GENETIC ANALYSIS OF BIOLOGICAL NITROGEN FIXATION TRAITS AND YIELD COMPONENTS IN COWPEA
(*Vigna unguiculata* (Linn). Walp).

By

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DECLARATION

I hereby declare that this thesis entitled "Genetic analysis of biological nitrogen fixation traits and yield components in cowpea (*Vigna unguiculata* (Linn). Walp)." 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 "Genetic analysis of biological nitrogen fixation traits and yield components in cowpea (*Vigna unguiculata* (Linn). Walp)." is a record of research work done independently by Sri.K.Sreekumar, under my guidance and supervision and that it has not previously formed the basis for the award of any degree, fellowship or associateship to him.

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INTRODUCTION

INTRODUCTION

The population on earth is expected to reach around 6253 million by 2000 AD. About 2600 million tons of cereals and 520 million tons of grain legumes will be needed to constitute just part of the food required to feed this increased growth of population. This does not take into account food input provided by meat from animals. To reach targets for grain production, the calculated figure for fertilizer consumption by grain crop is about 307 million tons by 2000 AD, of which nitrogenous fertilizer alone constitutes 56 million tons (Subba Rao, 1988).

Prospects for meeting nitrogen requirements in developing countries through the creation of new fertilizer plants are meagre on account of high cost of machinery and escalating cost of natural gas and the lack of less energy consuming industrial processes other than the Haber-Bosch process to convert nitrogen and hydrogen into ammonia.

Industrial nitrogen fixation in addition to being expensive and time consuming is heavily dependant on energy derived at a very fast rate. On the other hand, biological nitrogen fixation requires approximately half the quantum of energy needed for industrial fixation and is dependant on energy from renewable resources such as products of photosynthesis and soil organic matter. Therefore, the need for less expensive and realistic programmes to improve biological nitrogen fixation becomes more and more important for enhancing agricultural production.

In developing countries where the per capita income is low, people depend on vegetable protein, richest source of which is legumes. Even in the developed countries, the trend is in favour of substituting animal protein by vegetable protein in view of its nutritional qualities.

Majority of Indians depend on vegetable protein, and the grain pulses form an important part in their diet. Eventhough, India is the world's largest producer of grain legumes, the production is not adequate to meet the per capita requirement of 80 g recommended by World Health Organisation and FAO. In fact, there is a stagnation in area, production and productivity of pulses over the past three decades as against the increasing demand entailed by a growing population.

Grain legumes supply up to 20 per cent of the world's dietary protein needs. Legumes are popular in agriculture on account of their potential for reducing gaseous nitrogen into a biologically usable form. More over, cultivation of legumes are reported to be beneficial to the succeeding cereal crops (Nambiar *et al.*, 1988). Legumes in association with appropriate *Rhizobium* species contribute about 40 per cent of the total nitrogen fixed, which is affected by genotype of the legume, genotype of the *Rhizobium*, the environment and the genetic interaction between the legume and the *Rhizobium*. An appropriate symbiosis may result in higher nitrogen fixation. Hence, increase in nitrogen fixation could be achieved by genetic improvement of the legume and *Rhizobium*.

Cowpea forms an important component in the tropical cropping system of India, especially Kerala. It is grown for its green pods as vegetables, seeds as pulse and foliage as fodder. It is a major source of protein, energy, minerals and vitamins. Its importance is realised on account of its drought tolerance and adaptation to wide range of soil types.

The nitrogen fixing ability of cowpea will be an added advantage especially in subsistance agriculture. It is estimated that cowpea fixes 73-240 kg nitrogen per hactare per year in tropical conditions (Subba Rao, 1988). Till today much work was reported on different aspects of genetic improvement on yield components in cowpea, but practically little study has been done with respect to genetic basis of nitrogen fixation traits. Thus the present study is outlined to assess the genetic variability for nitrogen fixation traits along with the yield components in cowpea and to analyse the genetic basis of these traits as a prelude to breeding for improved nitrogen fixing varieties.

REVIEW OF LITERATURE

REVIEW OF LITERATURE

Geneticists and plant breeders have been successful in utilizing genetic variability to develop cultivars with high yield potential and other attributes including insect and pest resistance. However, very limited attention has been given to improve the nitrogen nutrition of legumes by breeding for increased biological nitrogen fixation. According to a model proposed by Mytton *et al.* (1984), nirtogen fixation by a legume- *Rhizobium* association is affected by the host genotype, *Rhizobium* strain, host X *Rhizobium* interaction, environment and interaction of environment with the other factors. Nambiar and Dart (1980) reported the variation in nitrogen fixation among groundnut cultivars. He concluded that virginia types of *Arachis hypogaea* formed more nodules and fixed more nitrogen than the valencia and spanish types. Groundnut had shown significant additive effects for traits indicative of nitrogen fixation (Nambiar *et al.* 1988) and they concluded that such selections are advantageous to improve the host first and then to identify superior strains for the improved host cultivar. The importance of selecting for traits related to nitrogen fixation was emphasized by Arunachalam *et al.* (1984). They observed that relative performance of genotypes based on nitrogenase activity and nodule mass alone agreed closely with that based on a number of characters measured from the seedling to the harvest stage. They concluded that nitrogenase activity and nodule mass have a good predictive value of the relative performance of genotypes based on a whole range of plant characters associated with the growth and yield of groundnut.

Islam (1978) and Rupela and Dart (1981) had established large differences among chickpea (*Cicer arietinum L.*) genotypes in nodulation and nitrogen fixation and found that correlation between nodulation parameters and grain yield were statistically significant and the inheritance of nodulation indicated segregation for nodulation in the F_2 population.

Kumar Rao and Dart (1979) studied in detail about the genetic variability for nodulation and nitrogen fixation in pigeonpea and concluded that cultivars differ with respect to nodulation and nitrogen fixation. *In vitro* studies coducted by Sreekumar (1982) proved that two cultivars *viz*, T 24 and Bahar differed significantly with nitrogen fixation in controlled conditions in pigeonpea.

Nutman (1967) observed in redclover that nodule number and size differed several fold among cultivars. Inheritance was polygenic with the abundantly nodulating habit showing some dominance over sparse nodulation. No specificity was detected with respect to strain of *Rhizobium*. In hybrids, selection for sparseness in succeeding generations recovered the sparse parent phenotype whereas selection for abundance often produced plants bearing very many more (and smaller) nodules than the abundantly nodulating parent. The relationship between average nodule size and number per plant is hyperbolic so that the same amount of nodule tissue can be produced by the different selection irrespective of the number of nodules formed.

Nutman (1984) reported that early nodulation (compared with late nodulation) and sparse nodulation (compared with abundant nodulation) in redclover are inherited independently. He concluded that early and sparse nodulation was associated with larger nodules.

The highly effective plants in redclover nodulated slightly earlier and had more nodules of a larger aggregate weight than the original cultivar, but plant yield per unit of nodule weight was similar (Nutman, 1984).

Hardarson and Jones (1979) reported in whiteclover that the host plant can influence with *Rhizobium* strains to form nodules. This specificity in nodulation is broadly heritable and can be enhanced by plant selection. The mechanism has potential to bring favourable plant - *Rhizobium* gene combination under control and its value should be explored by operational breeding programmes in which both the plant and *Rhizobium* genotypes which constitute the elite phenotype are selected and carried forward for further cycles of selection and hybridization.

In a systematic examination of six *Medicago sativa* cultivars grown in all possible combinations with eight *Rhizobium meliloti* strains of contrasting effectiveness, Mytton *et al.* (1984) measured host genotype, *Rhizobium* genotype and host X strain genotype interaction as accounting for, respectively, 4.8, 21 and 61 per cent of total phenotypic variance. Such results indicate low heritability of general symbiotic effectiveness in the host with interaction effects being large enough to mask general genetic differences.

2.1 Heritability and correlation of nitrogen fixation characters.

The selective capacity of the breeder's material depends upon the amount of heritable variability present in it. Heritability is an index of transmissibility of characters from one generation to the next and it provides a measure of the value of selection for different attributes in various types of progenies. The total variance of a character in segregating populations consists of (1) a heritable portion (2) an environmental portion and (3) a portion due to genotype-environment interaction. The heritable portion of the variable in turn is composed of the additive genetic variance which is fixable and dominance and epistatic variance which are non-fixable. Fisher (1918) first introduced the term heritability and defined it as the ratio of the fixable (additive genetic) variance to the total genetic variance. This concept was then strongly expressed by Kempthorne (1957). Robinson *et al.* (1949) defined heritability as the "additive genetic variance in per cent of the total variance". Lush (1940) has defined heritability both in broad and narrow sense as the percentage of total genotypic variance over phenotypic variance. In the narrow sense, heritability is the ratio of additive genetic variance to total variance and takes into account only average effects of genes transmitted from parents to offsprings.

Correlation studies provide estimates of the degree of the association of one character with its components and also among the components. Another aspect of this inter-relationship between various attributes is that this phenomenon often provides information as to the nature, extent and direction of selection pressure which should be exerted from the practical considerations. It is therefore, essential before initiating a breeding programme to obtain information regarding the inter- relationship among various attributes.

Correlation studies regarding the biological nitrogen fixation have been conducted in a set of varieties of pulse crops and these are reviewed in the ensuing paragraphs.

Mytton (1981) reported in lucerne that first consideration in identifying phenotypes with different fixing ability is the method of measuring nitrogen fixation. Several indirect criteria are available including plant appearance, colour, number, size and weight of nodules, dry matter accumulation, acetylene reduction and methods using measurement of nitrogen by mass spectrometry. Accuracy is assessed by correlation with total nitrogen accumulated by plants grown under conditions free from combined nitrogen. Correlation can be substantially less than unity for some criteria. Poorly correlated criteria limit ability to identify genetic differences with certainty and will thus reduce the rate of genetic advances under selection in uncontrolled mixed populations. In general, dry matter yield where combined nitrogen is relatively unavailable gives accurate assessment of fixation coupled with ease of measurement. It is recognised that the role of the plant in fixing nitrogen is confounded with its capacity to use it. It is, therefore, essential that the yield of crops selected for improvement is generally limited by symbiotic nitrogen fixation.

According to him there is a range of quantitative variation in nitrogen fixation which is broadly genetic, but precise methods of exploiting it have not been fully developed. Particular difficulties occur because amounts of nitrogen fixed are liable to change in an unpredictable way when cultivars are nodulated by different *Rhizobium* genotypes and as different environments are encountered. There is evidence to suggest scope for host determined improvements but it is clearly impossible by conventional methods of genetic manipulation to eliminate a certain amount of *Rhizobium* strain dependence in nitrogen fixation. Thus, rapid genetic advance under selection would result from coincidential selection of plant and *Rhizobium* genotypes.

Barnes *et al.*(1984) reported that alfalfa genotypes varied for nitrogenase activity and that the relative differences among genotypes were reproducible. Nitrogenase activity was positively correlated with shoot weight, root weight, number of fibrous roots and nodule mass.

Sudagar Singh and Ghai (1984) reported in pea that nitrogen fixation was positively associated with plant height, nodes on the main stem, first pod bearing node, internode length, grains per plant, total plant weight and grain yield. Nitrogen fixation was reported to be closely associated with plant weight followed by internode length, harvest index, chlorophyll content and nodes on the main stem.

Miller *et al.* (1986) observed in cowpea that positive and significant correlation existed among nitrogenase activity and both nodule weight and nodule number. A significant correlation was also observed between nodule weight and number. The results confirmed that nitrogenase activity among these parental genotypes is controlled in large part by the plants ability to form large efficient nodules and not by its ability to form vegetative matter. However, the correlation coefficients between top dry weight and the other three nitrogen fixation variables were not significant suggesting that top dry weight per plant at the time of flowering is not a good indicator in nitrogen fixation potential. Narrow sense heritability estimates were moderately high for nodule number and nitrogenase activity and low for nodule weight and top dry weight.

Rosaiah *et al.*(1987) studied the coefficient of variation, heritability and correlation of nitrogen fixation characters in greengram. The nodules per plant, nodule fresh weight per plant and yield per plant showed high heritability coupled with high genetic advance whereas nitrogen content of nodules, shoot and seed protein content showed high heritability coupled with low genetic gain. The seed yield per plant was significantly and positively associated with dry weight of nodules per plant, nitrogen content of nodules and of the shoot. Nodules per plant and seed protein content showed no correlation with yield, indicating that the nodule size and not the number was an important trait, and the seed yield would be improved without sacrificing the protein content of the seed. The positive correlation of nitrogen content of shoot with seed yield per plant, seed protein and dry weight of nodules suggest that the nitrogen content of a plant should be maximum at anthesis, because the onset of reproductive growth signals a decline of nitrogen fixation by nodules.

Singh and Murty (1988) reported in greengram that there was no evidence of an antagonistic relationship between grain yield and total nitrogen per plant. Thus a selection for total dry weight or nodule fresh weight may improve the total nitrogen fixed in greengram without any adverse effect on its yield or yield traits. A high heritability estimate was observed for total nitrogen per plant, total dry weight per plant and nodule fresh weight per plant indicating the control of host plant over both *Rhizobium* as well as environment.

Seetin and Barnes (1977) reported high heritability estimate for nitrogen fixation characters in alfalfa.

Smith *et al.* (1982) reported high heritability estimate for nitrogen fixation characters like nodule number, nodule fresh weight, plant dry weight and nitrogen content in crimson clover. High heritability estimate with large variation present for nitrogen fixation gave feasibility for the selection for increased nitrogen fixation in the species.

2.2 Combining ability and gene action in nitrogen fixation characters

The term "general combining ability" (gca) was used by Spraque and Tatum (1942) to designate the average performance of a line in a number of hybrid combinations. They used "specific combining ability" (sca) to designate those cases in which certain hybrid combination did relatively better or worse than would be expected on the basis of average performance of the lines involved. Various methods have been used for testing gca of inbred lines. Davis (1927) tested the gca of inbred lines by means of inbred X variety cross (top cross). Hayes and Johnson (1939) studied the segregates from the crosses of high and low combining lines and concluded that lines of good combining ability were obtained more frequently from crosses involving good combiners than from crosses involving lines having low combining ability. Allard (1960) pointed out that one among the early decision to be made in a plant breeding programme is the choice of parents for hybridization. Certain combinations of parents nick well to produce many superior offsprings, while hybrids, between apparently desirable parents produce disappointing progeny.

Griffing (1956) demonstrated the method of working out gca and sca effects along with their variances. He pointed out that twice the GCA variance contains not only the additive genetic variance but also a portion of the epistatic variance (additive X additive) and SCA includes all of the dominance and the remaining epistatic variance.

Several workers have estimated the combining ability and gene action in different pulses with regard to biological nitrogen fixation and these are reviewed in the following section.

Miller *et al.* (1986) carried out diallel analysis in cowpea for general combining ability, specific combining ability and reciprocal effects for nitrogen fixation variables such as nitrogenase activity, nodule number, nodule weight and plant dry weight. They observed that the estimates of sca were highly significant for nirtogenase activity, nodule weight and nodule number while non-significant for dry weight of the plant. The gca was significant only for nodule weight. Generation mean analysis revealed that additive gene action was more prominent than dominance and interallelic gene action for nodule number and nitrogenase activity, while non additive gene action was prominent for nodule weight and plant dry weight.

Combining ability analysis of the 8 X 8 diallel progeny by Singh and Murty (1988) revealed that both gca and sca were significant for nitrogen fixation traits such as total nitrogen content per plant, dry weight of the plant and nodule fresh weight indicating the importance of both additive and non-additive gene effects in the control of nitrogen fixation traits.

Hely (1972) reported significant gca and sca effects for nitrogen fixation traits such as total nitrogen content per plant, dry weight of the plant and nodule fresh weight in *Trifolium ambiguum*.

Significant gca and sca effects for biological nitrogen fixation traits in crimson clover were reported by Smith *et al.* (1982) and the importance of both additive and non additive gene effects were proposed for total nitrogen content per plant, dry weight of the plant and nodule fresh weight.

In alfalfa, Tan (1981) found significant gca and sca effects for biological nitrogen fixation traits such as total nitrogen content, dry weight, nodule fresh weight and nodule dry weight.

The importance of only additive gene effects for the biological nitrogen fixation traits such as nitrogen content per plant, nodule fresh and dry weight and plant dry weight in spanish clover was reported by Pinchbeck *et al.* (1980).

2.3 YIELD AND YIELD ATTRIBUTING CHARACTERS

2.3.1 Genotypic and phenotypic coefficients of variation, heritability and genetic advance

Singh and Mehndiratta (1969) studied forty varieties of cowpea and reported that number of pods per plant had the maximum genotypic coefficient of variation followed by number of pod clusters per plant and grain yield per plant. The number of days to maturity had the minimum value in their studies. They also reported high heritability estimates for days to flowering (88.8), length of pod (80.5) and days to maturity (78.3) and low heritability for seed yield per plant (31.6) and seed yield per plant (27.6).

Veeraswamy *et al.* (1973) reported high genotypic coefficient of variation in cowpea for grain yield per plant, number of pods per plant, number of branches per plant, height of the plant and number of pod clusters per plant. Maximum heritability was recorded for pod length and the minimum for number of seeds per pod. Genetic advance was high for pod length followed by number of pods per plant and grain yield per plant.

Rajendran *et al.* (1979) studied the heritability and intercorrelation of cowpea grown for seed purpose. All the characters examined were found to have high heritability. They also reported that an ideal plant which gives higher seed yield should preferably flower early, have longer peduncles and more number of seeds per pod.

Ramachandran *et al.* (1980) from their studies on variability in selected cowpea types reported that the range of variation for varietal means was quite large in respect of days to first harvest, internodal length, weight of pods, seeds per pod, pods per plant and yield per pod. The genotypic coefficient of variation was found to be maximum for yield per plant followed by number of pods per plant and internodal length. Heritability was highest for days to flower followed by days to harvest. Genetic advance as percentage of mean was found to be maximum for seeds per pod followed by yield per plot and pods per plant.

Radhakrishnan and Jebaraj (1982) reported in cowpea that the number of pods per plant had the maximum genotypic coefficient of variation followed by number of pod clusters per plant and number of branches per plant.

The results of studies conducted by Kumar *et al.* (1983) on cowpea indicated that the selection for pods per peduncle, pod length and width, peduncle length and days to 50 per cent maturity would increase seed yield.

Variability studies undertaken on forty genotypes of cowpea by Dharmalingam and Kadambavanasundaram (1984) had shown that there existed greater variability for the traits like harvest index, number of pods and seed yield. Genetic variability was low for the traits like number of seed per pod, pod length and hundred seed weight. Maximum heritability was observed for length of the pod followed by harvest index.

Apte *et al.* (1987) reported high heritability estimate for hundred seed weight, seeds per pod and days to maturity in cowpea. Percentage of genetic gain was greatest for hundred seed weight, followed by plant height, branches per plant and seeds per pod. Hundred seed weight and seeds per pod were suggested as selection criteria.

Patil and Baviskar (1987) in variability studies in cowpea reported high genotypic and phenotypic coefficients of variation for pod clusters per plant, pods per plant, seed yield per plant and hundred seed weight.

Sharma *et al.* (1988) have reported that the maximum genotypic coefficient of variation among genotypes of *Vigna unguiculata* was seen for dry matter yield followed by plant height, green forage yield, pods per plant, seed weight and green pod yield. High heritability was recorded for days to 50 per cent flowering.

Thiyagarajan (1989) had studied the genetic variability of yield and component characters on yield and nine related traits in seven parents and their F_1 hybrids in cowpea. The estimates of heritability and genetic advance were found to be high for plant height, number of seeds per pod and 100 seed weight.

Savithri Amma (1992) studied the genetic variability in cowpea and observed high genotypic variances for all characters except seeds per pod. Heritability values ranged from 15.23 per cent for number of pods per plant to 71.41 per cent for hundred seed weight. High heritability was observed for plant height, pod length and hundred seed weight. High genetic advance was recorded for plant height, seed weight per plant and hundred seed weight.

2.3.2 Correlation

Singh and Mehndiratta (1969) reported high positive genotypic correlation among number of pods per plant, number of pod clusters per plant, days to flowering and days to maturity in cowpea. Negative genotypic correlation was reported for length of pod with number of pod clusters per plant and number of pods per plant.

In cowpea, Angadi (1976) reported positive genotypic correlation between number of seeds per pod and height of plant and negative genotypic correlation between number of pods per plant and seeds per pod.

A study conducted by Sreekumar *et al.* (1979) in cowpea showed that characters such as number of days to flowering, number of grains per pod, hundred grain weight and grain yield had positive phenotypic and genotypic correlations with yield.

Rajendran *et al.* (1979) evaluated nineteen varieties of cowpea and reported significant positive genotypic correlation of grain yield with height of the plant, number of days to first flowering, number of pod clusters per plant, number of primary branches per plant and number of seeds per pod.

Dumbre *et al.* (1982) studied the genotypic and phenotypic correlations of six quantitative characters in twentyfour cultivars of cowpea and reported that height and pods per plant were significantly correlated with yield.

Natarajaratnam *et al.* (1985) estimated phenotypic correlation of yield and yield components in ten varieties of cowpea and found that grain yield showed positive phenotypic correlation with number of pods per plant, number of pod clusters per plant and height of the plant.

Natarajaratnam *et al.* (1986) reported in cowpea that the seed yield was strongly associated with pod weight per plant, number of pods per plant, number of pod clusters per plant and plant height.

Positive correlation of grain yield with 100 grain weight in cowpea was reported by Chikkadyavaiah (1985) and Choulwar and Borikar (1987).

Patil and Bhapkar (1987) made correlation studies in cowpea and observed that seed yield was positively and significantly correlated with number of pods per plant and seeds per pod while pods per plant and seeds per pod were negatively correlated with each other.

Rosaiah *et al.* (1987) reported that there was no correlation between seed protein content and seed yield in greengram.

Sharma *et al.* (1988) have reported in chickpea that seed yield was positively and significantly correlated with days to first flowering, and days to 50 per cent maturity. Green pod yield was positively correlated with days to first flowering and green pod yield was positively and significantly correlated with pods per plant and seeds per pod.

Senanayake and Wijeratne (1988) have reported that the yield of cowpea was positively correlated with hundred seed weight and pod length.

Positive and significant correlation between seeds per pod and yield in cowpea was observed by Tyagi and Koranne (1988).

Thiyagarajan and Rajasekaran (1989) reported in cowpea that a positive and highly significant phenotypic and genotypic correlations existed among yield and days to maturity, plant height, branches per plant, clusters per plant, pod length and seeds per pod while there was a negative association among yield and days to 50 per cent flowering and hundred seed weight.

High positive correlation between the number of pods per plant and seed production in cowpea was reported by Oliveira *et al.* (1990) and Sudhakumari (1994).

Raut *et al.* (1990)havereported high positive correlation with seed yield per plant and pod number per plant in blackgram.

2.3.3 Path analysis

The two characters whose relationship is being measured, do not exist by themselves alone, but a very intricate system of path way is involved, in which various other attributes also participate. Therefore, in order to get a clear picture, it would be desirable to seperate out the direct contribution of each yield component and also the indirect contribution it makes through its relationship with other attributes.

In the present study, this has been attempted by path coefficient analysis developed by Wright (1921). Li (1956) discussed the concept of path coefficient and its implication on population genetics. According to him, when the casual factors are uncorrelated, the path coefficient is simply the ordinary correlation between two variables concerned and seperation of the correlation coefficient in to various components is one of the main objects of path coefficient analysis. This technique has been utilized by various workers in a set of varieties of various pulse crops.

Patel and Telang (1976) made path analysis of yield components in cowpea and reported that seed number per pod had a largest direct effect on seed yield, followed by hundred seed weight and pod number per plant. Pod length had a marked negative direct effect on yield.

In pea Narasinghani *et al.* (1978) reported maximum direct effect of number of seeds per plant on yield followed by hundred seed weight, number of days to maturity, height and protein per cent.

In cowpea, Hanchinal *et al.*(1979) reported that the number of branches per plant had direct effect on yield and that number of seeds per plant had indirect effect acting through number of branches. Rajendran *et al.* (1979) observed that in cowpea, days to first flowering had positive direct effect on seed yield.

Jagadish Murthy (1986) reported in cowpea that the selection for all the characters was better in improving yield than selection based on seed yield alone. Path coefficient analysis has shown the number of pods per plant as the major yield contributing character.

Natarajaratnam *et al.*(1986) reported in cowpea that the pod weight per plant had the greatest direct effect on seed yield.

Thiyagarajan and Rajasekharan (1989) observed direct positive effect of branches per plant, days to 50 per cent flowering, plant height, number of pods per plant and pod length on grain yield in cowpea. Days to maturity, number of seeds per pod, 100 grain weight and number of clusters per plant recorded negative direct effect. Number of pods per plant recorded lowest positive direct effect.

Tyagi and Koranne (1988) reported that number of seeds per pod had positive direct effect on seed yield.

2.3.4 Combining ability

Combining ability studies with respect to yield and yield attributing characters have been conducted by various workers on pulses and these are reviewed in the ensuing paragraphs.

2.3.4.1 Number of days to 50 per cent flowering

Anilkumar (1992) while analysing the combining ability for number of days to flowering in a line X tester analysis in cowpea found significant variance due to GCA and SCA, while Jayarani (1993) observed that only gca effects were significant for this character in *Vigna unguiculata.*

Rejatha (1992) in a 6 X 6 diallel analysis of vegetable cowpea found significant GCA and SCA variance for number of days to 50 per cent flowering.

Both general and specific combining ability variances were found significant for this character in mungbean (Deshmukh and Manjare 1980 and Patel *et al.* 1988), cowpea

(Zaveri *et al.* 1983), chickpea (Katiyar *et al.* 1988), peas (El-Muraba *et al.* 1988 and Moitra *et al.* 1988) and blackgram (Sivan Pillai 1980).

A line X tester analysis involving 4 testers and 10 lines of *Vigna unguiculata* indicated that both general combining ability and specific combining ability were important for days to 50 per cent flowering (Mishra *et al.* 1987). In another line X tester analysis using chickpea varieties, Mandal and Bahl (1987) reported that gca estimates were non-significant for this character.

Saxena *et al.*(1989) observed in a diallel crossing system of redgram that the ratio of general to specific combining ability mean squares was high. This is in agreement with the findings of Singh and Dhaliwal (1970) and Fooland and Bassiri (1983) in blackgram Wilson *et al.* (1985) in greengram, Csizmadia (1985) and Ranalli *et al.* (1989) in pea and Cheralu *et al.* (1989) in redgram.

However, in a diallel crossing system of chickpea, Pande *et al.* (1979) observed that the SCA variance was higher than GCA variance.

2.3.4.2 Number of pods per plant

Jayarani (1993) reported significant GCA and SCA variance for number of pods per plant in cowpea.

Rajatha (1992) reported that both GCA and SCA variances were not significant for number of pods per plant in vegetable cowpea.

Anilkumar (1992) reported significant gca and sca effects for number of pods per plant in cowpea.

Mak and Yap (1977) in cowpea, Deshmuk and Manjare (1980) in mungbean, Zaveri *et al.*(1983) in cowpea, De-silva and Omaran (1986) in wingedbean, Katiyar *et al.*(1988) in chickpea, Hazarika *et al.* (1988) in redgram and Moitra *et al.* (1988) in pea observed that the variances due to GCA and SCA were significant. But the variance due to general combining ability was found to be predominant (Chauhan and Joshi 1981) in cowpea (Wilson *et al.* 1985), in greengram (Habib *et al.* 1985), in groundnut and pea (Naumkina 1987). The variance due to specific combining ability was reported to be higher than GCA (Pande *et al.* 1979) in chickpea, (Fooland and Bassiri 1983) in fieldbean, (Singh *et al.* 1987) in blackgram, (Kumar and Bahl 1988 and Bahl and Kumar 1989) in chickpea and (Rajarathinam and Rathnasamy 1990 and Sivan Pillai 1980) in urdbean.

Only GCA variance was found highly significant in a 12 X 12 partial diallel cross of peas by Tewatia *et al.* (1988). Similar results were obtained by Ranallil *et al.* (1989) in the same crop and Cheralu *et al.* (1989) and Saxena *et al.* (1989) in redgram. On the contrary, only SCA mean square was found significant in broadbean by Mahmoud and Al-Ayobi (1987), in greengram by Saxena and Sharma (1989) and in blackgram by Kalia *et al.* (1991).

2.3.4.3 Length of pod

Rejatha (1992) reported significant GCA variance for length of pod in vegetable cowpea while SCA variance was non-significant. Jayarani (1993) observed similar results and suggested the importance of general combining ability alone for length of pod in cowpea.

Combining ability analysis of a diallel cross of cowpea by Singh and Jain (1972) indicated the importance of both general and specific combining ability variances for length of pod. Similar results were also obtained by Mak and Yap (1977) in the same crop; Patel *et al.*(1988) in greengram and Kaila *et al.* (1991) in blackgram. Eventhough both GCA and SCA mean squares were important, GCA variance was found higher than SCA variance in cowpea by Chauhan and Joshi (1981) and in greengram by Wilson *et al.* (1985). But in wingedbean, the variance due to SCA (Erskine,1981) and in pea variance due to GCA (Tweatia *et al.* 1988) were found highly significant.

2.3.4.4 Number of seeds per pod

Rejatha (1992) reported in cowpea that the variances due to GCA and SCA were significant. The magnitude of GCA variance was greater than that of SCA variance suggesting the importance of general combining ability for the character.

Anilkumar (1992) reported significant gca effects for this character in cowpea. The sca was reported to be non significant. Jayarani (1993) observed in cowpea that the GCA variance for number of seeds per pod was non- significant while SCA variance was highly significant. The magnitude of SCA variance was reported to be higher than GCA variance.

Both GCA and SCA variances were important for this trait. This was reported by Mak and Yap (1977) in longbean, Pande *et al.* (1979) in chickpea, Chauhan and Joshi (1981) in cowpea, De-silva and Omran (1986) in winged bean, Katiyar *et al.* (1988) in chickpea and El-Muraba *et al.* (1988) in pea and Saxena and Sharma (1989) in mungbean.

Combining ability studies of 25 chickpea hybrids derived from crosses of 5 lines and 5 testers with their F_2 and parents by Bahl and Kumar (1989) revealed that the SCA variances were greater than those for GCA. Mahmoud and Al-Ayobi (1987) in fababean, Saxena *et al.*(1989) in redgram and Ranalli *et al.*(1989) in pea observed that variance due to GCA was significant for this character. But Singh and Jain (1972) in cowpea and Kalia *et al.*(1991) in blackgram noted the importance of SCA variance only.

2.3.4.5 Hundred seed weight

Jayarani (1993) reported significant gca and sca effects for the control of this character in cowpea. However, SCA variance was reported to be greater than GCA variance suggesting the importance of specific combining ability for 100 seed weight.

Anilkumar (1992) obsreved significant GCA variance for this character while SCA variance was non-significant in cowpea.

Singh and Jain (1972) in cowpea, Mak and Yap (1977) in longbean, Deshmukh and Manjare (1980) and Patel *et al.* (1988) in mungbean, Singh *et al.* (1985) in fieldpea, Katiyar *et al.*(1988) in chickpea, Jhorar *et al.*(1988) in clusterbean and Moitra *et al.*(1988) in pea reported that, variances due to GCA and SCA were important for this trait. Combining ability analysis in a diallel analysis of F_1 and F_2 generations involving seven diverse derivatives of soybean by Srivastava *et al.* (1977) revealed that both GCA and SCA variances were significant, the estimate of GCA variance being higher than SCA variance. Similar results were obtained by Pande *et al.* (1979) and Bahl and Kumar (1989) in chickpea, Chauhan and Joshi (1981) in cowpea, Fooland and Bassiri (1983), Singh *et al.*(1986) and Nienhuis and Singh,(1986) in bean, Sivan Pillai (1980) in blackgram and Fleck and Ruckenbauer (1989) in *Vicia faba*. On the contrary, in a line X tester analysis in chickpea revealed that gca estimates were non significant for 100 seed weight (Mandal and Bahl 1987).

2.3.4.6 Grain yield per plant

Jayarani (1993) reported significant sca effects for the seed yield per plant in cowpea, while gca effects were non significant. The variance due to SCA was higher in magnitude than variance due to GCA indicating the importance of specific combining ability alone for this trait.

Anilkumar (1992) observed significant gca and sca effects for yield in cowpea. Data from an 8 line X 4 tester analysis of *Cajanus cajan* indicated that both GCA and SCA variances were significant for seed yield per plant (Hazarika *et al.* 1988). This is in conformity with the findings of Singh and Jain (1972) and Zaveri *et al.* (1983) in cowpea, Deshmukh and Manjare (1980) and Saxena and Sharma (1989) in mungbean, Singh *et al.*(1985) in fieldpea, Singh *et al.*(1987) and Moitra *et al.*(1988) in pea, Arora and Pandya (1987) and Katiyar *et al.*(1988) in chickpea, Haque *et al.* (1988) and Sivan Pillai (1980) in blackgram.

