



## GENETIC ANALYSIS OF YIELD AND ITS CONTRIBUTING TRAITS IN BRINJAL (*Solanum melongena* L.)

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**ABSTRACT** : The experiment was conducted with parent, 45 F<sub>1</sub>s and 45 F<sub>2</sub>s population developed through diallel excluding reciprocals along with 10 parents viz., Azad B-1, Type-3, KS-224, KS-235, DVR-8, Azad Kranti, KS-331, PPL, KS-503 and KS-504 in 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* 2010. The observations were recorded on 5 randomly selected plants from each row for ten quantitative traits namely, days to flowering, height of plant, number of branches per plant, length of leaf, width of leaf, length of fruit, width of fruit and number of fruits per plant. Genetic component of variance showed significant value for additive component (D) which was significant for width of leaf, length of fruit, width of fruit, number of fruits per plant and weight per fruit on both the generation except days to flowering and plant height based on F<sub>1</sub> and number of branches per plant based on F<sub>2</sub> only. The dominance components (H) were also highly significant for all the characters under study in both the generations. The degree of dominance (H<sub>1</sub>/D)<sup>0.5</sup> showed over dominance for all the characters in both the generations. The ratio of KD/KR showed presence of more dominant alleles for all the characters based on F<sub>1</sub> and F<sub>2</sub> generation, while less than unity in F<sub>2</sub> generation only for days to flowering and length of fruit. Other characters showed more amount of successive alleles. The ratio of (h<sup>2</sup>/H<sub>2</sub>) showed more than two gene group for length of leaf and width of fruit in F<sub>1</sub> and F<sub>2</sub> generation, respectively. More than three gene groups for length of leaf and weight of brinjal fruit in F<sub>2</sub> & F<sub>1</sub> & F<sub>2</sub> generation, respectively. More than five gene groups for width of leaf in F<sub>1</sub>, more than six gene groups for width of leaf in F<sub>2</sub> generation and other characters showed at least one gene group with some modification for controlling the traits.

**Keywords** : Genetic component, diallel cross, brinjal.

Brinjal or egg plant (*Solanum melongena* L.) is one of the most important vegetable crops grown in India. It belongs to the family Solanaceae with chromosome number 2n = 24. It is an important commercial crop grown all over the country except on higher altitudes. It has high yielding potential and adaptability to various agro-climatic conditions throughout the country and grows throughout the year. Brinjal is native of India, one of the most popular vegetable grown throughout the country especially in north east region, where there are wild relatives of brinjal and are being grown in their kitchen garden. The unripe fruits are used as a cooked vegetable. It is adopted wider range of climatic condition from north to south and west to east. Brinjal is used in variety of culinary preparations. Pickles and industrially processed food are also produced from brinjal. Brinjal has *ayurvedic* medicinal properties. The fruits of brinjal are excellent remedies for those suffering from liver troubles. White brinjal is good for diabetic patients. Brinjal is good source of vitamin A, B and C. The green

leaves of brinjal are excellent source of vitamin C. The bitter source of brinjal is due to glycoalkaloids. The national share of brinjal in overall total production of vegetables is 8% during 2009-2010. In India, overall ranking wise production of brinjal, West Bengal possesses the top rank from the production of 2.99 million tonnes with 1.56 million hectare area followed by Odisha and Bihar. Brinjal has three main botanical varieties under the species *melongena*, the round or egg shaped cultivars group under *var. esculantum*, the long slender type are under *var. serpentinum*, and the dwarf brinjal plants are put under *var. depressum*.

The knowledge of nature and magnitude of gene action controlling the characters under consideration, general combining ability of the parents and degree of heterosis are helpful in determining the efficient conventional breeding and hybrid breeding procedures. The genetic diversity of the parent influence the performance of hybrids and segregating generations and increase the chance of recovering

desirable transgressive segregates and thus enhancing the effectiveness of selections.

