Genetics of Seed Yield and its Components in Bottle gourd (*Lagenaria siceraria* (Mol.) Standl.)

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Introduction: Bottlegourd [*Lagenaria siceraria* (Mol.) Standl.] is the cultivated species among the six species of *Lagenaria* having a diploid chromosome number of 22. The plants are annual viny pubescent herb with large white flower borne on slender peduncles. Breeding objectives of bottlegourd are based on seed production problems and consumer preference. In bottle gourd increasing attention is being paid towards breeding of superior cultivars with greater focus on development of hybrid seeds. F_1 hybrid breeding is prominent among the methods used in the improvement of bottle gourd. Diallel analysis helps in estimating the genetic components of variation, the degree of dominance, the proportion of dominant and recessive genes, the distribution of genes with positive and negative effects governing the expression of a particular trait. Diallel analysis using the inbreds from the local indigenous germplasm of bottlegourd assumes significance .With this viewpoint eight divergent genotypes were mated in a diallel fashion to study the genetics of seed yield and its component traits into bottlegourd.

Materials and Methods: The eight diverse genotypes of bottle gourd (*Lagenaria siceraria* (Mol.)Standl.) were chosen as representing a fixed sample of the best germplam/ advanced line 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 (28lines)was grown in a furrow irrigated experiment at Vegetable Research Centre of G.B. Pant Uni. of Agric. and Technology, Pantnagar, UK, India, at an altitude of 243.84m above mean sea level and 29^0 N altitude and 79.3^0 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 28F_1 hybrids. Each treatment had one rows of 5 meter length with plant to plant distance of 1 meter and row to row distance of 3meter. There were 5 hills per entry. The sowing of seeds was done directly in the field. The parental lines were PBOG 13(round fruited), PBOG22, PBOG 54 (segmented leaf), PBOG 61, PBOG 76, PBOG 117, PBOG 119 and Pusa Naveen. The data obtained from half diallel with seven characters viz., days to first male flower, node number to first female flower, number of primary branches per vine, fruit weight, pedicel diameter, number of seeds per fruits and 100 seed weight. Genetic analysis of diallel data for genetic components of variation was according to method of(3,9). The first three assumptions of the additive/ dominance genetic model underlying an analysis of the diallel cross (4) 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 (12) are (4) independent effect of non- allelic genes (i.e. no epistasis) ; (5) no multiple allelisam and (6) genes independently distributed between parents. Estimation of Genetics Components were done as follows:

The expected values of main components of genetic variance were estimated by solving the above equations for F_1 generation (3). In F_1 generation the expected values of main components are

$$\hat{D} = V_0L_0 - \hat{E}$$

$$\hat{F} = 2V_0L_0 - 4W_0L_{01} - 2(n-2)\hat{E}/n$$

$$\hat{H}_1 = V_0L_0 - 4W_0L_{01} + 4V_1L_1 - 3(n-2)\hat{E}/n$$

$$\hat{H}_2 = 4V_1L_1 - 4V_0L_1 - 2\hat{E}$$

$$\hat{h}^2 = 4(ML_1 - ML_0)^2 - 4(n-1)\hat{E}/n^2$$

$$E = M'e$$

Where,

N = number of parents

D = variance component due to additive gene effects

F = mean of the covariance of additive and dominance effects over all the arrays

H_1 = variance component due to dominance deviation

H_2 = dominance indicating asymmetry of positive and negative effect of genes

$$H_2 = H_1[1-(\mu-v)^2]$$

Where,

μ = proportion of positive genes in parents

v = proportion of negative genes in parents

h^2 =dominance effect (as the algebraic sum over all loci in heterozygous phase in all crosses)

V_0L_0 = variance of parents

V_r = variance of all the progenies in each parent of array

V_1L_1 = mean of all the V_r values

Wr = co-variance between parents and their off springs in one array

W_0L_{01} = mean of all W_r values

$(ML_1 - ML_0)^2$ = dominance relationship i.e. difference between the mean of the parents and the mean of their n(n-1) progenies.