A half diallel of seven short duration pigeonpea lines were evaluated by Saxena *et al.*(1989) and the results indicated that GCA variance predominated. Similar results were obtained in a 5 X 5 diallel cross of *Dolichos lablab* by Singh *et al.*(1980), in cowpea by Chauhan and Joshi (1981), in greengram by Wilson *et al.*(1985), in groundnut by Habib *et al.* (1985) in drybean, by Nienhuis and Singh (1986), in pea by Naumkina (1987) and

Tewatia *et al.*(1988) and in pigeonpea by Cheralu *et al.* (1989). In longbean, Mak and Yap (1977) observed that only gca was significant.

The estimates of mean squares due to SCA were greater than their respective mean squares due to GCA as reported by Pandey and Tiwari (1989) in chickpea, Fooland and Bassiri (1983) in fieldbean, De-silva and Omran. (1986) in winged bean, Mishra *et al.* (1987) in cowpea, Mehetre *et al.*(1988) in pigeonpea, Kumar and Bahl (1988) and Bahl and Kumar (1989) in chickpea and Singh *et al.* (1987), Rajarathinam and Rathnasamy (1990) and Kalia *et al.*(1991) in blackgram.

2.3.5 Gene action

The development of a plant breeding strategy hinges mainly on the support provided by genetic information on the inheritance and behaviour of major quantitive characters.

The combining ability is determined by two types of gene action namely additive and non-additive. The additive effects are mainly due to poly-genes which act in additive manner, producing fixable effects. The non-additive gene action results from dominance, epistasis and various other interaction effects, which are non fixable.

2.3.5.1 Number of days to 50 per cent flowering

Jayarani (1993) and Rejatha (1992) reported in cowpea that both additive and non-additive gene actions were important in governing this character. But, they observed that GCA variance was more than SCA variance indicating the predominance of additive gene action. However, Anilkumar (1992) and Sreekumar (1993) observed the predominance of non additive gene action for this character in cowpea and greengram respectively.

Studies by Mehtre *et al.*(1988) in pegionpea, Pandey and Tiwari (1989) in chickpea and Singh and Singh (1990) in pea revealed that both additive and non-additive gene effects were important for days to flowering. Combining ability analysis of chickpea varieties showed the existance of both additive and non-additive gene actions, but additive gene was predominant (Pandey and Tiwari 1989). Similar results were obtained by Kanarakaya and Kalinia (1981) in *Vica sativa*, Dubey and Lal (1983) in pea, Rao *et al.* (1984) and Wilson *et al.* (1985) in greengram, Salimath and Bahl (1989) and Katiyar *et al.*(1988) in chickpea, Patil and Bhapkar (1986) in cowpea, Singh *et al* (1986) in *Lalab purpureus*, Das and Dana (1990) in ricebean and Sivan Pillai (1980) in blackgram.

Singh and Dhaliwal (1970), Venkateswarlu and Singh (1981), Csizmadia (1985), Yadavendra and Sudhirkumar (1987), Gil and Martin (1988) and Tawar *et al.* (1989) opined that, only additive gene effects controlled days to flowering in blackgram, pigeonpea, pea, chickpea, *Vicia faba* and soybean respectively.

High SCA variance over GCA variance reported in chickpea (Pande *et al.* 1979), in mungbean (Deshmukh and Manjare 1980), and in cowpea (Zaveri *et al.* 1983) indicated that this character was controlled by non-additive genes.

Complementary type of epistasis was observed for the expression of this character in greengram as reported by Rao *et al.* (1984) and Muker *et al.* (1988).

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Singh and Dhaliwal (1970), Venkateswarlu and Singh (1981), Csizmadia (1985), Yadavendra and Sudhirkumar (1987), Gil and Martin (1988) and Tawar *et al.* (1989) opined that, only additive gene effects controlled days to flowering in blackgram, pigeonpea, pea, chickpea, *Vicia faba* and soybean respectively.

High SCA variance over GCA variance reported in chickpea (Pande *et al.* 1979), in mungbean (Deshmukh and Manjare 1980), and in cowpea (Zaveri *et al.* 1983) indicated that this character was controlled by non-additive genes.

Complementary type of epistasis was observed for the expression of this character in greengram as reported by Rao *et al.* (1984) and Muker *et al.* (1988).

2.3.5.2 Number of pods per plant

Jayarani (1993) reported in cowpea that variance due to SCA was greater in magnitude than variance due to GCA. The possibility of a predominance of non additive gene action was reported.

Anilkumar (1992) observed that number of pods per plant in cowpea was controlled by non additive gene action. Results from analysis of a diallel cross involving 10 varieties of pea indicated the importance of additive and non-additive genetic effects for number of pods per plant (Singh and Singh 1990). This is in conformation with the findings of Mehtre *et al.* (1988) in redgram, Onkar Singh and Paroda (1989) in chickpea and Natarajan *et al.*(1990) and Sreekumar (1993) in greengram.

Combining ability studies revealed that both general and specific combining ability variances were important, but magnitude of GCA variance seemed to be comparatively much higher for number of pods per plant, which suggested additive gene action in the inheritance of this trait in pulses like cowpea (Chauhan and Joshi 1981 and Thiyagarajan *et al.* 1990), blackgram (Sivan Pillai 1980, Dahiya and Waldia 1982 and Sharma and Rao 1990), pea (Dubey and Lal 1983), Soybean (Sharma and Nishi Sharma 1988), greengram (Wilson *et al.* 1985), pigeonpea (Patel *et al.* 1987) and chickpea (Sharma *et al.* 1988, Katiyar *et al.* 1988 and Salimath and Bahl 1989).

In chickpea (Pande *et al* 1979, Singh and Ramanujam 1981 and Yadavendra and Sudhirkumar 1987), cowpea (Zaveri *et al.* 1983 and Thiyagarajan *et al.* 1990), pigeonpea (Singh *et al.* 1983), greengram (Saxena and Sharma 1989 and Deshmukh and Manjare

1980) and blackgram (Rajarathinam and Rathnasamy, 1990) it was observed that, the SCA variance was predominant, indicating the preponderance of non-additive gene action. But according to Sandhu *et al.* (1981) and Habib *et al.* (1985), only non-additive gene effects were significantly influencing this character in blackgram and groundnut respectively.

Complementary and duplicate type of epistasis were found to be important for the expression of this character in mungbean as reported by Rao *et al.*(1984). The preponderance of duplicate type of epistasis was observed in greengram by Muker *et al.* (1988) and complementary type of epistasis in chickpea by Pandey and Tiwari (1989). Tawar *et al.* (1989) reported that overdominance was important in soybean for number of pods per plant.

Scaling test with 5 generation means showed the involvement of epistatic and dominance gene action for number of pods per plant in pea (Singh and Singh 1990) and chickpea (Sinde and Deshmukh 1990). But among epistasis, additive X additive interaction component contributes more in pea (Singh and Singh 1990) but in chickpea, additive and dominance gene effects, dominance X dominance and additive X additive interactions were important (Sinde and Deshmukh 1990).

2.3.5.3 Length of pod

Rejatha (1992) reported significant GCA variance for length of pod in vegetable cowpea. The GCA variance was found to be more than the SCA variance indicating additive gene action for this character.

Trials in pea by Singh *et al.* (1987) and Singh and Singh (1990) revealed that both additive and non-additive genetic variances were important for length of pod.

Eventhough both additive and non-additive gene effects were significant, a preponderance of additive variance was noticed by Chauhan and Joshi (1981) and Thiyagarajan *et al.* (1990) in cowpea, Malhotra (1983) in blackgram, Dubey and Lal (1983) in pea and Singh *et al.* (1986) in *Lablab purpureus.*

Patel *et al.* (1987) evaluated 39 hybrids along with 3 lines and 13 testers as parents in pigeonpea and reported that, only additive gene action was found operative for pod length. Similar result was reported in urdbean by Sharma and Rao (1990) and in greengram by Natarajan *et al.*(1990).

Duplicate type of epistasis was observed for this trait in mungbean (Rao *et al* (1984). But according to Muker *et al.* (1988) duplicate type of epistasis and complementary type of epistasis were important in different crosses of the same crop. Additive and dominance components were also found positive and significant.

2.3.5.4 Number of seeds per pod

Rejatha (1992) reported the importance of both additive and non-additive type of gene action for number of seeds per pod in cowpea. The GCA variance was found to be higher than SCA variance suggesting the predominance of additive type of gene action.

Anilkumar (1992) observed the influence of additive gene action in the control of number of seeds per pod in cowpea. Jayarani (1993) recorded the importance of non additive gene effect in number of seeds per pod in cowpea. The variance due to GCA was found to be less than that of SCA variance.

In crosses of chickpea by Pande *et al.* (1979), in pea by Singh *et al.* (1987) and Singh and Singh. (1990) and in greengram by Natarajan *et al.* (1990) observed that the character, number of seeds per pod was conditioned by both additive and non-additive genetic variances.

The ratio of variance due to GCA to SCA was found to be high, indicating the predominance of additive gene effects as reported by Syr'eva (1981), Venkateswarlu and Singh (1981) and Dubey and Lal (1983) in pea, Malhotra (1983) in blackgram, Wilson *et al.* (1985) and Saxena and Sharma (1989) in greengram, Sharma and Nishi Sharma (1988) in soybean, Katiyar *et al.* (1988) and Onkar Singh and Paroda (1989) in chickpea, Saxena *et al.* (1989) in pigeonpea.

This ratio was found to be low in soybean (Kaw and Madhava Menon 1977), mungbean (Deshmukh and Manjare, 1980), chickpea (Salimath and Bahl 1989) and cowpea (Thiyagarajan *et al.* 1990), and showed the preponderance of non-additive genes. Mehtre *et al.* (1988) opined that only non-additive gene effect was significant for number of seeds per pod in pigeonpea. Similar results were reported by Das and Dana (1981) in ricebean where dominance component was important.

Pandey and Tiwari (1989) observed that complementary type of epistasis was exhibited for this trait in chickpea.

2.3.5.5 Hundred seed weight

Jayarani (1993) reported the influence of both additive and non-additive gene action for hundred seed weight in cowpea.

Anilkumar (1992) reported additive gene action for hundred seed weight in cowpea. According to Sharma *et al.* (1988) the inheritance of hundred seed weight, appeared to be under the additive, dominance and epistatic effects in chickpea. A 12 X 12 diallel of pea indicated that both additive and non additive gene effects were important for this character (Singh and Singh, 1990). This was in agreement with the findings of Kamatar (1985) in chickpea.

Hundred seed weight was under the influence of additive gene effects as reported by Deshmukh and Manjare (1980) and Wilson *et al.* (1985) in greengram, Chauhan and Joshi (1981) and Patil and Bhapkar (1986) in cowpea, Venkateswarlu and Singh (1981) and Dubey and Lal (1983) and Singh and Singh (1990) in pea, Malhotra (1983) and Sharma and Rao (1990) in blackgram, Singh *et al.* (1983) in pigeonpea, Manoharan *et al* (1985) in groundnut, Tawar *et al* (1989) in soybean.

Pandey *et al.* (1979), Katiyar *et al.* (1988) and Salimath and Bahl (1989) reported that non-additive gene effect was predominant, though both additive and non-additive gene effects were present in chickpea. Similar results were obtained by Thiyagarajan *et al.* (1990) in cowpea and Sreekumar (1993) in greengram.

Complementary type of epistasis was found important for this character in mungbean (Rao *et al.* 1984). Muker *et al.* (1988) suggested that this character was under the control of duplicate type of epistatic gene action in the same crop, while additive X dominant component of epistasis was also found positive and significant.

In 5 crosses of chickpea, scaling test with five generation means showed the involvement of epistatic gene action. In four out of five crosses, additive gene effect was involved in the inheritance of 100 seed weight. But, additive and dominance gene effects, dominance X dominance and additive X additive interactions were important (Sinde and Deshmukh, 1990).

2.3.5.6 Seed yield per plant

Jayarani (1993) observed the importance of non- additive gene action for the expression of this character in cowpea due to the presence of higher SCA variance than GCA variance.

Anilkumar (1992) reported the non-additive gene action of seed yield per plant in cowpea. The ratio of variance due to GCA to SCA showed a value less than unity. Combining ability studies using 12 parent diallel F_1 progenies of pea revealed that both additive and non- additive genetic variances were important (Singh and Singh, 1990). Similar results were obtained by Rao *et al.* (1984) in mungbean. Habib *et al.* (1985) in groundnut, Jhorar *et al.* (1985) in clusterbean, Dasgupta and Das,(1987) in blackgram, Mehtre *et al.* (1988) in redgram, Singh *et al.* (1987) in pea and Onkar Singh and Paroda (1989) in chickpea.

Although gca and sca effects were significant, gca effects predominated for seed yield per plant, showing the preponderance of additive gene action in *Dolichos lablab* (Singh *et al.* 1980), ricebean (Das and Dana 1981), cowpea (Chauhan and Joshi 1981), pea (Venkateswarlu and Singh 1981, Dubey and Lal 1983, Singh *et al.* 1987) and Thiyagarajan *et al.* 1990) , blackgram (Malhotra 1983), greengram (Wilson *et al.* 1985, Saxena and

Sharma 1989 and Natarajan *et al.* 1990), groundnut (Manoharan *et al.* 1985) and in soybean (Loiselle *et al.* 1990 and Sharma and Nishi Sharma 1983).

Importance of non-additive genetic variance was noticed by Pande *et al.* (1979), Katiyar *et al.* (1988), Salimath and Bahl (1989) and Yadavendra and Sudhirkumar (1987) in chickpea, Deshmukh and Manjare (1980) and Sreekumar (1993) in mungbean, Sandhu *et al.* (1981) and Singh *et al.* (1987) in blackgram, Zavari *et al.* (1983) and Thiyagarajan *et al.* (1990) and Patil and Bhapkar (1986) in cowpea, Singh *et al.* (1983) and Patel *et al.* (1987) in pigeonpea.

According to Singh and Ramanujam (1981) significant additive, dominance and epistatic effects were involved in the inheritance of seed yield per plant in chickpea. However, in blackgram Dahiya and Waldia (1982) noted higher magnitude of dominance variance. Rao *et al.* (1984) stated that duplicate type of epistasis was important for this character in mungbean.

Ram *et al.* (1986) reported in pea that best crosses involved additive X dominance or dominance X dominance type of epistatic interactions. The inheritance of the character appeared to be under the control of dominance and epistasis in soybean (Gupta *et al.* 1982) and chickpea (Sharma *et al.* 1988). But over- dominance was observed to be important for seed yield per plant in soybean (Tawar et al., 1989). Pandey and Tiwari (1989) reported that this trait was conditioned by complementary type of epistasis in chickpea.

The analysis using means of 6 basic populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of pea by Singh and Singh (1990) indicated the importance of dominance (h) gene effect for yield per plant. However, additive (d) effects were pronounced in some crosses, whereas, additive, dominance and epiststic interactions were found significant in some other crosses. Among digenic epistatic interactions, additive X additive appeared to contribute more for this trait.

2.3.6 Heterosis

The presence of heterosis was reported by various workers in cowpea. Rejatha (1992) reported a very high heterosis for the characters like yield per plant and number of pods per plant in cowpea when it was calculated over mid parent and better parental values. From the study of a cross of two cowpea varieties, Hofman (1962) reported heterosis for flowering time. The F_1 hybrid flowered earlier than that of the better parent. Premsekar (1964) reported manifeststion of heterosis with respect to flowering duration, length of pod and 100 seed weight. With respect to flowering duration, the F_1 hybrid showed 6 per cent heterosis over the better parent. Singh and Jain (1972) from the study of diallel set involving 5 parents in cowpea, observed that heterosis manifested for seed yield resulted from heterosis for pod length and seeds per pod.

Singh and Jain (1971) reported considerable heterosis for yield in greengram. Their study showed that hybrid vigour over mid parent was present for grain yield, pod length etc. Although heterosis was found for cluster number and seeds per pod, the mean difference were insignificant. Negative heterosis was also observed for seed size. Sivan Pillai (1980) observed heterosis over mid parent, better parent and standard parent in yield seed size showed heterosis in F_1 for these characters. But crosses between varietiaes of different pod and seed size generally gave intermediate values for these characters. Heterosis was also observed for the number of flowers, pods and seeds per pod and seed yield per plant. In soybean Weber *et al.* (1970) reported heterosis. The hybrid showed an average of 13.4 per cent heterosis for seed yield over their respective high parent in the 85 crosses evaluated.

Premsager and Chandra (1977 reported heterosis for height and pod number per plant in F_1 hybrids of blackgram. According to Samia Ali Mohmoud (1977) the broad bean hybrids NA 47 X Romi and Roni X 253/556/03 exceeded their better parents in seed yield per plant by 158 per cent and 157 per cent respectively, while the comparable figures for all other combinations ranged between -25 and 90 per cent. No combination surpassed its better parent in 100 seed weight and the greater part of the heterosis in yield observed depended on the increase in number of pods per plant. Reddy *et al.* (1979) in pigeon pea reported that out of seven yield components, only pod number per plant and seed yield showed positive heterosis. Heterosis was also reported for number of seeds per pod and seed yield in wingedbean by De-Silva and Omran (1986).

In pea, Pandey and Gritton (1975) observed significant positive as well as negative heterosis for 100 seed weight over mid parent and better parent. Chaudhary and Singh (1974) reported that among 17 hybrids of soybean, one hybrid showed significant better parent heterosis of 19.5 per cent. Most of the hybrids were intermediate between the parents with respect to seed size and showed negative heterosis over better parent.

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Pandey and Gritton (1975) reported in pea that F_1's averaged very near the mid parent for protein, showing little heterosis. Furedi (1970) observed in pea that F_1 plants produced seed that averaged 10 to 15 per cent lower in protein than their parents. Kurnik *et al.* (1970) observed that F_1's resulting from crossing high protein parents were often lower in protein than either parent. However, they felt that genotypes with higher protein level could be selected from progenies derived from crossing two protein parents.

In greengram, Tiwari and Ramanujam (1976) using ten parents and twenty five F_1 hybrids reported that none of the crosses had a higher protein content than the best among the ten parents. Singh and Singh (1973) also reported heterosis of low magnitude for grain protein in greengram.

Mak and Yap (1977) reported in longbean that few hybrids exhibited heterosis for protein content as compared to their better parent.

MATERIALS AND METHODS

MATERIALS AND METHODS

3.1 Materials

3.1.1 Preliminary evaluation

The genetic material consisted of fifty three varieties/types of grain type cowpea collected from different sources and maintained at the Department of Plant Breeding, College of Agriculture, Vellayani. The details are presented in the Table 1.

3.1.2 Rhizobium inoculation

Rhizobium strain KAU 12 received from the Department of Plant Pathology, College of Agriculture, Vellayani was used for the seed inoculation purpose.

3.1.3 Choice of parents for hybridization

The material comprised of three high nitrogen fixing types, two low nitrogen fixing types, three high yielders and two low yielders which were selected from preliminary evaluation programme.

3.1.4 Combining ability analysis

The study involved six lines and four testers and their 24 hybrids as detailed in Table 1a.

3.1.5 Study of F_2 generation

The genetic material consisted of 24 F_2 populations (families) derived from the hybrids listed in Table 1a.

Table 1. Source of varieties/ types tested for initial evaluation trial.

Sl No	Varieties/ types	Source
1	C 88	Regional Agrl. Research Station, Pattambi
2	C 152	"
3	C 190	"
4	Charrodi	"
5	Co 3	Rice Research Station, Kayamkulam
6	CoVu 4	"
7	CoVu 358	"
8	CoVu 771	"
9	CoVu 810	"
10	CoVu 841	"
11	CoVu 869	"
12	CoVu 882	"
13	CoVu 8420	"
14	CoVu 8447	"
15	CoVu 8456	"
16	CoVu 8478	"
17	CoVu 85020	"
18	Culture 7	Regional Agril. Research Station, Pattambi
19	Culture 9	"
20	DPLC 198	College of Agriculture, Vellayani
21	DPLC 210	"
22	DPLC 216	"
23	GC 82-7	"
24	Guj 2	"
25	HG 23	"
26	IC 38956	"

Contd....2

Table 1. (Contd..)

Sl No	Varieties/ types	Source
27	IITA	Regional Agril. Research Station, Pattambi
28	New era	,,
29	PTB 1	,,
30	PTB 2	,,
31	RC 19	,,
32	S 488	,,
33	V 16	Rice Research Station, Kayamkulam
34	V 23	,,
35	V 27	,,
36	V 38	,,
37	V 87	,,
38	V 118	,,
39	V 130	,,
40	V 218	Regional Agril. Research Station, Pattambi
41	V 265	,,
42	V 266	Rice Research Station, Kayamkulam
43	V 269	,,
44	V 271	,,
45	V 276	,,
46	V 317	,,
47	V 322	,,
48	V 327	,,
49	V 385	,,
50	Varkala local	,,
51	VCM 8	Regional Agril. Research Station, Pattambi
52	VCP 4	,,
53	1-26	,,

3.2 Methods

3.2.1 Experimental procedure

3.2.1.1 Preliminary evaluation

The 53 types were evaluated during summer, 1991 at the College of Agriculture, Vellayani, Thiruvananthapuram. The experiment was laid out in a randomized block design in two replications with a plot size of 3x2 m^2. No nitrogen was applied, either in the organic or inorganic form. All other plant nutrients were applied and cultural practices were followed as per the Package of practices, recommendations of the Kerala Agricultural University (Anonymous, 1989). Seed treatment method was followed for Rhizobium inoculation. The data on biological nitrogen fixation were recorded by the destructive sampling of five plants selected at random and yield characters recorded from ten plants taken at random excluding the border plants in each replication. Observations on the following characters were recorded.

Biological nitrogen fixation characters

1. Number of days to flower
2. Length of primary root
3. Number of secondary roots
4. Number of nodules in the primary root
5. Number of nodules in the secondary roots
6. Total number of nodules
7. Weight of effective nodules in the primary root

Table 1a. Details of parents and their hybrids

Sl no	Treatments	Parents/Hybrids	Remarks
A.	Lines : 6		
	L1	VCP 4	High nitrogen fixer
	L2	CoVu 358	,,
	L3	DPLC 210	,,
	L4	V 322	High yielder
	L5	V 27	,,
	L6	V 271	,,
B.	Testers : 4		
	T1	PTB 2	Low nitrogen fixer
	T2	C 190	,,
	T3	C 152	Low yielder
	T4	CoVu 85020	,,
C.	Hybrids : 24		
	L1 T1	VCP 4 X PTB 2	
	L1 T2	VCP 4 X C 190	
	L1 T3	VCP 4 X C 152	
	L1 T4	VCP 4 X CoVu 85020	
	L2 T1	CoVu 358 X PTB 2	
	L2 T2	CoVu 358 X C 190	
	L2 T3	CoVu 358 X C 152	
	L2 T4	CoVu 358 X CoVu 85020	
	L3 T1	DPLC 210 X PTB 2	
	L3 T2	DPLC 210 X C 190	
	L3 T3	DPLC 210 X C 152	
	L3 T4	DPLC 210 X CoVu 85020	
	L4 T1	V 322 X PTB 2	
	L4 T2	V 322 X C 190	
	L4 T3	V 322 X C 152	
	L4 T4	V 322 X CoVu 85020	
	L5 T1	V 27 X PTB 2	
	L5 T2	V 27 X C 190	
	L5 T3	V 27 X C 152	
	L5 T4	V 27 X CoVu 85020	
	L6 T1	V 271 X PTB 2	
	L6 T2	V 271 X C 190	
	L6 T3	V 271 X C 152	
	L6 T4	V 271 X CoVu 85020	

8. Weight of nodules in the secondary roots
9. Total weight of nodules
10. Nitrogen content in the plant at 50 per cent flowering
11. Plant dry weight at 50 per cent flowering

Yield characters

1. Grain yield per plant
2. Length of pods
3. Number of pods per plant
4. Number of seeds per pod
5. Weight of 100 seeds
6. Seed protein content

3.2.1.1.1 Estimation of genetic parameters

Genetic parameters such as coefficient of variation, heritability and genetic advance as per cent of mean were estimated for the 17 characters recorded.

3.2.1.1.2 Correlation

The phenotypic and genotypic coefficients of correlation were estimated among different characters under study.

3.2.1.1.3 Direct and indirect effect

Direct and indirect effects on nitrogen content and grain yield per plant were estimated. The components of nitrogen content per plant included number of secondary roots, number of nodules in the primary root, number of nodules in the secondary roots, total number of nodules, weight of effective nodules in the primary root, weight of effective nodules in the secondary roots, total nodule weight and plant dry weight. The components of grain yield per plant included length of pod, number of pods per plant, weight of 100 seeds and dry weight of the plant.

3.2.1.2 Choice of parents and hybridization

The ten selected varieties/types were crossed in a line X tester model, keeping the three high nitrogen fixing types and three high yielding types as lines (L1 to L6) and two low nitrogen fixing and two low yielding types as testers (T1 to T4). The lines were used as the ovule parents. Parents for crossing were raised during Kharif, 1992 in three sets at weekly intervals. Emasculation was done in the flower buds, which were due to open on the next day, by splitting open the keel petals and removing stamens one by one holding the filaments. Emasculation was done in the evening between 4 and 6 pm followed by artificial pollination on the next morning between 6 and 8 am. The covered emasculated flowers were opened on the next day and pollination was done by dusting pollen from the tester plants to the stigmatic surface of the emasculated flower of the lines. Artifically pollinated flowers were tagged and covered with paper cover. The seeds of each crosses were collected separately and grown in the main plot for collection of data on different characters for the estimation of combining ability and gene action.

3.2.1.3 Combining ability

The six lines, four testers and their 24 hybrids were evaluated in a randomised block design with three replications at the College of Agriculture, Vellayani during August-November 1992. In each plot of $3X2\ m^2$ area, the seeds were dibbled at a spacing of 25 X 15 cm. Data on the nitrogen fixation characters were recorded by destructive sampling of 5 plants from each treatment and yield data recorded from a random sample of ten plants per treatment per replication. The observational plants were scored for the characters and the mean value used for statistical computation.

Nitrogen fixation characters

1. Number of days to flower
2. Number of nodules in the primary root
3. Number of nodules in the secondary roots
4. Total number of nodules
5. Weight of nodules in the primary root
6. Weight of nodules in the secondary roots
7. Total weight of nodules
8. Weight of effective nodules
9. Dry weight of the plant at 50 per cent flowering
10. Dry weight of the root
11. Nitrogen content per plant at 50 per cent flowering

Yield characters

1. Length of pod
2. Number of seeds per pod
3. Number of pods per plant

4. Grain yield per plant
5. 100 seed weight
6. Seed protein content

3.2.1.4 Study of F_2 generation

The 24 F_2 populations (families) were raised in RBD with two replications in a plot size of 3x2 m^2 at the College of Agriculture, Vellayani during November,1992 to February 1993. Observations on the following characters were recorded.

1. Nitrogen content per plant at 50 per cent flowering
2. Total nodule weight
3. Weight of effective nodules
4. Dry weight of the root
5. Dry weight of the plant
6. Grain yield per plant
7. Length of pod
8. Number of pods per plant
9. Number of seeds per pod
10. Weight of 100 seeds
11. Seed protein content (per cent)

3.2.1.5 Details of characters studied and estimations made

1. Number of days to flower

Number of days taken from the date of sowing to 50 per cent of the plants flowered in each plot was observed and recorded in days.

2. Length of primary root

Plants were uprooted carefully on the first day of the flowering and length of the tap root measured in centimeters.

3. Number of secondary roots

Number of secondary roots were counted on the each observational uprooted plants and recorded.

4. Number of nodules in the primary root

Uprooted plants were washed in tap water carefully and the nodules on the primary root were taken out with the help of a forceps after spreading it on a blotting paper and counted.

5. Number of nodules in the secondary roots

Nodules found on the secondary roots were taken out carefully with the help of a forceps and counted.

6. Total number of nodules

Number of nodules in the primary root as well as the number of nodules in the secondary roots were added and recorded as the total number of nodules.

7. Weight of effective nodules in the primary root

Pink coloured effective nodules were separated out from the nodule collections obtained from the primary root and its fresh weight recorded.

8. Weight of nodules in the secondary root

Nodules received from the secondary roots of the each observational plant were pooled together and fresh weight taken.

9. Total weight of nodules

Weight of nodules from the primary root and secondary roots were added together to get the total weight of nodules.

10. Plant dry weight

Each uprooted observational plants along with the seperated nodules were initially sundried for 2 days and then ovendried at 60-70 ° C for 24 hours and the dry weight recorded.

11. Nitrogen content in plant at 50 per cent flowering

Total nitrogen in the observational plants were estimated by the modified Kjeldahl method.

12. Grain yield per plant

Total grain yield from each observational plant was recorded and expressed on grams per plant.

13. Length of pod

Single pod from each observational plant was measured in centimeter for its length and averaged.

14. Number of pods per plant

Number of pods in each observational plant was counted and averaged.

15. Number of seeds per pod

Ten pods selected at random in each plant was threshed separately and the number of seeds in each pod was counted and averaged.

16. Weight of 100 seeds

A random sample of 100 grain was selected from the bulk in each plot, weighed and the mean weight was recorded in grams.

17. Seed protein content

Seed samples were drawn from each plot and the total nitrogen was estimated by the modified kjeldahl method. Total protein was estimated as follows.

Total protein = Total nitrogen X 6.25

3.2.2 Statistical methods used

Analysis of variance-covariance was performed to estimate the genotypic and environmental components of phenotypic variance and covariance. From these the coefficient of variation, phenotypic, genotypic and environmental correlation coefficients, heritability coefficient and genetic advance were worked out (Singh and Chowdhary, 1979).

Selection indices were worked out based on multiple biological nitrogen fixation characters like total nodule weight, plant dry weight and nitrogen content to discriminate the superior genotypes from the inferior ones by fitting discriminant function (Smith, 1936). If 'n' component characters are involved, the genetic worth of a genotype was defined as

$$H = a_1 x_1 + a_2 x_2 + \dots\dots + a_n x_n$$

Where $x_1,x_2,\dots x_n$ stands for the phenotypic values and $a_1,a_2,\dots a_n$ are the weight assumed to each variable which is taken as unity in this present case.

The discriminant function is defined as $I = b_1G_1 + b_2G_2 + \ldots\ldots + b_n G_n$ Where $G_1, G_2, \ldots\ldots G_n$ are the genotypic values with respect to the 'n' characters. The coefficients 'b' are estimated such that the correlation between H and I is maximum. The maximisation of this correlation results in a system of equation as

$$\underset{\sim}{P}\ \underline{a} = \underset{\sim}{G}\ \underline{b}$$

Where P and G are the n X n phenotypic and genotypic variance-covariance matrix. 'a' is the colum vector of the known weights and 'b' is the colum vector of 'b' coefficients. The solution of this matrix system of equation estimates the 'b' coefficients and the selection index is defined as

$$I = b_1 x_1 + b_2 x_2 + \ldots\ldots + b_n x_n$$

Then indices were arranged in descending order of magnitude and those with high index values were selected for further selection.

Correlation coefficient

Correlation coefficients were estimated as follows (Prem Narain 1990).

$$\text{Genotypic correlation coefficient } r_{gij} = \frac{\sigma gij}{\sigma gi\ \sigma gj}$$

$$\text{Phenotypic correlation coefficient } r_{pij} = \frac{\sigma pij}{\sigma pi\ \sigma pj}$$

σgij, σpij and σeij are the co-variances and σgi, σgj, σpi, σei and σej are the standard deviations.

Environmental correlation coefficient $r_{eij} = \dfrac{\sigma eij}{\sigma ei\, \sigma ej}$

Path analysis

Path coefficient method invented by Wright (1923) is applied to study the cause and effect relationship in a system of correlated variables.

The path coefficients were estimated from the solution of the matrix equation

$$\underset{\sim}{A}\ \underline{P} = \underline{B}$$

Where $\underset{\sim}{A}$ is the genotypic intercorrelation matrix of indepentent variables and $\underline{B}$ is the column vector of the genotypic correlation between depentent and indepentent variables and $\underline{P}$ is the vector of path coefficients. The path coefficient means the direct effect of each component character on the dependent character and $r_{ij}\, P_j$ means the indirect effect of the component character X_j via X_i and r_{ij} is the correlation between the component characters X_i and X_j. The residue facter R is estimated as $R^2 = (1 - \sum_{j} r_{ij}\, P_j)$.

Combining ability

Line X Tester analysis

Analysis of variance

Analysis of variance was done for all the characters and significance of differences among the types including parents and crosses was tested . The split up of the degrees of freedom due to various components of variation are given below (Table 2).