## MATERIALS AND METHODS

A set of 10 varieties/strains namely Azad B-1, Type-3, KS-224, KS-235, DVR-8, Azad Kranti, KS-331, PPL, KS-503 and KS-504, showing wide phenotypic diversity maintained in the germplasm section at the Department of Vegetable Science of Chandra Shekhar Azad University of Agriculture and Technology, Kalyanpur, Kanpur through selfing were collected for the study. These comprised of commercial varieties and indigenous collections from different parts of India. The soil fertility was homogenous in the field in which experiment was conducted. The field was ploughed twice with the soil turning plough followed by four ploughings with the cultivator. Each ploughing was followed by planking for making the soil friable and suitable for sowing. While preparing the land, due precautions were taken to maintain uniform level of the experimental field for proper drainage. Fertilizer @ 120 kg nitrogen, 60 kg phosphorus and 60 kg potash per hectare were given to the crop during the whole crop season. Half quantity of nitrogen, whole of phosphorus and potash were applied through basal dressing in the form of fertilizers at the time of last ploughing. Rest of the nitrogen was applied as top dressing in the form of urea after one month of transplanting. All the homozygous parents were sown at Research Farm of the Department of Vegetable Science of CSAUA & T, Kalyanpur, Kanpur during *kharif* 2008. All the possible 45 F<sub>1</sub> hybrids, excluding reciprocals were made among these ten parents. For building up of the F<sub>2</sub> population of these, F<sub>1</sub> hybrids were sown during *Kharif* 2009. All these F<sub>1</sub> hybrids were selfed for producing the F<sub>2</sub> seeds. All the 45 F<sub>1</sub> hybrids and 45 F<sub>2</sub> populations along with 10 parents were shown in Randomized Block Design with three replications in during *Kharif* 2010. Parents and F<sub>1</sub>s were sown in single rows while F<sub>2</sub>s in two rows, with ten plants in each row. The rows distance of 75 cm row to row and the plant to plant spacing was maintained at 60 cm.

## RESULTS AND DISCUSSION

It is illustrated from Table 1 that additive genetic component (B) was significant for width of leaf, length of fruit, width of fruit, number of fruits per plant and weight per fruit in both the generations except days to flowering and plant height based on F<sub>1</sub> and number of branches per plant based on F<sub>2</sub> only. Phase estimate indicates the preponderance role of additive genetic component for controlling these characters. The findings of Salimath *et al.* (4), Chadha and Sharma (1)

were in accordance with above results. The dominance components (H<sub>1</sub> and H<sub>2</sub>) were also highly significant for all the characters under study based on F<sub>1</sub> and F<sub>2</sub> generation. The H<sub>1</sub> is higher than H<sub>2</sub> for all the characters in both the generation which suggested that positive and negative genes at the loci governing the characters were not in equal proportion in parents selected for study. The F component was highly significant for width of fruit and weight per fruit based on F<sub>1</sub> and F<sub>2</sub> generation, while width of leaf only on F<sub>2</sub> based and days to flowering, plant height and number of fruits per plant under study based on only F<sub>1</sub> generation. The significantly negative value of F<sub>2</sub> components revealed that the recessive genes were more frequent in comparison to dominant for expression of their characters among parents. The estimated values of dominance effects of parents ( $h^2$ ) was positive and significant for days to flowering, plant height, length of leaf, width of leaf, length of fruit, width of fruit and weight per fruit based on both the generations and for number of branches per plant and fruit yield per plant based on F<sub>1</sub> generation only and non significant positive values for other characters also indicated that the preponderance genes were consistent in nature. The environmental component (E) was significant for days to flowering based on F<sub>2</sub> generation and fruit yield per plant based on F<sub>1</sub> generation only indicated the role of environment for expression of their characters. Other characters showed non-significant values for this component indicating the nominal effect of environment on the traits. The average degree of dominance of gene  $(H_1/D)^{0.5}$  showed higher the value (more than unity) for all the characters revealing the presence of over dominance for all the traits in both the generations which was also confirmed by higher the values of H<sub>1</sub> and H<sub>2</sub> in comparison to D (additive component). Over dominance for all the traits in both the generation showed partial dominance. The proportion of positive and negative allele in parents  $(H_2/4H_1)$  showed the values less than its theoretical value i.e. 0.25 for all the characters in both the generations revealing the asymmetrical distribution of positive and negative alleles among parents. It is also indicated that the distribution of loci among the parents was not in balanced form for these characters. The proportion of dominance and recessive alleles in parents  $(4DH_1)^{0.5} + F/(4DH_1)^{0.5}$  showed that the values of this statistics is more than unity in both the generation for all the characters based on F<sub>1</sub> and F<sub>2</sub> generations both, while less than unity in F<sub>2</sub> generation only for days to flowering and length of fruit, which reflect that dominant alleles were more frequently distributed than recessive

