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Inheritance of Genetic variability, Combining Ability and Heterosis for Yellow Mosaic Virus Disease Resistance and Yield Improvement in Blackgram [*Vigna mungo* (L.) Hepper]

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A B S T R A C T

Pulses are the second most important group of crops grown worldwide. Among pulses, black gram (*Vigna mungo* L. Hepper) occupies a prominent place in India. Black gram grain contains about 24% protein, 60% carbohydrates, 1.3% fat with desirable amount of minerals like calcium, phosphorus, iron and certain vitamins. Yellow mosaic virus is one of the most important constraints for blackgram production. To identify genetic sources of resistance to yellow mosaic virus (YMV) in blackgram, the genetic variability is lost and it is this genetic potential for high yield needs to be regenerated. Four parents *viz.*, Vamban 4, Vamban 2, LBG 17 and CO 5 and their 12 hybrids, obtained through full diallel mating design were evaluated for important quantitative traits during *Rabi*, 2010-2011 for YMV and improvement of yield. Genetic variability, the PCV value was found higher in all the characters studied except days to 50 percent flowering, days to maturity and number of seeds per pod than the GCV. Based on *per se* performance, *gca* effects and *sca* effects, CO 5 x VBN 2 cross combination was found to be superior which combine yield and quality characters and these hybrid can be utilized for recombination breeding. Based on *per se* performance, *sca* effects and standard heterosis, two cross combinations *viz.*, LBG 17 x CO 5 and VBN 2 x LBG 17 was found to be superior which combine yield and quality characters and these hybrids can be utilized for heterosis breeding. Investigation on the magnitude of heterosis helps to identify promising hybrid combination and also possible to exploit to new recombinant type for yield and attributing traits from segregants.

Introduction

Pulses are the second most important group of crops grown worldwide. Indian has the largest area of about 34 per cent and total production of about 26 per cent of pulses globally. The Mungbean Yellow Mosaic Virus disease (MYMV) is a highly devastating disease in tropical and sub-tropical Asia. MYMV belongs to genus *Begomovirus* of the family Geminiviridae (Bos, 1999). The virus has geminate particle morphology (20 x 30 nm) and the coat protein encapsulates spherical, single stranded DNA genome of approximately 2.8 Kb (Hull, 2004). The first symptom appears on young leaves as yellow specks or spots. The leaf emerging from the apex shows bright yellow patches interspersed with green areas. In severe cases there is a complete yellowing of the leaves and infected

plants stunted. They bear few flowers and pods and mature late. The yield losses in naturally infected susceptible cultivars varied with time of infection (Singh *et al.*, 1982). Early infected plants had more severe symptoms than late infected ones. Chlorosis, stunting and reduced branching contributed to yield loss. The concept of combining ability analysis helps in selection of superior parents (general combining ability) as well as crosses (specific combining ability) when considered along with the mean performances. It also tells about the nature of gene action involved and thus helps in framing a suitable breeding scheme for the amelioration of the characters under consideration. General combining ability is used to designated those crosses in which certain combinations do relatively better or worse than would expected on the basis of the average performance of the lines involved. Different mating systems have been developed for estimating the combining ability and to derive the gene action in the inheritance of polygenic characters. This technique has been extensively used in almost all the major field crops to estimate GCA and SCA variances and effects and to understand the nature of gene action involved in the expression of various quantitative traits. The breeders need sound information on variability consisting of phenotypic and genotypic variance to obtain better results for selecting superior genotypes. Heritability refers to 'the extent of transmission of variation for any trait to the progeny'. Estimate of heritability helps in discriminating the variance in a population into the genotypic component and environment interaction component and explain the relative importance of environment effect and inheritance levels for the variation in population. Genetic advance is a measure of the gain for the character that could be achieved by further selection. Heritability along with genetic advance estimates helps in programming the breeding programme to obtain best results of genetic gain for any economic trait. Heterosis refers to the increased or decreased vigour of F_1 hybrid over its parents. The term heterosis was coined by Shull (1914). According to him, the term heterosis refers to the increased vigour, growth, yield or functions of hybrid over the parents those results from crossing genetically diverse individuals. The possibility of commercial exploitation of hybrid vigour in crops like green gram and black gram depends upon the substantial heterosis for YMV and seed yield coupled with economically viable method of producing hybrid seeds.

Materials and Methods

The present investigation was conducted at the Agricultural College and Research Institute, Madurai during 2010-2011 at the experimental farm in the Department of Plant Breeding and Genetics. Four varieties of blackgram obtained from National Pulses Research Centre, Vamban, Tamil Nadu. Among the parents, four genotypes *viz.*, Vamban 4, Vamban 2, LBG 17 and CO 5 were used as the materials of the present study. Twelve hybrids were raised during *Rabi*, 2011 in ridges of three meter length with an inter row spacing of 40 cm and intra-row spacing of 20 cm. The hybrids were raised in a Randomized Block Design with three replications. For estimating heterosis, the parents were also raised in adjacent plot with above mentioned spacing in three replications. The recommended agronomic and plant protection practices were followed to maintain healthy stand of the plants. The Yellow Mosaic Virus Disease (YMV) incidence was recorded on all the plants based on the visual scores on 50^{th} day while the susceptible check C0 5 recorded scale 6.9. The classification was made into scales 1 – 9 as follows based on the scale adopted by Singh *et al.*, (1988). Combining ability

analysis of cultivars is thus important to exploit the relevant type of gene action for a breeding programme. Combining ability estimates can be used to evaluate the number of promising lines in F_1 and F_2 generations, which is quite helpful in selecting the potential parents for hybridization. Combining ability study is useful in classifying the parental lines in terms of their hybrid performance (Dhillon, 1975). It also helps in identifying the parents suitable for hybridization programme and deciding suitable breeding methodology (Table 12).

Results and Discussion

Success in any breeding programme largely depends on the knowledge of the genetic architecture of the population handled by the breeder. The estimate of components of variance provides an idea about additive and non-additive (dominant) types of gene action (Baker, 1978). Panse (1942) suggested that if additive variance is greater than non-additive variance, the chance of fixing superior genotypes in the early segregating generations would be greater. Recent developments in the biometrical methods have led to the formulation of a number of statistical procedures for the genetic analysis of quantitative characters. Diallel analysis is one among them, which provides information on additive and non-additive gene action, inferred from Diallel analysis. The magnitude of H_1 variances was higher than D variances for all the traits. The number of days to 50 percent flowering ranged between 34.33 to 37.33 days. The grand mean for this trait was 35.83days. Among the parent P_2 was the earliest in flowering and for this trait all other parents recorded non-significant value with that of the respective mean. Days to 50 per cent flowering among the hybrids varied from 34.66 (P_2 x P_3) to 37.00 days (P_1 x P_4 and P_4 x P_1). The grand mean for this trait was 35.77 days. Out of this 12 hybrids, only one hybrid namely P_2 x P_3 recorded significantly early in flowering than the grand mean. The *gca* effects ranged from (-0.729) P_2 to (0.771) P_4. Significant negative values of *gca* was obtained by P_2 and in the parent P_4 showed significantly positive *gca* effects for this trait. The *sca* effects for days to 50 per cent flowering ranged from -0.436 (P_4 x P_2) to 0.649 (P_2 x P_1). Out of 12 crosses, three combinations *viz.*, P_2 x P_1 alone registered positively significant *sca* effects (Fig. 3). The hybrids P_3 x P_4 and P_4 x P_2 had exhibited negative significant *sca* effect for this trait. In combining ability analysis, the estimate of the additive genetic variance (D) was found higher than the dominant genetic variance (H_1). It implied the preponderance of additive gene action for days to 50 per cent flowering. Srividhya *et al.,* (2005) and Barad *et al.,* (2008) obtained similar gene action in their studies, whereas preponderance of non-additive gene action was reported by Vaithiyalingam (2002), Pooran Chand and Raghunadha Rao (2002), Anbumalarmathi *et al.,* (2004), Abdul Ghaffor and Zahoor Ahmad (2005), Bhagirath *et al.,* 2013, Yashpal *et al.,* 2015, Kachave *et al.,* 2015 and Thamodharn *et al.,* 2016 for this trait. The relative heterosis for this trait ranged from -0.47 (P_3 x P_2) to 1.87 percent (P_4 x P_2). Out of 12 hybrids, all hybrids exhibited non-significant relative heterosis. Maximum heterobeltiosis was observed within range -4.46 (P_2 x P_4) to 0.00 per cent (P_3 x P_1 and P_4 x P_1). Hybrids P_2 x P_4 showed highly significant negative heterobeltiosis and P_2 x P_3, P_4 x P_3 and P_3 x P_4 showed significant negative heterobeltiosis. The heterosis percentage over standard variety varied from -3.57 (P_3 x P_1 and P_3 x P_4) to -7.14 percent (P_2 x P_3). In this trait seven crosses P_2 x P_3, P_1 x P_2, P_2 x P_1, P_3 x P_2, P_1 x P_3, P_2 x P_4 and P_4 x P_3 showed highly significant negative standard heterosis and the hybrids P_3 x P_1 and P_3 x P_4 recorded significant negative heterosis (Table 5) (Figs. 4, 5, 6).

The grand mean for days to maturity was (62.33) P_2 x P_1 to (72.33 days) P_4 x P_1 and with this trait only one cross P_2 x P_1 showed significantly early in maturity than their grand mean (66.14 days) (Table 1). For days to maturity, the lowest value of *gca* was showed by the parent (-3.042) and the highest value by (2.208). Significantly negative *gca* effects were recorded by P_2 and the parent P_4 and P_1 registered significantly positive *gca* effects for this trait (Table 2). Among twelve crosses, five showed significant and positive *sca* effects while six showed significantly negative *sca* effects (Table 3). The cross, (P_3 x P_2), (P_4 x P_3) exhibited the lowest *sca* effect (-0.83) whereas (P_2 x P_3) showed the highest *sca* effect (3.16). In Diallel analysis, dominant genetic variance (H_1) was found lesser than that of additive genetic variance (D) indicating the additive gene action for this trait. Aher *et al.,* (2001) and Abdul Ghaffor and Zahoor Ahmad (2003) noticed the additive gene action for days to maturity. Some authors namely, Abdul Ghaffor and Zahoor Ahmed (2003 and 2005), Jayapradha *et al.*, (2005), Srividhya *et al.*, (2005) and Barad *et al.*, (2008), Vijay kumar *et al.*, 2014, Thamodharn *et al.*, 2016 reported dominant gene action for this trait. The relative heterosis ranged from -3.70 (P_3 x P_4) to 10.80 percent (P_3 x P_2) and eight hybrids namely P_3 x P_2, P_1 x P_2, P_2 x P_3, P_4 x P_1, P_2 x P_4, P_4 x P_2 and P_2 x P_1 registered highly significant positive relative heterosis and P_3 x P_4 alone showed highly significant negative heterosis. Heterobeltiosis ranged between -3.38 (P_4 x P_3) and 4.83 percent (P_4 x P_1). Out of 12 hybrids, a total of five crosses P_3 x P_4, P_2 x P_1, P_2 x P_4, P_4 x P_2 and P_4 x P_3 showed highly significant negative heterobeltiosis and P_4 x P_1 alone exhibited highly significant and positive heterobeltiosis. Standard heterosis varied from -3.38 (P_3 x P_2 and P_4 x P_3) to 4.83 percent (P_4 x P_1). The crosses namely P_2 x P_1, P_1 x P_3, P_2 x P_3, P_3 x P_4, P_1 x P_2, P_3 x P_1, P_2 x P_4, P_4 x P_2, P_3 x P_2 and P_4 x P_3 showed highly significant negative standard heterosis and P_4 x P_1 alone recorded significantly positive standard heterosis (Table 5).

