DIALLEL ANALYSIS IN RICE BEAN
(Vigna umbellata (Thunb.) Ohwi & Ohashi)

By
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THESIS
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1999

*Dedicated
to
my Parents*

DECLARATION

I hereby declare that this thesis entitled, " Diallel analysis in ricebean (*Vigna umbellata* (Thunb.) Ohwi & Ohashi)", is a bonafide record of research work done by me during the course of research and that the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title of any other university or society.

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Certificate

Certified that this thesis entitled, " Diallel analysis in ricebean

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independently by Ms. Preeti. S.V. under my guidance and supervision and that

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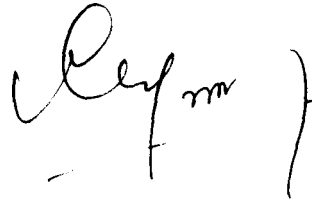and Genetics,
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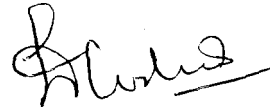
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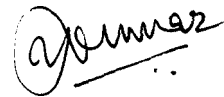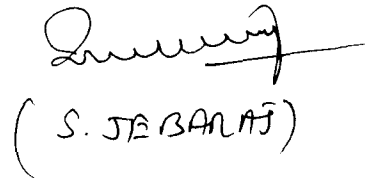
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Introduction

INTRODUCTION

India holds rich diversity in grain legumes. The grain legumes assume great importance as a source of protein rich food particularly in the tropics. Apart from traditional tropical pulses, many other non-traditional under-utilised legumes such as winged bean, marama bean, bambara nut and ricebean have recently gained attention as supplementary food crops (Chandel and Singh, 1984). These beans possess immense potential due to their high nutritional quality, high grain yield and their multi-purpose usage as food, animal feed, cover crop, green manure and as soil enrich.

Rice bean *(Vigna umbellata* (Thunb.) Ohwi & Ohashi Syn. *Phaseolus Calcaratus* Roxb.) is a native of South and South East Asia. As a cultigen, ricebean occurs in India, Burma, Malaysia, China, Korea, Indonesia and Philippines. In India, its distribution is mainly confined to the tribal regions of North Eastern hills, Western and Eastern ghats in peninsular India, often in hilly tracts (Arora *et al.,* 1980).

Rice bean is known by different local names like Sutri in Hindi and Gaimung in Bengali . Ricebean can be grown upto an elevation of 1800m above mean sea level, and is drought tolerant. In North India, it is grown during the Kharif and is photosensitive . In comparison with soyabean, rice bean is rich in essential aminoacids like lysine, methionine, histidine and minerals like iron.

Regarding the morphology, ricebean is an annual crop with stem erect/suberect or flexuose, tending to be viny usually clothed with fine deciduous deflexed hairs. The leaflets are entire or lobed, the infloresence is a raceme. Flowers are medium sized, and yellow in colour. The pods are glabrous, cylindrical and contain 8-12 seeds.

Similar to other *Vigna sp.* of Asian origin, ricebean is also truly diploid species with $2n = 2x = 22$ chromosomes. However, the primary base number for *Vigna umbellata* is $n = 11$. Rice bean flower is cleistogamous in nature and hence enforces self fertilisation.

In the pursuit of rendering a permanent genetic improvement in crops, it is necessary to possess an adequate knowledge of gene action, especially components of genetic variance(ie., additive, dominance and epistasis) and combining ability. Sprague and Tatum (1942) developed the concept of combining ability and coined the two terms: (i) general combining ability and (ii) specific combining ability. The concept of combining ability is especially useful in connection with 'testing' procedures which involve the study and comparison of the performance of parents in hybrid combinations. Several methods of progeny testing are available where different kinds of progenies are produced following different mating designs such as line x tester, diallel, partial diallel, etc.

Diallel analysis has been extensively used in both self and cross-pollinated species. Diallel cross refers to all possible crosses among 'n' lines, and the analysis of such a set of crosses is known as diallel analysis. In the present study, such an attempt of diallel analysis has been made, to understand the nature of gene action and to get reliable information on the components of variance and on general combining ability and specific combining ability variances and effects.

Review of literature

REVIEW OF LITERATURE

Rice bean, a potential grain legume crop, is one of the non-traditional under-utilised legumes, which has been recently gained attention as a supplementary food crop. Rice bean possesses immense potential due to its nutritional quality, high grain yield and its multipurpose usage as food, animal feed, cover-crop, green manure and as soil enrichers. It has been found that this crop possesses rich genetic diversity in its enormous forms, which provides ample scope for breeding. Information on the combining ability of the divergent parents involved in hybridisation and also on the nature of gene action play an important role in the production of superior hybrids. A review of the reports on research already made in the above context is being attempted here. However, the available published works on this crop is limited. Hence this review is extended to aspects of similar nature in other pulse crops also.

2. 1. Combining ability

Information on the general combining ability and specific combining ability with respect to parents and hybrids will facilitate the breeder to plan the breeding programmes effectively.

Deshmukh and Manjare (1980) worked on the combining ability in a diallel cross in green gram and observed highly significant variances due to general combining ability and specific combining ability (GCA and SCA) for number of pods per plant.

Pillai (1980) conducted a quantitative genetic study of yield and its components in blackgram, and observed high general combining ability for plant height and high specific combining ability for seed yield.

Chauhan and Joshi (1981) analysed a half diallel cross of eight cowpea varieties and revealed that both GCA and SCA were important, but the magnitude of GCA seemed to be comparatively much higher.

A study on the inheritance of seed yield components in rice bean revealed that, SCA was more significant for number of seeds per pod (Das and Dana, 1981).

Srivastava (1982) estimated that, both GCA and SCA were highly significant in pea for plant height, pod length, number of pods per plant, number of seeds per pod, number of branches per plant, 100 seed weight and grain yield per plant.

A diallel analysis in blackgram by Malhotra (1983) revealed the significance of GCA for number of seeds per pod and the importance of both GCA and SCA for 100 seed weight and seed yield.

Combining ability of a diallel set of mutant pea was studied by Rao *et al.*(1985) and found that, specific combining ability was more significant for days to maturity, number of pods per plant, 100 seed weight and seed yield.

In a diallel analysis of five greengram varieties by Wilson *et al.* (1985) revealed that, both specific and general combining ability was significant for number of seeds per pod.

Chowdhury (1986) conducted the combining ability analysis for seed yield and its components in a half diallel cross in greengram, and reported that both GCA and SCA were significant for seed yield per plant and number of pods per plant.

Singh and Dabas (1986) studied inheritance of yield and its components in cowpea and revealed that specific combining ability was significant for grain yield and general combining ability for 100 seed weight.

A 8 x 8 half diallel cross in blackgram revealed that both GCA and SCA were significant for pod length (Dasgupta and Das, 1987).

Combining ability analysis involving nine diverse parents and their 36 F_1 crosses in pigeonpea, revealed that cultivars - 13428-17-1-9 and 4839-3 were the best general combiners for grain yield per plant. The crosses involving diverse types of parents and showing high specific combining ability effects for grain yield per plant could be successfully utilized for exploitation in this crop (Mahetre *et al.*, 1988).

In mungbean, Patil *et al.* (1988) reported that general combining ability was significant for plant height, number of pods per plant, number of seeds per pod, pod length, root weight, seed yield, 100 seed weight, and protein content while specific combining ability was significant for number of branches per plant.

Natarajan *et al.*(1989) found that the SCA was much higher than GCA for seed yield, plant height, and number of pods per plant in mungbean.

Das and Dana (1990) studied combining ability in a diallel set of crosses in rice bean and reported that general combining ability was more significant for plant height.

Pathak *et al.* (1990) revealed that both general and specific combining ability were significant for plant height, pod length, seed yield, and 100 seed weight in mungbean.

Thiyagarajan *et al.* (1990) while analysing the combining ability and inheritance in cowpea suggested that specific combining ability was more significant in the number of branches per plant.

In a combining ability analysis in pea, Singh *et al.*(1991) reported that both GCA and SCA were highly significant for number of pods per plant, number of seeds per pod and grain yield per plant.

Combining ability for grain yield per plant, number of branches per plant, number of pods per plant and number of seeds per pod was estimated by Saxena and Sharma (1992) in a diallel set of eight mungbean varieties.He found that both general and specific combining ability were significant for all the above characters.

Twenty F_1's derived from four lines and five testers in mungbean were evaluated and their combining ability were studied by Naidu and Satyanarayana (1993 a). It was found that GCA was more important for days to maturity, number of pods per plant and seed protein content. Specific combining ability was more significant for plant height, 100 seed weight and seed yield. Both general and specific combining ability were important for number of branches per plant, pod length and number of seeds per pod. High yielding heterotic crosses were obtained from parents with high general combining ability.

A combining ability analysis of a 4 x 3, line x tester analysis in cowpea revealed that, specific combining ability was more significant for days to maturity, plant height, pod length, number of seeds per pod, 100 seed weight and grain yield per plant, while general combining ability was more significant for number of primary branches per plant and number of pods per plant (Thiyagarajan et al., 1993).

Combining ability studies in mungbean conducted by Tiwari et al. (1993) reported that the best general combiners were MeTM 11/395 for earliness, PS11

Sekhar *et al.* (1994) worked on a set of 8 x 8 diallel crosses excluding reciprocals in mungbean, reported that ML 267 x K851 cross is the best specific combiner for grain yield per plant and pods per plant.

Shanmughasundaram and Rangaswamy (1994) reported significant differences in general combining ability and specific combining ability in both F_1 and F_2 generations. General combining ability estimates indicated that CO-4, CO-5 and T9 were good general combiners for grain yield per plant.

Aravindan *et al.* (1995) evaluated crude protein content in fodder cowpea and found that, CS-55 performed best for crude protein content (23.6%) with the crosses, CS 55 x CO-5 and IFC 901 x C 152 giving values of 24.6 % and 31.5% respectively.

Information on combining ability in a 10 x 10 diallel cross (excluding reciprocals) in cowpea revealed that both GCA and SCA were hightly significant for plant height, number of branches, seed yield, number of pods per plant, number of seeds per pod, and days to maturity (Sawant, 1995).

In cowpea, Aravindan and Das (1996) reported that variances due to specific combining ability were predominant for seed yield per plant.

In ricebean, variances due to general and specific combining ability were highly significant in F_1 and F_2 generations. General combining ability was higher than

for number of pods per plant and seed yield per plant, EC 213012 for number of branches per plant and CO-2 for protein content. The cross McTM 11/395 x EC 213012 showed highly significant specific combining ability for earliness, number of branches per plant, seed yield per plant and protein content.

Malar (1994) while studying the combining ability analysis in greengram reported that specific combining ability was greater in magnitude than general combining ability for plant height, number of branches per plant, number of pods per plant, number of seeds per pod, pod length, root weight, seed yield, 100 seed weight, and protein content.

In a combining ability study on sprout quality traits in mungbean, Rosaiah et al. (1994) revealed that, estimates of GCA were higher than those due to SCA for 100 seed weight and seed yield. Lines Pusa 105 and K851 had good general combining ability for 100 seed weight and seed yield. Pusa 105 x PD M54, Pusa 105 x LGG 410, K 851 x LGG 410 and K851 x PDM 54 were the best specific combinations.

Ten greengram cultivars were crossed in a half diallel to generate 45 hybrids. Mean squares due to general combining ability for protein content was higher than those due to specific combining ability. Best general combiners for protein content were ML 65, J 45 and ML131 (Sandhu et al., 1994).

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In ricebean, variances due to general and specific combining ability were highly significant in F_1 and F_2 generations. General combining ability was higher than

specific combining ability for plant height, number of branches, number of pods per plant, seed yield, 100 seed weight, days to flowering, days to maturity, root weight, nodule weight and protein content (Singh and Singh, 1996).

Halkude *et al.* (1996) worked on combining ability analysis, in a 8 x 8 half diallel of green gram and reported that most of the parents which showed good GCA for seed yield were poor general combiners for 100 seed weight.

Ponmariammal and Das (1996) reported high GCA for days to flowering and high SCA for plant height, number of branches and crude protein content in cowpea.

In a 8 x 8 diallel cross set in cluster bean, Mathur and Mathur (1997) reported that both general and specific combining ability were highly significant for seed yield, days to flowering, plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, days to maturity and 100 seed weight. However, general combining ability was higher than specific combining ability for all the above traits.

Bhardwaj and Kohli (1998) in a combining ability analysis in pea reported that both general and specific combining ability were important for number of pods per plant, number of seeds per pod and seed yield per plant.

2.2. Gene Action.

Hayman's (1954) graphical and numerical approach to diallel analysis provides information on several valuable aspects of the genetic make up of a quantitative

character such as the adequacy of additive-dominance model, average degree of dominance involved in the action of genes, preponderence of dominant and recessive genes among the parental lines, symmetrical or asymmetrical distribution of genes with positive and negative effects on the attribute, etc.

In a 6 x 6 diallel cross of blackgram, the magnitude of specific combining ability was very high suggesting the predominance of non-additive gene action for number of pods per plant, while predominance of additive gene action was observed for plant height (Sagar and Chandra, 1977).

Preponderence of additive gene action was reported by Chaudhary (1979) for days to flowering, plant height, and number of branches per plant.

Lal and Waldia (1980) while studying combining ability in blackgram, reported that both additive and non-additive genetic variances were important for number of branches per plant and number of seeds per pod. However non-additive gene effects were of greater importance for both traits.

Basheeruddin and Nagur (1981) studied the combining ability analysis in greengram and revealed that SCA was much higher than GCA indicating operation of non-additive gene action for seed yield, plant height, and number of pods per plant.

Das and Dana (1981) carried out inheritance studies of seed yield components in ricebean and reported that non-additive gene effect was significant for number of seeds per pod, indicating that dominance component was more important.

Inheritance studies by Singh (1981) in cluster bean, revealed that ratio of GCA and SCA was more than unity for seed yield, days to flowering, plant height, pod length, number of seeds per pod, days to maturity and 100 seed weight, indicating preponderence of additive gene action.

Gupta (1982) in pea, reported that the ratio between GCA and SCA was found to be below one for crude protein content indicating non-additive gene action.

Marangappanavar (1984) estimated the gene action in cowpea and reported that additive, dominance and epistatic gene action were in operation for plant height.

In cowpea, Hebbal (1985) reported that variances due to specific combining ability were predominant for seed yield, indicating the predominance of non-additive gene action.

While studying the genetic architecture of seed yield and its components in cowpea, Neupane(1986) reported that additive, dominance and epistatic gene action was found to be in operation for plant height.

In a study conducted on the combining ability in cowpea, it was found that additive and epistatic gene action was in operation for days to maturity and 100 seed

weight, while non-additive gene action was controlling pod length (Patil and Bhapkar, 1986).

Patil and Patil (1986) reported in cowpea, additive variance for the characters, plant height, pod length, 100 seed weight, and seed yield, while dominance variance was reported for number of pods per plant. Both general and specific combining ability was significant for number of seeds per pod, but since, the ratio between GCA and SCA was more than one, it indicated additive gene action for that character.

Patil et al. (1987) while conducting the variability studies in some quantitative characters in mungbean, revealed that additive gene action was operative in governing the characters, viz., days to flowering, days to maturity, plant height and number of branches per plant.

While studying the combining ability analysis for yield and its components in blackgram, Singh et al. (1987) reported that, additive and non-additive components were important for the inheritance of the characters, viz., grain yield and 100 seed weight.

In blackgram, the characters like days to flowering, days to maturity, plant height and number of branches per plant were governed by additive gene action (Waldia et al., 1987).

Haque *et al.* (1988) studied the combining ability analysis in urd bean, and reported that seed yield per plant was governed by both additive and non-additive gene action. Number of branches per plant, 100 seed weight and plant height were predominantly controlled by additive genes, while days to maturity, number of pods per plant and number of seeds per pod were controlled by non-additive gene action.

In a diallel analysis of cowpea, conducted by Arunkumar (1989), it was reported that, additive, dominance and epistatic gene action governed plant height.

Seenaiah *et al.* (1989) reported that in blackgram, additive and non-additive components were important for the inheritance of grain yield and 100 seed weight.

In a combining ability analysis in pea, Singh and Singh (1989) reported that both general and specific combining ability were highly significant for number of pods per plant, number of seeds per pod and seed yield per plant. So both additive and non-additive components were important, but additive variance was more significant for the above traits.

While conducting studies on the gene effects in the metric traits in rice bean, Das and Dana (1990) reported that additive genetic variance was higher than dominance variance for plant height.

In a 8 x 8 half diallel analysis in blackgram, Gupta and Das (1991) reported that, both additive and non-additive genetic variances were important for number

of branches per plant and number of seeds per pod. However, non-additive gene effects were of greater importance for both characters.

Gowda *et al.* (1991) in a study on the genetic parameters in intervarietal crosses of cowpea, suggested predominance of additive gene effects in the expression of days to flowering, days to maturity, plant height, number of seeds per plant and 100 seed weight. Non-additive gene effects were found to be predominant for seed yield per plant.

Kalia *et al.* (1991) observed significant mean squares due to specific combining ability indicating non-additive gene action for seed yield per plant, while estimating combining ability for seed yield and its components over environment in blackgram.

While conducting studies on gene effects and heterosis in forage cowpea by Sanghi and Kandalkar (1991) it was observed that the ratio between general and specific combining ability was below one indicating the predominance of non-additive gene action for plant height.

In blackgram, additive and non-additive components were important for the inheritance of grain yield and 100 seed weight, while non-additive component was important for plant height, number of pods per plant and number of seeds per pod (Sood and Gartan, 1991).

A study was conducted by Govindaraj and Subramanian (1992) in blackgram to assess the combining ability and gene action of the parents and hybrids. The ratio between the general and specific combining ability indicated that the characters viz., plant height, primary branches per plant, number of pods per plant, pod length, number of seeds per pod, 100 seed weight and seed yield, were found to be predominantly controlled by non-additive gene action.

Combining ability analysis in a 6 x 6 diallel cross of chickpea indicated that both additive and non-additive types of gene action were important for grain yield per plant, number of pods per plant and number of seeds per pod. Predominance of additive gene action was also observed for 100 seed weight and days to maturity. Normal pedigree method for exploitation of additive genetic variability and the diallel selective mating system for population building have been suggested for improvement of this crop (Shinde and Deshmukh, 1992).

Jayarani (1993) in cowpea reported that plant height was governed by both additive and non-additive components.

Seenaiah *et al.* (1993) conducted combining ability studies in urd bean and observed that non-additive gene action was more important than additive gene action for seed yield, number of pods per plant, pod length and number of seeds per pod.

In a combining ability study in adzuki bean, Chaudhary *et al.* (1994) reported that additive gene action was operative in governing the characters, viz., days to flowering, days to maturity, plant height, number of branches per plant.

Sawant (1994) in cowpea, reported that plant height, number of branches per plant, number of pods per plant, seed yield, number of seeds per pod and days to maturity were controlled by at least one group of dominant genes.

In pea, general and specific combining ability variances were highly significant (Singh *et al.,* 1994 a). However, additive gene effects were predominant for plant height, pod length, number of pods per plant, number of seeds per pod, number of branches per plant, 100 seed weight, and seed yield per plant.

In cowpea, Madhusudan *et al.* (1995) observed that, additive and non-additive genetic variances were important in the inheritance of plant height, days to maturity, number of pods per plant, seed yield, number of seeds per pod, and protein content.

Mallikarjun *et al.* (1995) reported additive, dominance and epistatic gene action for plant height, number of pods per plant, seed yield, and protein content in cowpea. Additive and epistatic gene action was observed for days to maturity and 100 seed weight, while additive gene action governed for the character, pod length and epistatic gene action for number of branches per plant.

Heterosis and combining ability studies in cowpea was conducted by Selvalakshmi (1995) and reported that plant height, number of branches per plant, number of pods per plant, pod length, 100 seed weight and seed yield were controlled by non-additive gene action, while number of seeds per pod was governed by additive and non-additive gene action.

Singh and Singh (1996) conducted genetic analysis of 3 mung bean crosses involving parents with different photothermal response for grain yield and component traits. They observed that the characters, number of pods per plant, days to flowering, seed yield per plant and plant height were governed predominantly by additive genes.

Singh and Singh (1996) in a combining ability study for yield and its components in rice bean, reported that both general and specific combining ability were highly significant indicating importance of additive and non-additive gene action for all the characters, viz., plant height, number of branches per plant, days to flowering, number of pods per plant, number of seeds per pod, 100 seed weight, seed yield, days to maturity, and nodule weight. However, GCA was higher than SCA for all the above traits, except number of seeds per pod.

Genetic information for a set of 22 lines of adzuki bean obtained from a line x tester cross and triple test cross revealed that both additive and non-additive genetic variances were important for plant height, number of branches per plant, number of pods per plant, number of seeds per pod and seed yield (Chaudhary,1997).

Paralkar *et al.* (1997) while analysing the degree of dominance for yield and its components in blackgram reported, both additive and dominance gene effects for seed yield per plant. As regards relative magnitude of additive - dominance gene effects, higher values of (D) than those of (H) were observed for days to maturity, number of primary branches per plant, number of pods per plant, number of seeds per pod and 100 seed weight. Dominance (H) gene effects were found to be more important for plant height.

In a diallel analysis for yield and its components in blackgram, Shrivastava and Rao (1997) revealed that additive genetic variance had an important role in the expression of days to maturity and plant height. However, the characters, number of pods per plant, 100 seed weight, length of pod, number of seeds per pod and seed yield were under the control of additive and non-additive genetic variances. They concluded that, dominant genes were responsible for the expression of the characters, plant height, days to maturity, number of pods per plant, 100 seed weight and pod length.

In pigeonpea, Manivel and Rangaswamy (1998) observed that both additive as well as non-additive effects were predominant for seed yield per plant, plant height and number of pods per plant, while non-additive effects was predominant only for number of branches per plant.

2.3 Heterosis

Reddy and Sreeramulu (1982) estimated heterosis for yield and its components in greengram and reported positive and significant heterosis for number of pods per plant, seed yield per plant and negative heterosis for 100 seed weight.

In a heterosis and combining ability study in cowpea, Zaveri et al. (1983) reported the highest heterosis for number of pods per plant, significant heterosis for seed yield and 100 seed weight, and low heterosis for pod length.

Shanmugam (1984) in greengram reported that magnitude of heterosis was high for plant height, number of pods per plant and seed yield.

From a study of 6 x 6 diallel cross in cowpea, Patil and Shete (1987) reported positive heterosis of 89 % over better parent for number of pods per plant. Mylsamy (1988) in cowpea, reported positive heterosis over mid parent for pod length.

Heterosis for dry matter components in mungbean was studied by Natarajan (1989) and observed significant positive heterosis of seed yield over better parent and significant magnitude of heterosis in negative direction was observed for root weight.

Lodhi et al. (1990) conducted heterosis studies for fodder yield and quality characters in cowpea and reported both positive and negative heterosis for days to flowering.

Maximum heterosis over better parent was observed for number of pods per plant, number of seeds per pod, seed yield per plant, and pod length in urd bean, while negative heterosis was observed for days to flowering, plant height and 100 seed weight (Rao,1991).

While studying heterosis in cowpea, Savithramma (1991) recorded positive heterotic values for plant height.

Six mungbean cultivars were crossed in a diallel mating pattern excluding reciprocals and heterosis studies were conducted by Reddy *et al.* (1992). Reports of this study revealed positive heterosis for days to flowering, days to maturity, number of pods per plant and seed yield.

In cowpea, it was revealed that the frequency and level of heterosis was related more to specific combining ability than to the genetic divergence of the parents (Hazra *et al.*, 1993).

Mahetre *et al.* (1993) in pigeonpea reported positive heterosis over mid and better parent for days to flowering (early flowering), days to maturity and plant height, and highly significant positive heterosis over mid parent for number of pods per plant, number of seeds per pod, seed yield per plant and number of branches per plant.

Naidu and Satyanarayana (1993 a) studied heterosis and combining ability in mungbean and observed that average heterosis over mid and better parent were positive for seed yield per plant, number of pods per plant, and number of branches per plant, and that average heterosis was negative for days to maturity. In another study about heterosis for yield and its components in mungbean, Naidu and Satyanarayana (1993 b) reported that heterosis for seed yield varied from 1.77 to 32.95% and from 8.49 to 25.81% over mid and better parent values respectively. Naidu and Satyanarayana (1993 c) reported that the average heterosis and heterobeltiosis were high for seed yield (18.83 and 7.92%), and for number of pods per plant (10.04 and 1.09%), in mungbean.

In mungbean, heterobeltiosis was significant and positive for plant height, number of pods per plant and seed yield per plant. Negative and significant heterosis was reported for 100 seed weight (Sharma and Yadav, 1993).

Bajpai *et al.* (1994) reported significant positive heterosis (9.32 to18%) for days to maturity and considerable degree of heterosis for seed yield in pigeonpea.

Damarany (1994) estimated heterosis and drought tolerance in cowpea and reported that seed yield and 100 seed weight showed high heterosis in the F_1 hybrids.

Malar (1994) reported that magnitude of heterosis was high for number of pods per plant and seed yield in greengram.

Sawant et al.(1994) worked on 45 cowpea hybrids and their 10 parents of diverse origin to investigate heterosis for seed yield and its yield components. The greatest positive heterosis over mid parent was observed for seed yield per plant (140.5%) followed by number of pods per plant (132.5%), number of branches per plant (85.6%) and plant height (73.4%).

A set of diallel crosses excluding reciprocals was made using 8 cultivars in mungbean and heterosis over mid parent and better parent for yield and yield components was recorded for 28 F_1 hybrids. In most cases, significant positive heterosis for grain yield was associated with heterosis for number of pods per plant and number of seeds per pod (Sekhar et al., 1994).

Singh et al. (1994 b) in pea reported that relative heterosis indicated considerable amount of heterosis for grain yield followed by number of seeds per pod, number of pods per plant and pod length.

Heterosis and combining ability studies in cowpea by Selvalakshmi (1995) reported significant heterosis over better parent for plant height, number of branches per plant and 100 seed weight.

Hegde et al. (1996) in mungbean reported significant heterosis over mid parent and better parent for plant height, number of branches per plant, number of pods per plant, number of seeds per pod, seed yield and days to maturity.

Bhor *et al.* (1997) reported significant heterobeltiosis for grain yield in cowpea.

High heterosis over better parent was observed in grain yield per plant in rice bean (Madal and Dana, 1998).

Reddy (1998) in greengram, reported significant positive heterosis over mid and better parent for grain yield, negative heterosis over better parent (early parent) for days to maturity and positive heterosis for number of pods per plant. Significant heterosis and heterobeltiosis were observed for number of seeds per pod, and seed yield but their magnitude and direction was low. Heterosis in grain yield was associated with heterosis in number of pods per plant and number of seeds per pod.

Materials and Methods

MATERIALS AND METHODS

The present study was taken up in the Department of Plant Breeding & Genetics, College of Agriculture, Vellayani during 1997-98 with a view to understand the gene action through combining ability analysis for yield and yield attributing characters in ricebean and to determine the extent of heterosis manifested by the hybrids.

3.1. Materials

The six parents utilized were selected from the genetic analysis of the germplasm done as per PG project entitled, "Genetic analysis of productivity and quality parameters in rice bean, *Vigna umbellata* (Thunb.) Ohwi and Ohashi," and from the outstanding varieties obtained from the germplasm collections maintained at the NBPGR Regional Station, Vellanikkara. The varieties were 3LG, 5LG,6 LG,8LG, 9LG and 100LG (LG → Long green). These varieties were selected based on their high yielding characters. These six selected parents were crossed in all possible combinations in a diallel fashion such that the experimental material consisted of parents, F_1's and reciprocals. The six parents and the 30 hybrids are listed in Table 1.

3.2. Methods

3.2.1. Intervarietal Hybridization.

The six selected parents were raised in pots during the month of August, 1997. Fifteen plants per parent were raised in separate pots so that sufficient seeds could

be obtained for each parent . At the time of flowering the parents were crossed in all possible combinations to obtain 30 hybrids. For crossing, the flower buds due to open on the next day were selected and emasculated on the previous evening. For emasculation, the rest of the flowers and buds in a branch, except for the selected bud, are removed. The stamens of the selected bud, was removed with a pair of fine forceps by gently pushing the keels apart (Plate 1). The emasculated floral branch was then bagged. Ripe anthers were collected in the following morning and pollination was done by gently pressing the ripe anthers against the stigma (Plate 2). The flowers were again bagged after pollination (Plate 3). The covers were removed a day after pollination. Pollination was done in the early morning between 6.30 and 8.00 am. For selfing also, the flowers were covered, with butter paper covers, to avoid contamination from foreign pollen. The crossed as well as selfed flowers were labelled. The labelled pods were harvested separately on maturity, and parent and hybrid seeds were collected.

3.2.2. Estimation of combining ability.

The six parents along with the 30 hybrids were laid out in a Randomised Block Design with three replications during the month of July, 1998. Ricebean being a season bound crop will come to flowering only when sown in between the month of June and August. The crop was raised with a spacing of 45 x 45cm, with 25 plants per replication. Cultural and manurial practices were done as per the package of practice recommendations (Anonymous,1996). Observations on the

Plate 1. Emasculation of the selected flower bud

Plate 2. Dusting of the pollen on the selected flower

Plate 3. Bagging of the crossed flower

Table.1. Parents and hybrids used in the 6 x 6 diallel in *Vigna umbellata* along with the treatments.

Sl.No	Name of variety/cross	Treatment Number.
1.	P1 (3LG)	T1
2.	P1xP2	T2
3.	P1xP3	T3
4.	P1xP4	T4
5.	P1xP5	T5
6.	P1xP6	T6
7.	P2xP1	T7
8.	P2 (5LG)	T8
9.	P2xP3	T9
10.	P2xP4	T10
11.	P2xP5	T11
12.	P2xP6	T12
13.	P3xP1	T13
14.	P3xP2	T14
15.	P3 (6LG)	T15
16.	P3XP4	T16
17.	P3xP5	T17
18.	P3xP6	T18
19.	P4xP1	T19
20.	P4xP2	T20
21.	P4xP3	T21
22.	P4 (8 LG)	T22
23.	P4xP5	T23
24.	P4xP6	T24
25.	P5xP1	T25
26.	P5xP2	T26
27.	P5xP3	T27
28.	P5xp4	T28
29.	P5 (9LG)	T29
30.	P5xP6	T30
31.	P6xP1	T31
32.	P6xP2	T32
33.	P6xP3	T33
34.	P6xP4	T34
35.	P6xP5	T35
36.	P6(100LG)	T36

following characters were recorded, from five plants at random in each treatment per replication for the estimation of combining ability.

3.2.2.1. Biometric observations

(i)   **Plant Height :**

The plant height on 60 th day after sowing was measured from ground level to the tip of the terminal bud and expressed in centimeters.

(ii)   **Number of branches :**

All the branches in the observational plants were counted and recorded on 60 th day after sowing.

(iii)   *Days to first flowering :*

The number of days taken for the first flower to open from the date of sowing was recorded on plot basis from individual plots.

(iv)   **Length of pods :**

The pods from individual observational plants were collected and the length measured in centimeters.

(v)   **Number of pods per plant :**

The total number of pods harvested from the observational plants were recorded.

(vi)   **Number of seeds per pod :**

The pods from observational plants were collected and the number of seeds per pod was recorded from each pod.

(vii)   Seed yield

Seed yield from each observational plant in each plot was weighed after normal drying and expressed in grams.

(viii)   100 seed weight

Hundred well dried seeds chosen at random from each treatment were weighed and expressed in grams.

(ix)   Days to maturity

The number of days taken for maturity from the date of sowing was noted for each treatment, when majority of the pods became fully dried up.

(x)   Root weight

The observational plants were uprooted without damaging roots, root portion removed, washed in water, dried and weighed which was expressed in grams.

(xi)   Nodule weight

The uprooted observational plants were taken and nodules removed by hand after cleaning the roots free of soil. Nodules from each plant were weighed and expressed in milligrams.

(xii)   Fodder acceptability

This was studied in the dairy farm of the Department of Animal Husbandary, College of Agriculture, Vellayani . For this 1 Kg fodder of each variety was given to the cattle during its usual feeding time. Those varieties consumed by cattle were taken as acceptable and others unacceptable.

(xiii)   Protein content

The seeds were oven dried at 80 ± 5 ^{0}C and ground finely in Wiley mill.
The total nitrogen was calculated employing modified microkjeldahl method
(Jackson, 1967).

Protein content of the grain was calculated by multiplying the percentage
of nitrogen by the factor 6.25 (Simpson *et al.*, 1965)

3.2.3 Statistical Techniques

Data recorded from the parents, F_i's and reciprocals were initially
subjected to analysis of variance for each character so as to detect the genotypic
differences. The characters for which genotypic differences detected were further
subjected to diallel analysis to estimate the additive components of heritable
variation. The following parameters were estimated.

(i)   Combining ability through Griffing's Approach

        - General combining ability.

        - Specific combining ability.

(ii)   D,H,E components through Hayman's approach

(iii)   Vr. - Wr graph

        -Graphical analysis of diallel cross as suggested by Hayman (1954)

3.2.3.1 Combining ability analysis

The different genotypes were subjected to combining ability analysis only
if they showed significant difference for the character under study. The analysis

was carried out according to the Method I, Model I of Griffing's approach (1956).