Table 2. Anova for line X tester

Source	df	MS	Expected mean squares
Replication	r-1		
Treatments	n-1		
I. Parents	l+t-1		
II. Parents vs crosses	1		
III. Crosses	lt-1		
a. Lines	l-1	Ml	$\sigma^2 e + r\sigma^2 sca + rt\,\sigma^2 gca(l)$
b. Testers	t-1	Mt	$\sigma^2 e + r\sigma^2 sca + rl\,\sigma^2 gca(t)$
c. Line X Tester	(l-1) (t-1)	Mlt	$\sigma^2 e + r\sigma^2 sca$
Error	(n-1) (r-1)	Me	$\sigma^2 e$
Total	nr-1		

Where n = number of treatment materials = l+t+lt

r = number of replication

l = number of lines

t = number of testers

$$\text{Cov.H.S. (lines)} = \frac{M_l - M_{lt}}{rt} = \sigma^2 \text{gca (lines)}$$

$$\text{Cov.H.S. (testers)} = \frac{M_t - M_{lt}}{rl} = \sigma^2 \text{gca (testers)}$$

$$\text{Cov.H.S (average)} =$$

$$\frac{1}{r\,(2lt - 1 - t)} \times \left[\frac{(l-1)\,M_l + (t-1)\,M_t}{1 + t - 2} - M_{lt} \right]$$

$$\text{Cov.F.S} =$$

$$\frac{(M_l - M_o) + (M_t - M_o) + (M_{lt} - M_o)}{3r} + \frac{6r.\text{Cov.H.S} - (rl+t)\,\text{Cov.H.S}}{3r}$$

$$\sigma^2 \text{gca} = \text{Cov.H.S. (average)}$$

$$\sigma^2 \text{sca} = \frac{M_{lt} - M_o}{r}$$

When $F = 0$, $\sigma^2 D = 4\,\sigma^2 \text{sca}$, $= \sigma^2 A = 4\,\sigma^2 \text{gca}$

$F = 1$, $\sigma^2 D = \sigma^2 \text{sca}$, $= \sigma^2 A = \sigma^2 \text{gca}$

Where l = number of lines

t = number of testers

r = number of replications

F = inbreeding coefficient

Estimation of gca and sca effects

The model used to estimate the gca and sca effects of ijkth observation was as follows

$X_{ijk} = \mu + g_i + g_j + s_{ij} + e_{ijk}$

$i = 1, 2, 3, \ldots\ldots, l$

$j = 1, 2, 3, \ldots\ldots, t$

$k = 1, 2, 3, \ldots\ldots, r$

where μ = population mean

g_i = gca effect of ith line

g_j = gca effect of jth tester

s_{ij} = sca effect of ijth combination

e_{ijk} = random error component associated with ijkth observation

The individual effects were estimated as follows

1. Mean $= \dfrac{X\ldots}{ltr}$

2. gca effect of lines gi $= \dfrac{X_{i..}}{tr} - \dfrac{X_{...}}{ltr}$

3. gca effect of testers $= \dfrac{X_{j.}}{lr} - \dfrac{X_{...}}{ltr}$

4. sca effect in combinations

$$S_{ij} = \frac{X_{ij}}{r} - \frac{X_{i..}}{tr} - \frac{X_{j.}}{lr} + \frac{X_{...}}{ltr}$$

Where $X_{...}$ = total of all hybrid combinations

$X_{i..}$ = total of i^{th} line over t testers and r replications

$X_{j.}$ = total of j^{th} tester over l lines and r replications

$X_{ij.}$ = total of the hybrids i^{th} line and j^{th} tester over r replications.

The standard error pertaining to gca effect of lines and testers and sca effects in different combination were calculated as follows.

Lines = $SE(g_i) = (M_e/rt)^{1/2}$

Testers = $SE(g_j) = (M_e/rl)^{1/2}$

Crosses = $SE(s_{ij}) = (M_e/r)^{1/2}$

Proportional contribution of lines, testers and line X tester to total variance are as follows.

standard parent which ever is the case.

Significance for the three types of heterosis was tested by using CD values calculated as

$$\text{C.D. for relative heterosis} = t_{df(e)} \sqrt{\frac{3\ Me}{2\ r}}$$

$$\text{C.D for heterobeltiosis and standard heterosis} = t_{df(e)} \sqrt{\frac{2\ Me}{r}}$$

Where

C.D = Critical difference

Me = Mean square for error

r = Number of replications

$t_{df(e)}$ = t value corresponding to error degree of freedom

RESULTS

RESULTS

The data collected from the different experiments were subjected to statistical analysis whereever required. The results obtained are interpreted and presented hereunder.

4.1 Preliminary evaluation

Analysis of variance on 17 characters had shown that characters such as length of primary root, number of secondary roots and number of seeds per pod did not exhibit significant treatment effects. Hence they were excluded from further analysis. The mean value of each character is presented in Table 3.

4.1.1 Genetic parameters

Coefficient of variation, heritability, genetic advance and genetic advance as percentage of mean were estimated for all the 14 traits from the analysis of variance. The estimates are presented in Table 4 and Fig 1 and 2.

The number of days to 50 per cent flowering ranged from 43.50 days (V 16) to 32.50 days (VCM 8) with a mean value of 32.50 days. The phenotypic coefficient of variation was 8.26 while the genotypic coefficient of variation was 8.08 indicating a low degree of environmental influence. A very high heritability of 95.70 per cent was also recorded with a low value of genetic advance as per cent of mean (16.28).

The number of nodules in the primary root ranged between 10.40 and 30.30 with a mean value of 17.61. The variety VCP 4 recorded the maximum value of 30.30

Table 3. Mean value of various nitrogen fixation and yield contributing characters in cowpea.

Sl No	Cultivar	Number of days to flower	Length of primary root (cm)	Number of secondary roots	Number of nodules in the primary root	Number of nodules in the secondary root	Total number of nodules	Weight of nodules in the primary root (g)	Weight of nodules in the secondary root (g)	Total nodule weight (g)	Plant dry weight (g)	Nitrogen content in plant (%)
1	2	3	4	5	6	7	8	9	10	11	12	13
1	C 88	38.00	21.39	22.40	20.00	45.00	65.00	1.97	1.56	3.53	8.19	2.47
2	C 152	40.50	16.14	31.50	15.40	17.80	33.20	2.08	0.92	3.00	8.26	2.40
3	C 190	37.50	16.71	30.30	12.60	19.00	31.60	0.56	0.45	1.01	5.56	2.03
4	Charrodi	36.50	20.02	30.00	23.20	15.00	38.20	1.96	0.33	2.29	5.96	2.26
5	CO 3	41.50	17.57	27.70	14.30	24.10	38.40	2.09	1.10	3.19	6.31	2.44
6	CoVu 4	41.00	13.40	29.20	16.60	28.30	44.90	1.22	0.76	1.98	5.01	2.23
7	CoVu 358	41.00	17.98	37.10	18.70	10.90	29.60	3.12	1.48	4.60	6.65	2.73
8	CoVu 771	41.00	14.95	33.90	14.30	15.60	29.90	1.82	1.38	3.20	10.06	2.45
9	CoVu 810	37.00	16.07	26.10	16.20	13.40	29.60	1.55	0.72	2.27	5.68	2.25
10	CoVu 841	38.50	20.98	28.90	10.40	18.00	28.40	1.20	1.12	2.32	9.40	2.27
11	CoVu 869	36.00	17.79	23.10	24.20	23.80	48.00	1.68	0.51	2.16	4.97	2.25
12	CoVu 882	37.50	18.54	31.10	12.80	17.20	30.00	1.81	0.61	2.42	5.74	2.29
13	CoVu 8420	40.50	16.91	38.80	13.20	19.10	32.30	1.91	1.25	3.16	7.89	2.41
14	CoVu 8447	38.00	19.98	26.80	13,60	20.70	34.30	1.49	0.49	1.98	6.29	2.22
15	CoVu 8456	40.00	17.99	45.80	16.60	37.80	52.60	1.22	1.22	2.44	8.90	2.29
16	CoVu 8478	37.00	19.71	27.00	19.60	16.70	36.30	1.25	0.37	1.62	6.01	2.16
17	CoVu 85020	41.50	20.01	26.80	16.70	17.40	34.10	2.37	1.29	3.66	7.46	2.54

Contd....2.

Table. 3 (Contd.)

1	2	3	4	5	6	7	8	9	10	11	12	13
17	CoVu 85020	41.50	20.01	26.80	16.70	17.40	34.10	2.37	1.29	3.66	7.46	2.54
18	Culture 7	36.00	17.13	26.90	24.10	21.60	45.70	1.76	0.65	2.41	4.88	2.29
19	Culture 9	33.00	17.68	23.80	21.80	31.20	53.00	1.00	0.50	1.49	3.87	2.13
20	DPLC 198	34.00	17.95	26.20	18.40	55.80	74.20	0.77	1.37	2.14	5.53	2.22
21	DPLC 210	40.50	20.65	22.20	22.70	18.50	41.20	3.33	1.19	4.52	6.70	2.77
22	DPLC 216	33.00	19.26	26.30	23.40	33.20	56.66	1.09	0.66	1.75	4.03	2.18
23	GC 82 7	39.50	16.99	31.40	16.10	21.50	37.60	1.76	0.73	2.49	6.00	2.31
24	Guj 2	36.50	20.14	27.70	28.70	15.10	43.80	1.32	0.17	1.50	4.32	2.13
25	HG 23	43.00	17.65	21.50	12.60	26.40	39.00	0.91	0.57	1.48	6.96	2.18
26	IC 38956	33.00	18.57	25.70	22.50	47.90	70.40	1.05	0.79	1.84	4.82	2.18
27	IITA	40.50	16.65	34.90	24.50	19.00	43.50	2.31	1.02	3.33	6.40	2.47
28	New era	39.50	17.38	23.20	13.00	7.40	47.00	1.96	0.99	2.96	6.82	2.42
29	PTB 1	40.50	16.61	34.10	20.60	25.40	46.00	1.86	0.74	2.60	5.99	2.34
30	PTB 2	33.00	15.06	22.10	21.30	31.60	52.90	1.13	0.34	1.47	3.52	2.15
31	RC 19	37.50	20.66	24.20	15.70	26.00	41.70	1.75	1.14	2.89	8.35	2.34
32	S 488	33.00	18.77	23.00	22.70	10.70	33.40	1.56	0.32	1.87	4.07	2.18
33	V 16	43.50	19.46	19.40	14.40	37.80	52.20	1.20	1.35	2.55	9.75	2.36
34	V 23	41.50	17.51	27.00	15.10	22.80	37.90	1.28	0.74	2.02	8.64	2.21
35	V 27	41.00	18.14	28.50	10.50	16.10	26.60	0.68	0.71	1.19	9.47	2.08

Contd...3.

Table 3. (Contd.)

1	2	3	4	5	6	7	8	9	10	11	12	13
36	V 38	40.50	19.21	34.30	12.80	20.50	33.30	0.87	0.30	1.18	8.08	2.07
37	V 87	41.00	16.33	22.90	12.10	14.10	26.20	1.19	0.56	1.74	9.22	2.15
38	V 118	33.00	20.60	23.60	18.90	13.80	32.70	1.73	0.38	2.11	4.61	2.26
39	V 130	36.50	15.11	32.00	18.00	7.20	25.20	2.41	0.29	2.69	7.00	2.37
40	V 218	34.00	17.24	30.90	21.30	14.30	35.60	2.14	0.49	2.62	4.65	2.34
41	V 265	36.00	17.63	27.20	19.80	13.80	33.60	1.40	0.30	1.70	5.21	2.22
42	V 266	34.00	17.45	34.80	19.80	18.90	38.70	2.36	0.76	3.11	6.32	2.44
43	V 269	41.00	15.75	21.40	11.30	15.90	27.20	1.12	0.55	1.67	10.54	2.15
44	V 271	41.00	19.94	29.10	14.00	18.30	32.30	1.46	0.42	1.89	10.77	2.20
45	V 276	41.00	18.07	19.90	15.80	13.00	28.80	1.90	0.51	2.41	6.65	2.31
46	V 317	41.50	18.91	22.30	15.10	19.30	34.40	1.80	0.69	2.49	6.38	2.30
47	V 322	40.50	17.47	27.10	22.70	27.00	49.70	1.86	0.56	2.43	9.14	2.29
48	V 327	40.50	16.57	25.60	15.40	26.00	41.40	1.44	0.91	2.39	8.48	2.29
49	V 385	40.00	17.34	26.80	13.70	39.10	52.80	1.21	2.41	3.62	5.76	2.56
50	Varkalalocal	40.50	21.10	27.90	19.20	35.20	54.40	1.06	0.79	1.84	7.00	2.21
51	VCM 8	32.50	15.16	22.40	13.50	16.10	29.60	1.10	0.37	1.47	5.58	2.06
52	VCP 4	38.50	17.18	24.70	30.30	30.00	60.30	3.78	1.43	5.21	10.61	2.88
53	1 26	34.00	18.64	23.20	13.00	7.40	20.40	1.54	0.36	1.89	4.86	2.21
		**			**	**	**	**	**	**	**	**
	F Value	45.33	0.996	1.10	4.50	4.06	4.66	7.73	7.82	13.12	2.004	11.46
	CD (0.05)	1.32	-	-	6.26	14.40	15.53	0.65	0.44	0.69	3.85	0.15
	SE	0.46	-	-	2.20	5.07	5.46	0.23	0.16	0.24	1.36	0.05

Contd...4.

Table 3. (contd.)

Sl No	Cultivar	Length of pod (cm)	Number of pods per plant	Number of seeds per pod	Weight of 100 seeds (g)	Seed protein content (%)	Grain yield per plant (g)	Selection index	Rank
		14	15	16	17	18	19	20	21
1	C 88	14.26	13.15	13.84	23.66	21.10	13.31	-5.82	4
2	C 152	13.58	10.60	12.59	11.21	27.38	8.56	-7.52	9
3	C 190	11.78	43.55	11.70	14.83	26.03	32.19	-14.75	52
4	Charrodi	11.53	56.70	12.67	6.86	30.02	32.19	-10.82	31
5	CO 3	14.09	14.05	13.04	11.83	26.90	11.25	-8.26	12
6	CoVu 4	15.43	21.05	12.84	14.39	26.89	21.96	-12.54	40
7	CoVu 358	13.24	9.20	11.15	10.07	27.99	9.00	-4.41	2
8	CoVu 771	13.78	11.10	11.40	11.69	27.99	10.75	-6.11	5
9	CoVu 810	13.99	35.30	12.40	11.27	28.12	26.83	-10.96	32
10	CoVu 841	15.09	35.90	12.84	10.19	28.29	30.94	-8.73	17
11	CoVu 869	10.74	54.65	10.92	7.03	30.19	28.91	-11.91	37
12	CoVu 882	14.71	34.10	13.48	10.48	27.71	29.18	-10.58	29
13	CoVu 8420	13.98	21.95	11.59	9.19	27.11	15.20	-7.06	7
14	CoVu 8447	14.33	34.60	12.38	9.95	27.47	25.75	-11.74	35
15	CoVu 8456	19.64	25.30	14.63	14.07	26.08	24.81	-8.66	16
16	CoVu 8478	11.86	39.60	12.47	8.05	29.34	25.41	-12.91	45
17	CoVu 85020	14.61	10.00	13.00	9.15	28.24	8.56	-6.37	6

Contd...5.

Table 3. (Contd.)

		14	15	16	17	18	19	20	21
18	Culture 7	12.00	38.25	11.74	8.54	28.87	24.25	-11.26	33
19	Culture 9	14.48	14.90	11.39	10.34	27.74	21.44	-14.48	51
20	DPLC 198	15.19	32.65	11.59	19.19	21.12	30.91	-11.38	34
21	DPLC 210	13.02	9.25	11.67	10.73	27.92	9.40	-5.23	3
22	DPLC 216	14.20	22.10	12.11	15.94	25.90	21.59	-13.67	48
23	GC 82 7	15.46	17.50	13.84	11.51	27.09	17.94	-10.35	27
24	Guj 2	11.56	45.40	12.07	7.64	28.59	35.19	-14.24	50
25	HG 23	15.42	21.40	14.30	10.78	28.34	13.25	-12.94	46
26	IC 38956	15.23	21.10	12.99	13.26	25.95	23.38	-12.83	43
27	IITA	15.66	24.90	12.25	17.24	24.49	30.94	-7.88	11
28	New Era	16.78	12.35	14.50	11.60	28.07	15.68	-8.82	18
29	PTB 1	18.14	18.15	13.17	13.56	26.15	28.50	-10.23	25
30	PTB 2	11.84	27.10	11.73	8.42	29.10	16.21	-15.12	53
31	RC 19	14.27	31.80	13.17	10.92	27.92	28.50	-7.36	8
32	S 488	17.67	28.95	13.32	12.13	27.11	28.00	-13.08	47
33	V 16	13.31	32.20	13.00	5.73	5.73	30.11	-8.43	13
34	V 23	15.55	27.25	14.09	10.42	27.89	26.20	-9.99	23
35	V 27	15.68	27.95	14.50	12.81	26.87	37.93	-12.05	38

Contd...6.

Table 3. (Contd.)

		14	15	16	17	18	19	20	21
36	V 38	14.48	33.25	13.25	10.05	28.10	30.28	-12.86	44
37	V 87	16.57	25.30	14.42	11.96	27.33	30.74	-10.35	28
38	V 118	16.91	31.60	12.24	14.56	25.40	25.00	-12.54	39
39	V 130	15.44	31.80	13.70	10.18	27.91	23.84	-9.49	21
40	V 218	17.27	31.80	12.15	12.07	26.72	32.13	-10.81	30
41	V 265	14.77	41.90	13.94	9.77	28.37	29.69	-13.70	49
42	V 266	17.19	24.30	12.72	12.28	26.71	26.25	-8.57	14
43	V 269	15.11	27.65	13.50	12.54	27.44	30.88	-9.88	22
44	V 271	15.42	28.70	13.00	12.44	26.95	35.39	-9.21	20
45	V 276	15.39	25.35	13.09	11.58	28.37	31.60	-10.34	26
46	V 317	15.22	16.80	13.97	13.08	25.95	19.19	-10.01	24
47	V 322	16.28	28.35	13.13	13.63	26.25	41.53	-8.65	15
48	V 327	15.70	28.20	14.09	10.55	27.23	22.46	-9.15	19
49	V 385	16.81	14.00	13.34	13.50	24.28	19.60	-7.83	10
50	Varkalalocal	13.43	44.85	12.09	8.89	29.10	34.69	-11.88	36
51	VCM 8	13.05	22.95	11.79	8.10	27.44	17.06	-12.76	41
52	VCP 4	18.43	16.00	14.30	15.33	24.10	23.13	-0.69	1
53	1 26	14.82	23.15	13.08	10.31	27.45	15.31	-12.80	42
	F value	6.08**	5.82**	0.95	6.81**	17.21	2.68		
	CD (.05)	2.16	13.13	-	0.11	1.23	14.33		
	SE	0.76	4.62	-	0.04	0.43	5.04		

Table 4. Mean, range, components of variance, coefficient of variation, heritability, genetic advance and genetic gain for various characters in cowpea.

Sl No	Character	Mean	Range	Variance		Coefficient of variation		Herita bility (%)	Genetic advance	Genetic advance as per cent of mean
				Geno typic	Pheno typic	Geno typic	Pheno typic			
1	Number of days to flower	38.26	32.5-43.5	9.55	9.98	8.08	8.26	95.70	6.23	16.28
2	Number of nodules in the primary root	17.61	10.4-30.3	16.75	26.47	23.24	29.21	63.30	6.71	38.10
3	Number of nodules in the secondary roots	22.21	7.2-55.8	78.60	129.91	39.92	51.32	60.50	14.21	63.98
4	Total number of nodules	40.30	20.4-74.2	109.38	169.11	25.95	32.27	64.70	17.33	43.00
5	Weight of effective nodules in the primary root (g)	1.63	0.56-3.78	0.35	0.454	36.26	41.29	77.10	1.07	65.64
6	Weight of nodules in the secondary roots (g)	0.79	0.17-2.41	0.16	0.21	51.63	58.72	77.30	0.73	92.41
7	Total nodule weight (g)	2.41	1.01-5.21	0.71	0.82	34.82	37.58	85.80	1.60	66.39
8	Plant dry weight (g)	6.78	3.52-10.77	1.85	5.52	20.04	34.66	33.40	1.62	23.89
9	Nitrogen content per plant (%)	2.30	2.03-2.88	0.03	0.03	7.18	7.83	83.90	0.31	13.48
10	Length of pods (cm)	14.80	10.7-19.64	2.93	4.08	11.56	13.65	71.80	2.99	20.20
11	Number of pods per plant	26.79	9.2-56.7	103.01	145.72	37.88	45.06	70.69	17.58	65.62
12	Weight of 100 seeds (g)	11.61	5.73-23.66	9.66	9.66	26.76	26.77	99.90	6.40	55.12
13	Seed protein content (%)	27.19	21.1-30.19	3.04	3.42	6.42	6.80	89.00	3.39	12.47
14	Grain yield (g)	23.94	8.56-41.53	42.77	93.63	27.32	40.42	45.70	9.11	38.05

X 1 - Number of nodules in the primary root.

X 2 - Number of nodules in the secondary roots.

X 3 - Total number of nodules.

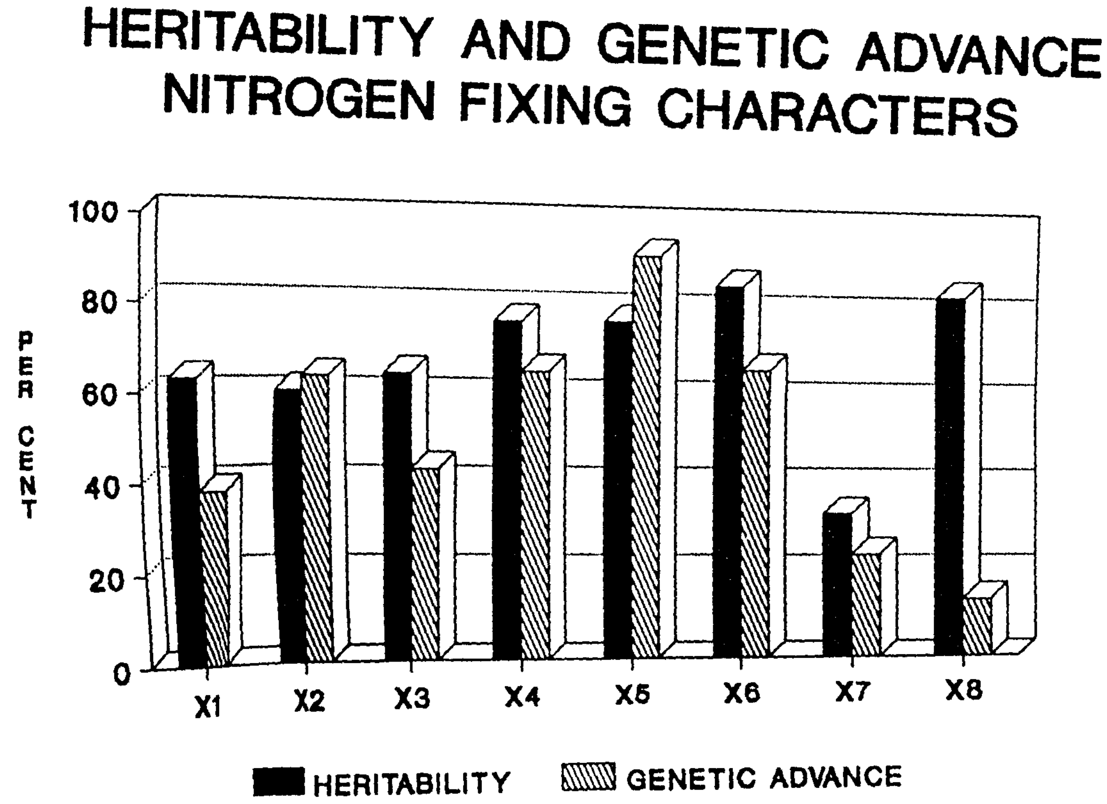
X 4 - Weight of effective nodules in the primary root.

X 5 - Weight of nodules in the secondary roots.

X 6 - Total nodule weight.

X 7 - Plant dry weight.

X 8 - Nitrogen content in plant.



HERITABILITY AND GENETIC ADVANCE NITROGEN FIXING CHARACTERS

Fig 1

X 1 - Number of days to flower.

X 2 - Length of pod.

X 3 - Number of pods per plant.

X 4 - Weight of 100 seeds.

X 5 - Seed protein content.

X 6 - Grain yield.

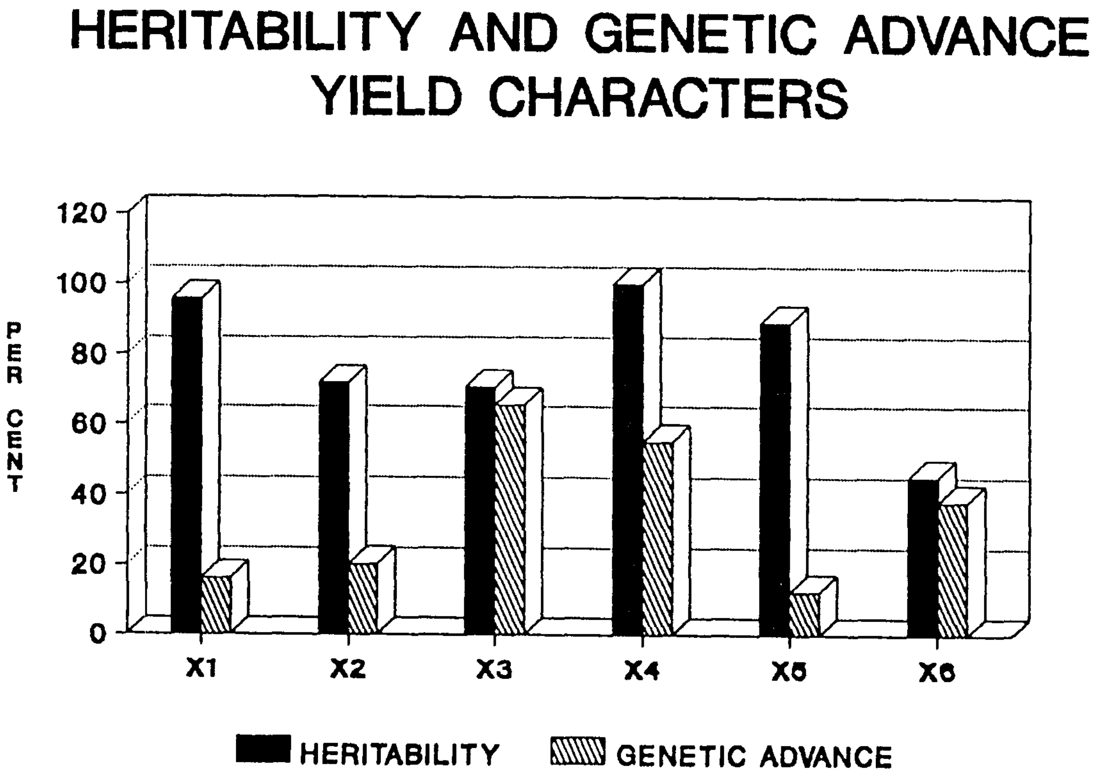

HERITABILITY AND GENETIC ADVANCE
YIELD CHARACTERS
PER CENT
120
100
80
60
40
20
0
X1
X2
X3
X4
X5
X6
HERITABILITY
GENETIC ADVANCE

Fig 2

whereas the minimum value was recorded by CoVu 841 (10.40). The phenotypic and genotypic coefficient of variations were 29.21 and 23.24 per cent respectively with a high heritability of 63.30 per cent. The genetic advance as percentage of the mean was 38.10 which was a medium value.

The number of nodules in the secondary roots ranged from 55.80 (DPLC 198) to 7.20 (V 130) with a mean value of 22.21. The phenotypic coefficient of variation was 51.32 per cent whereas, genotypic coefficient of variation was 39.92 per cent with a high heritability of 60.50 per cent and high genetic advance as percentage of mean (63.98). The relative magnitude of PCV and GCV indicated a moderate degree of environmental influence. This character also recorded a high genetic advance as percentage of mean (63.98).

The total number of nodules ranged from 74.20 (DPLC 198) to 20.40 (1 26) with a mean value of 40.30. The phenotypic coeffecient of variation and genotypic coefficient of variation were 32.27 per cent and 25.95 per cent respectively. The relative magnitude of PCV and GCV indicated a moderate degree of environmental influence on this character. High heritability estimate of 64.70 per cent was recorded with a medium genetic advance of 43 per cent.

The weight of effective nodules in the primary root ranged from 3.78 g (VCP 4) to 0.56 g (C 190) with a mean value of 1.63 g. The phenotypic and genotypic coefficients of variation were 41.29 per cent and 36.26 per cent respectively. The relative magnitude of PCV and GCV indicated a low degree of environmental influence on this character.

High heritability estimate of 77.10 per cent was recorded with a high genetic advance of 65.64 per cent.

The weight of nodules in the secondary roots ranged from 2.41 g (V 358) to 0.17 g (Guj 2) with a mean value of 0.79 g. The phenotypic coefficient of variation was 58.72 per cent while genotypic coefficient of variation was 51.63 per cent indicating a low degree of environmental influence on this character. High heritability of 77.30 per cent was recodred, with a very high genetic advance of 92.41 per cent.

The total nodule weight ranged from 5.21 g (VCP 4) to 1.01 g (C 190) with a mean value of 2.41 g. The phenotypic coefficient of variation was 37.58 per cent whereas genotypic coefficient of variation recorded 34.82 per cent. The relative magnitude of PCV and GCV indicated a low degree of environmental influence on this character. High heritability of 85.80 per cent was recorded with a high genetic advance of 66.39 per cent.

The nitrogen content in plant at 50 per cent flowering ranged from 2.85 per cent (VCP 4) to 2.03 per cent (C 190) with a mean value of 2.30 per cent. The phenotypic coefficient of variation was 7.83 per cent while the genotypic coefficient of variation recorded 7.18 per cent indicating a low degree of environmental influence. A high heritability of 83.9 per cent was recorded with a low value of genetic advance (13.48 per cent).

Plant dry weight ranged from 10.77 g (V 271) to 3.52 g (PTB 2) with an average value of 6.78 g. The phenotypic and genotypic coefficients of variation were 34.66 and

20.04 per cent respectively. The relative magnitude of PCV and GCV indicated a high degree of environmental influence . A low magnitude of heritability (33.40 per cent) was recorded with a low genetic advance of 23.89 per cent.

The grain yield per plant ranged from 41.53 g (V322) to 8.56 g (C 152) with a mean value of 23.94 g. The phenotypic coefficient of variation was 40.42 per cent while genotypic coefficient of variation was 27.32 per cent indicating a fair amount of environmental influence. A medium magnitude of heritability (45.7 per cent) was recorded with a moderately good genetic advance.

The length of pods ranged from 19.64 cm (CoVu 8456) to 10.74 cm (CoVu 869) with an average value of 14.8 cm. The phenotypic coefficient of variation was 13.65 per cent while the genotypic coefficient of variation was 11.56 per cent indicating a low degree of environmental influence on length of pod. A high heritability of 71.80 per cent was also recorded with a low value of genetic advance.

The number of pods per plant ranged from 56.7 (Charrodi) to 9.20 (CoVu 358) with a mean value of 26.79. The phenotypic coefficient of variation was 45.06 per cent, whereas genotypic coefficient of variation recorded 37.88 per cent indicating a low degree of environmental influence. High heritability of 70.69 per cent was recorded with a high genetic advance of 65.62 per cent.

The weight of hundred seeds ranged from 23.66 g (C 88) to 5.73 g (V 16) with a mean value of 11.61 g. The phenotypic coefficient of variation was 26.77 per cent while genotypic coefficient of variation was 26.76 per cent, almost same as that of PCV indicating a very low degree of environmental influence. A very high heritability of 99.9 per cent was recorded with a high genetic advance of 55.12 per cent.

The seed protein content ranged from 30.19 per cent (V 130) to 21.1 per cent (C 88) with a mean value of 27.19 per cent . The phenotypic coefficient of variation was 6.8 per cent while the genotypic coefficient of variation was 6.42 per cent indicating a low degree of environmental influence. A very high heritability of 89 per cent was recorded with a very low value of genetic advance (12.47 per cent).

4.1.2 Selection index

Application of discriminant function as a basis for making selection on several characters simultaneously is aimed at discriminating the desirable genotypes from the undesirable ones on the basis of their phenotypic performance. A selection index for the fiftythree genotypes was worked out considering the biological nitrogen fixing characters such as total nodule weight, plant dry weight and nitrogen content in plant at 50 per cent flowering. These characters had positive and significant genotypic correlation with nitrogen content. Based on the selection index, top ranking three genotypes viz. VCP 4, CoVu 358 and DPLC 210 were selected as lines and bottom ranking two genotypes viz. PTB 2 and C 190 were selected as testers (Table 3).

Selections were made based on the grain yield per plant for the yield character. Top yielders such as V 322,V27 and V 271 were selected as lines and two low yielders such as C 152 and CoVu 85020 were selected as the testers. Since nitrogen fixation characters and grain yield are negatively correlated, indepentent selection criteria were used for these two groups of characters.

4.1.3 Correlations

Phenotypic and genotypic correlations were estimated among nine characters for nitrogen fixation traits and five characters, with respect to yield traits (Table 5).