The minimum and maximum plant height was recorded in the hybrid (30.75) P_2 x P_1 to (45.00 cm) P_4 x P_3. The crosses P_4 x P_3, P_3 x P_2, P_3 x P_1, P_2 x P_4, P_4 x P_1, P_4 x P_2, P_1 x P_4, P_1 x P_2, P_2 x P_3 and P_2 x P_1 recorded significantly higher plant height compared to their grand mean (39.43 cm). The *gca* effect for plant height varied from P_1 (-2.193) to P_3 (2.895). However, in general, it was observed that all of the parents showed significant *gca* effects for this trait. Significantly negative *gca* effects were observed in P_1 and P_2. The parent P_3 and P_4 recorded significantly positive *gca* effects for this trait. For the trait plant height, the *sca* values fell between -1.29 (P_3 x P_1) to 3.71 (P_1 x P_3). Of these, seven hybrids P_1 x P_3, P_2 x P_4, P_4 x P_2, P_2 x P_3, P_2 x P_1, P_1 x P_2, and P_1 x P_4 showed significant and positive *sca* effects. Four crosses exhibited significantly negative effects for this trait. The estimate of dominance genetic variance (H_1) was greater than additive genetic variance (D) for plant height. This inferred that non-additive gene action governed this trait. Manivannan (2002), Vaithiyalingam *et al.*, (2002), Anbumalarmathi *et al.*, (2004), Srividhya *et al.*, (2005), Barad *et al.*, (2008), Supriyo Chakraborty *et al.*, (2010, Vijay kumar *et al.*, 2014, Kachave *et al.*, 2015 Thamodharn *et al.*, 2016 observed predominance of the non-additive gene action in controlling this trait. The relative heterosis for this trait ranged from 2.98 (P_1 x P_4) to 37.51 percent (P_3 x P_2). A total of 12 crosses registered highly significant positive relative heterosis. The heterosis percentage over better parent ranged from -9.45 (P_1 x P_4) to 21.12 percent (P_4 x P_3) and the hybrids such as P_4 x P_3, P_3 x P_2, P_1 x P_2, P_3 x P_1, P_2 x P_4, P_4 x P_1, P_2 x P_1, P_1 x P_3, P_3 x P_4 and P_4 x P_2 showed highly significant positive heterobeltiosis and only two cross P_2 x P_3 and P_1x P_4 recorded

highly significant negative heterosis over better parent. The minimum and maximum standard heterosis was observed in-10.03 (P_1x P_4) and 21.12 percent (P_4 x P_3). Seven hybrids exhibited highly significant positive standard heterosis and P_4 x P_2 alone showed significant positive heterosis. Four crosses showed highly significant negative standard heterosis (Table 5).

The number of branches per plant ranged from (2.52) P_2 to (3.21) P_4. The grand mean for this trait was 3.31. The parent P_2 alone registered significantly positive mean value for this trait. The variation for this trait ranged from 3.00 to 4.19. Out of 12 hybrids, two hybrids P_2 x P_3 and P_3 x P_4 recorded significantly more number of branches with that of the grand mean (3.69). Among the parents, *gca* effects for number of branches varied from -0.215 to 0.218. Positive and significant *gca* effects were observed in P_4. The *gca* effects were significant and negative for the parent P_2. The hybrids had the lowest and the highest *sca* effects of P_4 x P_1 (-0.317) and P_3 x P_4 (0.40) respectively. The *sca* effects were significant and positive in the hybrids namely P_3 x P_4, P_2 x P_4, P_1 x P_3, P_1 x P_2 and P_4 x P_2 and three cross P_1 x P_4, P_4 x P_1 and P_3 x P_2 showed significant and negative *sca* effects for the trait number of branches. The values of dominant genetic variance (H_1) exceeded the values of additive genetic variance (D) in combining ability analysis, thus exhibiting the presence of non-additive gene action for this trait. This was in conformity with earlier findings of Abdul Ghaffor and Zahoor Ahmed (2005) and Kachave *et al.,* 2015. The preponderance of additive gene action was confirmed by Khattak *et al.,* (2001), Anbumalarmathi *et al.,* (2004) and Vijay kumar *et al.,* 2014 for number of branches per plant. The hybrids expressed a range of relative heterosis from 24.89 (P_1 x P_3) to 37.49 percent (P_4 x P_3) and the crosses showing highly significant and positive heterosis were P_4 x P_3, P_4 x P_1, P_3 x P_4, P_1 x P_2, P_3 x P_1, P_2 x P_4, P_4 x P_2, P_3 x P_2 and P_1 x P_3. Heterobeltiosis ranged from 19.00 (P_4 x P_2) to 36.11 percent (P_4 x P_3). Hybrids such as P_4 x P_3, P_4 x P_1, P_3 x P_4, P_3 x P_1, P_2 x P_4, P_1 x P_3, P_1 x P_2 and P_4 x P_2 recorded highly significant positive heterobeltiosis. The heterosis percentage over the standard variety varied from 19.17 (P_3 x P_1) to 30.47 percent (P_3 x P_4). Hybrids namely P_3 x P_4, P_4 x P_3, P_2 x P_4, P_4 x P_1 and P_3 x P_1 showed highly significant positive standard heterosis (Table 5).

The mean value of this Number of clusters per plant ranged from 12.39 to 16.98 with a grand mean 14.76. The parents P_2 and P_4 recorded significantly superior mean values than the grand mean. The mean values of number of clusters per plant among the hybrids range from 16.50 (P_3 x P_1) to 23.50 (P_1 x P_2). The hybrids P_1 x P_2, P_3 x P_4, P_2 x P_3, P_4 x P_3, P_1 x P_4, P_2 x P_4, P_1 x P_3, P_3 x P_2, P_4 x P_1, P_2 x P_1 and P_3 x P_1 recorded significantly more number of clusters with that of the mean (19.88). The *gca* effect observed for this trait ranged from -0.556 (P_1 and P_2) to 0.880 (P_4). Significant and positive effects were noticed in P_4 (0.880) and P_3 (0.232). Significant and negative effects were observed in P_1 and P_2 (-0.556). The lowest value of *sca* effect was shown by P_1 x P_3 (-0.52) and P_3 x P_4 the highest by (2.54).The hybrids with significant and positive *sca* effects were P_3 x P_4, P_2 x P_4, P_2 x P_1, P_3 x P_1,P_4 x P_3 and P_1 x P_4. Five registered negatively significant *sca* effects. Higher estimates of dominant genetic variance (H_1) than additive genetic variance (D) indicated the presence of dominant gene action for this trait. Singh and Dikshit (2003), Srividhya *et al.,* (2005), Barad *et al.,* (2008), Thamodharn *et al.,* 2016 found similar type of gene action controlling this trait whereas the predominance of additive and non-additive type of gene action was reported by some

workers in earlier findings *viz*., Jahagirdar (2001) Vijay kumar *et al.,* 2014 and Tantasawat *et al.,* 2015. The relative heterosis varied from 11.76 (P_4 x P_1) to 78.08 percent (P_1 x P_2). Out of 12 hybrids, all hybrids recorded highly significant positive relative heterosis. The minimum and maximum heterobeltiosis were observed in P_3 x P_1 (10.00) and P_1 x P_2 (67.86 percent) with 11 hybrids showing highly significant positive heterobeltiosis. Standard heterosis varied between 7.22 (P_3 x P_2) to 38.40 percent (P_1 x P_2) with nine crosses showed highly significant positive heterosis such as P_1 x P_2, P_3 x P_4, P_2 x P_3, P_4 x P_3, P_1 x P_4, P_1 x P_3, P_2 x P_4, P_4 x P_2 and P_3 x P_2 (Table 6).

Pod length of parents varied from 3.96 to 4.73 cm.The grand mean for this trait was 4.50 cm. Among the parents P_2 alone produced significant mean value than the grand mean. Among the hybrids the lowest and the highest pod length was observed in P_2 x P_1 (4.50) to P_3 x P_1 (5.53 cm) and out of this 12 hybrids, four hybrids P_3 x P_1, P_4 x P_3, P_1 x P_2 and P_2 x P_1 recorded significantly higher pod length than that of the mean (5.13 cm). Among the parents, the *gca* values ranged from P_2 (-0.253) to P_3 (0.192). The parent P_3 had significantly positive *gca* effects and P_2 recorded significantly negative *gca* effects for this trait. The *sca* effects for pod length ranged from P_4 x P_1 (-0.10) to P_2 x P_4 (0.31). The four crosses P_2 x P_4, P_1 x P_3, P_2 x P_1, and P_3 x P_4 showed significant and positive *sca* effects and three crosses P_2 x P_3, P_1 x P_4 and P_4 x P_1 exhibited significantly negative *sca* effects for this trait. In combining ability analysis, the estimate of the additive genetic variance (D) was lesser than the dominant genetic variance (H_1). It indicated the preponderance of dominant gene action. Similar result was reported by Anbumalarmathi *et al.,* (2004) Barad *et al.,* (2008) and Baradhan and Thangavel (2011). Additive gene action was predominant in pod length and it was suggested by Srividhya *et al.,* (2005), Saif Ullah Ajmal *et al.,* (2007), Vijay kumar *et al.,* 2014 and Yashpal *et al.,* 2015. The relative heterosis for this trait ranged from 6.00 percent (P_4 x P_1) to 19.53 percent (P_2 x P_3). Ten hybrids recorded highly significant positive heterosis and other two crosses P_1 x P_4 and P_2 x P_1 showed non-significant positive relative heterosis. The minimum and maximum heterobeltiosis were observed in P_3 x P_4 (5.47 percent) and P_3 x P_1 (10.67 percent) and the hybrids P_3 x P_1, P_2 x P_3, P_2 x P_4, P_4 x P_3, P_1 x P_3 and P_3 x P_4 showed positive and significant heterobeltiosis. The heterosis percentage over standard variety varied from P_3 x P_2 (6.62) to P_4 x P_3 (14.87 percent) and the hybrids namely P_4 x P_3, P_1 x P_3, P_3 x P_4, P_3 x P_1, P_2 x P_3, P_4 x P_1, P_4 x P_2 and P_2 x P_4 recorded highly significant positive standard heterosis. Hybrids P_3 x P_2 showed significant and positive heterosis (Table 6).

Number of pods per plant varied from (23.79) P_2 to (37.70) P_4. The parents P_4, P_3, P_1 and P_2 recorded significantly more number of pods per plant than their grand mean (29.92). For this trait the minimum number of pods was recorded in the hybrid P_1 x P_4 (28.50) and maximum in the hybrid P_4 x P_2 (39.19) and out of 12 hybrids, nine hybrids *viz*., P_4 x P_2, P_3 x P_4, P_4 x P_3, P_3 x P_1, P_4 x P_1, P_2 x P_4, P_1 x P_3, P_1 x P_2 and P_1 x P_4 exhibited significantly higher mean value when compared to their grand mean (34.93). For number of pods per plant, the *gca* values fell between P_2 (-1.806) and P_4 (2.661). The parents P_4 and P_3 recorded significant and positive effect and P_1 and P_2 registered negative significant for this trait. The *sca* effects varied from P_1 x P_4 (-1.34) to P_1 x P_2 (3.18). With this trait the hybrids that showed significant and positive *sca* effects were P_1 x P_2, P_4 x P_2, P_3 x P_4, P_2 x P_4, P_1 x P_3, and P_2 x P_3 and the hybrid P_4 x P_1, P_3 x P_2, P_2 x P_1, P_3 x P_1 and P_1 x P_4 registered negatively significant *sca* effects for number of pods per plant.

