

Short Communication

## Genetic analysis of yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt) for vegetative and yield characters

Merin Elza George\* and S. Sarada

College of Agriculture, Vellayani, Kerala Agricultural University, Thiruvananthapuram- 695 522, Kerala, India.

Received 24 September 2018; received in revised form 18 February 2019; accepted 19 February 2019

### Abstract

Gene action involved in the inheritance of vegetative and yield characters in yard long bean was estimated using generation mean analysis. Six basic generations, viz.,  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$  of the cross VS 50 (Kakkamoola Local) x VS 26 (Vellayani Jyothika) were used for the study. Significance of scaling test revealed the presence of epistasis for all the characters under investigation. Pod yield/ plant was highest for  $F_1$  (1116.83 g) and lowest for  $P_2$  (584.00 g) among the generations. The predominance of dominance x dominance gene action for the characters pod length, pod weight and yield/ plant indicated that the traits could be improved through hybridization followed by selection. Presence of dominance gene action for vine length at final harvest, days to first flowering, pods/ plant and days to harvest pointed out the suitability of resorting to heterosis breeding. Duplicate type of epistasis was observed for most of the traits studied. High heritability was observed for pod length and pods per plant. High degree of transgressive segregants was observed for pod length.

**Keywords:** Gene action, Generation mean analysis, Yard long bean.

Yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt), also known as 'asparagus bean', 'chinese long bean' and 'snake bean', is one of the most popular and remunerative vegetable crops, traditionally grown in the humid tropics of Kerala. It is a distinct form of cowpea grown for its immature pods. The traditional vernaculars viz., 'achinga-payar', 'kurutholapayar', 'vallipayar' and 'pathinettumaniyan' are used to refer to yard long bean in Kerala. The crop, native to central West Africa, is now extensively cultivated in many countries in South East Asia such as Taiwan, Philippines, Indonesia, Thailand, India, Pakistan, Bangladesh and South China. It is a rich and inexpensive source of vegetable protein.

Understanding the mode of inheritance of the vegetative and yield components is a pre-requisite for the effective choice of breeding methodology

for developing elite varieties. Appropriate breeding procedure can be used for the improvement of the trait, based on the gene action involved in its expression. The magnitude of heritability indicates the effectiveness with which the selection of the accessions can be made based on the phenotype. The present project was undertaken to estimate the genetic variability among the six generations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$ ) of the elite cowpea cross VS 50 x VS 26, to investigate the genetic basis and inheritance pattern of vegetative, flowering, yield and quality characters of the generations in the cross, to estimate the gene effects controlling yield and quality components using six parameter model and to identify the most suitable breeding methods for improving the traits.

The present investigation was carried out at the Department of Vegetable Science, College of

Agriculture, Vellayani, Kerala during 2017- 2018. The materials for the study comprised 6 populations ( $P_1, P_2, F_1, F_2, BC_1$  and  $BC_2$  of the hybrids) developed using the parents, VS 50 (Kakkamoola Local) and VS 26 (Vellayani Jyothika). The superior  $F_1$  hybrid with high yield and quality characters was selected based on specific combining ability and *per se* performance from the previous M.Sc. (Hort.) programme “Development of hybrids in yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt)”. The  $F_1$ s were raised in the crossing block. The selected hybrid was selfed to produce  $F_2$  progeny. Simultaneously, the  $F_1$  hybrid was backcrossed with female parent to produce  $BC_1$  generation, and male parent to produce  $BC_2$  generation. The six generations ( $P_1, P_2, F_1, F_2, BC_1$  and  $BC_2$ ) from the cross combination were raised in Randomized Block Design with a spacing of 1m x 1 m. One replication consisted of one row of parents and  $F_1$ , two rows of the back cross generations  $BC_1$  and  $BC_2$  and four rows of  $F_2$ . Each row consisted of 10 plants. Five plants from each treatment in the experimental field were randomly selected and tagged. Observations were recorded and the average of these five plants was worked out in each replication for statistical analysis. Mean performance and gene action were studied for the vegetative characters *viz.*, vine length at final harvest (cm), primary branches/ plant and reproductive traits like days to first flowering and yield characters like pod length (cm), pod weight (g), pods/ plant, yield (g/ plant) and days to harvest. Vine length was recorded at the time of final harvest from the ground level to the top most leaf of the plants and presented in centimetres whereas for primary branches/ plant, number of branches arising from the main stem from all the observational plants at the peak harvest stage was recorded and average was worked out. Number of days from the date of sowing to the first flowering of observational plants was recorded, and the