The combining ability analysis under this approach was made by using the following fixed effects linear mathematical model.

$$Y_{ij} = m + g_i + g_j + r_{ij} + s_{ij} + \frac{1}{bc} \sum_k \sum_l e_{ijkl}$$

where m - Population mean

g_i and g_j	=	General combining ability effects of i th and j th inbred lines respectively.
s_{ij}	=	Specific combining ability effect of ij th cross such that $s_{ij} = s_{ji}$
r_{ij}	=	Reciprocal effect such that $r_{ij} = -r_{ji}$
$\frac{1}{bc} \sum_k \sum_l e_{ijkl}$	=	Mean error effect
b	=	Number of replications
c	=	Number of observational plants
i,j	=	1,2,.............,n
k	=	1,2,.................,b
l	=	1,2,.................,c

Restrictions are imposed on combining ability effects such that $\sum_i g_i = 0$ and $\sum_i s_{ij} = 0$ (for each j) for making the estimations possible.

Combining ability analysis with 'n' parents.

Sources of variation	df	M.S.	F
General combining ability (GCA)	$(n - 1) = 5$	Mg	Mg/Me
Specific combining ability (SCA)	$\dfrac{n(n-1)}{2} = 15$	Ms	Ms/Me
Reciprocal effects	$\dfrac{n(n-1)}{2} = 15$	Mr	Mr/Me
Error	$M = (n^2 - 1)(r-1) = 70$	Me	

The combining ability effects were estimated as follows :

General combining ability effect (gca) of i [th] parent.

$$g_i = \frac{1}{2} n (Y_{i.} + Y_{.j}) - \frac{1}{n^2} Y_{..}$$

Specific combining ability effects (sca) in i x j cross

$$s_{ij} = \frac{1}{2} n (Y_{ij} + Y_{ji}) - \frac{1}{2} n (Y_{i.} + Y_{.i} + Y_{j.} + Y_{.j}) + \frac{1}{n^2} Y_{..}$$

Reciprocal effect for the i x j cross

$$r_{ij} = \frac{1}{2} (Y_{ij} - Y_{ji})$$ Where Y_{ij} is the mean value with respect to i x j cross.

$$Y_{i.} = \lesssim_j Y_{ij}, \; Y_{.j} = \lesssim_i Y_{ij} \text{ and } Y_{..} = \lesssim_{ij} Y_{ij}$$

The following standard errors are used to test the significance of the estimates.

$$\text{gca} \ : \ SE \ \hat{g_i} = \left(\frac{(n-1) \ Me}{2n^2} \right)^{\frac{1}{2}}$$

$$SE \ (\hat{g_i} - \hat{g_j}) = \left(\frac{1}{n} \ Me \right)^{\frac{1}{2}}$$

$$\text{sca} : SE \ (\hat{s_{ij}}) = \left(\frac{1}{2n^2} \ (n^2 - 2n + 2) \ Me \right)^{\frac{1}{2}}$$

$$SE \ (\hat{s}_{ij} - \hat{s}_{ik}) = \left(\frac{(n-1)}{n} \ Me \right)^{\frac{1}{2}}$$

$$SE \ (\hat{s}_{ij} - \hat{s}_{kl}) = \left(\frac{(n-2)}{n} \ Me \right)^{\frac{1}{2}}$$

The significance of gca, sca and reciprocal effects are tested using students 't' test with the following test criteria :

$t = |g_i| \ /SE \ (g_i)$ for the significance of g_i.

$t = | g_i - g_j | \ /SE \ (g_i - g_j)$ for the significant difference between g_i and g_j.

$t = | s_{ij}| \ /SE \ (s_{ij})$ for the significance by s_{ij}

$t = | s_{ij} - s_{ik} | \ /SE \ (s_{ij} - s_{ik})$ for the significant difference between s_{ij} and s_{ik} (one parent common)

$t = | s_{ij} - s_{kl} | \ /SE \ (s_{ij} - s_{kl})$ for the significant difference between s_{ij} and s_{kl} (no common parent)

$t = | r_{ij}| \ /SE \ (r_{ij})$ for significance of r_{ij}, the degrees of freedom for 't' being equal to the error degrees of freedom at the chosen level of significance (generally 5% or 1%)

3.2.3.2 Estimate of additive and dominance components (Hayman's numerical approach)

The estimation of additive and dominace components ie.D, H components was done through Hayman's Approach which provides information on the genetic make up of a character based on an additive - dominance model.

Hayman's approach was used to estimate the following components.

Variance components and their estimates	Standard Error Estimates

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

$$\left(\frac{(n^5 + n^4)}{n^5} \times Me\right)^{1/2}$$

$$H_1 = 4\,\overline{V}r + Vp - 4\overline{W}_r - \left(\frac{3n - 2}{n}\right)\hat{E}$$

$$\left(\frac{(n^5 + 41n^4 - 12\,n^3 + 4\,n^2)}{n^5} \times Me\right)^{1/2}$$

$$H_2 = 4\,\overline{V}r - 4\,Vr - 2\,\hat{E}$$

$$\left(\frac{36\,n^4 \times Me}{n^5}\right)^{1/2}$$

$$F = 2\,Vp - 4\,Wr - \frac{2(n-2)}{n}\hat{E}$$

$$\left(\frac{(4\,n^5 + 20\,n^4 - 16\,n^3 + 16\,n^2)}{n^5} \times Me\right)^{1/2}$$

$$h^2 = 4(M_{L_1} - M_{L_0})^2 - \frac{4(n-1)}{n^2}\hat{E}$$

$$\left(\frac{16n^4 + 16\,n^2 - 32n + 16}{n^5} \times Me\right)^{1/2}$$

$$E = \frac{SSB + SSE}{n^2 r (r-1)} \qquad \left(\frac{n^4}{n^5} \times Me\right)^{1/2}$$

where D	=	Variance due to additive effect
H_1 and H_2	=	Variance due to dominance effect of positive and negative genes respectively
F	=	Average covariance between additive and dominance effect over all the parental arrays.
h^2	=	Dominance effect
E	=	Environment effect
Vp	=	Variance of parents
$\overline{Vr}$	=	Mean variance over arrays
$\overline{Wr}$	=	Mean covariance between parents and offsprings over the arrays.
SSB	=	Replication sum of squares
SSE	=	Error sum of squares
n	=	Number of parents
r	=	Number of replications
M_{L_1}	=	Mean of n^2 progeny families
M_{L_o}	=	Parental mean
Me	=	Environmental variance

The following ratios were also derived.

$$\text{Average degree of dominance} = \left(\frac{H_1}{D}\right)^{\frac{1}{2}}$$

If this ratio equals unity, complete dominance is indicated. A value of less than unity and more than unity suggests partial dominance and overdominance respectively.

Distribution of increasing (positive effects) and decreasing (negative effects) genes among the common parents of arrays $= \dfrac{H_2}{4\,H_1}$

A symmetrical distribution of these genes is indicated if the ratio attains a value of 0.25 and deviation from this value implies an asymmetical distribution.

Proportion of Dominant and Recessive Genes among parents (P.D.R.G.).

$$= \frac{(4\,DH_1)^{\frac{1}{2}} + F}{(4\,DH_1)^{\frac{1}{2}} - F}$$

This ratio will attain unit value if the dominant and recessive genes are symmetrically distributed among parents. Deviation from unity indicates an asymmetrical distribution of these genes.

3.2.3.3.   Hayman's Graphical Approach

The Wr-Vr graph was drawn using a regression relationship between Wr and Vr where Wr is the covariance between the parents and offsprings in the r th array and Vr is the variance of the r th array. A parabola was constructed with Vr and Wr values.

In the linear regression of Wr = a + b Vr, 'b' is the regression coefficient of Wr on Vr and 'a' the constant term which is taken as an indication of the type of gene action governing the character.

If the regression line passes through the origin ie., (a = o) it can be taken as an indication of complete dominance. But if it passes above the origin (ie., a >0) it can be taken as an indication of absence of dominance ie., partial dominance while the line passing below the origin (ie., a < 0) indicates the presence of overdominance.

3.2.3.4 Heterosis

Heterosis was calculated as the percent deviation of the mean performance of F_1's ($\overline{F}_1$) from their mid parent (MP) and better parent (BP) for each cross combination as suggested by Hayes *et al.* (1955) and Briggle (1963).

$$\text{Relative heterosis} = \frac{\overline{F}_1 - \overline{MP}}{\overline{MP}} \times 100$$

$$\text{Heterobeltiosis} = \frac{\overline{F}_1 - \overline{BP}}{\overline{BP}} \times 100$$

Where, $\overline{F}_1$ = Mean performance of F_1's

$\overline{MP}$ = Mean performance of the average of two parents

$\overline{BP}$ = Mean performance of the better parent

The significance of heterosis (F_1's mean over MP and BP mean) over MP and BP are compared using the following critical difference (CD) values.

$$CD\ (0.05\ ) = t_{e\ (0.005)} \times \left(\frac{3\ Me}{2r}\right)^{\frac{1}{2}}$$

$$CD\ (0.05) = t_{e\ (0.005)} \times \left(\frac{2Me}{r}\right)^{\frac{1}{2}}$$

Where Me is the estimated error variances with respect to each character.

Results

RESULTS

Statistical analysis of the experiment was done and the results are presented.

4.1. Mean Performance

The mean performance of the six parents and the 30 hybrids for the 12 characters are presented in Table 2.

Significant differences were observed among the genotypes with respect to all characters.

Considering the character, viz., plant height, the mean values of the parents ranged from 105 cm (P_2) to 163.33 cm (P_6), and that of crosses ranged from 109 cm (P_3 x P_6) to 192 cm (P_6 x P_2). The crosses P_6 x P_3 (190.67 cm), P_4 x P_1 (190.00cm), P_2 x P_1 (186.67 cm), P_3 x P_1 (175.00 cm), P_4 x P_2 (171.67 cm), P_4 x P_5 (169.00 cm), P_1 x P_5 (168.33 cm) and P_4 x P_3 (165.00 cm) were found to be on par with P_6 x P_2.

With respect to number of branches per plant, P_1 recorded the maximum number of branches (6.33) and the minimum number of branches (4.67) was recorded by P_2, P_3 and P_5. In hybrids, it ranged from 4.0 -10.0. The maximum number of branches (10.0) was recorded by P_4 x P_1.

In the case of days to first flowering, the mean performance of the parents ranged from 40 (P_5) to 42 (P_2) and that of the crosses ranged from 38.33 to 41.67.

Table. 2 Mean performance of the genotypes.

Parents/ Crosses	Plant height	Number of branches/ plant	Days to first flowering	Length of pods	Number of pods/ plant	Number of seeds/ pod
P_1	108.33	6.33	41.00	7.27	42.00	5.33
P_2	105.00	4.67	42.00	8.07	45.33	5.33
P_3	109.00	4.67	41.00	8.40	47.00	7.00
P_4	143.33	5.33	41.33	7.67	47.67	6.33
P_5	161.00	4.67	40.00	8.27	45.00	7.67
P_6	163.33	5.33	41.00	7.60	38.33	6.33
$P_1 \times P_2$	158.33	5.33	39.67	8.77	51.33	7.33
$P_1 \times P_3$	118.33	6.00	41.00	8.90	58.33	6.33
$P_1 \times P_4$	162.33	4.00	40.33	9.33	51.33	7.00
$P_1 \times P_5$	168.33	4.67	40.33	8.53	32.67	7.00
$P_1 \times P_6$	149.67	4.33	40.67	7.50	35.33	8.67
$P_2 \times P_3$	115.00	6.67	38.67	8.67	58.33	7.00
$P_2 \times P_4$	155.00	6.00	39.33	9.23	65.00	6.33
$P_2 \times P_5$	133.33	6.00	40.00	8.57	30.67	6.33
$P_2 \times P_6$	140.33	8.00	38.33	9.53	60.33	6.67
$P_3 \times P_4$	146.67	6.67	40.33	8.97	66.33	6.33
$P_3 \times P_5$	118.33	9.00	38.33	8.23	91.00	5.00
$P_3 \times P_6$	109.00	8.67	39.67	8.23	61.67	7.00
$P_4 \times P_5$	169.00	9.00	38.33	9.60	106.67	6.67
$P_4 \times P_6$	126.67	9.00	40.33	9.23	78.33	7.00
$P_5 \times P_6$	138.33	7.00	39.00	8.00	58.33	6.33
$P_2 \times P_1$	186.67	5.67	41.00	9.40	58.67	8.00
$P_3 \times P_1$	175.00	8.00	40.33	8.80	76.67	6.33
$P_3 \times P_2$	152.67	7.33	38.33	8.43	70.33	6.00
$P_4 \times P_1$	190.00	10.00	39.00	10.10	91.00	7.67
$P_4 \times P_2$	171.67	6.00	41.00	8.57	61.00	6.33
$P_4 \times P_3$	165.00	6.00	41.00	8.60	53.33	7.67
$P_5 \times P_1$	140.00	6.00	39.67	9.80	39.00	7.67
$P_5 \times P_2$	128.33	4.67	39.67	8.13	40.67	6.67
$P_5 \times P_3$	128.67	5.00	41.33	8.23	55.67	6.00
$P_5 \times P_4$	125.00	4.33	41.00	8.57	34.33	7.33
$P_6 \times P_1$	125.00	6.00	39.67	8.87	51.00	8.00
$P_6 \times P_2$	192.00	4.33	38.33	8.20	43.33	5.67
$P_6 \times P_3$	190.67	4.33	39.67	7.27	49.00	6.67
$P_6 \times P_4$	140.00	8.33	40.67	7.80	87.33	6.00
$P_6 \times P_5$	151.67	5.33	41.67	9.17	48.67	6.33
F	6.38^{**}	4.48^{*}	1.60^{*}	2.53^{**}	8.35^{**}	1.57^{*}
S.E.	14.11	1.09	1.17	0.62	8.78	0.91
C.D. (5%)	28.22	2.18	2.34	1.24	17.56	1.82

Parents/ Crosses	Seed yield	100 Seed weight	Days to maturity	Root weight	Nodule weight	Protein content
P_1	12.70	5.71	104.67	3.52	60.00	17.85
P_2	18.18	6.03	105.33	4.27	76.67	17.68
P_3	17.34	5.79	105.33	3.76	63.33	17.04
P_4	14.72	5.37	107.00	4.42	80.00	17.79
P_5	13.35	5.27	103.67	3.38	76.67	17.68
P_6	13.95	5.42	104.33	4.67	70.00	17.27
$P_1 \times P_2$	21.80	6.57	102.67	4.43	70.00	17.56
$P_1 \times P_3$	23.94	6.09	103.00	6.01	116.67	17.85
$P_1 \times P_4$	22.36	5.80	103.67	6.29	180.00	19.08
$P_1 \times P_5$	12.21	5.49	102.67	4.29	150.00	18.03
$P_1 \times P_6$	16.85	5.83	102.67	4.52	73.33	18.20
$P_2 \times P_3$	24.09	6.27	100.33	5.00	175.00	18.67
$P_2 \times P_4$	24.61	6.16	101.67	12.33	93.33	18.79
$P_2 \times P_5$	18.52	5.78	103.33	6.08	90.00	18.84
$P_2 \times P_6$	22.56	5.89	100.33	7.26	133.33	18.90
$P_3 \times P_4$	20.48	6.57	104.67	4.06	170.00	19.19
$P_3 \times P_5$	24.67	5.59	101.33	4.52	200.00	17.80
$P_3 \times P_6$	22.50	5.54	103.00	4.46	170.00	17.91
$P_4 \times P_5$	36.32	5.81	100.67	4.29	80.00	18.32
$P_4 \times P_6$	26.99	5.83	103.00	4.10	100.00	19.14
$P_5 \times P_6$	21.78	5.88	101.00	4.30	93.33	18.32
$P_2 \times P_1$	24.84	6.05	103.00	6.45	83.33	19.02
$P_3 \times P_1$	30.28	6.14	104.33	11.53	106.67	17.56
$P_3 \times P_2$	25.16	5.92	101.00	5.14	130.00	19.08
$P_4 \times P_1$	39.29	6.43	101.33	9.29	213.33	17.74
$P_4 \times P_2$	23.55	6.31	106.00	7.79	160.00	18.32
$P_4 \times P_3$	27.51	6.39	107.33	4.94	163.33	19.25
$P_5 \times P_1$	18.52	6.28	101.67	4.95	123.33	18.49
$P_5 \times P_2$	16.34	6.10	101.00	4.50	80.00	18.20
$P_5 \times P_3$	20.01	5.92	103.67	6.47	93.33	19.72
$P_5 \times P_4$	16.01	6.01	100.67	5.19	170.00	19.02
$P_6 \times P_1$	20.56	5.37	101.67	6.32	68.33	18.49
$P_6 \times P_2$	14.37	5.77	100.33	4.95	96.67	17.50
$P_6 \times P_3$	16.21	5.75	102.00	7.40	73.33	18.49
$P_6 \times P_4$	29.58	5.86	101.33	8.88	150.00	17.27
$P_6 \times P_5$	17.77	5.75	104.00	4.55	120.00	18.90
F	3.29**	2.12**	4.43**	3.07**	4.89**	3.26**
S.E.	4.86	0.32	1.27	1.69	27.95	0.53
C.D. (5%)	9.72	0.64	2.54	3.38	55.90	1.06

The length of the pods recorded by the parents ranged from 7.27 cm in P_1 to 8.40 cm in P_3. Among the hybrids, it ranged from 7.27cm in P_6 x P_3 to 10.10 cm in P_4 x P_1.

The maximum number of pods per plant among the parents was exhibited by P_4 (47.67) and the minimum by P_6 (38.33). The hybrids showed a wider variability for this charcter, ranging from 30.67 (P_2 x P_5) to 106.67 (P_4 x P_5). The crosses, P_4 x P_1 (91.00) and P_3 x P_5 (91.00) were on par with P_4 x P_5.

The number of seeds per pod ranged from 5.33 to 7.67 among the parents. The highest number of seeds per pod among the parents was recorded by P_5. While the range for this character was from 5.00 (P_3 x P_5) to 8.67 (P_1 x P_6) in the hybrids.

The seed yield per plant was the highest in P_2 (18.18 g) and the lowest in P_1 (12.70 g) among the parents. Among the hybrids, the maximum yield of seeds was recorded by P_4 x P_1 (39.29g) and the minimum yield was recorded by P_1 x P_5 (12.21 g). The crosses, P_4 x P_5 (36.32 g) and P_3 x P_1 (30.28 g) were on par with P_4xP_1.

With regard to 100 seed weight, the highest was recorded by P_2 (6.03g) and the lowest recorded by P_5 (5.27g) among the parents and among the hybrids, variability ranged from 5.37 g (P_6 x P_1) to 6.57g (P_1 x P_2 and P_3 x P_4).

Considering the character, days to maturity, the lowest number of days was recorded by P_5 (103.67 days) and the highest by P_4 (107days). Among the hybrids,

the lowest was recorded by P_2 x P_3, P_2 x P_6, and P_6 x P_2 (100.33 days) and the highest recorded by P_4 x P_3 (107.33 days).

The root weight recorded by the parents ranged from 3.38g (P_5) to 4.67g (P_6). Among the hybrids, it ranged from 4.06 g (P_3 x P_4) to 12.33g (P_2 x P_4). P_3 x P_1 (11.53g) and P_4 x P_1 (9.29 g) were on par with P_2 x P_4.

Among the parents, P_1 recorded the lowest nodule weight (60mg) and P_4 recorded the highest nodule weight of 80.00mg. The hybrids showed a wider range of variability from 70mg (P_1 x P_2) to 213.33 mg (P_4 x P_1).

Protein content among parents and hybrids showed narrow range of variability. Parents ranged from 17.04 % (P_3) to 17.85 % (P_1) and hybrids ranged from 17.27 % (P_6 x P_4) to 19.72 % (P_5 x P_3).

Fodder acceptability studies showed that all the parents and crosses were acceptable by the cattle.

In general, considering the mean performance of the 12 characters studied, P_2 showed better performance when compared to other parents. Among hybrids, P_4 x P_5 showed better performance for plant height, number of pods per plant, number of branches, days to first flowering, length of pods, seed yield and days to maturity. Among reciprocals, P_4 x P_1 showed good performance for number of branches per plant, length of pods, number of pods per plant, number of seeds per pod, seed yield, 100 seed weight and nodule weight.

4.2. Combining ability

Combining ability analysis was carried out by the method as suggested by Griffing (1956). The analysis of variance for combining ability is presented in Table 3.

The general combining ability variance (GCA) was significant for plant height, number of branches, length of pods, number of pods per plant, seed yield, 100 seed weight, days to maturity, root weight and nodule weight.

The specific combining ability variance (SCA) was significant for all the characters studied.

The mean squares due to reciprocals were significant for plant height, number of branches, length of pods, number of pods per plant, seed yield, days to maturity, root weight, nodule weight and protein content.

The estimates of the general combining ability effects (gca) of the six parents and the specific combining ability effects (sca) of the F_1 hybrids and the reciprocal crosses are presented in Tables 4,5 and 6.

4.2.1. Plant height

The combining ability analysis for plant height showed highly significant GCA, SCA and reciprocal effects. The SCA was highly significant indicating the importance of non-additive effect for this character.

Table. 3 Analysis of variance for combining ability for the 12 characters

Sl.no.	Character	Mean squares			
		GCA	SCA	Reciprocal effects	Error
1.	Plant height	405.96**	680.70**	666.18**	99.51
2.	Number of branches	1.43*	1.70**	4.01**	0.59
3.	Days to first flowering	0.45	1.33	1.07	0.69
4.	Length of pods	0.46*	0.57**	0.42*	0.19
5.	Number of pods/plant	395.12**	292.23**	326.08**	38.51
6.	Number of seeds/pod	0.58	1.06**	0.27	0.41
7.	Seed yield	48.39**	41.09**	33.66**	11.83
8.	100 seed weight	0.26**	0.10*	0.07	0.05
9.	Days to maturity	4.27**	4.93**	1.98**	0.81
10.	Root weight	4.08*	5.15**	3.75**	1.43
11.	Nodule weight	2236.75**	2312.79**	1403.89**	390.65
12.	Protein content	0.23	0.47**	0.51**	0.14

*Significant at 5% level

**Significant at 1% level

Table. 4 Estimates of general combining ability effects (gca) of the six parents

Sl.no:	Character	P_1	P_2	P_3	P_4	P_5	P_6
1.	Plant height	3.06	-0.86	-9.69**	7.03**	-2.56	3.03
2.	Number of branches	-0.13	-0.41*	0.23	0.48*	-0.32	0.15
3.	Days to first flowering	0.22	-0.22	-0.03	0.25	-0.14	-0.08
4.	Length of pods	0.14	0.07	-0.14	0.21	0.04	-0.32**
5.	Number of pods/plant	-3.97*	-3.89*	4.81**	9.42**	-4.11*	3.44*
6.	Number of seeds/pod	0.35	-0.29	-0.18	0.05	0.02	0.05
7.	Seed yield	-0.05	-0.37	1.08	3.29**	-2.32*	-1.63
8.	100 seed weight	0.05	0.16**	0.07	0.08	-0.15*	-0.22**
9.	Days to maturity .	0.12	-0.35	0.56*	0.81**	-0.60*	-0.55*
10.	Root weight	0.25	0.36	-0.09	0.66*	-1.02**	-0.17
11.	Nodule weight	-6.62	-9.95	11.71*	21.30**	-2.59	-13.84*
12.	Protein content	-0.16	0.05	0.00	0.17	0.11	-0.17

*Significant at 5% level

**Significant at 1% level

Table. 5 Estimates of specific combining ability effects (sca) of the 30 hybrids

Parents/ Crosses	Plant height	Number of branches	Days to first flowering	Length of pods	Number of pods/ plant	Number of seeds/ pod
F_1's						
$P_1 \times P_2$	24.17**	-0.15	0.25	0.31	6.44	0.90
$P_1 \times P_3$	7.17	0.71	0.39	0.28	10.25*	-0.55
$P_1 \times P_4$	19.94*	0.46	-0.89	0.80*	9.31	0.23
$P_1 \times P_5$	7.53	-0.40	-0.17	0.41	-12.50*	0.26
$P_1 \times P_6$	-14.89	-1.04	-0.06	-0.21	-7.03	1.23*
$P_2 \times P_3$	-1.75	0.99	-1.33	0.06	7.00	0.26
$P_2 \times P_4$	11.03	-0.26	0.06	0.06	1.06	-0.13
$P_2 \times P_5$	-11.89	-0.12	0.11	-0.33	-12.75*	0.06
$P_2 \times P_6$	17.86*	0.24	-1.44*	0.55	1.56	-0.30
$P_3 \times P_4$	12.36	-0.56	0.36	0.15	-10.81*	0.43
$P_3 \times P_5$	-10.39	0.91	-0.08	-0.24	16.22**	-1.05*
$P_3 \times P_6$	10.36	-0.06	-0.31	-0.36	-3.64	0.26
$P_4 \times P_5$	-3.61	0.32	-0.53	0.26	8.78	0.23
$P_4 \times P_6$	-22.86**	1.85**	0.25	0.06	19.25**	-0.30
$P_5 \times P_6$	-1.61	0.16	0.47	0.29	3.44	-0.44
Reciprocals						
$P_2 \times P_1$	14.17	0.17	0.67	0.32	3.67	0.33
$P_3 \times P_1$	28.33**	1.00	-0.33	-0.05	9.17	0.00
$P_3 \times P_2$	18.83*	0.33	-0.17	-0.12	6.00	-0.50
$P_4 \times P_1$	13.83	3.00**	-0.67	0.38	19.83**	0.33
$P_4 \times P_2$	8.33	0.00	0.83	-0.33	-2.00	0.00
$P_4 \times P_3$	9.17	-0.33	0.33	-0.18	-6.50	0.67
$P_5 \times P_1$	-14.17	0.67	-0.33	0.63	3.17	0.33
$P_5 \times P_2$	-2.50	-0.67	-0.17	-0.22	5.00	0.17
$P_5 \times P_3$	5.17	-2.00**	1.50*	0.00	-17.67**	0.50
$P_5 \times P_4$	-22.00*	-2.33**	1.33	-0.52	-36.17**	0.33
$P_6 \times P_1$	12.33	0.83	-0.50	0.68	7.83	-0.33
$P_6 \times P_2$	25.83**	-1.83**	0.00	-0.67	-8.50	-0.50
$P_6 \times P_3$	40.83**	-2.17**	0.00	-0.48	-6.33	-0.17
$P_6 \times P_4$	6.67	-0.33	0.17	-0.72*	4.50	-0.50
$P_6 \times P_5$	6.67	-0.83	1.33	0.58	-4.83	0.00

Table. 5 continued

Parents/ Crosses	Seed yield	100 Seed weight	Days to maturity	Root weight	Nodule weight	Protein content
F_1's						
$P_1 \times P_2$	2.35	0.19	0.19	-0.85	-22.13	0.10
$P_1 \times P_3$	4.70	0.09	0.10	2.93**	-8.80	-0.43
$P_1 \times P_4$	6.20*	0.08	-1.31	1.20	66.62**	0.09
$P_1 \times P_5$	-3.66	0.08	-0.23	-0.29	30.51	0.00
$P_1 \times P_6$	-1.00	-0.14	-0.29	-0.34	-24.07	0.37
$P_2 \times P_3$	2.53	-0.05	-2.43**	-0.88	35.37*	0.52
$P_2 \times P_4$	-0.23	0.08	0.49	3.36**	-0.05	0.03
$P_2 \times P_5$	-1.27	0.01	0.24	0.27	-17.82	0.06
$P_2 \times P_6$	-0.92	-0.02	-1.65*	0.23	23.43	0.02
$P_3 \times P_4$	-1.76	0.42*	1.74*	-1.74	18.29	0.75*
$P_3 \times P_5$	2.20	-0.07	-0.34	0.92	22.18	0.35
$P_3 \times P_6$	-1.48	-0.12	-0.40	0.51	8.43	0.07
$P_4 \times P_5$	3.80	0.06	-2.43**	-0.58	-9.07	0.08
$P_4 \times P_6$	5.24	0.07	-0.98	0.33	2.18	-0.11
$P_5 \times P_6$	2.33	0.27	0.77	-0.06	7.73	0.36
Reciprocals						
$P_2 \times P_1$	1.52	-0.26	0.17	1.01	6.67	0.73*
$P_3 \times P_1$	3.17	0.02	0.67	2.76**	-5.00	-0.15
$P_3 \times P_2$	0.53	-0.17	0.33	0.07	-22.50	0.20
$P_4 \times P_1$	8.47**	0.32	-1.17	1.50	16.67	-0.67*
$P_4 \times P_2$	-0.53	0.08	2.17**	-2.27*	33.33*	-0.23
$P_4 \times P_3$	3.52	-0.09	1.33	0.44	-3.33	0.03
$P_5 \times P_1$	3.16	0.39*	-0.50	0.33	-13.33	0.23
$P_5 \times P_2$	-1.09	0.16	-1.17	-0.79	-5.00	-0.32
$P_5 \times P_3$	-2.33	0.17	1.17	0.97	-53.33*	0.96**
$P_5 \times P_4$	-10.15**	0.10	0.00	0.45	45.00**	0.35
$P_6 \times P_1$	1.86	-0.23	-0.50	0.90	-2.50	0.14
$P_6 \times P_2$	-4.10	-0.06	0.00	-1.16	-18.33	-0.70*
$P_6 \times P_3$	-3.14	0.10	-0.50	1.47	-48.33**	0.29
$P_6 \times P_4$	1.30	0.02	-0.83	2.39*	25.00	-0.93**
$P_6 \times P_5$	-2.01	-0.07	1.50*	0.13	13.33	0.29

Table. 6 Standard Error (S.E.) and Critical Differences (C.D.) of general and specific combining ability effects (gca and sca)

Sl. no.	Character	S.E. (g_i)	C.D (g_i)	S.E. $(g_i - g_j)$	C.D. $(g_i - g_j)$	S.E. (s_i)	C.D. (s_i)
1.	Plant height	2.63	5.15 6.99	4.07	7.98 10.83	8.31 8.31	16.29 22.10
2.	Number of Branches	0.203	0.398 0.539	0.31	0.62 0.84	0.64	1.25 1.71
3.	Days to first flowering	0.22	0.43 0.59	0.34	0.66 0.90	0.69	1.35 1.84
4.	Length of pods	0.12	0.23 0.31	0.18	0.35 0.48	0.37	0.72 0.97
5.	Number of pods per plant	1.64	3.21 4.36	2.53	4.96 6.73	5.17	10.13 13.75
6.	Number of seeds per pod	0.17	0.33 0.45	0.26	0.51 0.69	0.54	1.05 1.42
7.	Seed yield	0.91	1.78 2.41	1.40	2.74 3.72	2.87	5.63 7.61
8.	100 seed weight	0.06.	0.12 0.16	0.09	0.18 0.24	0.19	0.37 0.51
9.	Days to maturity	0.24	0.47 0.63	0.37	0.72 0.98	0.75	1.47 1.98
10.	Root weight	0.32	0.62 0.84	0.49	0.96 1.30	0.99	1.95 2.65
11.	Nodule weight	5.21	10.21 13.85	8.07	15.79 21.47	16.47	32.28 43.81
12.	Protein content	0.09 0.09	0.19 0.23	0.15	0.30 0.39	0.31	0.61 0.82

$g_i \rightarrow$ SE of gca of the ith parent

$s_{i,j} \rightarrow$ SE of sca of the $i \times j^{th}$ parent

$r_{i,j} \rightarrow$ SE of reciprocal effect

C.D $\rightarrow$ 5% level (first entry)

$\rightarrow$ 1% level (second entry)

Table. 6 Continued

Sl. no.	Character	S.E. $s_{ij}-s_{jk}$	C.D $s_{ij}-s_{jk}$	S.E. $s_{ij}-s_{kl}$	C.D. $s_{ij}-s_{kl}$	S.E. $r_{ij}-r_{kl}$	C.D. $r_{ij}-r_{kl}$
1.	Plant height	9.11	17.84 24.23	8.14	15.97 21.65	9.98	19.56 26.55
2.	Number of Branches	0.70	1.38 1.86	0.62	1.23 1.65	0.77	1.51 2.07
3.	Days to first flowering	0.76	1.48 2.02	0.68	1.32 1.81	0.83	1.62 2.21
4.	Length of pods	0.40	0.79 1.06	0.36	0.70 0.96	0.44	0.86 1.17
5.	Number of pods per plant	5.66	11.09 15.06	5.08	9.94 13.51	6.21	12.17 16.52
6.	Number of seeds per pod	0.59	1.15 1.57	0.52	1.03 1.38	0.64	1.26 1.70
7.	Seed yield	3.14	6.15 8.35	2.81	5.51 7.47	3.44	6.74 9.15
8.	100 seed weight	0.21	0.41 0.56	0.19	0.36 0.51	0.23	0.45 0.61
9.	Days to maturity	0.82	1.61 2.18	0.73	1.44 1.94	0.90	1.75 2.39
10.	Root weight	1.09	2.14 2.89	0.98	1.91 2.61	1.19	2.33 3.17
11.	Nodule weight	18.04	35.36 47.9	16.14	31.63 42.93	19.76	38.73 52.56
12.	Protein content	0.34	0.67 0.90	0.30	0.60 0.79	0.37	0.73 0.98

The parent P_3 showed significant negative gca of -9.69 and parent P_4 showed significant positive gca of 7.03. P_3 was found to be significantly different from all other parents. The crosses, $P_6 \times P_3$ (40.83), $P_3 \times P_1$ (28.33) and $P_6 \times P_2$ (25.83) were found to show highly significant effects and these crosses were on par. Thus the parent P_4 can be considered as the best general combiner, while the crosses, $P_6 \times P_3$ and $P_3 \times P_1$ can be considered as the best specific combinations for this character (Fig. 1 & Fig. 2).