4.1.3.1 Correlation of nitrogen fixation traits

Significant positive correlation was observed for nitrogen content in plant at 50 per cent flowering with number of nodules in the primary root, weight of effective nodules in the primary root, weight of nodules in the secondary roots, total nodule weight, number of days to 50 per cent flowering and plant dry weight. It was seen that between the phenotypic and genotypic correlations, the magnitude of the latter was higher in all the cases except the correlation between number of nodules in the primary root and nitrogen content thereby indicating the predominance of genetic relationship. Highest positive correlation with nitrogen content was shown by total nodule weight followed by weight of effective nodules in the primary root and weight of nodules in the secondary roots. Plant dry weight at 50 per cent flowering had shown significant positive correlation with weight of nodules in the secondary roots, total nodule weight, number of days to flower and nitrogen content in plant at 50 per cent flowering in which number of days to flower had shown highest positive phenotypic and genotypic correlations followed by weight of nodules in the secondary roots and total nodule weight.

As for the correlations with grain yield,

Table 5. Phenotypic and genotypic correlation on biological nitrogen fixation and yield characters in cowpea.

Character	Number of nodules in the primary root	Number of nodules in the secondary root	Total number of nodules	Weight of effective nodules in the primary root	Weight of nodules in the secondary root	Total nodule weight	Number of days to flower	Nitrogen content in plant	Plant dry weight	Grain yield per plant	Length of pods	Number of pods per plant	Weight of hundred seeds	Seed protein content
	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	-	0.199	0.560	0.386	-0.072	0.242	-0.484	0.275	-0.552	0.312	-0.095	0.205	0.094	-0.098
2	0.113	-	0.924	-0.311	0.478	0.016	-0.035	-0.004	-0.061	-0.208	0.109	-0.253	0.487	-0.566
	**	**												
3	0.496	0.919	-	-0.111	0.376	0.109	-0.220	0.105	-0.270	-0.055	0.051	-0.135	0.448	-0.517
	**	*												
4	0.429	-0.228	-0.029	-	0.384	0.896	0.149	0.902	0.208	-0.386	0.165	-0.423	0.050	-0.045
		**	**	*										
5	-0.119	0.496	0.386	0.232	-	0.755	0.415	0.741	0.454	-0.667	0.236	-0.629	0.364	-0.463
	**			**	**									
6	0.265	0.085	0.179	0.869	0.682	-	0.303	0.998	0.358	-0.603	0.234	-0.604	0.211	-0.256
	**	*			**	**								
7	-0.369	-0.253	-0.169	0.122	0.367	0.272	-	0.310	0.969	-0.182	0.102	-0.309	-0.033	0.111
	**			**	**	**	**							
8	0.284	0.092	0.193	0.865	0.659	0.984	0.284	-	0.322	-0.622	0.212	-0.597	0.181	-0.219
	**				**	**	**	*						
9	-0.318	0.026	-0.105	0.107	0.306	0.230	0.555	0.214	-	-0.275	0.400	-0.475	0.118	-0.058
	**			**	**	**		**						
10	0.345	-0.014	0.002	-0.336	-0.314	-0.417	-0.114	-0.407	0.181	-	0.138	0.721	0.075	-0.035
								*						
11	-0.087	0.128	0.074	0.129	0.188	0.187	0.119	0.198	0.191	0.139	-	-0.469	0.518	-0.521
				**	**	**	**	**		**	**			
12	0.131	-0.090	-0.027	-0.348	-0.457	-0.493	-0.265	-0.404	-0.052	0.683	-0.341	-	-0.400	0.434
		**	**		**	*					**	**		
13	0.073	0.379	0.360	0.044	0.320	0.195	-0.032	0.166	0.069	0.049	0.438	-0.336	-	-0.953
		**	**		**	**		**			**	**	**	
14	-0.096	-0.416	-0.401	-0.086	-0.406	-0.270	0.110	-0.232	-0.041	0.008	-0.440	0.332	-0.900	-

* Significant at 5% level
** Significant at 1% level

The lower diagonal values are the phenotypic correlation coefficients and the upper diagonal values are the genotypic correlation coefficients.

characters such as weight of effective nodules in the primary root, weight of nodules in the secondary roots, total weight of nodules and nitrogen content in plant at 50 per cent flowering had shown significant and negative phenotypic and genotypic correlations whereas none of the characters had shown positive correlation.

Plant dry weight and characters such as weight of nodules in the secondary roots, total nodule weight, number of days to flower and nitrogen content in plant at 50 per cent flowering had shown significant and positive correlation with number of days to flower.

4.1.3.2 Correlation of yield and yield components

An estimate of interrelationship between yield of seeds and yield contributing characters is vital for an effective selection for simultaneous improvement of one or more yield contributing components. The intensity and direction of association between characters may be measured by genotypic and phenotypic correlation coefficients.

The genotypic and phenotypic correlations for grain yield with number of pods per plant were positive and highly significant. On the other hand the genotypic and phenotypic correlation coefficients for grain yield with length of pod, weight of hundred seeds and seed protein content were found to be non-significant.

The genotypic and phenotypic correlation coefficients for length of pod with number of pods per plant and seed protein content were significantly negative, while correlations with weight of hundred seeds were found to be positively correlated. When the length of pod increased, the hundred seed weight also increased while number of pods per plant and seed protein content decreased. The impact of length of pod on total yield was little. The genotypic and phenotypic correlation coefficients of weight of hundred seeds with number of pods per plant and seed protein content were found to be significant and negative.

4.1.4 Direct and indirect effects (Path analysis)

The direct and indirect effects of component characters on nitrogen fixation and grain yield are presented in Tables6 and 7 and in Fig.1 and 2.

4.1.4.1 Nitrogen fixation traits

The direct and indirect effects of eight components on nitrogen content per plant, and four components on grain yield along with their respective genotypic correlation coefficients are presented in Tables6 and 7. Path diagram with path coefficients (direct effects) and the genotypic correlations are presented in Fig. 3 and 4. Total number of nodules had maximum direct effect on nitrogen content per plant (3.076) followed by weight of effective nodules in the primary root (1.228). The total number of nodules exerted negative indirect effect (-0.137) though weight of effective nodules in the primary root which in turn had negative indirect effect through total number of nodules (-0.342).

Very high positive genotypic correlation was recorded (0.998) for total nodule weight with nitrogen content per plant,but the direct effect is negative (-0.812). The high positive indirect effect of this trait through weight of effective nodules in the primary root (1.099), weight of effective nodules in the secondary roots (0.707) and total number of nodules (0.335) justifies the high positive correlation. Besides, these three traits have positive direct effects with nitrogen content in plant.

Table 6. Direct and indirect effects of the components on nitrogen content per plant in cowpea.

Sl No	Components	Indirect effects via								Genotypic correlation with nitrogen content per plant
		Number of Secondary roots	Number of nodules in the primary root	Number of nodules in the secondary root	Total number of nodules	Weight of effective nodules in the primary root	Weight of effective nodules in the secondary root	Total nodule weight	Plant dry weight	
		X1	X2	X3	X4	X5	X6	X7	X8	
	X1	**-0.003**	0.922	0.392	-1.428	0.532	0.983	-0.652	-0.027	0.719
	X2	0.002	**-1.141**	-0.533	1.722	0.474	-0.068	-0.197	0.015	0.275
	X3	0.0004	-0.227	**-2.674**	2.841	-0.381	0.449	-0.013	0.002	-0.004
	X4	0.001	-0.638	-2.470	**3.076**	-0.137	0.353	-0.088	0.008	0.105
	X5	-0.001	-0.440	0.831	-0.342	**1.228**	0.360	-0.727	-0.006	0.902
	X6	-0.003	0.082	-1.279	1.157	0.472	**0.938**	-0.613	-0.013	0.741
	X7	-0.002	-0.276	-0.043	0.335	1.099	0.708	**-0.812**	-0.010	0.998
	X8	-0.003	0.629	0.163	-0.829	0.255	0.425	-0.291	**-0.028**	0.322

Residual effect 0.0268

Diagonal values are the direct effect.

N C - Nitrogen content in plant at 50 per cent flowering.

1 - Number of secondary roots.

2 - Number of nodules in the primary root.

3 - Number of nodules in the secondary roots.

4 - Total number of nodules

5 - Weight of effective nodules in the primary root.

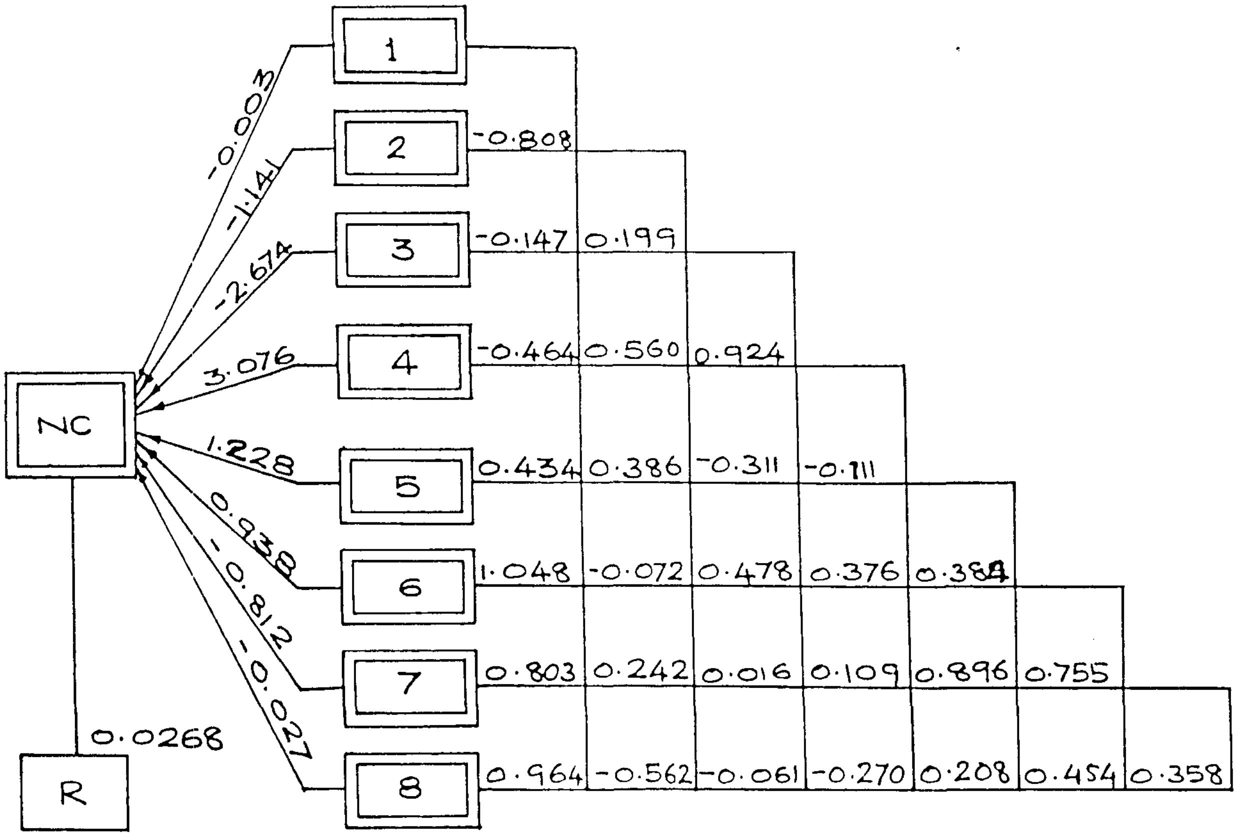
6 - Weight of effective nodules in the secondary root.

7 - Total nodule weight.

8 - Plant dry weight.

R - Residual effect.

Fig 3. Path diagram showing the direct effect and interrelationship between nitrogen content per plant and eight selected components in cowpea.



NC
R
0.0268
1
2
3
4
5
6
7
8
-0.003
-1.141
-2.674
3.076
1.228
0.938
-0.812
-0.027
-0.808
-0.147
0.199
-0.464
0.560
0.924
0.434
0.386
-0.311
-0.111
1.048
-0.072
0.478
0.376
0.384
0.803
0.242
0.016
0.109
0.896
0.755
0.964
-0.562
-0.061
-0.270
0.208
0.454
0.358

Direct effects shown in arrows and genotypic correlation shown in steps

Table 7. Direct and indirect effects of the components on grain yield in cowpea.

Components	Indirect effects via				Genotypic correlation with grain yield
	Length of pod	Number of pods per plant	Weight of hundred seeds	Plant dry weight	
	X1	X2	X3	X4	
X1	**1.917**	0.039	-0.369	-0.586	0.138
X2	-0.899	**-0.082**	0.285	0.695	0.721
X3	0.992	0.033	**-0.714**	-0.173	0.075
X4	0.766	0.039	-0.085	**-1.464**	-0.275

Residual effect 0.488

Diagonal values are the direct effect

G Y - Grain yield per plant.

1 - Length of pod.

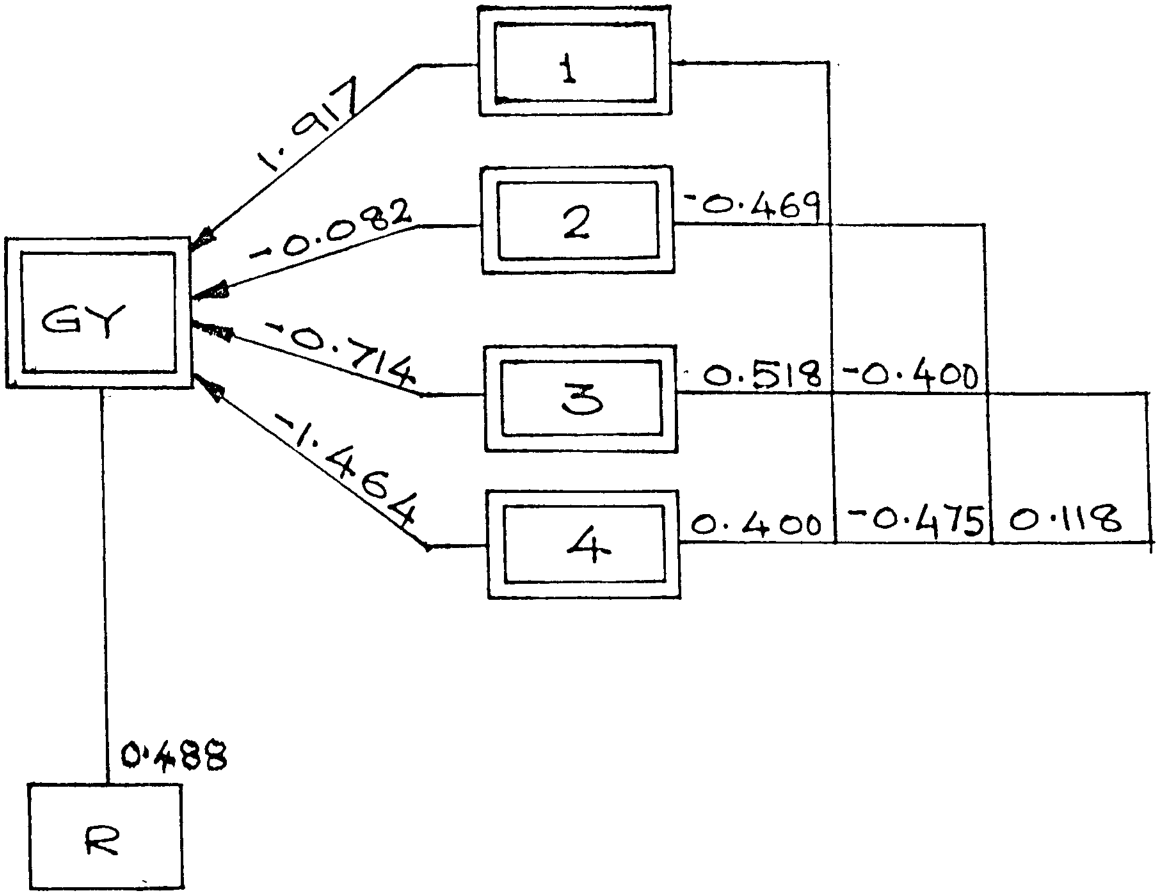
2 - Number of pods per plant.

3 - Weight of hundred seeds.

4 - Plant dry weight.

R - Residual effect.

Fig 4. Path diagram showing the direct effects and interrelationship between grain yield and four selected components in cowpea.


1
2
3
4
GY
R
1.917
-0.082
-0.714
-1.464
0'488
-0.469
0.518
-0.400
0.400
-0.475
0.118

Direct effects shown in arrows and genotypic correlation shown in steps

The highest negative direct effect was produced by number of nodules in the secondary root (-2.67) which recorded a negative correlation (-0.004), balancing the position.

Number of secondary roots recorded a significant positive correlation (0.719) with nitrogen content, but its direct effect was negative (-0.003). The high positive indirect effect of this trait through weight of effective nodules in the secondary roots (0.983), number of nodules in the primary root (0.922), weight of effective nodules in the primary root (0.532) and number of nodules in the secondary roots (0.392) justifies the positive correlation in which weight of effective nodules in the primary root and weight of effective nodules in the secondary roots have positive direct effects on nitrogen content.

Plant dry weight recorded significant positive genotypic correlation (0.322) with nitrogen content per plant, but its direct effect was negative (-0.028). High positive indirect effect of plant dry weight through number of nodules in the primary root (0.629), weight of effective nodules in the secondary roots (0.425), weight of effective nodules in the primary root (0.255) and number of nodules in the secondary roots (0.163) justifies the significant positive correlation, in which weight of effective nodules in the primary root, total number of nodules and weight of effective nodules in the secondary roots have positive direct effects.

Although total nodule weight displayed very high genotypic correlation with nitrogen content per plant at 50 per cent flowering, its direct effect was negative; whereas weight of effective nodules in the primary root was showing very high positive genotypic correlation (0.902) along with positive direct effect with nitrogen content per plant at 50 per cent flowering. Likewise weight of effective nodules in the secondary root was significantly and positively correlated (0.741) with nitrogen content along with a positive direct effect (0.938). At the same time weight of effective nodules in the primary root exerted positive indirect effect ((0.36) through weight of effective nodules in the secondary roots which in turn had positive indirect effect (0.472) through weight of effective nodules in the primary root.

Genotypic correlation of weight of effective nodules in the primary root (0.902) and weight of effective nodules in the secondary roots (0.741) with nitrogen content was found to be almost equal to its direct effect. The low value of residual factor indicate that 97 per cent of the variation in nitrogen content may be attributed to the above characters.

4.1.4.2 Yield characters

Number of pods per plant had very low negative direct effect (-0.082) eventhough the character recorded very high positive genotypic correlation with yield (0.7212). Very high positive indirect effect of this trait through plant dry weight (0.695) and weight of hundred seeds (0.285) justifies the high positive correlation (Table 7, Fig 2).

Length of pod recorded the highest positive direct effect with the grain yield (1.917), but the indirect effects *via*, plant dry weight (-0.586) and weight of hundred seed (-0.369) were negative whereas the indirect effect through number of pods per plant was positive (0.039). The reduced non significant genotypic correlation as compared to the direct effect was due to the significant negative indirect effect of length of pod through weight of hundred seeds and plant dry weight.

Plant dry weight had the highest negative direct effect on grain yield (-1.464) even though it exerted positive indirect effects through length of pods (0.767) and number of pods per plant (0.039). Whereas the indirect effect through weight of hundred seed was negative (-0.085). This justifies the negative genotypic correlation (-0.275) of this character with the grain yield.

Weight of hundred seeds though exhibited positive genotypic correlations with grain yield (0.08), it had a negative direct effect (-0.71). The indirect effects of weight of hundred seeds via length of pod (0.99) and number of pods per plant (0.03) were found to be positive, whereas the indirect effect via plant dry weight was negative (-0.17).

Number of pods per plant exhibited a very strong positive correlation with yield (0.721). On partitioning the total correlation it was observed that the direct effect was negative and negligible. The positive indirect effect through plant dry weight and weight of hundred seeds seem to be the cause of significant positive correlation. Fifty one per cent of the variation in general may be attributed to these factors.

4.2 Combining ability analysis

4.2.1 Analysis of variance

The analysis of variance for characters studied are presented in Table 8. The results showed that all the characters except number of nodules in the primary root, number of nodules in the secondary roots, total number of nodules and weight of nodules in the secondary roots recorded significant treatment effects. The characters which showed

Table 8. Analysis of variance (line x tester) for seventeen characters under study.

Source	df	Number of days to 50% flowering	Number of nodules in the primary root	Number of nodules in the secondary roots	Total number of nodules	Weight of nodules in the primary root	Weight of nodules in the secondary roots	Total weight of nodules	Weight of effective nodules
					M S S				
Replication	2	25.60**	33.79	273.93	303.18	3.02**	0.25	1.84**	1.87**
Treatment	33	26.39**	30.49	50.35	72.04	0.78**	0.08	0.90**	0.90**
Parents	9	24.73**				1.45**		1.81**	1.82**
Crosses	23	24.54**				0.53**		0.58**	0.57**
Parent Vs Crosses	1	83.77**				0.29		0.01	0.01
Lines	5	20.72**				0.49		0.47	0.46
Testers	3	136.78**				1.07		1.82**	1.83**
Line X Tester	15	3.37**				0.44*		0.37*	0.36*
Error	66	1.24	20.72	35.93	46.52	0.19	0.07	0.20	0.20

Contd....2.

Table 8. (Contd.)

Source	df	Dry weight of the plant	Dry weight of the root	Nitrogen content per plant (%)	Length of pod	Number of seeds per pod	Number of pods per plant	Hundred seed weight (%)	Seed protein content	Yield per plant
		M S S								
Replication	2	25.45**	0.37	0.064**	0.20	2.43	62.17*	0.37	0.28*	31.71
Treatment	33	28.92**	0.28*	0.034**	6.01**	10.55**	428.36**	6.44**	1.48**	180.65**
Parents	9	12.16	0.28	0.067**	6.39**	6.31**	12.99	6.69**	1.68**	3.41
Crosses	23	25.66**	0.25	0.023**	5.67**	11.60**	490.49**	6.42**	1.42**	206.45**
Parent Vs crosses	1	254.86**	0.91*	0.0003	10.56**	24.62**	2737.79**	4.57**	0.95**	1182.44**
Lines	5	18.65		0.017	7.19**	4.50	401.53*	12.23**	2.58**	228.09*
Testers	3	101.48**		0.076**	23.76**	64.77**	2305.70**	19.60**	4.40**	792.24**
Line X Tester	15	12.83*		0.014*	1.54**	3.33*	157.10**	1.85**	0.44**	82.08**
Error	66	6.49	0.16	0.007	0.60	1.55	18.76	0.22	0.069	12.43

* Significant at 5% level

** Significant at 1% level

significant genotypic differences were subjected to line x tester analysis. The mean performance of lines, testers and line X testers are presented in Table 9 and Plate 1 to 6.

4.2.1.1 Number of days to 50 per cent flowering

The combining ability analysis for number of days to flowering showed that both lines and testers differed significantly in their general combining ability. Among lines CoVu 358 and DPLC 210 showed highly significant positive gca effects of 1.722 and 1.389 respectively, but the gca effect of V 322 was non-significant. Lines such as VCP 4, V 27 and V 271 recorded significant negative gca effect of -0.851,-1.444 and -0.944 respectively. Among testers, only PTB 2 showed significant negative gca of -4.0 while it was positive and significant for C 152 (2.056) and CoVu 85020 (1.556). C 190 showed non-significant gca of 0.389. The hybrid DPCL 210 X C 190 differed significantly from all other hybrids with a positive sca of 1.611. Apart from the above hybrid, the sca effect was positive for VCP 4 X C 152, VCP 4 X CoVu 85020, CoVu 358 X PTB 2, CoVu 358 X CoVu 85020, V 322 X C 190, V 322 X C 152, V 27 X PTB 2, V 27 X CoVu 85020 and V 271 X C 152. The gca and sca effects for number of days to flower are presented in the Table 10 and Fig 5 and 6.

The ratio of variance due to GCA and SCA showed a value which was less than unity (0.755) indicating the predominance of non-additive gene action. The proportional contribution of tester to the total variance of the number of days to flower was high (72.70 per cent) followed by lines (18.36 per cent) and line X tester (8.95 per

Plate 1. Line VCP 4, tester PTB 2 and its F_1.

VCP-4
×
PTB-2
F_1

Plate 2. Line CoVu 358, tester PTB 2 and its F_1.

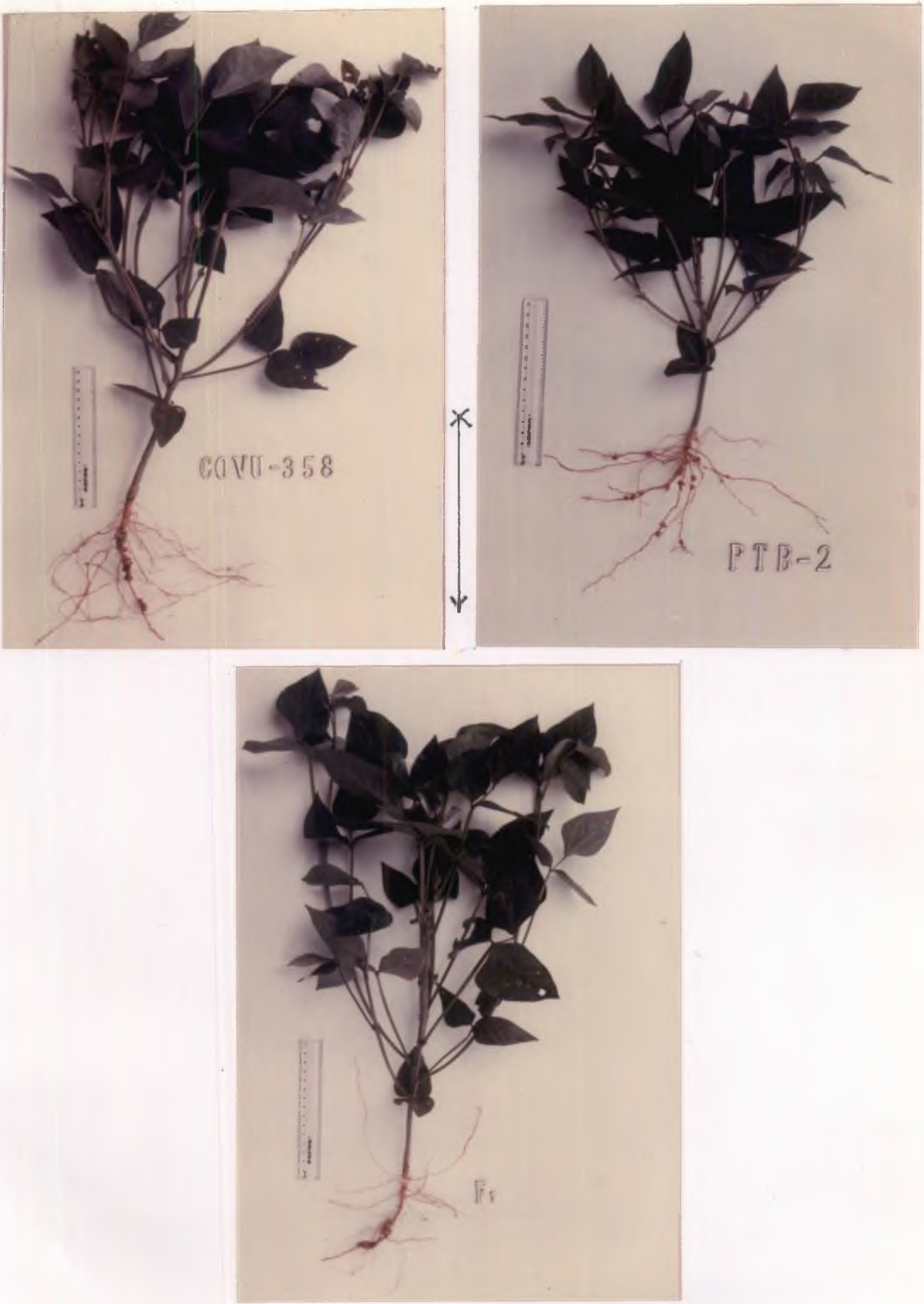

COVU-358
×
PTB-2
F1

Plate 3. Line DPLC 210, tester PTB 2 and its F_1.

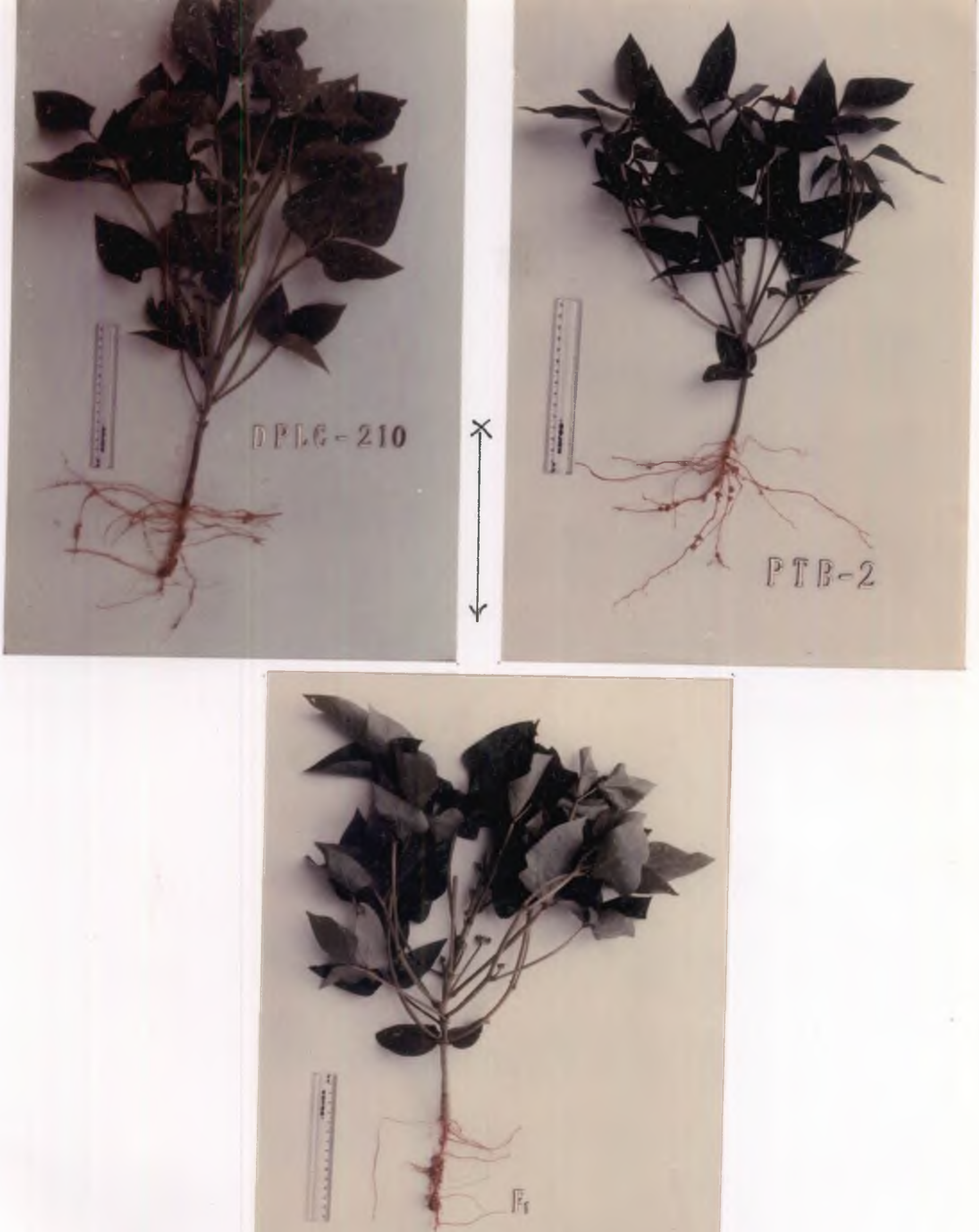

DPLC-210
×
PTB-2
F_1

Plate 4. Line V 322, tester PTB 2 and its F_1.