average used for calculating days to first flowering. Five pods were selected at random from each observational plant at peak harvest period for recording mean pod length and pod weight. Pods/ plant was recorded by counting total number of pods produced per plant till the last harvest from each observational plant and average was worked out. Average weight of all pods harvested from the observational plants were utilised for calculating yield and expressed in grams/ plant. Days to harvest was counted from the date of sowing to the first harvest of the observational plants and the average was calculated. Heritability percentage was estimated for each character (Jain, 1982). The data was subjected to generation mean analysis (Hayman, 1958), followed by scaling test (Mather, 1949).

The type of epistasis was revealed by the significance of specific scales as given in Table 1.

The observations were analyzed statistically and the results obtained from the present study are given below (Tables 2 and 3). Analysis of variance showed significant differences among the generations of the cross VS 50 x VS 26, for most of the characters studied.

#### *Vine length at final harvest (cm)*

Significant variation was observed among the generations for vine length at final harvest as shown by the significant value of ‘m’. Highest vine length at final harvest was reported in  $P_2$  (536.67 cm) and lowest in  $F_2$  (367.33 cm). Mean value of  $F_1$  was higher than that of  $F_2$ . Significance of all the scales except scale A suggested the inadequacy of additive-dominance model and presence of non-allelic interaction. Detailed analysis showed the significance of dominance, additive x additive and additive x dominance in favorable positive direction,

**Table 1.** Significance of specific scales

Sl. No	Scales	Significance
1	A, B or both scales	Presence of all three types of epistasis, <i>viz.</i> A x A, A x D and D x D
2	C scale	Dominance x Dominance type of epistasis ( <i>l</i> )
3	D scale	Additive x Additive type of epistasis ( <i>i</i> )
4	C and D scales	Additive x Additive ( <i>i</i> ) and Dominance x Dominance ( <i>l</i> )

**Table 2.** Generation means ( $\pm$ SE), scale values ( $\pm$ SE), and estimates of genetic components ( $\pm$ SE) in yard long bean