V_0L_1 = variance of the means of arrays

E = the expected environmental component of variation

In order to test the significance of the main component: D, F, H_1, H_2, h^2 and E, the standard errors (SE) are calculated for each of mean as follows:

$$S_E(D) = (S^2 \times CD)^{1/2}$$

$$S_E(F) = (S^2 \times CF)^{1/2}$$

$$S_E(H_1) = (S^2 \times CH_1)^{1/2}$$

$$S_E(H_2) = (S^2 \times CH_2)^{1/2}$$

$$S_E(h^2) = (S^2 \times Ch^2)^{1/2}$$

$$S_E = (S^2 \times CE)^{1/2}$$

The above genetic components were used in computation of following genetic ratios :

1. Mean Degree of Dominance was calculated as $(H_1D)^{1/2}$. If the ratio obtained is equal to 1, this indicated presence of complete dominance; if more than 1, it indicates presence of over dominance and if less than 1, it reveals presence of partial dominance.
2. The proportion of dominant genes with positive or negative effects in parents is determined by the ratio : $H_2/4H_1$ with the maximum theoretical value of 0.25, which arises when p = q = 0.5 at all loci. A deviation from 0.25 would seem when $p \neq q$. Thus, $H_2/4H_1 \approx 0.25$ would means symmetrical distribution of positive and negative dominant genes in parents; and when $H_2/4H_1 \neq 0.25$ it means asymmetrical distribution (p = proportion of dominant alleles and q = proportion of recessive alleles).
3. The proportion of dominant and recessive genes in parents. It was calculated as $\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F}$. When this ratio is equal to 1 it indicates nearly equal proportion of dominant and recessive alleles in parents (i.e. p = q = 0.5). If the ratio is greater than 1 it refers to excess of dominant alleles and minority of recessive alleles (p > q). When this ratio is less than 1, it means minority of dominant alleles and excess of recessive alleles (p < q).

4. Number of dominant gene blocks is estimated by h^2/H_2 ratio.

Result and Discussions: The analysis of variance revealed highly significant differences among progenies indicating that the parents were diverse for the characters studied and diversity was transmittable to the offspring. The component analysis data is given in table 1.For days to first male flower in the kharif season experiment, only additive (D) variance was

significant, signifying the involvement of additive gene action in the inheritance of days to first male flower. The $(H_1/D)^{1/2}$ estimate was 1.17 which was greater than unity, and suggested the presence of over dominance. The proportion of dominant and recessive alleles pooled over parents $(4\ DH_1)^{1/2} + F\ /(4DH_1)^{1/2}–F$ was 1.11, suggesting almost equal proportion of dominant and recessive alleles. The proportion of dominant genes with positive and negative effects was 0.18, which was less than the theoretical maximum value of 0.25 which arises when u (alleles with positive effects) and V (alleles with negative effects) = 0.5. This indicating asymmetrical distribution of positive and negative dominant genes in the parents. In the summer season, the degree of dominance $(H_1/D)^{1/2}$ was found to be greater than one (1.85) indicating over dominance. The proportion of dominant and recessive alleles pooled over was 0.79 suggesting unequal preparation of dominant and recessive alleles. The proportion of dominant genes with positive and negative effects was 0.17 indicating asymmetrical distribution of positive and negative dominant genes in the parents. For node number to first female flower in both the seasons, the significant D and H_1 variances were observed. This indicated the role of both additive and dominance gene action in the inheritance of node number to first female flower. The estimate of $(H_1/D)^{1/2}$ was more than unity i.e. 1.90 in the kharif and 1.81 in the summer, indicating the over dominance. An asymmetrical distribution of positive and negative dominant genes for this trait was seen in the parents as $H_2/4H_1$ was 0.16 and 0.19 in the kharif and summer season, respectively. The value of relative frequency of dominant and recessive alleles in the parents was 3.35 in the kharif season and 2.42 was in the summer season, suggesting an excess of dominant alleles. For number of primary branches per vine dominance (H_1 and H_2) of genetic variance were significant in both the seasons. Mean degree of dominance $(H_1/D)^{1/2}$ was greater than unity (3.60 in the kharif season and 3.09 in the summer season) and thus suggested the presence of over dominance. The values $H_2/4H_1$ (0.22) were almost equal to the maximum theoretical value of 0.25 indicating symmetrical distribution of u (alleles with positive effects) and v (alleles with negative effects) in both the seasons. Proportion of dominant and recessive alleles was 0.86 in the kharif season and 1.29 in the summer season, suggesting almost equal proportion of dominant and recessive alleles in the parents. For fruit weight additive genetic component of variance (D) was non-significant. Dominance components (H_1 and H_2) were found to be significant. The $(H_1/D)^{1/2}$ estimate was (3.60 in the kharif season and 3.84 in the summer season) more than unity implying over dominance. The estimate of $H_2/4H_1$ (0.21) were almost equal to its maximum value of 0.25, indicating symmetrical distribution of dominant genes. Proportion of dominant and recessive alleles was more than one, suggesting excess of the dominant alleles. For pedicel diameter in both the seasons, none of the estimates was significant. For number of seeds per fruits, the analysis of variance component indicated that in both the season experiments, additive (D) and dominance variances (H_1) were significant. That follows that the expression of number of seeds per fruits was conditioned by both additive and dominance gene action. However, dominance component was predominant than the additive component. $(H_1/D)^{1/2}$ was 3.65 (kharif season) and 1.72 (summer season) and showed over dominance. $(H_2/4H_1)$ (0.17) was less than its maximum theoretical value. 0.25 showing asymmetrical distribution of positive and negative alleles over both the seasons. The value of $(4DH_1)^{1/2} + F/(4DH_1)^{1/2}$-F was 2.31 and 2.84 during the kharif and summer seasons, respectively, indicating the excess of dominant alleles over both the seasons. For 100 seed weight dominance variances (H_1) was significant, signifying the involvement of dominance gene action to govern 100 seed weight. However, h^2 was significant in the both season. This indicated that there was presence of overall dominance effect. The $(H_1/D)^{1/2}$ estimate was more than unity i.e. (3.35 in the kharif season and 3.56 in the summer season), suggesting the presence of over dominance for 100 seed weight. An asymmetrical distribution