Table.1 Mean performance of parents and hybrids

Entries	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	No. of branches per plant	No. of clusters per plant	Pod length (cm)	No. of pods per plant	No. of seeds per pod	100 grain weight (g)	Protein content (%)	Single plant yield (g)
Parents											
P1	35.66	65.66	28.15*	2.86	14.49	4.73	25.03*	6.05	4.78	20.05*	8.90
P2	34.33*	54.33*	25.97*	2.52*	12.39*	3.96*	23.79*	6.02	4.63	16.17*	7.13*
P3	36.00	66.00	37.15*	2.94	15.17	4.72	33.16*	6.14	4.95	17.70	8.67
P4	37.33	69.00	36.91*	3.21	16.98*	4.60	37.70*	6.84*	5.91*	19.35*	10.06*
Hybrids											
P1 X P2	35.00	65.33	32.75*	3.67	23.50*	4.87*	29.90*	6.30	4.97	18.69*	8.29*
P1 X P3	35.66	65.00	39.90	3.69	19.00*	5.35	32.33*	6.19	5.95	17.14*	11.83*
P1X P4	37.00	68.00	33.42*	3.34	21.39*	4.94	28.50*	6.94	5.10	20.20	14.24
P2 X P1	35.00	62.33*	30.75*	3.35	17.39*	4.50*	35.16	6.44	5.83	18.63*	12.58*
P2 X P3	34.66*	65.00	33.15*	3.00*	22.09*	5.21	34.40	6.97	5.10	17.63*	11.01*
P2 X P4	35.66	66.00	41.56*	4.05	19.00*	5.05	33.55*	6.32	5.57	19.86	13.43*
P3 X P1	36.00	65.33	42.50*	3.83	16.5*	5.53*	36.87*	7.29*	5.27	20.48	14.98*
P3 X P2	35.00	66.66	43.29*	3.49	18.20*	5.04	35.18	6.87	5.49	20.65	13.19*
P3 X P4	36.00	65.00	39.26	4.19*	23.02*	5.27	39.13*	6.50	4.78*	19.06*	18.64*
P4 X P1	37.00	72.33	41.46*	3.97	17.59*	5.15	36.44*	6.52	5.61	17.54*	17.15*
P4 X P2	36.33	66.00	38.04*	3.57	19.39	5.12	39.19*	6.63	6.03*	21.15*	14.19
P4 X P3	35.66	66.66	45.00*	4.08	21.50*	5.43*	38.50*	6.43	5.93	20.14	20.69*
Mean of parents	**35.83**	**63.75**	**32.05**	**3.31**	**14.76**	**4.50**	**29.92**	**6.07**	**5.07**	**18.32**	**8.69**
Mean of hybrids	**35.77**	**66.14**	**39.43**	**3.69**	**19.88**	**5.13**	**34.93**	**6.62**	**5.47**	**20.26**	**14.19**
SEd	**0.54**	**0.60**	**0.38**	**0.24**	**0.38**	**0.12**	**0.67**	**0.33**	**0.26**	**0.33**	**0.37**
CD(P=05)	**1.104**	**1.24**	**0.782**	**0.50**	**0.79**	**0.25**	**1.37**	**0.67**	**0.53**	**0.67**	**0.76**

* Significant at 5% level

Table.2 General combining ability effects of parents for different traits

Parents	Days to 50 per cent flowering	Days to maturity	Plant height	No. of branches per plant	No. of clusters per plant	Pod length	No. of pods per plant	No. of seeds per pod	100 grain weight	Protein content	Single plant yield
Parents											
Vamban 4	0.104	0.667*	-2.193*	-0.038	-0.556*	0.007	-2.520*	-0.056	-0.081	0.070	-0.702*
Vamban 2	-0.729*	-3.042*	-2.895*	-0.215*	-0.556*	-0.253*	-1.806*	-0.081	-0.087	-0.408*	-1.942*
LBG 17	-0.146	0.167	2.846*	0.034	0.232*	0.192*	1.665*	0.039	-0.068	-0.216*	0.647*
CO 5	0.771*	2.208*	2.242*	0.218*	0.880*	0.054	2.661*	0.099	0.236*	0.554*	1.997*
SE(gi)	**0.117**	**0.131**	**0.082**	**0.053**	**0.083**	**0.026**	**0.145**	**0.072**	**0.056**	**0.080**	**0.071**

*Significant at 5% level

Table.3 Specific combining ability effects of hybrids for different traits

Hybrids	Days to 50 per cent flowering	Days to maturity	Plant height	No. of branches per plant	No. of clusters per plant	Pod length	No. of pods per plant	No. of seeds per pod	100 grain weight	Protein content	Single plant yield
P1 x P2	-0.146	0.667*	0.007	0.278*	2.957*	-0.038	3.180*	-0.022	0.210*	-0.031	0.266*
P1 X P3	0.104	-1.208*	3.717*	0.279*	-0.526*	0.275*	1.779*	0.227	0.392*	-0.075	0.696*
P1 X P4	0.354*	1.750*	0.566*	-0.011	0.569*	0.017	-1.349*	0.157	-0.167	-0.779*	1.592*
P2 X P1	0.201	1.500*	0.998*	0.157	3.052*	0.187*	-2.630*	-0.068	-0.430*	0.032	-2.143*
P2 X P3	-0.063	3.167*	1.441*	-0.062	1.872*	-0.498*	1.255*	0.435*	0.078	0.738*	0.585*
P2 X P4	0.187	1.292*	3.621*	0.319*	0.270	0.317*	1.837*	-0.068	0.284*	1.331*	0.947*
P3X P1	-0.167	-0.167	-1.298*	-0.070	1.253*	-0.088*	-2.270*	-0.550*	0.340*	-1.670*	-1.573*
P3 X P2	-0.175	-0.833*	-5.073*	-0.245*	1.945*	0.085*	-3.843*	0.050	-0.197	-1.512*	-1.088*
P3 X P4	-0.562*	-2.083*	0.212*	0.400*	2.544*	0.137*	0.810*	-0.201	-0.182	0.230	4.209*
P4 X P1	-0.015	-2.167*	-4.020*	-0.317*	1.900*	-0.108*	-3.968*	0.210	-0.285*	1.330*	-1.455*
P4 X P2	-0.333*	-0.071	1.760*	0.240*	-0.198	-0.032	-2.822*	-0.157	-0.223*	-0.648*	-0.380*
P4 X P3	0.167	-0.833*	-2.868*	0.057	0.760*	-0.080*	0.315	0.033	-0.577*	-0.540*	-1.028*
SE(S_{ij})	**0.210**	**0.240**	**0.151**	**0.096**	**0.153**	**0.048**	**0.266**	**0.133**	**0.103**	**0.147**	**0.134**

* Significant at 5% level

Table.4 Variability parameters for different traits

S.No.	Characters	PCV (%)	GCV (%)	Heritability (%)	Genetic advance as per cent of mean
1.	**Days to 50 per cent flowering**	2.84	2.15	57.35	3.35
2.	**Days to maturity**	5.71	5.59	96.03	11.29
3.	**Plant height**	15.29	15.23	99.30	31.27
4.	**Number of branches per plant**	15.67	13.08	69.78	22.53
5.	**Number of clusters per plant**	17.11	16.92	97.78	34.46
6.	**Pod length**	8.41	7.83	86.83	15.04
7.	**Number of pods per plant**	14.23	14.02	97.04	28.46
8.	**Number of seeds per pod**	7.63	4.28	31.54	4.96
9.	**Hundred grain weight**	10.15	8.22	65.58	13.71
10.	**Protein content**	7.87	7.50	90.75	14.73
11.	**Single plant yield**	30.07	29.90	98.88	61.26

Table.5 Percentage of heterosis for days to 50 percent flowering, Days to maturity, Plant height, Number of branches per plant

S.No.	Cross	Days to 50 per cent flowering			Days to maturity			Plant height			Number of branches per plant		
		Relative heterosis (di)	Heterobeltiosis (dii)	Standard heterosis (diii)	Relative heterosis (di)	Heterobeltiosis (dii)	Standard heterosis (diii)	Relative heterosis (di)	Heterobeltiosis (dii)	Standard heterosis (diii)	Relative heterosis (di)	Heterobeltiosis (dii)	Standard heterosis (diii)
1	P1 X P2	-0.47	-2.78	-6.25**	8.59**	-1.01	-5.31**	21.36**	16.96**	-11.85**	32.89**	22.33**	14.09
2	P1 X P3	-0.93	-0.93	-4.46**	-1.52	-1.52	-5.80**	22.49**	7.46**	7.46**	24.89**	23.11**	14.82
3	P1X P4	0.91	-0.89	-0.89	0.74	-1.45	-1.45	2.98**	-9.45**	-10.03**	7.45	3.83	3.83
4	P2 X P1	0.48	-1.87	-6.25**	4.18**	-5.08**	-9.66**	13.57**	9.22**	-17.23**	14.43	11.89	4.35
5	P2 X P3	-0.95	-3.70*	-7.14**	8.33**	-1.52	-5.80**	4.98**	-10.78**	-10.78**	1.01	0.00	-6.74
6	P2 X P4	0.00	-4.46**	-4.46**	7.32**	-4.35**	-4.35**	32.11**	12.58**	11.86**	30.29**	25.91**	25.91**
7	P3 X P1	0.47	0.00	-3.57*	-0.76	-1.01	-5.31**	30.45**	14.86**	14.39**	30.68**	27.78**	19.17**
8	P3 X P2	-0.47	-2.78	-6.25**	10.80**	1.01	-3.38**	37.51**	17.02**	16.54**	26.37**	16.33	8.50
9	P3 X P4	-1.82	-3.57*	-3.57*	-3.70**	-5.80**	-5.80**	6.24**	6.12**	5.68**	35.01**	30.47**	30.47**
10	P4 X P1	1.83	0.00	-0.89	7.43**	4.83**	4.83**	27.28**	12.07**	11.61**	35.45**	32.44**	23.52**
11	P4 X P2	1.87	-1.80	-2.68	7.03**	-4.35**	-4.35**	20.81**	2.81*	2.39*	29.27**	19.00**	10.98
12	P4 X P3	-2.28	-3.60*	-4.46**	-1.23	-3.38**	-3.38**	21.34**	21.12**	21.12**	37.49**	36.11**	26.94**
	SE	**0.46**	**0.54**	**0.54**	**0.52**	**0.60**	**0.60**	**0.33**	**0.38**	**0.38**	**0.21**	**0.24**	**0.24**

* Significant at 5% level, ** Significant at 1% level.

Table.6 Percentage of heterosis for Number of cluster per plant, pod length, Pod per plant, Number of seeds per pod

S.No.	Cross	Number of cluster per plant			pod length			Pod per plant			Number of seeds per pod		
		Relative heterosis (di)	Heterobeltiosis (dii)	Standard heterosis (diii)	Relative heterosis (di)	Heterobeltiosis (dii)	Standard heterosis (diii)	Relative heterosis (di)	Heterobeltiosis (dii)	Standard heterosis (diii)	Relative heterosis (di)	Heterobeltiosis (dii)	Standard heterosis (diii)
1	P1 X P2	78.08**	67.86**	38.40**	8.70**	-2.53	3.03	22.56**	19.61**	-20.69**	4.85	4.65	-7.85
2	P1 X P3	30.29**	25.24**	11.94**	10.28**	7.18**	13.25**	11.17**	-2.51	-14.24**	1.92	0.70	-9.50
3	P1X P4	38.13**	26.01**	26.01**	2.85	-1.20	4.44	-9.09**	-24.40**	-24.40**	8.10	1.46	1.46
4	P2 X P1	31.35**	20.06**	2.45	3.09	-4.86	-4.86	43.44**	40.48**	-6.74**	6.83	6.33	-5.85
5	P2 X P3	62.61**	45.60**	30.13**	19.53**	10.37**	10.22**	20.37**	3.74	-8.74**	14.82**	13.45**	1.95
6	P2 X P4	31.12**	11.90**	11.90**	17.51**	9.77**	6.91**	8.75**	-11.02**	-11.02**	-1.51	-7.55	-7.75
7	P3 X P1	11.90**	10.00**	-2.83	13.74**	10.67**	16.98**	27.08**	11.74**	-2.20	20.93**	20.36**	6.58
8	P3 X P2	32.93**	21.38**	7.22**	12.49**	0.87	6.62*	23.88**	6.61**	-6.69**	14.33**	14.11*	0.49
9	P3 X P4	43.96**	35.57**	35.57**	9.78**	5.47**	11.49**	10.69**	3.78*	3.78*	1.25	-4.97	-4.97
10	P4 X P1	11.76**	3.51	3.63	6.00**	3.13	9.02**	15.63**	-4.11*	-3.35	-0.13	-6.87	-4.68
11	P4 X P2	31.98**	14.10**	14.23**	14.20**	2.40	8.25**	26.85**	3.14	3.95*	1.92	-5.19	-2.97
12	P4 X P3	33.64**	26.47**	26.62**	11.76**	8.67**	14.87**	8.20**	1.32	2.11	-2.13	-8.10	-5.95
	SE	**0.33**	**0.38**	**0.38**	**0.10**	**0.12**	**0.12**	**0.58**	**0.67**	**0.67**	**0.29**	**0.33**	**0.33**

* Significant at 5% level, ** Significant at 1% level.