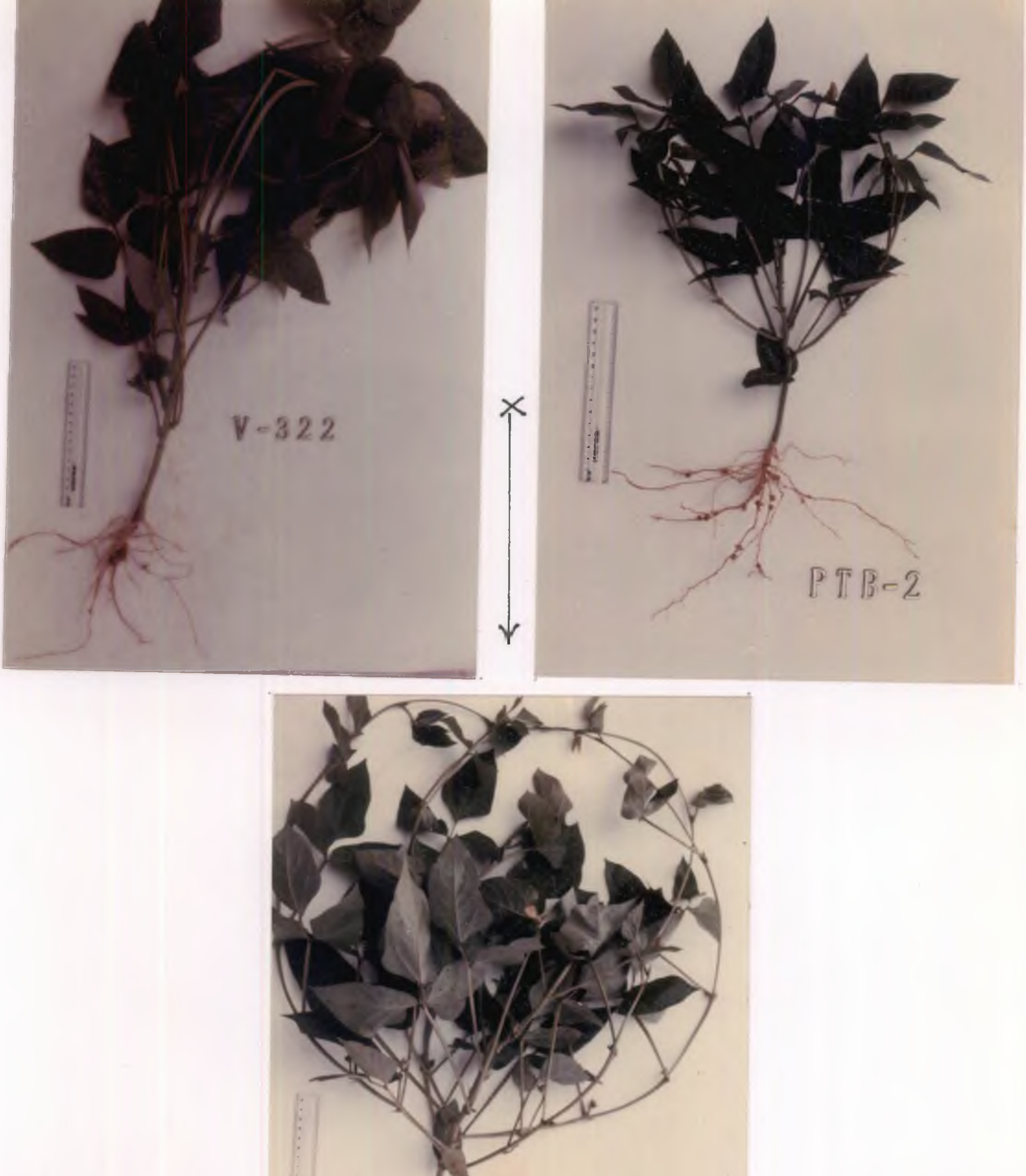
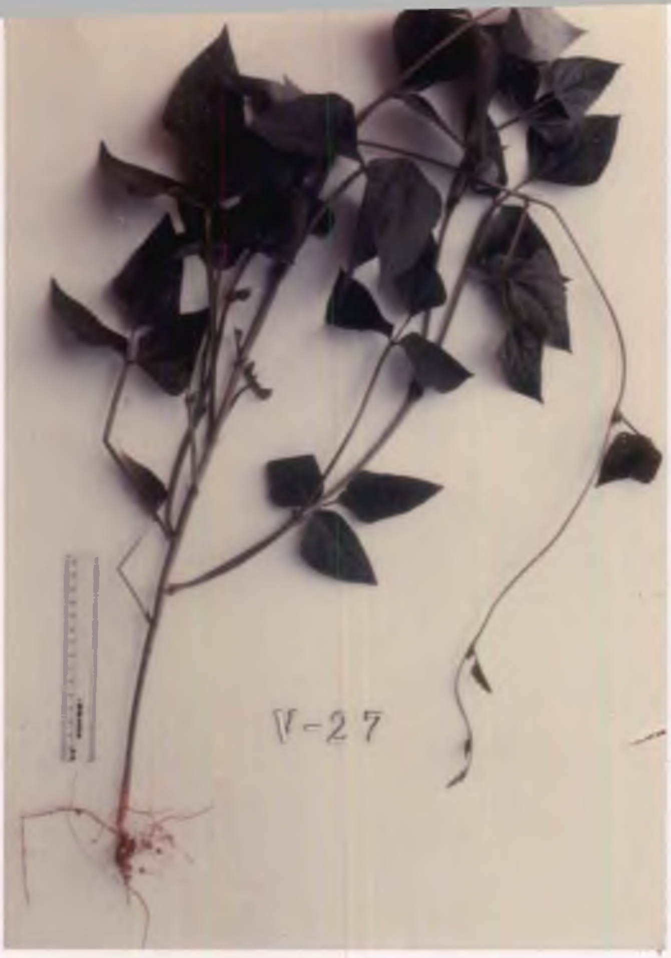
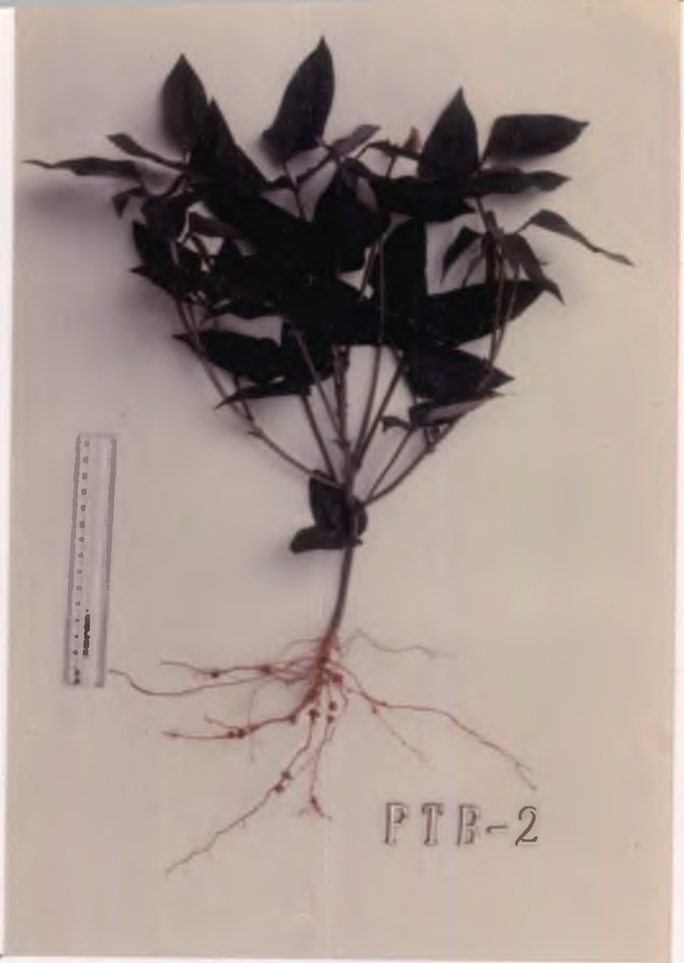

V-322
×
PTB-2
F1

Plate 5. Line V 27, tester PTB 2 and its F_1.


V-27

×


PTB-2

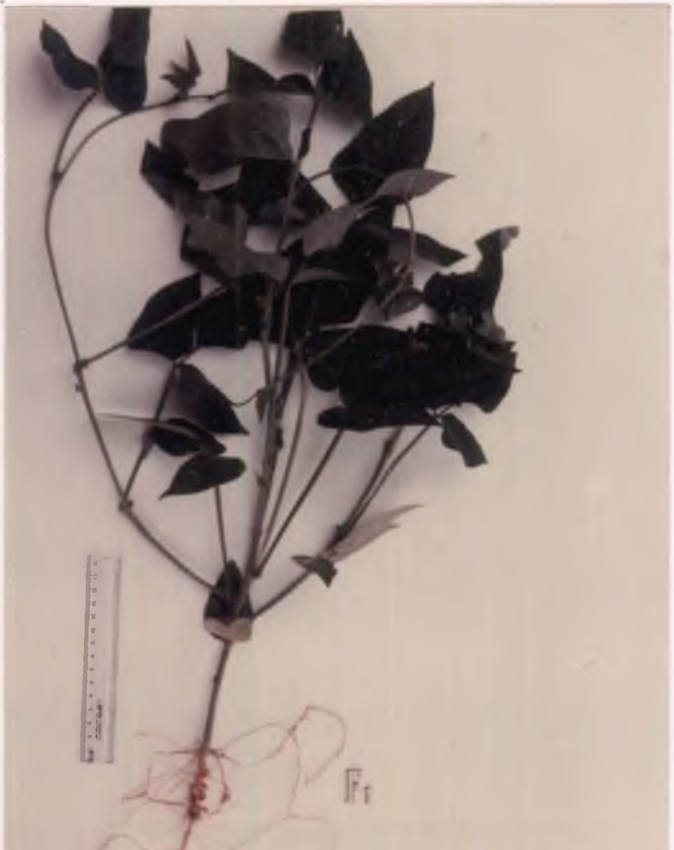
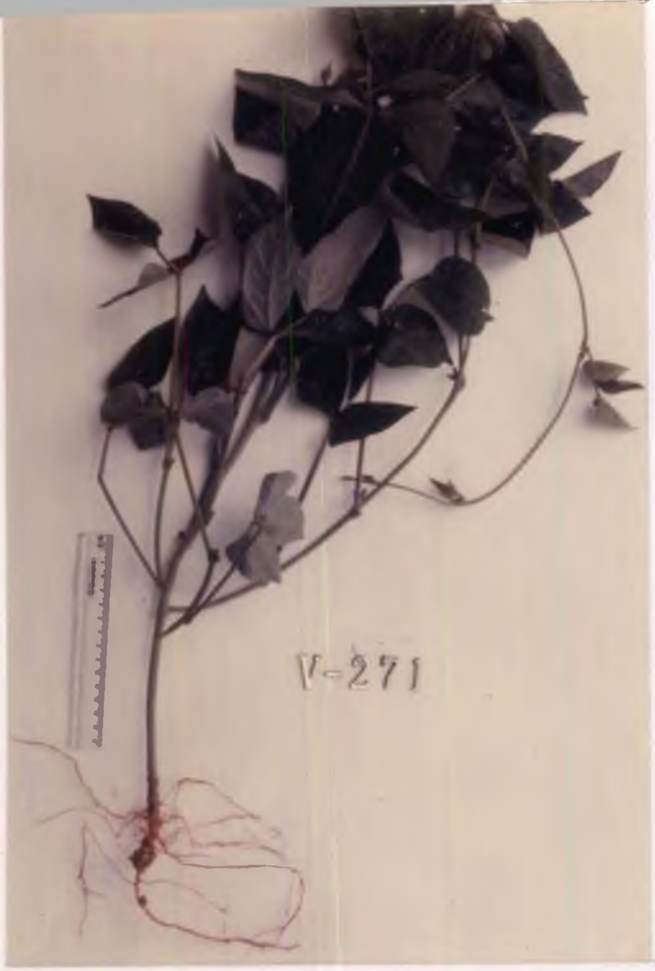
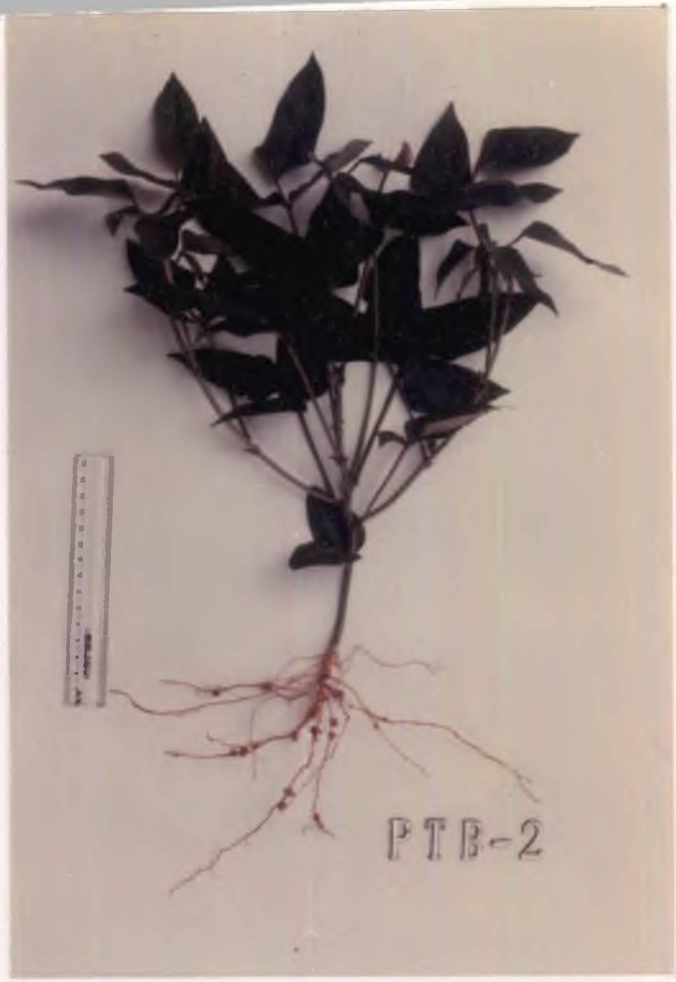

F_1

Plate 6. Line V 271, tester PTB 2 and its F_1.


V-271

×


PTB-2

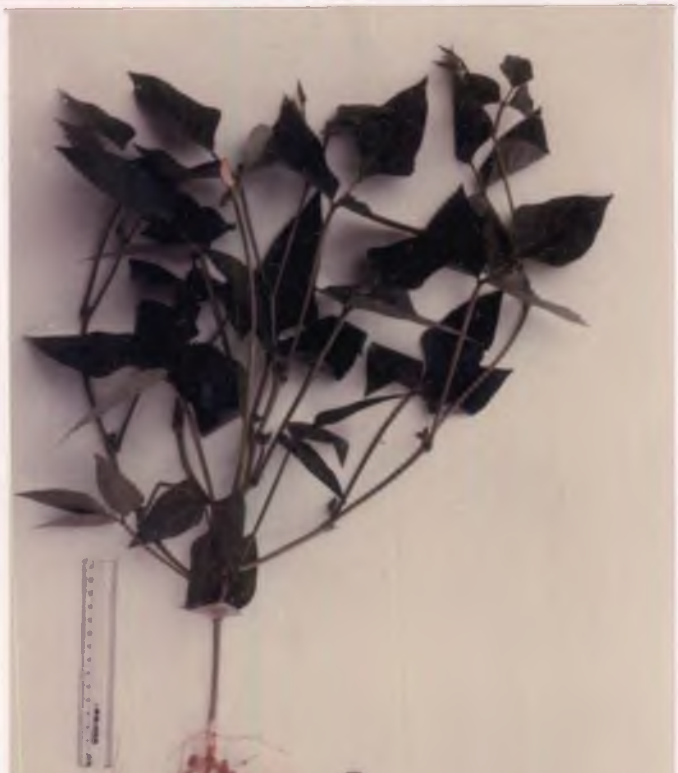

F_1

Table 9. Mean performance of lines, testers and line x testers.

	Number of days to 50% flowering	Number of nodules in the primary root	Number of nodules in the secondary roots	Total number of nodules (g)	Weight of nodules in the primary root (g)	Weight of nodules in the secondary roots (g)	Total weight of nodules	Weight of effective nodules (g)
Lines								
VCP-4 (L1)	41.33	21.27	12.00	33.27	2.50	0.32	2.82	2.82
CoVu-358 (L2)	41.33	13.80	9.27	23.07	2.35	0.33	2.69	2.68
DPLC-210 (L3)	42.33	13.27	13.87	27.13	2.06	0.71	2.77	2.76
V-322 (L4)	42.67	15.40	14.80	30.20	1.41	0.33	1.73	1.72
V-27 (L5)	41.33	7.00	11.00	18.00	0.69	0.22	0.91	0.91
V-271 (L6)	41.33	10.13	8.80	18.93	1.14	0.31	1.45	1.44
Testers								
PTB-2 (T1)	33.67	10.60	11.67	22.27	0.44	0.21	0.65	0.64
C-190 (T2)	37.33	11.27	6.87	18.13	1.04	0.52	1.23	1.23
C-152 (T3)	42.33	15.47	8.00	23.47	1.83	0.33	2.15	2.14
CoVu-85020(T4)	42.33	10.60	11.20	21.80	1.21	0.48	1.69	1.67
Crosses								
L1 X T1	33.67	16.13	11.93	28.07	1.13	0.31	1.43	1.41
L1 X T2	37.00	17.27	15.07	32.33	1.37	0.39	1.75	1.74
L1 X T3	41.00	17.67	10.40	28.07	2.33	0.43	2.76	2.73
L1 X T4	39.33	15.20	7.73	22.93	1.79	0.39	2.18	2.14
L2 X T1	37.33	13.67	17.80	31.47	1.48	0.52	2.00	1.89
L2 X T2	39.67	11.60	9.40	21.00	0.98	0.41	1.39	1.38
L2 X T3	41.67	12.53	12.53	25.07	1.51	0.67	2.18	2.18
L2 X T4	42.67	16.07	11.07	27.13	1.92	0.41	2.34	2.30
L3 X T1	35.33	14.20	13.40	27.60	1.70	0.62	2.32	2.31
L3 X T2	42.00	13.60	13.40	27.00	1.30	0.33	1.62	1.62
L3 X T3	41.33	9.73	15.87	25.60	1.00	0.74	2.07	2.07
L3 X T4	41.33	8.73	12.80	21.53	1.20	0.61	1.81	1.80
L4 X T1	34.00	14.67	16.53	31.20	1.18	0.35	1.53	1.51
L4 X T2	40.00	13.33	27.87	41.20	0.94	0.58	1.52	1.51
L4 X T3	41.00	13.20	17.00	30.20	1.26	0.68	1.94	1.94
L4 X T4	40.00	20.40	7.87	28.27	2.20	0.29	2.49	2.48
L5 X T1	33.67	12.60	17.53	30.13	0.74	0.42	1.15	1.14
L5 X T2	37.33	15.00	6.53	21.53	0.82	0.14	0.96	0.95
L5 X T3	38.00	11.47	11.33	22.80	1.25	0.69	1.94	1.94
L5 X T4	39.67	14.60	8.73	23.33	1.80	0.44	2.24	2.22
L6 X T1	33.67	13.27	10.93	24.20	1.01	0.31	1.33	1.31
L6 X T2	38.00	18.47	11.53	30.00	1.36	0.37	1.74	1.72
L6 X T3	41.00	9.00	14.73	23.73	0.94	0.83	1.77	1.76
L6 X T4	38.00	12.87	12.80	25.67	1.16	0.42	1.57	1.56
CD (5%)	1.82	7.43	9.79	11.13	0.72	0.46	0.73	0.72
SE	0.64	2.63	3.46	3.94	0.25	0.16	0.26	0.26

Contd...2.

Table 9. (Contd.)

	Dry weight of the plant (g)	Dry weight of the root (g)	Nitrogen content per plant (%)	Length of pod (cm)	Number of seeds per pod	Number of pods per plant	Hundred seed weight (g)	Seed protein content (%)	Yield per plant (g)
Lines									
VCP-4 (L1)	10.37	1.28	2.46	17.97	16.23	7.25	13.37	26.79	6.85
CoVu-358 (L2)	10.72	1.31	2.43	14.69	16.50	7.98	9.35	28.71	5.94
DPCL-210 (L3)	6.88	1.06	2.46	14.58	16.10	8.72	9.18	28.92	6.49
V-322 (L4)	11.07	1.05	2.25	15.79	14.33	7.66	11.77	27.63	5.63
V-27 (L5)	7.99	0.86	2.11	15.52	14.33	9.50	11.56	27.67	6.88
V-271 (L6)	9.08	0.84	2.19	15.21	15.27	9.27	10.92	28.20	7.44
Testers									
PTB-2 (T1)	4.76	0.55	2.05	12.47	13.13	11.14	8.90	29.17	5.77
C-190 (T2)	9.31	0.92	2.14	13.34	12.10	14.00	11.77	27.72	8.08
C-152 (T3)	7.44	0.81	2.34	14.93	15.70	7.19	9.74	28.63	4.42
CoVu-85020(T4)	10.33	1.60	2.24	14.78	15.80	9.58	9.40	28.74	7.32
Crosses									
L1 X T1	7.96	0.88	2.19	15.45	13.87	13.08	10.03	28.63	9.92
L1 X T2	17.39	1.98	2.25	14.32	13.57	39.58	13.21	26.96	23.52
L1 X T3	12.84	1.12	2.45	16.47	16.27	9.91	12.14	27.45	9.94
L1 X T4	9.02	1.22	2.34	16.05	15.30	7.66	11.21	27.94	7.18
L2 X T1	10.43	1.01	2.30	11.82	11.07	13.71	10.13	28.52	8.41
L2 X T2	16.03	1.52	2.18	14.04	14.77	22.88	10.12	28.39	16.17
L2 X T3	14.77	1.16	2.34	14.27	15.63	6.87	9.72	28.68	4.63
L2 X T4	10.39	1.08	2.37	14.59	15.37	6.94	9.47	28.51	5.61
L3 X T1	10.86	1.69	2.37	12.08	11.67	35.38	8.85	28.93	19.81
L3 X T2	11.14	0.94	2.23	13.76	12.77	35.29	11.15	28.04	20.88
L3 X T3	9.24	1.09	2.32	14.97	16.33	6.89	9.16	28.92	5.16
L3 X T4	10.60	1.08	2.27	14.54	15.73	7.61	10.11	28.50	4.11
L4 X T1	11.61	1.29	2.21	13.64	12.03	38.37	10.89	28.24	24.33
L4 X T2	15.60	1.14	2.20	12.97	10.82	50.44	15.48	25.90	37.91
L4 X T3	16.78	1.53	2.29	15.92	15.00	19.41	11.39	27.70	15.04
L4 X T4	12.39	1.22	2.40	16.36	16.63	12.65	11.07	28.04	10.45
L5 X T1	7.51	1.26	2.14	12.49	11.17	19.31	11.07	28.06	12.25
L5 X T2	13.09	1.33	2.10	11.95	10.33	22.74	12.99	27.04	12.77
L5 X T3	15.28	1.61	2.29	15.28	15.50	20.11	11.08	27.98	19.46
L5 X T4	14.82	1.50	2.35	14.76	15.07	19.29	11.77	27.67	11.67
L6 X T1	7.92	1.02	2.17	13.07	12.60	27.17	10.24	28.41	14.51
L6 X T2	14.36	1.33	2.25	13.25	12.17	38.25	12.54	27.50	26.08
L6 X T3	13.63	0.96	2.26	15.16	15.00	9.29	10.70	28.14	7.13
L6 X T4	10.71	0.69	2.24	14.11	14.27	11.59	10.95	28.00	7.97
CD (5%)	4.16	0.65	0.14	1.26	2.04	7.07	0.76	0.43	5.76
SE	1.47	0.23	0.05	0.45	0.72	2.50	0.27	0.15	2.04

Table 10. Combining ability effects of lines, testers and crosses for the character number of days to flower.

Testers Lines		PTB 2	C 190	C 152	CoVu 85020
	gca of Testers	-4.000**	0.389	2.056**	1.556**
	gca of Lines	sca effects of combinations			
VCP 4	-0.861*	-0.083	-1.139	1.194	0.028
CoVu 358	1.722**	1.000	-1.056	-0.722	0.778
DPLC 210	1.389**	-0.667	1.611*	-0.722	-0.222
V322	0.139	-0.750	0.861	0.194	-0.306
V 27	-1.444**	0.500	-0.222	-1.222	0.944
V271	-0.944**	0.000	-0.056	1.278	-1.222

SE			CD		
gca	Lines	0.322	gca	Lines	1.090
	Testers	0.263		Testers	0.890
sca		0.644	sca		2.180

* Significant at 5% level

** Significant at 1% level

LINES

L1 - VCP 4

L2 - CoVu 358

L3 - DPLC 210

L4 - V 322

L5 - V 27

L6 - V 271

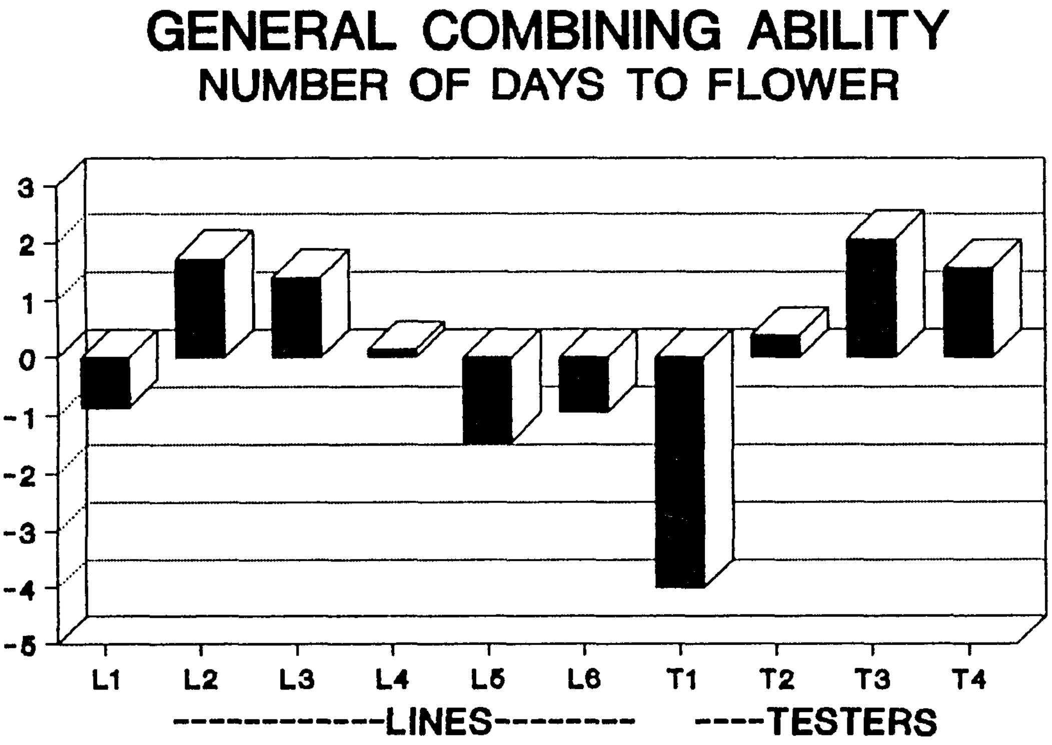
TESTERS

T1 - PTB 2

T2 - C 190

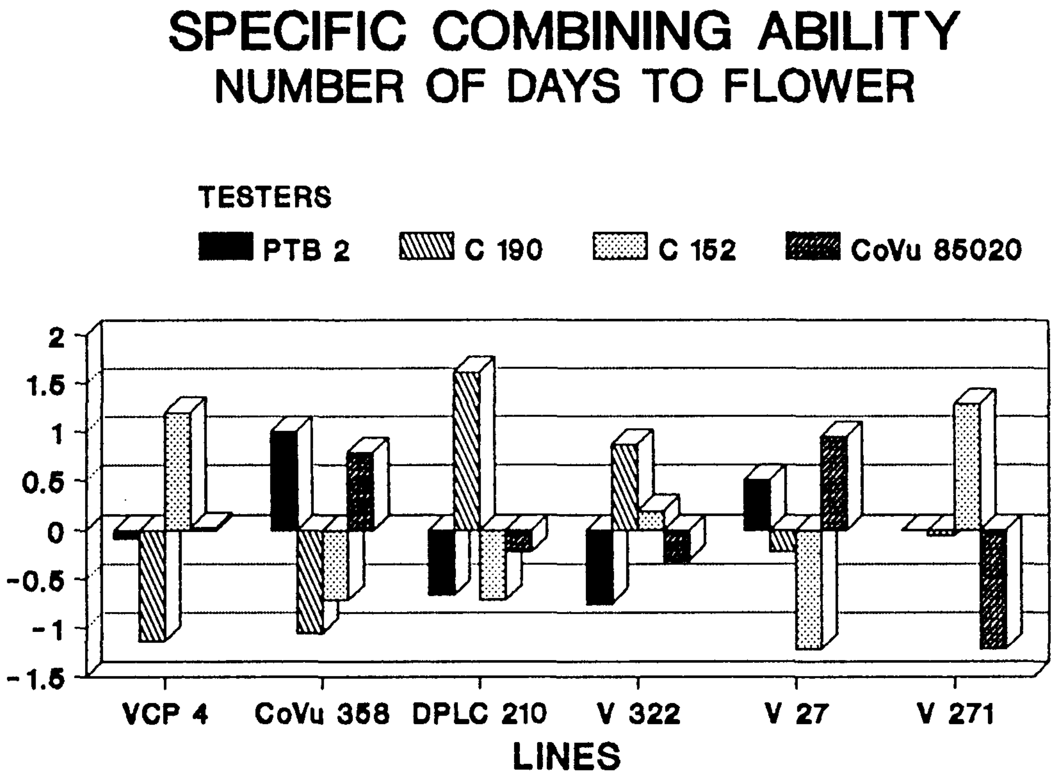
T3 - C 152

T4 - CoVu 85020



CD 5% LINE 1.090 TESTER 0.890
SE LINE 0.322 TESTER 0.263

Fig 5



SPECIFIC COMBINING ABILITY
NUMBER OF DAYS TO FLOWER

CD 5% :2.180   SE :0.644

Fig 6

cent) indicating the importance of tester in contributing to the total variance.

4.2.1.2 Weight of nodules in the primary root

The combining ability analysis for weight of nodules in the primary root showed that both lines and testers differed significantly in their general combining ability. Among the lines, VCP 4 displayed significant positive gca of 0.304 whereas, the gca of all other lines were nonsignificant. Among testers, CoVu 85020 recorded positive gca effect of 0.329 where as, C 190 showed negative gca effect of -0.220. The hybrids VCP 4 X C 152 and DPLC 210 X PTB 2 differed significantly from all other hybrids with significant positive sca of 0.647 and 0.543 respectively. The gca and sca effects for weight of nodules in the primary root is given in Table 11 and graphically represented in Fig 7 and 8.

The ratio of variance due to GCA and SCA was found to be less than unity (0.028) . The proportional contribution of line X tester to the total variance of the weight of nodules in the primary root was highest (54.013 per cent) followed by tester (25.987 per cent) and lines (20 per cent) indicating the importance of hybrid combinations in contributing to the total variance.

4.2.1.3 Total weight of nodules

Both lines and testers differed significantly in their gca effects. Among lines, none of them had recorded significant positive gca effects while only V 27 showed a significant negative gca effect of -0.262. Among testers all of them differed significantly in which C 152 and CoVu 85020 had shown positive gca of 0.275 and 0.268 respectively

Table 11. Combining ability effects of lines, testers and crosses for the character weight of nodules in the primary root.