of positive and negative dominant genes for 100 seed weight was reflected in the parents as $H_2/4H_1$ was 0.18 (kharif season) and 0.16 (summer season). The proportion of dominant and recessive alleles pooled over parents $(4DH_1)^{1/2}$ + $F/(4DH_1)^{1/2}$-F was 2.64 (kharif season) and 3.21 (summer season) suggesting an excess of dominant alleles. It is worth nothing that bottle gourd like several other cucurbits does not respond to inbreeding (16). The cost of production of hybrid seed in bottle gourd is substantially low, as the F_1 seeds can be produced on commercial scale by the removal of male buds from the female parent and allowing insect pollination. The breeding methods for the improvement of crop depend on nature and magnitude of the components of genetic variances, combining ability of the parents and crosses and the extent of heterosis for quantitative traits. Choice of the parents is considered an important aspect in bottle gourd breeding programme aimed at improving yield and its components because superior parents may not necessarily transfer their superiority to the progenies (1). The theory of diallel crosses and the usefulness of diallel cross technique in genetic analysis of population have received sufficient attention in the past. Several diallel cross techniques have been proposed and applied to diverse problems. For example (2,6,13,17) have considered the utility of diallel crosses. The theory of diallel crosses and procedures for estimating certain genetic parameters in terms of gene models in varying degrees of complexity, have been discussed by (2,3,7,8,9,10). In addition to have an understanding of the combining ability and the genetic components of variation one gets information on the average degree of dominant and recessive alleles in the parents. Therefore, diallel cross analysis in totality is a useful biometrical technique in bottle gourd breeding. The higher proportion of dominant genes observed in most of the characters are in agreement with the findings of (14,15).The proportion of genes with positive and negative effects ($H_2/4H_1$) in the parents was less than 0.25 for days to first male flower, node number to female flower, number of seeds per fruit and 100 seed weight consistently over both the seasons. This suggested asymmetrical distribution of dominant genes with positive and negative effects. It is in accordance with the findings of (11, 15). The parents for making crosses could be selected on the basis of gca effects. Overall, both additive and non additive components of variation were found to play important roles in the inheritance of economic traits in bottle gourd as it evident from component analysis. The t^2 values were non-significant for the traits in the F_1, indicating the validity of assumptions underlying the diallel analysis. However, presence of non-additive interaction for the same traits was intriguing but, as suggested by (3) even if a traits exhibits a partial failure of assumptions, analysis could be carried out for such characters, though the results would not be as reliable as they would have been had all assumptions been fulfilled. In a cross-pollinated crop like bottle gourd, exploitation of non-additive genetic variance as such would be practical worth. However, conventional selection, is likely to lead to substantial trait improvement.

