity and the estimate of relative frequency of dominant and recessive genes in parents (-43.005) was negative and non-significant.

Days to 50 per Cent Flower: The value of degree of dominance (1.436) was greater than unity, estimate of heritability (0.238) was low. The value of ratio of proportion of dominant and recessive genes in the parents (1.739) was more than unity and the estimate of relative frequency of dominant and recessive genes in parents (39.333) was positive and non-significant. The proportion of positive and negative alleles was (0.207).

Number of Branches per Plant: Estimates of additive component (0.131) were positive and non-significant. The value of the ratio of proportion of dominant and recessive genes in parents (0.117) was less than unity and the estimate of relative frequency of dominant and recessive genes in parents (-0.781) was negative and non-significant. The value for degree of dominance (3.762) was in over dominance range and heritability (0.128) was low.

Number of Flowers per Branch: Estimate of additive component (2.153) was non-significant. The estimate of net dominance effect (11.585) was significant and the degree of dominance (4.119) was in over dominance range. The estimate of the ratio of proportion of dominant and recessive genes (0.891) was less than unity and that of relative frequency of dominant and recessive genes in parents (-1.023) was negative and non-significant. The heritability estimate (0.206) was low.

Number of Fruits per Plant: Non-significant estimates of additive component (10.616) showed for fruit numbers. The value of degree of dominance (2.086) was in over dominance range and estimate of heritability (0.357) was moderate.

Fruits Length: An estimate of additive component (0.229) was non-significant and estimates of environmental effects (0.446) were statistically significant. The value for degree of dominance (4.212) was in over dominance range and heritability (0.179) was low.

Fruit Diameter: Significant estimates of additive component (2.271). The value of degree of dominance (1.334) was greater than unity, pointing to dominance and estimate of heritability (0.186) was low. The value of ratio of proportion of dominant and recessive genes in the parents (3.009) was greater than unity and the estimate of relative frequency of dominant and recessive genes in parents (3.037) was positive and significant.

Fruit Weight: The magnitude of additive component (1384.164) was non-significant, whereas net dominance variance expressed over all loci (8811.545) were significant. The value of degree of dominance (2.372) was in over dominance range. Estimate of heritability (0.355) was moderate. The value of ratio of proportion of dominant and recessive genes in the parents (1.080) was more than unity and the estimate of relative frequency of dominant and recessive genes in parents (251.539) was positive and non-significant.

Yield per Plant: For yield per plant, both additive (0.076) and dominance (0.271) component were significant and latter was greater in magnitude than former. The estimates of net dominance variance expressed over all loci (1.575) and environment effect (0.050) were also significant. Further, the degree of dominance (1.882) was in over dominance range accompanied by low heritability estimates (0.293).

Yield per Plot and Yield per Hectare: Similar trend was observed for yield per plot and yield per hectare, further, the degree of dominance (1.874) and (1.875) was in over dominance range accompanied by low heritability estimates (0.293) and (0.993) respectively.

Chlorophyll Content: The magnitude of additive component (4.160) was significant whereas net dominance variance expressed over all loci (-0.067) was non-significant. The value of degree of dominance (2.279) was in over dominance range. Estimate of heritability (0.080) was low. The proportion of positive and negative alleles was (0.197).

DISCUSSION

In this present investigation, the mean squares due to general combining ability were observed to be significant for all the characters except for number of branches per plant, infestation of shoot and fruit borer and protein content and those for specific combining ability were also significant for all these traits except for plant height, days to first flower, branches per plant, infestation of shoot and fruit borer and protein content indicates the importance of both additive and non-additive gene action.

In the analysis of components of genetic variation, the non-significant values of t^2 test (Hayman, 1954[a]) showed that the assumptions underlying diallel analysis were valid for all the traits (Table 1). The additive component was highly significant for all the characters except number of branches per plant, number of flowers per branch, number of fruits per plant, fruit length and fruit weight for which it was non-significant.