Tester		PTB 2	C 190	C 152	CoVu 85020
Lines	gca of Testers	-0.142	-0.22*	0.033	0.329**
	gca of Lines	sca effects of combinations			
VCP 4	0.304*	-0.385	-0.067	0.647*	-0.196
CoVu 358	0.126	0.151	-0.271	-0.001	0.121
DPLC 210	-0.049	0.543*	0.216	-0.330	-0.429
V 322	0.047	-0.073	-0.235	-0.169	0.476
V 27	-0.197	-0.274	-0.110	0.066	0.318
V 271	-0.231	0.039	0.467	-0.215	-0.291

SE			CD		
gca	Lines	0.127	gca	Lines	0.431
	Testers	0.104		Testers	0.352
sca		0.255	sca		0.862

LINES

L1 - VCP 4

L2 - CoVu 358

L3 - DPLC 210

L4 - V 322

L5 - V 27

L6 - V 271

TESTERS

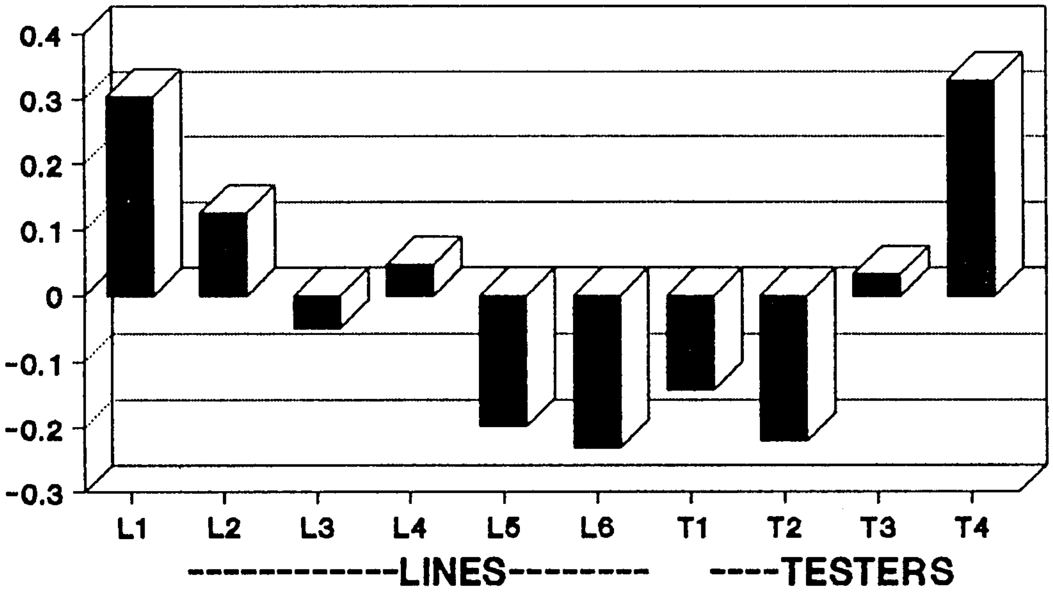
T1 - PTB 2

T2 - C 190

T3 - C 152

T4 - CoVu 85020

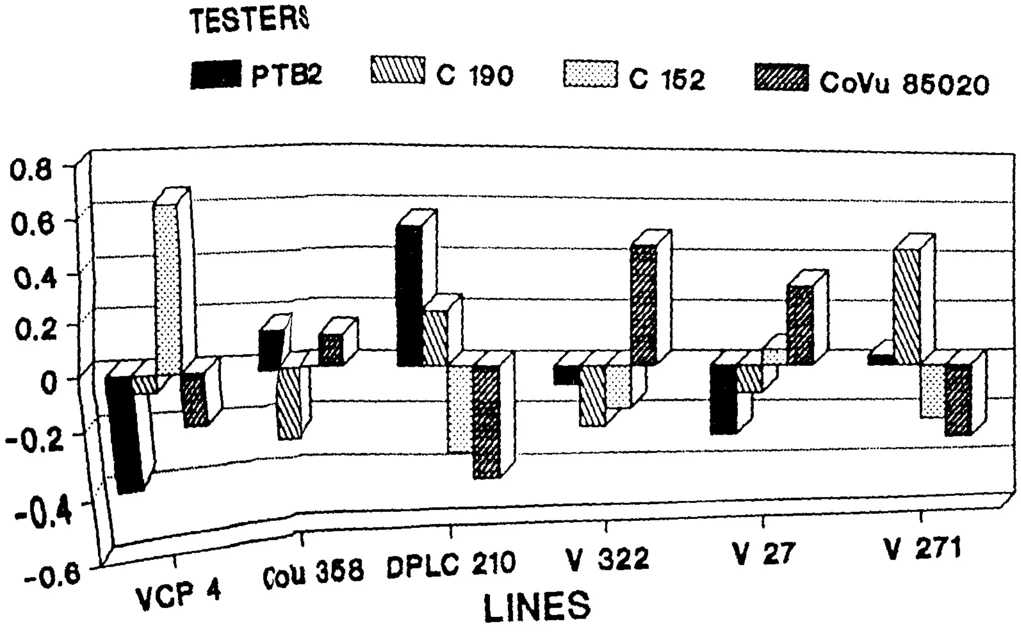
GENERAL COMBINING ABILITY
WEIGHT OF NODULES IN THE PRIMARY ROOT



CD 5% LINE 0.431 TESTER 0.352
SE LINE 0.127 TESTER 0.104

Fig 7

SPECIFIC COMBINING ABILITY
WEIGHT OF NODULES IN THE PRIMARY ROOT



CD 5% :0.862 SE :0.254

Fig 8

where as negative gca of -0.207 and -0.337 was observed for PTB 2 and C 190. Hybrid combinations of DPLC 210 X PTB 2 differed significantly from all other hybrids with a positive sca of 0.574. Apart from the above hybrid, positive sca was recorded in CoVu 358 X PTB 2, VCP 4 X C 190, DPLC 210 X C 190, V 271 X C 190, VCP 4 X C 152, V 27 X C 152, CoVu 358 X CoVu 85020, V 322 X CoVu 85020 and V 27 X CoVu 85020 hybrid combinations (Table 12, Fig 9 and 10). The ratio of variance due to GCA and SCA showed a value which is less than unity (0.096) indicating the predominance of non- additive gene action. The proportional contribution of line x tester to the total variance of the total weight of nodules was highest (41.222 per cent) followed by tester 40.99 per cent and lines (17.788 per cent) indicating the importance of line x tester in contributing to the total variance.

4.2.1.4 Weight of effective nodules

The combining ability analysis for weight of effective nodules revealed that both lines and testers differd significantly in their gca. Among lines, none of them had recorded significant positive gca effects where as V 27 showed a significant negative gca effect of -0.259. Among testers all of them differed significantly in which C 152 and CoVu 85020 had shown positive gca effects of 0.28 and 0.265 respectively, whereas, negative gca of -0.211 and -0.333 was observced for PTB 2 and C 190 respectively. Hybrid combination, DPLC 210 X PTB 2 differed significantly from all other hybrids with a positive sca effect of 0.57. Apart from the above hybrid, positive sca was recorded in CoVu 358 X PTB 2, VCP 4 X C 190, DPLC 210 X C 190, V 271 X C 190, VCP 4

Table 12. Combining ability effects of lines, testers and crosses for the character total weight of nodules.

Testers		PTB 2	C 190	C 152	CoVu 85020
Lines	gca of Testers	-0.207*	-0.337**	0.275*	0.268*
	gca of Lines	sca effects of combinations			
VCP 4	0.196	-0.391	0.06	0.454	-0.123
Covu 358	0.143	0.232	-0.251	-0.072	0.091
DPLC 210	0.121	0.574*	0.003	-0.16	-0.417
V 322	0.035	-0.133	-0.011	-0.204	0.349
V 27	-0.262*	-0.214	-0.273	0.092	0.396
V 271	-0.234	-0.068	0.473	-0.109	-0.296

SE			CD		
gca	Lines	0.129	gca	Lines	0.437
	Tester	0.105		Tester	0.357
sca		0.258	sca		0.874

LINES

L1 - VCP 4

L2 - CoVu 358

L3 - DPLC 210

L4 - V 322

L5 - V 27

L6 - V 271

TESTERS

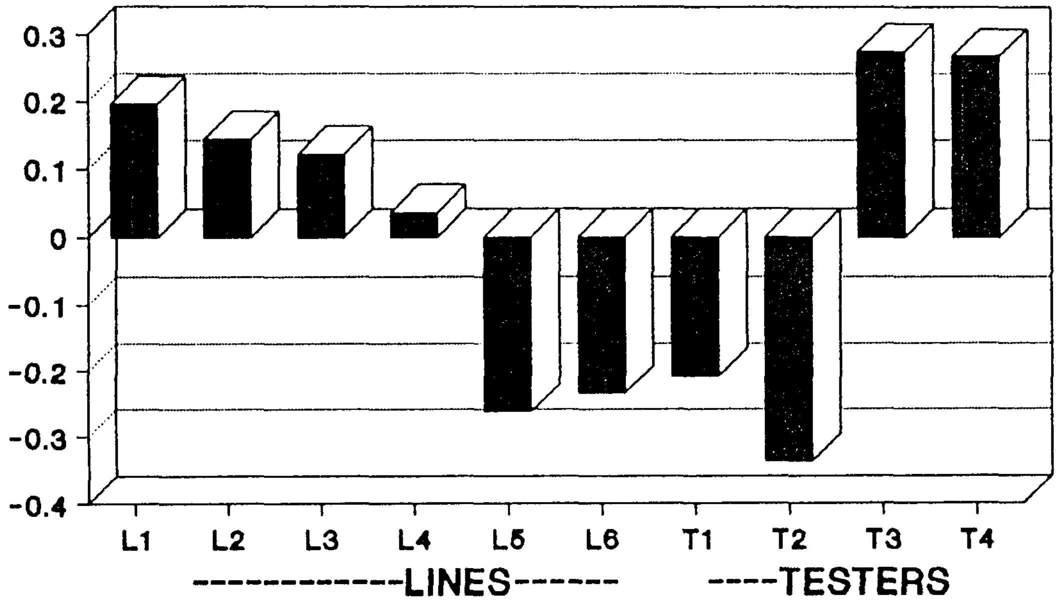
T1 - PTB 2

T2 - C 190

T3 - C 152

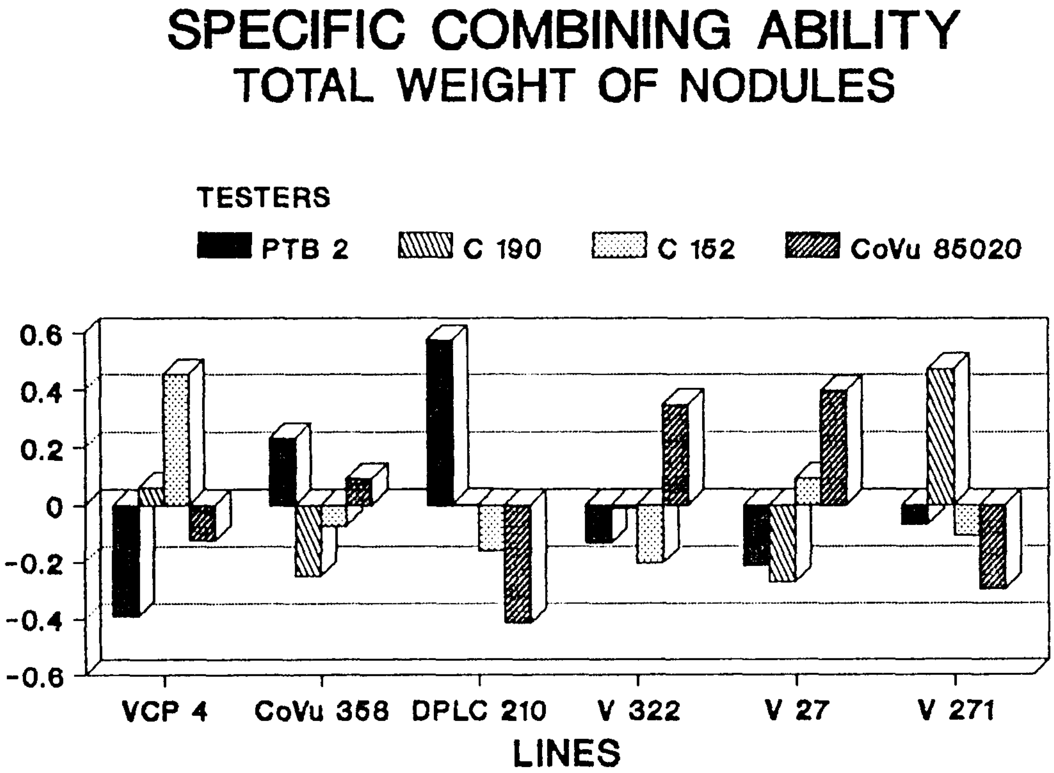
T4 - CoVu 85020

GENERAL COMBINING ABILITY
TOTAL WEIGHT OF NODULES



CD 5% LINE 0.437 TESTER 0.357
SE LINE 0.129 TESTER 0.105

Fig 9



CD 5% :0.874   SE :0.258

Fig 10

X C 152, V 27 X C 152, CoVu 358 X CoVu 85020, V 322 X CoVu 85020 and V 27 X CoVu 85020 hybrid combinations(Table 13, Fig 11 and 12). The ratio of variance due to GCA and SCA recorded a value less than unity (0.098). The proportional contribution of the tester to the total variance of the weight of effective nodules was highest (41.415 per cent) followed by line x tester (41.038 per cent) and line (17.788 per cent) indicating the importance of tester in contributing to the total variance.

4.2.1.5 Dry weight of plant at 50 per cent flowering

The combining ability analysis for the dry weight of plant at 50 per cent flowering revealed that both lines and testers differed significantly in their gca. Among lines, V 322 had recorded significant positive gca effect of 1.831 where as, DPLC 210 had shown significant negative gca effect of -1.804. Among testers, both C 190 and C 152 had shown significant positive gca of 2.338 and 1.492 each, but PTB 2 recorded a significant negative gca of -2.886. The hybrids DPLC 210 X PTB 2, VCP 4 X C 190 and V 27 X CoVu 85020 differed significantly with all other hybrids with a significant positive sca of 3.286, 3.251 and 3.088 respectively. Hybrids like VCP 4 X PTB 2, V 27 X PTB 2, V 271 X PTB 2, DPLC 210 X C 190, V 322 X C 190, V 27 X C 190, VCP 4 X C 152, DPLC 210 X C 152, VCP 4 X CoVu 85020, CoVu 358 X CoVu 85020, V 322 X CoVu 85020 and V 271 X CoVu 85020 recorded non significant negative sca (Table 14, Fig 13 and 14). The ratio of variance due to GCA and SCA displayed a value less than unity (0.153). The proportional contribution of line x tester to the total variance of the dry weight of the plant at 50 per cent flowering was highest

Table 13. Combining ability effects of lines, testers and crosses for the character weight of effective nodules.

Testers		PTB 2	C 190	C 152	CoVu 85020
Lines	gca of Testers	-0.211*	-0.333**	0.280**	0.265*
	gca of Lines	sca effects of combinations			
VCP 4	0.186	-0.388	0.07	0.446	-0.127
CoVu 358	0.14	0.231	-0.247	-0.062	0.078
DPLC 210	0.127	0.570*	0.003	-0.164	-0.409
V 322	0.04	-0.139	-0.016	-0.201	0.356
V 27	-0.259*	-0.21	-0.278	-0.093	0.396
V 271	-0.233	-0.064	0.468	-0.112	-0.293

SE			CD		
gca	Lines	0.128	gca	Lines	0.433
	Testers	0.105		Testers	0.354
sca		0.256	sca		0.867

LINES

L1 - VCP 4

L2 - CoVu 358

L3 - DPLC 210

L4 - V 322

L5 - V 27

L6 - V 271

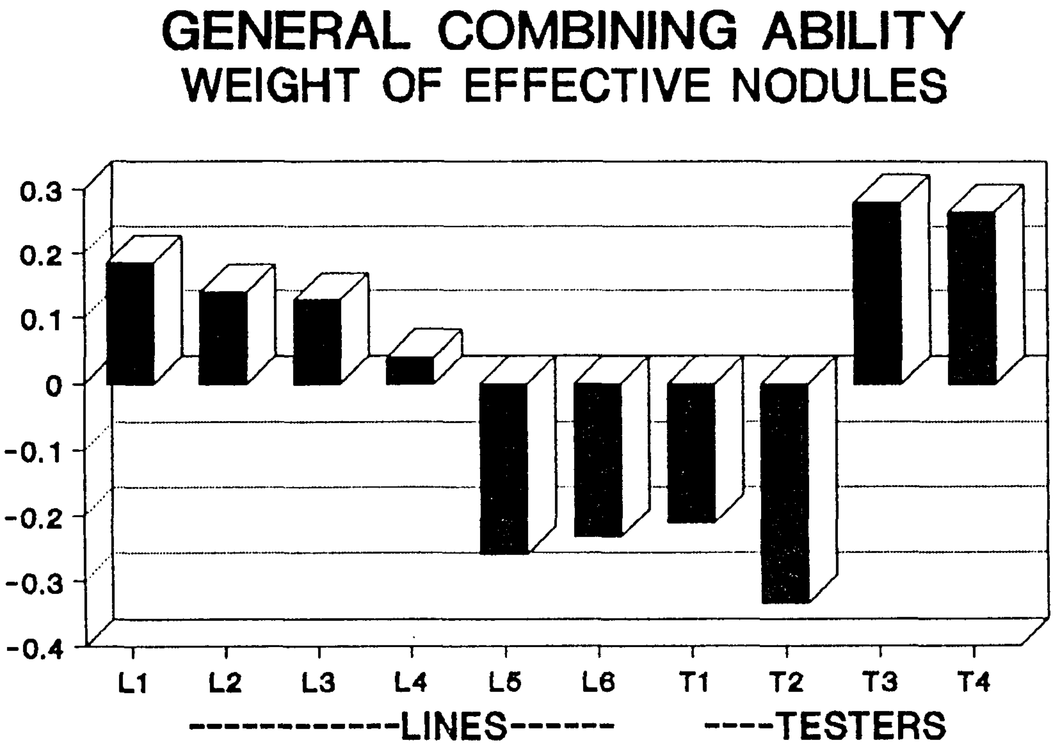
TESTERS

T1 - PTB 2

T2 - C 190

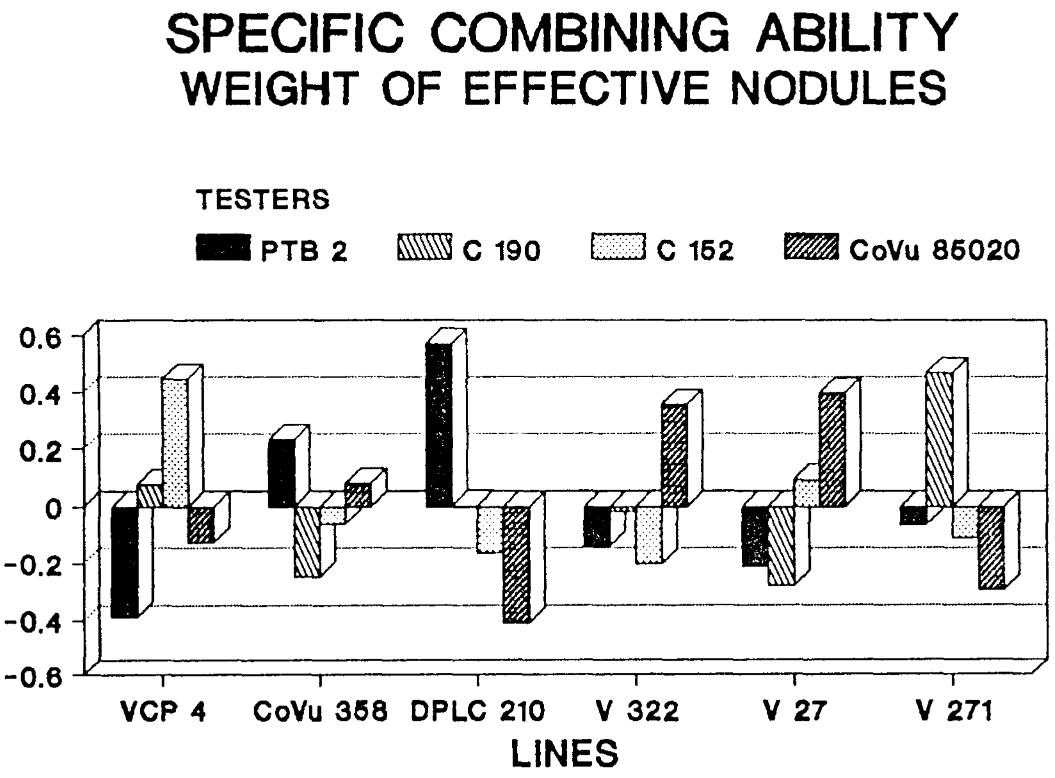
T3 - C 152

T4 - CoVu 85020


GENERAL COMBINING ABILITY
WEIGHT OF EFFECTIVE NODULES

CD 5% LINE 0.433 TESTER 0.354
SE LINE 0.128 TESTER 0.105

Fig 11



CD 5% :0.867 SE :0.256

Fig 12

Table 14. Combining ability effects of lines, testers and crosses for the character dry weight of the plant at 50 per cent flowering.

Testers		PTB 2	C 190	C 152	CoVu 85020
Lines	gca of Testers	-2.886**	2.338**	1.492*	-0.944
	gca of Lines	sca effects of combinations			
VCP 4	-0.465	-0.958	3.251*	-0.453	-1.839
CoVu 358	0.639	0.410	0.786	0.374	-1.570
DPLC 210	-1.804*	3.286*	-1.655	-2.715	1.083
V 322	1.831*	0.396	-0.834	1.195	-0.757
V 27	0.409	-2.282	-1.917	1.111	3.088*
V 271	-0.611	-0.852	0.369	0.488	-0.004

SE			CD		
gca	Lines	0.735	gca	Lines	2.489
	Testers	0.60		Testers	2.032
sca		1.471	sca		4.978

LINES

L1 - VCP 4

L2 - CoVu 358

L3 - DPLC 210

L4 - V 322

L5 - V 27

L6 - V 271

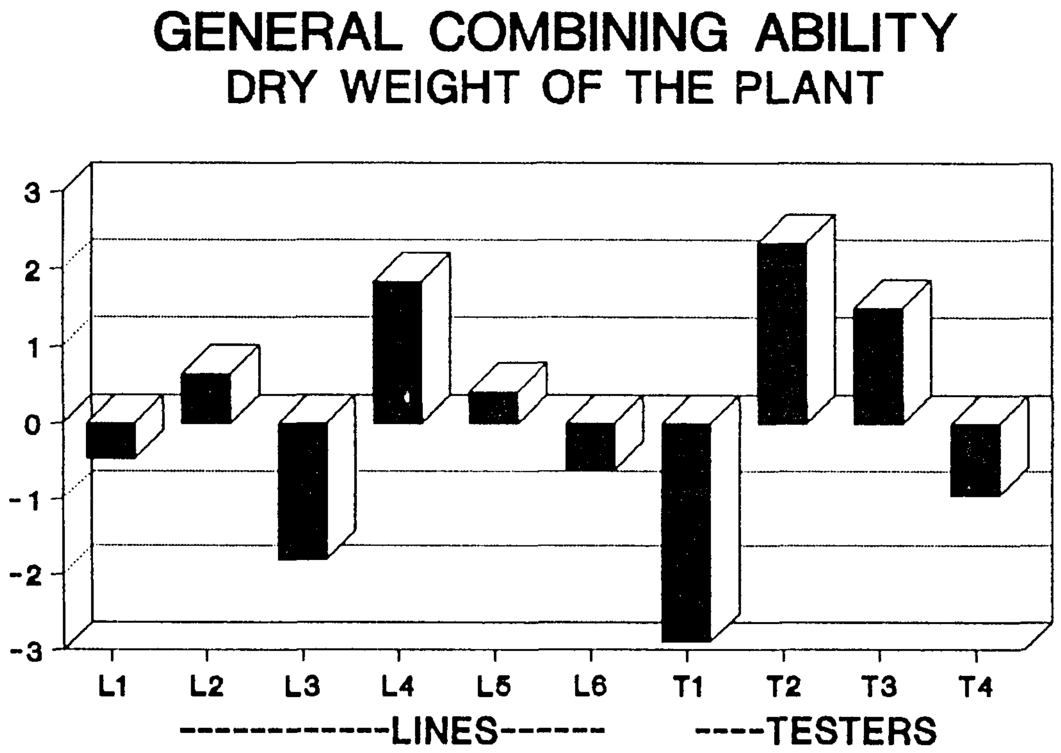
TESTERS

T1 - PTB 2

T2 - C 190

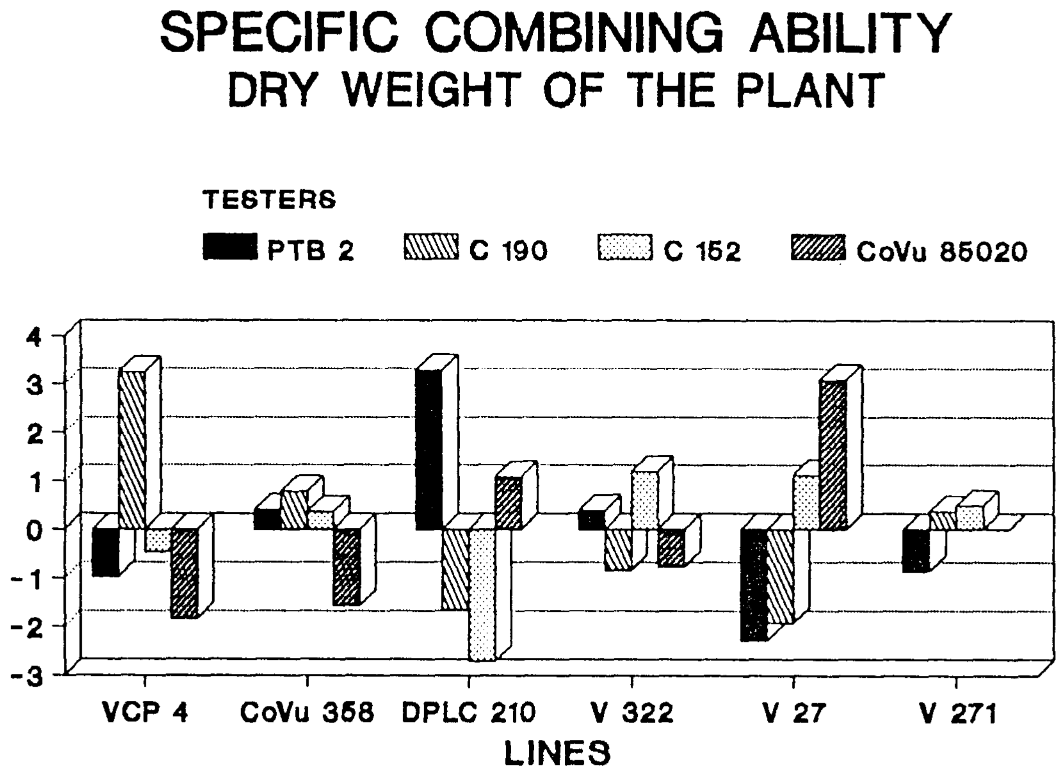
T3 - C 152

T4 - CoVu 85020



CD 5% LINE 2.489 TESTER 2.032
SE LINE 0.735 TESTER 0.600

Fig 13



CD 5% :4.978 SE :1.471

Fig 14

(32.61 per cent) followed by lines (15.8 per cent) and tester (15.59 per cent) indicating the importance of line x tester in contributing to the total variance.

4.2.1.6 Nitrogen content in plant at 50 per cent flowering

The combining ability analysis for nitrogen content in plant at 50 per cent flowering displayed that both lines and testers differed significantly in their general combining ability. Among lines, V 27 recorded significant negative gca effect of -0.05 whereas gca of other lines were non- significant. Among testers, C 152 and CoVu 85020 recorded positive significant gca of 0.055 and 0.056 respectively while PTB 2 and C 190 recorded significant negative gca of -0.042 and -0.069 respectively. The hybrid combination DPLC 210 X PTB 2 had recorded significant and positive sca of 0.112 (Table 15, Fig 15 and 16). The ratio of variance due to GCA and SCA showed a value which is less than unity (0.103) indicating the predominance of non-additive gene action. The proportional contribution of tester and line x tester was almost equal (40.896 per cent and 40.125 per cent) indicating the importance of these two in contributing to the total variance. Contribution of lines was only 15.98 per cent.

4.2.1.7 Length of pod

As regards to the length of pod, the lines and testers differed significantly with general combining ability. Among lines VCP 4 and V 322 had shown significant positive gca of 1.354 and 0.501 respectively whereas, CoVu 358, DPLC 210 and V 27 had shown significant negative gca of -0.539, -0.394 and -0.6 respectively. Among testers, C 152 and CoVu 85020 had shown positive significant gca of 1.122 and 0.848 each, but PTB 2 and

Table 15. Combining ability effects of lines, testers and crosses for the character nitrogen content in plant (per cent).

Testers		PTB 2	C 190	C 152	CoVu 85020
Lines	gca of Testers	-0.042*	-0.069**	0.055**	0.056**
	gca of Lines	sca effects of combinations			
VCP 4	0.036	-0.079	0.013	0.092	-0.026
CoVu 358	0.027	0.046	-0.049	-0.014	0.017
DPLC 210	0.025	-0.112*	0.001	-0.027	-0.086
V 322	0.005	-0.024	-0.003	-0.041	0.068
V 27	-0.050*	-0.040	-0.052	0.018	0.074
V 271	-0.042	-0.015	0.090	-0.027	-0.047

SE			CD		
gca	Lines	0.025	gca	Lines	0.071
	Testers	0.02		Testers	0.058
sca		0.05	sca		0.141

LINES

L1 - VCP 4

L2 - CoVu 358

L3 - DPLC 210

L4 - V 322

L5 - V 27

L6 - V 271

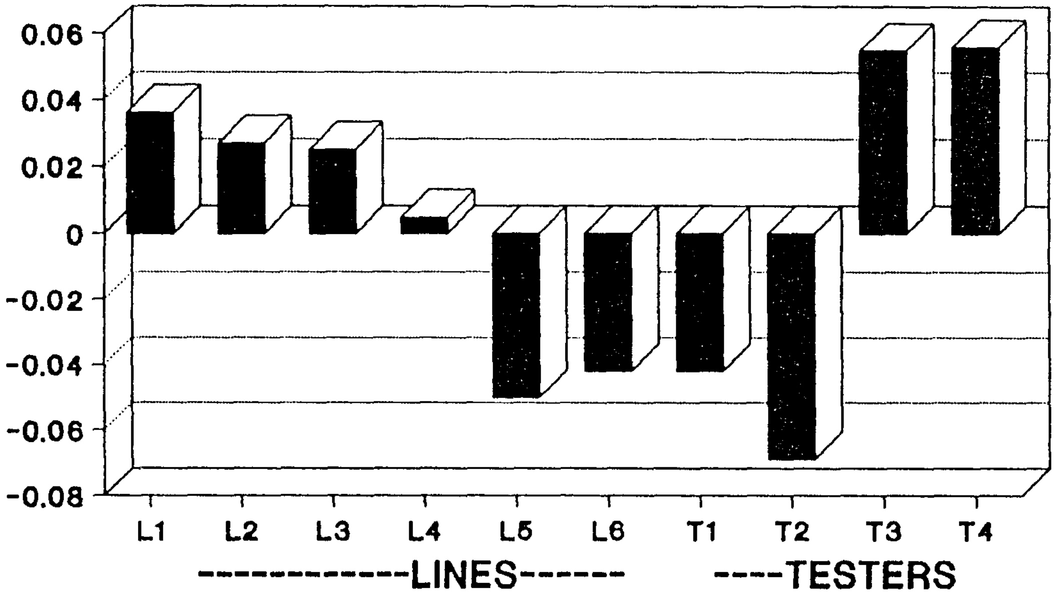
TESTERS

T1 - PTB 2

T2 - C 190

T3 - C 152

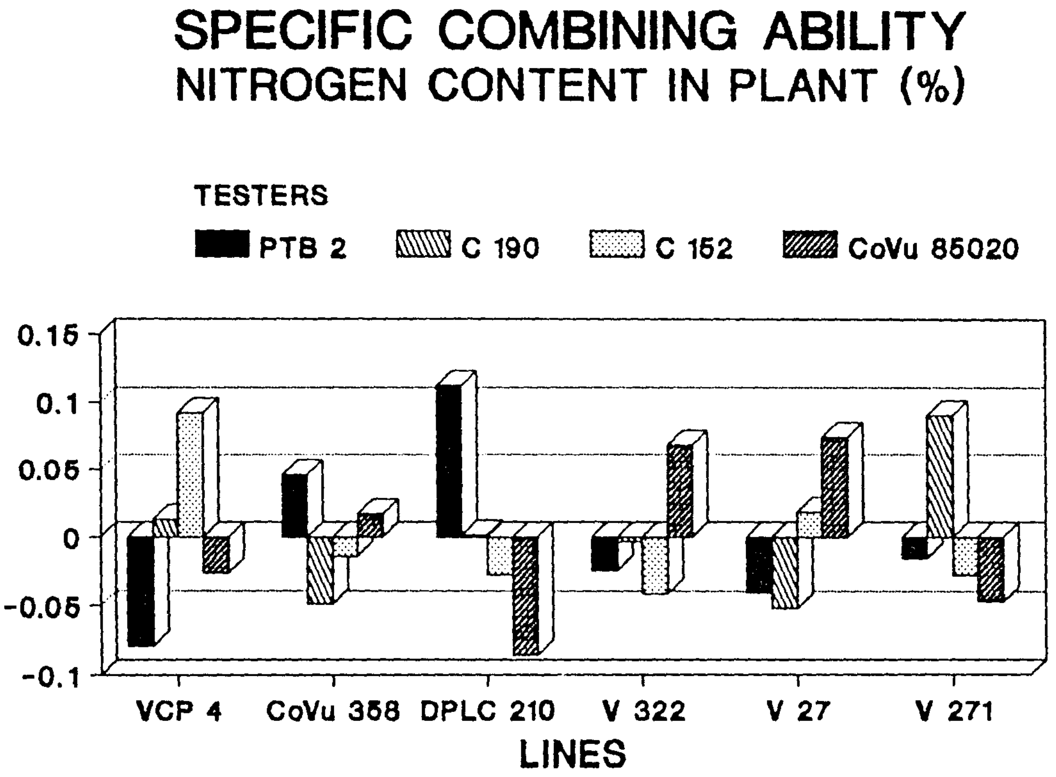
T4 - CoVu 85020



GENERAL COMBINING ABILITY
NITROGEN CONTENT IN PLANT (%)

CD 5% LINE 0.071 TESTER 0.058
SE LINE 0.025 TESTER 0.020

Fig 15



CD 5% :0.141 SE :0.050

Fig 16

C 190 had shown negative significant gca of -1.13 and -0.84 respectively. Hybrid combinations *Viz.* VCP 4 X PTB 2 and CoVu 358 X C 190 differed significantly from all other hybrids with positive significant sca of 1.001 and 1.202 respectively, whereas all other hybrids had shown insignificant sca effects (Table 16, Fig 17 and 18). The ratio of variance due to GCA and SCA showed a value which is less than unity (0.33) indicating the predominance of non additive gene action. The proportional contribution of tester to the total variance of length of pod was highest (54.688 per cent) followed by lines (27.579 per cent) and line x tester (17.733 per cent) indicating the importance of tester in contributing to the total variance.

