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

Rakesh K. Dubey[1,2*] • Hari Har Ram[3]

[1] Department of Vegetable Science, G.B. Pant University of Agriculture and Technology, Pantnagar 263145, US Nagar, (UK), India
[2] Current corresponding address: College of Horticulture and Forestry, Pasighat-791102 Arunachal Pradesh, India
[3] Krishidhan Seeds Pvt. Ltd., Pune, India

Corresponding author: * rksdubey@yahoo.co.in

ABSTRACT

A Hayman analysis for eleven characters of yield and related traits of eight parent half-diallel set of crosses was conducted in bottlegourd (*Lagenaria siceraria* (Mol.) Standl.). Vr-Wr graphical analysis demonstrated that dominant genes were responsible for earliness while a recessive gene accounted for the round shape of fruit. The components of variation indicated that the dominance components H_1 and H_2 were significant for all the characters while additive genetic variance (D) was significant for all the characters except for fruit weight, suggesting the involvement of both additive and non-additive gene action.

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 an 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 (Sharma *et al.* 1993; Pandey *et al.* 2004). Development of commercial F_1 hybrid cultivars is a major aim of cucurbit breeders (Padma *et al.* 2002). The Jinks and Hayman (1953) method of analysis was employed by Sivakami *et al.* (1987), Sirohi and Gourui (1993) and Kushwaha and Ram (1996) in genetic study of bottlegourd.

The present study investigated whether the genetic control of the commercially important characters which were subjected to selection was different in Pantnagar-bred material, and what additional genetic resources, if any, were present in the available germplasm/cultivar to allow further progress to be made. The merits of diallel analysis in plant breeding have been hotly debated but it remains a popular technique for combining a detailed genetic analysis of a small fixed set of genotypes with the production of the hybrid seed for further breeding work (Wright 1985). While other designs in themselves may require less labour and be able to test a larger number of genotypes (Pooni *et al.* 1984) but 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

Eight diverse genotypes of bottle gourd (*Lagenaria siceraria* (Mol.) Standl.) were chosen as representing a fixed sample of the best germplasm/cultivar available for a range of characters of commercial importance including yield and other related traits. The parents were crossed by hand, reciprocal hybrids were excluded. The eight parental lines and 28 F_1 lines were grown in a furrow irrigated experiment at Vegetable Research Centre of G.B. Pant Uni. of Agri. and Techno., Pantnagar, UK, India, at an altitude of 243.84 m above mean sea level and 29°N altitude and 79.3° longitude in the kharif (i.e. the Autumn harvest in India), 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 28 F_1 hybrids. Each treatment had one row 5 m long with a plant-to-plant distance of 1 m and a row-to-row distance of 3 m. There were 5 hills per entry. The sowing of seeds was done directly in the field. The parental lines were PBOG 13 (round fruited), PBOG 22, PBOG 54, PBOG 61, PBOG 76, PBOG 117, PBOG 119 and Pusa Naveen. Data was obtained from half diallel using eleven characters viz., days to first female flower, node number of 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. Genetic analysis of diallel data for graphical approach (Vr-Wr graph) as well as genetic components of variation was according to the method of Hayman (1954a) and Jinks (1956). Plotting of the Vr-Wr graph was done with the help of a sigma plotting package. The first three assumptions of the additive/dominance genetic model underlying an analysis of the diallel cross (Hayman 1954b) were tested as: (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 (Mather and Jinks 1982) are (4) independent effect of non-allelic genes (i.e. no epistasis); (5) no multiple allelism and (6) genes independently distributed between parents.

