

# INFLUENCE OF GENE ACTION IN DIALLEL CROSSING ON BOTTLE GOURD [*LAGENARIA SICERARIA* (MOL.) STANDL] HYBRIDS

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## KEYWORDS

Gene action  
Diallel crossing  
*Lagenaria siceraria*

## Received on :

14.12.2013

## Accepted on :

17.03.2014

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## ABSTRACT

In present study, diallel cross analysis was carried out for development of Hybrid in Bottle Gourd (*Lagenaria siceraria* (Mol.) Standl). The gene effects with respect to its nature and magnitude for yield and yield contributing traits (12 characters) were studied by involving 45 hybrids obtained by crossing 10x10 half diallel pattern. The estimates components of variance and their related statistic for different characters especially fruits per plant ( $6.45 \pm 0.97$ ) and fruit yield per plant ( $2.12 \pm 0.43$ ) have been found significant ( $p < 0.05$ ) for dominance components  $H_1$ . The values of additive components D were also significant ( $p < 0.05$ ) for most of the characters except for no. of fruits per plant and fruit yield per plant (kg). These results indicate importance of both additive and dominance gene action in expression of these characters. The average degree of dominance ( $H_1/D$ )<sup>1/2</sup> involved in the action of genes was found as over dominance for all the traits.

## INTRODUCTION

Recent developments in agriculture have contributed significantly to the improvement of vegetable production throughout the world. In India, varied agro-climatic conditions have made it possible to grow a wide variety of vegetable crops all the year round in one or the other part of the country. Bottle Gourd (*Lagenaria siceraria* (Mol.) Standl) is one amongst the major vegetable crops grown throughout the country. The origin of bottle gourd is Africa. According to Cutler and Whitaker (1961), this plant is probably indigenous to tropical Africa. De Candolle reported its occurrence in wild form in South Africa and India.

To estimate the average gene action one may construct models involving different types of gene interaction and choose the model which best fits the experimental data. In thus reducing the total gene action entering into the expression of a complex characteristic to that of a simple model, it cannot be assumed that all genes behave in the manner prescribed by the chosen model. In fact, it has been suggested that quantitative genes probably have as diverse types of action as the so called qualitative ones and differ from qualitative genes only in magnitude of effect reported by Dubey and Maurya (2003). However, it has been shown in various quantitative traits that the system of genes involved does have average properties which are measurable. Estimation of these group genetic parameters is the objective of a statistical analysis, and these estimated parameters are associated with a gene model also supported by Askel and Johnson (1963). The principal approach that has developed over the years involves, a description of frequency distributions resulting from segregating populations by use and a partitioning of variances

into components

Considering the importance of such information, an experiment was conducted to understand the gene effects governing various yield and related traits in bottle gourd. Among the biometrical techniques, diallel analysis has been used extensively for deciphering nature of gene action and selection of large number of parents for hybridization. It seems that information on genetic architecture of parents, their combining ability, transmissibility of characters and expected genetic advance will be of immense value to ascertain the selection of desirable parents in the choice of suitable breeding methodology for the improvement of bottle gourd. Therefore, the present study was undertaken to elucidate the nature and magnitude of gene action involved in inheritance of fruit yield and its component in bottle gourd.

## MATERIALS AND METHODS

The selected parental lines i.e. Pusa Naveen ( $P_1$ ), NDBG-202 LF ( $P_2$ ), NDBG-70-2 ( $P_3$ ), NDBG-517 ( $P_4$ ), NDBG-601 ( $P_5$ ), NDBG-603 ( $P_6$ ), NDBG-624 ( $P_7$ ), NDBG-625 ( $P_8$ ), NDBG-749-2 ( $P_9$ ) and NDBG-751 ( $P_{10}$ ) were taken for the present study. All the line were hand-pollination with each other to produce all possible combinations of  $F_1$  hybrids were obtained in half-diallel cross techniques according to Griffing's Method -2, Model-1. Pollen for crossing was obtained from freshly dehisced anther. The seeds of 45  $F_1$  hybrids along with 10 parental lines were sown in randomized complete block design with three replications at Vegetable Research Farm, N.D. University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad (U.P.) during August, 2010 to assess