	Vine length at final harvest (cm)	Primary branches / plant	Days to first flowering	Pod length (cm)	Pod weight (g)	Pods/plant	Yield (g /plant)	Days to harvest
Generation means								
P <sub>1</sub>	508.67 $\pm$ 4.84	4.00 $\pm$ 0.10	53.50 $\pm$ 0.17	65.99 $\pm$ 0.04	35.33 $\pm$ 0.17	32.67 $\pm$ 0.73	707.95 $\pm$ 2.62	64.00 $\pm$ 0.87
P <sub>2</sub>	536.67 $\pm$ 18.78	3.66 $\pm$ 0.10	54.00 $\pm$ 0.25	60.58 $\pm$ 0.46	30.33 $\pm$ 0.10	27.67 $\pm$ 0.44	584.00 $\pm$ 19.34	64.33 $\pm$ 0.17
F <sub>1</sub>	440.00 $\pm$ 14.43	2.88 $\pm$ 0.20	49.50 $\pm$ 0.14	68.56 $\pm$ 0.21	49.00 $\pm$ 0.39	69.00 $\pm$ 0.58	1116.83 $\pm$ 31.29	63.00 $\pm$ 0.50
F <sub>2</sub>	367.33 $\pm$ 15.45	3.66 $\pm$ 0.13	50.17 $\pm$ 0.20	68.44 $\pm$ 0.10	50.89 $\pm$ 0.17	62.67 $\pm$ 0.30	881.22 $\pm$ 24.80	64.33 $\pm$ 0.61
BC <sub>1</sub>	479.00 $\pm$ 21.17	3.66 $\pm$ 0.07	50.41 $\pm$ 0.13	67.09 $\pm$ 0.30	46.22 $\pm$ 0.21	66.00 $\pm$ 0.52	771.97 $\pm$ 10.32	63.00 $\pm$ 0.34
BC <sub>2</sub>	405.00 $\pm$ 3.57	3.11 $\pm$ 0.10	49.92 $\pm$ 0.18	64.01 $\pm$ 0.36	44.22 $\pm$ 0.36	74.67 $\pm$ 0.70	818.38 $\pm$ 19.07	63.00 $\pm$ 0.34
Scale values								
A	9.33 $\pm$ 44.99	0.45 $\pm$ 0.26	-2.17* $\pm$ 0.34	-0.37 $\pm$ 0.65	8.11* $\pm$ 0.60	30.33* $\pm$ 1.40	-280.84* $\pm$ 37.57	-1.00 $\pm$ 1.21
B	-166.67* $\pm$ 24.74	-0.33 $\pm$ 0.30	-3.66* $\pm$ 0.46	-1.11 $\pm$ 0.88	9.11* $\pm$ 0.83	52.67* $\pm$ 1.57	-64.07 $\pm$ 52.99	-1.33 $\pm$ 0.87
C	-456.00* $\pm$ 70.90	1.23 $\pm$ 0.68	-5.83* $\pm$ 0.93	10.09* $\pm$ 0.75	39.88* $\pm$ 1.03	52.33* $\pm$ 1.88	-0.73 $\pm$ 118.91	3.00 $\pm$ 2.76
D	-149.33* $\pm$ 37.62	0.56 $\pm$ 0.30	0.00 $\pm$ 0.00	5.78* $\pm$ 0.51	11.33* $\pm$ 0.54	-15.33* $\pm$ 1.06	172.09* $\pm$ 54.14	2.67* $\pm$ 1.30
Genetic components								
m	224.00* $\pm$ 75.87	4.94* $\pm$ 0.58	53.75* $\pm$ 0.94	74.85* $\pm$ 1.05	55.49* $\pm$ 1.08	-0.50 $\pm$ 2.16	990.16* $\pm$ 108.71	69.50* $\pm$ 2.64
d	-14.00 $\pm$ 9.70	0.17* $\pm$ 0.07	-0.25 $\pm$ 0.15	2.71* $\pm$ 0.23	2.50* $\pm$ 0.10	2.50* $\pm$ 0.43	61.98* $\pm$ 9.76	-0.17 $\pm$ 0.44
h	357.33* $\pm$ 181.44	-3.06* $\pm$ 1.31	-10.07* $\pm$ 2.15	-19.34* $\pm$ 3.02	-11.93* $\pm$ 2.89	183.17* $\pm$ 5.93	-562.41* $\pm$ 241.11	-14.17* $\pm$ 5.82
i	298.67* $\pm$ 75.24		0.00 $\pm$ 0.93	-11.57* $\pm$ 1.02	-22.66* $\pm$ 1.07	30.67* $\pm$ 2.12	-344.18* $\pm$ 108.27	-5.33* $\pm$ 2.61
j	176.00* $\pm$ 47.12		1.49* $\pm$ 0.53	0.74 $\pm$ 1.05	-0.10 $\pm$ 0.86	-22.33* $\pm$ 1.94	-216.78* $\pm$ 47.56	0.17 $\pm$ 0.66
l	-141.33 $\pm$ 111.37		5.83* $\pm$ 1.26	13.05* $\pm$ 2.02	5.44* $\pm$ 1.98	-113.67* $\pm$ 3.96	689.09* $\pm$ 147.18	7.67* $\pm$ 3.38
E			D	D	D	D	D	D

*m*- mean effects, *d*- additive effects, *h*- dominance effects, *i*- additive x additive gene interaction, *j*- additive x dominance gene interaction, *l*- dominance x dominance gene interaction, E- Epistasis, D- Duplicate type of epistasis, \*Significant at 5% level

**Table 3.** Heritability (%) and transgressive segregants in the cross VS 50 x VS 26

Sl.No.	Characters	Heritability (%)	Transgressive segregants (%)
1.	Vine length at final harvest (cm)	58.5	Nil
2.	Primary branches/ plant	28.9	Nil
3.	Days to first flowering	59.9	23.33%
4.	Pod length (cm)	92.3	56.6%
5.	Pod weight (g)	52.2	40%
6.	Pods/ plant	89.7	Nil
7.	Yield (g/ plant)	52.5	Nil
8.	Days to harvest	56.7	Nil

among which dominance gene action had the highest magnitude. The predominance of dominance gene action suggested the usefulness of heterosis breeding for improving this trait. Sawant (1994), Nagaraj et al. (2002), Subbiah et al. (2013) and Jithesh (2009) reported the presence of dominance effect in controlling the trait in cowpea. Duplicate nature of epistasis was present in the cross as indicated by opposite signs of dominance (*h*) and dominance x dominance (*l*) type of interaction. Heritability was 58.5%.