4.2.2. Number of branches

Significant, GCA, SCA, and reciprocal effects were observed for this character. Variation due to reciprocal effects was found to be higher than that of GCA and SCA.

Significant positive gca was shown by P_4 (0.48) and significant negative gca was shown by P_2 (-0.41). Among the direct crosses, $P_4 \times P_6$ showed significant positive sca of 1.85. Significant sca effects were also seen in the reciprocal crosses, $P_4 \times P_1$ (3.0), $P_5 \times P_3$ (-2.0), $P_5 \times P_4$ (-2.3), $P_6 \times P_2$ (-1.83) and $P_6 \times P_3$ (-2.17). The cross, $P_4 \times P_1$ was found to be significantly different from the other crosses, and hence can be considered as the best specific combination for this character (Fig. 3 & Fig. 4.).

4.2.3. Days to first flowering

The combining ability analysis for days to first flowering showed significant SCA. The cross, $P_2 \times P_6$ only showed significant negative effect (Fig. 5).
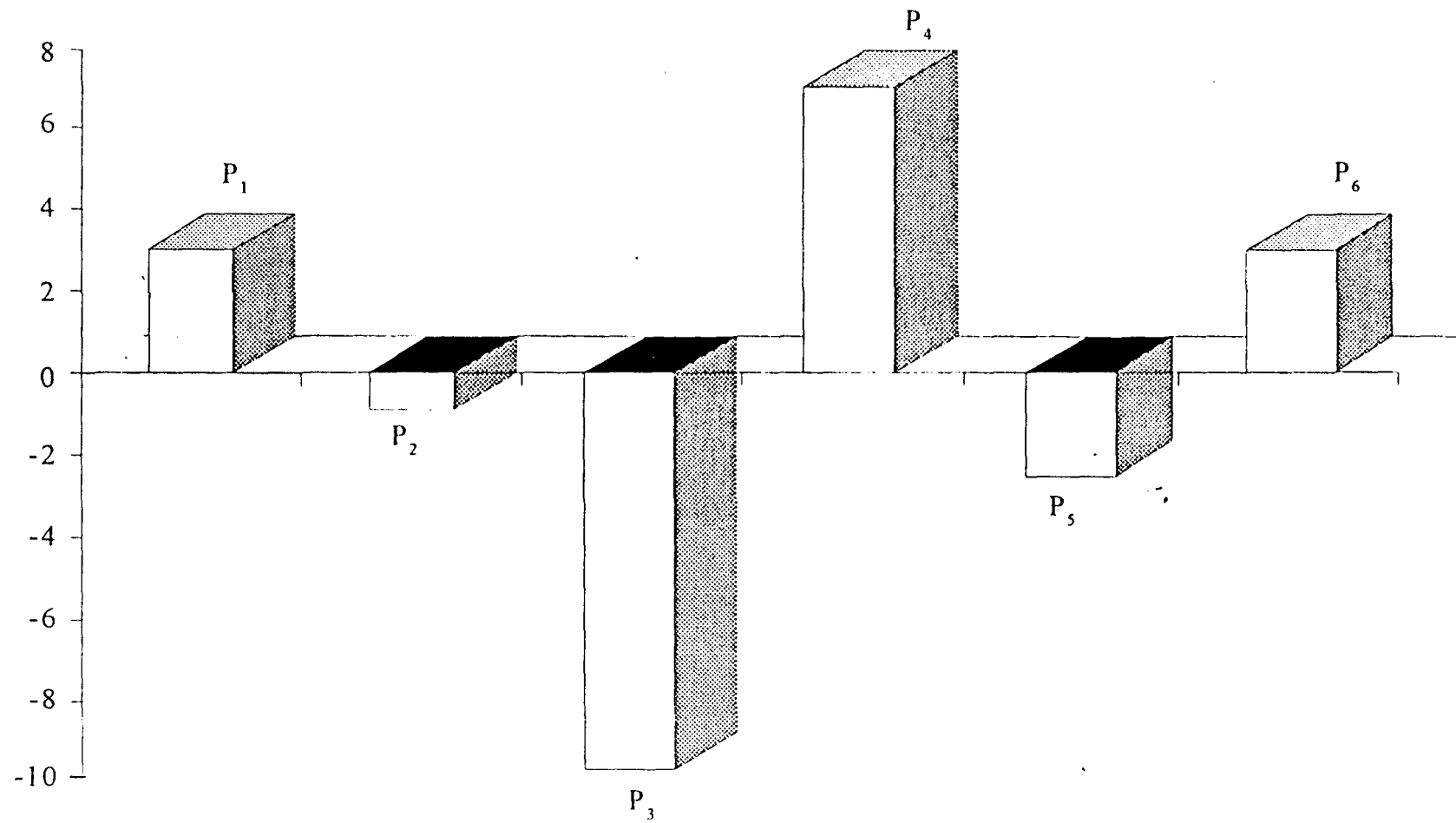
Fig 1. Plant Height - general combining ability effects (gca)
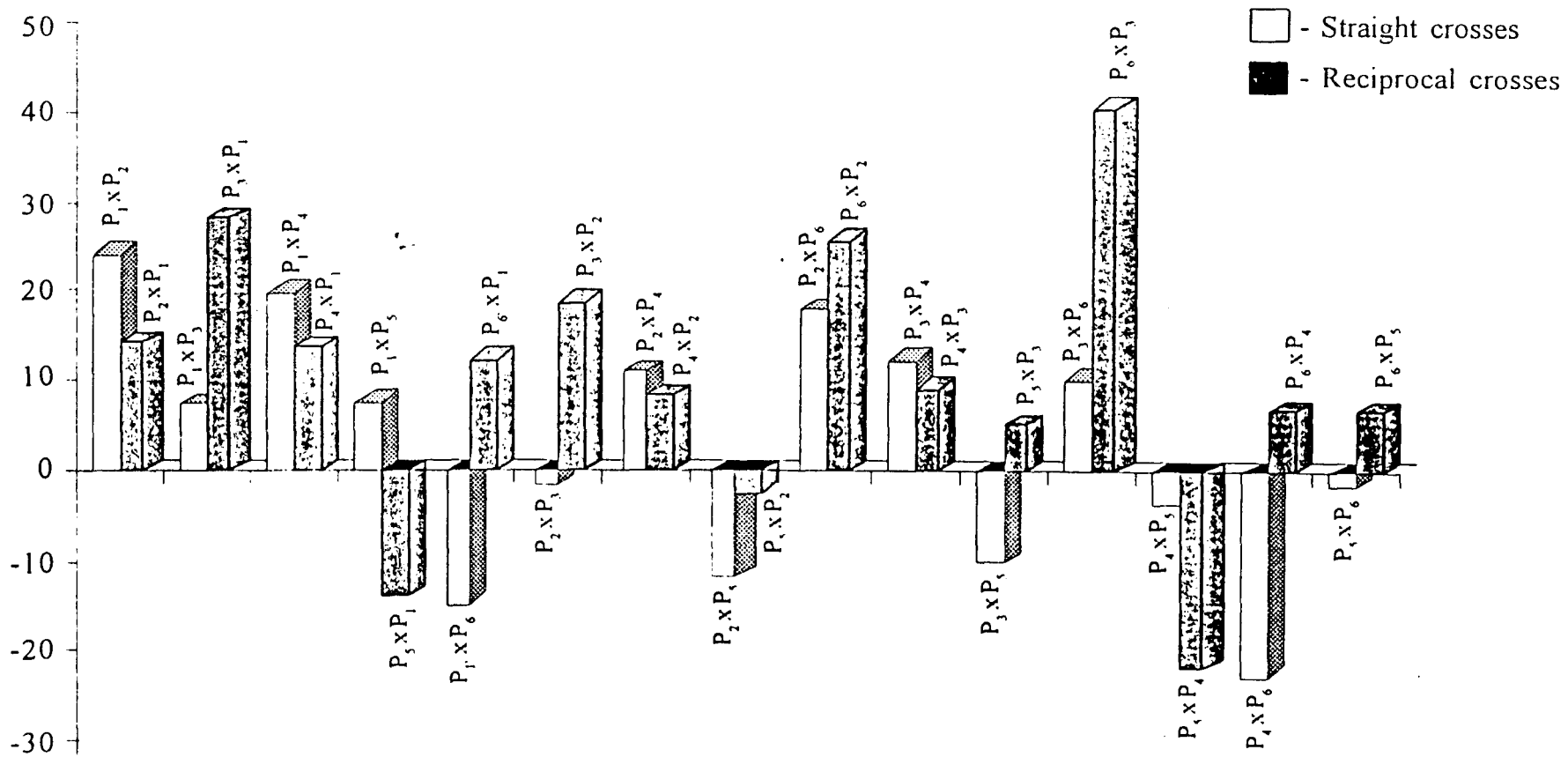
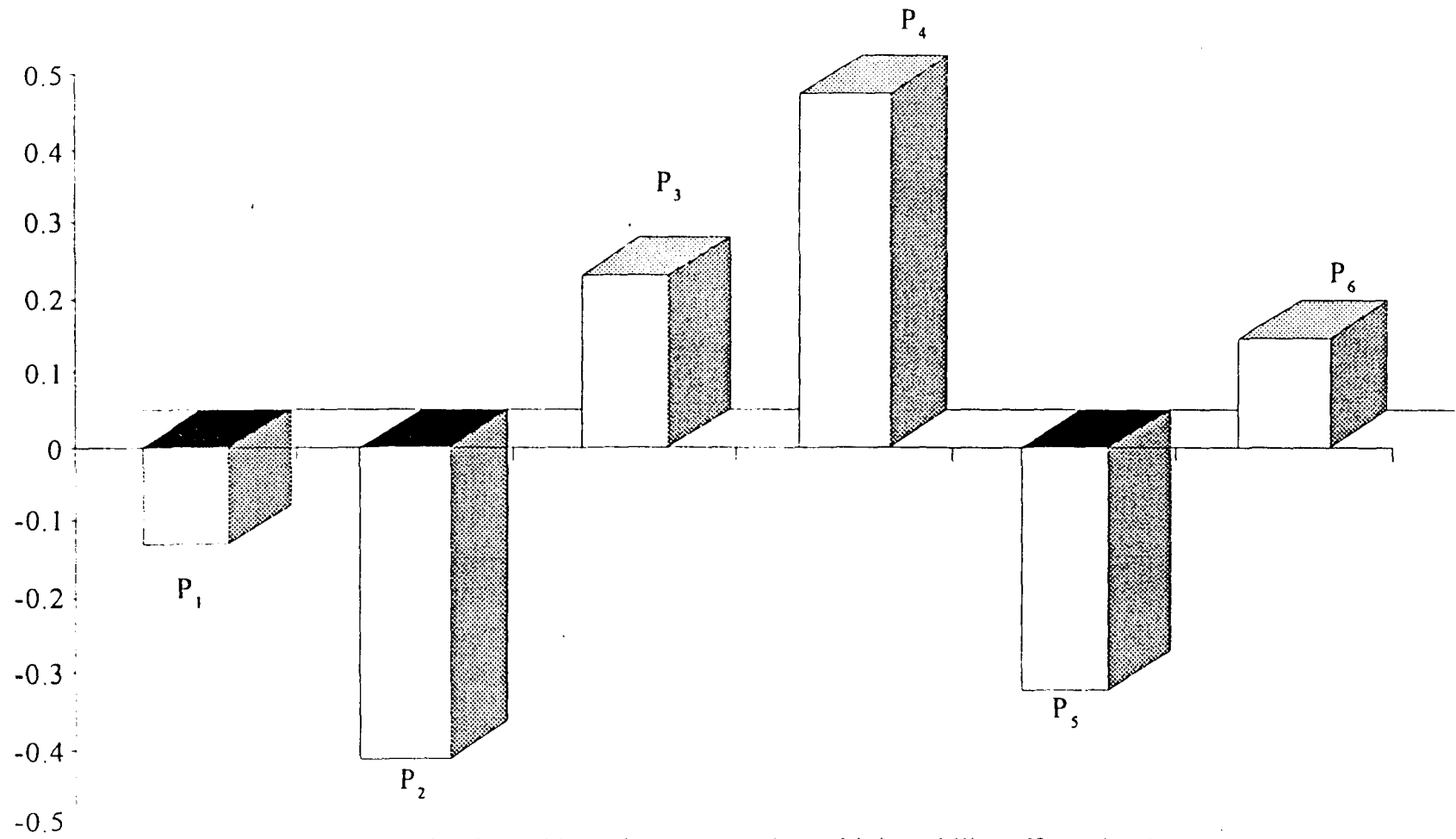Fig. 2. Plant Height - specific combining ability effects (sca)

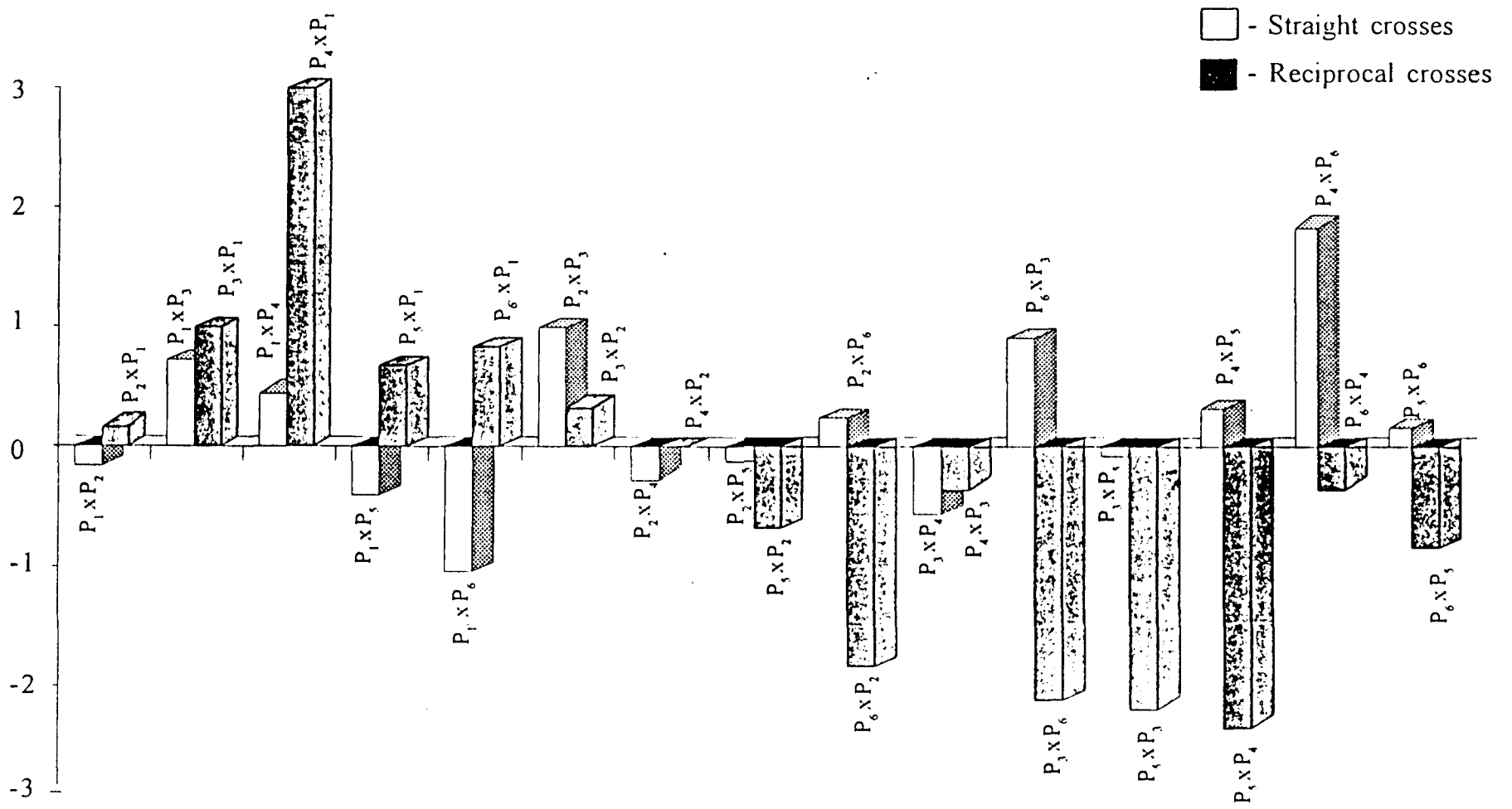Fig 3. Number of branches - general combining ability effects (gca)

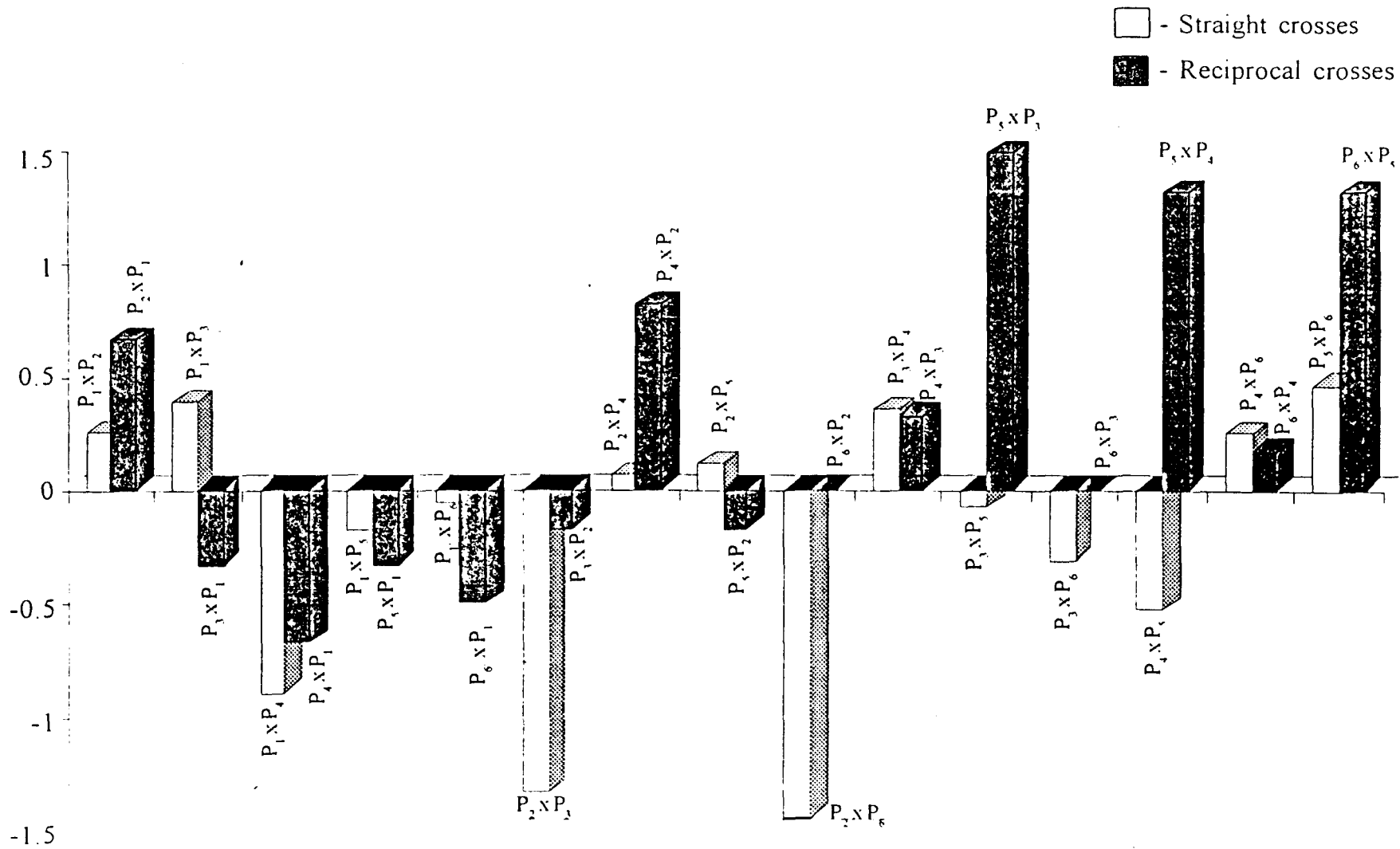Fig. 4. Number of branches - specific combining ability effects (sca)

Legend:
☐ - Straight crosses
■ - Reciprocal crosses

Fig. 5. Days to first flowering - specific combining ability effects (sca)

4.2..4. Length of pods

The combining ability analysis showed highly significant SCA, significant GCA and reciprocal effects.

The parent P_6 showed significant negative gca of -0.32. Among the hybrids $P_1 \times P_4$ showed significant positive sca of 0.80, and among reciprocals $P_6 \times P_4$ showed significant negative sca of -0.72. Thus it can be seen that the parent P_6 was the best general combiner and the hybrid $P_1 \times P_4$ was the best specific combination for length of pods (Fig. 6 & Fig. 7).

4.2.5. Number of pods per plant.

The combining ability analysis showed highly significant GCA, SCA and reciprocal effects.

The parent P_4 showed highly significant positive effect of 9.42, which was on par with P_3 (4.81). P_5 showed highly significant negative effect of -4.11. Among the hybrids, $P_4 \times P_6$ was found to be showing significantly high positive effects of 19.25, which was on par with $P_3 \times P_5$ (16.22). $P_2 \times P_5$ showed highly significant negative effect of -12.75. Among the reciprocals, $P_4 \times P_1$ was found to be positively significant with 19.83 and $P_5 \times P_4$ showed highly significant negative effect of -36.17. Hence P_4 can be considered as the best general combiner, and the cross $P_4 \times P_1$ can be considered as the best specific combination for this trait (Fig. 8 & Fig. 9).
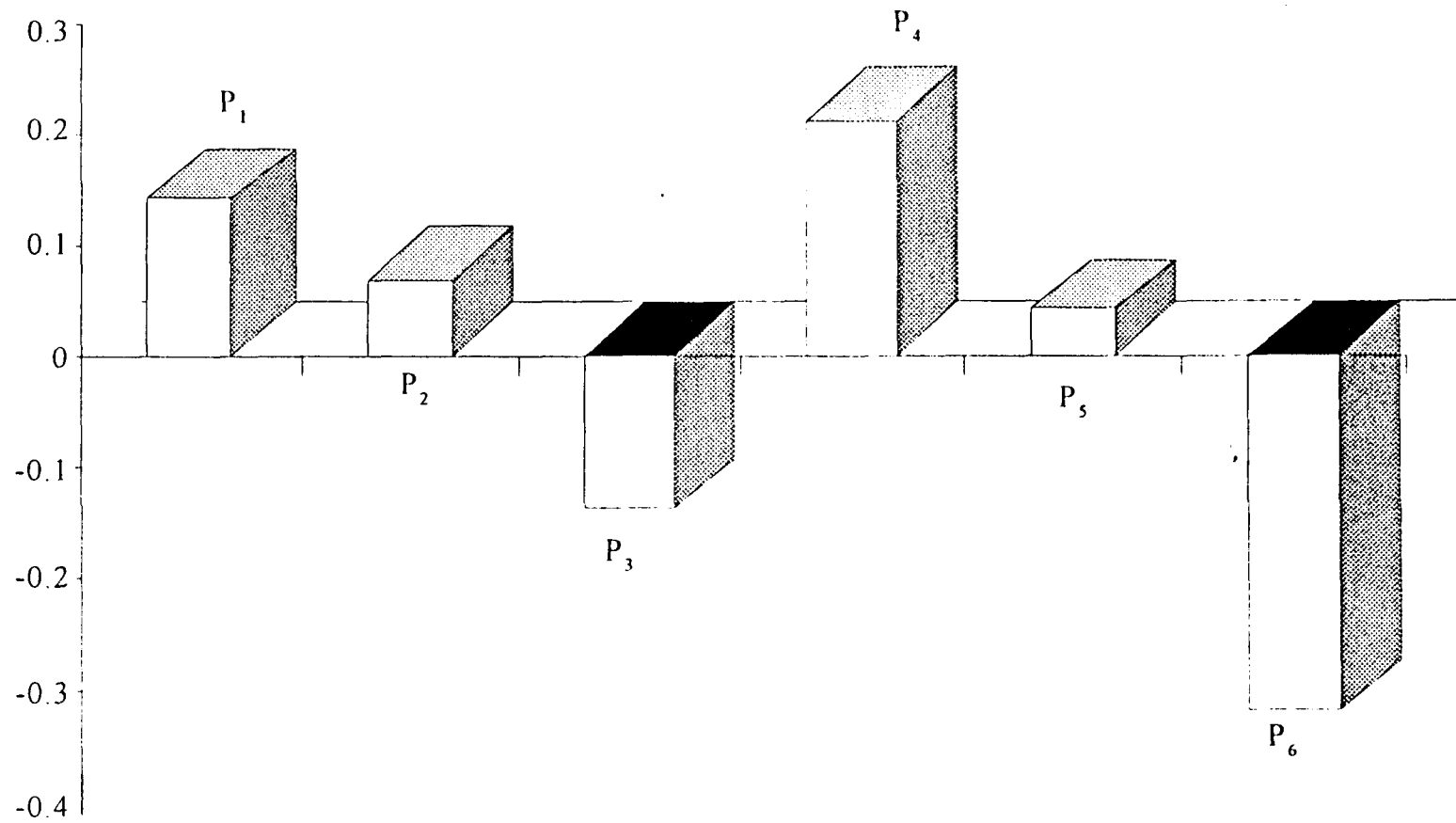
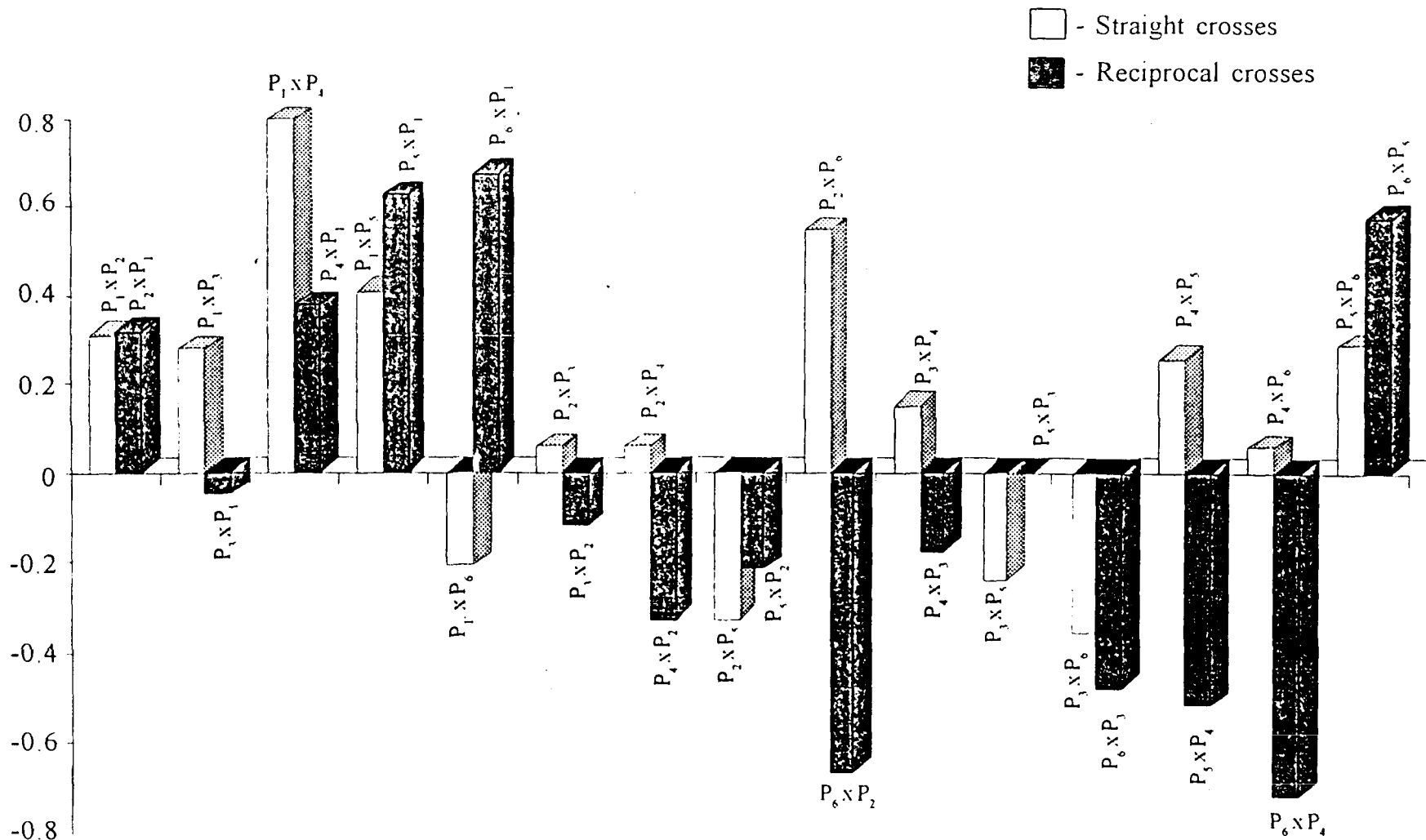Fig 6. Length of pods - general combining ability effects (gca)

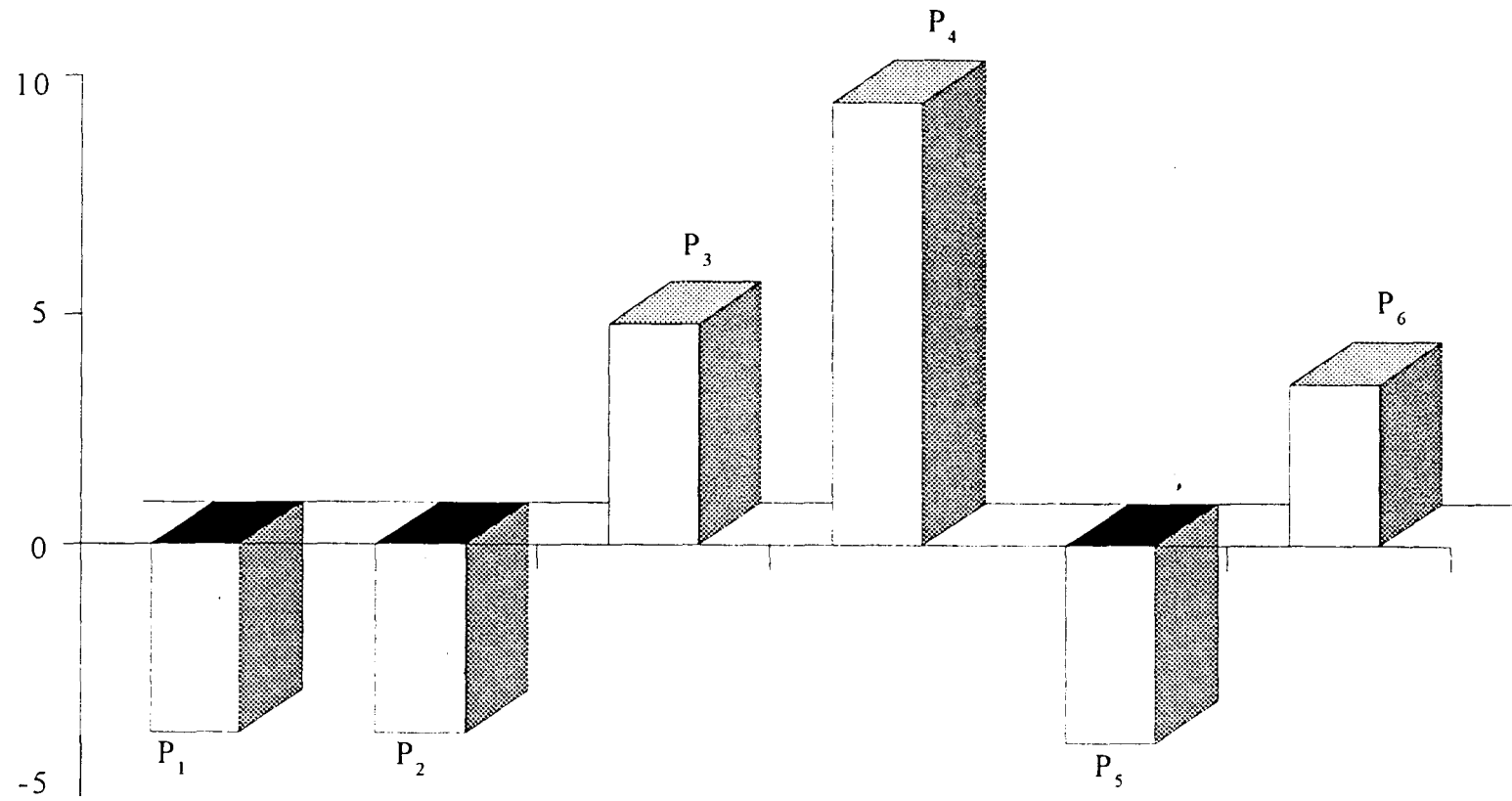Fig. 7. Length of pods - specific combining ability effects (sca)

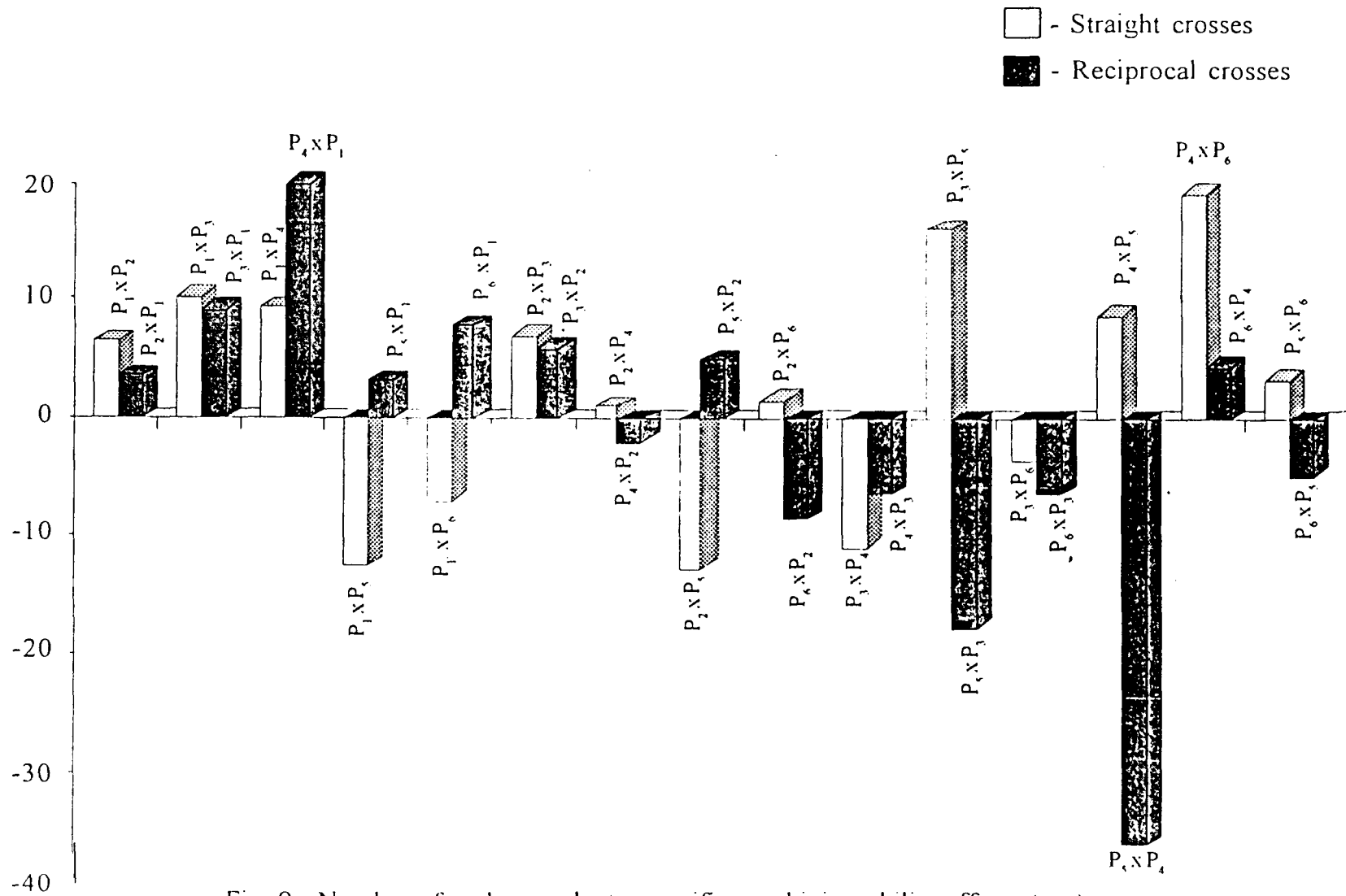Fig 8. Number of pods per plant - general combining ability effects (gca)

Fig. 9. Number of pods per plant - specific combining ability effects (sca)

4.2.6. Number of seeds per pod

The analysis of variance for combining ability showed significance for SCA only.