Table.7 Percentage of heterosis for Hundred grain weight, Protein content and Single plant yield

S.No.	Cross	Hundred grain weight			Protein content			Single plant yield		
		Relative heterosis (di)	Heterobeltiosis (dii)	Standard heterosis (diii)	Relative heterosis (di)	Heterobeltiosis (dii)	Standard heterosis (diii)	Relative heterosis (di)	Heterobeltiosis (dii)	Standard heterosis (diii)
1	P1 X P2	3.29	-0.47	-15.79**	3.34	-6.53**	-6.80**	2.81	-7.85*	-17.56**
2	P1 X P3	19.73**	19.13**	0.79	-9.09**	-14.30**	-14.54**	33.95**	31.48**	17.63**
3	P1X P4	-6.39	-13.59**	-13.59**	2.63	1.03	0.75	49.49**	41.62**	41.62**
4	P2 X P1	19.28**	16.73**	-1.24	3.34	-7.11**	-7.11**	58.17**	41.24**	25.05**
5	P2 X P3	2.51	2.00	-13.71**	4.63	-0.41	-12.08**	40.61**	27.07**	9.51
6	P2 X P4	2.23	-5.64	-5.64	12.34**	2.60	-0.98	57.52**	33.57**	33.57**
7	P3 X P1	7.83	5.53	10.72*	7.63**	2.11	2.11	67.31**	66.44**	48.91**
8	P3 X P2	14.01**	9.87	-7.05	20.88**	14.76**	2.99	63.55**	46.59**	31.15**
9	P3 X P4	-12.31**	-19.06**	-19.06**	2.04	-1.53	-4.97*	95.59**	85.29**	85.29**
10	P4 X P1	4.14	-6.39	-4.96	-10.15**	-12.51**	-12.51**	81.49**	71.57**	70.54**
11	P4 X P2	13.51**	0.61	2.14	20.29**	11.35**	5.48**	65.72**	41.97**	41.12**
12	P4 X P3	8.43	-1.06	0.45	9.73**	6.00**	0.42	121.71**	106.97**	105.73**
	SE	**0.22**	**0.26**	**0.26**	**0.32**	**0.37**	**0.37**	**0.28**	**0.33**	**0.33**

* Significant at 5% level, ** Significant at 1% level.

Table.8 Hybrids selected for recombination breeding

S.no	Characters	Mean	Non-significant of *gca* effects	Significant of *sca* effects	Standard heterosis	Overall performance of mean, Non-significant of *gca* effects, *sca* effects and standard heterosis
1.	**Days to 50 per cent flowering**	VBN 2 x LBG 17	VBN 4, LBG 17,CO 5	VBN 4 x CO 5, LBG 17x CO 5, CO 5 x VBN 2	VBN 4 x VBN 2,VBN 4 x LBG 17, VB,N 2 x VBN 4,VBN 2 x LBG 17, VBN 2 x CO 5, LBG 17 x VBN 4, LBG 17 x VBN 2, LBG 17 x CO 5 CO 5 x LBG 17	LBG 17x CO 5
2.	**Days to maturity**	VBN 2 x VBN 4	VBN 4, LBG 17,CO 5	VBN 4 x VBN 2,VBN 4 x LBG 17, VBN 4 x CO 5,VBN 2 x VBN 4, VBN 2 x LBG 17, VBN 2 x CO 5, LBG17 x VBN4, LBG 17 x CO 5, CO 5 x VBN 4, CO 5 x VBN 2, CO 5 x LBG 17	VBN 4 x VBN 2,VBN 4 x LBG 17, VBN 4 x CO 5, VBN2 x VBN 4, VBN 2 x LBG 17, VBN 2 x CO 5, LBG 17 x VBN 4, LBG 17x VBN2, LBG 17 x CO 5, CO 5 x VBN 4, CO 5 x VBN 2, CO 5 x LBG 17	VBN 4 x LBG 17,VBN 4 x CO 5, LBG 17 x VBN 4, LBG 17 x CO 5, CO 5 x VBN 4, CO 5 x LBG 17
3.	**Plant height**	VBN4 x VBN2, VBN 4 x CO 5, VBN2 x VBN4, VBN 2 x LBG 17, VBN 2 x CO 5, LBG17x VBN4, LBG 17 x VBN 2, CO 5 x VBN 4, CO 5 x VBN 2, CO5 x LBG 17	-	VBN 4 x VBN 2,VBN 4 x LBG 17, VBN 4 x CO 5, VBN 2 x VBN 4, VBN 2x LBG 17, VBN 2x CO 5, LBG 17x VBN 4, LBG 17x VBN 2, LBG 17x CO 5, CO 5 x VBN 4, CO 5 x VBN 2, CO 5 x LBG 17	VBN 4 x VBN 2,VBN 4 x LBG 17, VBN 4 x CO 5, VBN 2 x VBN 4, VBN 2 x LBG 17, VBN 2 x CO 5, LBG 17 x VBN 4, LBG 17 x VBN 2, LBG 17 x CO 5, CO 5 x VBN 4, CO 5 x VBN 2, CO 5 x LBG 17	-
4.	**Number of branches per plant**	VBN 2 x LBG 17, LBG 17 x CO5,	VBN 4, LBG 17,CO 5	VBN 4 x VBN 2,VBN 4 x LBG 17, VBN 2x CO 5,LBG 17x VBN 2, LBG 17 x CO 5, CO 5 x VBN 4, CO 5 x VBN 2.	VBN 2 x CO 5, LBG 17 x VBN 4, LBG 17 x CO 5, CO 5 x VBN 4, CO 5 x LBG 17	LBG 17 x CO 5, CO 5 x VBN 4
5.	**Number of clusters per plant**	VBN 4 x VBN 2,VBN 4 x LBG 17, VBN 4 x CO 5, VBN 2 x VBN 4, VBN 2 x LBG 17, VBN 2 x CO 5, LBG 17 x VBN 4,LBG 17 x VBN 2, LBG 17 x CO 5, CO 5 x VBN 4, CO 5 x LBG 17.	VBN 4,LBG 17	VBN 4 x VBN 2,VBN 4 x LBG 17, VBN 4 x CO 5, VBN 2 x VBN 4, VBN 2 x LBG 17, LBG 17 x VBN 4, LBG 17 x VBN 2, LBG 17x CO 5, CO 5 x LBG 17.	VBN 4 x VBN2,VBN 4 x LBG 17, VBN 4 x CO 5,VBN 2 x LBG 17, VBN 2 x CO5,LBG 17 x VBN 2, LBG 17 x CO 5, CO 5 x VBN 2, CO 5 x LBG 17.	VBN 4 x LBG 17

Table.9 Hybrids selected for recombination breeding

S.no	Characters	Mean	Non-significant of *gca* effects	Significant of *sca* effects	Standard heterosis	Overall performance of mean, Non-significant of *gca* effects, *sca* effects and standard heterosis
6.	**Pod length**	VBN 4 x VBN 2, VBN 2 x VBN 4, LBG 17x VBN 4, CO5 x LBG 17.	VBN 4, LBG 17,CO 5	VBN 4 x LBG 17, VBN 2 x VBN4, VBN 2 x LBG 17, VBN 2 x CO 5.	VBN 4 x LBG 17, VBN 2 xLBG17, VBN 2 x CO 5, LBG 17x VBN 4, LBG 17 x VBN 2, LBG 17 x CO 5, CO 5 x VBN 4, CO 5 x VBN 2, CO 5 x LBG 17	VBN 4 x LBG 17
7.	**Number of pods per plant**	VBN 4 x VBN2,VBN 4 x LBG 17, VBN 4 x CO 5, VBN 2 x CO5 LBG 17x VBN 4, LBG 17 x CO 5, CO 5 x VBN 4,CO 5 x VBN 2, CO 5 x LBG 17	-	VBN 4 x VBN 2,VBN 4 x LBG 17, VBN 4 x CO 5, VBN 2 x VBN 4, VBN 2x LBG17, VBN 2x CO 5, LBG 17x VBN 4, LBG 17x VBN 2, LBG 17x CO 5, CO 5 x VBN 4, CO 5 x VBN 2	VBN 4 x VBN 2,VBN 4 x LBG 17, VBN 4 x CO 5, VBN 2 xVBN 4, VBN 2 x LBG 17, VBN 2 x CO 5, LBG 17 x VBN 2, LBG 17 x CO 5, CO 5 x VBN 2	-
8.	**Number of seeds per pod**	LBG 17x VBN 4	VBN 4,VBN 2, LBG17	VBN 2 x LBG 17, LBG 17 x VBN 4	-	VBN 2x LBG 17, LBG 17x VBN 4
9.	**Hundred grain weight**	LBG 17x CO 5, CO 5 x VBN 2	VBN 4,VBN 2, LBG17	VBN 4 x VBN 2,VBN4 x LBG17, VBN 2 x VBN 4,VBN 2 x CO5, CO5 x VBN 4, CO5 x VBN2, CO5 x LBG 17	VBN 4 x VBN 2, VBN 4 x CO 5, VBN2x LBG 17,LBG 17x VBN 4, LBG 17x CO 5	VBN 4 x VBN 2

Table.10 Hybrids selected for recombination breeding

S.no	Characters	Mean	Non-significant of *gca* effects	Significant of *sca* effects	Standard heterosis	Overall performance of mean, Non-significant of *gca* effects, *sca* effects and standard heterosis
10.	**Protein content**	VBN 4 XVBN 2, VBN 4 x LBG17, VBN 2 x VBN 4, VBN 2 x LBG 17 LBG 17x CO 5, CO 5 x VBN 4, CO 5 x VBN 2	LBG17	VBN 4 x CO 5, VBN 2x LBG 17, VBN 2 x CO 5, LBG 17 x VBN 4, LBG 17x VBN 2, CO 5 XVBN 4, CO 5 XVBN 2, CO 5 x LBG 17	VBN 4 XVBN 2, VBN 4 x LBG17, VBN 2 x VBN 4, VBN 2 x LBG 17, LBG 17x CO 5, CO 5 x VBN 4, CO 5 x VBN 2	VBN 2 x LBG 17
11.	**Single plant yield**	VBN 4x VBN 2, VBN 4 x LBG17, VBN 2 x VBN 4, VBN 2x LBG17, VBN 2x CO 5, LBG 17x VBN 4, LBG 17x VBN 2, LBG 17x CO 5, CO 5 x VBN 4, CO 5 x LBG 17	VBN 4,LBG 17	VBN 4 x VBN 2,VBN 4 x LBG 17 VBN 4 x CO 5, VBN 2 x VBN 4, VBN 2 x LBG 17, VBN 2 x CO 5, LBG 17 x VBN 4, LBG 17x VBN 2 LBG 17x CO 5, CO 5 x VBN 4, CO 5 x VBN 2, CO5 x LBG 17	VBN 4 x VBN 2,VBN 4 x LBG 17, VBN 4 x CO 5, VBN 2 x VBN 4, VBN 2 x CO 5, LBG 17x VBN 4, LBG 17 x VBN 2, LBG 17 x CO 5, CO 5 x VBN4, CO 5 x VBN 2, CO 5 x LBG 17	VBN 4 x LBG 17, LBG 17x VBN 4
Over all effcet		VBN 4x VBN 2, VBN 2 x VBN 4 VBN 2x LBG17, LBG 17x VBN 4, LBG 17x CO 5	LBG 17,VBN 4	VBN 2 x LBG 17, VBN 4 x LBG 17, VBN 2 x CO 5, LBG 17x VBN 4, LBG 17x CO 5	LBG 17 x CO 5, VBN 4x VBN 2 VBN 4 x LBG 17,VBN 2 x LBG 17, VBN 2 x CO 5,	**VBN 4 x LBG 17**

