

Graphical Analysis (Wr-Vr) and Numerical Approach for a Diallel analysis of Yield Components in Bottlegourd (*Lagenaria siceraria* (Mol.) standl.)

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Introduction: Detailed information concerning the genetic control of the characters under selection is important if plant breeders are to conduct their programme efficiently by the choice of appropriate parents and selection methodology. Moreover, it is highly desirable that the information is obtained under the same conditions where selection is to take place. A breeding effort was initiated at Pantnagar in 2003 and 2004 to complement exiting programme, with the aim of producing hybrids of bottle gourd (*Lagenaria siceraria* (Mol.) standl.) with particular emphasis as production problems and consumer preference including high yielding varieties having greater fruit number, weight, earliness, non fibrous flesh at edible stage. The present diallel study was conducted to assist the breeding of high yield cultivars. A considerable number of diallel studies have been reported in bottlegourd. Most have been heterosis and combining ability analysis (9, 10) since the development of commercial F₁ hybrids cultivar is a major aim of cucurbit breeders (8). Some studies (7, 11, 12) have employed the Jinks Hayman method of analysis (3, 4, 5, 6).

This study investigated whether the genetic control of the commercially important characters which are subjected to selection was different at Pantnagar bred material, and what additional genetic resources, if any, were present in the available germplasm to allow further progress to be made. The merits of diallel analysis in plant breeding have been hotly debated (16) but it remains a popular technique for combining a detailed genetic analysis of a small fixed set of

genotypes (usually commercial cultivars) with the production of the hybrid seed for further breeding work. While other designs in themselves may require less labour and be able to test a larger number of genotypes (13) they do not produce all possible hybrids. This means that after analysis a further round of hybridization and seed production may be needed before the hybrids with the greatest potential can be exploited. In addition, the accumulation of information in the literature is of considerable assistance with planning, executing and analyzing diallel experiments.

Materials and Methods: The eight diverse genotypes of bottle gourd (*Lagenaria siceraria* (Mol.) standl.) were chosen as representing a fixed sample of the best germplasm available for a range of characters of commercial importance, including yield and other related components. The parents were crossed by hand, reciprocal hybrids were excluded. The parental (8 lines) and F₁ (28 lines) was grown in a furrow irrigated experiment at Vegetable Research Centre of G.B. Pant Uni. of Agric. and Technology, Pantnagar, UA, India, at an altitude of 243.84m above mean sea level and 29° N altitude and 79.3° longitude in the kharif, 2003 and summer, 2004. The experiment received standard agronomic practices. The experiment consisted of three randomized complete blocks with 36 treatments consisting of 8 parents and 28F₁ hybrids. Each treatment had one row of 5 meter length with plant to plant distance of 1 meter and row to row distance of 3 meter. There were 5 hills per entry. The sowing of seeds was done directly in the field. The parental lines were PBOG 13 (round fruit), PBOG22,

PBOG 54, PBOG 61, PBOG 76, PBOG 117, PBOG 119 and Pusa Naveen. The data obtained from half diallel with eleven characters viz., days to first female flower, node number to first male flower, days to first fruit harvest, main vine length, number of nodes on main vine, internodal length, fruit length, fruit diameter, pedicel length, number of fruit per plant and fruit yield (q/ha). Genetic analysis of diallel data for graphical approach (W_r - V_r graph) as well as genetic components of variation was according to method of Hayman (2,6). Plotting of W_r - V_r graph was done with the help of sigma plotting package. The first three assumptions of the additive/dominance genetic model underlying an analysis of the diallel cross (3) were tested as follows:

- (1) diploid segregation; (2) homozygous parents each parent was maintained by inbreeding and was assumed to be homozygous; and (3) no reciprocal differences. The remaining assumptions of the simple additive dominance genetic model (4) are (4) independent effect of non-allelic genes (i.e. no epistasis); (5) no multiple allelism and (6) genes independently distributed between parents.