the performance of 45  $F_1$  hybrids and their 10 parental lines. The crop was planted in rows spaced at 3.0 meter with plant to plant spacing of 0.5 meter apart. All the recommended agronomic package of practices and plant protection measures were followed to raise a good crop. The observation were recorded on randomly selected five plants for twelve economically important traits namely (1) Days to first staminate flower anthesis, (2) Days to first pistillate flower anthesis, (3) Node number to first staminate flower anthesis, (4) Node number to first pistillate flower anthesis, (5) Days to first fruit harvest, (6) Vine length (m), (7) Primary branches per plant, (8) Fruit length (cm), (9) Fruit circumference (cm), (10) Fruit weight (kg), (11) Fruits per plant, (12) Fruit yield per plant (kg). Data collected were subjected to analysis of variance, having observed significant differences in the crosses, the genetic components of variation were partitioned into additive gene action, dominance gene action, dominance components, maternal influence by various environmental and genetical factors using the method of Hayman (1954).

## RESULTS AND DISCUSSION

The diallel cross analysis was carried out for all the twelve characters, using analytical approach in terms of components of variation i.e.  $D$ ,  $H_1$ ,  $H_2$ ,  $F$ ,  $h^2$  and  $E$  along with their respective standard errors. The estimates of these components have been presented in Table 1. These genetic components were used in estimation of average degree of dominance  $(H_1/D)^{1/2}$ , proportion of dominant and recessive genes  $(KD/KR)$  in parents i.e.  $(4DH_1)^{1/2} + F/(4DH_1) - F$  and number of gene groups, which control the character and exhibit dominance  $(h^2/H_2)$ . The coefficient of correlation ( $r$ ) between parental order of dominance ( $Wr - Vr$ ) and parental measurements ( $Yr$ ) was calculated to get an idea about the dominance genes with positive and negative effects. The estimate of genetic components of variation and various statistical parameters for different characters have been presented in Table -1. The results pertaining to days to first staminate flower anthesis the estimates of  $D$ ,  $H_1$ ,  $H_2$  and  $h^2$  were found significant and  $F$ ,  $E$  was non significant. The higher value of  $H_1$  as compared to  $D$  indicates preponderance of non additive gene action. The value of  $F$  was found to be negative and the value of  $E$  was no significant. Mean degree of dominance  $(H_1/D)^{1/2}$  was more than unity suggest over dominance. The proportion of genes with positive and negative effects  $(H_2/4H_1)$  in the parents was found to be 0.22 denoting asymmetrical distribution of loci showing dominance, is reported Sharma *et al.* (1983). The genetic component of variation for days to first pistillate flower anthesis, the estimate of  $D$ ,  $H_1$ ,  $H_2$ ,  $F$  components were significant while  $h^2$  and  $E$  were non significant. The values of  $H_1$  was higher than  $D$  indicated the major role of dominance component in the expression of this trait. The degree of dominance for this traits, the ratio of  $(H_2/4H_1)$  indicated asymmetrical distribution of dominant and recessive genes in the parent. The number of dominant and recessive genes in parents as indicated by  $(KD/KR)$  was (1.66) shows excess of dominance genes. The estimates of  $(h^2/H_2)$  showed that the number of gene group, which control the character and exhibited dominance was 0.13. The positive value of correlation coefficient suggested the preponderance of

recessive gene agreed with Sharma *et al.* (1983).