Table.11 Estimation of genetic parameters

Characters	D	F	H_1	H_2	h^2	E
Days to 50 per cent flowering	1.00	-0.42	-0.7	-0.56	-0.36	0.51
Days to maturity	40.97	26.78	27.12	22.19	12.32	0.68
Plant height (cm)	33.31	-1.49	49.05	49.09	90.99	0.62
No. of branches per plant	0.02	-0.09	0.628	0.65	1.40	0.05
No. of clusters per plant	3.42	2.33	33.87	33.12	58.96	0.16
Pod length (cm)	0.11	-0.00	0.44	0.43	0.84	0.02
No. of pods per plant	43.49	21.67	39.16	35.37	55.90	0.68
No. of seeds per pod	0.07	0.10	0.23	0.21	0.22	0.07
100 grain weight (g)	0.29	0.26	0.41	0.35	0.34	0.03
Protein content (%)	2.63	3.84	4.59	3.33	1.71	0.38
Single plant yield (g)	1.31	-4.69	48.08	42.60	67.88	0.13

* Significant at 5% level, ** Significant at 1% level, D - Additive effects of genes, F - Covariance of additive and dominance effects, H_1 - Dominance effects of genes, H_2 - Dominance indicating symmetry of positive and negative effects of genes, h^2 - Dominance effects over all loci, E - Environmental component

Table.12 Qualitative traits

Scales	**Percentage of plant foliage affected**	**Reaction**
1	Mottling of leaves covering 0.1 to 5.0 per cent of the leaf area.	Resistant
3	Mottling of leaves covering 5.1 to 10.0 per cent of the leaf area.	Moderately resistant
5	Mottling and yellow discoloration of 10.1to 25.0 per cent of the leaf area.	Moderately susceptible
7	Mottling and yellow discoloration of 25.1to 50.0 per cent of the leaf area.	Susceptible
9	Severe yellow mottling on more than 50.0 per cent and up to 100 per cent of the leaf area.	Highly susceptible

The mean disease scale of parents and $F_1$was calculated as follows (Singh, 1980). Mean scale = $\sum$ (Infection rate x Frequency) / Total number of plants scored. The plants in the F_2 and back cross generations were classified as resistant (1-3) and susceptible (5-9) following Reddy and Singh (1993).

Table.13 YMV scores in parents and hybrids

Code no.	Genotypes	Mean YMV score	Reaction
P1	Vamban 4	1.0	Resistant
P2	Vamban 2	1.0	Resistant
P3	LBG 17	3.8	Moderately resistant
P4	CO 5	9.0	Highly Susceptible
Hybrids			
P1 x P2	VBN4 x VBN2	1.2	Resistant
P1 X P3	VBN4 X LBG 17	4.3	Moderately resistant
P1X P4	VBN4 X CO 5	3.8	Moderately resistant
P2 X P1	VBN2 X VBN 4	1.8	Resistant
P2 X P3	VBN2 X LBG 17	3.4	Moderately resistant
P2 X P4	VBN2 X CO 5	7.6	Susceptible
P3 X P1	LBG 17 X VBN 4	4.2	Moderately resistant
P3 X P2	LBG 17 X VBN 2	1.5	Resistant
P3 X P4	LBG 17 X CO5	5.8	Moderately susceptible
P4 X P1	CO 5 X VBN4	4.2	Moderately resistant
P4 X P2	CO 5 X VBN 2	4.5	Moderately resistant
P4 X P3	C0 5 X LBG 17	9.2	Highly Susceptible

Fig.1 Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) for single plant yield & its components

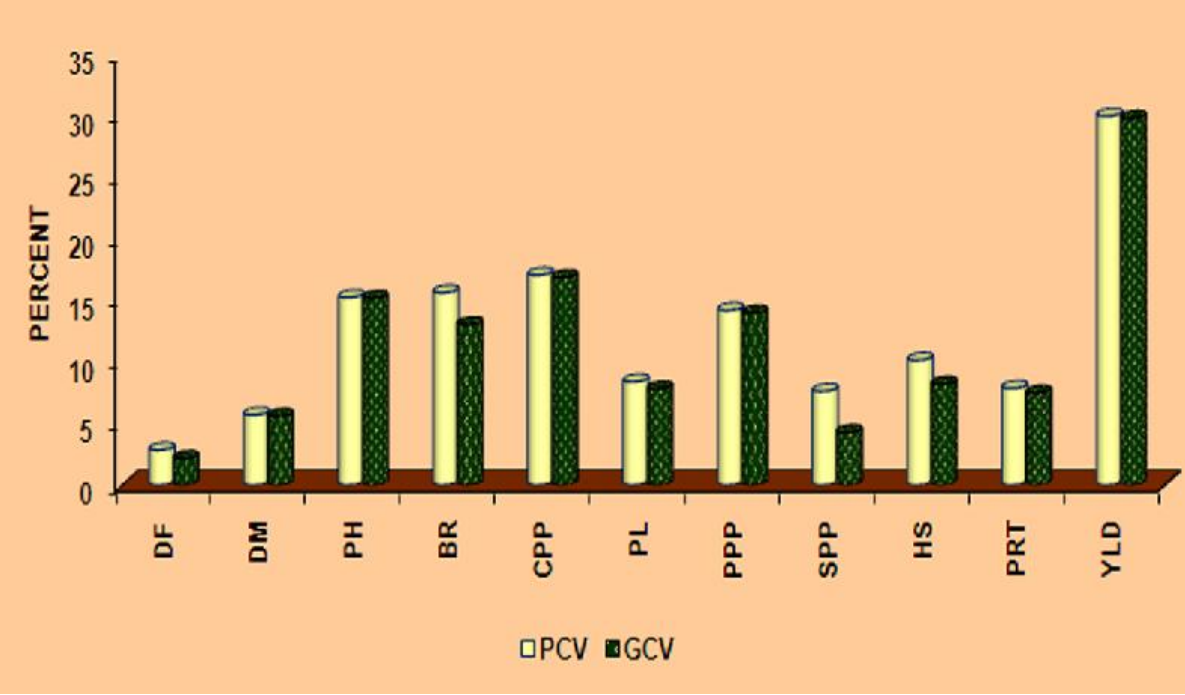


Fig.2 Heritability and Genetic Advance for single plant yield & its components

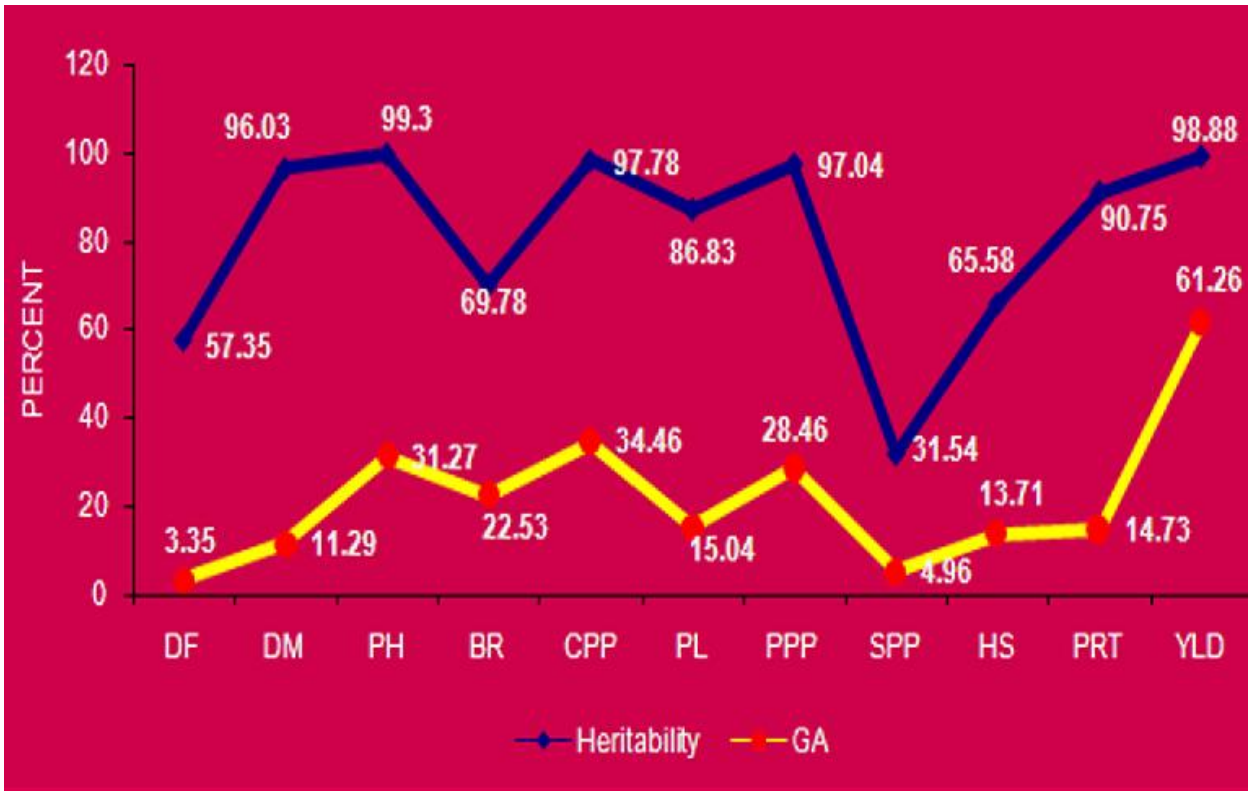
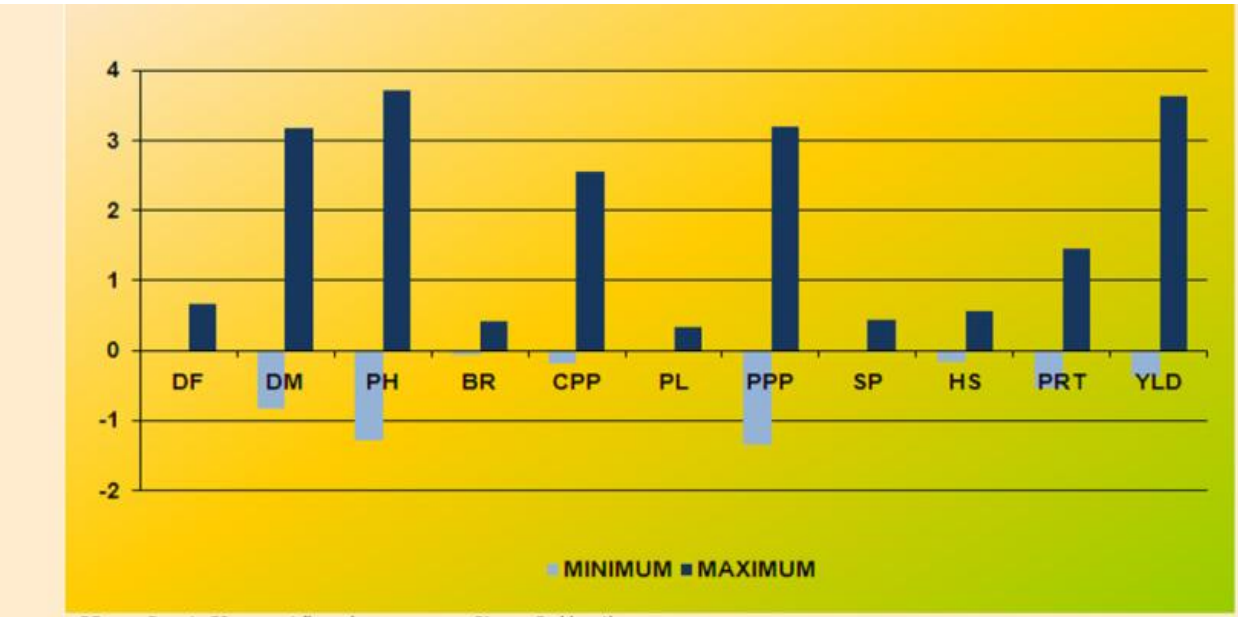
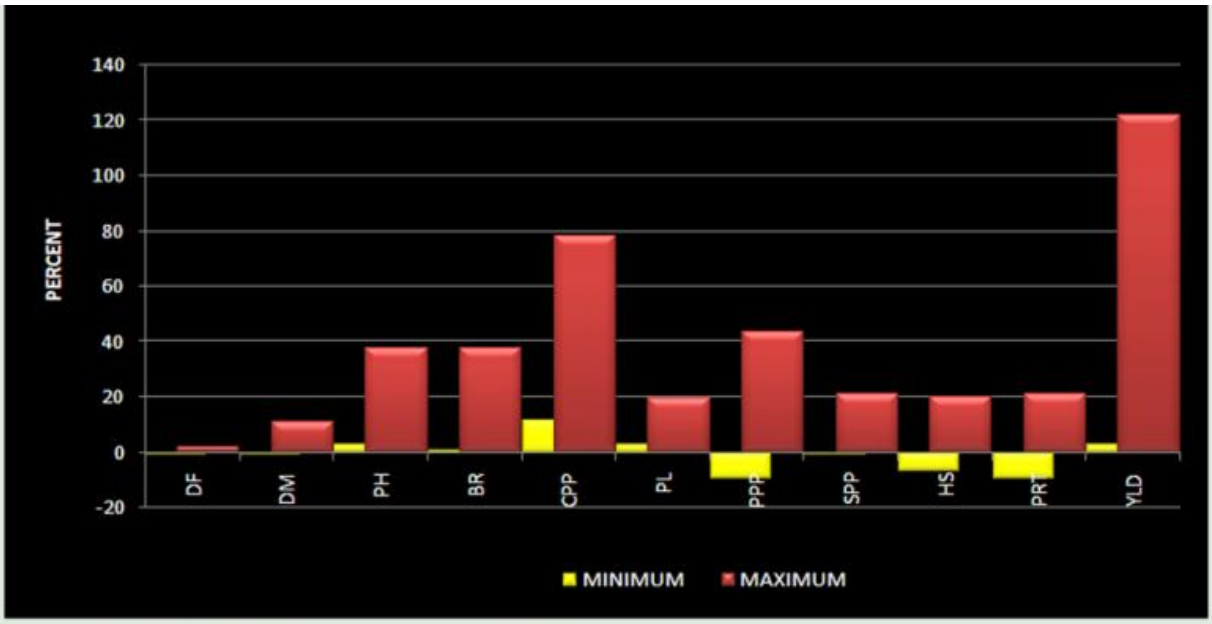