Table 1: Estimate of genetic components and related statistics for 10 characters in 10 x 10 diallel cross of F<sub>1</sub>S and F<sub>2</sub>S in brinjal.

Characters	Gene ration	D	H <sub>1</sub>	H <sub>2</sub>	F	h <sup>2</sup>	E	(H <sub>1</sub> /D) <sup>0.5</sup>	(H <sub>2</sub> /4H <sub>1</sub> )	$\frac{(4DH_1)^{0.5} + F}{(4DH_1)^{0.5} - F}$	h <sup>2</sup> /H <sub>2</sub>	KD/KR
Days to flowering	F <sub>1</sub>	10.000*	36.126*	29.494*	12.662*	34.556*	0.358	1.901	0.204	1.998	1.172	0.812
	SE ±	2.163	4.604	3.913	4.991	2.619	0.652					
Plant height (cm)	F <sub>2</sub>	7.250	160.750*	115.608*	30.582	73.108*	3.108*	2.354	0.180	0.206	0.632	0.029
	SE ±	4.514	38.435	32.665	20.831	21.865	1.361					
Plant height (cm)	F <sub>1</sub>	38.671*	300.236*	222.231*	93.813*	142.242*	0.355	2.786	0.185	2.542	0.640	0.028
	SE ±	17.243	36.703	31.194	39.785	20.880	5.199					
Number of branches /plant	F <sub>2</sub>	38.627	1312.714 *	1048.020*	177.346	999.367*	0.400	2.915	0.200	8.415	0.954	0.110
	SE ±	20.610	175.482	149.140	95.107	99.829	6.214					
Number of branches /plant	F <sub>1</sub>	0.795	5.893*	4.888*	1.247	3.070*	0.212	2.724	0.207	1.809	0.628	0.158
	SE ±	0.574	1.223	1.039	1.325	0.696	0.173					
Length of leaf (cm)	F <sub>2</sub>	0.848*	17.109*	13.227*	3.425	-0.088	0.159	2.246	0.193	18.892	-0.007	0.156
	SE ±	0.428	3.641	3.095	1.974	2.071	0.129					
Length of leaf (cm)	F <sub>1</sub>	3.885	26.234*	24.915*	1.840	61.899*	0.382	2.599	0.237	1.200	2.484	0.685
	SE ±	2.321	4.941	4.199	5.356	2.811	0.700					
Width of leaf (cm)	F <sub>2</sub>	4.026	130.742*	130.817*	10.140	441.970*	0.241	2.849	0.231	2.584	3.658	0.738
	SE ±	2.234	19.018	16.163	10.307	10.819	0.673					
Width of leaf (cm)	F <sub>1</sub>	3.853*	25.744*	23.618*	4.690	132.062*	0.267	2.585	0.229	1.616	5.591	0.829
	SE ±	1.085	2.310	1.964	2.504	1.314	0.327					
Width of leaf (cm)	F <sub>2</sub>	3.856*	105.784*	94.488*	11.414*	575.492*	0.264	2.619	0.223	3.600	6.091	0.891
	SE ±	1.156	9.846	8.368	5.336	5.601	0.349					

continued .....

Table 1: Contd....