The dominance component was significant and had high value for all the characters except days to first flower and number of branches per plant for which it was non-significant, showing thereby the more pronounced effect of dominance in the expression of these characters. Three measures of dominance variance i.e. the estimates of H_1, H_2 and h^2 showed significant differences for plant spread, number of flowers per branch, yield per plant, per plot and for yield per hectare. The remaining characters exhibited non-significant difference.

The estimates of F were positive for six characters. Fruit diameter and chlorophyll content had significant F estimates whereas others were non-significant. Similar results were reported earlier by Mittal *et al.* (1976). Further, the estimates of degree of dominance were greater than unity for all the characters which showed over-dominance except plant height for which it is less than unity showed partial to no dominance. The proportion of positive and negative alleles and dominant and recessive genes indicates the asymmetrical and symmetrical distribution of alleles in parents and respective genes for the characters.

Exploitation of heterosis on a commercial scale through hybrid seed production, although theoretically possible, may not be achieved on a practical scale due to the high cost involved in the production of hybrid seed by emasculation and pollination technique, till a suitable male sterile line is found. For this reason the breeder has to make use of the fixable component of genetic variance. In the present study on the basis of results from different

biometrical analysis, yield was found to be governed more by the non-fixable (dominance) component of genetic variance and showed the fair heritability. Gotoh (1953 [6, 7] and 1954) and Baha-Eldin [8] *et al.* (1968) also observed the role of dominant component of genetic variance for yield in eggplant. The higher magnitude of specific combining ability, highly significant dominance component and low estimates of heritability revealed that yield was genetically a complex character. The high heritability estimates for all the characters except chlorophyll content indicated that these component characters can be used for component breeding. Results are conformity with findings of Mittal *et al.* (1976). The study of combining ability is useful in selecting parents which, when crossed would give to more desirable segregates. Parents AKL-11, Asond Round and Local C-1 seemed to be good general combiner for the maximum characters. These parents appears to be worthy of exploitation. The sca effects between the crosses revealed that good general combiners did not produce the best hybrid. Mittal *et al.* (1976) reported similar results in brinjal.

The proportion of total number of dominant to recessive genes among the parents determines the extent of genetic advance that can be made in particular direction, because, if the genes present in the population are of predominantly of recessive nature, while the expression of the characters towards which the selection is directed is determined by dominant action, the extent of genetic advance will be limited and vice-versa. The ratio between recessive and dominant alleles was obtained close to unity only for maximum characters except days to per cent flower, number of fruits per plant, fruit length, fruit diameter, fruit weight and chlorophyll content implying the equality between the number of dominant and recessive alleles in the present study for this trait.

The estimates of ratio of positive and negative alleles among the parents indicated asymmetrical distribution of positive and negative alleles for the traits. It is possible that a dominant allele may or may not be associated with a positive allele and same may hold true for recessive one.

The estimates of environmental component was significant for all the characters except for number of flowers per branch, number of fruits per plant, fruit diameter, fruit weight and chlorophyll content indicating that the environment imposed more influence in the expression of these traits.

One major gene group appeared to control the inheritance of total yield, plant spread, fruit diameter, fruit weight and plant height thereby indicating dominance.

Similar results were recorded by Mittal *et al.* (1976) [9]. But too much reliance on the estimate of the ratio of number of alleles or gene groups showing dominance provides little information about the group of genes exhibiting little or no dominance (Griffing, 1956) [10] because it tends to under estimate number of genes. The character of less number of effective factors with additive type of gene action and higher number of additive genes is desirable in self-pollinated crops (Lupton, 1961) [11].

CONCLUSION

The higher magnitude of specific combining ability, highly significant dominance component and low estimates of heritability revealed that yield was genetically a complex character. The high heritability estimates for all the characters except chlorophyll content indicated that these component characters can be used for component breeding. Results are conformity with findings.

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