#### Primary branches/plant

Significant 'm' denoted wide variation for primary branches/ plant among the generations. Highest number of primary branches/ plant was observed in P<sub>1</sub> (4.00) and lowest in F<sub>1</sub> (2.88). All the scales A,

B, C and D were found to be non-significant, which indicated the absence of non-allelic interaction and adequacy of additive-dominance model in accordance with earlier report of Lovely (2005). All the genetic components m, d and h were significant and dominance effect was in negative direction. Direct selection could improve the trait primary branches/ plant, since additive effect was positive and significant. Predominance of additive gene action for primary branches/ plant was reported by Anbuselvam et al. (2000), Nagaraj et al. (2002), Philip (2004) and Romanus et al. (2008) in cowpea. Heritability was 28.9%.

#### Days to first flowering

'm' was significant and greater than all other effects,

denoting the significant variation between the treatments for days to first flowering.  $F_1$  was the earliest to flower (49.50 days) while  $P_2$  (54.00 days) was late. Scales A, B and C were significant and acting in favourable negative direction, among which value of scale C was the highest, which implied the superiority of  $F_2$  over the parents. Dominance, additive x dominance and dominance x dominance were significant, among which dominance effect had the highest negative value indicating the need for exploitation of heterosis to get early flowering types. Similar results of predominance of dominance gene effect was reported by Sawant (1994), Jithesh (2009) and Gupta et al. (2017). Philip (2004) and Lakshmi (2016) reported the predominance of non-additive gene action in controlling the trait. Duplicate type of epistasis was recorded for the trait, as observed from the opposite signs of dominance (h) and dominance x dominance (l) type of interaction. Heritability was 59.9%.

#### *Pod length*

Significant variation was observed among the generations for pod length as shown by the significant value of 'm'. Pod length was highest in  $F_1$  (68.56 cm) and lowest in  $P_2$  (60.58 cm). Cross VS 50 x VS 26 witnessed positive significance for scales C and D, among which scale C had the highest magnitude which implied the superiority of  $F_2$  over both the parents. Even though additive, dominance and all epistatic effects except additive x dominance interactions were significant, dominance x dominance gene action was in the favourable positive direction and had the highest magnitude which underlined the efficient utility of heterosis and selection for the improvement of pod length, as reported by Philip (2004) and Lovely (2005). The predominance of non-additive gene action for pod length in cowpea was earlier reported by Ushakumari et al. (2010), Chaudhari et al. (2013) and Lakshmi (2016). Opposite signs of dominance (h) effect and dominance x dominance (l) type of interaction indicated the presence of duplicate type of epistasis. Heritability was 92.3%.

#### *Pod weight (g)*

Significance of 'm' denoted wide variation for pod weight among the generations. The highest mean values for pod weight was recorded by  $F_2$  (50.89 g) and the lowest by  $P_2$  (30.33 g). Significance was observed for all the scales A, B, C and D in favourable positive direction, highest magnitude of scale C indicating betterment of  $F_2$  over the parents. Further analysis in the cross VS 50 x VS 26 showed positive significance in additive and dominance x dominance gene action and negative in dominance and additive x additive interaction. Hybridization followed by selection could be used for the improvement of the trait, since dominance x dominance type of interaction was predominant. The above result was in conformity with that of Lovely (2005) in vegetable cowpea. Predominance of non-additive gene action was suggested by Rahman and Saad (2000) and Manivannan and Sekar (2005) in vegetable cowpea. Duplicate type of epistasis was observed for the trait which was evident from the opposite signs of dominance (h) and dominance x dominance (l) type of interaction. Heritability was 52.2%.