The result pertaining to node number to first staminate flower anthesis the estimates of  $D$ ,  $H_1$  and  $H_2$  were significant for this character while the value  $F$ ,  $h^2$  and  $E$  were found to be non significant for this character. However, the higher values of  $H_1$  than  $D$  indicated the major role of dominance components for this character. Mean degree of dominance was over dominance. The proportion of gene with positive and negative effects  $(H_2/4H_1)$  in parents was found to be 0.10 suggested asymmetrical distribution of positive and negative allele among the parents. The proportion of dominant and recessive alleles among the parents was more than one, which shows excess of dominant gene. The number of major gene group  $(h^2/H_2)$ , which control the character and exhibited dominance was 0.11 indicated that at least one gene group showing dominance was involve in the inheritance this trait. The positive values of correlation coefficient indicated preponderance of recessive gene, also reported earlier Kushwaha and Ram (1997). The genetic component of variation for node number to first pistillate flower anthesis viz.  $D$ ,  $H_1$ ,  $H_2$  and  $F$  were significant except  $h^2$  and  $E$  were non significant. The higher value of  $H_1$  as compared to  $D$  indicated preponderance of non additive gene action. The mean degree of dominance  $(H_1/D)^{1/2}$  was more than one showed over dominance. The proportion of gene with positive and negative effects  $(H_2/4H_1)$  in the parents was found to be 0.19, denoting asymmetrical distribution of loci showing dominance. The proportion of dominant and recessive gene  $(KD/KR)$  was found more than one which showed excessive genes. The number of gene group  $(h^2/H_2)$  which control the character and exhibit dominance was 0.27 indicated that at least one major gene group was involved in the inheritance of this trait. The positive value of correlation coefficient indicated the preponderance of recessive genes.

Singh *et al.* (2000). Reported the importance of pure line for days to first fruit harvest, the estimates of days to first fruit harvest  $D$ ,  $H_1$  and  $H_2$  were significant for this traits while the value of  $F$ ,  $h^2$  and  $E$  were found to be non significant. The value of  $H_1$  was higher than the  $D$  value indicated the major role of dominance component for this character. The value of overeager of dominance  $(H_1/D)^{1/2}$  showed over dominance for this traits. The ratio of  $(H_2/4H_1)$  was found to be less than 0.25 indicating the asymmetrical distribution of positive and negative alleles among the parents. The ratio of  $(KD/KR)$  was found more than one, which shows excess of dominant gene and the number of group of gene which controlled a character and exhibiting dominance  $(h^2/H_2)$  was 0.19. The positive value of correlation coefficient suggested the preponderance of recessive genes.

For vine length the genetic parameter like  $D$ ,  $H_1$ ,  $H_2$  and  $h^2$  were found significant while  $F$  and  $E$  were found to be non significant. The higher valve of  $H_1$  than  $D$  indicated preponderance of non additive gene action. The value of average degree of dominance  $(H_1/D)^{1/2}$  showed over dominance for these traits. The ratio of  $(H_2/4H_1)$  was found to be less than 0.25 indicating the asymmetrical distribution of positive and negative alleles among the parents in the population. The ratio of  $(KD/KR)$  was found more than one which shows excess of dominant genes and exhibiting dominance  $(h^2/H_2)$  was 0.43. The positive value of correlation

**Table 1: Estimates of genetic components of variation and their related statistics for twelve characters in 10 × 10 diallel cross of bottle gourd**

Components of variation and related statistics	1	2	3	4	5	6
D (Additive effect)	24.61* ± 4.52	31.57* ± 3.94	1.29* ± 0.42	3.65* ± 0.61	18.72* ± 4.18	0.41* ± 0.16
H <sub>1</sub> (Dominance effect)	70.63* ± 9.61	63.47* ± 8.37	4.19* ± 0.89	7.03* ± 1.29	51.39* ± 8.89	2.25* ± 0.33
H <sub>2</sub> (Dominance indicating asymmetry of +/-effect of genes)	61.43* ± 8.17	52.79* ± 7.12	3.51* ± 0.75	5.17* ± 1.10	44.87* ± 7.56	1.84* ± 0.28
F (Mean Fr over arrays)	10.97 ± 10.42	22.04* ± 9.07	0.73 ± 0.96	3.71* ± 1.41	12.89 ± 9.64	0.32 ± 0.36
h <sup>2</sup>	1.38 ± 0.74	0.78* ± 0.19	0.22 ± 0.19	11.06* ± 5.47	6.39 ± 4.76	0.36 ± 0.50
E (Environmental component)	0.21 ± 1.37	0.18 ± 0.13	0.18 ± 1.26	0.08 ± 0.05		
(H <sub>1</sub> /D) <sup>1/2</sup> (Mean degree of dominance)	1.69	1.42	1.79	1.39	1.66	2.34
H <sub>2</sub> /4H <sub>1</sub> (Proportion of genes with +/-effects in parents)	0.22	0.21	0.1	0.19	0.22	0.21
(4 DH <sub>1</sub> ) <sup>1/2</sup> + F/(4DH <sub>1</sub> ) <sup>1/2</sup> F (Proportion of dominant and recessive genes in parents)	1.3	1.66	1.37	2.16	1.53	1.39
h <sup>2</sup> /H <sub>2</sub> (Number of gene groups)	0.18	0.13	0.11	0.27	0.19	0.43
r (correlation coefficient)	0.804	0.856	0.625	0.206	0.75	0.74