Original Research Paper

RESULTS AND DISCUSSION

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 (bwr, vr) for eleven characters – presented as Vr-Wr graphs in **Figs. 1-11**, respectively – viz. days to first female flower (**Fig. 1**), node number of first male flower (**Fig. 2**), days to first fruit harvest (**Fig. 3**), main vine length (**Fig. 4**), number of nodes on main vine (**Fig. 5**), internodal length (**Fig. 6**), fruit length (**Fig. 7**), fruit diameter (**Fig. 8**), pedicel length (**Fig. 9**), number of fruit per plant (**Fig. 10**) and fruit yield (**Fig. 11**) did not differ significantly from unity indicating the absence of epistasis. This indicated the fulfillment of the assumption that epistasis is absent for these characters. For almost all the characters, the parental array points were scattered all along the regression line in the Vr-Wr graph. This indicates the genetic diversity among the parents for all the traits studied. Distribution of array points in the Vr-Wr graph also decides the relative proportions of dominant and recessive alleles present in the parent.
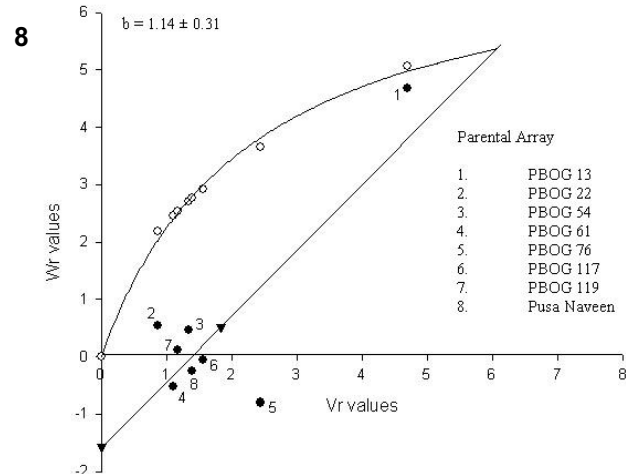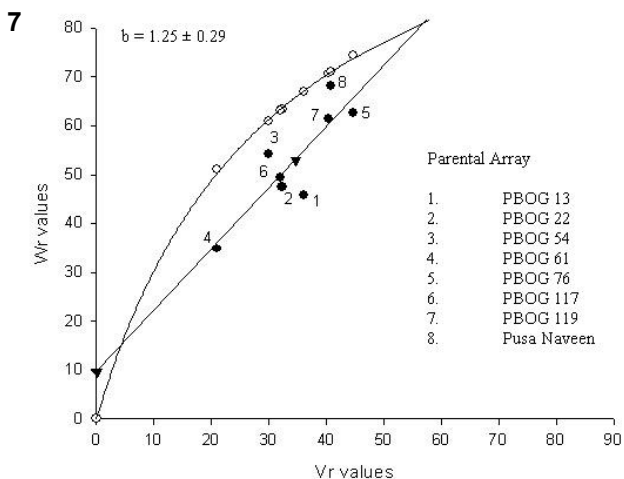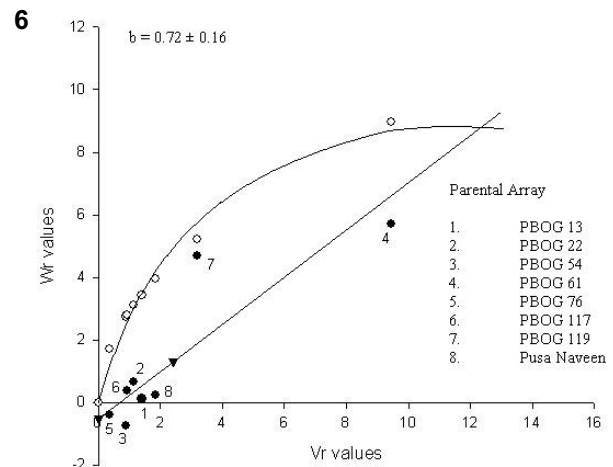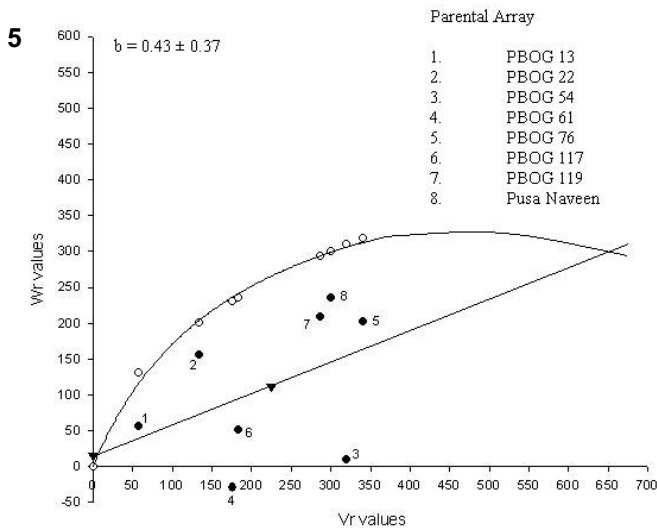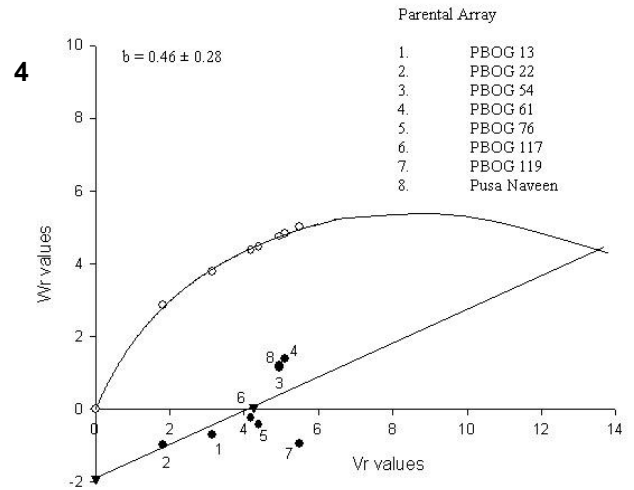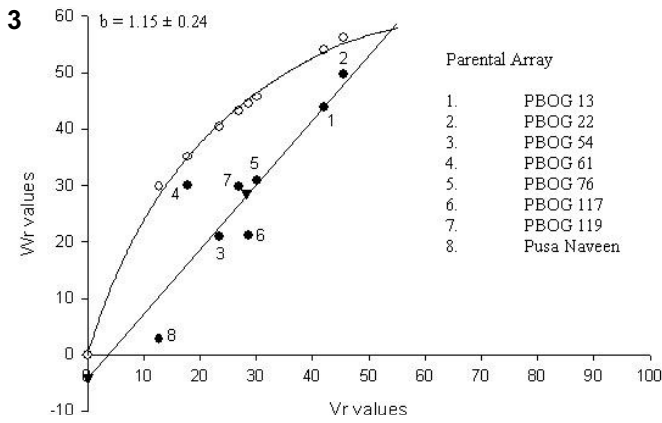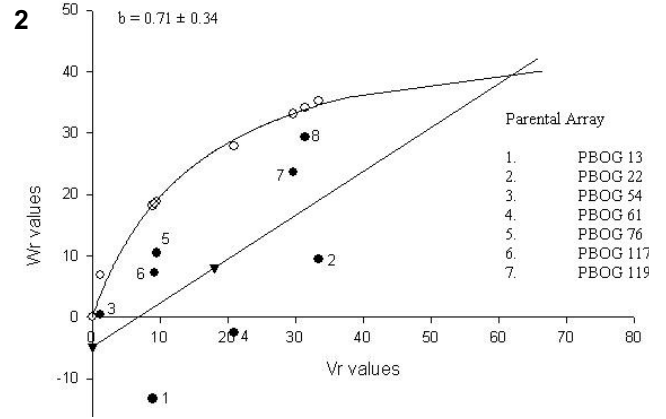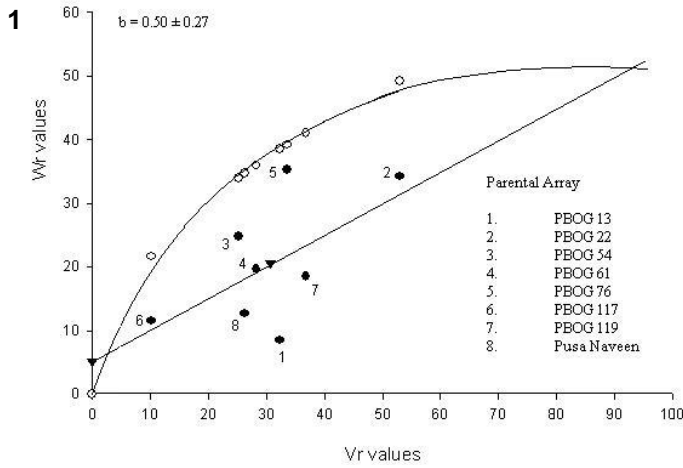
For days to first female flower (**Fig. 1**) the regression coefficient did not differ significantly from unity suggesting absence of epistasis. The regression line passed above the origin indicating the presence of partial dominance. The parent PBOG 117 had more number of dominant alleles while PBOG 22 which was located at the opposite end of regression line had maximum number of recessive alleles. For node number of first male flower (**Fig. 2**) the 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. PBOG 54 had