Characters	Genera- ation	D	H <sub>1</sub>	H <sub>2</sub>	F	h <sup>2</sup>	E	(H <sub>1</sub> /D) <sup>0.5</sup>	(H <sub>2</sub> /4H <sub>1</sub> )	$\frac{(4DH_1)^{0.5} + F}{(4DH_1)^{0.5} - F}$	h <sub>2</sub> /H <sub>2</sub>	KD/KR
Length of fruit (cm)	F <sub>1</sub>	9.069*	26.253*	25.278*	-2.996	6.644*	0.246	1.701	0.241	1.823	0.263	0.986
	SE ±	2.256	4.803	4.082	5.206	2.732	0.680					
	F <sub>2</sub>	9.030*	109.970*	104.217*	-6.456	36.501*	0.284	1.745	0.237	0.669	0.350	0.990
Width of fruit (cm)	SE ±	1.893	16.117	13.698	8.735	9.169	0.571					
	F <sub>1</sub>	17.347*	16.816*	14.291*	11.679*	23.671*	0.274	0.985	0.212	2.039	1.656	0.710
	SE ±	1.884	4.010	3.408	4.346	2.281	0.568					
Number of fruits per/plant	F <sub>2</sub>	17.354*	73.195*	59.902*	27.462*	149.430*	0.267	1.027	0.205	7.716	2.495	0.565
	SE ±	1.932	16.453	13.983	8.917	9.360	0.583					
	F <sub>1</sub>	6.885*	37.276*	29.218*	13.586*	4.684	0.266	2.327	0.196	2.473	0.160	0.280
Weight per fruit (g)	SE ±	2.935	6.247	5.309	6.771	3.554	0.885					
	F <sub>2</sub>	6.815*	152.402*	124.487*	18.902	7.113	0.335	2.364	0.204	3.837	0.057	0.521
	SE ±	2.507	21.346	18.142	11.569	12.143	0.756					
Fruit yield per plant (kg)	F <sub>1</sub>	2096.115*	2683.090*	2123.669*	757.972*	7172.660*	22.736	1.131	0.198	1.380	3.377	0.946
	SE ±	126.591	269.460	229.011	292.083	153.291	38.168					
	F <sub>2</sub>	2100.649*	12758.060*	10130.670*	3212.091*	40307.070*	18.202	1.232	0.199	4.270	3.979	0.925
Fruit yield per plant (kg)	SE ±	155.272	1322.046	1123.592	716.520	752.089	46.816					
	F <sub>1</sub>	0.332	3.239*	2.666*	0.716	1.200*	0.178*	3.122	0.206	2.053	0.450	0.038
	SE ±	0.213	0.454	0.386	0.492	0.258	0.064					
Fruit yield per plant (kg)	F <sub>2</sub>	0.360	16.206*	13.818*	1.147	1.099	0.150	3.355	0.213	2.809	0.080	-0.378
	SE ±	0.683	5.817	4.944	3.153	3.309	0.206					

ones among parents in corresponding generations. The other characters showed its value less than one, which indicates that there are more frequency of recessive alleles in comparison of dominant ones among parents. The ratio of dominant and recessive alleles among the parents is determined to the extent of genetic advance, which can be estimated in a population. If the genes are dominant in nature the magnitude of genetic advance will be less, if the recessive general pre dominant. The proportion of dominant genes was fairly moderate for all the characters except, mentioned is finding, which denoted moderate amount of genetic gain for fruit yield and same yield contributing traits. The ratio of  $h^2/h^2$  may also be less due to complement genes interaction therefore, the number of groups of genes reported may be higher/lower than the actual number of genes involved. The ratio of ( $h^2/H_2$ ) i.e. the number of group of genes control the character and exhibited dominance showed that more than two gene groups were responsible for length of leaf and width of fruit per plant in  $F_1$  generation in  $F_2$  generation respectively more than three gene groups for length of leaf and weight per fruit in  $F_2$  and  $F_1$  &  $F_2$  generation, respectively more than five gene groups for width of leaf in  $F_1$  and more than six gene groups for width of leaf in  $F_2$  generations and at least one gene group was responsible for expression of other characters in respective generation. These findings are also supported with Goto (2), Robinson *et al.* (3), Singh and Gautam (6), Shull (5), Vadivel and Bapu (8), and Srivastava and Singh (7).

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