

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

Rakesh K. Dubey^{1,2*} • Hari Har Ram³

¹ Department of Vegetable Science, GB Pant University of Agriculture and Technology, Pantnagar 263145 US Nagar, India

² Current corresponding address: College of Horticulture and Forestry, Central Agricultural University, Pasighat 791102 Arunachal Pradesh, India

³ Krishidhan Seeds Pvt. Ltd., Pune, India

Corresponding author: * rksdubey@gmail.com

ABSTRACT

Genetic studies on seven traits of bottle gourd viz. days to first male flower, node to first female flower, number of primary branches per vine, fruit weight, pedicel diameter, number of seeds per fruit and 100-seed weight, were studied. Dominance components (H_1 and H_2) were significant for node number to first female flower and number of primary branches per vine. The degree of dominance averaged over two seasons (kharif and summer) $(H_1/D)^{1/2}$ was observed to be greater than unity for node number to first female flower, number of primary branches per vine, fruit weight, pedicel diameter, number of seeds per fruit and 100-seed weight, suggesting the presence of overdominance. The ratio of dominant and recessive alleles $(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$ was greater than unity for days to first male flower, node number to first female flower, fruit weight, pedicel diameter, number of seeds per fruit and 100-seed weight. The proportion of positive and negative effects of genes ($H_2/4H_1$) in the parents was not less than its maximum theoretical value (0.25) for the characters, i.e., number of primary branches per vine, fruit weight and pedicel diameter. However $(H_1/4H_1)$ was almost equal to its maximum theoretical value in this investigation. In the F_1 , additive gene action was predominant, thus suggesting seed yield improvement through selection in bottle gourd.

Keywords: components of variation, diallel analysis, gene action, inheritance, seed

INTRODUCTION

Bottle gourd [*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 herbs with large, white flowers borne on slender peduncles. Breeding objectives of bottle gourd are based on seed production problems and consumer preference. In bottle gourd increasing attention is being paid towards breeding of superior cultivars with a greater focus on the development of hybrid seeds. F_1 hybrid breeding is prominent among the methods used in the improvement of bottle gourd (Pandey *et al.* 2004; Ram 2007). Diallel analysis helps to estimate the genetic components of variation, the degree of dominance, the proportion of dominant and recessive genes, and the distribution of genes with positive and negative effects governing the expression of a particular trait. Diallel analysis using inbred from local, indigenous germplasm of bottle gourd assumes significance. The present study investigated whether the genetic control of the commercially important characters, which were subjected to selection, was different in Pantnagar-bred material for seed yield, 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). 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/cultivar available for a range of characters of commercial importance; including seed 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 the Vegetable Research Center of G. B. Pant University of Agriculture and Technology, Pantnagar, UA, India, at an altitude of 243.84 m above mean sea level and 29°N altitude and 79.3° longitude in 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 eight parents and 28 F_1 hybrids. Each treatment had one row 5 m in length 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 (segmented leaf), PBOG 61, PBOG 76, PBOG 117, PBOG 119 and Pusa Naveen. Data was 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 Hayman (1954a). 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 in which 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.

Estimation of genetic components was done as follows:

Between crosses with both parents different	Genetic interpretation (expectations) F ₁					
	D	F	H ₁	H ₂	h ²	E
V ₀ L ₀ (V _p)	1					1
V ₀ L ₁ (V _m)	1/4	-1/4	1/4	1/4		1+(n-2)/2n ²
V ₁ L ₁ (V _i)	1/4	-1/4	1/4			[1+(n-2)/2n]
W ₀ L ₀₁ (W _r)	1/2	-1/4				1/n
(ML ₁ -ML ₀) ²					1/4	(n-1)/n ²
V _r	1/4	-1/4				1
W _r	1/2					1/n

The expected values of main components of genetic variance were estimated by solving the above equations for the F₁ generation (Hayman 1954a). In the F₁ 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

H₁ = variance component due to dominance deviation

H₂ = dominance indicating asymmetry of positive and negative effect of genes.

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

where

μ = proportion of positive genes in parents

ν = proportion of negative genes in parents

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

V₀L₀ = variance of parents

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

V₁L₁ = mean of all the V_r values

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

W₀L₀₁ = mean of all W_r values

(ML₁ - ML₀)² = dominance relationship i.e. difference between the mean of the parents and the mean of their n (n-1) progenies.

V₀L₁ = variance of the means of arrays \hat{E}

E = the expected environmental component of variation

In order to test the significance of the main component: D, F, \hat{h}^2 , H₁, H₂, and E, the standard errors (SE) are calculated for each of mean as follows:

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

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

$$SE(H_1) = (S^2 \times C H_1)^{1/2}$$

$$SE(H_2) = (S^2 \times C H_2)^{1/2}$$

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

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

The above genetic components were used to compute the following genetic ratios:

1. Mean Degree of Dominance was calculated as (H₁/D)^{1/2}. If the ratio obtained is equal to 1, this indicates the presence of complete dominance; if more than 1, it indicates the presence of over-dominance and if less than 1, it reveals the presence of partial dominance.