Among the hybrids, $P_1 \times P_6$ showed significant positive sca of 1.23, and $P_3 \times P_5$ showed significant negative sca of -1.05. So $P_1 \times P_6$ can be considered as the best specific combiner for this character (Fig. 10).

4.2.7. Seed Yield

The analysis of variance for combining ability revealed highly significant variance for GCA, SCA and reciprocal effects. The GCA was more indicating the importance of additive effect.

Among the parents, P_4 was found to be significantly different from all other parents. P_4 showed significantly high positive gca of 3.29. Among the hybrids, $P_1 \times P_4$ showed significant positive effects of 6.20 which was on par with $P_4 \times P_6$ (5.24), $P_1 \times P_3$ (4.70), $P_4 \times P_5$ (3.80), $P_2 \times P_3$ (2.53), $P_1 \times P_2$ (2.35), $P_5 \times P_6$ (2.33) and $P_3 \times P_5$ (2.20). In the reciprocals, $P_4 \times P_1$ (8.47) showed significant positive sca, which was on par with $P_4 \times P_3$ (3.52), $P_3 \times P_1$ (3.17), $P_5 \times P_1$ (3.16) and $P_6 \times P_1$ (1.86). So P_4 can be considered as the best general combiner and $P_4 \times P_1$ can be considered as the best specific combiner for this character (Fig.11 & Fig.12).
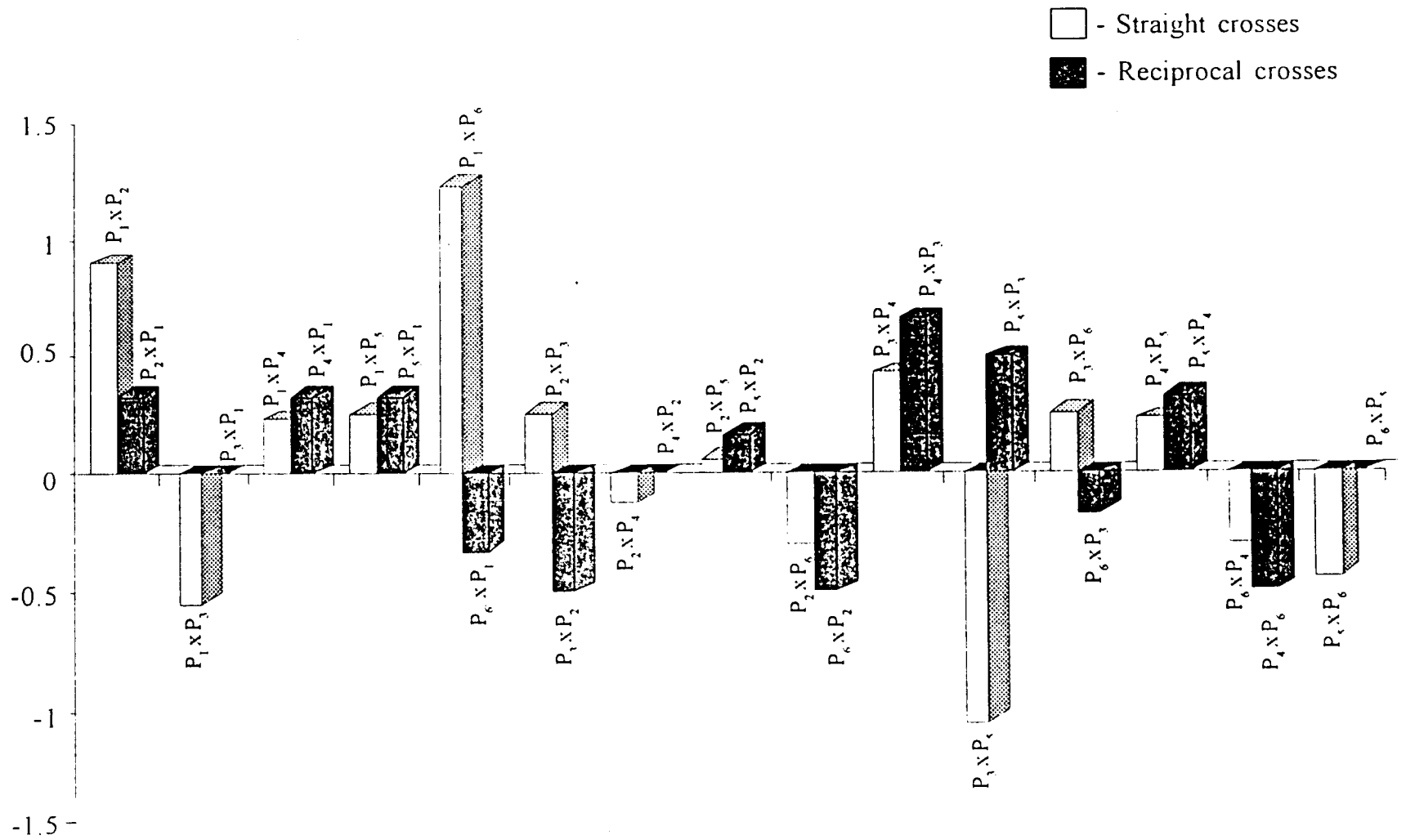
Fig. 10. Number of seeds per pod - specific combining ability effects (sca)
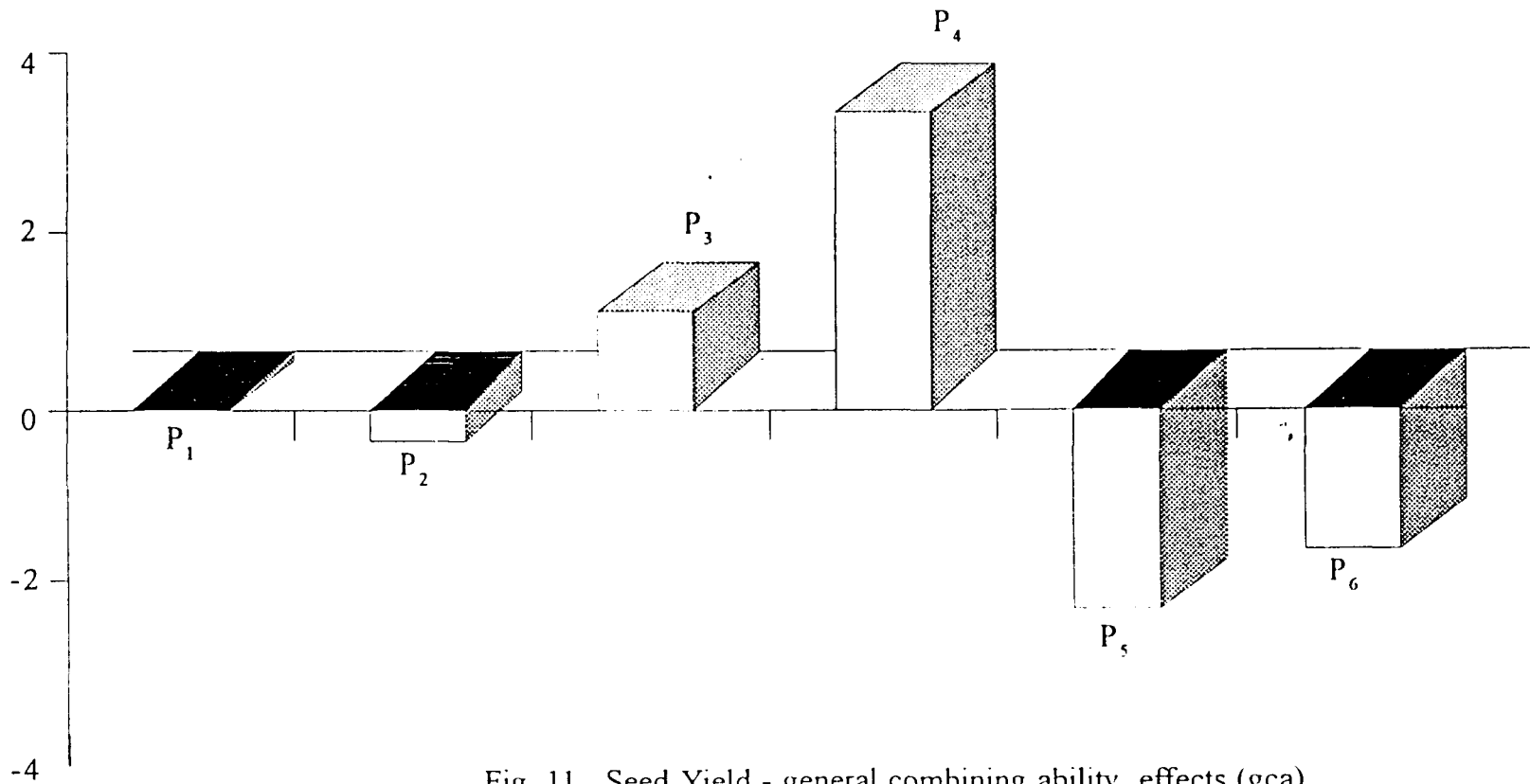
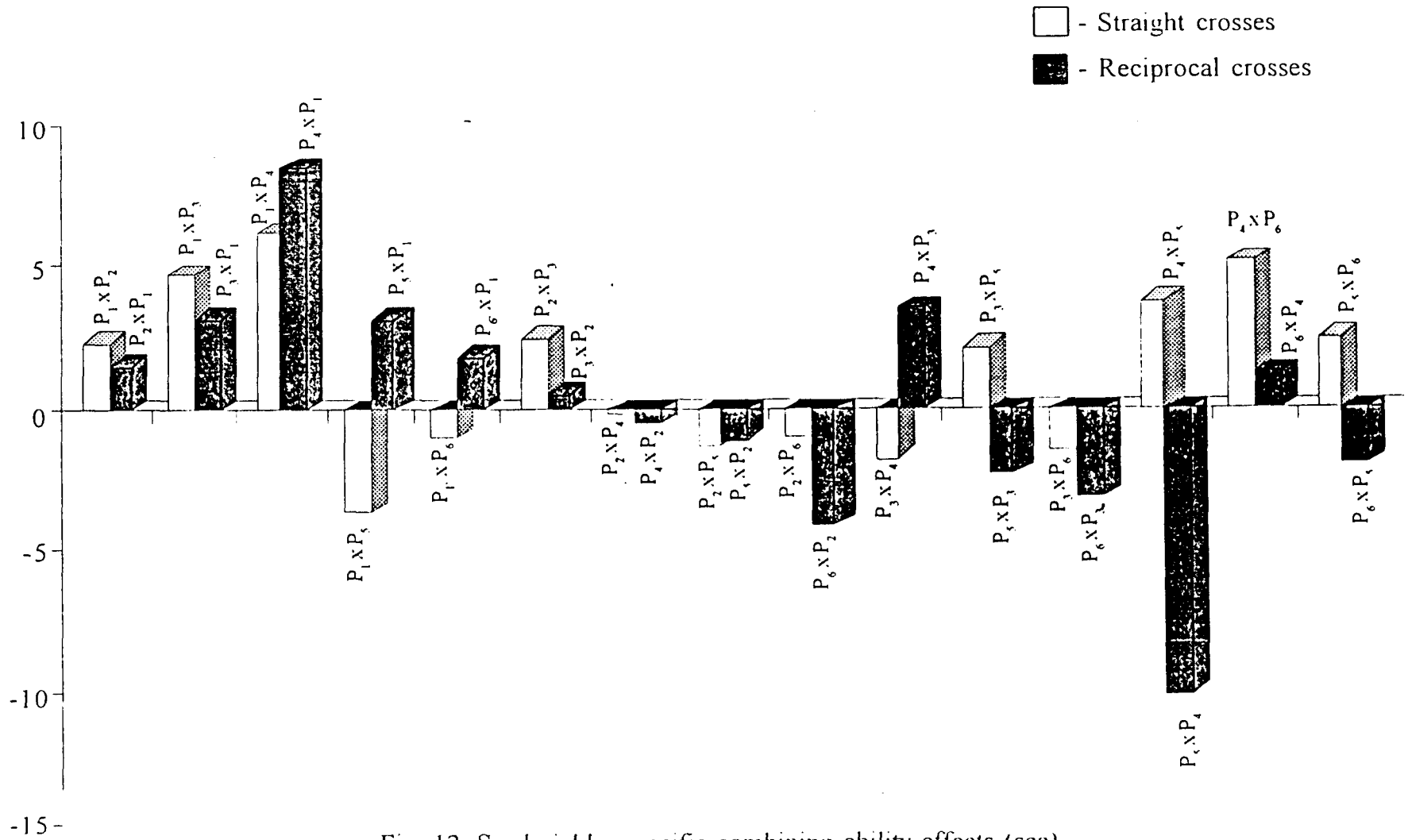Fig. 11. Seed Yield - general combining ability effects (gca)

Fig. 12. Seed yield - specific combining ability effects (sca)

4.2.8. 100 seed weight

The combining ability analysis revealed that, this character showed significant GCA and SCA. The GCA was more indicating the preponderence of additive effect for this character.

The parent, P_2 showed significant positive effect of 0.16, and the parent P_6 showed highly significant negative effect of -0.22. Among the hybrids, $P_3 \times P_4$ showed significant positive effect of 0.42. Among the reciprocals, $P_5 \times P_1$ showed significant positive effect of 0.39. So P_2 can be considered as the best general combiner, and $P_3 \times P_4$, the best specific combiner for this character (Fig. 13 & Fig.14).

4.2.9. Days to maturity

The analysis of combining ability revealed high significance for GCA, SCA and reciprocal effects.

The parent P_4 showed highly significant positive effect of 0.81 and P_5 showed significant negative effect of -0.60. Among the hybrids, $P_3 \times P_4$ (1.74) showed significant positive effect. $P_2 \times P_3$ and $P_4 \times P_5$ showed highly significant negative effects of -2.43 which were on par with $P_2 \times P_6$ (-1.65) and $P_1 \times P_4$ (-1.31). Among the reciprocals, $P_4 \times P_2$ showed significantly high positive effect of 2.17. Hence P_5 can be considered as the best general combiner and $P_2 \times P_3$ and $P_4 \times P_5$ can be considered as the best specific combiners for this trait (Fig.15 & Fig.16).
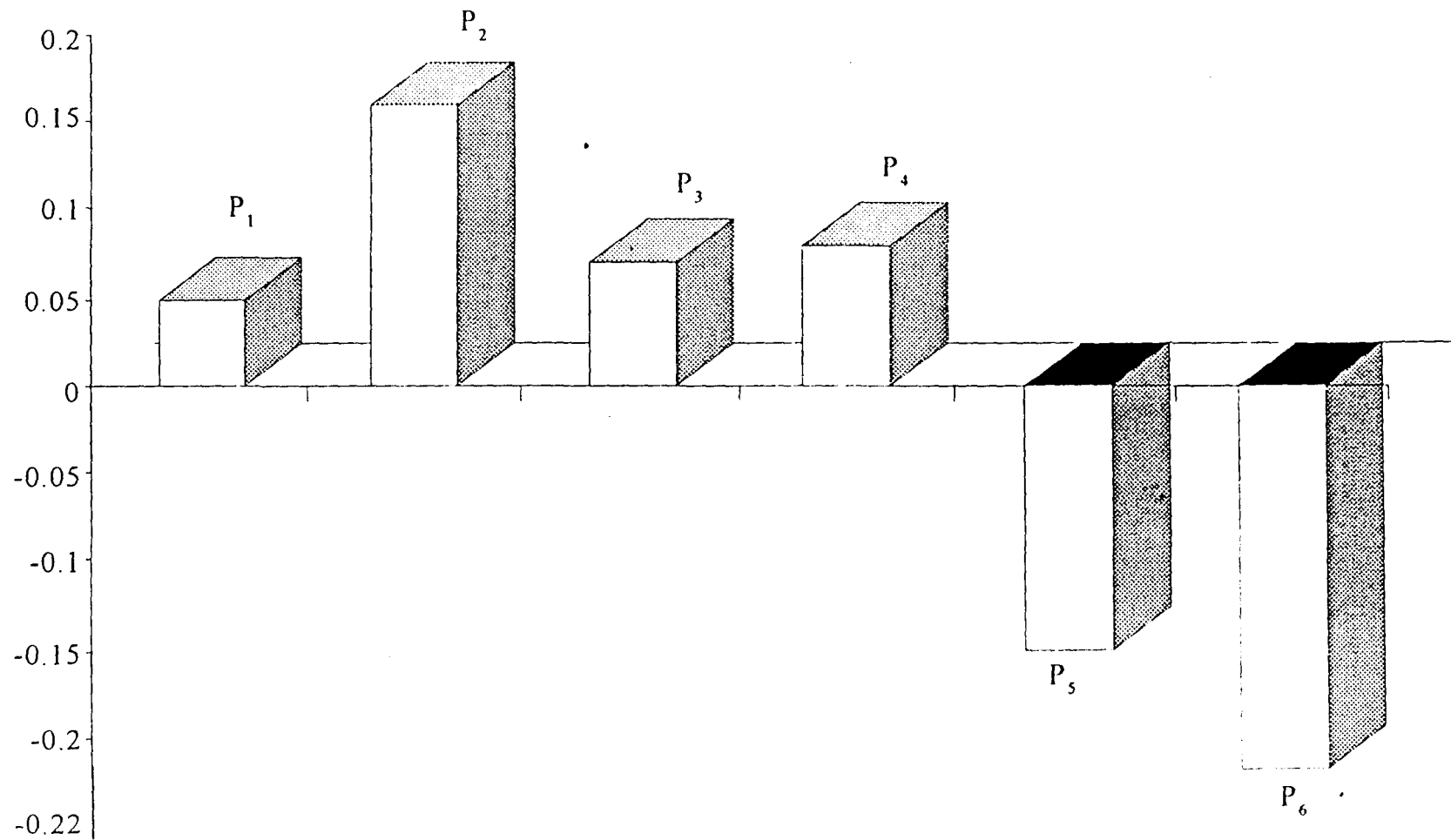
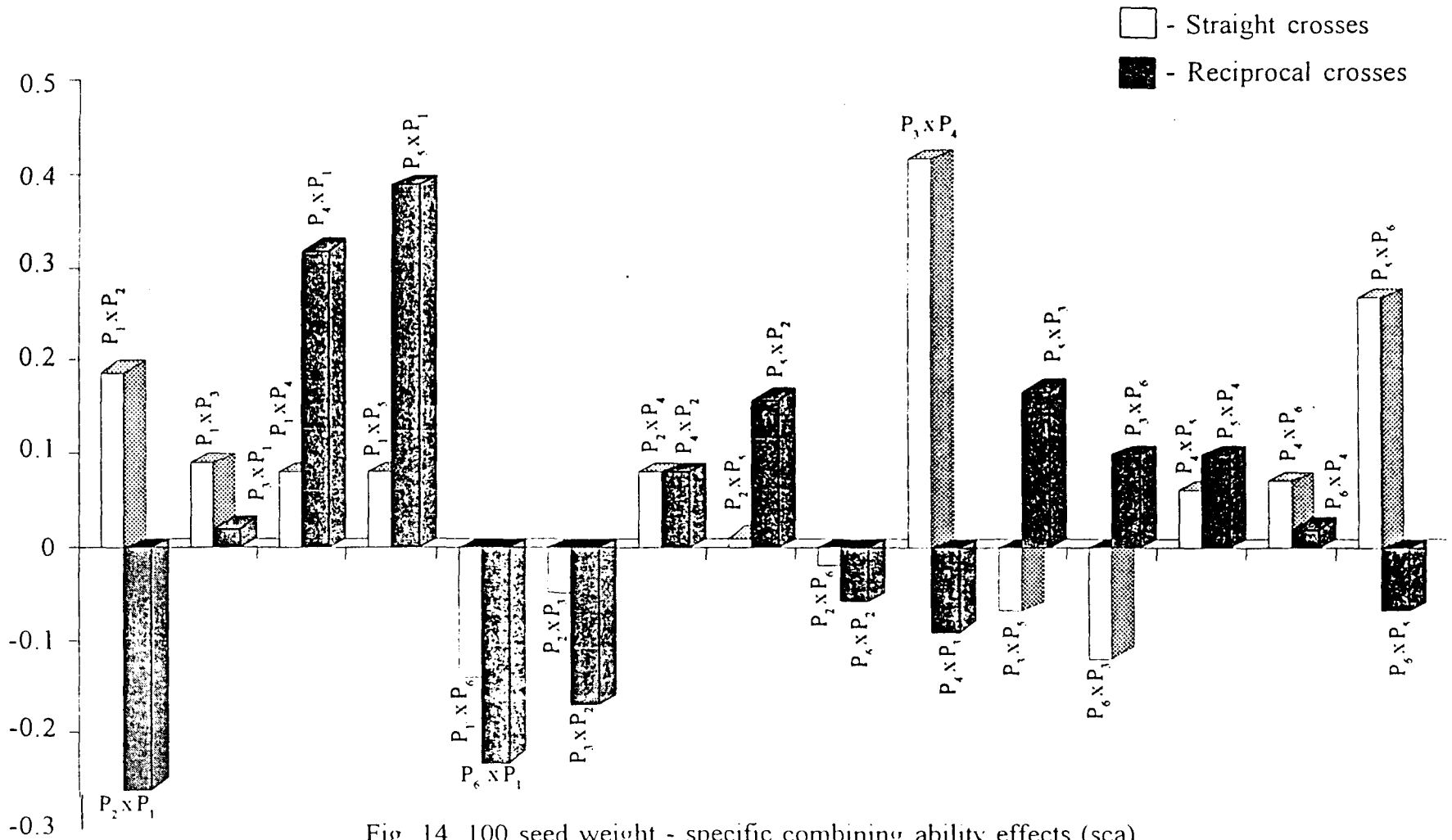Fig. 13. 100 seed weight - general combining ability effects (gca)

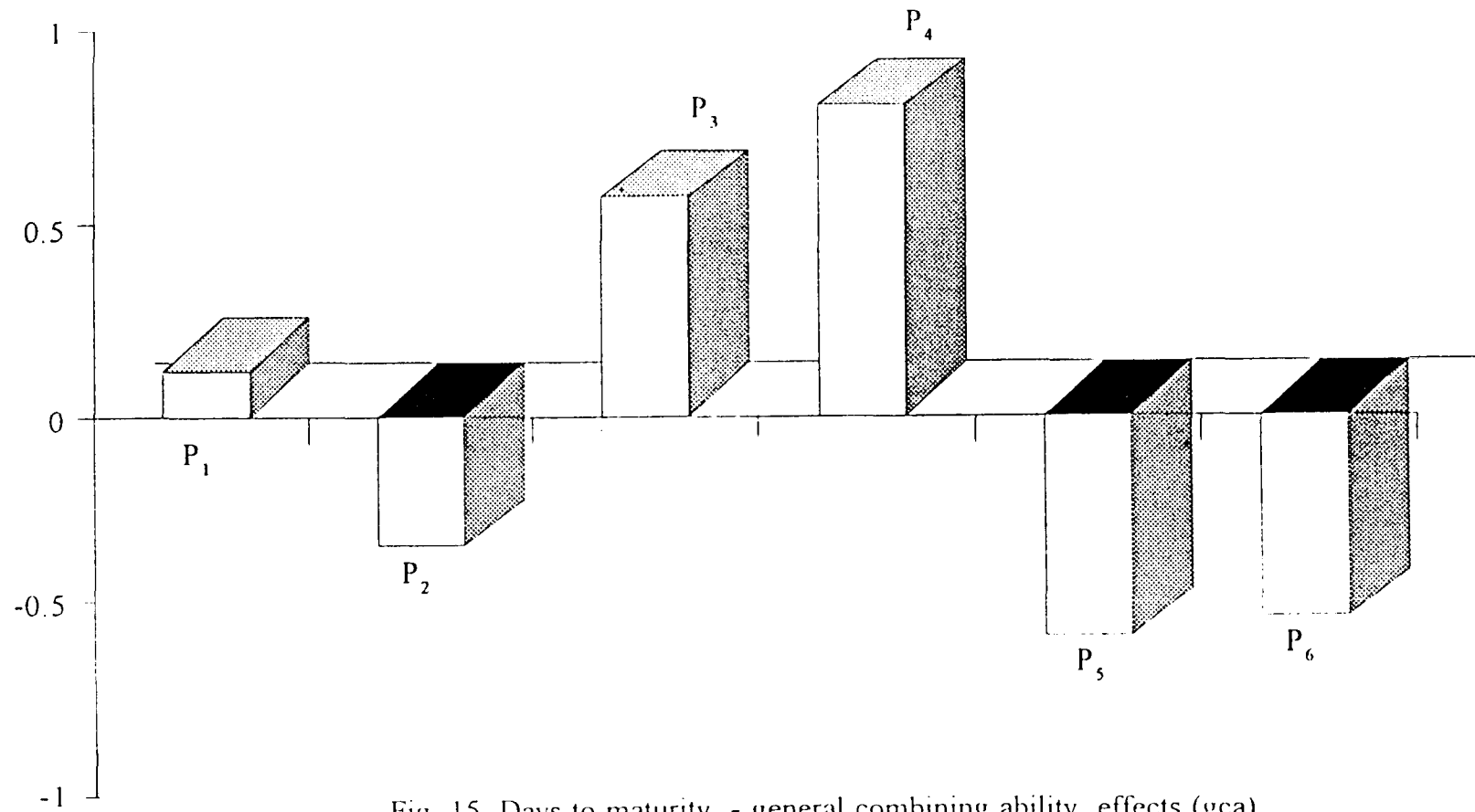Fig. 14. 100 seed weight - specific combining ability effects (sca)

Fig. 15. Days to maturity - general combining ability effects (gca)

Fig. 16. Days to maturity - specific combining ability effects (sca)

4.2.10. Root weight

The combining ability analysis revealed that, GCA, SCA and reciprocal effects were significant for this character. .

The parent P_4 showed significant positive gca of 0.66 and P_5 showed significant negative effect of -1.02. Among the hybrids, P_2 x P_4 showed significantly high positive effect of 3.36 which was on par with P_1 x P_3 (2.93). Among the reciprocals, P_3 x P_1 showed significantly high positive effect of 2.76, which was on par with P_6 x P_4 (2.39), P_4 x P_1 (1.50), P_6 x P_3 (1.47), P_2 x P_1 (1.01), P_5 x P_3 (0.97), P_6 x P_1 (0.90), P_5 x P_4 (0.45) and P_4 x P_3 (0.44). P_4 x P_2 showed significantly high negative effect of -2.27. Hence P_4 can be considered as the best general combiner and P_2 x P_4, the best specific combiner for this character (Fig.17 & Fig. 18).

4.2.11. Nodule weight

The combining ability analysis revealed, highly significant GCA, SCA and reciprocal effects.