Fig.3 Range of *sca* effects of hybrids for different traits



DF – Days to 50 per cent flowering
DM – Days to maturity
PH – Plant height
BR – Number of branches per plant
CPP – Number of clusters per plant
PPP – Number of pods per plant
PL – Pod length
SPP – Number of seeds per pod
HS – Hundred seed weight
PRT – Protein content
YLD – Seed yield per plant

Fig.4 Range of relative heterosis for different traits



DF – Days to 50 per cent flowering
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CPP – Number of clusters per plant
PPP – Number of pods per plant
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SPP – Number of seeds per pod
HS – Hundred seed weight
PRT – Protein content
YLD – Seed yield per plant

Fig.5 Range of heterobeltiosis for different traits

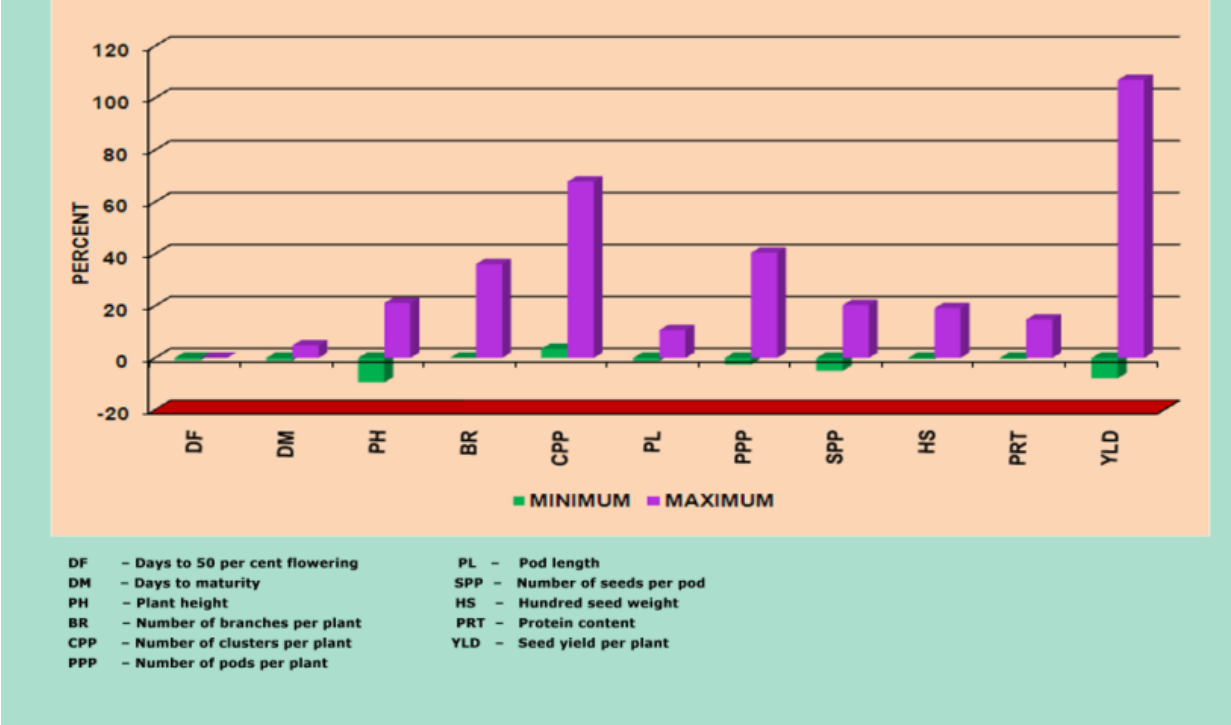

Fig.6 Range of standard heterosis for different traits

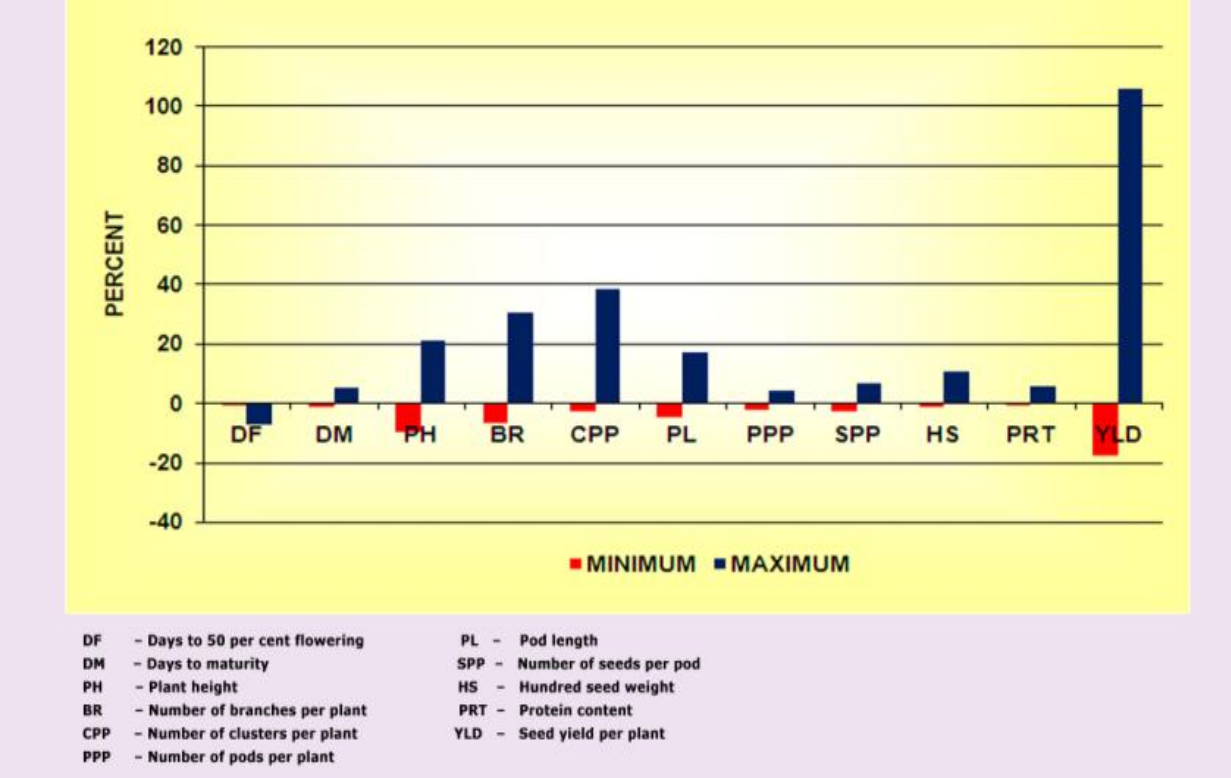

Fig.7 Magnitude of additive and dominance variance for single plant yield and its components traits

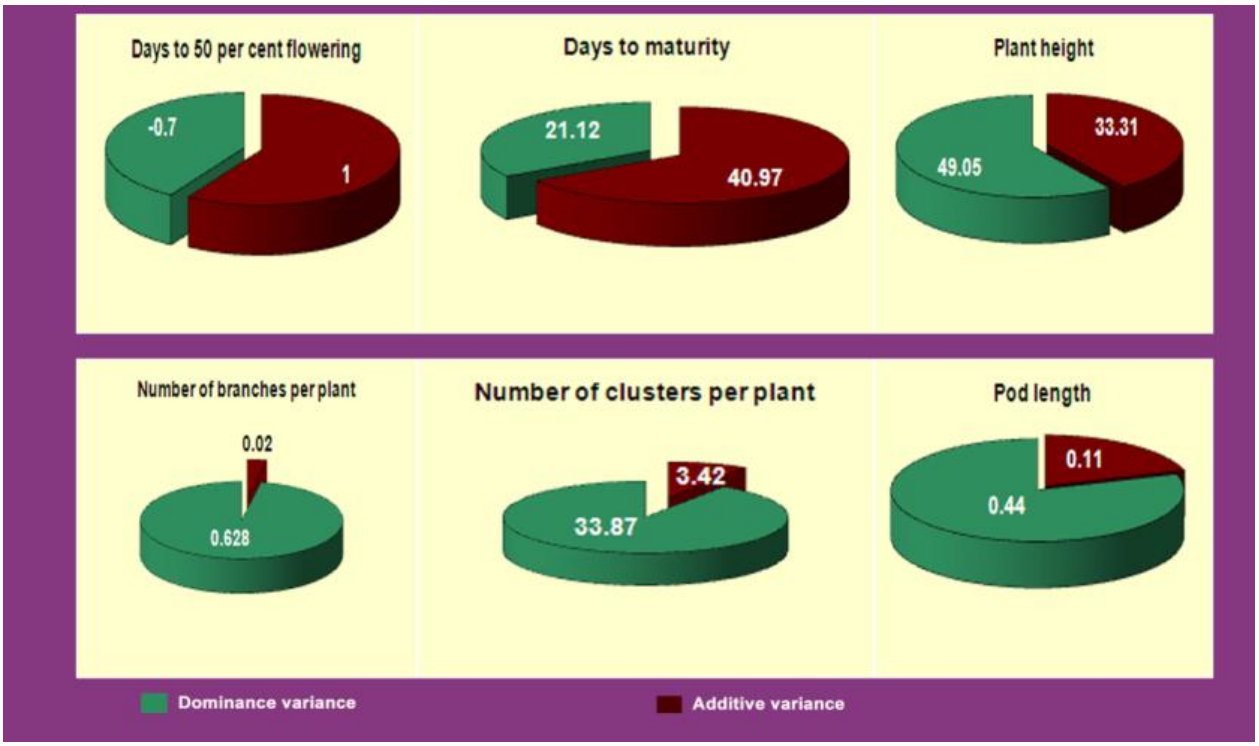

Fig.8 Magnitude of additive and dominance variance for single plant yield and its components traits