#### *Pods/ plant*

The generations did not differ significantly for pods/plant, as given by non-significant 'm' value. Highest magnitude and significance of scale B in favourable positive direction over all other scales revealed the superiority of  $F_1$  over the second parent. All the types of epistatic interactions were significant, among which dominance type of gene action had the highest positive value. Hence, the improvement of the trait could be done by heterosis breeding. These results were in agreement with the findings of Smitha (1995), Valarmathi et al. (2007), Ushakumari et al. (2010), Yadav et al. (2010), Chaudhari et al. (2013), Lakshmi (2016) and Gupta et al. (2017), who suggested the presence of non-additive gene action for controlling the trait. Epistasis was revealed to be duplicate, due to opposite signs of dominance (h) effect and dominance x dominance (l) interactions. Heritability was 89.7%.

### *Yield (g/plant)*

Significant difference was observed among the six generations for pod yield/plant, since 'm' value was significant and greater than all other effects. Among the treatments, pod yield/plant was highest for  $F_1$  (1116.83 g) and lowest for  $P_2$  (584.00 g). Though scales A and D were significant, A was negative and D positive, which implied that  $F_2$  was better than the backcrosses. Detailed analysis of genetic components revealed the significance of additive, dominance and all the epistatic interactions, among which dominance x dominance gene action had the highest magnitude in positive direction. Hence, hybridization followed by selection could be used for the improvement of yield/plant in accordance with the studies of Rahman and Saad (2000), Philip (2004), Lovely (2005), Manivannan and Sekar (2005), Jithesh (2009) and Meena et al. (2010). Dominance (h) and dominance x dominance (l) type of interaction with opposite signs indicated duplicate nature of epistasis. Heritability was 52.5%.

### *Days to harvest*

The treatments differed significantly for days to harvest as given by significant 'm' value. The generations  $F_1$ ,  $BC_1$  and  $BC_2$  (63.00 days) were found to be earlier, and  $P_2$  and  $F_2$  (64.33 days) late. All the scales were found to be non-significant, except scale D. Highest positive significance was noticed in scale D, which indicated the superiority of  $F_2$  over the backcrosses. Further analysis showed significance of dominance and additive x additive gene action in negative direction and dominance x dominance in positive direction. Dominance effect showed the highest magnitude in the favourable negative direction. This showed the possibility of getting early harvesting varieties through heterosis breeding. The predominance of non-additive gene action in controlling days to harvest was observed in the studies of Pal et al. (2007) and Uma and Kalubowila (2010). Epistasis was revealed to be duplicate due to opposite signs of dominance (h) and dominance x dominance (l) interaction. Heritability was 56.7%.

Heritability estimates were moderate for all the characters except for pod length and pods per plant, which had high heritability (92.3% and 89.7% respectively). Low heritability was observed for primary branches per plant (28.9%). Transgressive segregants were observed for pod length (56.6%), pod weight (40%) and days to first flowering (23.33%) (Table 3). High degree of transgressive segregants for pod length indicated the possibility for utilizing these desirable segregants to develop superior varieties. Predominance of dominance x dominance gene action was observed for the characters pod length, pod weight and yield/plant in the cross VS 50 x VS 26, which suggested the use of hybridization followed by selection as the appropriate breeding method for the improvement of the traits. Presence of dominance gene action for vine length at final harvest, days to first flowering, pods/plant and days to harvest pointed out the suitability of resorting to heterosis breeding for the improvement of the traits. Primary branches/plant was controlled by additive gene effect. Simple selection procedure would be more rewarding for improving the characters governed by additive type of gene effects. Heterosis breeding and hybridization followed by selection could be the appropriate breeding methods for the crosses since predominance of dominance and dominance x dominance interaction was observed for most of the characters.

### **Acknowledgement**

The authors hereby acknowledge the financial assistance and research facilities extended by Kerala Agricultural University.

### **References**

- Anbuselvam, Y., Manivannan, N., Murugan, S., Thangavelu, P., and Ganesan, J. 2000. Variability studies in cowpea (*Vigna unguiculata* (L.) Walp.). Legume Res., 23: 279-280.
- Chaudhari, S.B., Naik, M.R., Patil, S.S., and Patel, J.D. 2013. Combining ability for pod yield and seed