the maximum number of dominant alleles, being nearest to the origin. However, PBOG 22, PBOG 119 and Pusa Naveen carried the maximum number of recessive alleles being farthest from the origin. For days to first fruit harvest (**Fig. 3**), the regression coefficient value was 1.15. The regression line intercepted the Wr axis below the origin. This confirmed that overdominance 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 PBOG 22 had maximum frequency of dominant alleles for main vine length (**Fig. 4**) while PBOG 119, PBOG 61, Pusa Naveen and PBOG 54 had high number of recessive alleles. The line of regression intercepted Wr axis below the origin indicates the presence of over dominance in the inheritance of the main vine length. The rest of the parents PBOG 13, PBOG 76 and PBOG 117 possessed an almost equal proportion of dominant and recessive alleles for main vine length. For number of nodes on the main vine (**Fig. 5**), complete dominance was found as the regression line passed close to the origin; distribution of parental arrays along the regression line showed that parent PBOG13 had the maximum number of dominant alleles while the maximum frequency of recessive alleles was observed in PBOG 76. For internodal length (**Fig. 6**), overdominance was observed since the regression line passed below the origin. Parent PBOG 76 had the maximum frequency of domiant alleles. However, parents PBOG 61 and PBOG 119 had the maximum number of recessive alleles. For fruit length (**Fig. 7**), 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. Distribution of the parental arrays along the regressions line showed that PBOG 61 exhibited maximum frequency of dominant alleles, while Pusa Naveen had maximum frequency of recessive alleles. The parents with the balanced proportion of dominant and recessive alleles were PBOG 13, PBOG 22, PBOG 54 and PBOG 119. The regression coefficient was 1.14 and the regression line intercepted the Wr axis below the origin, indicating the involvement of over dominance in the inheritance of fruit diameter (**Fig. 8**).