Results and Discussions: Graphical analysis of the experimental data recorded was done in order to get information about allelic constitution of the parents used in the diallel cross. In the present study, regression coefficient values (b , w_r , v_r) for eleven characters viz; days to first female flower, node number to first male flower, days to first fruit harvest, main vine length, number of nodes on the main vine, internodal length, fruit length, fruit diameter, pedicel length, number of fruit per plant and fruit yield (q/ha) did not differ significantly from unity indicating the absence of epistasis. This indicated the fulfilment of the assumption that epistasis is absent for these characters. The W_r - V_r graphs for these characters have been presented in Figures

(Fig.1-11). But for the rest characters regression value differs significantly. So, for these characters epistatic gene action may be present. For almost all the characters, the parental array points were scattered all along the regression line in the W_r - V_r graph. This indicates the genetic diversity among the parents for all the traits studied. Distribution of array points in W_r - V_r graph also decides relative proportions of dominant and recessive alleles present in parent. For days to first female flower regression coefficient did not differ significantly from unity, suggesting absence of epistasis. The regression line passed above the origin indicating the presence of partial dominance. The parent PBOG117 had more number of dominant alleles while PBOG 22 which was located at the opposite end of regression line had maximum number of recessive alleles. For node number to first male flower regression line passed below the origin indicating that this trait was conditioned by over dominance, confirmed by the estimated value of $(H_1/D)^{1/2}$, where it was more than unity (1.42). PBOG 54 had the maximum number of dominant alleles, being nearest to the origin. However, PBOG22, PBOG119 and Pusa Naveen carried maximum number of recessive alleles being farthest from the origin. For days to first fruit harvest, regression coefficient value was 1.15. The regression line intercepted the W_r axis below the origin. This confirmed that over dominance was involved in the expression of days to first fruit harvest in the parents. Pusa Naveen exhibited maximum frequency of dominant alleles being nearest to the origin, while PBOG 22 and PBOG 13 had the maximum recessive alleles, being farthest from origin. Parent PBOG22 had maximum frequency of dominant alleles for main vine length while PBOG 119, PBOG 61, Pusa Naveen and PBOG 54 had high number of recessive alleles. The line of regression intercepted W_r axis below the origin indicates the presence of over dominance in the inheritance of main vine length. Rest of the parents PBOG13, PBOG76 and PBOG117 possessed an almost

equal proportion of dominant and recessive alleles for main vine length. For number of nodes on the main vine, complete dominance was found as the regression line passed close to the origin; distribution of parental arrays along the regression line showed that parents PB0G13 had maximum number of dominant alleles while maximum frequency of recessive alleles was in parent PB0G 76. For internodal length, over dominance was found as regression line passed below the origin. Parent PBOG 76 had maximum frequency of dominant alleles. However, parent PBOG 61 and PBOG 119 had number of recessive alleles. For fruit length, partial dominance was found, as the regression line passed above the origin. The result confirmed by the estimated value of $(H_1/D)^{1/2}$, where it was less than unity i.e. (0.56). Distribution of the parental arrays along the regressions line showed that PB0G61 exhibited maximum frequency of dominant alleles, while PB0G13 had maximum frequency of recessive alleles. The parents with the balanced proportion of dominant and recessive alleles were, PB0G22, PB0G 54, PB0G119 and Pusa Naveen. Regression coefficient was 1.14 and regression line intercepted the W_r axis below the origin, indicating the involvement of over dominance in the inheritance of fruit diameter. This result was in conformity with the value of $(H_1/D)^{1/2}$, where it was more than unity (1.37). The distribution of parental arrays along the regression line suggested that PB0G22, PB0G54, PB0G61, PB0G117, PB0G 119 and Pusa Naveen had the maximum number of dominant alleles and parent PBOG 13 had maximum number of recessive alleles. The parent, PB0G76 had the equal proportion of dominant and recessive alleles for fruit diameter. For pedicel length regression line passed above the origin, indicating almost partial dominance to control the inheritance of pedicel length. This results was confirmed by the estimated value of $(H_1/D)^{1/2}$; where it was less than unity (0.87). The parent PB0G117 possessed maximum number of