The parent P_4 showed significantly high positive gca of 21.30, and P_6 showed significant negative gca of -13.84. Among the hybrids, P_1 x P_4 (66.62) was found to be highly significant and it was par with P_2 x P_3 (35.37). Among the reciprocals, P_5 x P_4 showed high positive sca of 45.00 and P_5 x P_3 showed high negative sca of -53.33. So P_4 can be considered as the best general combiner and P_1 x P_4 as the best specific combiner for this trait (Fig.19 & Fig. 20).
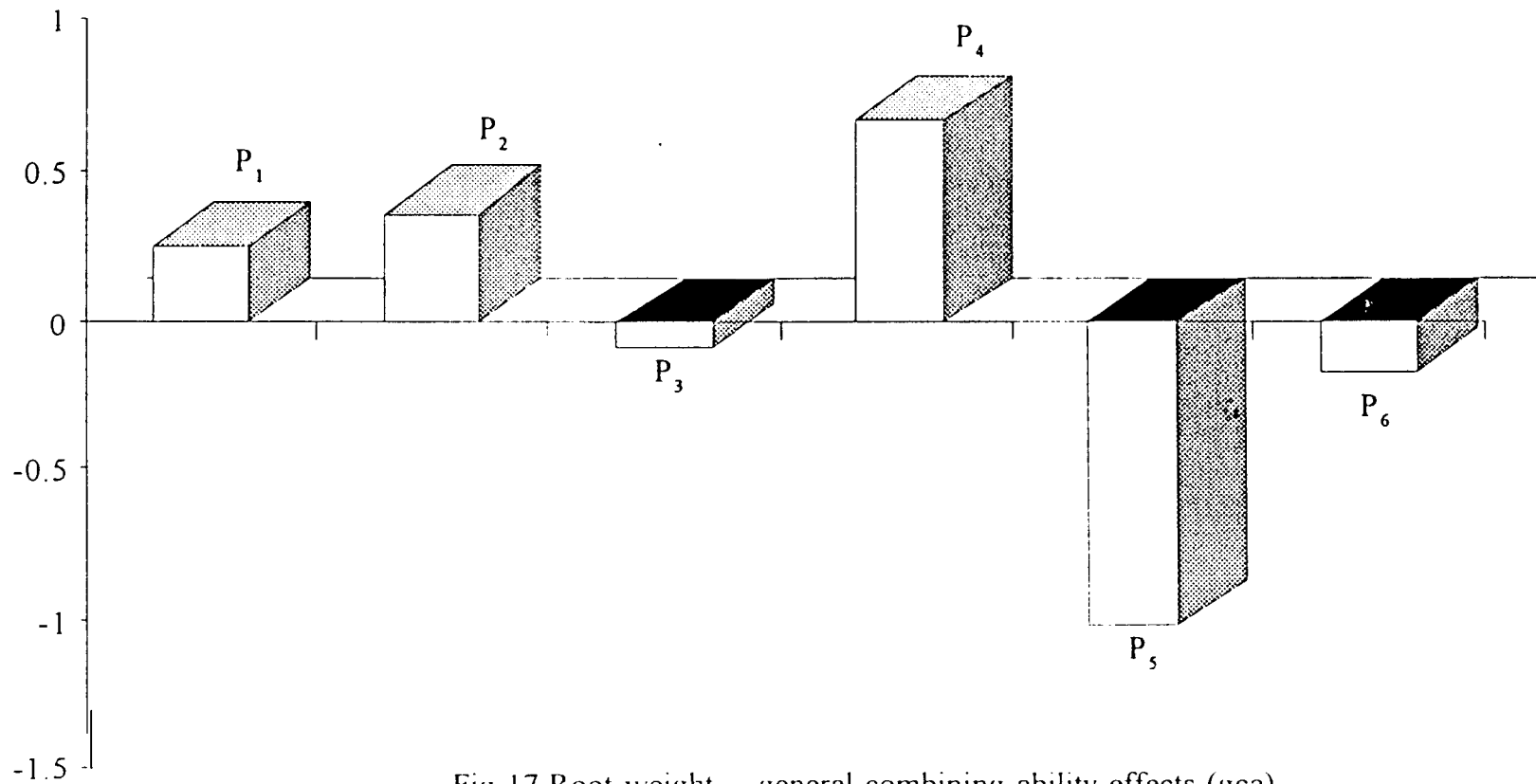
Fig 17 Root weight - general combining ability effects (gca)
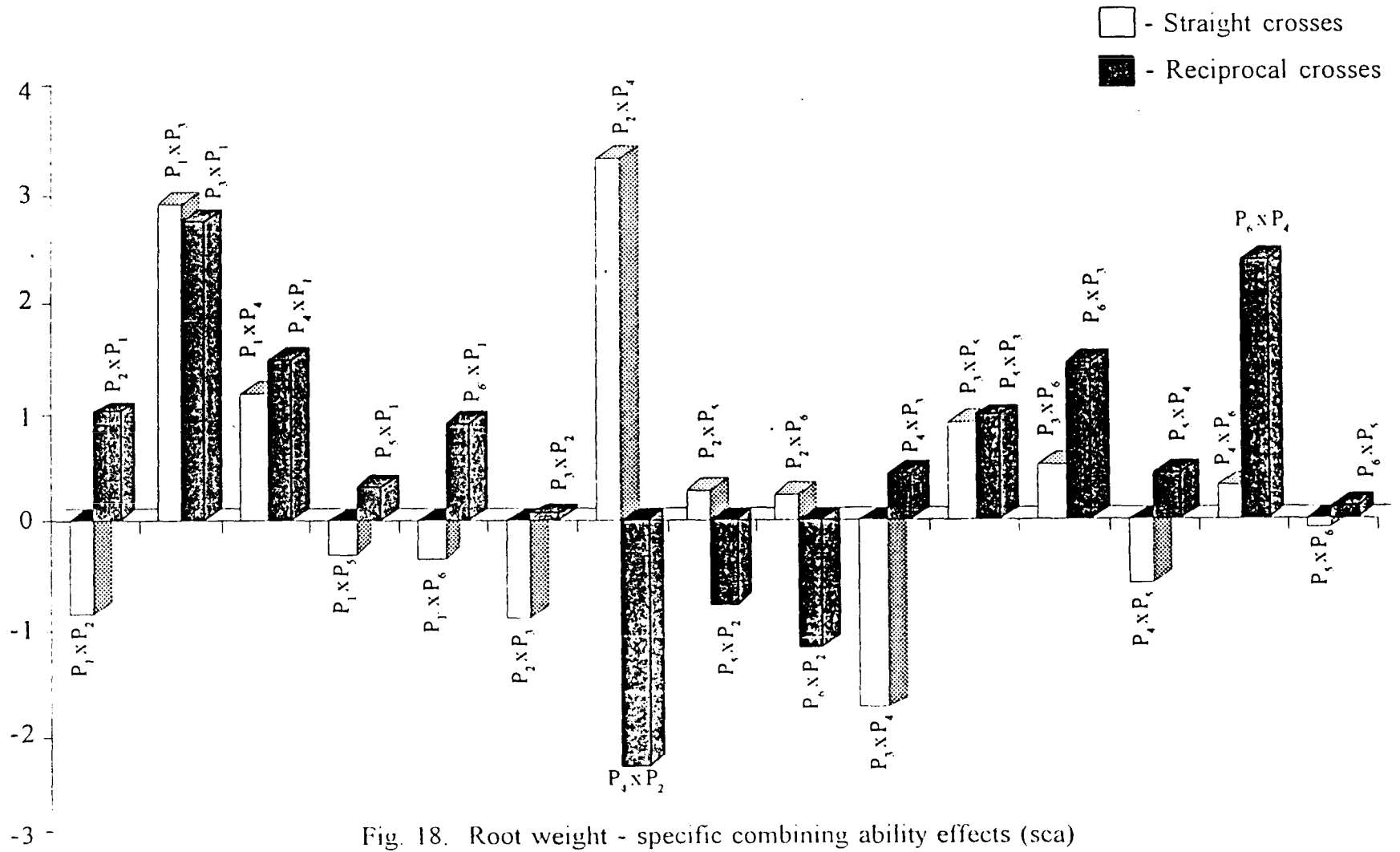
Fig. 18. Root weight - specific combining ability effects (sca)
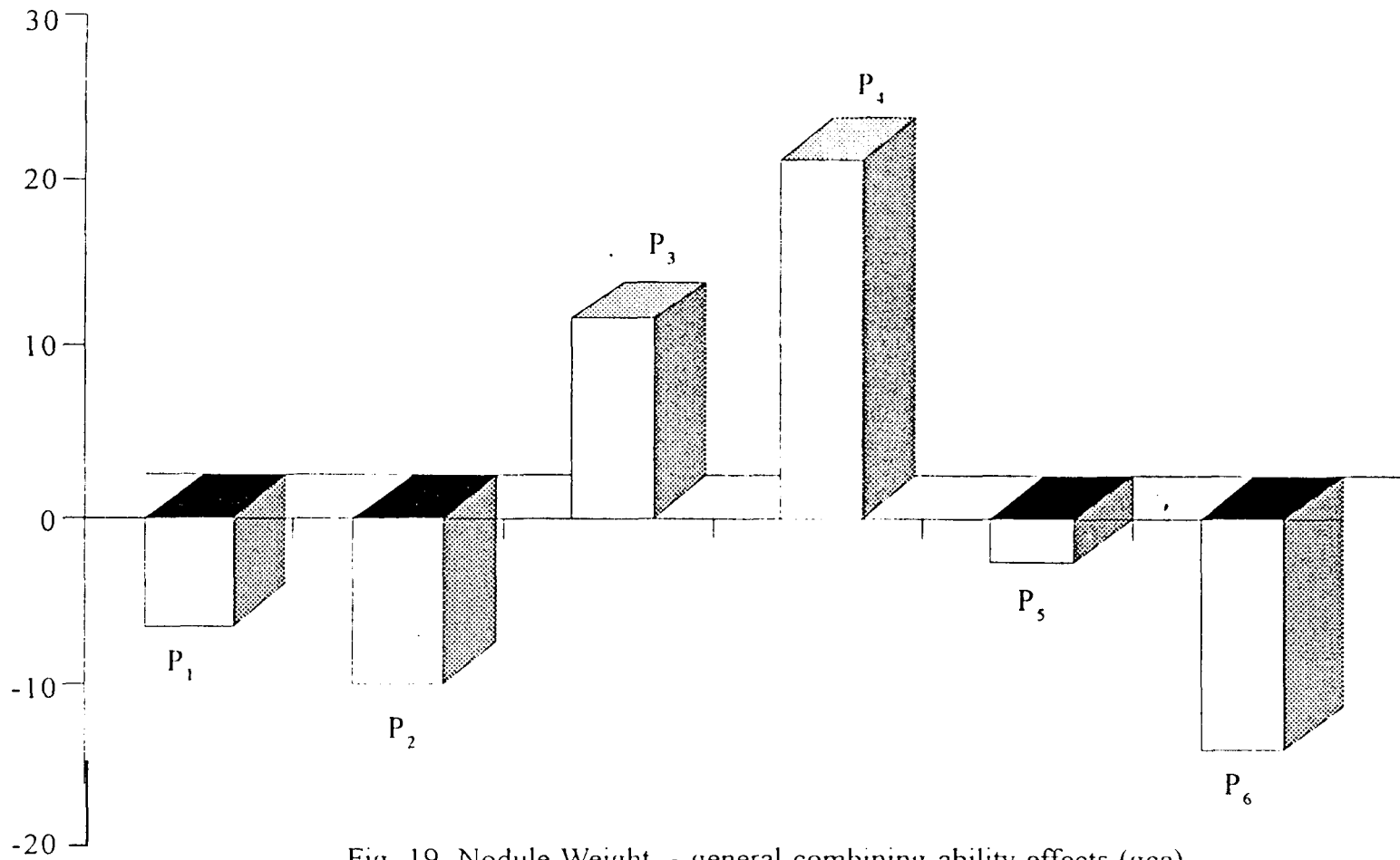
Fig. 19. Nodule Weight - general combining ability effects (gca)

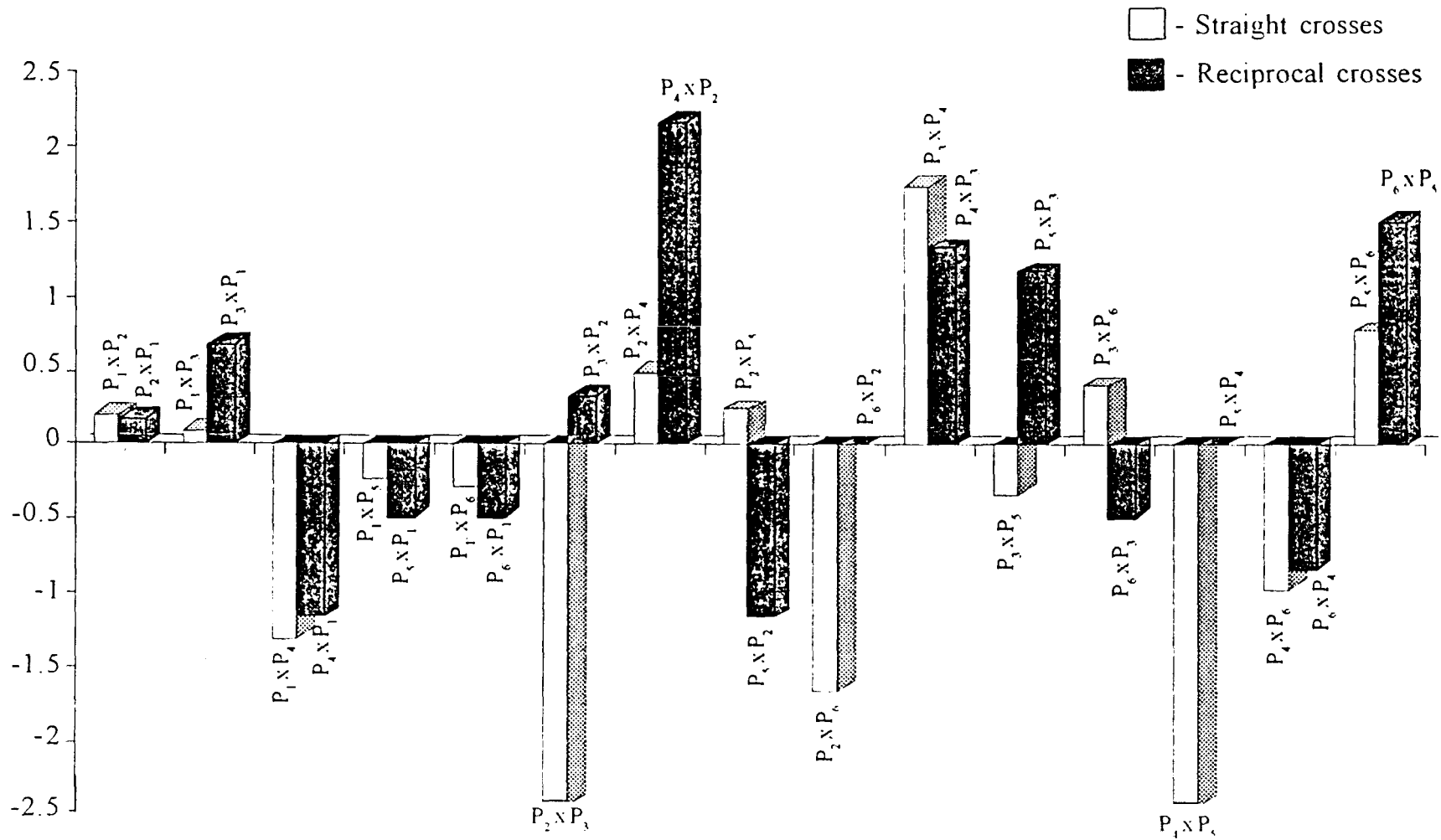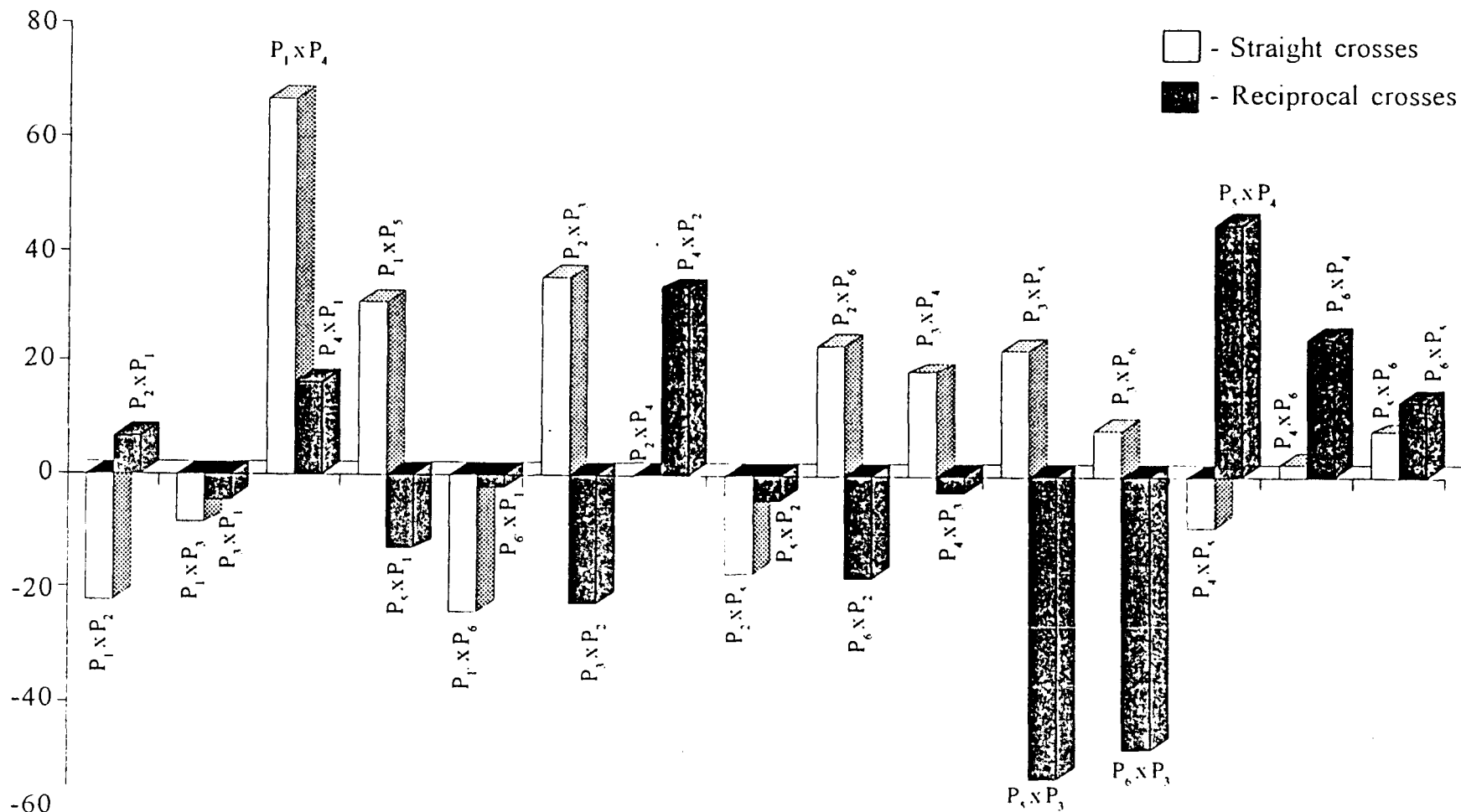Fig. 20. Nodule Weight - specific combining ability effects (sca)

4.2.12. Protein content

The combining ability analysis for protein content showed that the SCA and reciprocal effects were significant.

Among the hybrids, $P_3 \times P_4$ showed significantly high positive effect of 0.75. Among the reciprocals, $P_5 \times P_3$ showed significantly high positive effect of 0.96 and $P_6 \times P_4$ showed highly significant negative effect of -0.93. Hence, $P_5 \times P_3$ can be considered as the best specific combiner, while a good general combiner could not be suggested for this character (Fig. 21).

4.3. Gene action

The data related to the 12 characters under study were subjected to analysis by Hayman's Approach (1954), both numerically and graphically to determine the type of gene action governing the different characters.

4.3.1. Numerical and Graphical analysis

The data were subjected to numerical analysis to estimate the variance due to additive effect (D), variance due to dominance effect of positive and negative genes (H_1 and H_2), average covariance between additive and dominance effect over all the parental arrays (F), dominance effect (h^2), environmental effect (E). The other parameters such as average degree of dominance $[(H_1/D)^{1/2}]$, proportion of genes with positive and negative effects in the parents ($H_2/4H_1$) and proportion of
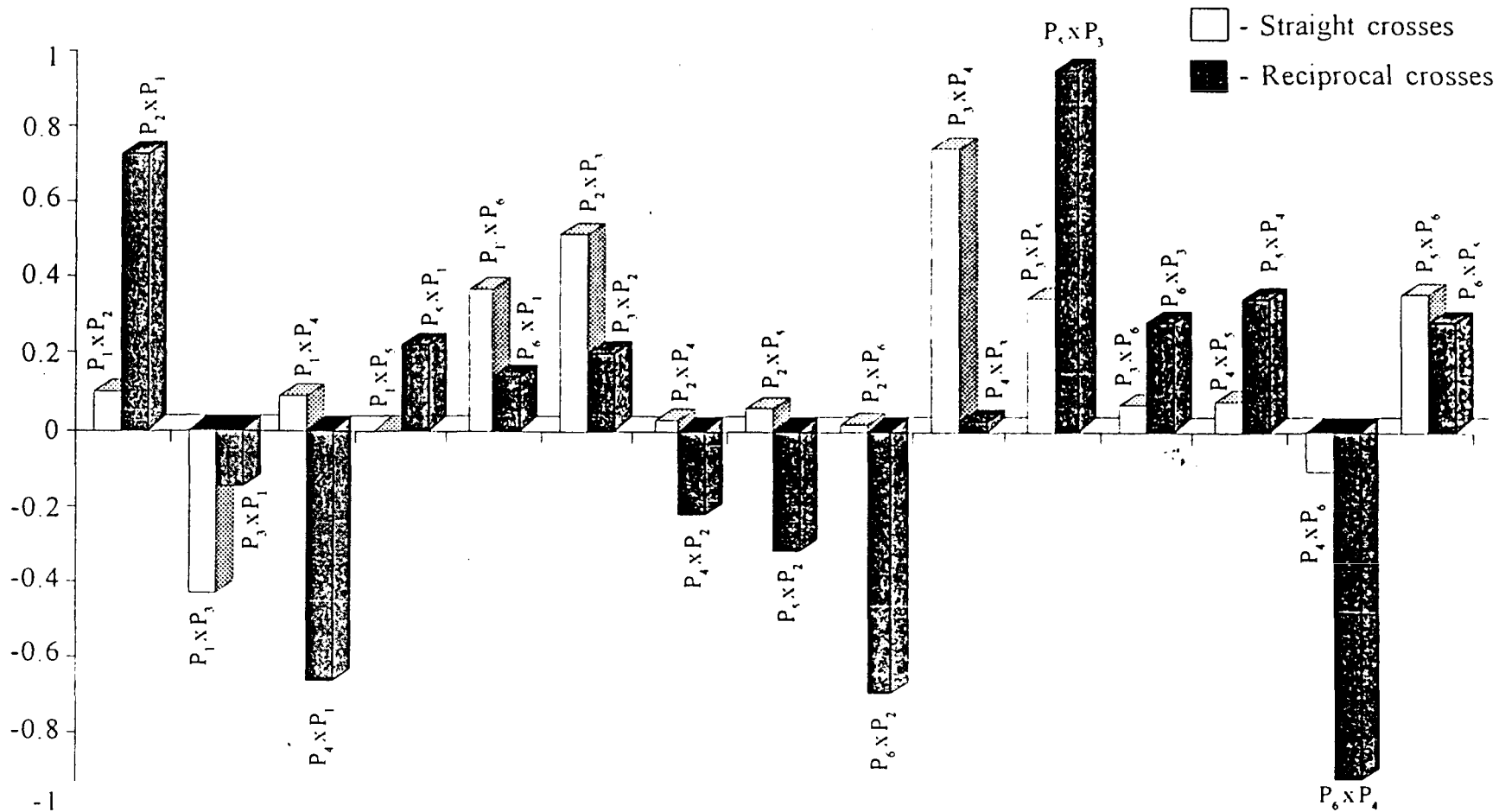
Fig. 21. Protein content - specific combining ability effects (sca)

dominant and recessive genes among parents were also estimated. The estimates

of the variance components and their proportions for the 12 characters are

presented in Table 7.

The data with respect to each of the 12 characters were also subjected to

graphical analysis by using variance-covariance graph (Vr-Wr graph).

4.3.1.1. Plant Height

.   Considering the parents, F_1's and reciprocals, the estimates of E (99.51) was

not significant. All other parameters, viz., D (654.22), F (1155.34), H_1(1765.64),

H_2(1162.38) and h^2(782.50) were significant. The positive value of F indicated

that increasing alleles were dominant in the parents. The value of H_1 was

significantly greater than D indicating overdominance for this character. The

average degree of dominance (1.64) and the proportion of dominant and recessive

genes in the parents (3.32) deviated from unit value. The value of $H_2/4H_1$ (0.16)

was lesser than the maximum attainable value of 0.25.

In the Vr - Wr graph, the regression coefficient (b) did not differ significantly

from unity (0.39), indicating absence of non-allelic interaction. The intercept of

regression line on the covariance axis being below the origin, shows a clear cut

case of overdominance. The array points along the regression line were not much

scattered. The parents, P_3, P_4, P_5 and P_6 appeared to possess most of the dominant

Table. 7 Estimates of genetic parameters and their proportions for parents and hybrids

Sl.no.	Character	D $\pm$ SE	$H_1 \pm$ SE	$H_2 \pm$ SE	F $\pm$ SE	$h^2 \pm$ SE
1.	Plant height	654.22* $\pm$ 186.67	1765.64* $\pm$ 473.87*	1162.38* $\pm$ 423.32	1155.34* $\pm$ 456.03	782.50* $\pm$ 284.92
2.	Number of branches	-0.16 $\pm$ 0.35	2.58* $\pm$ 0.89	2.22* $\pm$ 0.80	-0.09 $\pm$ 0.86	3.82* $\pm$ 0.54
3.	Days to first flowering	-0.27 $\pm$ 0.44	1.40 $\pm$ 1.12	1.29 $\pm$ 1.00	-0.08 $\pm$ 1.08	3.40* $\pm$ 0.67
4.	Length of pods	0.00 $\pm$ 0.10	1.04* $\pm$ 0.26	0.75* $\pm$ 0.23	0.19 $\pm$ 0.25	1.81* $\pm$ 0.16
5.	Number of pods/plant	-26.30 $\pm$ 45.15	577.43* $\pm$ 114.62	507.46* $\pm$ 102.39	-75.20 $\pm$ 110.30	573.43* $\pm$ 68.92
6.	Number of seeds/pod	0.43 $\pm$ 0.24	2.17* $\pm$ 0.61	1.28* $\pm$ 0.54	1.26* $\pm$ 0.58	0.32 $\pm$ 0.36
7.	Seed yield	-6.88 $\pm$ 8.54	66.85* $\pm$ 21.67	58.51* $\pm$ 19.36	-10.73 $\pm$ 20.86	154.50* $\pm$ 13.03
8.	100 seed weight	0.03 $\pm$ 0.02	0.11* $\pm$ 0.05	0.10* $\pm$ 0.05	-0.02 $\pm$ 0.05	0.36* $\pm$ 0.03
9.	Days to maturity	0.50 $\pm$ 0.61	8.17* $\pm$ 1.55	8.24* $\pm$ 1.38	-0.72 $\pm$ 1.49	18.49* $\pm$ 0.93
10.	Root weight	-1.16 $\pm$ 1.41	7.48* $\pm$ 3.57	7.44* $\pm$ 3.19	-2.00 $\pm$ 3.44	10.37* $\pm$ 2.15
11.	Nodule weight	-325.46 $\pm$ 537	4300.68* $\pm$ 1363.23	3844.3* $\pm$ 1217.81	-484.44 $\pm$ 1311.90	7618.51* $\pm$ 819.66
12.	Protein content	-0.04 $\pm$ 0.12	0.69* $\pm$ 0.30	0.65* $\pm$ 0.27	-0.03 $\pm$ 0.29	2.19* $\pm$ 0.30

*Significant at 5% level

Table. 7 continued

Sl.no.	Character	E ± SE	$\sqrt{\dfrac{H_1}{D}}$ (1)	$\dfrac{H_2}{4H_1}$ (2)	P.D.R.G. in parents (3)	Regression coefficient 'b' (4)
1.	Plant height	99.51 ± 70.55	1.64	0.16	3.32	0.3900
2.	Number of branches	0.59* ± 0.13	—	0.22	—	-0.1608
3.	Days to first flowering	0.69* ± 0.17	—	0.23	—	0.1900
4.	Length of pods	0.19* ± 0.04	0.00	0.18	—	0.5124
5.	Number of pods/plant	38.51* ± 17.07	—	0.22	—	0.2623
6.	Number of seeds/pod	0.41* ± 0.09	2.24	0.15	4.76	0.1917
7.	Seed yield	11.83* ± 3.23	—	0.22	—	0.2408
8.	100 seed weight	0.05* ± 0.01	1.82	0.22	0.68	0.5223
9.	Days to maturity	0.81* ± 0.23	4.04	0.25	0.70	0.6418
10.	Root weight	1.43* ± 0.53	—	0.25	—	0.0411
11.	Nodule weight	390.65* ± 202.97	—	0.22	—	0.1057
12.	Protein content	-0.14* ± 0.04	—	0.24	—	0.3316

*Significant at 5% level

(1)   Dominance action of genes
(2)   Asymmetry in the distribution of genes
(3)   Proportion of dominant and recessive genes in the parents

genes (>75%) while the parents, P_1 and P_2 had almost equal proportion of dominant and recessive genes (Fig. 22).

4.3.1.2. Number of branches

Considering the parents, F_1's and reciprocals, the estimates of E (0.59), H_1(2.58), H_2(2.22) and h^2(3.82) were significant, while the other parameters viz., D (-0.16) and F (-0.09) were not significant. The negative value of F indicated that decreasing alleles were dominant in the parents. The average degree of dominance and the proportion of dominant and recessive genes in the parents deviated from unity. The value of $H_2/4H_1$ (0.22) approached the maximum attainable value of 0.25.

In the Vr - Wr graph, b (-0.1608) differed significantly from unity. However, the interception of regression line on the covariance axis being above the origin, indicated partial dominance. The array points along the regression line were not much scattered (Fig. 23).

4.3.1.3. Days to first flowering

The estimates of E (0.69) and h^2 (3.40) were significant, while the other parameters viz., D (-0.27), F(-0.08), H_1(1.40) and H_2(1.29) were found to be not significant. The negative value of F indicated that decreasing alleles were dominant in the parents. The value of H_1 was greater than D, indicating overdominance for

Fig 22 . Vr-Wr graph of plant height
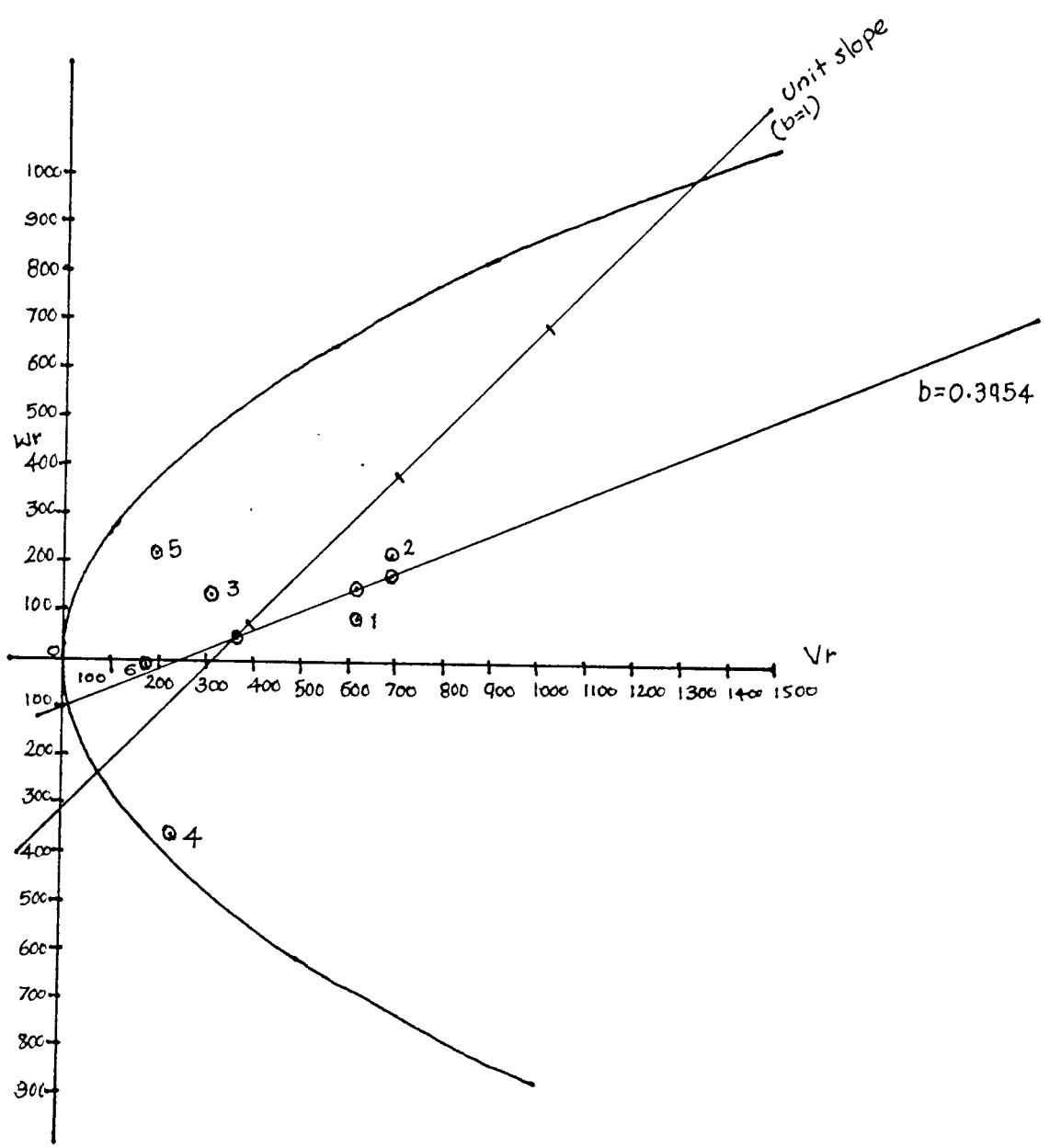
Fig: 23. Vr-Wr graph of number of branches
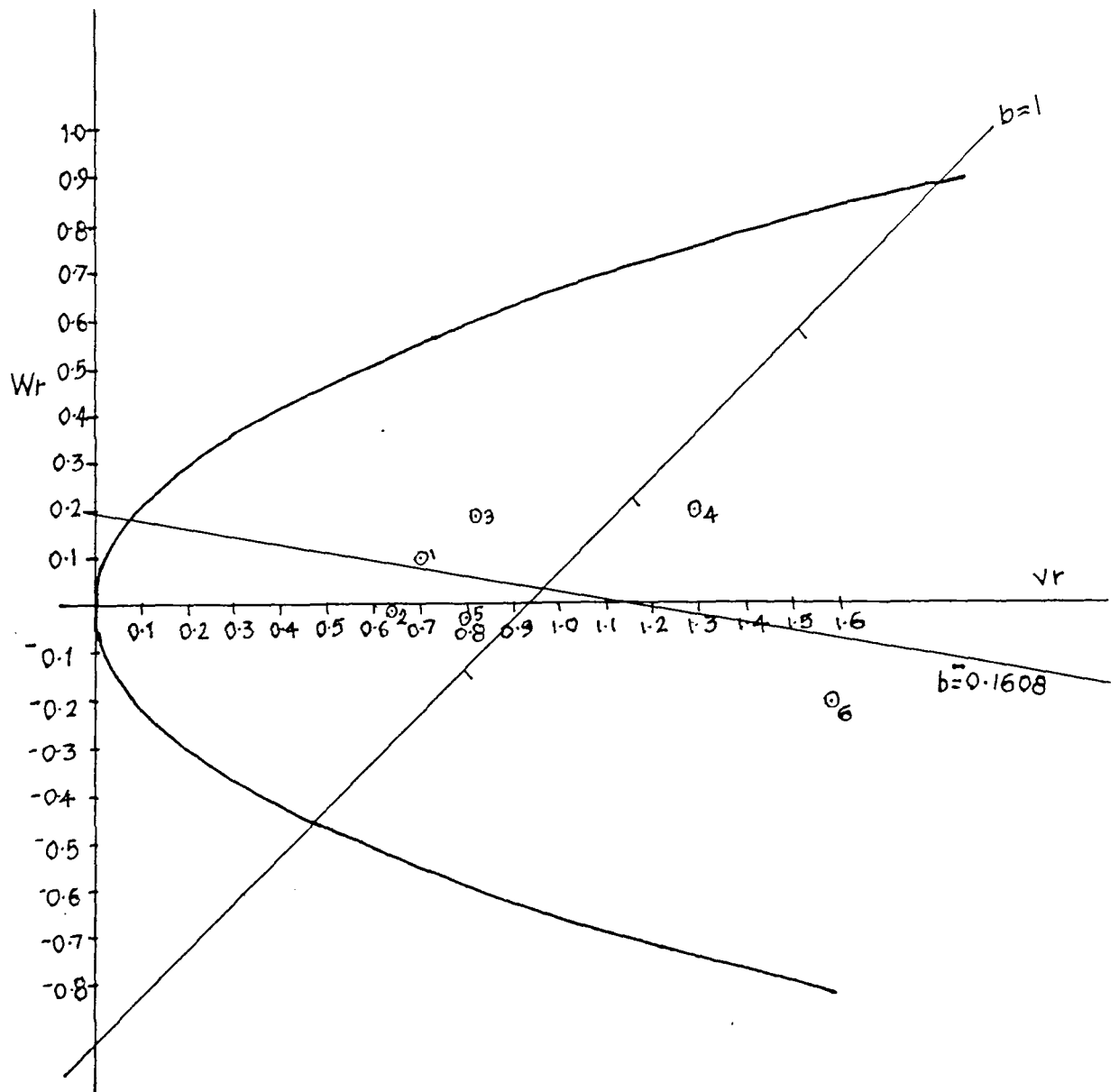
this character. The value of $H_2/4H_1$ was 0.23 which almost approached the maximum attainable value of 0.25 indicating equal distribution of positive and negative genes at all loci.