Literature Cited

1. Allard, R.W. (1960). Principles of Plant Breeding. John Willey and Sons Inc. New York, pp. 227-228.
2. Griffing, B. (1956). Concept of general and specific combining ability in relation to diallel crossing system. Aust. J. Biol. Sci. 9:463-493.
3. Hayman, B.I. (1954a). The analysis of variance of diallel tables. Biometrics 10(2): 235-244.
4. Hayman, B. I. (1954 b). The theory and analysis of diallel crosses. Genetics 39:789-809.
5. Heisher, C.B. (1973). Variation in bottlegourd. In: B.J. Meggers, E.S. Ayensu and W.D. Duckwarths eds; Tropical Forest Ecosystem in Africa and South America. A

Comparative Review,. Simthosonian. Institute Press, Washington, D.C. p 121-128.
6. Henderson, C.R. (1952). Specific and general combining ability. In: J. W. Gowen Heterosis (eds.) Iowa State College Press, Ames, Iowa. pp. 522.
7. Hulll, F.H. (1945). Recurrent selection for specific combining ability in corn. J. Amer. Soc. Agron. 37:134-145.
8. Jinks, J.L. (1954). A survey of the genetical basis of heterosis in a variety of diallel crosses. Heredity 9:223-238.
9. Jinks, J.L. (1956.) The F_2 and backcross generations from a set of diallel crosses. Heredity 10:1-30.
10. Kempthorne, O. (1956). The theory of the diallel cross. Genetics 41:451-459.
11. Kushawaha, M.L. and Ram, H.H. (1997). Combining ability studies in indigenous inbreds of bottlegourd. Rec. Hort. 4:163-165.
12. Mather, K. and Jinks, J.L. (1982): Introduction to biometrical Genetics 3rd Edn. Chapman and Hall, Londan . p231
13. Matzinger, D.F., Sprague, G.F. and Cockheram, C.C. (1959). Diallel crosses of maize in experiments repeated over locations and years. Agron. J. 51:346-350.
14. Maurya, I.B. and Singh, S.P. (1994). Studies on gene action in long-fruited bottlegorud [*Lagenaria siceraria* (Molina) Standl.]. Crop Res. 8:100-104.
15. Pandey, S.K., srivastava, A.K., tiwari, J.K. and srivastava, J. P. (2004). Studies on heterosis and combining ability for earliness in bottlegourd. International seminar on rec. Trend Hi-Tech. Hort. and PHT, Kanpur. Feb. 4-6 p 45.
16. Robinson, R.W. and Whitaker, T.W. (1974). *Cucumis*. In : R.C. King ed; Handbook of Genetics. Vol. 2: Plenum Press, New York.pp145-150.
17. Sprague, G.F. and Tatum, L.A. (1942). General versus specific combining ability in single cross of corn. J. Amer Soc. Agron. 3:923-932.

Estimation of Genetics Components Example.

between crosses with both parents different	Genetic interpretation (expectations) F_1					
	D	F	H_1	H_2	h^2	E
V_0L_0 (Vp)	1					1
V_0L_1 (V_m)	1/4	-1/4	1/4	1/4		$1+(n-2)/2n^2$
V_1L_1 ($\overline{V}_r$)	1/4	-1/4	1/4			[1+(n-2)/2n]
W_0L_{01} ($\overline{W}_r$)	½	-1/4				1/n
$(ML_1\text{-}ML_0)^2$					1/4	$(n-1)/n^2$
V_r	¼	-1/4				1
W_r	½					1/n

Table 2. Mean Squares for Seed Yield and its Components in Bottle gourd.