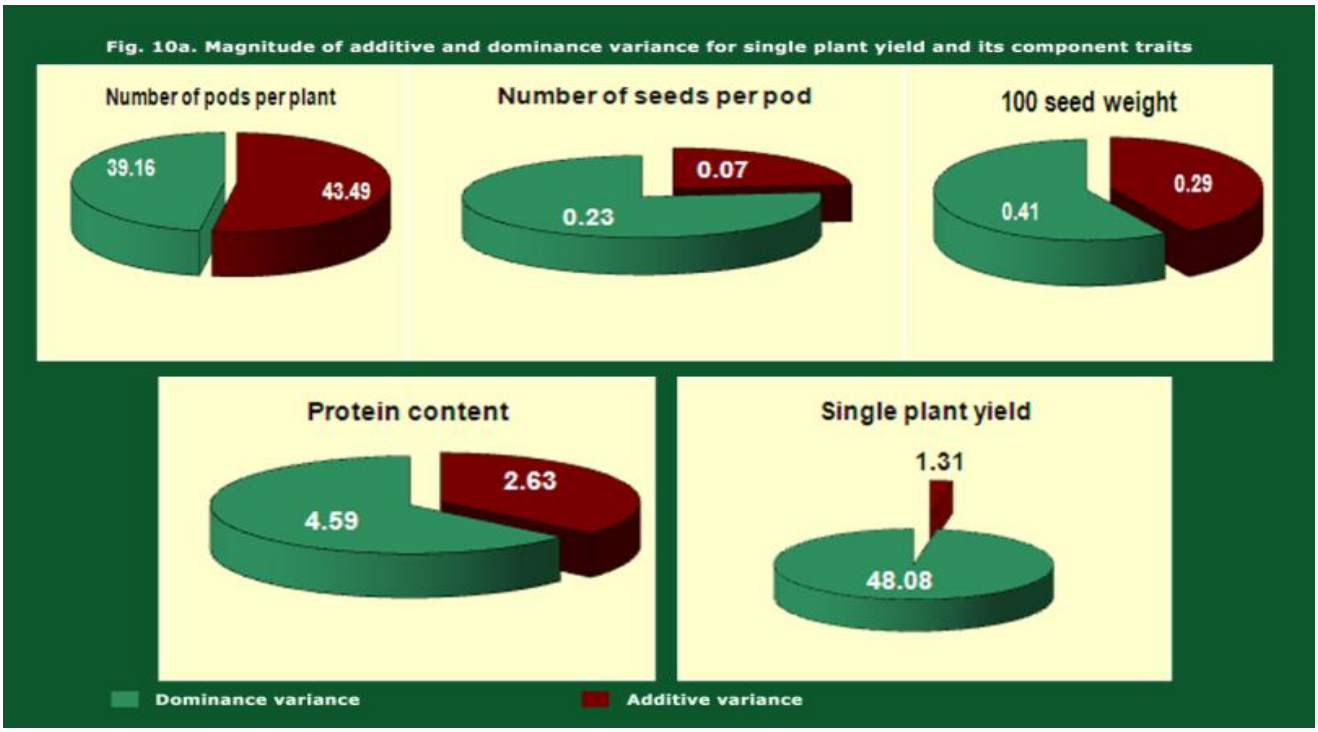

Plate.1 Hybrid selected for recombination breeding P2 X P4 (VBN 2 X CO 5)

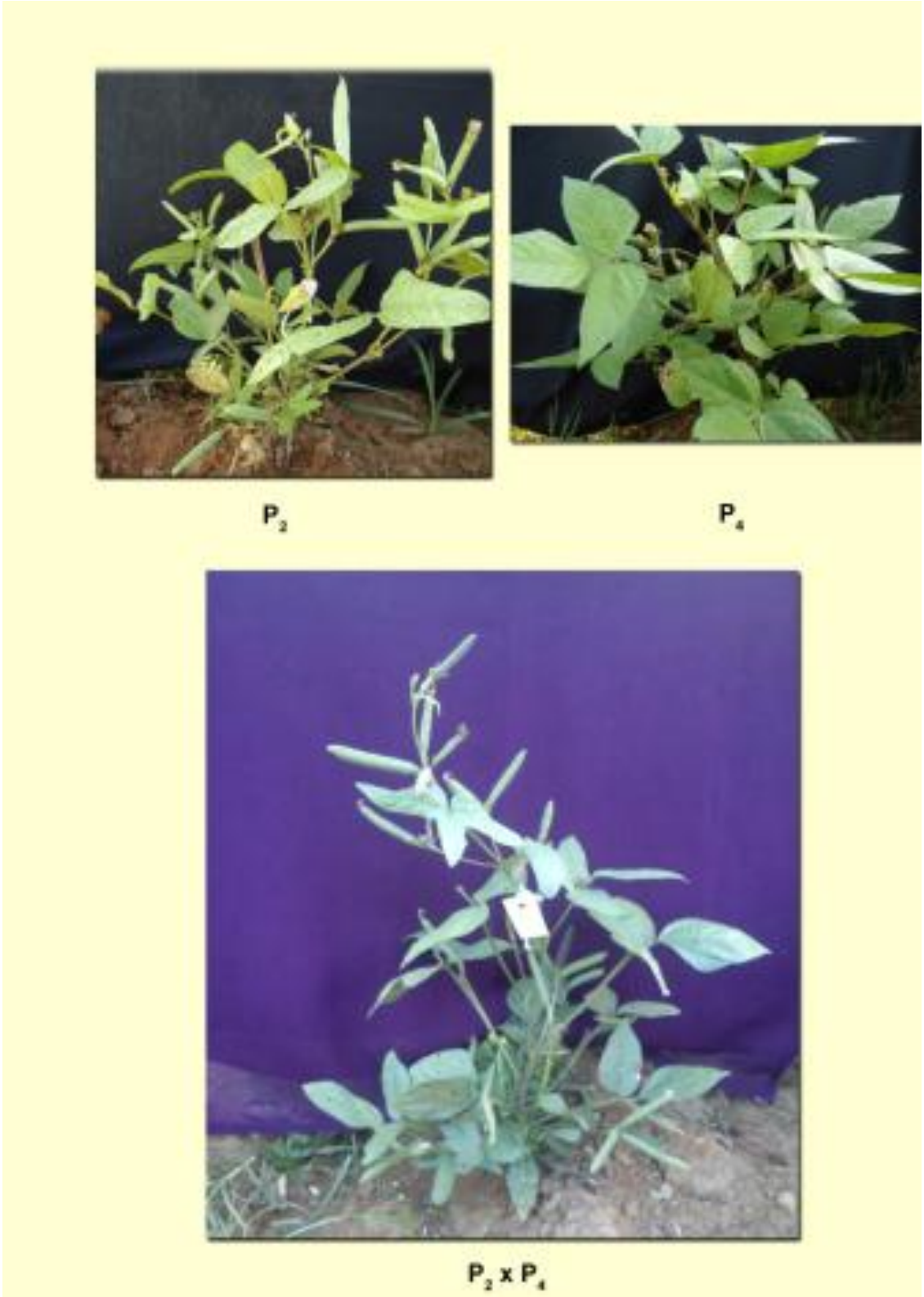

Plate.2 Hybrid selected for recombination breeding P2 X P3 (VBN 2 X LBG 17)

P_2

P_3

$P_2 \times P_3$

Plate.3 Hybrid selected for recombination breeding P3 X P4 (LBG 17 X CO 5)

The estimate of additive genetic variance (D) in combining ability analysis was more than dominant genetic variance (H_1) indicating the predominance of additive gene action for this trait. Abdul Ghaffor and Zahoor Ahmed (2005) and Yashpal *et al.*, 2015 found additive type of gene action for number of pods per plant. The cross P_1 x P_4 (-9.09) had the lowest relative heterosis and the hybrid P_2 x P_1 (43.44 percent) had the highest relative heterosis for number of pods per plant. The hybrids P_2 x P_1, P_3 x P_1, P_4 x P_2, P_3 x P_2, P_1 x P_2, P_2 x P_3, P_4 x P_1, P_1 x P_3, P_3 x P_4, P_2 x P_4 and P_4 x P_3 recorded highly significant positive relative heterosis. P_1 x P_4 (-9.09 percent) only showed highly significant negative relative heterosis. Heterobeltiosis ranged between -4.11 (P_4 x P_1) to 40.48 percent (P_2 x P_1) and with this six hybrids recorded highly positive and significant heterobeltiosis such as P_2 x P_1, P_1 x P_2, P_3 x P_1 and P_3 x P_2. Out of 12 hybrids, a total of three hybrids showed highly negative significant heterobeltiosis. Hybrids P_3 x P_4 and P_4 x P_1 showed significant positive heterosis over better parent. Standard heterosis ranged from -6.69 (P_3 x P_2) to 3.95 percent (P_4 x P_2). Hybrids showing highly significant and negative heterosis over standard check were P_1x P_4, P_1 x P_2, P_1 x P_3, P_2 x P_4, P_2 x P_3, P_2 x P_1 and P_3 x P_2 and P_4 x

P_2 and P_3 x P_4 showed positive significant heterosis (Table 6).

The range for this Number of seeds per pod varied from 6.02 (P_2) to 6.84 (P_4). The mean value for this trait was 6.07. Among the parents P_4 alone showed significantly superior mean performance than the grand mean for this trait. The variation for this trait ranged from (6.19) P_1 x P_3 to (7.29) P_3 x P_1. The grand mean for this trait was (6.07). Out of 12 hybrids, P_3 x P_1 alone registered significantly more number of seeds per pod with that of the grand mean (6.62). The *gca* effects for number of seeds per pod ranged from P_1 (-0.056) to P_4 (0.099) in the parents. Among the four parents all the traits showed non-significant *gca* effects. The *sca* effects for seeds per pod ranged from -0.32 (P_4 x P_2) to 0.43 (P_2 x P_3). The only three crosses P_2 x P_3 alone showed significantly positive *sca* effects and P_3 x P_1 and P_4 x P_2 exhibited significant negative effect for this trait. The cross (P_3 x P_1) had the highest value for all the three types in this two heterosis for the trait seeds per pod (20.93 and 20.36 percent) respectively. The estimate of dominance genetic variance (H_1) was greater than additive genetic variance (D). This showed preponderance of dominance gene action for this trait. Vaithiyalingam *et al.,* (2002), Barad *et al.,* (2008) and Baradhan and Thangavel (2011), Thamodharn *et al.,* (2016) suggested the importance of non-additive gene action in determining this character. The importance of additive gene action for number of seeds per pod was confirmed by Khattak *et al.,* (2001), Pooran Chand and Raghunadha Rao (2002), Srividhya *et al.,* (2005), Isha Parveen *et al.,* (2013) and Thamodharn *et al.,* (2016). Both additive and non-additive type of gene action for determining this character was supported by Jahagirdar (2001) and Singh *et al.,* (2007). The hybrid (14.33 percent) P_3 x P_2 showed the lowest relative heterosis and the hybrids namely P_3 x P_1, P_2 x P_3 and P_3 x P_1 recorded highly significant positive relative heterosis. The lowest percentage of heterobeltiosis was observed in the hybrid P_2 x P_3 (13.45 percent). Three hybrids recorded highly significant and positive heterobeltiosis *viz.,* P_3 x P_1, P_3 x P_2 and P_2 x P_3 over the better parent (Table 6).