In the Vr-Wr graph, the interception of regression line on the covariance axis being below the origin, showed overdominance for this character. The absence of non-allelic interaction was not satisfactory, since b (0.19) differed significantly from unity. The scattered array points on regression line indicated diversity among the parents (Fig. 24).

4.3.1.4. Length of pods

Considering the parents, F_1's and reciprocals, the estimates of D (0.00), and F (0.19) were not significant, while the other parameters, E (0.19), H_1(1.04), H_2(0.75) and h^2 (1.81)were found to be significant. The positive value of F indicated that increasing alleles were dominant in the parents. The average degree of dominance and the proportion of dominant and recessive genes in the parents deviated from unity. The value of $H_2/4H_1$ (0.18) was less than the maximum attainable value of 0.25.

In the Vr-Wr graph, assumption of absence of non-allelic interaction appeared to be satisfactory. The regression coefficient did not differ significantly from unity (0.5124). The intercept of regression line on the covariance axis being

Fig: 24. Vr-Wr graph of days to first flowering
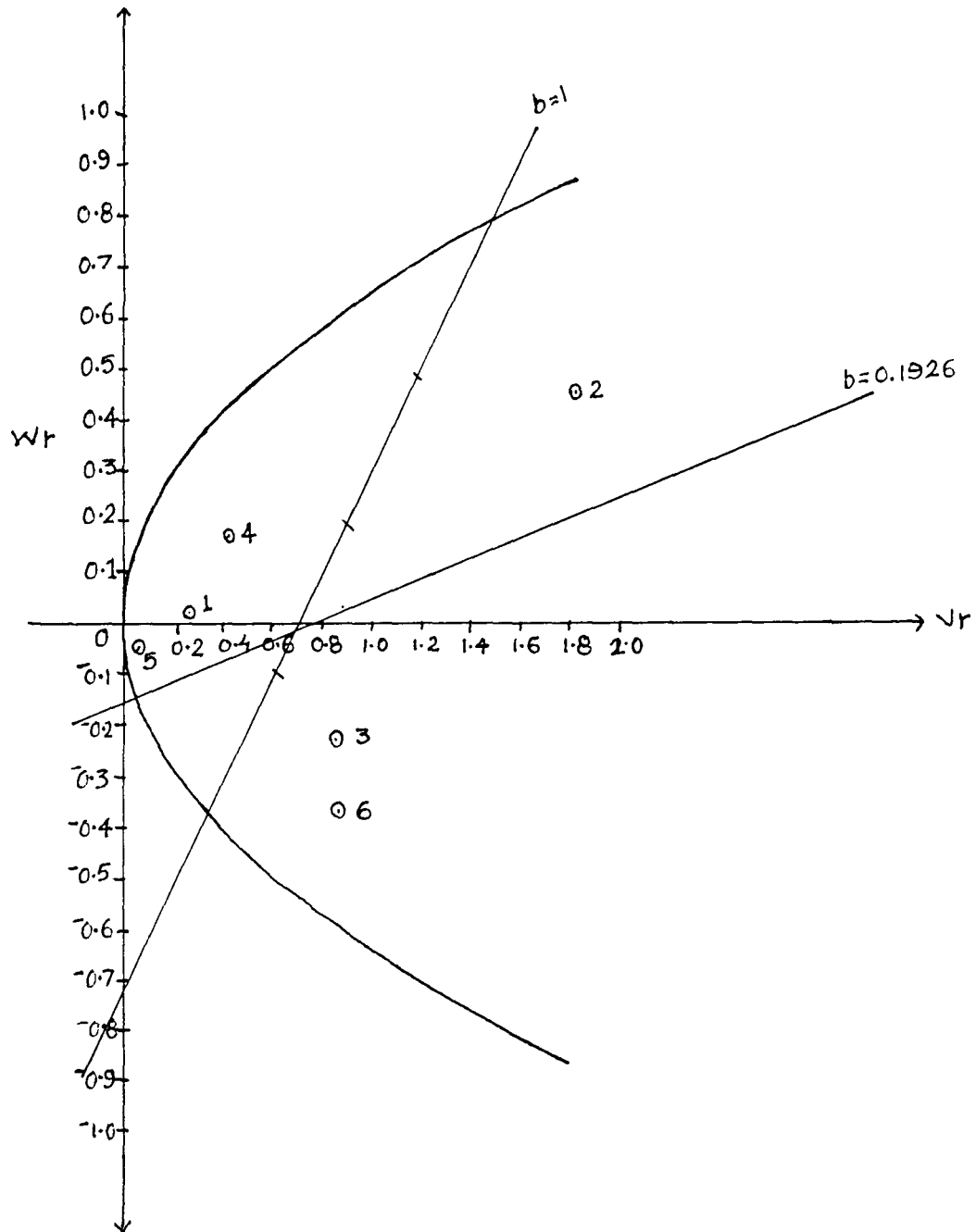
below the origin, showed a clear cut evidence of overdominance. The array points on the regression line were not much scattered, indicating less diversity among the parents. The parents, P_2, P_3 and P_5 were found to possess mostly dominant genes (>75%). P_4 and P_6 possessed 50-75% of dominant genes, while the parent, P_1 contained an excess of recessive genes (Fig. 25).

4.3.1.5. Number of pods per plant

The estimates of D (-26.30) and F (-75.20) were found to be non-significant for this character, while the other parameters E(38.51), H_1(577.43),H_2(507.46) and h^2 (573.43) were found to be highly significant. The negative value of F indicated that decreasing alleles were dominant in the parents. The value of H_1 was significantly greater than D, indicating overdominance for this character. The value of $H_2/4H_1$ (0.22) seemed to approach the maximum attainable value of 0.25, indicating equal distribution of positive and negative genes to all loci.

In the Vr-Wr graph, b (0.2623) was significantly different from unity. The intercept of regression line on the covariance axis being below the origin, showed overdominance for this character. The array points along the regression line were found to be scattered on the regression line, indicating diversity among the parents (Fig. 26).

Fig:25. Vr-Wr graph of length of pods
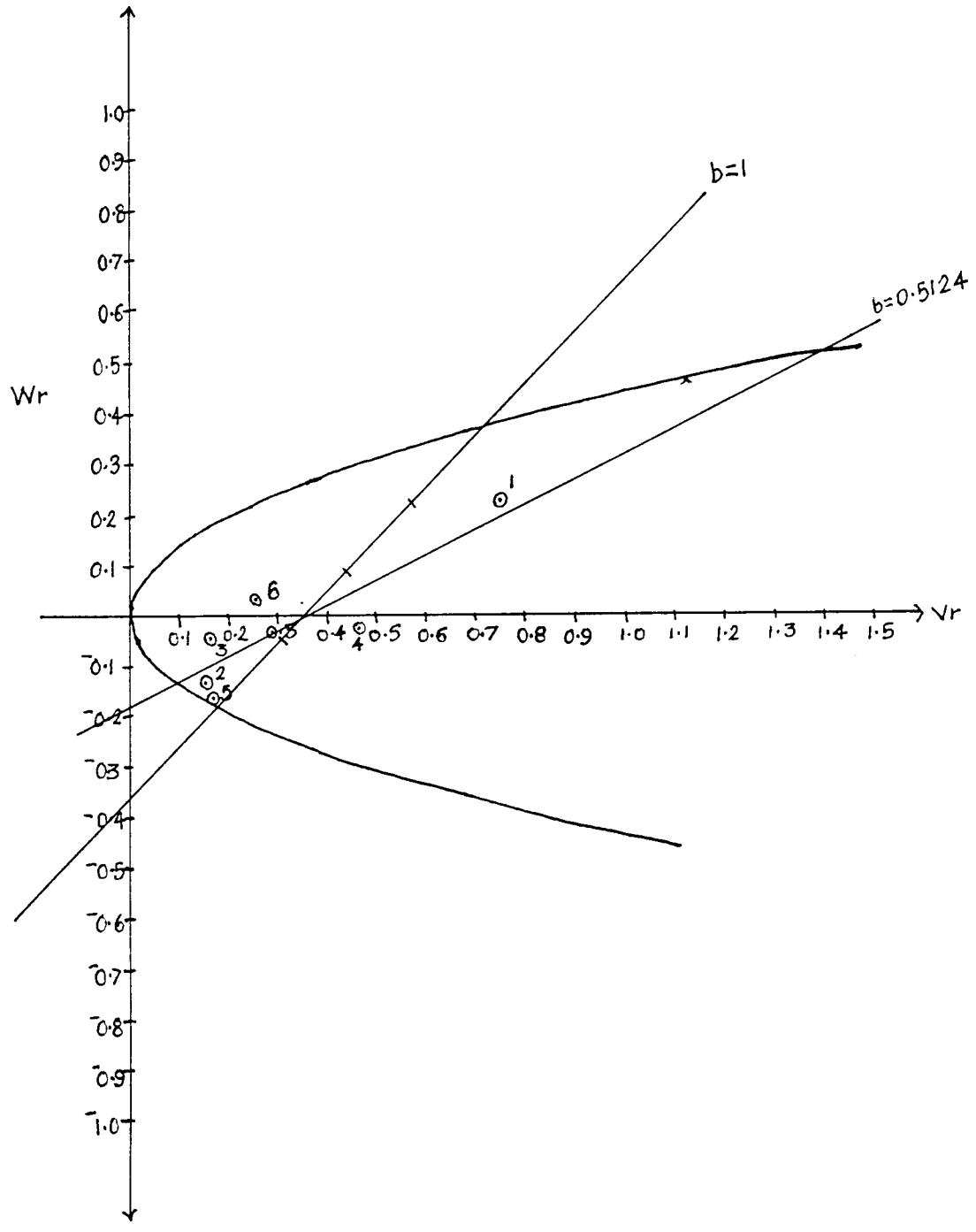
Fig: 26. Vr-Wr graph of number of pods per plant
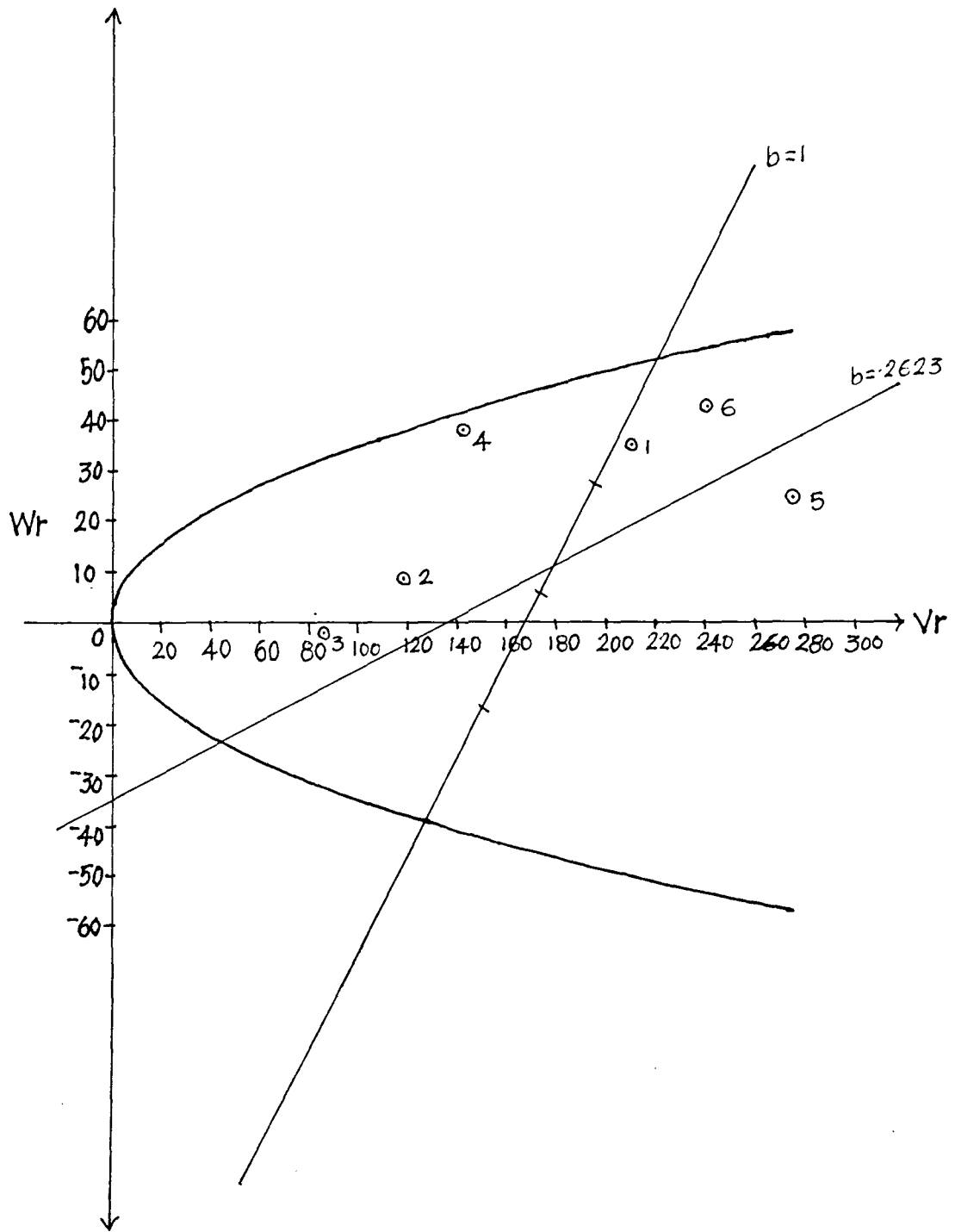
4.3.1.6. Number of seeds per pod

In this character, the estimates of D (0.43) and h^2 (0.32) were found to be not significant, while the other parameters viz., E (0.41), F (1.26), H_1 (2.17) and H_2 (1.28) were found to be significant. The positive value of F indicated that increasing alleles were dominant in the parents. The average degree of dominance (2.24) and the proportion of dominant and recessive genes in the parents (4.76) deviated from unity. The value of $H_2/4H_1$ (0.15) was found to be lesser than 0.25.

In the Vr-Wr graph, the intercept of regression line on the covariance axis being below the origin, indicated overdominance. The array points along the regression line were scattered, indicating diversity among the parents. All the parents except P_1, were found to possess mostly dominant genes. But the assumption of absence of non-allelic interaction was not satisfactory, since b (0.1917) was significantly different from unity (Fig. 27).

4.3.1.7. Seed yield

The estimates of D (-6.88) and F (-10.73) were found to be non-significant for this character, while the other estimates were found to be significant, viz., E (11.83), H_1 (66.85), H_2 (58.51) and h^2 (154.50). The negative value of F indicated that decreasing alleles were dominant in the parents. The value of H_1 was significantly greater than D indicating overdominance for this character. The value of $H_2/4H_1$ (0.22) seemed to approach the maximum attainable value of 0.25.

Fig: 27. Vr-Wr graph of number of seeds per pod
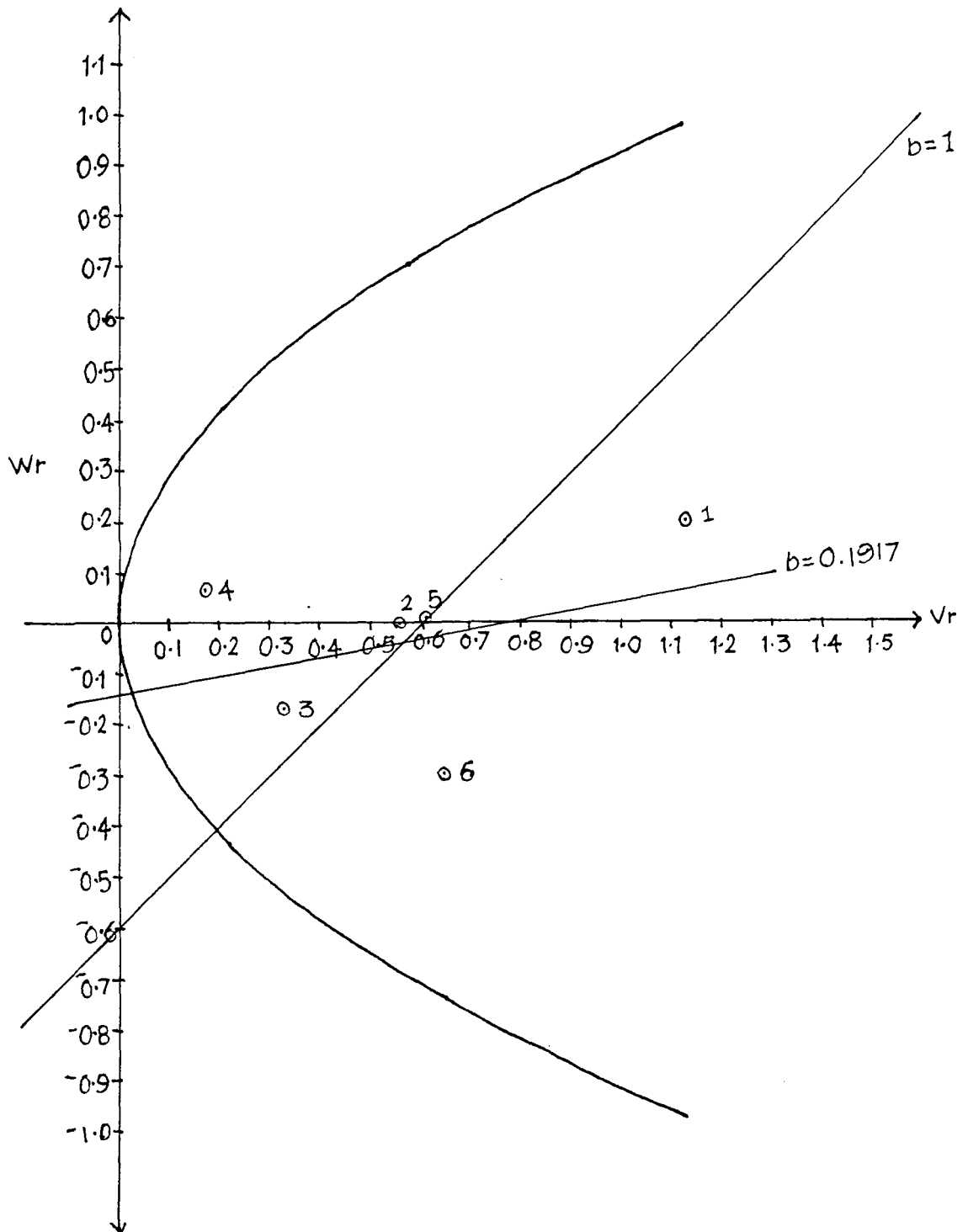
The regression coefficient (b = 0 .2408) did not differ significantly from unity, indicating that absence of non-allelic interaction was satisfactory. In the Vr-Wr graph, the intercept of regression line on the covariance axis being below the origin, shows a clear cut case of overdominance. The array points on the regression line were not much scattered. The parents, P_2 and P_3 appeared to possess most of the dominant genes (>75%). The parents P_4, P_5 and P_6 were found to contain equal proportions of dominant and recessive genes and the parent P_1 possessed mostly recessive genes (Fig . 28).

4.3.1.8. Hundred seed weight

Considering the parents, F_1's and reciprocals, the estimates of D (0.03) and F (-0.02) were found to be non-significant. All other parameters, viz., E (0.05), H_1(0.11), H_2(0.10) and h^2(0.36) were found to be significant. The negative value of F indicated that decreasing alleles were dominant for this character. The average degree of dominance (1.82) and the proportion of dominant and recessive genes (0.68) deviated from unity. The value of $H_2/4H_1$ (0.22) approached the maximum attainable value of 0.25, which indicated equal distribution of positive and negative genes at all loci.

In the Vr-Wr graph, assumption of absence of non-allelic interaction appears to be satisfied. The regression coefficient did not differ significantly from unity (0.5223). The interception of regression line on the covariance axis being below

Fig:28. Vr-Wr graph of seed yield
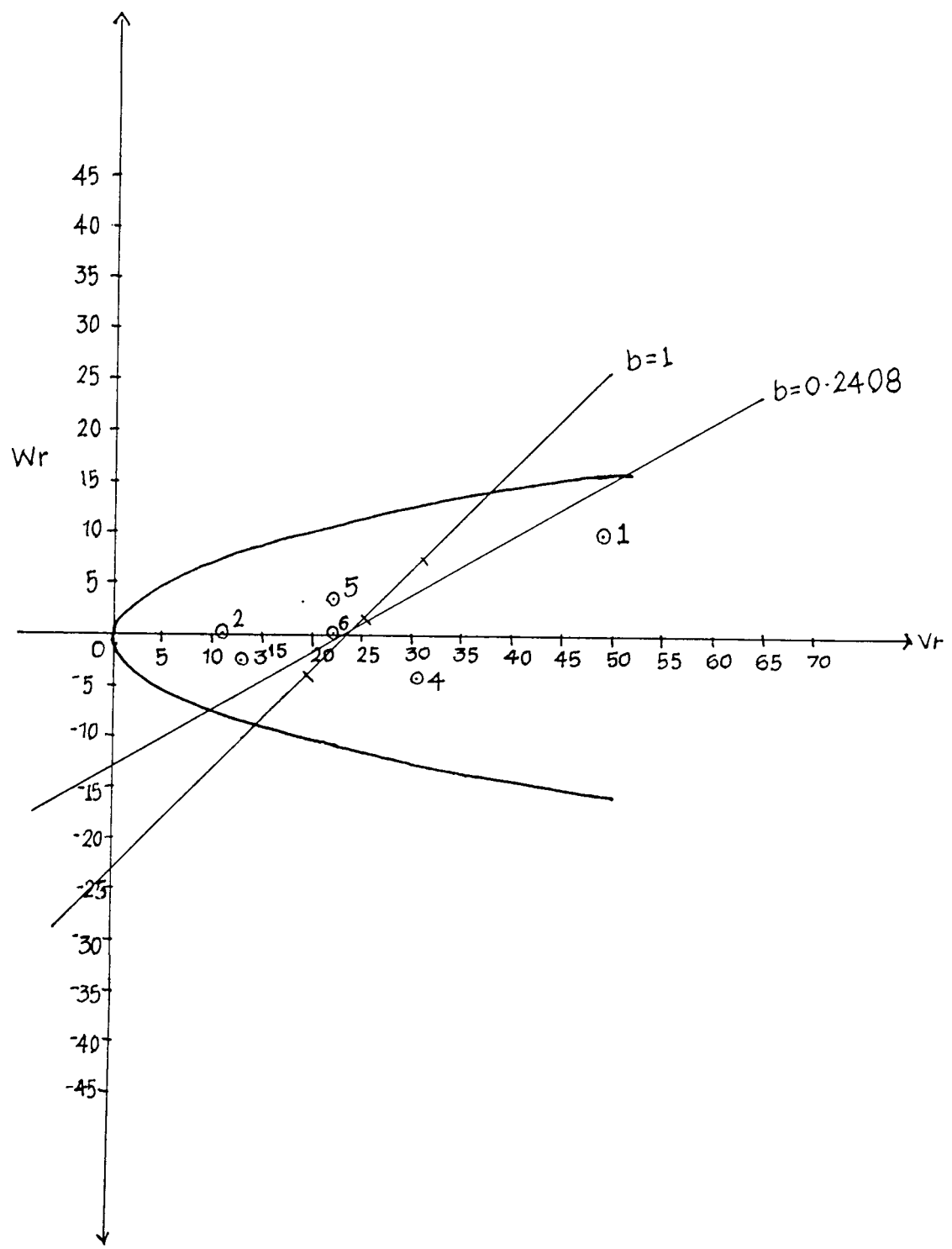
the origin, showed overdominance for this character. The scattered array points on the regression line indicated diversity among parents. The parents, P_2 and P_6 seemed to possess most of the dominant genes (>75%). The parents, P_1, P_3 and P_5 appeared to possess equal proportion of dominant and recessive genes, while the parent P_4 possessed mostly recessive genes for this character (Fig. 29).

4.3.1.9. Days to maturity

In this character, the estimates of D (0.50) and F (-0.72) were not significant. The other parameters viz., E (0.81), H_1(8.17), H_2(8.24) and h^2 (18.49) were significant. The negative value of F indicated that decreasing alleles were dominant in the parents. The value of H_1 was significantly greater than D indicating overdominance for this character. The average degree of dominance (4.04) and the proportion of dominant and recessive genes in the parents (0.70) deviated from unit value. However, the value of $H_2/4H_1$ equal to the maximum attainable value of 0.25 indicated equal proportion of genes with positive and negative effects.

In the Vr-Wr graph, the interception of regression line on the covariance axis being below the origin, shows a clear cut case of overdominance. The array points along the regression line were scattered, indicating diversity among the parents. The assumption of absence of non-allelic interaction appears to be satisfied. The regression coefficient did not differ significantly from unity (0.6418). The parents, P_1, P_5 and P_6 were found to possess most of the dominant genes (>75%).

Fig: 29. Vr-Wr graph of 100 seed weight
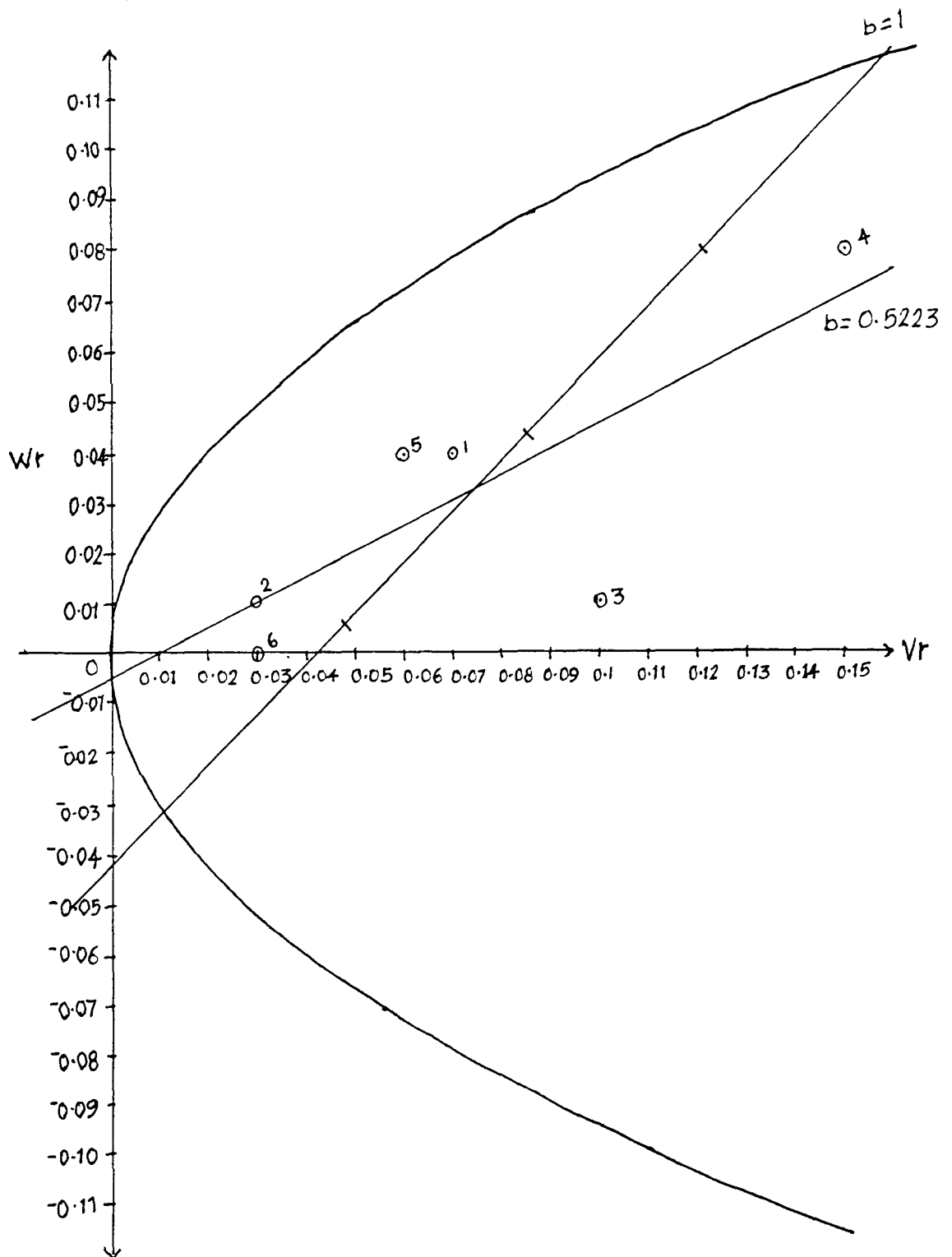
The parents P_2 and P_3 were found to possess 25-50% dominant genes, while the parent, P_4 appeared to possess most of the recessive genes (Fig. 30).

4.3.1.10. Root weight

The estimates of D (-1.16) and F (-2.00) are not significant, in this character. All other parameters viz., E (1.43), H_1(7.44), H_2(7.48) and h^2 (10.37) were found to be significant. The negative value of F indicated that decreasing alleles were dominant in the parents. The value of H_1 was significantly greater than D indicating overdominance for this charcter. The value of $H_2/4H_1$ (0.25) reached the maximum attainable value of 0.25.

In the Vr-Wr graph, the intercept of regression line on the covariance axis being below the origin, shows a clear cut case of overdominance. The array points along the regression line were scattered, indicating diversity among the parents. However, b (0.0411) differed significantly from 1. Hence assumption of non-allelic interaction was not satisfactory (Fig. 31).