Source of variation	Degree of freedom	Season	Days to first male flower	Node no. to first female flower	Number of primary branches /vine	Fruit weight (Kg)	Pedicel diameter (Cm)	Number of seeds per fruits	100 seed weight (g)
Replication	**2**	**Kharif**	**6.68**	**2.25**	**24.45**	**0.0098**	**0.0025**	**11797.8**	**12.61**
		Summer	**4.52**	**6.34**	**23.58**	**0.0168**	**0.0186**	**13980.2**	**21.84**
Genotypes	**35**	**Kharif**	**302.5****	**57.83***	**100.51****	**0.037***	**0.06***	**33953.3****	**16.67***
		Summer	**107.3***	**46.77***	**96.51***	**0.040***	**0.04***	**179051.2***	**21.43***
Error	**70**	**Kharif**	**11.63**	**9.36**	**2.07**	**0.0079**	**0.005**	**4062.1**	**2.15**
		Summer	**14.07**	**11.24**	**1.48**	**0.0039**	**0.018**	**4171.1**	**2.91**

*** Significant at 0.05 level of probability**
**** Significant at 0.01 level of probability**

Table 1.Genetic Components of Variation and their Proportions for Seed Yield and its Components in Bottle gourd

Components / proportions	Days to first male flower		Node no. to first female flower		Number of primary branches/vine		Fruit weight (kg)		Pedicel diameter (Cm)		Number of seeds per fruits		100 seed weight (g)	
	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer
D	123.50* ± 30.7	15.8 ±8.0	26.1* ±7.9	10.1** ±2.9	8.4 ±1.1	5.5 ±3.5	0.0 ±0.01	0.01 ±0.01	0.00 ±0.03	0.00 ±0.00	3376.4* ±4542.4	8110.7** ±191.82	2.45 ±3.0	3.18 ±3.72
F	15.7 ±12.6	6.9 ±9.1	53.4* ±18.6	15.2 ±6.3	4.4 ±2.2	4.3 ±2.8	0.00 ±0.02	0.01 ±0.02	0.00 ±0.06	0.00 ±0.01	9747.0 ±1033.4	13337.8* ±4515.9	7.40 ±7.80	11.88 ±8.80
H_1	169.61 ±70.68	54.28 ±18.61	93.79** ±18.16	33.04** ±6.19	109.71* ±44.01	52.90** ±8.63	0.05* ±0.02	0.07** ±0.02	0.08 ±0.06	0.02 ±0.00	44943.74** ±10442.86	23899.99** ±4392.69	27.43* ±7.59	40.26** ±8.56
H_2	124.13 ±61.49	37.47 ±16.20	61.35** ±15.80	24.47** ±5.38	86.05* ±38.29	51.58** ±7.51	0.04 ±0.02	0.05* ±0.02	0.07 ±0.05	0.01 ±0.00	32111.97* ±9085.28	16415.47** ±3821.64	19.56* ±6.60	26.20** ±7.45
h^2	0.00 ±0.24	-0.57 ±10.87	18.88 ±10.60	9.10 ±3.61	15.78 ±25.68	38.07** ±5.04	0.01 ±0.01	0.01 ±0.01	0.02 ±0.03	0.00 ±0.00	45112.67* ±6092.98	32299.32** ±2562.15	20.16 ±4.43	25.62** ±4.99
E	3.88 ±10.25	1.36 ± 2.70	3.12 ±2.63	0.65 ±0.90	0.69 ±6.38	0.50 ±1.25	0.00 ±0.00	0.00 ±0.00	0.00 ±0.01	0.00 ±0.00	1354.18 ±1514.21	247.15 ± 636.94	0.39 ±1.10	0.98 ±1.25
$(H_1/D)^{1/2}$	1.17	1.85	1.9	1.81	3.6	3.09	3.6	3.84	8.38	2.97	3.65	1.72	3.35	3.56
$(H_2/4H_1)$	0.18	0.17	0.16	0.19	0.22	0.24	0.21	0.21	0.21	0.23	0.18	0.17	0.18	0.16
$\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F}$	1.11	0.79	3.35	2.42	0.86	1.29	1.29	2.25	1.06	1.75	2.31	2.84	2.64	3.21