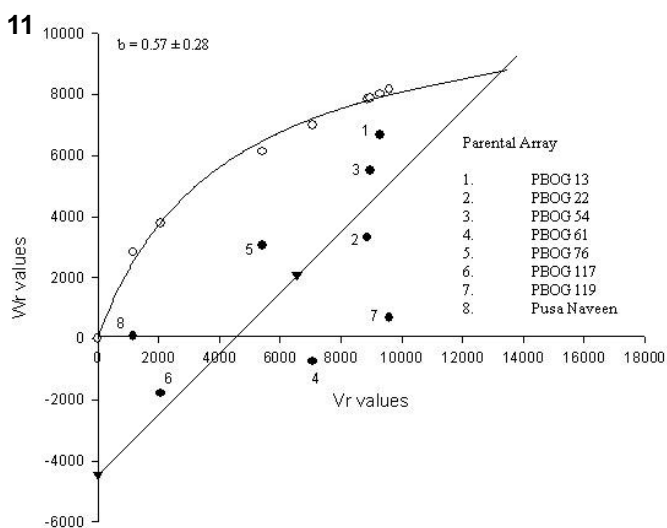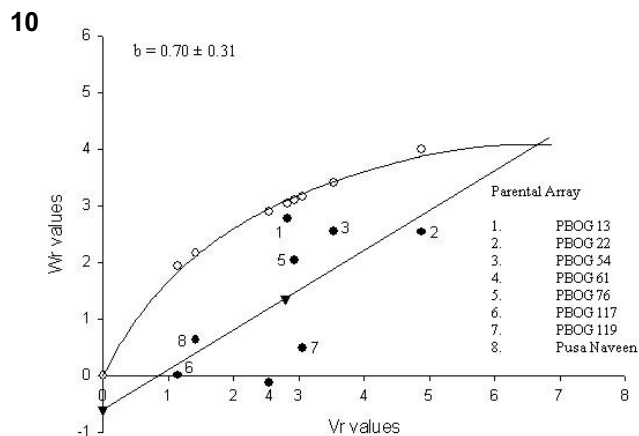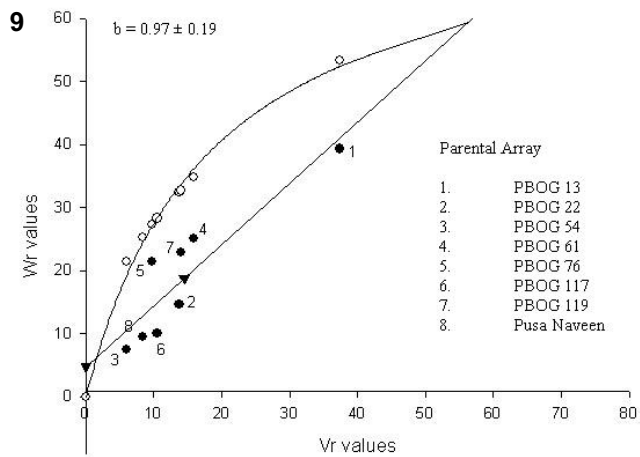
This result was in conformity with the value of $(H_1/D)^{1/2}$ where it was more than unity. The distribution of parental arrays along the regression line suggested that PBOG 22, PBOG 54, PBOG 61, PBOG 117, PBOG 119 and Pusa Naveen had the maximum number of dominant alleles and parent PBOG 13 had the maximum number of recessive alleles for the fruit diameter trait. Parent PBOG76 had an equal proportion of dominant and recessive alleles for fruit diameter. For pedicel length (**Fig. 9**) the 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. Parent PBOG117 possessed the maximum number of dominant alleles and maximum number of recessive alleles was shown by PBOG 13. Parents PBOG 22, PBOG 54, PBOG 61, PBOG76, PBOG 119 and Pusa Naveen, which had a balanced proportion of dominant and recessive alleles. For the number of fruits per plant (**Fig. 10**), parents PBOG 117 and PusaNaveen had the maximum frequency of dominant alleles whereas the parent with the maximum frequency of recessive alleles was PB0G 22. Parents PBOG 13, PBOG 54, PBOG 61, PBOG 76 and PBOG 119 had an intermediate proportion of dominant and recessive alleles. The regression line passed below the origin, indicating overdominance in the control of expression of number of fruits per plant. For fruit yield (**Fig. 11**) overdominance was found to control this trait, 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 PBOG 117 had a maximum frequency of dominant alleles. However, parents PBOG 13 and PBOG 54 had a greater number of recessive alleles. Parents PBOG 22, PBOG 61, PBOG 76 and PBOG 119 showed a balanced proportion of dominant and recessive alleles. The genetic components of variation are presented in **Table 1**.