2. The proportion of dominant genes with positive or negative effects in parents is determined by the ratio H₂/4H₁ with the maximum theoretical value of 0.25, which arises when p = q = 0.5 at all loci. A deviation from 0.25 would occur when p ≠ q. Thus, H₂/4H₁ ≈ 0.25 would mean symmetrical distribution of positive and nega-

tive dominant genes in parents; and when H₂/4H₁ ≠ 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: $(4DH_1)^{1/2} + F$ / $(4DH_1)^{1/2} - F$

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. The number of dominant gene blocks is estimated by the \hat{h}^2 / H₂ ratio.

5. The t² values were non-significant for the traits in the F₁, indicating the validity of assumptions underlying the diallel analysis

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among progenies indicating that the parents were diverse for the characters studied and that diversity was transmittable to the offspring. The component analysis of data is presented in **Table 1** and mean squares for seed yield is presented in **Table 2**. For days to first male flower in the kharif experiment, only additive (D) variance was significant, signifying the involvement of additive gene action in the inheritance of days to first male flower. In case of additive gene action it is suggested that a modified reciprocal recurrent selection procedure with an inbred tester, would be have a greater potential for simultaneously improving breeding populations and developing elite single crosses. The (H₁/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 an 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 indicates the asymmetrical distribution of positive and negative dominant genes in the parents. In summer, the degree of dominance (H₁/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 seasons, significant D and H₁ variances were observed. This indicated the role of both additive and dominance gene action in the inheritance of node number to first female flower. For this trait reciprocal recurrent selection will be useful, since it exploits both the components of genetic variance, for practical breeding of bottle gourd it is suggested that first select lines on the basis of gca effects, with further selection by an evaluation for specific effects. Thus, rapid progress could be made by a family selection. The estimate of (H₁/D)^{1/2} was more than unity i.e. 1.90 in kharif and 1.81 in summer, indicating over-dominance. An asymmetrical distribution of positive and negative dominant genes for this trait was seen in the parents as H₂/4H₁ was 0.16 and 0.19 in kharif and summer, respectively. The value of the relative frequency of dominant and recessive alleles in the parents was 3.35 in kharif and 2.42 in summer, suggesting an excess of dominant alleles. For the number of primary branches per vine dominance (H₁ and H₂) of genetic variance were significant in both seasons. Mean degree of dominance (H₁/D)^{1/2} was greater than unity (3.60 in kharif and 3.09 in summer) and thus suggested the presence of over-dominance. For this trait selection of sca is likely to be the most effective method to exploit hybrid vigour. The val-

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 № to first female flower		№ of primary branches/vine		Fruit weight (kg)	
	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
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
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**
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*
\hat{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
E	3.88 ± 10.25	1.36 ± 2.70	3.12 ± 2.63	0.65 ± 0.90	0.696.38	0.50 ± 1.25	0.00 ± 0.00	0.00 ± 0.00
(H ₁ /D) ^{1/2}	1.17	1.85	1.90	1.81	3.60	3.09	3.60	3.84
(H ₂ /4H ₁)	0.18	0.17	0.16	0.19	0.22	0.24	0.21	0.21
$\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F}$	1.11	0.79	3.35	2.42	0.86	1.29	1.29	2.25

* Significant at 0.05 level of probability

** Significant at 0.01 level of probability

Table 1 (cont.)

Components/ proportions	Pedicel diameter (cm)		№ of seeds/fruit		100-seed weight (g)	
	Kharif	Summer	Kharif	Summer	Kharif	Summer
D	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	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	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	0.07 ± 0.05	0.01 ± 0.00	32111.97 ± 9085.28*	16415.47 ± 3821.64*	19.56 ± 6.60*	26.20 ± 7.45**
\hat{h}^2	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	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}	8.38	2.97	3.65	1.72	3.35	3.56
(H ₂ /4H ₁)	0.21	0.23	0.18	0.17	0.18	0.16
$\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F}$	1.06	1.75	2.31	2.84	2.64	3.21

* Significant at 0.05 level of probability

** Significant at 0.01 level of probability

Table 2 Mean squares for seed yield and its components in bottle gourd.