4.2.1.8 Number of seeds per pod

The combining ability analysis for number of seeds per pod had shown that both lines and testers differed significantly in their gca. Among lines, VCP 4 had shown significant positive gca effect (0.878) whereas, V 27 had shown negative gca effect of -0.855. Among testers, C 152 and CoVu 85020 had shown positive gca effects of 1.750 and 1.523 whereas PTB 2 and C 190 had shown significant negative gca effects of -1.805 and -1.468 respectively. Only one hybrid combination CoVu 358 X C 190 had shown significant positive sca effect of 2.026 (Table 17, Fig 19 and 20). The ratio of variance due to GCA and SCA showed a value which is less than unity (0.353) indicating the predominance of non-additive gene action. The proportional contribution of tester to the total variance of number of seeds per pod was highest (72.84 per cent) followed by line x tester (18.73 per cent) and lines (8.43 per cent) indicating the

Table 16. Combining ability effects of lines, testers and crosses for the character length of pod.

Testers		PTB 2	C 190	C 152	CoVU 85020
Lines	gca of Testers	-1.13**	-0.84**	1.122**	0.848**
	gca of Lines	sca effects of combinations			
VCP 4	1.355**	1.001*	-0.419	-0.211	-0.371
CoVu 358	-0.539*	-0.732	1.202**	-0.533	0.063
DPLC 210	-0.394	-0.621	0.769	-0.009	-0.139
V 322	0.501*	0.048	-0.915	0.080	0.787
V 27	-0.60**	-0.001	-0.831	0.538	0.294
V 271	-0.322	0.304	0.194	0.136	-0.634

SE			CD		
gca	Lines	0.223	gca	Lines	0.754
	Testers	0.182		Testers	0.616
sca		0.446	sca		1.508

LINES

L1 - VCP 4

L2 - CoVu 358

L3 - DPLC 210

L4 - V 322

L5 - V 27

L6 - V 271

TESTERS

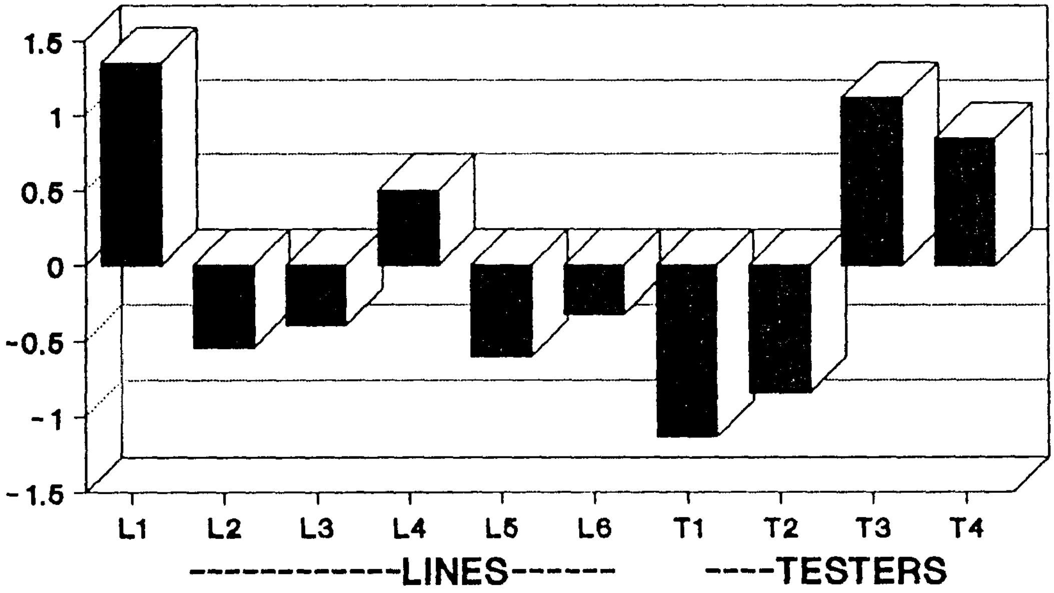
T1 - PTB 2

T2 - C 190

T3 - C 152

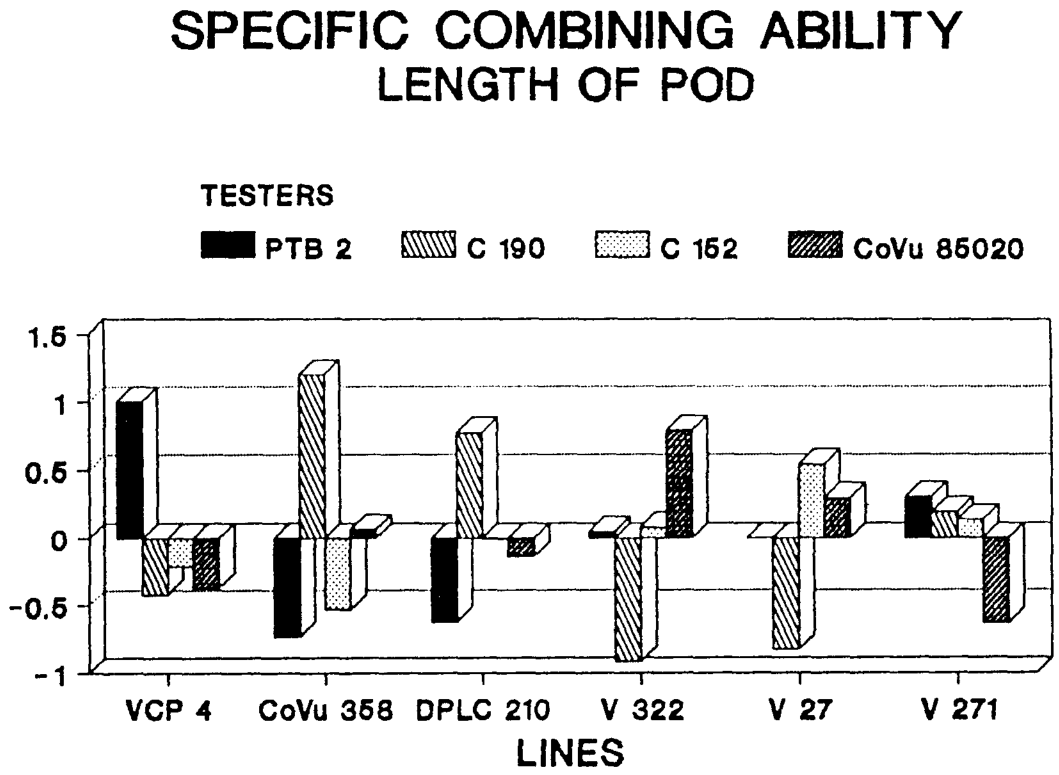
T4 - CoVu 85020

GENERAL COMBINING ABILITY
LENGTH OF POD



CD 5% LINE 0.754 TESTER 0.516
SE LINE 0.223 TESTER 0.182

Fig 17



CD 5% :1.508 SE :0.446

Fig 18

Table 17. Combining ability effects of lines, testers and crosses for the character number of seeds per pod.

Testers		PTB 2	C 190	C 152	CoVu 85020
Lines	gca of Testers	** -1.805	** -1.467	** 1.75	** 1.523
	gca of Lines	sca effects of combinations			
VCP 4	* 0.878	0.922	0.285	-0.234	-0.973
CoVu 358	0.337	-1.337	** 2.026	-0.325	-0.364
DPLC 210	0.253	-0.653	0.110	0.458	0.086
V 322	-0.249	0.216	-1.331	-0.373	1.488
V 27	* -0.855	-0.045	-1.215	0.733	0.527
V 271	-0.364	0.897	0.126	-0.259	-0.764

SE			CD		
gca	Lines	0.359	gca	Lines	1.218
	Testers	0.294		Testers	0.995
sca		0.719	sca		2.437

LINES

L1 - VCP 4

L2 - CoVu 358

L3 - DPLC 210

L4 - V 322

L5 - V 27

L6 - V 271

TESTERS

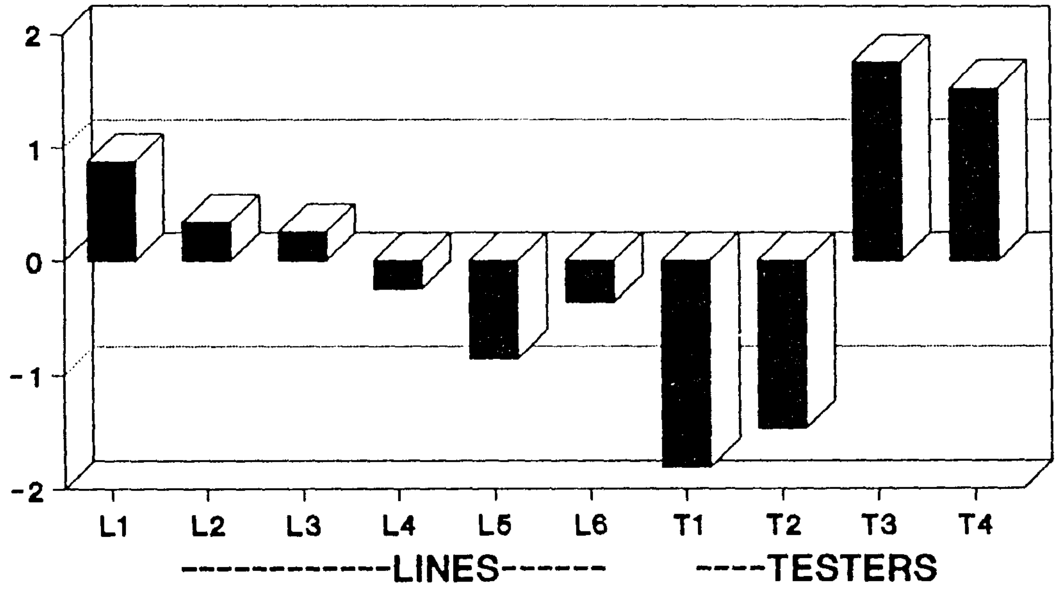
T1 - PTB 2

T2 - C 190

T3 - C 152

T4 - CoVu 85020

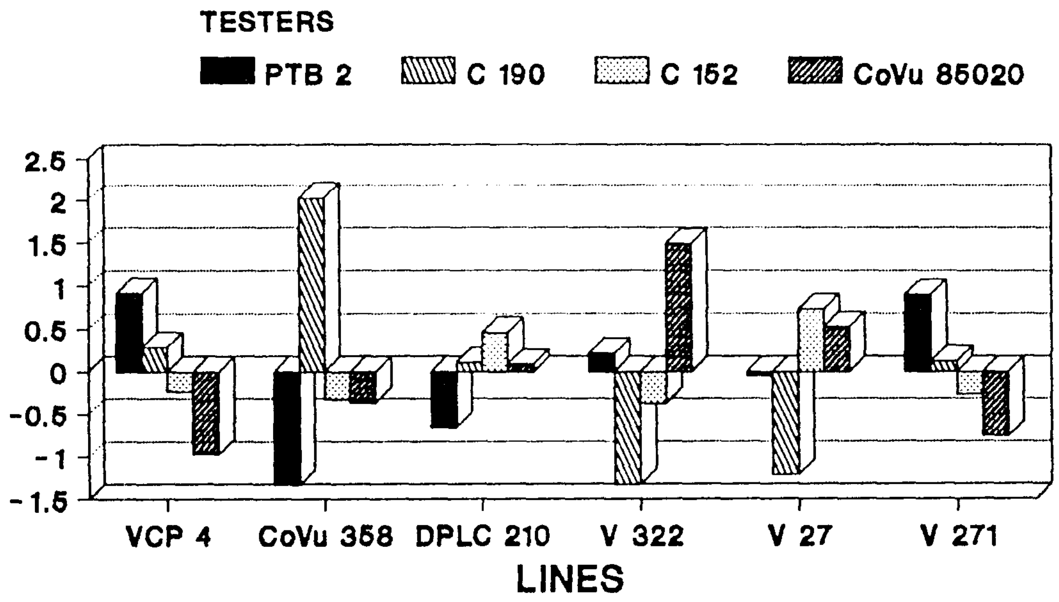
GENERAL COMBINING ABILITY
NUMBER OF SEEDS PER POD



CD 5% LINE 1.218 TESTER 0.995
SE LINE 0.360 TESTER 0.294

Fig 19

SPECIFIC COMBINING ABILITY
NUMBER OF SEEDS PER POD



CD 5% :2.437 SE :0.720

Fig 20

importance of tester in contributing to the total variance.

4.2.1.9 Number of pods per plant

The combining ability analysis for number of pods per plant displayed that both lines and testers differed significantly in their gca. Among lines, V 322 had shown significant positive gca of 9.618 whereas, gca was significant and negative for VCP 4 (-3.044) and CoVu 358 (-8.003). All testers had shown significant gca effects in which PTB 2 and C 190 had shown positive effects of 3.904 and 14.262 respectively whereas gca effects were significant and negative for C 152 (-8.521) and CoVu 85020 (-9.645). Specific combining ability effects were significant and positive for hybrid combinations viz., DPLC 210 X PTB 2 (10.186), VCP 4 X C 190 (7.759), V 322 X C 190 (5.964), V 27 X C 152 (8.270) and V 27 X CoVu 85020 (8.573) whereas significant and negative for VCP 4 X PTB 2 (-8.377), V 27 X C 190 (-11.889), DPLC 210 X C 152 (-5.881) and V 322 X CoVu 85020 (-7.922) (Table 18, Fig 21 and 22). The ratio of varience due to GCA and SCA showed a value which is less than unity (0.182) indicating the predominance of non-additive gene action. The proportional contribution of tester to the total varience of the number of pods per plant was highest (61.315 per cent) followed by line x tester (20.889 per cent) and lines (17.796 per cent).

4.2.1.10 Grain yield per plant

The combining ability analysis for yield per plant exhibited that both lines and testers differed significantly in their gca. Among lines, V 322 showed significant positive gca effect of 7.976 while CoVu 358 had shown significant negative gca effect of -5.29.

Table 18. Combining ability effects of lines, testers and crosses for the character number of pods per plant.

Testers		PTB 2	C 190	C 152	CoVu 85020
Lines	gca of Tester	3.904**	14.262**	-8.521**	-9.645**
	gca of Lines	sca effects of combinations			
VCP 4	-3.044*	-8.377**	7.759**	0.87	-0.252
CoVu 358	-8.003**	-2.78	-3.982	2.789	3.982
DPLC 210	0.692	10.186**	-0.265	-5.881*	-4.041
V 322	9.618**	4.242	5.964*	-2.284	-7.922**
V 27	-0.238	-4.954	-11.889**	8.27**	8.572**
V 271	0.976	1.690	2.413	-3.764	-0.340

SE			CD		
gca	Lines	1.250	gca	Lines	3.537
	Testers	1.021		Testers	2.888
sca		2.501	sca		7.073

LINES

L1 - VCP 4

L2 - CoVu 358

L3 - DPLC 210

L4 - V 322

L5 - V 27

L6 - V 271

TESTERS

T1 - PTB 2

T2 - C 190

T3 - C 152

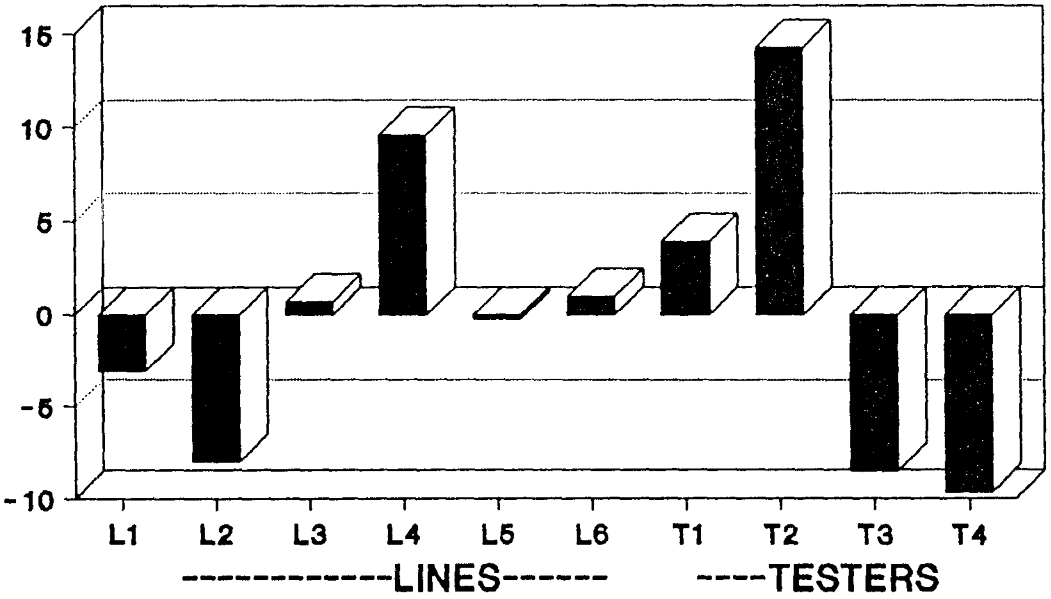
T4 - CoVu 85020

Among testers, C 190 had shown positive significant gca effect of 8.934 while C 152 and CoVu 85020 had shown significant negative gca effects of -3.73 and -6.122 respectively. The hybrid combinations such as DPLC 210 X PTB 2, V 322 X C 190, V 27 X C 152 had shown positive significant sca effects of 6.405, 7.046 and 9.148 respectively while V 27 X C 190 and V 322 X CoVu 85020 had recorded -10.198 and -5.358 respectively (Table 19, Fig 23 and 24). The ratio of variance due to GCA and SCA showed a value which is less than unity (0.135) indicating the predominance of non-additive gene action. The proportional contribution of tester to the total variance of the grain yield per plant was highest (50.054 per cent) followed by line x tester and lines in almost equal proportion of 25.928 and 24.018 respectively indicating the importance of tester in contributing to the total variance.

4.2.1.11 Hundred seed weight

The combining ability analysis for hundred seed weight displayed that both lines and testers differed significantly in their gca. Among lines VCP 4, V 322 and V 27 recorded positive significant gca effects of 0.587, 1.147 and 0.667 respectively, while CoVu 358 and DPLC 210 had shown significant negative gca effects of -1.202 and -1.244 respectively. Among testers, C 190 recorded significant and positive gca effect of 1.519 while PTB 2, C 190 and CoVu 85020 recorded negative gca effects of -0.86, -0.363 and -0.297 respectively. Positive and significant sca effects were recorded by hybrid combinations such as CoVu 358 X PTB 2 (1.127), V 322 X C 190 (1.753) VCP 4 X C 152 (0.852) and DPLC 210 X CoVu 85020 (0.59) while VCP 4 X PTB 2, CoVu

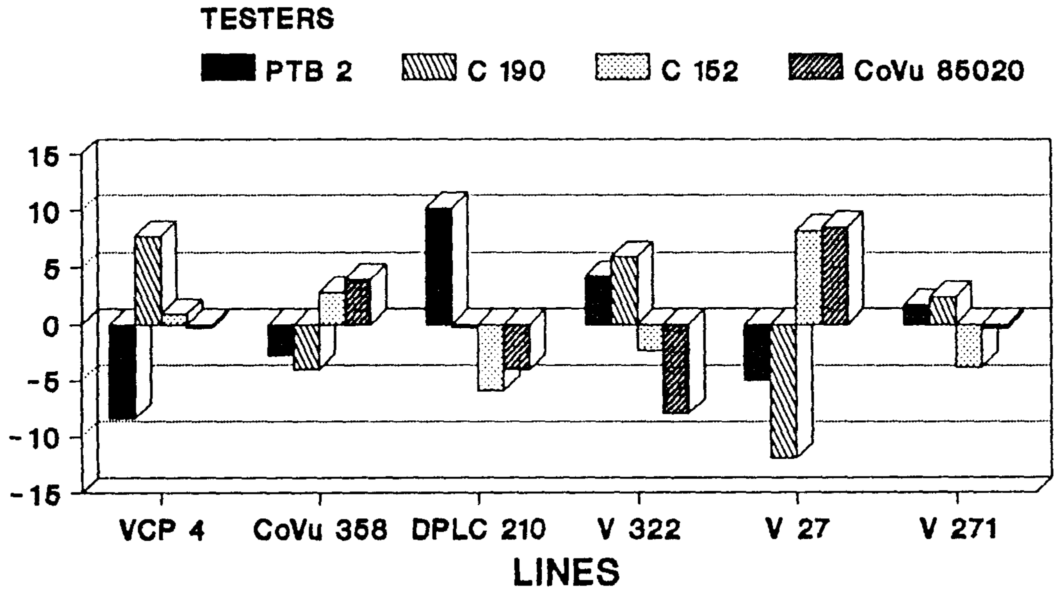
GENERAL COMBINING ABILITY
NUMBER OF PODS PER PLANT



CD 5% LINE 3.537 TESTER 2.888
SE LINE 1.250 TESTER 1.021

Fig 21

SPECIFIC COMBINING ABILITY
NUMBER OF PODS PER PLANT



CD 5% :7.073 SE :2.501

Fig 22

170796

Table 19. Combining ability effects of lines, testers and crosses for the character grain yield per plant.

Testers		PTB 2	C 190	C 152	CoVu 85020
Lines	gca of Testers	0.917	8.934**	-3.73**	-6.122**
	gca of Lines	sca effect of combinations			
VCP 4	-1.312	-3.636	1.944	1.031	0.610
CoVu 358	-5.25**	-1.209	-1.472	-0.347	3.029
DPLC 210	-1.465	6.405**	-0.544	-3.604	-2.257
V 322	7.976**	1.478	7.046**	-3.166	-5.358**
V 27	0.083	-2.704	-10.198**	9.148**	3.754
V 271	-0.033	-0.334	3.224	-3.062	0.171

SE			CD		
gca	Lines	1.018	gca	Lines	2.879
	Testers	0.831		Testers	2.351
sca		2.036	sca		5.758

THRISSUR

LINES

L1 - VCP 4

L2 - CoVu 358

L3 - DPLC 210

L4 - V 322

L5 - V 27

L6 - V 271

TESTERS

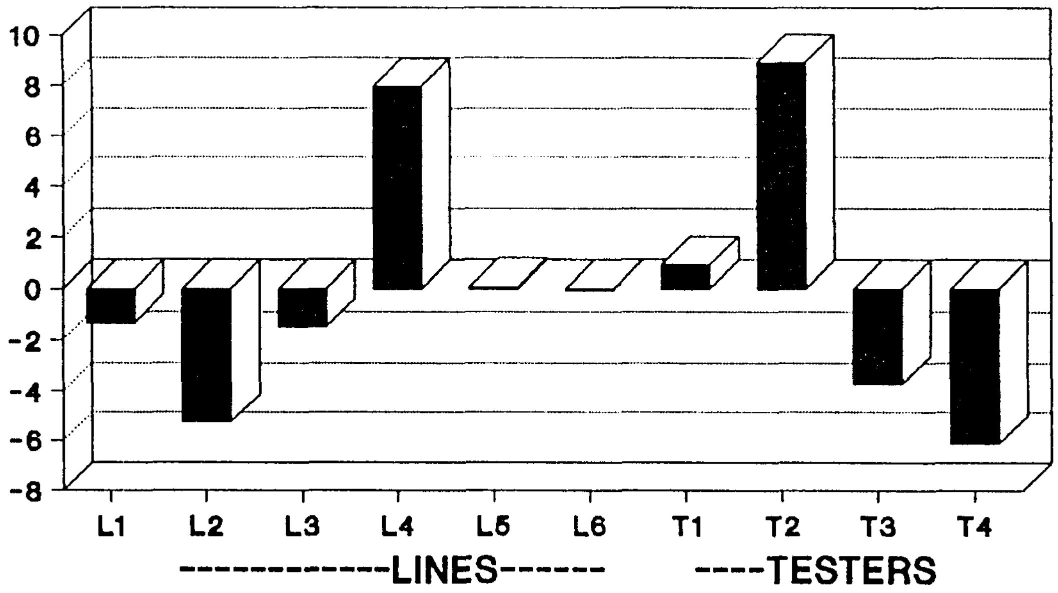
T1 - PTB 2

T2 - C 190

T3 - C 152

T4 - CoVu 85020

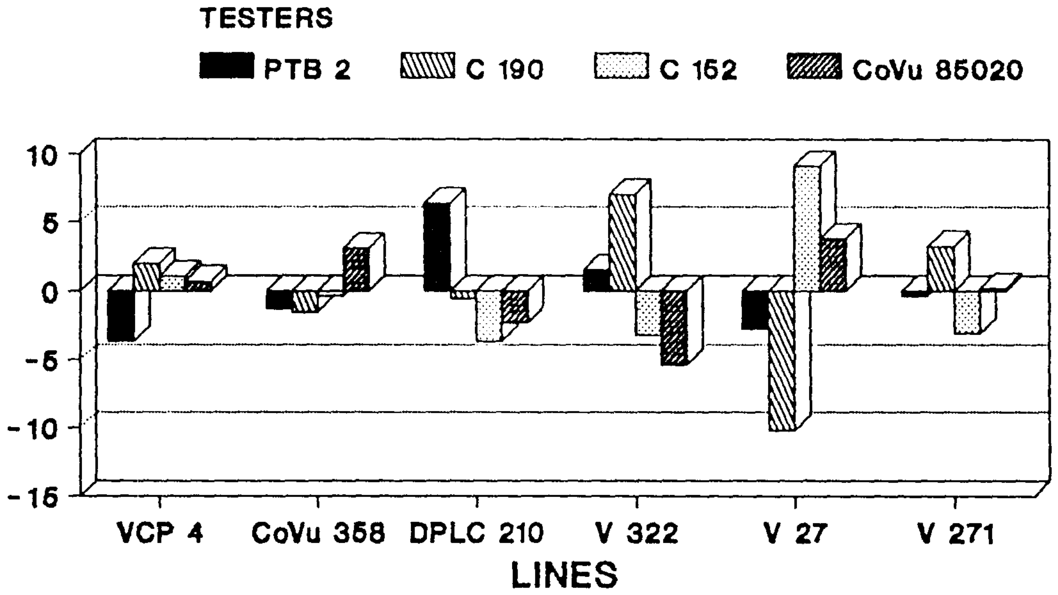
GENERAL COMBINING ABILITY
GRAIN YIELD PER PLANT



CD 5% LINE 2.879 TESTER 2.351
SE LINE 1.018 TESTER 0.831

Fig 23

SPECIFIC COMBINING ABILITY
GRAIN YIELD PER PLANT



CD 5% :5.758 SE :2.036

Fig 24

358 X C 190 and V 322 X CoVu 85020 recorded significant negative sca effects of -0.758, -1.262 and -0.841 respectively (Table 20, Fig 25 and 26).

4.2.1.12 Seed protein content (per cent)

The combining ability analysis for seed protein content (per cent) showed that both lines and testers differed significantly in their gca. Among lines, CoVu 358 and DPLC 210 had recorded significant and positive gca effects of 0.518 and 0.589 respectively while VCP 4, V 322 and V 27 had displayed significant and negative gca effects of -0.262, -0.535 and -0.32 respectively. Among testers, PTB 2 and C 152 displayed positive significant gca effects of 0.46 and 0.138 respectively while C 190 had recorded significant and negative gca effect of -0.701. Significant and positive sca effects were shown by the hybrids such as VCP 4 X PTB 2 (0.428), V 322 X PTB 2 (0.313), CoVu 358 X C 190 (0.566) and V 322 X CoVu 85020 (0.465) where as hybrids such as CoVu 358 X PTB 2, V 322 X C 190 and VCP 4 X C 152 had recorded significant negative sca effects of -0.464, -0.867 and -0.435 respectively (Table 21, Fig 27 and 28). The ratio of variance due to GCA and SCA showed a value which is less than unity (0.198) indicating the predominance of non-additive gene action (Table 23). The proportional contribution of lines and tester to the total variance of the seed protein content was almost equal (39.32 per cent and 40.31 per cent) indicating the importance of lines and testers in contributing to the total variance. The proportional contribution of line x tester to the total variance was only 20.37 per cent (Table 22, Fig 29).

Table 20. Combining ability effects of lines, testers and crosses for the character hundred seed weight.

Testers		PTB 2	C 190	C 152	CoVu 85020
Lines	gca of Testers	-0.86**	1.519**	-0.363**	-0.297**
	gca of Lines	sca effects of combinations			
VCP 4	0.587**	-0.758**	0.043	0.852**	-0.137
CoVu 358	-1.202**	1.127**	-1.262**	0.223	-0.089
DPLC 210	-1.244**	-0.107	-0.189	-0.294	0.590*
V 322	1.147**	-0.461	1.753**	-0.452	-0.841**
V 27	0.667**	0.20	-0.257	-0.285	0.33
V 271	0.046	-0.007	-0.089	-0.042	0.140

SE			CD		
gca	Lines	0.134	gca	Lines	0.379
	Testers	0.109		Testers	0.309
sca		0.268	sca		0.758

LINES

L1 - VCP 4

L2 - CoVu 358

L3 - DPLC 210

L4 - V 322

L5 - V 27

L6 - V 271

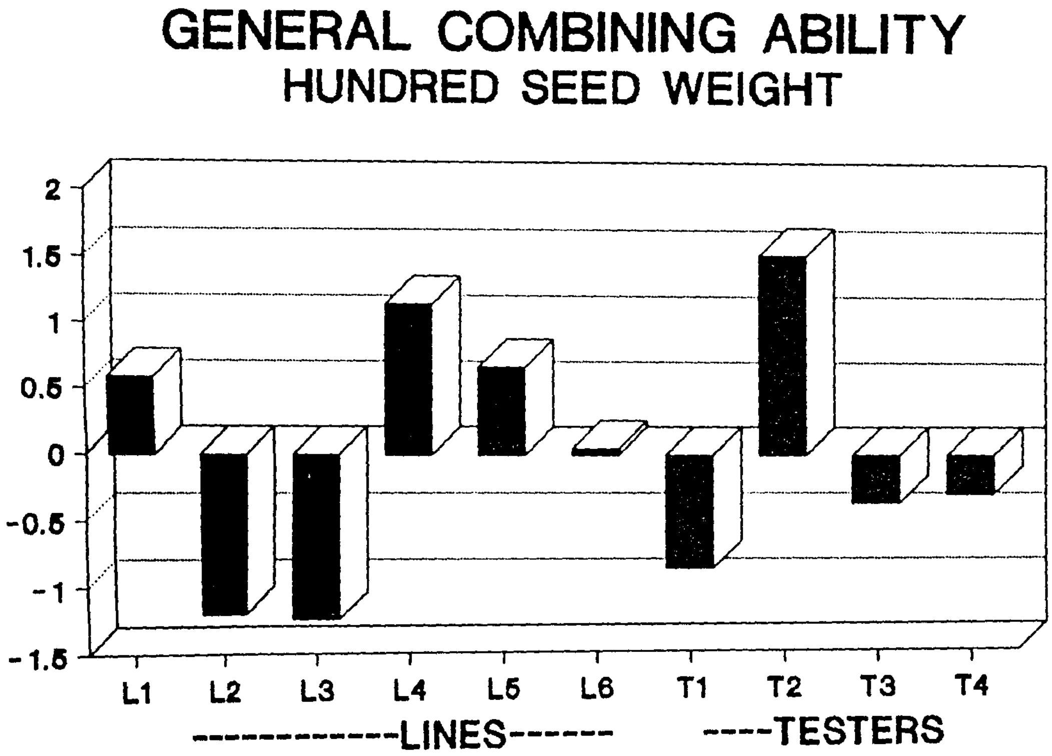
TESTERS

T1 - PTB 2

T2 - C 190

T3 - C 152

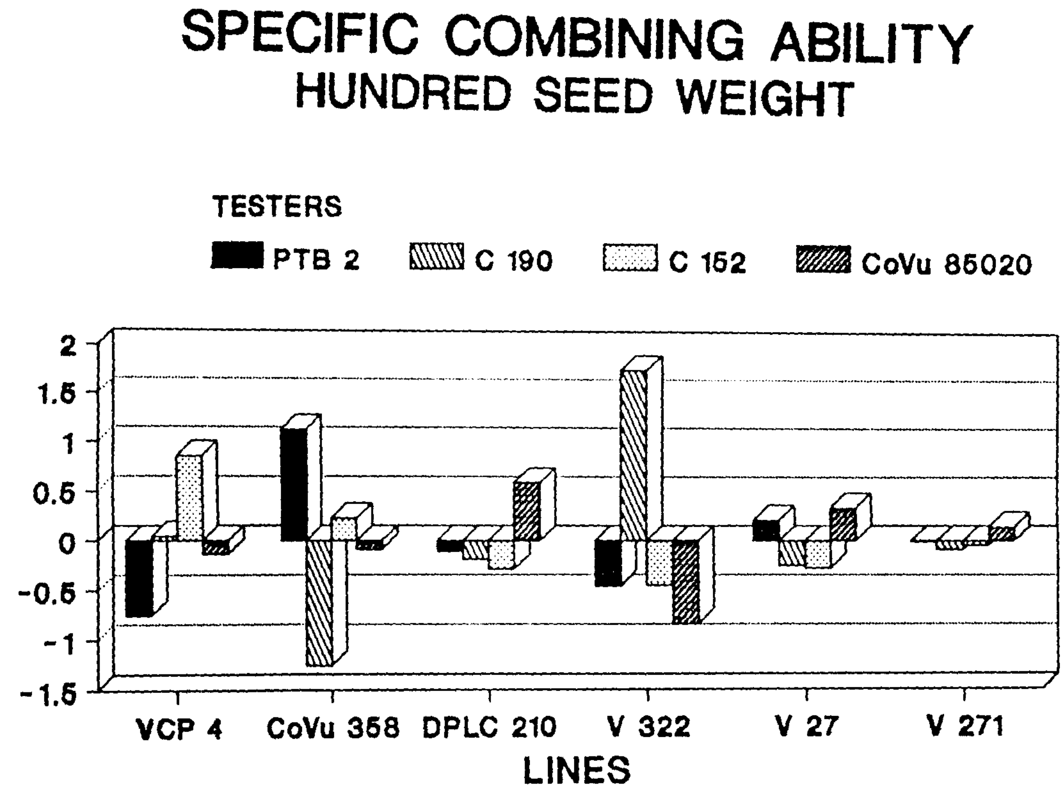
T4 - CoVu 85020



GENERAL COMBINING ABILITY
HUNDRED SEED WEIGHT

CD 5% LINE 0.379 TESTER 0.309
SE LINE 0.134 TESTER 0.109

Fig 25



CD 5% :0.758 SE :0.268

Fig 26

Table 21 Combining ability effects of lines, testers and crosses for the character seed protein content (per cent).