4.3.1.11. Nodule weight

The estimates of D (-325.46) and F (-484.44) were not significant, in this character. All other parameters viz., E (390.65), H_1(4300.68), H_2(3844.30) and h^2 (7618.51) were found to be significant. The negative value of F indicated that decreasing alleles were dominant in the parents. The value of H_1 was greater

Fig:30. Vr-Wr graph of days to maturity
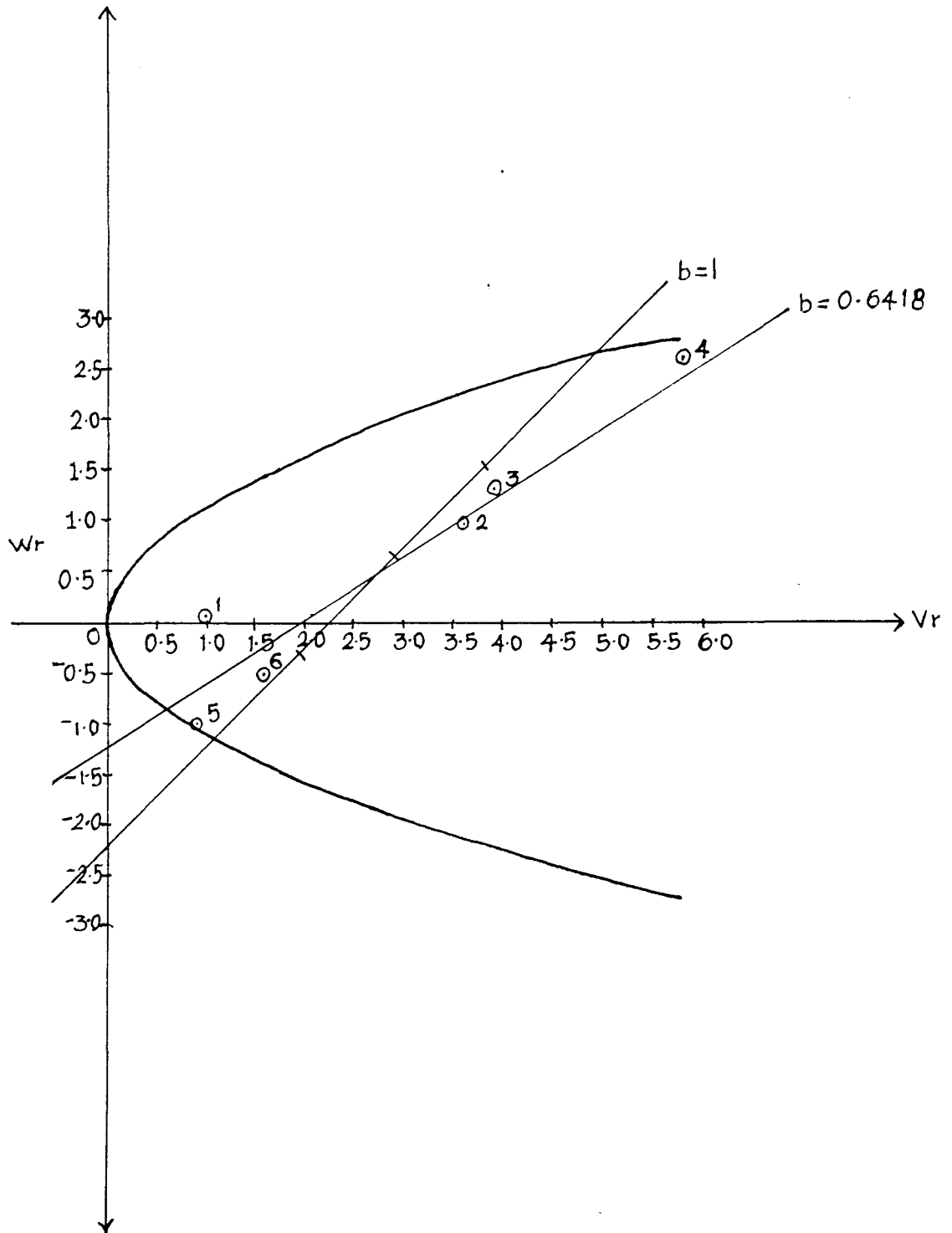
Fig: 31. Vr-Wr. graph of root weight
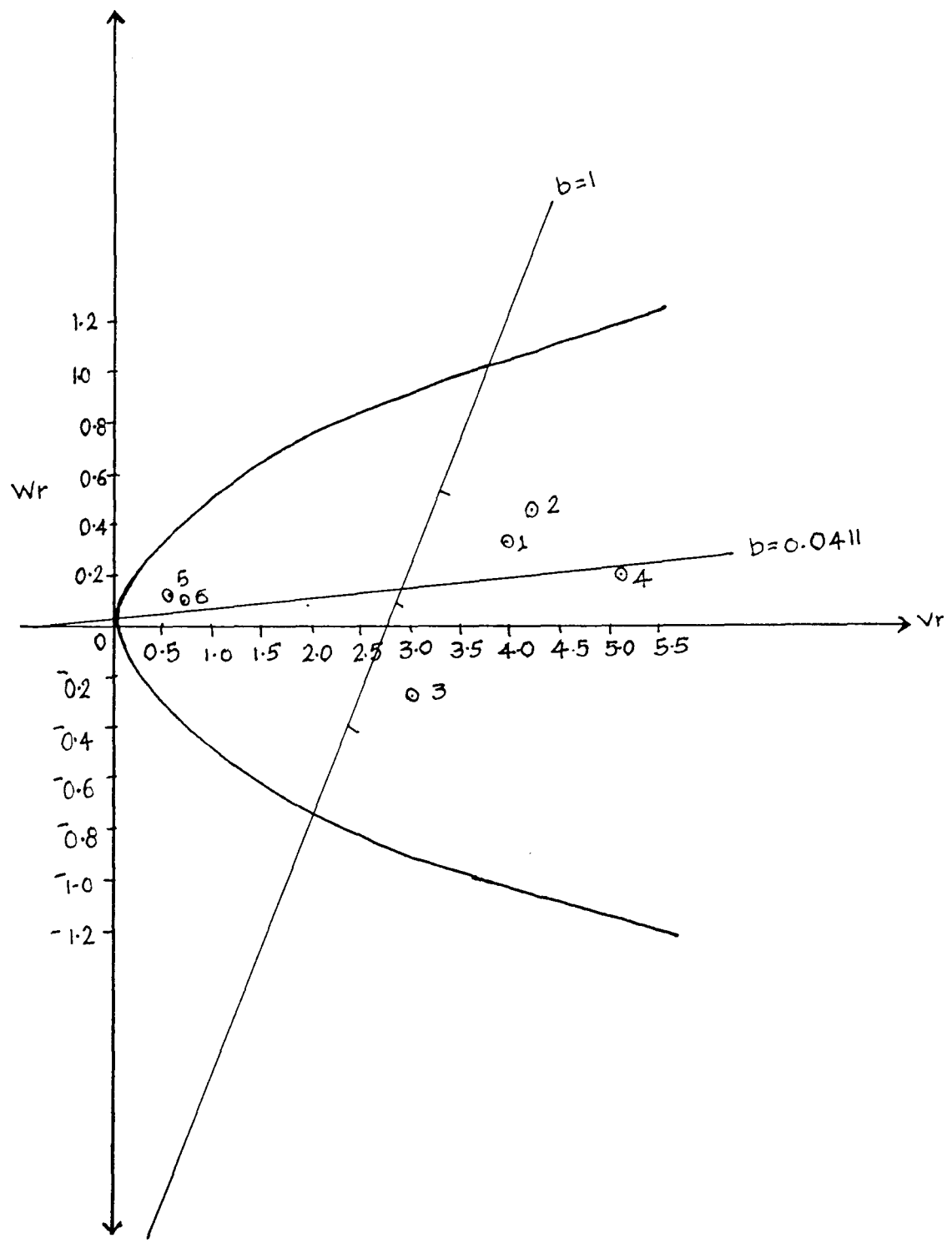
than D indicating overdominance for this character. The value of $H_2/4H_1$ (0.22) was lesser than 0.25.

In the Vr-Wr graph, the intercept of regression line on the covariance axis being below the origin, showed overdominance for this character. The array points along the regression line were scattered indicating diversity among the parents. The regression coefficient , b (0.1057) was significantly different from unity (Fig. 32).

4.3.1.12. Protein content

Considering the parents, F_1's and reciprocals, the estimates of D (-0.04) and F (-0.03)were found to be non-significant. The other parameters viz., E (-0.14) H_1(0.69), H_2 (0.65) and h^2 (2.19) were found to be significant. The negative value of F indicated that decreasing alleles were dominant in the parents. The value of H_1 was significantly greater than D indicating overdominance for this character. The value of $H_2/4H_1$ (0.24) almost approached the maximum attainable value of 0.25, indicating equal proportion of genes with positive and negative effects.

In the Vr-Wr graph, the intercept of regression line on the covariance axis being below the origin, showed overdominance for this character. The array points along the regression line were found to be less scattered. The parents, P_1,P_2, P_4 and P_5 were found to possess most of the dominant genes (>75%), while the parent, P_6 appeared to possess 50-75% dominant genes and the parent, P_3 possessed most of

Fig:32. Vr-Wr graph of nodule weight

Fig:32. Vr-Wr graph of nodule weight
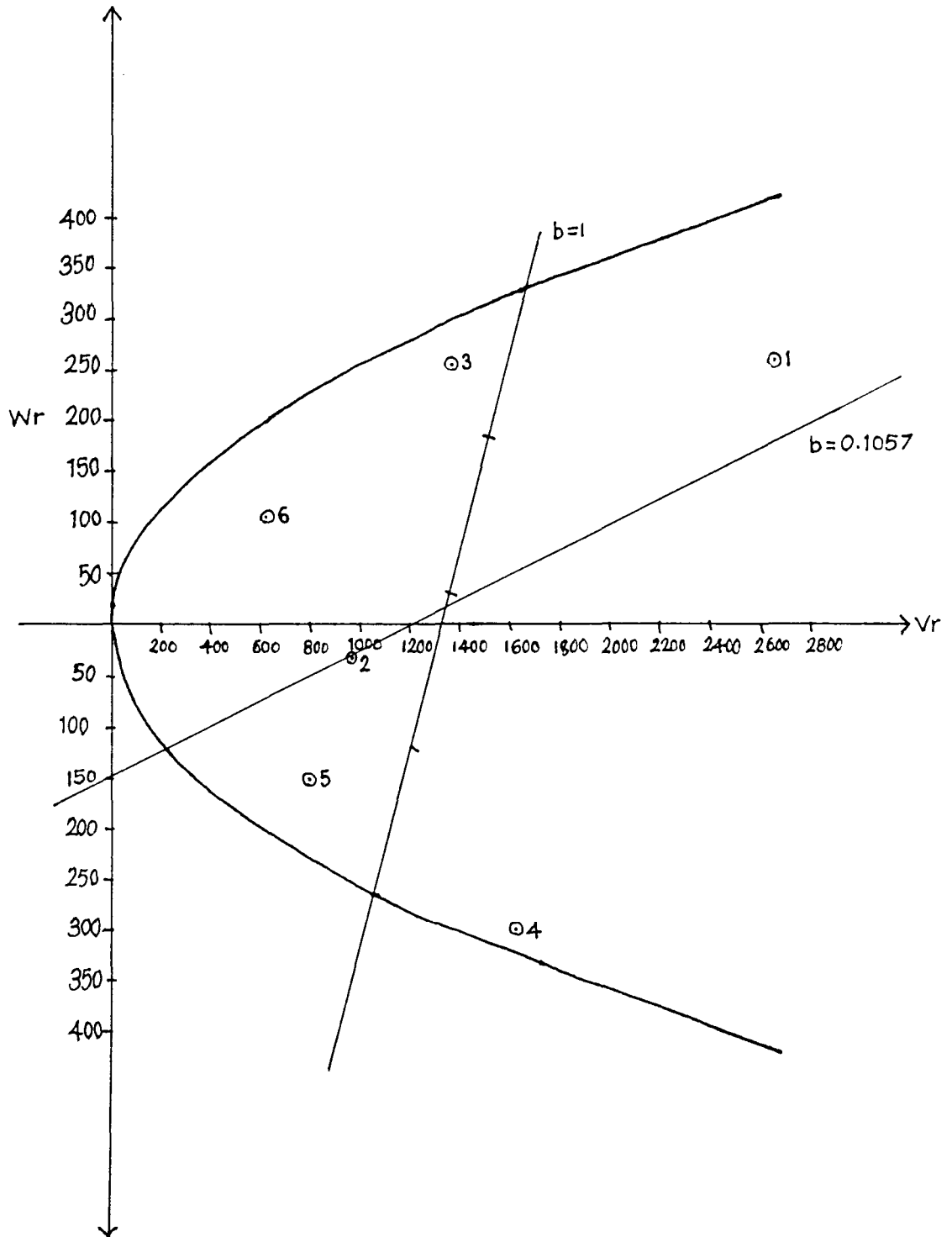
Fig. 33. Vr -Wr graph of protein content
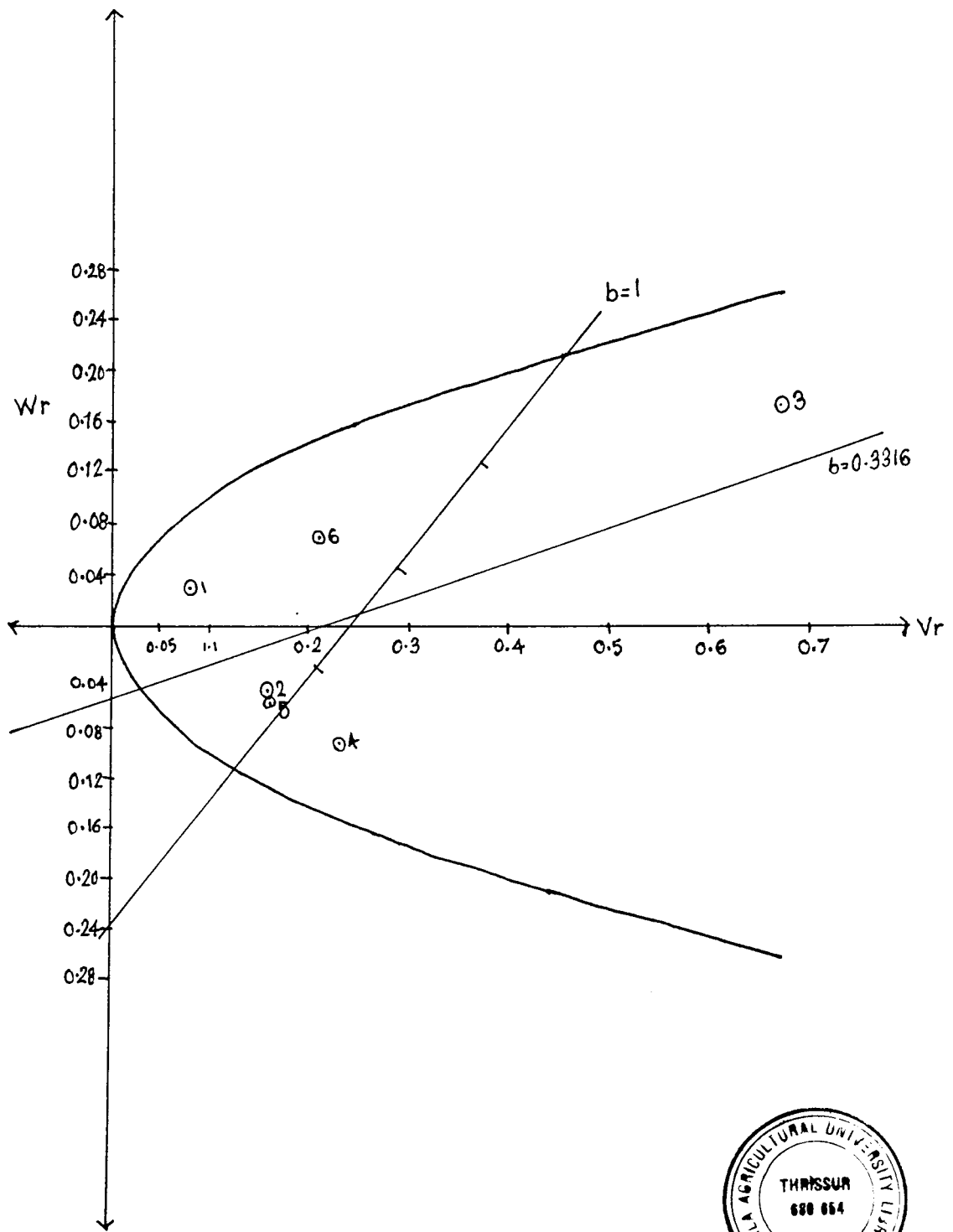
the recessive genes. The assumption of absence of non-allelic interaction was satisfactory, as b (0.3316) did not significantly differ from unity (Fig. 33).

4.4. Heterosis

The mean values of the parents and hybrids were used to determine the heterosis manifested by the hybrids for each character. The results are presented below:

Data on the percentage of heterosis over mid parent (MP) and better parent (BP) for the 12 characters are furnished in Table 8.

4.4.1. Plant Height

The relative heterosis for plant height ranged from -17.9% (P_5 x P_4) to 75.01% (P_2 x P_1). Significant positive heterosis were shown by 12 hybrids. Of these, maximum positive heterosis was exhibited by P_2 x P_1 (75.01%), followed by P_3 x P_1 (61.05%) and P_4 x P_1 (51.00%) both of them being on par with P_2 x P_1. Only three hybrids showed significant negative heterosis, of which P_5 x P_4 (-17.90%) showed maximum negative heterosis followed by P_4 x P_6 (-17.40%) . Regarding heterobeltiosis, seven hybrids showed significant positive heterosis. Of these, P_2 x P_1 showed maximum heterosis of 72.32% which was on par with P_3 x P_1 (60.55%). Seven hybrids showed significant negative heterosis. P_3 x P_6 showed maximum heterosis in the negative direction (-33.3%).

Table. 8 Percentage Heterosis over mid parent (MP) and better parent (BP)

Crosses	Plant Height Heterosis (%) over		Number of Branches Heterosis (%) over		Days to first flowering Heterosis (%) over		Length of Pods Heterosis (%) over	
	MP	BP	MP	BP	MP	BP	MP	BP
$P_1 X P_2$	48.44**	46.16**	-3.10	-15.80	-4.41	-3.24	14.34**	8.67
$P_1 X P_3$	8.89	8.56	9.09	-5.21	0.00	0.00	13.59	5.95
$P_1 X P_4$	29.01**	13.26	-31.00	-36.81	-2.03	-1.63	24.90**	21.60**
$P_1 X P_5$	25.00**	4.55	-15.00	-26.22	-0.42	0.82	9.78	3.14
$P_1 X P_6$	10.19	-8.36	-26.00	31.60	-0.80	-0.80	0.87	-1.30
$P_2 X P_3$	7.48	5.51	42.80	42.83	-6.82**	-5.68	5.28	3.20
$P_2 X P_4$	24.83*	8.42	20.00	12.57	-5.60*	-4.84	17.28*	14.40
$P_2 X P_5$	0.25	-17.20	28.50	28.48	-2.44	0.00	4.90	3.63
$P_2 X P_6$	4.60	-14.10	60.00	50.09	-7.64**	-6.51*	21.63**	18.10*
$P_3 X P_4$	16.25	2.33	33.40	25.14	-2.03	-1.63	11.64	6.79
$P_3 X P_5$	-12.30	-26.50**	92.70**	92.72**	-5.36*	-4.18	-1.26	-2.00
$P_3 X P_6$	-20.00*	-33.30**	73.40**	62.66**	-3.24	-3.24	2.88	-2.00
$P_4 X P_5$	11.06	4.97	80.00**	68.86**	-5.74*	-4.18	20.45**	16.10*
$P_4 X P_6$	-17.40*	-22.40**	68.90**	68.86**	-2.03	-1.63	20.89**	20.30*
$P_5 X P_6$	-14.70	-15.30	40.00	31.33	-3.70	-2.50	0.82	-3.30

Crosses	Plant Height Heterosis (%)over		Number of Branches Heterosis (%) over		Days to first flowering Heterosis (%) over		Length of Pods Heterosis (%) over	
	MP	BP	MP	BP	MP	BP	MP	BP
$P_2X P_1$	75.01**	72.32**	3.09	-10.43	-1.20	0.00	22.56**	16.50*
$P_3X P_1$	61.05**	60.55**	45.50*	26.38*	-1.63	-1.63	12.32	4.76
$P_3X P_2$	42.68**	40.06**	57.00**	56.96*	-7.64**	-6.51*	2.37	0.36
$P_4X P_1$	51.00**	32.56**	71.50**	57.98**	-5.26*	-4.88	35.21**	31.70**
$P_4X P_2$	38.26**	19.77*	20.00	12.57	-1.60	-0.80	8.89	6.20
$P_4X P_3$	30.78**	15.12	20.00	12.57	-0.40	0.00	7.03	2.38
$P_5X P_1$	3.96	-13.00	9.09	-5.21	-2.05	-0.82	26.13**	18.50**
$P_5X P_2$	-3.51	-20.30*	0.00	0.00	-3.24	-0.82	-0.49	-1.70
$P_5X P_3$	-4.69	-20.10*	7.07	7.07	2.05	3.33	-1.26	-2.00
$P_5X P_4$	-17.90*	-22.40*	-13.00	-18.76	0.82	2.50	7.53	3.63
$P_6X P_1$	-7.97	-23.50**	2.92	-5.21	-3.24	-3.24	19.30**	16.70*
$P_6X P_2$	43.11**	17.55*	-13.00	18.76	-7.64**	-6.51*	4.66	1.61
$P_6X P_3$	40.03**	16.74	-13.00	-18.76	-3.24	-3.24	-9.13	-13.00
$P_6X P_4$	-8.69	-14.30	56.30*	56.29**	-1.20	-0.80	2.16	1.69
$P_6X P_5$	-6.47	-7.14	6.60	0.00	2.89	4.18	15.56	10.90
CD(5%)	24.43	28.21	1.88	2.18	2.03	2.34	1.08	1.24
(1%)	32.49	37.54	2.55	2.89	2.69	3.18	1.43	1.65

4.4.2. Number of branches

The percentage heterosis over mid parent for the 30 hybrids ranged from -31.00% to 92.7%. The maximum heterosis over mid parent was exhibited by P_3 x P_5 (92.7%) followed by P_4 x P_5 (80%), P_3 x P_6 (73.4%), P_4 x P_1 (71.5%), P_4 x P_6 (68.9%), P_2 x P_6 (60%), P_3 x P_2 (57%), P_6 x P_4 (56.3%) and P_3 x P_1 (45.5%) all of which were on par with P_3 x P_5. Compared to the better parent, the range of heterosis was from -36.81% to 92.72%. None of the hybrids showed significant negative heterosis. P_3 x P_5 showed the maximum heterobeltiosis of 92.72%.

4.4.3. Days to first flowering

The crosses, P_2 x P_6, P_3 x P_2 and P_6 x P_2, exhibited the highest negative heterosis over mid parental value (-7.64%) for days to first flowering. None of the crosses showed significant positive heterosis. Considering heterobeltiosis, the least heterosis was shown by the crosses, P_2 x P_6 , P_3 x P_2 and P_6 x P_2 (-6.51%) and the highest by P_6 x P_5 (4.18). Only the above mentioned three crosses exhibited significant heterosis in the negative direction. None of the crosses showed significant positive heterosis.

4.4.4. Length of Pods

The relative heterosis for length of pods ranged from -9.14(P_6 x P_3) to 35.21 (P_4 x P_1). Ten hybrids showed significant positive heterosis. Of these, P_4 x P_1

(35.21%) and P_5 x P_1 (26.13%) showed highly significant positive heterosis. None of the hybrids showed significant negative heterosis. In comparison to the better parent, the heterosis ranged from -13% (P_6 x P_3) to 31.7% (P_4 x P_1). Significant positive heterosis was exhibited by eight hybrids. Of these crosses, P_4 x P_1 was found to be highly significant with 31.7% heterosis. As in relative heterosis, none of the hybrids showed significant negative heterosis.

4.4.5. Number of pods per plant

Significant heterosis over mid parent for number of pods per plant was exhibited by ten hybrids. Of these, P_4 x P_5 (130%) showed maximum relative heterosis followed by P_6 x P_4 (103.10%) and P_4 x P_1 (103%) which were on par with P_4 x P_5. Compared to the better parent, eight hybrids showed significant heterosis in the positive direction. Of these, P_4 x P_5 (123.8%) showed significant performance which was on par with P_4 x P_1 (90.9%). None of the hybrids showed significant heterosis in the negative direction, over mid parent and better parent.

4.4.6. Number of seeds per pod

Significant positive relative heterosis was expressed by five hybrids. The highest values were seen in the crosses, P_2 x P_1 (50.1%) followed by P_1 x P_6 (48.7%), P_1 x P_2 (37.5%), P_6 x P_1 (37.2%) and P_4 x P_1 (31.6%) all of them were on par with P_2 x P_1. Significant negative relative heterosis was exhibited by only one

Crosses	Number of pods/plant Heterosis (%) over		Number of seeds/ pod Heterosis (%) over		Seed yield Heterosis (%) over		100 seed weight Heterosis (%) over	
	MP	BP	MP	BP	MP	BP	MP	BP
$P_1 X P_2$	17.60	13.24	37.50**	37.50**	41.20	19.91	11.90*	8.96
$P_1 X P_3$	31.10	24.11	2.68	-9.60	59.40*	38.06	5.91	5.18
$P_1 X P_4$	14.50	7.68	20.10	10.60	63.10*	51.90	4.69	1.58
$P_1 X P_5$	-24.90	-27.40	7.69	-8.70*	-6.26	-8.54	0.00	-3.90
$P_1 X P_6$	-12.00	-15.90	48.70**	37.00**	26.50	20.79	4.76	2.10
$P_2 X P_3$	26.40	24.11	13.50	0.00	35.60	32.51	6.09	3.98
$P_2 X P_4$	39.80	36.35	8.58	0.00	49.60	35.37	8.07	2.16
$P_2 X P_5$	-32.10	-32.30	-2.62	-17.00	17.50	1.87	2.30	-4.10
$P_2 X P_6$	44.20*	33.09	14.40	5.37	40.40	24.09	2.88	-2.30
$P_3 X P_4$	40.10*	39.14*	-5.03	-9.60	27.80	18.17	17.70**	13.50*
$P_3 X P_5$	97.80**	93.62**	-31.80**	-35.00**	60.80*	42.27	1.08	-3.50
$P_3 X P_6$	44.50*	31.21	5.03	0.00	43.80	29.76	-1.20	-4.30
$P_4 X P_5$	130.00**	123.80**	-4.71	-13.00	159.00**	146.70**	9.21	8.19
$P_4 X P_6$	82.20**	64.32**	10.60	10.60	88.30**	83.36*	8.06	7.56
$P_5 X P_6$	40.00	29.62	-9.57	-17.00	59.60	56.13	10.00	8.49

Crosses	Number of pods/plant Heterosis (%) over		Number of seeds/ pod Heterosis (%) over		Seed yield Heterosis (%) over		100 seed weight Heterosis (%) over	
	MP	BP	MP	BP	MP	BP	MP	BP
$P_2 X P_1$	34.40	29.43	50.10**	50.10**	60.90*	36.63	3.07	0.33
$P_3 X P_1$	72.30**	63.13**	2.68	-9.60	102.00**	74.63*	6.78	6.04
$P_3 X P_2$	52.30**	49.64*	-2.68	-14.00	41.70	38.39	0.17	-1.80
$P_4 X P_1$	103.00**	90.90**	31.60*	21.20*	187.00**	166.90**	16.10**	12.60*
$P_4 X P_2$	31.20	27.96	8.58	0.00	43.20	29.54	10.70	4.64
$P_4 X P_3$	12.70	11.87	15.10	9.57	71.60**	58.65	14.50**	10.40
$P_5 X P_1$	-10.30	-13.30	18.00	0.00	42.20	38.73	14.40**	9.98
$P_5 X P_2$	-9.95	-10.30	2.62	-13.00	3.65	-10.10	7.96	1.16
$P_5 X P_3$	21.00	18.45	-18.20	-22.00*	30.40	15.40	7.05	2.25
$P_5 X P_4$	-25.90	-28.00	4.71	-4.40	14.10	8.76	13.00	11.90*
$P_6 X P_1$	27.00	21.43	37.20**	26.40 *	54.30	47.38	-3.50	-6.00
$P_6 X P_2$	3.59	-4.41	-2.74	-10.00	-10.60	-21.00	0.79	-4.30
$P_6 X P_3$	14.80	4.26	0.08	-4.70	3.61	-6.52	2.59	-0.70
$P_6 X P_4$	103.10**	83.20**	-5.21	-5.20	106.00**	101.00**	8.62	8.12
$P_6 X P_5$	16.80	8.16	-9.57	-17.00	30.20	27.38	7.58	6.09
CD(5%)	15.19	17.55	1.57	1.81	8.42	9.73	0.56	0.64
(1%)	20.20	23.34	2.09	2.42	11.21	12.94	0.74	0.85

hybrid, viz., P_3 x P_5 (-31.8%). In comparison with the better parent, P_2 x P_1 (50.1%) and P_1 x P_2 (37.5%) showed significant positive heterosis which were on par with P_1 x P_6 (37%), P_4 x P_1 (21.2%) and P_6 x P_1 (26.4%). Significant negative heterobeltiosis was noticed in P_3 x P_5 (-35%) and P_1 x P_5 (-8.7%).

4.4.7. Seed Yield

Significant positive heterosis over mid parent was exhibited by ten hybrids, over the better parent by five hybrids. Maximum relative heterosis for seed yield was seen in P_4 x P_1 (187%), which was on par with P_4 x P_5 (159%), which were significantly different from P_6 x P_4 (106%), P_3 x P_1 (102%) and other hybrids. Maximum heterobeltiosis for seed yield was exhibited by P_4 x P_1 (166.9%) followed by P_4 x P_5 (146.7%) and P_6 x P_4 (101%), both of which were on par with P_4 x P_1.

4.4.8. 100 Seed weight

Compared to the mid parental value, seven hybrids expressed significant positive heterosis. The hybrid P_3 x P_4 showed the maximum heterosis of 17.7%. The hybrid, P_3 x P_4 (13.5%) showed maximum heterosis over better parent which was on par with the other two significant hybrids viz., P_4 x P_1 (12.6%) and P_5 x P_4 (11.9%). None of the hybrids showed significant negative heterosis over mid parent or better parent.

4.4.9. Days to maturity

Seventeen of the 30 hybrids expressed significant negative relative heterosis for days to maturity. The superior crosses were P_2 x P_3 (-4.75%), P_4 x P_5 (-4.43%), P_5 x P_4 (-4.43%), P_2 x P_6 (-4.29%), P_6 x P_2 (-4.29%), P_4 x P_1 (-4.26%), P_2 x P_4 (-4.23%), P_3 x P_2 (-4.11%) and P_6 x P_4 (-4.10%) all of which were on par with each other. None showed significant positive heterosis. Ten hybrids expressed significant negative heterosis over the better parent. Maximum heterosis was exhibited by P_2 x P_3 (-4.75%). None of the hybrids showed significant positive heterosis over better parent also.

4.4.10. Root weight

Significant positive heterosis over mid parent was noticed in six crosses. Among these, highly significant heterosis was shown by P_3 x P_1 (217%), P_2 x P_4 (184%) and P_4 x P_1 (134%) three of which being on par with each other. Regarding heterobeltiosis, four crosses showed significant positive heterosis. The outstanding ones were P_3 x P_1 (207%), P_2 x P_4 (179%) and P_4 x P_1 (110%) which were on par. None of the crosses showed significant negative heterosis.

4.4.11. Nodule weight

Fifteen of the 30 hybrids showed significant positive heterosis over mid parent for nodule weight. The superior crosses were P_4 x P_1 (205%), P_3 x P_5 (186%),

Table. 8 continued

Crosses	Days to maturity Heterosis (%) over		Root weight Heterosis (%) over		Nodule weight Heterosis (%) over		Protein contents Heterosis (%) over	
	MP	BP	MP	BP	MP	BP	MP	BP
$P_1 X P_2$	-2.22*	-1.91	13.70	3.75	2.44	-8.70	-1.20	-1.60
$P_1 X P_3$	-1.90	-1.60	65.10	59.80	89.20**	84.20	2.32	0.00
$P_1 X P_4$	-2.05	-0.96	58.40	42.30	157.00**	125.00**	7.07**	6.89*
$P_1 X P_5$	-1.44	-0.96	24.30	21.90	120.00**	95.60*	1.49	1.01
$P_1 X P_6$	-1.75	-1.59	10.40	-3.20	12.80	4.76	3.64	1.96
$P_2 X P_3$	-4.75**	-4.75**	24.50	17.10	150.00**	128.00**	7.55**	5.60
$P_2 X P_4$	-4.23**	-3.47**	184.00**	179.00**	19.10	16.70	5.95*	5.62
$P_2 X P_5$	-1.12	-0.33	59.00	42.40	17.40	17.40	6.56*	6.56*
$P_2 X P_6$	-4.29**	-3.83	62.40	55.50	81.80*	73.90*	8.15**	6.90*
$P_3 X P_4$	-1.41	-0.63	-0.70	-8.10	137.00**	113.00**	10.20**	7.87*
$P_3 X P_5$	-3.03**	-2.26	26.60	20.20	186.00**	161.00**	2.53	0.68
$P_3 X P_6$	-1.75	-1.27	5.81	-4.50	155.00**	143.00**	4.40	3.71
$P_4 X P_5$	-4.43**	-2.89	10.00	-2.90	2.13	0.00	3.30	2.98
$P_4 X P_6$	-2.52*	-1.27	-9.80	-12.00	33.30	25.00	9.18**	7.59*
$P_5 X P_6$	-2.88**	-2.58*	6.83	-7.90	27.30	21.70	4.84	3.62

Crosses	Days to maturity Heterosis (%) over		Root weight Heterosis (%) over		Nodule weight Heterosis (%) over		Protein contents Heterosis (%) over	
	MP	BP	MP	BP	MP	BP	MP	BP
$P_2 X P_1$	-1.90	-1.60	65.60	51.10	21.90	8.69	7.06**	6.55*
$P_3 X P_1$	-0.64	-0.32	217.00**	207.00**	73.00	68.40	0.66	-1.60
$P_3 X P_2$	-4.11**	-4.11**	28.00	20.40	85.70*	63.60	9.91**	7.92*
$P_4 X P_1$	-4.26**	-3.19**	134.00**	110.00**	205.00**	167.00**	-0.40	-0.60
$P_4 X P_2$	-0.16	0.64	79.30*	76.20	104.00**	100.00**	3.30	2.98
$P_4 X P_3$	1.09	1.90	20.80	11.80	128.00**	104.00**	10.50**	8.21**
$P_5 X P_1$	-2.40*	-1.93	43.50	40.60	80.50*	60.90	4.08	3.59
$P_5 X P_2$	-3.35**	-2.58*	17.60	5.39	4.34	4.34	2.94	2.94
$P_5 X P_3$	-0.79	0.00	81.20	72.10	33.30	21.70	13.60**	11.50**
$P_5 X P_4$	-4.43**	-2.89*	33.10	17.40	117.00**	113.00**	7.25**	7.58*
$P_6 X P_1$	-2.71*	-2.55*	54.30	35.30	5.12	-2.40	5.30	3.59
$P_6 X P_2$	-4.29**	-3.83**	10.70	6.00	31.80	26.10	0.14	-1.00
$P_6 X P_3$	-2.70*	-2.23	75.60*	58.50	10.00	4.76	7.78**	7.06*
$P_6 X P_4$	-4.10**	-2.88*	95.40**	90.10**	100.00**	87.50*	-1.50	-2.90
$P_6 X P_5$	0.00	0.32	13.00	-2.60	63.60	66.50	8.15**	6.90*
CD(5%)	2.20	2.54	2.93	3.38	4839.00	55.88	0.91	1.05
(1%)	2.93	3.38	3.89	4.49	64.36	74.32	1.21	1.40

$P_1 \times P_4$ (157%), $P_3 \times P_6$ (155%), $P_2 \times P_3$ (150%) and $P_3 \times P_4$ (137%) all of them being on par with $P_4 \times P_1$. Significant positive heterosis over better parent was also noticed in 12 crosses. The superior ones were $P_4 \times P_1$ (167%), $P_3 \times P_5$ (161%), $P_3 \times P_6$ (143%), $P_2 \times P_3$ (128%), $P_1 \times P_4$ (125%), $P_3 \times P_4$ (113%), $P_5 \times P_4$ (113%) and $P_4 \times P_3$ (104%) , all of them being on par with $P_4 \times P_1$.