Source of variation	Degrees of freedom	Season	Days to first male flower	Node № to first female flower	№ of primary branches/vine	Fruit weight (Kg)	Pedicel diameter (cm)	№ of seeds/fruit	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

ues of H₂/4H₁ (0.22) were almost equal to the maximum theoretical value of 0.25 indicating a symmetrical distribution of u (alleles with positive effects) and v (alleles with negative effects) in both seasons. The proportion of dominant and recessive alleles was 0.86 in kharif and 1.29 in summer, suggesting almost equal proportion of dominant and recessive alleles in the parents. For fruit weight, the additive genetic component of variance (D) was non-significant. Dominance components (H₁ and H₂) were found to be significant. The (H₁/D)^{1/2} estimate was (3.60 in kharif and 3.84 in summer) more than unity implying over-dominance. The estimate of H₂/4H₁ (0.21) was almost equal to its maximum value of 0.25, indicating a symmetrical distribution of dominant genes. The proportion of dominant and recessive alleles was > 1, suggesting an excess of dominant alleles. For pedicel diameter in both seasons, none of the estimates was significant. For the number of seeds per fruit, the analysis of variance component indicated that in both seasonal experiments, additive (D) and dominance variances (H₁) were significant. This indicates that the expression of number of seeds per fruits was conditioned by both additive and dominant gene action. However, the dominance component was more predominant than the additive component. (H₁/D)^{1/2} was 3.65 (kharif) and 1.72 (summer) and showed over-dominance. (H₂/4H₁) (0.17) was less than its maximum theoretical value of 0.25 showing an asymmetrical distribution of positive and negative alleles over both seasons. The value of $(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$ was 2.31 and 2.84 during kharif and summer, respectively,

indicating an excess of dominant alleles over both seasons. For the 100-seed weight dominance variances (H₁) was significant, signifying the involvement of dominance gene action to govern 100-seed weight. However, \hat{h}^2 was significant in both seasons. This indicates that there was the presence of an overall dominant effect. The (H₁/D)^{1/2} estimate was more than unity i.e. (3.35 in kharif and 3.56 in summer), 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 H₂/4H₁ was 0.18 (kharif) and 0.16 (summer). The proportion of dominant and recessive alleles pooled over parents $(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$ was 2.64 (kharif) and 3.21 (summer) suggesting an excess of dominant alleles. It is worth nothing that bottle gourd, like several other cucurbits, does not respond to inbreeding (Robinson and Whitaker 1974). The cost of production of hybrid seed in bottle gourd is substantially low, as the F₁ seeds can be produced on a commercial scale by the removal of male buds from the female parent and allowing insect pollination. The breeding methods for the improvement of a crop depend on nature and on the magnitude of the components of genetic variances, combining the ability of the parents and crosses and the extent of heterosis for quantitative traits (Dubey 2004). The choice of parents is considered to be an important aspect in a bottle gourd breeding programme aimed at improving yield and its components because superior parents may not necessarily transfer their superiority to the progenies (Allard 1960). The theory of diallel crosses and

the usefulness of diallel cross technique in the genetic analysis of a population have received considerable attention in the past. For example (Griffing 1956; Matzinger *et al.* 1959; Robinson 2000; Pitrat *et al.* 2002; Gusmini and Wehner 2004; Sirohi *et al.* 2005) 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 claimed by several scientists (Griffing 1956; Hayman 1954a; Hull 1954; Jinks 1954, 1956; Kempthorne 1956; Ashok 2000; Bairagi *et al.* 2001; Dubey and Maurya 2002; Mehta *et al.* 2006; Munshi *et al.* 2006; Upadhyay and Ram 2006). In addition to having 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, a diallel cross analysis in its totality is a useful biometrical technique in bottle gourd breeding. The higher proportion of dominant genes in most of the characters in bottlegourd also explained by 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 for days to first male flower, node number to female flower, number of seeds per fruit and 100-seed weight consistently over both seasons. This suggested the asymmetrical distribution of dominant genes with positive and negative effects. Kushawaha and Ram (1997) and Pandey *et al.* (2004) also claimed asymmetrical distribution of dominant genes with positive and negative effects for days to first male flower, node number to female flower, number of seeds per fruit and 100-seed weight in bottle gourd. Both additive and non-additive components of variation were found to play important roles in the inheritance of economic traits in bottle gourd as evidenced 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 a non-additive interaction for the same traits was intriguing but, as suggested by (Hayman 1954a) even if a trait 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. In bottle gourd, increasing attention is being paid towards breeding of superior cultivar 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 for improving the traits.

ACKNOWLEDGEMENTS

The first author wishes to acknowledge the technical support rendered by the Dr Vikas Singh, SMS, Krishi Vigyan Kendra, College of Horticulture and Forestry, CAU, Pasighat.