dominant alleles and maximum recessive alleles was shown by PB0G 13. Parent PB0G22, PB0G54, PB0G 61, PB0G76 PB0G119 and Pusa Naveen had balanced proportion of dominant and recessive alleles. For number of fruits per plant, parents PBOG 117 and PusaNaveen had maximum frequency of dominant alleles, where as the parent with maximum frequency of recessive alleles was PB0G22. The parents PB0G 13, PB0G54, PB0G61, PB0G76 and PB0G119 had the intermediate proportion of dominant and recessive alleles. Due the regression line passed below the origin indicating over dominance to control the expression of number of fruits per plant. For fruit yield (q/ha) over dominance was found to control the inheritance of fruit yield; as the regression line passed below the origin. The result was in conformity with the estimated value of $(H_1/D)^{1/2}$ where it was more than unity. The parents Pusa Naveen and PB0G 117 had maximum frequency of dominant alleles. However, PB0G13 and PB0G 54 had a greater number of recessive alleles. Parent PBOG 22, PBOG 61, PBOG 76 and PB0G 119 showed a balanced proportion of dominant and recessive alleles. Genetic components of variation are presented in Table1. Additive genotypic variance (D) was significant for the characters viz., days to first female flower, node number to first female flower, days to first fruit harvest, fruit length, fruit diameter, pedicel length and fruit yield. Dominance component (H_1) was significant for the character viz., node number to first female flower, days to first fruit harvest, fruit length, fruit diameter, pedicel length, number of fruits per plant and fruit yield (q/ha). Thus, the additive and dominance both the variances were pre dominance component governing the expression of yield (q/ha) and other yield components. The mean squares due to gca and sca both were also found to be significant/ highly significant of most of the character except fruit weight indicating the presence of both additive and non-additive gene action. Involvement of both additive and non-

additive gene action in the inheritance of yield and related traits were also reported by (1, 7)

The contradiction between the approaches of as genetic component of variation and Wr-Vr graph analysis could be ascribed to the presence of correlated gene distribution (2). Ratio of dominant and recessive alleles $(4DH_1)^{1/2}+F / (4DH_1)^{1/2}-F$ was more than unity for days to first female flower, node number to first female flower, days to first fruit harvest, fruit length, fruit diameter, pedicel length, number of fruits per plant and fruit yield (q/ha). The higher proportions of dominant genes observed in most of the characters are in agreement with the findings of (9 and 15). The proportion of genes with positive and negative effects $(H_2/4H_1)$ in the parents was less than 0.25 days to first female flower, node number to first female flower, days to first fruit harvest, fruit diameter and pedicel length consistently over both the seasons. This suggested asymmetrical distribution of dominant genes with positive and negative effects.

Since the distribution of array points reflects the parental diversity, it is suggested that the crosses of Pusa Naveen with other potential lines should be the potential ones to derive high yielding genotypes. The parents for making crosses could be selected on the basis of gca effects. However, selecting the parents on the basis of genetic diversity can not be ignored. The crosses between the diverse parents shall be the potential ones for throwing out desirable segregants. So, the crosses should preferably between the parents located away from the origin in Wr-Vr graph analysis, subject to fulfilment of other criteria, namely good gca effect and the desirable mean values for the important traits. Wr-Vr graphical analysis indicated the involvement of dominant genes for earliness and recessive genes for fruit diameter i.e. the round shape fruit was conditioned by recessive genes. In bottle gourd, increasing attention is being paid towards breeding of

superior cultivars with greater focus on development of hybrids. This segment of research has gained momentum due to enactment of New Seed Policy Act-1998 where in among other things, the vegetable hybrid seed and those of the parental lines are allowed to be imported under open general license (OGL). A large number of private sector seed companies have entered in hybrid seed research and marketing. There is pressure on public sector institutions to contribute substantially on hybrid breeding on commercial scale. Along with this, it is also to be recognized that on bottle gourd, the local germplasm/inbred lines should be prominently used in breeding programmes. In this context the diallel analysis using the inbred from the local indigenous germplasm of bottle gourd assumes significance.

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Table 1: Genetic components of variation and their proportions for yield and yield attributing traits in bottlegourd (kharif, 2003 and summer, 2004).