- protein in cowpea [*Vigna unguiculata* (L.) Walp] over environments. Trends Biosci., 6 (4): 395-398.
- Gupta, R.P., Patel, S.R., Modha, K.G., and Wadekar, P.B. 2017. Generation mean analysis for yield and yield components in cowpea [*Vigna unguiculata* (L.) Walp.]. Int. J. Curr. Microbiol. Appl. Sci., 6(7): 2231-2240.
- Hayman, B. 1958. The separation of epistatic from additive and dominance variation in generation means. Heredity 12: 371-390.
- Jain, J.P. 1982. Statistical Techniques in Quantitative Genetics. Tata Mc Graw Hill Co., New Delhi, 281 p.
- Jithesh, V.G. 2009. Genetic analysis of resistance to pod borers and yield in yard long bean [*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt]. Ph.D. thesis, Kerala Agricultural University, Thrissur, 218p.
- Lakshmi, K. M. 2016. Development of hybrids in yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt). M.Sc. (Hort) thesis, Kerala Agricultural University, Thrissur, 133p.
- Lovely, M. 2005. Genetic analysis of yield and mosaic resistance yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt.). Ph.D. thesis, Kerala Agricultural University, Thrissur, 147p.
- Manivannan, R. and Sekar, K. 2005. Combining ability for yield and different quality traits in vegetable cowpea (*Vigna unguiculata* (L.) Walp.). Indian J. Hortic., 62(2): 196-199.
- Mather, K. 1949. Biometrical Genet. Methuen and Co. Ltd., London, 153p.
- Meena, R., Pithia, M. S., Savaliya, J. J., and Pansuriya, A. G. 2010. Combining ability Studies in vegetable cowpea [*Vigna unguiculata* (L.) Walp]. Res. Crop. 11(2): 441-445.
- Nagaraj, K.M., Savithramma, D.L., and Ramesh, S. 2002. Triple test cross analysis in two crosses of vegetable cowpea. South Indian Hortic., 50: 98-104.
- Pal, A. K., Kumar, S., and Maurya, A. N. 2007. Genetic study for earliness in cowpea (*Vigna unguiculata* (L.) Walp.). Indian J. Hortic., 64 (1): 63-66.
- Philip, M. C. A. 2004. Genetic analysis of legume pod borer *Maruca vitrata* (Fab.) resistance and yield in cowpea (*Vigna unguiculata* (L.) Walp.). Ph.D. thesis, Kerala Agricultural University, Thrissur, 171p.
- Rahman, M. A. and Saad, M. S. 2000. Estimation of additive, dominance and digenic epistatic interaction effects for certain yield characters in *Vigna sesquipedalis*. Fruw. Euphytica, 114: 61-66.
- Romanus, K. G., Hussein, S., and Mashela, W. P. 2008. Combining ability analysis and association of yield and yield components among selected cowpea lines. Euphytica, 162 (2): 205-210.
- Sawant, D. S. 1994. Gene control for yield and its attributes in cowpea. Ann. Agric. Res., 15: 140-143.
- Smitha, S. 1995. Gene action and combining ability in grain cowpea (*Vigna unguiculata* (L.) Walp.) in relation to aphid borne mosaic virus resistance. M.Sc.(Ag.) thesis, Kerala Agricultural University, Thrissur, 83p.
- Subbiah, A., Prabhu, M., Rajangam, J., Jagadeesan, R., and Anbu, S. 2013. Genetic analysis of vegetable cowpea [*Vigna unguiculata* (L.) Walp.]. Legume Res., 36(1): 1-9.
- Uma, M. S. and Kalubowila, I. 2010. Line x tester analysis for yield and rust resistance in cowpea (*Vigna unguiculata* (L.) Walp.). Electr. J. Plant Breed. [e-journal]. 1(3): 254-267. Available: <http://sites.google.com/site/ejplantbreeding>. [June 2010].
- Ushakumari, R., Vairam, N., Anandakumar, C. R., and Malini, N. 2010. Studies on hybrid vigour and combining ability for seed yield and contributing characters in cowpea (*Vigna unguiculata* ). Electr. J. Plant Breed. [e-journal] 1(4): 940-947. Available: <http://sites.google.com/site/ejplantbreeding> [17 July 2010].
- Valarmathi, G., Surendran, C., and Muthiah, A. R. 2007. Studies on combining ability for yield and yield traits in inter subspecies crosses of cowpea (*Vigna unguiculata* ssp. *unguiculata* and *Vigna unguiculata* ssp. *sesquipedalis*). Legume Res., 30(3): 173-179.
- Yadav, K. S., Yadav, H. S. and Dixit, H. 2010. Heterosis and inbreeding depression in cowpea. Int. J. Agric. Sci., 2: 537-540.