**Table 1: Cont.....**

Components of variation and related statistics	7	8	9	10	11	12
D (Additive effect)	53.96* ± 5.25	35.86* ± 6.13	17.95* ± 1.19	0.03* ± 0.01	0.75 ± 0.46	0.33 ± 0.21
H <sub>1</sub> (Dominance effect)	34.88* ± 9.49	57.17* ± 11.08	11.97* ± 2.14	0.08* ± 0.01	4.59* ± 0.83	1.68* ± 0.37
H <sub>2</sub> (Dominance indicating asymmetry of +/-effect of genes)	58.29* ± 12.10	10.95 ± 14.13	25.74* ± 2.73	0.04* ± 0.02	1.35 ± 1.06	0.33 ± 0.47
F (Mean Fr over arrays)	9.29 ± 6.36	0.05 ± 7.42	10.13* ± 1.44	0.06* ± 0.01	6.88* ± 0.56	1.57* ± 0.25
h <sup>2</sup>	0.41 ± 1.59	0.29 ± 1.85	0.15 ± 0.36	0.01 ± 0.01	0.05 ± 0.14	0.03 ± 0.07
E (Environmental component)	1.02	1.39	1.11	2.28	2.94	2.55
(H <sub>1</sub> /D) <sup>1/2</sup> (Mean degree of dominance)	0.16	0.21	0.14	0.19	0.18	0.19
H <sub>2</sub> /4H <sub>1</sub> (Proportion of genes with +/-effects in parents)	3.26	1.25	4.68	2.26	1.89	1.49
(4 DH <sub>1</sub> ) <sup>1/2</sup> + F/(4DH <sub>1</sub> ) <sup>1/2</sup> F (Proportion of dominant and recessive genes in parents)	0.27	0.01	0.85	0.69	1.49	0.94
h <sup>2</sup> /H <sub>2</sub> (Number of gene groups)	0.76	0.57	0.95	0.59	0.43	0.18
r (correlation coefficient)						

(1) Days to first staminate flower anthesis (2) Days to first pistillate flower anthesis (3) Node number to first staminate flower anthesis (4) Node number to first pistillate flower Anthesis (5) Days to first fruits harvest (6) Vine length (m) (7) Primary branches per plant (8) Fruit length (cm) (9) Fruit circumference (cm) (10) Fruit weight (kg) (11) Fruits per plant (12) Fruit yield per plant (kg)

coefficient suggested excess of recessive genes for this character in the population. For primary branches per plant, the estimates of D, H<sub>1</sub>, H<sub>2</sub> and F were found significant while

h<sup>2</sup> and E were no significant. The greater value of H<sub>1</sub> as compare to D indicated the major role of non additive gene in the expression of this character. The value of average degree of