REFERENCES

- Allard RW (1960) *Principles of Plant Breeding*, John Willey and Sons Inc., New York, pp 227-228
- Ashok P (2000) Character association of seeds on plant morphology in snake-gourd. MSc thesis, Kerala Agricultural University, Vellanikkara, 143 pp
- Bairagi SK, Singh DK, Ram HH (2001) Diallel analysis for combing ability in cucumber. *Progressive Horticulture* **33**, 178-183
- Dubey RK (2004) Development of hybrids and seed protein electrophoresis in bottlegourd. PhD thesis, GB Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, 251 pp
- Dubey SK, Maurya IB (2002) Heterosis and combining ability in bottlegourd. In: *International Conference on Vegetables*, 11-14 November, 2002, Bangalore, p 4 (Abstract)
- Griffing B (1956) Concept of general and specific combining ability in relation to diallel crossing system. *Australian Journal of Biological Science* **9**, 463-493
- Gusmini G, Wehner TC (2004) Foundations of yield improvement in water melon. *Crop Science* **45**, 141-146
- Hayman BI (1954a) The analysis of variance of diallel tables. *Biometrics* **10**, 235-244
- Hayman BI (1954b) The theory and analysis of diallel crosses. *Genetics* **39**, 789-809
- Hull FH (1954) Recurrent selection for specific combining ability in corn. *Journal of American Society of Agronomy* **37**, 134-145
- Jinks JL (1954) A survey of the genetical basis of heterosis in a variety of diallel crosses. *Heredity* **9**, 223-238
- Jinks JL (1956) The F_2 and backcross generations from a set of diallel crosses. *Heredity* **10**, 1-30
- Kempthorne O (1956) The theory of the diallel cross. *Genetics* **41**, 451-459
- Kushawaha ML, Ram HH (1997) Combining ability studies in indigenous inbreds of bottlegourd. *Recent Horticulture* **4**, 163-165
- Mather K, Jinks JL (1982) *Introduction to Biometrical Genetics* (3rd Edn), Chapman and Hall, London, 231 pp
- Matzinger DF, Sprague GF, Cockheram CC (1959) Diallel crosses of maize in experiments repeated over locations and years. *Journal of Agronomy* **51**, 346-350
- Maurya IB, Singh SP (1994) Studies on gene action in long-fruited bottlegourd. *Crop Research* **8**, 100-104
- Mehta DR, Purohit VL, Golani I J, Dhaduk LK, Gajipara NN (2006) Genetics of fruit yield and its components in ridge gourd (*Luffa acutangula* L.) In: Gautam PL, Ram HH, Singh HP (Eds) *Cucurbits Breeding and Production Technology*, Gobind Ballabh Pant University of Agriculture and Technology, Pantnagar, India, pp 285-288
- Munshi AD, Kumar R, Panda B (2006) Heterosis for yield and its components in cucumber. In: Gautam PL, Ram HH, Singh HP (Eds) *Cucurbits Breeding and Production Technology*, Gobind Ballabh Pant University of Agriculture and Technology, Pantnagar, India, pp 237-241
- Pandey SK, Srivastava AK, Tiwari JK, Srivastava JP (2004) Studies on heterosis and combining ability for earliness in bottle gourd. In: *International Seminar on Recent Trend Hi-Tech Horticulture and Post Harvest Technology*, 4-6 Feb., 2004, Kanpur, p 45 (Abstract)
- Pitrat M, Chauvet C, Fouru C (2002) Diversity, history and production of cultivated cucurbits. In: *International Symposium on Cucurbits*, National Bureau of Plant Genetic Resources, pp 111-130
- Ram D (2007) Hybrid seed production in bottle gourd. Winter school on hybrid seed production of vegetable crops, 4-24 Dec., IIVR, Varanasi, pp 61-65
- Robinson RW (2000) Rational and methods for producing hybrid cucurbit seed. In: Basara AS (Ed) *Hybrid Seed Production in Vegetables: Rationale and Methods in Selected Crops*, Food Products Press, New York, pp 1-47
- Robinson RW, Whitaker TW (1974) *Cucumis*. In: King RC (Ed) *Handbook of Genetics*, Plenum Press, New York, pp 145-150
- Sirohi PS, Muni AD, Kumar G, Behara TK (2005) Cucurbits In: Dhillon BS, Tyagi RK, Saxena S, Randhawa GL (Eds) *Plant Genetic Resources: Horticultural Crops*, Narosa Publishing House Pvt. Ltd., New Delhi, pp 34-58
- Upadhyay R, Ram HH (2006) Breeding potential of indigenous lines of bottlegourd. In: Gautam PL, Ram HH, Singh HP (Eds) *Cucurbits Breeding and Production Technology*, Gobind Ballabh Pant University of Agriculture and Technology, Pantnagar, India, pp 233-236
- Wright AJ (1985) Diallel designs, analysis and reference populations. *Heredity* **54**, 307-311