Components / proportions	Days to first female flower		Node number to first male flower		Days to first fruit harvest		Main vine length		Number of nodes on main vine	
	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer
D	172.60** ±34.22	42.66** ± 7.55	34.26** ±8.36	0.89** ± 0.30	245.05** ±13.30	67.75** ±5.25	7.58 ±4.00	4.03** ±0.81	292.82* ±81.44	27.42 ±74.38
F	70.44 ±80.86	4.28 ± 17.83	37.50 ±19.75	0.78 ± 0.71	202.68 ±31.43	21.77* ±12.41	5.85 ±9.46	8.09** ±1.91	144.38* ±192.44	100.19* ±175.75
H ₁	181.36 ±78.67	77.55** ± 17.35	69.25* ±19.21	2.45** ±0.69	235.42** ±30.58	63.66** ±12.07	24.87* ±9.21	19.86** ±1.85	738.02** ±187.22	633.57** ±170.98
H ₂	139.21 ±68.44	64.19** ± 15.09	55.46* ±16.71	1.85** ±0.60	128.91** ±26.60	59.65** ±10.50	22.18* ±8.01	14.67** ±1.61	684.02** ±162.89	463.19** ±148.75
h ²	3.05 ±45.90	1.01 ± 10.12	-1.21 ±11.21	0.10 ± 0.40	10.37 ±17.84	-0.43 ±7.04	-0.06 ±5.37	1.60 ±1.08	47.92 ±109.24	292.40** ±99.76
E	7.07 ±11.41	3.11 ± 2.52	2.77 ±2.79	0.23 ±0.10	11.93* ±4.43	1.71 ±1.75	0.33 ±1.33	0.54 ±0.27	5.82 ±27.15	2.80 ±24.79
(H ₁ /D) ^{1/2}	1.03	1.35	1.42	1.66	0.98	0.97	1.81	2.22	1.59	4.81
(H ₂ /4H ₁)	0.19	0.21	0.20	0.19	0.14	0.23	0.22	0.18	0.23	0.18
$\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F}$	1.50	1.08	2.25	1.71	2.45	1.40	1.54	2.65	1.37	2.23

Components / proportions	Internodal length (cm)		Fruit length (cm)		Fruit diameter (cm)		Pedicel length (cm)		No. of fruits/plant		Fruit yield (q/ha)	
	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer
D	7.71** ±1.10	119.21** ±4.31	75.40** ±3.55	59.12** ± 3.14	5.02** ±0.75	7.52** ±0.80	108.50** ±9.69	5.07 ±3.69	9.55 ±4.16	3.21* ±0.72	16401.57** ±4934.65	6882.54** ±2058.49
F	10.51** ±2.59	28.84* ±10.19	75.84** ±8.38	53.15** ± 7.43	8.17** ±1.76	5.41** ±1.89	28.94 ±22.91	11.67 ±8.71	6.83 ±9.83	1.00 ± 1.71	19025.57 ±11660.12	5394.12 ±4864.01
H ₁	10.68** ±2.52	37.29** ±9.92	56.72** ±8.15	45.13** ±7.23	9.44** ±1.71	7.68** ±1.84	70.55* 22.29	37.41** ±8.48	42.07** ±9.57	8.79** ±1.67	53769.82** ±11344.03	24632.14** ±4732.16
H ₂	6.55* ±2.19	33.63** ±8.63	32.20** ±7.09	29.42** ± 6.29	5.21** ±1.49	5.95* ±1.60	64.65* ±19.39	28.15** ±7.37	38.24** ±8.32	6.65** ±1.45	47663.43** ±9869.3	20058.39** ±4116.97
h ²	4.82* ±1.47	8.73 ±5.79	-0.15 ±4.76	-0.17 ± 4.22	0.08 ±1.00	0.35 ±1.07	7.28 ±13.0	7.18* ±4.98	23.22** ±5.58	2.73* ±0.97	19778.62* ±6618.77	7946.55** ±2761.02
E	0.76 ±0.37	4.83 ±1.44	0.71 ±1.18	0.53 ± 1.05	0.45 ±0.25	0.17 ±0.27	2.52 ±3.23	0.74 ±1.23	0.38 ±1.39	0.07 ±0.24	138.93 ±1644.88	47.76 ±686.16
(H ₁ /D) ^{1/2}	1.18	0.56	0.87	0.87	1.37	1.01	0.81	2.72	2.10	1.65	1.81	1.89
(H ₂ /4H ₁)	0.15	0.23	0.14	0.16	0.14	0.19	0.23	0.19	0.23	0.19	0.22	0.20
$\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F}$	3.75	1.55	3.76	3.12	3.19	2.10	1.40	2.47	1.41	1.21	1.94	1.52