dominance ( $H_1/D$ )<sup>1/2</sup> was more than one indicated over dominance. The value of ( $H_2/4H_1$ ) in the parents was found to be less than 0.25 showing asymmetrical distribution of dominance and recessive genes among the parents. The ratio of (KD/KR) was found more than one which showed excess of dominant genes. The estimation of ( $h^2/H_2$ ) was found 0.27 indicated that no major gene group was involved in the inheritance of these characters. The positive value of correlation coefficient suggested excess of recessive gene for these characters in the population. The estimates of genetic parameters for fruit length, dominant components D,  $H_1$  and  $H_2$  were found to be significant while F,  $h^2$  and E were no significant. The value of  $H_1$  is more than D indicated preponderance of non additive gene action is also reported Sharma *et al.* (2010). The average degree of dominance ( $H_1/D$ )<sup>1/2</sup> suggested the role of dominance. The ratio of ( $H_2/4H_1$ ) suggested asymmetrical distribution of positive and negative alleles in the parents. The proportion of dominant and recessive genes among the parents (KD/KR) was more than unity, which showed excess of dominant gene in this population. The estimates of ( $h^2/H_2$ ) was found 0.01 indicated that no major gene group was involved in the inheritance of this characters. The positive value of correlation coefficient suggested excess of recessive gene for this character in the population. The genetic component of variation for fruit circumference, the significant value of D,  $H_1$ ,  $H_2$ , F and  $h^2$  indicated that presence of both additive as well as dominance gene effects for this inheritance of fruit circumference. The mean degree of dominance ( $H_1/D$ )<sup>1/2</sup> was greater than unity suggesting preponderance of dominant genes. The ratio of ( $H_2/4H_1$ ) indicated asymmetrical distribution of positive and negative alleles among the parents. The proportion of dominant and recessive genes in parents (KD/KR) shows excess of dominant alleles. The number of gene group which controlled the character and exhibited dominance was 0.85. The correlation coefficient value was positive which indicated direction for recessive gene. The genetic parameter for fruit weight was estimates of significant for D,  $H_1$ ,  $H_2$ , F and  $h^2$  indicated that both additive and non additive components of variation were important in the manifestation of fruit weight but the magnitude of  $H_1$  was greater than D indicated the major role of dominance component for this trait. The positive value of F suggested frequency of dominant alleles in the parent. The average degree of dominance ( $H_1/D$ )<sup>1/2</sup> was more than one suggesting over dominance for this character. The estimates of ( $H_2/4H_1$ ) was less than unity, suggesting asymmetrical distribution of genes with positive and negative effects among the parents. The proportion of dominant and recessive gene in parents (KD/KR) showed excess of dominant alleles. The correlation coefficient value was positive which indicated direction for recessive gene, Singh *et al.* (2013), Karthik *et al.* (2013). Thus the fruits per plant estimates of  $H_1$ ,  $H_2$  and  $h^2$  were significant for this character. The value of  $H_1$  was more than D which indicated presence of over dominance component for this trait. The mean degree of dominance ( $H_1/D$ )<sup>1/2</sup> shows over dominance for this traits. The ratio of ( $H_2/4H_1$ ) was found to be less than 0.25 indicated the asymmetrical distribution of positive and negative alleles among the parents. The proportion of dominant and recessive gene (KD/KR) in parents suggested that dominant gene were more frequent than

recessive genes. The estimate of ( $h^2/H_2$ ) 1.49 indicated that major gene group was involved in the inheritance for these characters. The positive estimates of correlation coefficient indicated that direction was toward negative side. The genetic effect for fruit per plant was reported earlier by Pitchaimuthu and Sirohi (1997). The genetic component of fruit yield per plant  $H_1$ ,  $H_2$  and  $h^2$  were found to be significant while D, F and E were found no significant. The greater value of dominance components than D indicated the major role of non additive gene in this expression of this character. The positive value of F also suggested more frequency of dominant genes. The average degree of dominance ( $H_1/D$ )<sup>1/2</sup> showed over dominance. The ( $H_2/4H_1$ ) ratio indicated symmetrical distribution of gene with positive and negative effects among the parent. The ratio of (KD/KR) showed that fruit yield was controlled by more number of dominant genes. The number of gene group which controlled the character and exhibit dominance ( $h^2/H_2$ ) was found 0.94. The positives estimates of correlation coefficient indicated that direction was toward recessive genes in population.

The result of present study revealed over dominance and dominance gene action for the entire yield and yield related traits under study. The predominance of non-additive gene action for these characters studied suggests that heterosis breeding would be advantageous to get higher gain in bitter gourd.

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