Additive genotypic variance (D) was significant for the characters viz., days to first female flower, node number of first male flower, days to first fruit harvest, fruit length, fruit diameter, pedicel length and fruit yield. Dominance component (H_1) was significant for the characters viz., node number of first male flower, days to first fruit harvest, fruit length, fruit diameter, pedicel length, number of fruits per plant and fruit yield. Thus, the additive and dominance both the variances were pre dominance component governing the expression of yield and other yield components. Kushwaha and Ram (1996) and Dubey and Maurya (2003) also claimed the involvement of both additive and non-additive gene action in the inheritance of yield and related traits in bottlegourd.

The contradiction between the approaches of as genetic component of variation and Vr-Wr graph analysis could be ascribed to the presence of correlated gene distribution (Hayman 1954). The 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 of first male flower, days to first fruit harvest, fruit length, fruit diameter, pedicel length, number of fruits per plant and fruit yield. The higher proportions of dominant genes observed in most of the characters are in agreement with the findings of Maurya and Singh (1994) and Pandey *et al.* (2004). The proportion of genes with positive and negative effects ($H_2/4H_1$) in the parents was less than 0.25 in days to first female flower, node number of the first male flower, days to first fruit harvest, fruit diameter and pedical length consistently over both seasons. This suggested asymmetrical distribution of dominant genes with both positive and negative effects.