Hundred seed weight varied from 4.63 (P_2) to 5.91g (P_4). The parent P_4 alone exhibited significantly more hundred seed weight than the grand mean (5.07 g). The highest value for this trait was registered by the hybrid (6.03 g) P_4 x P_2 and the lowest by the hybrid P_3 x P_4 (4.78 g). Out of 12 crosses, only two hybrids showed significantly more seed weight over the grand mean value (5.47 g). The range for this trait was from P_3 (-0.068) to P_4 (0.236). Positive and significant *gca* effects was observed in P_4. Among the parents, P_2, P_1 and P_3 registered non-significant *gca* effect for this trait. The minimum and maximum *sca* effects were recorded in -0.22 (P_4 x P_2) and 0.56 (P_3 x P_2). With this trait the hybrids P_3 x P_2, P_1 x P_3, P_3 x P_1 and P_2 x P_4 recorded significant and positive *sca* effects and the cross P_4 x P_3, P_2 x P_1, P_4 x P_1 and P_4 x P_2 showed significant and negative *sca* effects for this trait. The heterosis percentage over mid parent varied from – 12.31 (P_3 x P_4) to 19.73 percent (P_1 x P_3). The combining ability analysis clearly revealed the major role of non-additive gene action governing this character since H_1 was higher than D. Govindaraj and Subramanian (2001), Vaithiyalingam *et al.,* (2002), Pooran Chand Jayapradha *et al.,* (2005), Thangavel (2011), Bhagirathram *et al.,* (2013) and Tantasawat *et al.,* (2015) were of the opinion that 100 seed weight was controlled by non-additive gene action. However, Indrani Dana and Das Gupta (2001), Abdul Ghaffor and Zahoor Ahmed (2005) and Saif Ullah Ajmal *et al.,* (2007) indicated that this character was controlled by additive gene action.Five hybrids *viz.,* P_1 x P_3, P_2 x P_1, P_3 x P_2 and P_4 x

P_2 recorded highly significant and positive relative heterosis and (-12.31 percent) P_3 x P_4 alone showed highly significant and negative relative heterosis. Heterobeltiosis ranged between -13.59 (P_1 x P_4) and 19.13 percent (P_1 x P_3) with four hybrids this two hybrids P_3 x P_4 and P_1 x P_4 showed highly significant and negative heterobeltiosis over better parent. The standard heterosis over a standard variety ranged between -13.59 (P_1 x P_4) and 10.72(P_3 x P_1).The hybrids namely P_3 x P_4, P_1 x P_2, P_2 x P_3 and P_1 x P_4 recorded highly significant and negative standard heterosis. Hybrid P_3 x P_1 recorded significant positive standard heterosis (Table 7).

The range for protein content was from 16.17 (P_2) to 20.05 percent (P_1). The grand mean for this trait was 18.32 percent. The parent $P_1$was showed the maximum protein content followed by P_4 and P_2 recorded significantly positive mean performance than the grand mean for this trait. Protein content showed a wide range, from (17.14) P_1 x P_3 to (21.15 percent) P_4 x P_2. Out of 12 hybrids, seven hybrids exhibited significantly superior mean values than the grand mean (20.26 percent). Protein content of parents varied from P_3 (-0.216) to P_4 (0.554) (Table 11). Positive and significant *gca* effect was registered only in P_4 and other two parents P_2 and P_3 exhibited negatively significant *gca* effects for this trait. The hybrids had the lowest and the highest *sca* effects of -0.54 (P_4 x P_3) and 1.44 (P_4 x P_1). Hybrides P_4 x P_1, P_2 x P_4, P_2 x P_3, P_2 x P_1 and P_3 x P_4 showed significant and positive *sca* effects. Out of 12 hybrids, a total of five crosses registered significant and negative *sca* effects. The H_1 value was higher than D. This inferred the role of non-additive gene action for this trait. Anbumalarmathi *et al.,* (2004) and Barad *et al.,* (2008) also observed predominance of non-additive gene action in controlling this trait. Aher *et al.,* (2001) and Pooran Chand and Raghunadha Rao (2002) suggested that the character was controlled by additive type of gene action. The relative heterosis for this trait ranged from-9.09 (P_1 x P_3) to 20.88 percent (P_3 x P_2) with five hybrids P_3 x P_2, P_4 x P_2, P_2 x P_4, P_4 x P_3 and P_3 x P_1 recorded highly significant and positive relative heterosis and the hybrids P_4 x P_1 and P_1 x P_3 recorded highly significant negative heterosis over mid parent. The lowest and highest value for better parent heterosis was shown by the hybrids P_1 x P_2 (-6.53) and P_3 x P_2 (14.76 percent) respectively and the crosses which showed highly significant and positive heterosis were as follows P_3 x P_2, P_4 x P_2 and P_4 x P_3 and four hybrids registered highly significant and negative heterosis over better parent. Standard heterosis varied between -4.97 (P_3 x P_4) and 5.48 percent (P_4 x P_2) and six hybrids showed highly significant and positive heterosis, P_3 x P_4 alone recorded significantly negative heterosis and one cross P_4 x P_2 recorded highly significant positive heterosis over the check variety (Table 7).

The trait single plant yield ranged from 7.13 (P_2) to 10.06 g (P_4). The mean value for this trait was 8.69 g. The parents P_2 and P_4 registered significantly higher seed yield to their mean (Fig. 3). This trait also showed wide a range, which was from 8.29 (P_1x P_2) to 20.69 g (P_4 x P_3) and closely followed by the cross P_3 x P_4. Among the 12 hybrids studied, 11 hybrids showed significantly superior mean performance when compared to grand mean (14.19g). The parent P_1 had the lowest value of (-0.702), P_4 while exhibited the highest value of (1.997) for the *gca* effects. The parents P_4 and P_3 had significant and positive *gca* effects, and the parents P_2 and P_1 recorded significant and negative *gca* effects for this trait. The *sca* effects for yield ranged from -0.38 (P_4 x P_2) to 3.63 (P_3 x P_4). Five hybrids recorded significant and positive *sca* effects and the six hybrids recorded negative and significant *sca* effects for single plant yield. This was supported by the earlier reports of Govindaraj and Subramanian

(2001), Pooran Chand and Raghunadha Rao (2002), Vaithiyalingam *et al.,* (2002), Anbumalamathi *et al.,* (2004), Abdul Ghaffor and Zahoor Ahmad (2005), Kachave *et al.,* (2015) and Tnamodharn *et al.,* (2016), whereas the importance of additive gene action for seed yield was suggested by Aher *et al.,* (2001), Abdul Ghaffor and Zahoor Ahmad (2003) and Srividhya *et al.,* (2005). Khattak *et al.,* (2001), Indrani Dana and Das Gupta (2001), Singh *et al.,* (2007) and Yashpal *et al.,* (2015) reported both additive and non-additive type gene action for single plant yield. The cross (P_1 x P_3) showed the lowest value of heterosis for all the three traits this two for yield (-7.85 and -17.56 percent). Simultaneously hybrid (P_4 x P_3) recorded the maximum heterosis value for all the three bases (121.71, 106.97 and 105.73 percent). 11 crosses recorded highly significant and positive relative heterosis over mid parent. The crosses which showed highly significant and positive heterobeltiosis were P_4 x P_3, P_3 x P_4, P_4 x P_1, P_3 x P_1, P_3 x P_2, P_4 x P_2, P_1 x P_4, P_2 x P_1, P_2 x P_4, P_1 x P_3 and P_2 x P_3. Hybrids P_1 x P_2 recorded highly significant negative heterobeltiosis. P_4 x P_3, P_3 x P_4, P_4 x P_1, P_3 x P_1, P_1x P_4, P_4 x P_2, P_2 x P_4, P_3 x P_2, P_2 x P_1 and P_1 x P_3 were the hybrids showing highly significant and positive standard heterosis over the standard variety and hybrids P_1 x P_2 exhibited highly significant and negative standard heterosis. High value of dominance genetic variance (H_1) than the additive variance (D) indicated that the character was determined by non-additive gene action (Table 7) (Figs. 7, 8).

Among the hybrids, LBG 17 x CO 5 recorded significant standard heterosis for 10 traits except for number of seeds per plant. The hybrid VBN 2 x LBG 17 recorded desirable standard heterosis for eight traits except number of branches per plant and single plant yield and VBN 2 x CO 5 showed desirable standard heterosis for eight traits except 100 grain weight and protein content (Table 8 and 9). It was followed by VBN 4x VBN 2 and VBN 4 x LBG 17 which showed significant standard heterosis for eight traits except number of branches per plant, pod length and 100 grain weight (Plate 1, 2 & 3). Similar results were also reported by Jiji Joseph and Santhoshkumar (2000) for plant height and number of branches per plant, Loganathan *et al.,* (2001) and Barad *et al.,* (2008) for number of seeds per pod (Table 10).

The phenotypic coefficient of variation ranged from 2.84 to 30.07 per cent. Higher percent of PCV was recorded by single plant yield followed by, number of cluster per plant, number of branches per plant, plant height, number of pods per plant and 100 grain weight (Table 4) (Fig. 1). The lowest value of PCV was recorded by days to 50 percent flowering. The genotypic coefficient of variation ranged from 2.15 to 29.90 per cent. Higher per cent of GCV was recorded by single plant yield followed by number of clusters per plant, plant height, number of pods per plant and number of branches per plant (Fig. 2). The lowest value of GCV was recorded by days to 50 percent flowering. The heritability ranged from 31.54 to 99.30 per cent. The highest value of heritability was recorded in plant height followed by single plant yield, number of cluster per plant, number of pods per plant, days to maturity and protein content. The lowest percentage of heritability was recorded by number of seeds per pod. The genetic advance varied from 3.35 to 61.26 per cent. The highest value of genetic advance was observed in single plant yield followed by number of cluster per plant, plant height, number of pod per plant and number of branches per plant. The lowest value of genetic advance was recorded in days to 50 per cent flowering.

Among the 12 crosses, three hybrids showed complete resistance against YMV with high

yield performance. The hybrids are VBN 4 x VBN 2, VBN 2 x VBN 4 and VBN 2 x LBG 17. So the segregants from these crosses may be utilized for recombination breeding for hybridization and YMV resistant (Table 13). Four hybrids reacted as moderately resistant to YMV such as VBN 4 x LBG 17, VBN 2 x CO 5, LBG 17 x VBN 4 and CO 5 x VBN 2. Moderately susceptible reactions recorded by the hybrids were VBN 4 x CO5, LBG 17 x CO 5 and CO 5 x VBN 4. The hybrids *viz.*, LBG 17 x VBN 2 and CO 5 x LBG 17 was the two crosses showing susceptible reaction against YMV. Similar results were also reported by Shamim *et al.,* (2014) and Peeta *et al.,* (2016). From the foregoing discussion it may be concluded that the pod length and number of branches per plant expressed dominant gene action followed by number of pods per plant additive gene action found to be best selection criteria for yield improvement in blackgram as revealed by path analysis. Similar result was reported by Prasanthi *et al.,* (2013). The parents for general combiners and the cross involving the same will expect through useful segregants also the study revealed that the hybrid LBG 17 x CO 5 and VBN 2 x LBG 17 found to be superior which combiners yield and quality characters and this hybrids can be exploited for heterosis breeding. Among the above hybrids VBN 2 x LBG 17 which is having the parents resistance for YMV and powdery mildew respectively, expect through more yield combined with resistance and can be commercially exploited.

Yellow Mosaic Virus disease (YMV)

The Yellow Mosaic Virus Disease (YMV) incidence was recorded on all the plants based on the visual scores on 50th day while the susceptible check C05 recorded scale 6.9. The classification was made into scales 1 – 9 as follows based on the scale adopted by Singh *et al.,* (1988).

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