4.4.12. Protein Content

When compared to the mid parental value, positive heterosis was exhibited by 13 hybrids, and 11 hybrids expressed positive heterosis when compared to the better parent. The maximum relative heterosis of 13.6% was noticed in $P_5 \times P_3$, followed by $P_4 \times P_3$ with 10.5%, $P_3 \times P_4$ with 10.2%, $P_3 \times P_2$ with 9.91% and $P_4 \times P_6$ with 9.18%. The percentage heterobeltiosis was the highest in $P_5 \times P_3$ (11.5%).

R₁T₂₂

8 LG (Parent)

X

3 LG (Parent)

Plate 4. 8 LG x 3 LG hybrid

R₁T₁₅

X

6 LG (Parent)

3 LG (Parent)

R₂T₁₃

Plate 5. 6 LG x 3 LG hybrid

R₁T₁₅

X

R₁T₂₂

6 LG (Parent)

8 LG (Parent)

R₁T₁₆

Plate 6. 6 LG × 8 LG hybrid

Discussion

DISCUSSION

The diallel mating system involved in the present study is an effective method, for providing information on the nature and amount of genetic parameters and about the general and specific combining ability of parents and their crosses. The general and specific combining ability enables a rational choice of the parental material to be used in a heterosis breeding programme. This method also helps to study the nature of gene action governing the different characters based on which an appropriate breeding methodology can be adopted. In the present study, six parental lines and their 30 F_1 hybrids of ricebean were subjected to diallel analysis employing Griffing's method I for analysing combining ability and Hayman's numerical as well as graphical approach for estimating the gene actions involved.

5.1. Combining ability and gene action

The study of the combining ability of the parents is an effective technique that permits identification of superior varieties to be used as parents for hybridization and also pinpoints cross combinations likely to be superior in their performance. Results of the combining ability analysis of the six parental lines and their 30 F_1 hybrids are discussed below.

In the present study, the analysis of variance for combining ability revealed that the variances due to general combining ability (GCA) and variances due to specific combining ability (SCA) were significant for nine characters viz., plant height,

number of branches, length of pods, number of pods per plant, seed yield, 100 seed weight, days to maturity, root weight and nodule weight.

Significant GCA, SCA and reciprocal effects were observed for plant height, implying that both additive and non-additive components of genetic variance are operating for this character. Similiar observation was noticed by Patil and Patil (1986) and Mallikarjun *et al.* (1995) in cowpea. The SCA was however greater than GCA indicating a major role of non-additive gene action as was reported by Selvalakshmi(1995) in cowpea. But Seenaiah *et al.* (1993) in black gram and Chaudhary *et al.* (1994) in adzukibean observed additive gene action for this character. Here combining ability effects in the positive direction are desirable. Two crosses possessed significantly positive specific combining ability effects (sca), viz., P_6 x P_3 and P_3 x P_1. However, P_4 was found to be the good general combiner for this trait.

The regression coefficient (b) did not differ significantly from unity, indicating absence of non-allelic interaction. Significance of H_1 and H_2 as well as D suggests the operation of additive and dominant genes with respect to plant height. The positive value of $\bar{F}$ indicated that increasing alleles were dominant in the parents. The value of H_1 was significantly greater than D indicating overdominance for this character. From the Vr-Wr graph, the parents, P_3, P_4, P_5 and P_6 appeared to possess most of the dominant genes, while P_1 and P_2 had almost equal proportion of dominant and recessive genes.

For number of branches per plant, significant gca, sca and reciprocal effects were observed implying that both additive and non-additive components of genetic variance are operating for this character. Similar results were noticed by Singh *et al.* (1994 a) in pea. Parent, P_4 was the best general combiner. High sca effect was expressed in the direct cross, $P_4 \times P_6$. Reciprocal effects were also significant, for the crosses, $P_4 \times P_1$, $P_5 \times P_3$, $P_5 \times P_4$, $P_6 \times P_2$ and $P_6 \times P_3$. Hence, $P_4 \times P_1$ considered as the best specific combiner for this character

The character, number of branches had the preponderence of recessive genes as indicated by the negative value of F. The regression coefficient (b) differed significantly from unity. This character was under the environmental influence. The value of H_1 was significantly greater than D indicating overdominance for this character. But graphical analysis indicated the presence of partial dominance. The Vr-Wr graph showed lesser scattering of array points indicating lesser genetic divergence among the parents. The parent, P_1 appeared to possess most of the dominant genes.

Regarding the character, days to first flowering, only the SCA was significant. This emphasises the importance of non- additive genetic variance for the character. $P_2 \times P_6$ showed significant specific combining ability in the negative direction, which is more desirable. In cowpea, similar reports of importance of non- additive genetic variance was given by Thiyagarajan *et al.* (1993). However, both additive and non-additive genetic variance was reported by Mathur and Mathur (1997) in clusterbean.

Days to first flowering was also found to be influenced by environment. The absence of non-allelic interaction was not satisfactory, since 'b' differed from unity. The negative value of F indicated the presence of more of decreasing alleles in the parents. A symmetrical distribution of genes with positive and negative effects was indicated by the ratio, $H_2 / 4H_1$. Gene action was in the range of overdominance as revealed by the graphical analysis. The array points in this graph indicated genetically divergent parents for days to first flowering.

In the case of length of pods, the SCA, GCA and reciprocal effects were significant. Significant reciprocal difference may be attributed to cytoplasmic inheritance of the maternal effects. The SCA was found to be highly significant, emphasising the importance of non- additive genetic variance for this character. Similar reports were given by Thiyagarajan *et al.* (1993) in cowpea. Findings contradictory to this were also reported by Mathur and Mathur (1997) in clusterbean. It was seen that, only two crosses showed significant sca. P_1 x P_4 showed significant positive effects and P_6 x P_4 showed significant negative effects.

The absence of non-allelic interaction was found to be satisfactory since 'b' did not differ significantly from unity. It was evident from the significant values of H_1 and H_2 that dominant genes are operating for this character. Influence of environment was also reported for pod length. The positive value of F indicated that increasing alleles are dominant in the parents. The Vr-Wr graph clearly indicated overdominance for this character. The array points on the regression line

were not much scattered, indicating less diversity among the parents. The parent P_2, P_3, and P_5 were found to possess most of the dominant genes, P_4 and P_6 possessed 50 -75% of dominant genes while the parent, P_1 contained an excess of recessive genes.

With respect to number of pods per plant, GCA, SCA and reciprocal effects were found to be significant. Significant SCA and GCA indicated that both additive and non-additive genetic variance were operating for this character. This is in agreement with the report of Mathur and Mathur (1997) in cluster bean. However, the GCA was found to be slightly greater than SCA implying a major role of the additive component of genetic variance. This was reported by Thiyagarajan *et al.* (1993) in cowpea and Singh and Singh (1996) in ricebean . This character exhibited reciprocal differences also which may be due to cytoplasmic inheritance of maternal effect. An examination of the parents, crosses and reciprocals revealed that, P_4 was found to be a good general combiner, and the cross $P_4 \times P_6$ and reciprocal, $P_4 \times P_1$ were the best specific combiners for this trait.

Number of pods per plant was mainly governed by dominant genes as indicated by the significance of H_1 and H_2. Environmental influence was also seen. The regression coefficient differed significantly from unity. The negative value of F indicated that decreasing alleles were dominant in the parents. The proportion of dominant and recessive genes confirmed the unequal distribution of these genes.

An almost symmetrical positive and negative alleles was observed from the ratio, $H_2/4H_1$. The graphical analysis revealed overdominance for this character. The Vr-Wr graph revealed considerable genetic divergence among the parents.

Results of the combining ability analysis for number of seeds per pod revealed significance for SCA only indicating the predominant role of non-additive gene action. This is in confirmity with Thiyagarajan *et al.* (1993) in cowpea. Mathur and Mathur (1997) in clusterbean and Singh and Singh (1996) in ricebean reported additive gene action to be predominant. Among the crosses, P_1 x P_6 showed significant positive sca, and hence it can be considered as the best specific combiner for this character.

This character seemed to be under the control of dominance gene effects though the environmental influence was significant. Similar findings was reported by Thiyagarajan *et al.* (1993) in cowpea. Dominance of increasing alleles was noticed from the positive value of F. The regression coefficient differed significantly from unity, so assumption of non-allelic interaction was not satisfactory. The dominant and recessive genes were asymmetrically distributed. However, the genes with positive and negative effects were almost symmetrically distributed among the parents as observed from the ratio, $H_2/4H_1$. The graphical analysis indicated overdominance for this trait. The array points along the regression line were scattered, indicating diversity among the parents . All the parents except parent, P_1, were found to possess mostly dominant genes.

With respect to the seed yield, significant GCA and SCA were obtained indicating that both additive and non-additive genetic variance were operating for this character. This is in confirmity with the findings of Paralkar *et al.* (1997) and Lal and Waldia (1980) in blackgram. However, GCA was slightly greater than SCA implying a major role of the additive component of genetic variance. This was reported by Halkude *et al.* (1996) in greengram and Singh and Singh (1996) in ricebean. Whereas, Mathur and Mathur (1997) in clusterbean reported a major role of non-additive component of genetic variance for this trait. This character exhibited significant reciprocal differences also which may be due to cytoplasmic inheritance of maternal effect. Among the straight crosses, P_1 x P_4 showed significant positive sca, and among the reciprocals, P_4 x P_1 showed significant positive sca. P_4 was found to be the best general combiner and P_4 x P_1 as the best specific combiner for this character.

The seed yield was mainly governed by dominant genes as indicated by the significance of H_1 and H_2. Environmental influence was also seen. The absence of non-allelic interaction was satisfactory, since, 'b' did not differ significantly from unity. Dominant genes operating for this trait was reported by Thiyagarajan *et al.* (1993) in cowpea, while additive effects were stressed by Halkude *et al.* (1996) in greengram. An almost symmetrical distribution of positive and negative alleles was observed. The graphical analysis revealed overdominance for this character. The Vr-Wr graph revealed lesser divergence among the parents. The parents, P_2 and P_3

appeared to possess most of the dominant genes, P_4, P_5 and P_6 contained equal proportions of dominant and recessive genes and P_1 possessed mostly recessive genes.

Results of the combining ability analysis for 100 seed weight, revealed significance of GCA and SCA indicating the importance of additive and non-additive gene action. This is in confirmity with the findings of Mathur and Mathur (1997) in cluster bean. However in cowpea, non-additive gene action was reported by Thiyagarajan *et al.* (1993), while Mallikarjun *et al.* (1995) reported additive gene action for this trait. The parent, P_2 was the best general combiner and the hybrid $P_3 \times P_4$ showed the highest sca.

This character also seemed to be under the control of dominant gene effects, though there was environmental influence also. Similar reports were given by Thiyagarajan *et al.* (1993) in cowpea. The negative value of F indicated that decreasing alleles were dominant for this character. The genes with positive and negative effects were almost symmetrically distributed among the parents. The assumption of non-allelic interaction was satisfactory. The graphical analysis revealed overdominance for this trait. The scattered array points on the regression line indicated considerable genetic divergence among the parents. P_2 and P_6 possessed most of the dominant genes, P_1, P_3 and P_5 possessed equal proportion of dominant and recessive genes and P_4 possessed mostly recessive genes for this character.

The character, days to maturity showed significant GCA, SCA and reciprocal effects. Significant GCA and SCA indicated the importance of both additive and non-additive genetic variances. In clusterbean, similar reports was given by Mathur and Mathur (1997). However, importance of non-additive genetic variances was reported by Thiyagarajan *et al.* (1993) in cowpea and Mallikarjun *et al.* (1995) in cowpea. Significant reciprocal effects owed to cytoplasmic inheritance of maternal effect. The parent, P_5 was considered as the best general combiner and $P_2 \times P_3$ and $P_4 \times P_5$ as the best specific combiners for this trait.

Days to maturity was found to be influenced by environment. Dominance effect was indicated by the significance of H_1 and H_2. The negative value of F indicated that decreasing alleles were dominant in the parents. The value of 'b' did not differ significantly from unity. A symmetrical distribution of genes with positive and negative effects were observed. The graphical analysis indicated over dominance for this character. The array points on the regression line were scattered, implying considerable genetic divergence among the parents. P_1, P_5 and P_6 possessed most of the dominant genes, P_2 and P_3 possessed 25-50% dominant genes and P_4 possessed mostly recessive genes.

For root weight, significant GCA as well as SCA were obtained indicating the operation of both additive and non-additive types of gene action in the inheritance of root weight. This in confirmity with Singh and Singh (1996) in ricebean. However, the SCA was greater than GCA implying preponderence of

non-additive component than additive component. Root weight exhibited significant reciprocal differences also. Among the parents, P_4 was found to be the good general combiner, and among the crosses, P_2 x P_4 which had the good general combiner (P_4) was the best specific combiner for this character.

Root weight was under the influence of environment. The significance of H_1 and H_2 indicated dominance effect. The decreasing alleles were dominant in the parents, as indicated by the negative value of F. The regression coefficient differed significantly from unity, hence assumption of non-allelic interaction was not satisfactory. A symmetrical distribution of genes with positive and negative effects were noticed. The overdominance was confirmed by Vr-Wr graph.

Significant SCA and GCA were observed for the nodule weight, indicating the importance of both additive and non-additive genetic variances. This is in confirmity with the reports of Singh and Singh (1996) in ricebean. The character was influenced by reciprocal differences also. P_4 was the best general combiner and P_1 x P_4 which had the highest sca in the positive direction was the best specific combiner for nodule weight.

Nodule weight was governed by dominant gene effects, which was indicated by the significance of H_1 and H_2. There was considerable environmental influence also. Preponderance of decreasing alleles was denoted by the negative value of F. The Vr-Wr graph revealed overdominance for this trait. The regression coefficient

differed significantly from unity. This graph also indicated genetic divergence among the parents.

For the character, protein content, the SCA was significant implying the preponderence of non-additive genetic variance. Reports of Singh and Singh (1996) in rice bean, Madhusudan *et al.* (1995) and Mallikarjun *et al.* (1995) in cowpea showed the importance of both additive and non-additive genetic variance. P_5 x P_3 was found to be the best specific combiner.

Protein content was found to be under the control of non-additive effects as well as environmental effects, as indicated by the significance of H_1, H_2 and E. The regression coefficient did not differ significantly from unity. The negative value of F indicated dominance of decreasing alleles. The ratio of H_2 to $4H_1$ also indicated symmetrical distribution of genes with positive and negative effects among the parents. The overdominance character was confirmed by the Vr-Wr graph. The graph indicated lesser genetic divergence among the parents. P_1, P_2, P_4 and P_5 possessed mostly dominant genes, P_6 possessed 50-75% dominant genes and P_3 possessed most of the recessive genes.

An overall ranking of the lines for all the traits, indicated that P_4 was a good general combiner. The specific combinations involving P_4 showed high specific combining ability. However, there were also combinations, with P_4 which gave low specific combining ability. Combinations involving P_1 and P_3 also gave high specific combining ability effects.

5.2. Heterosis

Exploitation of hybrid vigour to increase the yield of crops is one of the most important techniques in plant breeding. Manifestation of heterosis for various economic traits in *Vigna sp.* has been reported by many researchers. The present study was also aimed to identify superior hybrids and to find out the magnitude of heterosis on yield and its components in *Vigna umbellata.*

In the present study for plant height, 12 hybrids were found to exhibit significant positive heterosis when compared to the mid parent value, and seven hybrids expressed significant positive heterobeltiosis. Mahetre *et al.* (1993) in pigeonpea, Sharma and Yadav (1993) in mungbean and Sawant *et al.* (1994) in cowpea reported heterosis over mid parental value in most of the hybrids, while heterobeltiosis for this trait was reported by Mahetre *et al.* (1993) in pigeonpea, Sharma and Yadav (1993) in mungbean and Selvalakshmi (1995) in cowpea. Of the hybrids, P_2 x P_1 showed significant heterosis over the mid and better parental value.

Considering the number of branches per plant, the maximum heterosis over mid parent was exhibited by P_3 x P_5 followed by P_4 x P_5. Significant heterosis over mid parent for this trait was reported by Mahetre *et al.* (1993) in pigeonpea, Naidu and Satyanarayana (1993 b) in mungbean and Sawant *et al.* (1994) in cowpea. Maximum heterosis over better parent was shown by P_3 x P_5. Hence P_3 x P_5 can be

considered as the outstanding one among the hybrids. In cowpea, significant heterobeltiosis was reported by Selvalakshmi (1995).

With regard to days to first flowering, maximum heterosis in the negative direction was shown by $P_2 \times P_6$, $P_3 \times P_2$ and $P_6 \times P_2$. Significant heterosis over mid parent was reported by Mahetre *et al.* (1993) in pigeonpea and Reddy *et al.* (1992) in mungbean. Significant heterobeltiosis was also shown by the above mentioned three hybrids. Mahetre *et al.* (1993) in pigeonpea reported significant heterobeltiosis for this trait.

For length of pods, ten hybrids showed significant positive heterosis, over mid parent value, and eight hybrids showed significant heterobeltiosis. Singh *et al.* (1994 b) in pea and Mylsamy (1988) in cowpea reported significant relative heterosis in the positive direction and Rao (1991) in blackgram reported significant positive heterobeltiosis. The cross $P_4 \times P_1$ was found to be the outstanding one, with regard to relative heterosis and heterobeltiosis for this trait.

In the case of number of pods per plant, $P_4 \times P_5$ showed maximum relative heterosis and maximum heterobeltiosis. Positive significant relative heterosis was reported by Mahetre *et al.* (1993) in pigeonpea, Naidu and Satyanarayana (1993 b), Sharma and Yadav (1993) and Malar (1994) in mungbean, Sawant *et al.* (1994) in cowpea and Singh *et al.* (1994 b) in pea. Significant heterobeltiosis was reported by Reddy (1998) in greengram, Rao (1991) in blackgram, Sharma and Yadav (1993) in greengram, Sawant *et al.* (1994) and Patil and Shete (1987) in cowpea.

For number of seeds per pod, positive heterosis over the mid parent value was exhibited by five hybrids, $P_2 \times P_1$, $P_1 \times P_6$, $P_1 \times P_2$, $P_6 \times P_1$ and $P_4 \times P_1$ and two hybrids , $P_2 \times P_1$ and $P_1 \times P_2$ exhibited positive heterosis over better parental value. High heterosis over mid parental value for number of seeds per pod was reported by Reddy *et al.* (1992) in greengram, Mahetre *et al.* (1993) in pigeonpea and Singh *et al.* (1994 b) in pea, while significant heterobeltiosis was reported by Rao (1991) in blackgram.

Significant positive heterosis over mid parent and better parent for seed yield was exhibited by ten and five hybrids respectively. Maximum relative heterosis was expressed by $P_4 \times P_1$. In greengram, Reddy (1998), Reddy *et al.* (1992), Naidu and Satyanarayana (1993 b), Sharma and Yadav (1993), and Malar (1994) obtained significant relative heterosis for seed yield. Significant heterobeltiosis for this character was also reported by Reddy (1998) in greengram, Rao (1991) in blackgram, Sharma and Yadav (1993) in mungbean and Sawant *et al.* (1994) in cowpea. Among the hybrids, $P_4 \times P_1$ was found to be having the highest seed yield, in comparison with the two types of heterosis .

Seven hybrids showed significant positive relative heterosis for hundred seed weight, the maximum being exhibited by $P_3 \times P_4$ closely followed by $P_4 \times P_1$. These two also showed significant heterobeltiosis for this character. The hybrid showing maximum heterobeltiosis was $P_3 \times P_4$. In mungbean, Sharma and Yadav (1993) reported presence of relative heterosis for hundred seed weight, while Selvalakshmi

(1995) in cowpea and Rao (1991) in blackgram found significant heterobeltiosis for this character. It is clear from the results that the hybrid P_3 x P_4 exhibited significant superiority for 100 seed weight in the two comparisons of heterosis.

Among the 30 hybrids, seventeen of them expressed significant negative relative heterosis for days to maturity. The maximum value was seen in P_2 x P_3 followed by P_4 x P_5, P_5 x P_4, P_2 x P_6, P_6 x P_2, P_4 x P_1, P_2 x P_4, P_3 x P_2 and P_6 x P_4. Significant negative relative heterosis was reported by Naidu and Satyanarayana (1993 b) in greengram. However Mahetre *et al.* (1993) and Bajpai *et al.* (1994)in pigeonpea reported positive relative heterosis. Regarding heterobeltiosis ten hybrids showed significant negative heterosis, maximum value being exhibited by P_2 x P_3. Hence, the hybrid P_2 x P_3 considered as the best for days to maturity.

Significant positive heterosis over mid and better parent for root weight was exhibited by six and four hybrids respectively. In mungbean, Natarajan(1989) reported negative relative heterosis for this trait. Maximum relative heterosis was noticed in the hybrid, P_3 x P_1 followed by P_2 x P_4 and P_4 x P_1. P_3 x P_1 and P_2 x P_4 showed similar trend for heterobeltiosis. The results revealed that P_3 x P_1 had the superiority in root weight when compared to other hybrids.

With regard to nodule weight, fifteen of the 30 hybrids showed significant positive relative heterosis, the maximum being in the cross P_4 x P_1 followed by P_3 x P_5. These two hybrids were found to exhibit significant heterobeltiosis also for nodule weight, thereby indicating that these two hybrids have higher nodule weight than the others.

When compared to the mid parental value, significant positive heterosis for protein content was observed in 13 hybrids. The maximum relative heterosis was noticed in P_5 x P_3 followed by P_4 x P_3. Twelve hybrids showed significant positive heterobeltiosis. P_5 x P_3 and P_4 x P_3 showed maximum heterobeltiosis for this trait, indicating that these two hybrids were the outstanding ones, in comparison with the two types of heterosis.

It was seen that among the 30 hybrids, P_4 x P_1 was the most outstanding one, when sca and heterosis were considered. P_4 x P_1 was significantly heterotic for all characters, except for protein content. The parent P_4, was found to be a good general combiner. The crosses with the combinations of P_4, viz., P_4 x P_5, P_4 x P_6 and P_6 x P_4 were found to excel than others, when compared with other crosses. P_3 x P_1 also showed good performance in sca and heterosis effect (Table. 9).

Table. 9 Overall performance of selected six crosses

Crosses/ parameters		Plant hieght	Number of branches	Days to first flowering	Length of pods	Number of pods/ plant	Number of seeds/ pod
P₄	Mean	190.00	10.00	39.00	10.10	91.00	7.67
	s.c.a.	13.83	3.00**	-0.67	0.38	19.83**	0.33
X	Heterosis (MP)	51.00**	71.50**	-5.26	35.21**	103.00**	31.60*
P₁	Heterosis (BP)	32.56**	57.98**	-4.88	31.70**	90.90**	21.20
P₄	Mean	169.00	9.00	38.33	9.60	106.67	6.67
	s.c.a.	-3.61	0.32	-0.53	0.26	8.78	0.23
X	Heterosis (MP)	11.06	80.00**	-5.74*	20.45**	130.00**	-4.71
P₅	Heterosis (BP)	4.96	68.86**	-4.18	16.10*	123.80**	-13.00
P₄	Mean	126.67	9.00	40.33	9.23	78.33	7.00
	s.c.a.	-22.86**	1.85**	0.25	0.06	19.25**	-0.30
X	Heterosis (MP)	-17.40*	68.90**	-2.03	20.89**	82.20**	10.60
P₆	Heterosis (BP)	-22.40**	68.86	-1.63	20.30**	64.32**	10.60
P₃	Mean	118.33	9.00	38.33	8.23	91.00	5.00
	s.c.a.	-10.39	0.91	-0.08	-0.24	16.22*	-1.05*
X	Heterosis (MP)	-12.30	92.70**	-5.36*	-1.26	97.80**	-31.80**
P₅	Heterosis (BP)	-26.50**	92.72**	-4.18	-2.00	93.62**	-35.00**
P₃	Mean	175.00	8.00	40.33	8.80	76.67	6.33
	s.c.a.	28.33**	1.00	-0.33	-0.05	9.17	0.00
X	Heterosis (MP)	61.05**	45.50*	-1.63	12.32	72.30**	2.68
P₁	Heterosis (BP)	60.55**	26.38*	-1.63	4.76	63.13**	-9.60
P₆	Mean	140.00	8.33	40.67	7.80	87.33	6.00
	s.c.a.	6.67	-0.33	0.17	-0.72*	4.50	-0.50
X	Heterosis (MP)	-8.69	56.30**	-1.20	2.161	103.00**	-5.21
P₄	Heterosis (BP)	-14.30	56.29	-0.80	1.69	83.20**	-5.20

Crosses/ parameters		Seed yield	100 seed weight	Days to maturity	Root weight	Nodule weight	Protein content
P_4	Mean	39.29	6.43	101.33	9.29	213.33	17.74
	s.c.a.	8.47**	0.32	-1.17	1.50	16.67	-0.67
x	Heterosis (MP)	187.00**	16.10**	-4.26**	134.00**	205.00**	-0.40
P_1	Heterosis (BP)	166.90**	12.60*	-3.19*	110.00*	167.00**	-0.60
P_4	Mean	36.32	5.81	100.67	4.29	80.00	18.32
	s.c.a.	3.80	0.06	-2.43**	-0.58	-9.07	0.08
x	Heterosis (MP)	159.00**	9.21	-4.43**	10.00	2.13	3.30
P_5	Heterosis (BP)	146.70**	8.19	-2.89	-2.90	0.00	2.98
P_4	Mean	26.99	5.83	103.00	4.10	100.00	19.14
	s.c.a.	5.24	0.07	-0.98	0.33	2.18	-0.11
x	Heterosis (MP)	88.30*	8.06	-2.52*	-9.80	33.30	9.18**
P_6	Heterosis (BP)	83.36*	7.56	-1.27	-12.00	25.00	7.59*
P_3	Mean	24.67	5.59	101.33	4.52	200.00	17.80
	s.c.a.	2.20	-0.07	-0.34	0.92	22.18	0.35
x	Heterosis (MP)	60.80*	1.08	-3.03**	26.60	186.00**	2.53
P_5	Heterosis (BP)	42.27	-3.50	-2.26	20.20	161.00**	0.68
P_3	Mean	30.28	6.14	104.33	11.53	106.67	17.56
	s.c.a.	3.17	0.02	0.67	2.76**	-5.00	-0.15
x	Heterosis (MP)	102.00**	6.78	-0.64	217.00**	73.00	0.66
P_1	Heterosis (BP)	74.63*	6.04	-0.32	207.00**	68.40	-1.60
P_6	Mean	29.58	5.86	101.33	8.88	150.00	17.27
	s.c.a.	1.30	0.02	-0.83	2.39*	25.00	-0.93**
x	Heterosis (MP)	106.00**	8.62	-4.10**	95.40**	100.00**	-1.50
P_4	Heterosis (BP)	101.00**	8.12	-2.88*	90.10**	87.50**	-2.90

Summary

SUMMARY

A diallel analysis in rice bean was carried out in the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during 1997-1998 in order to determine the combining ability of the parents, to study the nature of gene action and also to estimate the heterosis for different characters. The experimental material consisted of six parental lines, 30 F_1 hybrids obtained by crossing the parents in all possible combinations. The experiment was laid out in Randomised Block Design with three replications. The observations were recorded on yield and yield attributing characters.

Significant differences were detected among the mean performance of the genotypes, for all the characters studied. It was observed that P_2 showed better performance when compared to other parents. Among the hybrids, $P_4 \times P_5$ showed better performance for plant height, number of pods per plant, number of branches per plant, days to first flowering, length of pods, seed yield and days to maturity. Among reciprocals, $P_4 \times P_1$ showed good performance for number of branches per plant, length of pods, number of pods per plant, number of seeds per pod, seed yield, 100 seed weight and nodule weight. Regarding fodder acceptability, all the genotypes were found to be acceptable by cattle.

The combining ability analysis carried out by the Method I under Model I of Griffing's Approach (1956) indicated that variances due to general combining

ability (GCA) and variances due to specific combining ability (SCA) were significant for nine characters, viz., plant height, number of branches, length of pods, number of pods per plant, seed yield, 100 seed weight , days to maturity, root weight and nodule weight. Among these characters, the GCA was more than SCA for number of pods per plant, seed yield and 100 seed weight indicating the operation of additive gene action for these traits. Both additive and non-additive gene action were operating for the remaining characters. The characters, days to first flowering, number of seeds per pod and protein content, showed significant SCA only indicating prepondence of non- additive gene action.

The combining ability analysis revealed that the parent P_4 (8LG) was the best general combiner for most of the yield attributing traits. Among the crosses, P_4 x P_1 exhibited outstanding specific combining ability effects for seed yield per plant. The crosses involving P_4 were found to be good specific combiners. The combinations involving P_1 and P_3 also gave good specific combining ability effects.

The numerical analysis by Hayman's approach indicated overdominance for all characters under study. The dominance of decreasing alleles in the parents was indicated by the negative value of F for all characters except plant height, length of pods and number of seeds per pod, for which increasing alleles were predominant. An almost equal distribution of genes with positive and negative effects was indicated by the ratio of H_2 to $4H_1$ for all the characters under study. Environmental influence was seen for all characters, except for plant height.

The graphical analysis revealed overdominance for all except for the character, number of branches per plant. The regression coefficient of covariance between parents and their offsprings in each array (Wr) on variance of all progenies in each parental array (Vr) did not differ significantly from unity, for plant height, length of pods, seed yield, 100 seed weight, days to maturity and protein content. Hence the assumption to non- allelic interaction was satisfactory for these characters. For the remaining characters, the regression coefficients differed significantly from unity.

The Vr- Wr graph also indicated that the parents were genetically divergent for the characters, viz., days to first flowering, number of pods per plant, number of seeds per pod, 100 seed weight, days to maturity, root weight and nodule weight, while very little divergence was seen among the parents for the remaining characters. The parent, P_1 appeared to possess most of the recessive genes, for majority of the characters, while the parents, P_2, P_3, P_5, and P_6 possessed most of the dominant genes. The parent P_4 possessed most of the dominant genes for majority of the characters and recessive genes for the others.

Manifestation of heterosis was seen for all the characters studied. Among the 30 hybrids, the hybrid, P_4 x P_1 was the most outstanding for yield and yield related characters. It was found to be significantly heterotic for all characters, except for protein content. The crosses P_4 x P_5, P_4 x P_6, P_3 x P_5, P_6 x P_4 and P_3 x P_1 also performed better in yield and yield attributing characters. In general, the hybrids involving the parents, P_4 (8LG) and P_3 (6LG) were found to be heterotic.

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DIALLEL ANALYSIS IN RICE BEAN
(*Vigna umbellata (Thunb.) Ohwi & Ohashi*)

By
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ABSTRACT OF THE THESIS
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ABSTRACT

A diallel analysis in ricebean (*Vigna umbellata* (Thunb.) Ohwi and Ohashi) was carried out in the Department of Plant Breeding and Genetics, during 1997-'98. The experimental material consisted of six parental lines and 30 F_1 hybrids, laid out in Randomised Block Design with three replications. The six parents were 3 LG, 5 LG, 6 LG, 8 LG, 9 LG, and 100 LG obtained from the germ plasm collection maintained at NBPGR, Thrissur. The observations were recorded on yield and yield attributing characters.

Significant differences were detected among the mean performance of the genotypes, for all the characters studied. The combining ability analysis carried out by Method I, Model I of Griffing's approach (1956), revealed that the parent, 8LG was the best general combiner for most of the yield attributing traits. Among the crosses, 8LG x 3 LG exhibited outstanding sca for seed yield per plant. The crosses involving 8 LG were found to be good specific combiners. The combinations involving 3 LG and 6 LG also gave good specific combining ability effects.

The numerical analysis by Hayman's approach indicated overdominance for almost all characters, which was confirmed by graphical analysis. The

dominance of decreasing alleles in the parents was indicated by the negative value of F for all characters except, plant height, length of pods and number of seeds per pod. An almost equal distribution of genes with positive and negative effects was indicated by the ratio of H_2 to $4H_1$ for all the characters. The regression coefficient of covarince between parents and their offsprings in each array (Wr) on variance of all progenies in each parental array (Vr) did not differ from unity, for plant height, length of pods, seed yield, 100 seed weight, days to maturity and protein content, indicating that assumption of non-allelic interaction was satisfactory for these characters. The Vr - Wr graph indicated that the parents were genetically divergent for days to first flowering, number of pods per plant, number of seeds per pod, 100 seed weight, days to maturity, root weight and nodule weight.

Manifestation of heterosis was seen for all the characters studied. Among the hybrids, 8 LG x 3 LG was the most outstanding for yield and yield related characters. The crosses, 8 LG x 9 LG, 8 LG x 100 LG, 6 LG x 9 LG, 100 LG x 8 LG and 6 LG x 3 LG also performed better in yield and yield attributing characters. In general, hybrids involving 8 LG and 6 LG were found to be heterotic.