Since the distribution of array points reflects the parental diversity, it is suggested that the crosses of parent 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

9 b = 0.97 ± 0.19

Parental Array
1. PBOG 13
2. PBOG 22
3. PBOG 54
4. PBOG 61
5. PBOG 76
6. PBOG 117
7. PBOG 119
8. Pusa Naveen

10 b = 0.70 ± 0.31

Parental Array
1. PBOG 13
2. PBOG 22
3. PBOG 54
4. PBOG 61
5. PBOG 76
6. PBOG 117
7. PBOG 119
8. Pusa Naveen

11 b = 0.57 ± 0.28

Parental Array
1. PBOG 13
2. PBOG 22
3. PBOG 54
4. PBOG 61
5. PBOG 76
6. PBOG 117
7. PBOG 119
8. Pusa Naveen

Figs. 1-11 (this page and previous page) Regression coefficient values (bwr, vr) for eleven characters. Days to first female flower (**1**), node number of first male flower (**2**), days to first fruit harvest (**3**), main vine length (**4**), number of nodes on main vine (**5**), internodal length (**6**), fruit length (**7**), fruit diameter (**8**), pedicel length (**9**), number of fruit per plant (**10**) and fruit yield (**11**).

Table 1 Genetic component of variation and their proportions for yield and related traits in bottle gourd. Values significant at [*]0.05 or [**]0.01 level of probability.

Components/ Traits	Season	D	F	H_1	H_2	h^2	E	$(H_1/D)^{1/2}$	$(H_2/4H_1)$	$\frac{(4DH_1)^{1/2}+F}{(4DH_1)^{1/2}-F}$
Days to first	Kharif	172.60±34.2[**]	70.44±8.9	181.36±78.6	139.21±68.4	30.50±4.5	7.07±11.4	1.03	0.2	1.5
female flower	Summer	42.66±7.6[**]	4.28±1.8	77.55±17.3[*]	64.19±15.1[**]	10.10±1.0	3.11±2.5	1.35	0.2	1.0
Node number to	Kharif	34.26±8.4[**]	37.5±19.8	69.25±19.2[*]	55.46±16.8[*]	12.10±1.2	2.77±2.8	1.4	0.2	2.3
first male flower	Summer	0.89±0.3[**]	0.78±0.7	2.45±0.6[**]	1.85±0.6[**]	0.10±0.4	0.23±0.1	1.6	0.2	1.7
Days to first	Kharif	245.05±13.3[**]	202.68±31.4	235.42±30.6[**]	128.91±26.0[**]	10.37±1.7	11.93±4.4[*]	0.9	0.2	2.4
fruit harvest	Summer	67.75±5.3[**]	21.77±12.4[*]	63.66±12.0[**]	59.65±10.5[**]	-0.43±.04	1.71±1.7	0.9	0.2	1.4
Main vine	Kharif	7.58±4.0	5.85±0.5	24.87±9.2[*]	22.18±8.0[*]	-0.06±5.3	0.33±1.3	1.8	0.2	1.5
length	Summer	4.03±0.8[**]	8.09±1.9[**]	19.86±1.9[**]	14.67±1.6[**]	1.60±1.0	0.54±0.2	2.2	0.2	2.6
Number of nodes	Kharif	292.82±81.4[*]	144.38±19.4[**]	738.02±187.2[**]	684.02±162.9[**]	47.92±109.2	5.82±27.2	1.6	0.2	1.4
on main vine	Summer	27.42±4.4	100.19±17.8[*]	633.57±170.9[**]	463.19±148.6[**]	292.40±99.7[**]	2.80±24.8	4.8	0.2	2.2
Inter nodal	Kharif	7.71±1.1[*]	10.51±2.6[**]	10.68±2.5[**]	6.55±2.2[*]	4.82±1.5[*]	0.76±0.4	1.2	0.1	3.7
length	Summer	119.21±4.3[*]	28.84±10.2[*]	37.29±9.9[**]	33.63±8.6[**]	8.73±5.8	4.83±1.4	0.6	0.2	1.5
Fruit length	Kharif	75.40±3.6[*]	75.84±8.4[**]	56.72±8.6[**]	32.20±7.1[**]	-0.15±4.7	0.71±1.2	0.8	0.1	3.7
	Summer	59.12±3.1[**]	53.15±7.4[**]	45.13±7.2[**]	29.42±6.3[**]	-0.17±4.2	0.53±1.0	0.8	0.15	3.1
Fruit diameter	Kharif	5.02±0.8[**]	8.17±1.7[**]	9.44±1.7[**]	5.21±1.5[**]	0.08±1.0	0.45±0.6	1.4	0.15	3.2
	Summer	7.52±0.8[**]	5.41±1.8[**]	7.68±1.8[**]	5.95±1.6[*]	0.35±1.0	0.17±0.3	1.1	0.2	2.1
Pedicel length	Kharif	5.02±0.8[**]	8.17±1.7[**]	9.44±1.7[**]	5.21±1.5[**]	0.08±1.0	0.45±0.3	1.4	0.1	3.2
	Summer	7.52±0.8[**]	5.41±1.8[**]	7.68±1.8[**]	5.95±1.6[*]	0.35±1.0	0.17±0.3	1.1	0.19	2.1
Number of fruits	Kharif	9.55±4.2	6.83±1.8	42.07±9.6[**]	38.24±8.3[**]	23.22±5.5[**]	0.38±1.4	2.1	0.2	1.4
per plant	Summer	3.21±0.7[*]	1.00±0.71	8.79±1.7[**]	6.65±1.4[**]	2.73±0.9[*]	0.07±0.2	1.5	0.2	1.2
Fruit yield	Kharif	16401.57 ±4934.6[*]	19025.57 ±1160.1	53769.82 ±11344.0[**]	47663.43 ±9869.3[**]	19778.62 ±6618.7[*]	138.93±1644.8	1.8	0.2	1.9
	Summer	6882.54 ±2058.4[**]	5394.12 ±484.0	24632.14 ±4732.7[**]	20058.39 ±4116.9[**]	7946.55 ±2761.0[**]	47.76±686.2	1.8	0.2	1.5

segregants. So, the crosses should preferably be between the parents located away from the origin in Vr-Wr graph analysis, subject to fulfillment of other criteria, namely good gca effects and the desirable mean values for the important traits. Vr-Wr graphical analysis indicated involve-

ment of dominant genes for earliness and recessive genes for fruit diameter i.e. the round shape fruit was conditioned by recessive genes. In bottlegourd, increasing attention is being paid towards breeding of superior cultivars with greater focus on development of hybrids. Along with this, it

is also to be recognized that the local germplasm/inbred lines should be prominently used in breeding programmes. In this context the diallel analysis using inbreds from local indigenous germplasm assumes significance.

ACKNOWLEDGEMENTS

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