Testers		PTB 2	C 190	C 152	CoVu 85020
Lines	gca of Testers	0.46**	-0.701**	0.138*	0.103
	gca of Lines	sca effects of combinations			
VCP 4	-0.262**	0.428**	-0.084	-0.435**	0.091
CoVu 358	0.518**	-0.464**	0.566**	0.014	-0.116
DPLC 210	0.589**	-0.13	0.141	0.19	-0.200
V 322	-0.535**	0.313*	-0.867**	0.09	0.465**
V 27	-0.320**	-0.086	0.054	0.155	-0.123
V 271	0.008	-0.061	0.191	-0.014	-0.117

SE			CD		
gca	Lines	0.076	gca	Lines	0.215
	Testers	0.062		Testers	0.175
sca		0.152	sca		0.429

LINES

L1 - VCP 4

L2 - CoVu 358

L3 - DPLC 210

L4 - V 322

L5 - V 27

L6 - V 271

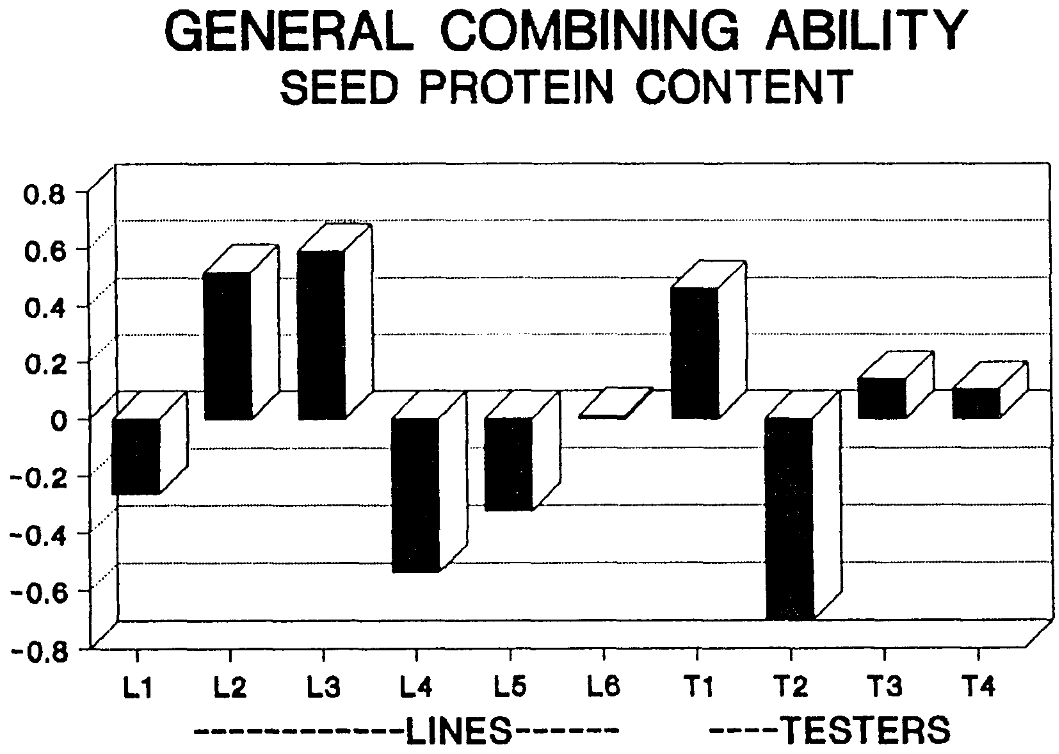
TESTERS

T1 - PTB 2

T2 - C 190

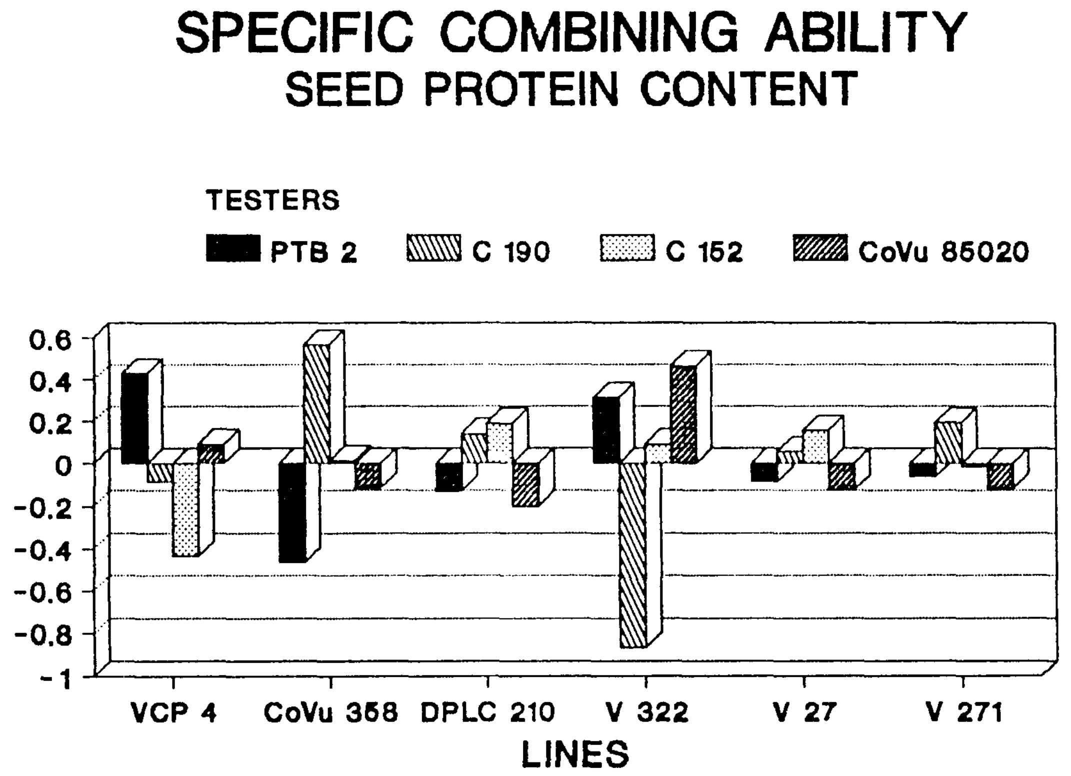
T3 - C 152

T4 - CoVu 85020



CD 5% LINE 0.215 TESTER 0.175
SE LINE 0.076 TESTER 0.062

Fig 27



CD 5% :0.429 SE :0.152

Fig 28

Table 22. Proportional contribution of line, tester and line x tester to the total variance.

Sl No	Character	Lines (%)	Tester (%)	Line x tester(%)
1.	Number of days to flower	18.357	72.696	8.947
2.	Wt. of nodules in the primary root	20.000	25.987	54.013
3.	Total weight of nodules	17.788	40.990	41.222
4.	Weight of effective nodules	17.547	41.415	41.038
5.	Dry weight of the plant	15.800	51.590	32.610
6.	Nitrogen content per plant (%)	15.980	43.896	40.125
7.	Length of pod	27.579	54.688	17.733
8.	Number of seeds per pod	8.430	72.840	18.730
9.	Number of pods per plant	17.796	61.315	20.889
10.	Hundred seed weight	41.410	39.804	18.787
11.	Seed protein content (%)	39.320	40.310	20.370
12.	Grain yield per plant	24.018	50.054	25.928

CHARACTERS

X 1 - Number of days to flower

X 2 - Weight of nodules in the primary root

X 3 - Total weight of nodules

X 4 - Weight of effective nodules

X 5 - Dry weight of the plant

X 6 - Nitrogen content in plant (%)

X 7 - Length of pod

X 8 - Number of seeds per pod

X 9 - Number of pods per plant

X 10- Hundred seed weight

X 11- Seed protein content (%)

X 12- Grain yield per plant

PROPORTIONAL CONTRIBUTION OF LINE,TESTER AND LINE X TESTER TO THE TOTAL VARIANCE

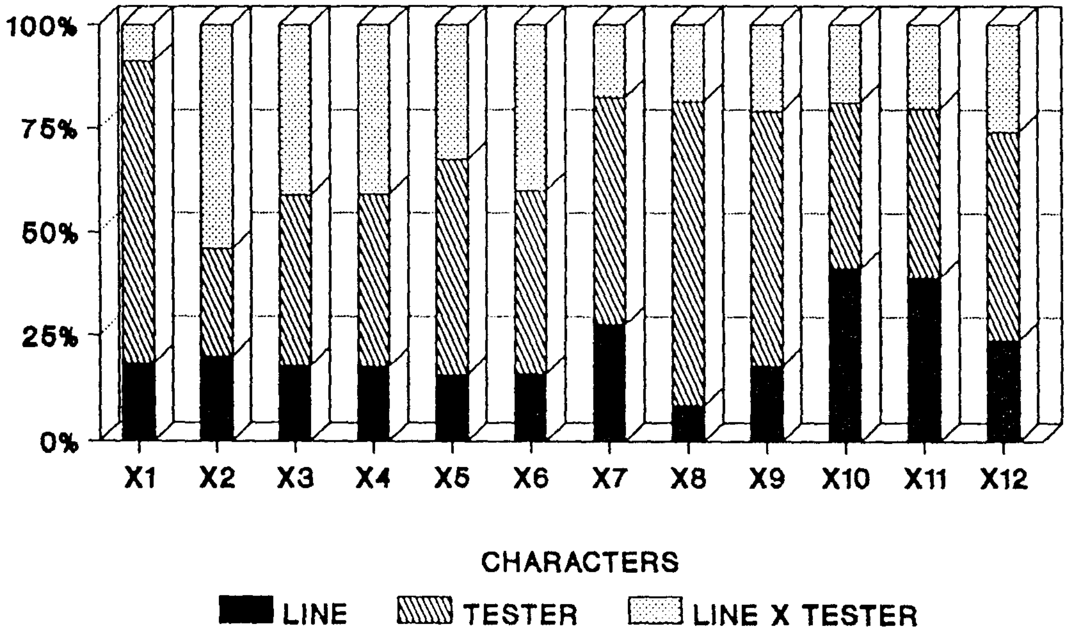


Fig 29

Table 23. Genetic components of variance of various characters.

Sl No	Character	A	D	Ratio of GCA to SCA variance
		F0	F0	
1.	Number of days to flower	2.136	2.830	0.755
2.	Wt of nodules in the primary root	0.009	0.331	0.028
3.	Total weight of nodules	0.022	0.222	0.096
4.	Weight of effective nodules	0.022	0.220	0.098
5.	Dry weight of the plant	1.294	8.456	0.153
6.	Nitrogen content per plant (%)	0.0009	0.009	0.103
7.	Length of pod	0.416	1.261	0.330
8.	Number of seeds per pod	0.834	2.369	0.353
9.	Number of pods per plant	33.631	184.45	0.182
10.	Hundred seed weight	0.461	2.180	0.211
11.	Seed protein content	0.099	0.501	0.198
12.	Grain yield per plant	12.55	92.86	0.135

A - Additive component D - Dominance component

F - Inbreeding coefficient

4.2.2 Heterosis

Heterosis is the amount by which, mean performance of F_1 exceeds mid parent (relative heterosis) or better parent (heterobeltiosis) or standard parent (standard heterosis). This phenomenon has been exploited in several agricultural crops for the increase in production.

Statistical analysis of the data relating to six lines and four testers and twentyfour hybrid combinations were presented. The extent of heterosis was calculated in percentage in comparision with the mid parent (relative heterosis), better parent (heterobeltiosis) and standard parent (standard heterosis). Variety PTB 2 was considered as the standard parent for the standard heterosis. Heterosis with respect to various characters are presented below.

4.2.2.1 Days to 50 per cent flowering

Days to flowering determines the duration of the varieties as such the character assumes importance. Short duration varieties are desirable for commercial cultivation. Hence negative relative heterosis as well as heterobeltiosis and standard heterosis are considered as important for this trait. For the estimation of heterobeltiosis, early flowering parent is considered as the better parent and for standard heterosis, PTB 2 was considered as the standard parent.

Significant negative relative heterosis was recorded by the hybrid combinations viz., VCP 4 X PTB 2, DPLC 210 X PTB 2, V 322 X PTB 2, V 27 X PTB 2, V 271 X PTB 2, VCP 4 X C 190,V 27 X C 190, V 27 X 152, VCP 4 X CoVu 85020, V 322 X

CoVu 85020, V 27 X CoVu 85020 and V 271 X CoVu 85020 in which V 322 X PTB 2 had recorded the highest negative relative heterosis of -10.92 per cent.

Significant negative heterobeltiosis was recorded by the hybrid combinations V 27 X C 152, VCP 4 X CoVu 885020, V 322 X CoVu 85020, and V 271 X CoVu 85020 in which V 27 X C 152 and V 271 X CoVu 85020 had recorded the highest negative heterobeltiosis of -8.06 per cent.

None of the hybrid combinations had recorded negative standard heterosis, while no standard heterosis was recorded by VCP 4 X PTB 2, V 27 X PTB 2 and V 271 X PTB 2 indicating that these hybrid combinations had same flowering duration as that of the standard variety PTB 2 (Table 24).

4.2.2.2 Weight of nodules in the primary root

Positive heterosis has paramount importance for the character weight of nodules in the primary root. Positive and significant relative heterosis was recorded by the hybrid combinations V 27 X CoVu 85020 (89.25 per cent) and V 322 X CoVu 85020 (68.27 per cent). Among hybrid combinations with significant negative heterosis, DPLC 210 X C 152 had recorded highest value of -48.43 per cent.

Significant and positive heterobeltiosis was displayed by only one hybrid combination V 322 X CoVu 85020 (56.52 per cent). Among the hybrid combinations with significant negative heterobeltiosis, CoVu 358 x C 190 recorded highest value of -58.14 per cent.

Positive standard heterosis was recorded by all hybrid combinations, in which

Table 24. Estimate of heterosis for number of days to 50 per cent flowering.

Lines	Testers											
	PTB 2			C 190			C 152			CoVu 85020		
	RH	HB	SH	RH	HB	SH	RH	HB	SH	RH	HB	SH
VCP 4	-10.22**	0	0	-5.93**	-0.884	9.89	-1.99	-0.798	21.77**	-5.98**	-4.84*	16.81**
CoVu 358	-0.44	10.87**	10.87**	0.85	6.27*	17.82**	-0.40	0.82	23.76**	1.99	3.42	26.73**
DPLC 210	-0.702**	4.93	4.93	5.44**	12.51**	24.74**	-2.36	-2.36	22.75**	-2.36	2.36	22.75**
V 322	-10.92**	0.98	0.98	0	7.15**	18.80**	-3.53	-3.14	21.77**	-5.88**	-5.50*	18.80**
V 27	-10.22**	0	0	-5.08*	0	10.87**	-9.16**	-8.06**	12.86**	-5.18**	-4.02	17.82**
V 271	-10.22**	0	0	-3.39	1.79	12.87**	-1.99	-0.80	21.77**	-9.16**	-8.06**	12.86**

CD	5 %	1%
RH	1.575	2.094
HB & SH	1.818	2.419

RH - Relative heterosis

HB - Heterobeltiosis

SH - Standared heterosis

CoVu 358 X PTB 2, DPLC 210 X PTB 2, V 322 X PTB 2, VCP 4 X C 190, DPLC 210 X C 190, V 271 X C 190, VCP 4 X C 152, CoVu 358 X C 152, V 322 X C 152, V 27 X C 152, VCP 4 X CoVu 85020, CoVu 358 X CoVu 85020 and V 27 X CoVu 85020 had recorded positive and significant values. Highest positive standard heterosis was recorded by VCP 4 X C 152 (429.55 per cent) (Table 25).

4.2.2.3 Total weight of nodules

Positive heterosis is important for total weight of nodules since it has got a positive correlation with other nitrogen fixation characters.

Among the hybrids tested, only two hybrid combinations,viz., V 27 X CoVu 85020 (71.93 per cent) and V 322 X CoVu 85020 (45.30 per cent) had recorded positive and significant relative heterosis whereas all other hybrid combinations had displayed only non-significant relative heterosis.

With regard to heterobeltiosis, significant positive value was displayed by the hybrid combination V 322 X CoVu 85020 (43.48 per cent) whereas VCP 4 X PTB 2 had recorded highest negative significant heterobeltiosis of -49.25 per cent.

Standard heterosis was found to be positive in all the cases wherein except V 27 X PTB 2, V 271 X PTB 2 and V 27 X C 190 had recorded significant and positive value. VCP 4 X C 152 had recorded the highest standard heterosis of 324.60 per cent followed by V 322 X CoVu 85020 (283.10 per cent) and CoVu 358 X CoVu 85020 (260 per cent) (Table 26).

Table 25. Estimate of heterosis for weight of nodules in the primary root.

Lines	Testers											
	PTB 2			C 190			C 152			CoVu 85020		
	RH	HB	SH	RH	HB	SH	RH	HB	SH	RH	HB	SH
VCP 4	-23.40	-54.94**	156.82	-22.82	-45.32**	211.36*	7.92	-6.60	429.55**	-3.67	-28.50	306.82**
CoVu 358	6.31	-36.88*	236.36**	-41.98*	-58.14**	122.73	-27.84	-35.90*	243.20**	8.09	-18.15	336.40**
DPLC 210	35.98	-17.48	286.40**	-16.46	-37.13*	195.50*	-48.43**	-51.38**	127.30	-26.64	-41.79*	172.70*
V 322	27.90	-16.01	168.20*	-23.08	-33.07	113.60	-22.08	-31.04	186.40*	68.27**	56.52*	400.00**
V 27	30.20	6.64	68.20	-5.08	-21.07	86.40	-0.59	-31.50	184.10*	89.25**	48.63	309.10**
V 271	28.46	-10.94	129.50	25.16	19.75	209.10*	-36.93	-48.78*	113.60	-1.59	-4.44	163.60*

CD	5%	1%
RH	0.616	0.820
HB & SH	0.712	0.947

RH - Relative heterosis

HB - Heterobeltiosis

SH - Standard heterosis

Table 26. Estimate of heterosis for total weight of nodules.

Lines	Testers											
	PTB 2			C 190			C 152			CoVu 85020		
	RH	HB	SB	RH	HB	SH	RH	HB	SH	RH	HB	SH
VCP 4	-17.61	-49.25**	120.00*	-13.44	-37.88**	169.20**	10.89	-2.230	324.60**	-3.56	-22.91	235.40**
CoVu 358	19.89	-25.44	207.70**	-29.01	-48.27**	113.81*	-9.90	-18.81	235.40**	6.81	-13.00	260.00**
DPLC 210	35.77	-16.05	256.90**	-18.84	-41.41**	149.20*	-15.84	-25.16	218.50**	-18.96	-34.74*	178.50**
V 322	28.10	-11.75	135.40*	2.76	-12.20	133.80*	-0.15	-9.910	198.50**	45.30*	43.48*	283.10**
V 27	47.03	26.30	76.90	-10.04	-21.63	47.70	26.51	-9.970	198.50**	71.93**	32.36	244.60**
V 271	25.99	-8.55	104.60	29.73	19.83	167.70**	-1.98	-18.01	172.30**	0.18	-6.94	141.50*

CD	5%	1%
RH	0.632	0.841
HB & SH	0.730	0.971

RH - Relative heterosis

HB - Heterobeltiosis

SH - Standard heterosis

4.2.2.4 Weight of effective nodules

Among the hybrids tested, only two hybrid combinations, viz., V 27 X CoVu 85020 (72.38 per cent) and V 322 x CoVu 85020 (46.37 per cent) had recorded positive and significant relative heterosis, whereas all other hybrid combinations had recorded non-significant relative heterosis.

Heterobeltiosis was significant and positive for the hybrid V 322 X CoVu 85020 (44.41 per cent) whereas VCP 4 X PTB 2 had recorded highest negative significant heterobeltiosis of -49.98 per cent.

Standard heterosis was found to be positive and significant in all the cases except V 27 X PTB 2, V 271 X PTB 2 and V 27 X C 190. VCP 4 X C 152 had displayed the highest standard heterosis of 362.60 per cent followed by V 322 X CoVu 85020 (287.5 per cent) and DPLC 210 X PTB 2 (260.9 per cent) (Table 27).

4.2.2.5 Dry weight of the plant at 50 per cent flowering

Positive heterosis is important for this character because of the positive association with the other nitrogen fixation characters.

In general relative heterosis was found to be positive in all cases except for the hybrid combinations VCP 4 X CoVu 85020 and CoVu 358 X CoVu 85020 with non-significant value. Among hybrid combinations with PTB 2 as tester parent, significant positive relative heterosis was recorded by DPLC 210 X PTB 2 (86.55 per cent) and V 322 X PTB 2 (46.59 per cent). With C 190 as tester parent, all hybrid

Table 27. Estimate of heterosis for weight of effective nodules.

Lines	Testers											
	PTB 2			C 190			C 152			CoVu 85020		
	RH	HB	SH	RH	HB	SH	RH	HB	SH	RH	HB	SH
VCP 4	-18.46	-49.98**	120.30*	-13.71	38.05**	171.90**	10.29	-2.89	362.60**	-4.40	-23.81	234.40**
CoVu 358	19.47	-26.03	209.40**	-29.28	-48.44**	115.60*	-9.59	-18.63	240.60**	5.90	-13.99	259.40**
DPLC 210	35.84	-16.36	260.90**	18.79	-41.33**	153.10**	-15.72	-25.12	223.40**	-18.57	-34.60*	181.25**
V 322	28.25	-12.05	135.90*	2.71	-11.97	135.90*	0.61	-9.44	203.10**	46.37*	44.41*	287.50**
V 27	47.62	25.78	78.10	-10.89	-22.52	48.40	26.94	-9.67	203.10**	72.38**	32.93	246.90**
V 271	26.56	-8.61	104.70	29.39	19.94	168.80**	-1.84	-18.01	175.00**	0.37	-6.68	143.80*

CD	5%	1%
RH	0.632	0.841
HB & SH	0.730	0.971

RH - Relative heterosis

HB - Heterobeltiosis

SH - Standard heterisis

combinations except DPLC 210 X C 190 had displayed significant positive relative heterosis. In the case of hybrid combinations with C 152 as tester, except DPLC 210 X C 152 recorded significant positive relative heterosis. When CoVu 85020 was considered as the tester parent only one hybrid combination, viz., V 27 X CoVu 85020 had shown significant positive relative heterosis of 61.7 per cent.

None of the hybrid combinations with PTB 2 as tester parent had recorded significant heterobeltiosis while three hybrid combinations, viz., VCP 4 X C 190, V 271 X C 190 and CoVu 358 X C 190 had recorded significant positive heterobeltiosis when C 190 was considered as the tester parent. Only two hybrid combinations, viz., V 27 X C 152 (91.13 per cent) and V 322 X C 152 (51.57 per cent) had shown significant positive heterobeltiosis when C 152 was considered as the tester parent. Among hybrid combinations with CoVu 85020 as tester, only one hybrid combination V 27 X CoVu 85020 had recorded significant and positive heterobeltiosis of 43.38 per cent.

Among 24 hybrid combinations tested, except VCP 4 X PTB 2, V 27 X PTB 2 and V 271 X PTB 2, all other hybrid combinations had shown significant and positive standard heterosis in which VCP 4 X C 190 had displayed highest standard heterosis of 265.3 per cent followed by V 322 X C 152 (252.52 per cent) and CoVu 358 X C 190 (235.75 per cent) (Table 28).

4.2.2.6 Dry weight of the roots

Positive and significant relative heterosis for dry weight of the root was recorded by the hybrid combinations DPLC 210 X PTB 2 (103.85 per cent), V 27 X C 152 (94.1

per cent) VCP 4 X C 190 (79.79 per cent) and V 322 X C 152 (64.66 per cent) while none of the hybrid combinations had displayed significant negative relative heterosis.

Two hybrid combinations, viz., VCP 4 X C 190 and V 27 X C 152 had recorded significant and positive heterobeltiosis of 54.815 and 88.46 per cent respectively while V 271 X CoVu 85020 had recorded significant and negative heterobeltiosis of -56.71 per cent.

Significant and positive standard heterosis was recorded by the hybrid combination, viz., V 271 X C 190 (439.67 per cent), VCP 4 X C 190 (260 per cent), DPLC 210 X PTB 2 (207.27 per cent), CoVu 358 X C 190 (176.36 per cent), V 27 X CoVu 85020 (172.73 per cent), V 27 X C 190 (141.82 per cent), V 322 X PTB 2 (134.55 per cent), V 27 X PTB 2 (129.09 per cent), V 322 X CoVu 85020 (121.82 per cent) and VCP 4 X CoVu 85020 (121.82 per cent). None of the hybrid combinations had recorded negative standard heterosis (Table 29).

4.2.2.7 Nitrogen content in plant at 50 per cent flowering

Relative heterosis was found to be positive and significant for hybrid combinations, viz., V 322 X CoVu 85020 (6.98 per cent) and V 27 X CoVu 85020 (8.08 per cent).

Positive and significant heterobeltiosis was registered by the hybrid combination V 322 X CoVu 85020 (6.62 per cent) while the crosses VCP 4 X C 190, CoVu 358 X C 190, DPLC 210 X C 190, DPLC 210 X C 152 and DPLC 210 X CoVu 85020 had displayed significant negative heterobeltiosis.

Table 29. Estimate of heterosis for dry weight of the root.

Lines	Testers											
	PTB 2			C 190			C 152			CoVu 85020		
	RH	HB	SH	RH	HB	SH	RH	HB	SH	RH	HB	SH
VCP 4	-4.00	-31.46	60.00	79.79**	54.81*	260.00**	7.51	-12.37	103.64	-15.16	-23.79	121.82*
CoVu 358	9.22	-22.52	83.64	36.45	16.45	176.36**	10.30	-10.83	110.91	-25.55	-32.48	96.36
DPLC 210	103.06**	54.43	207.27**	-4.01	-11.02	70.91	17.25	3.11	98.10	-19.31	-32.96	96.36
V 322	61.73	23.07	134.55*	16.21	9.29	107.27	64.66*	45.64	178.10**	-8.07	-24.02	121.82*
V 27	79.12	46.02	129.09*	50.01	44.51	141.02*	94.10**	88.46*	192.73**	22.71	-5.94	172.73**
V 271	47.10	21.23	85.45	50.74	44.26	439.67**	15.05	13.24	74.55	-43.26	-56.71*	25.45

CD	5%	1%
RH	0.566	0.752
HB & SH	0.653	0.869

RH - Relative heterosis

HB - Heterobeltiosis

SH - Standard heterosis

All the 24 hybrid combinations had recorded positive standard heterosis with PTB 2 as the standard parent. Among them, V 27 X PTB 2, V 271 X PTB 2, CoVu 358 X C 190, V 27 X C 190 and V 271 X C 190 had recorded non-significant positive standard heterosis. Highest positive standard heterosis was recorded by the hybrid combination VCP 4 X C 152 (19.51 per cent) followed by V 322 X CoVu 85020 (17.07 per cent), DPLC 210 X PTB 2 (15.61 per cent) and CoVu 358 X CoVu 85020 (15.61 per cent) (Table 30).

4.2.2.8 Length of pod

Among the twentyfour hybrid combinations tested, none of them had recorded significant and positive relative heterosis for the character length of pod while V 27 X C 190 (-17.19 per cent), CoVu 358 X PTB 2 (-12.95 per cent), V 322 X C 190 (-10.98 per cent), V 27 X PTB 2 (-10.73 per cent), DPCL 210 X PTB 2 (-10.70 per cent) and VCP 4 X C 190 (-8.55 per cent) had recorded significant and negative relative heterosis.

Likewise, none of the hybrid combinations had displayed significant positive heterobeltiosis while significant negative heterobeltiosis was recorded by 12 hybrid combinations. Among them V 27 X C 190 had displayed highest value of -22.99 per cent followed by VCP 4 X C 190 (-20.32 per cent) and CoVu 358 X PTB 2 (-19.54 per cent).

All the hybrid combinations with C 152 and CoVu 85020 as testers recorded significant positive standard heterosis with PTB 2 as the standard parent. When PTB 2 was considered as the tester parent, only one hybrid combination VCP 4 X PTB 2 had recorded significant positive standard heterosis of 23.9 per cent while three hybrid

Table 30. Estimate of heterosis for nitrogen content in plant (per cent).

Lines	Testers											
	PTB 2			C 190			C 152			CoVu 85020		
	RH	HB	SH	RH	HB	SH	RH	HB	SH	RH	HB	SH
VCP 4	-3.06	-11.24	6.83*	-2.17	-8.64**	9.76**	2.19	-0.38	19.51**	-0.54	-5.12	14.15**
CoVu 358	2.17	-5.43	12.20**	-4.61	-10.41**	6.34	-2.03	-3.93	14.15**	1.54	-2.57	15.61**
DPLC 210	5.09	-3.64	15.61**	-2.98	-9.26**	8.78*	-3.09	-5.39*	13.17**	-3.41	-7.72**	10.73**
V 322	2.82	-1.83	7.80*	0.43	-2.11	7.32*	-0.24	-2.11	11.71**	6.98*	6.62**	17.07**
V 27	2.78	1.17	4.39	-1.20	-1.74	2.44	3.01	-1.94	11.71**	8.08**	5.12	14.63**
V 271	2.51	-0.82	5.85	3.97	2.73	9.76	-0.36	-3.53	10.24**	1.12	0.07	9.27**

CD	5%	1%
RH	0.118	0.157
HB & SH	0.137	0.182

RH - Relative heterosis

HB - Heterobeltiosis

SH - Standard heterosis

combinations, viz., VCP 4 X C 190 (14.84 per cent), CoVu 358 X C 190 (12.59 per cent), DPLC 210 X C 190 (10.34 per cent) had shown significant positive standard heterosis when C 190 was taken as the tester parent. Highest standard heterosis was recorded by the hybrid combination VCP 4 X C 152 (32.08 per cent) followed by V 322 X CoVu 85020 (31.19 per cent) and VCP 4 X CoVu 85020 (28.71 per cent) (Table 31).

4.2.2.9 Number of seeds per pod

None of the hybrid combinations had recorded positive and significant relative heterosis for number of seeds per pod, while CoVu-358 X PTB-2 (-25.31 per cent) V 27 X C 190 (-21.82 per cent), DPLC-210 X PTB-2 (-20.18 per cent) and V-322 X C-190 (-18.11 per cent) had displayed significant negative relative heterosis.

Significant positive heterobeltiosis was not recorded by any of the hybrid combinations while all the hybrid combinations with PTB 2 and C 190 as tester had recorded significant negative heterobeltiosis except the crosses CoVu 358 X C 190.

Standard heterosis was found to be positive for hybrid combinations such as V 322 X CoVu 85020 (26.66 per cent), DPLC 210 X C 152 (24.37 per cent), VCP 4 X C 152 (23.932 per cent), DPLC 210 X CoVu 85020 (19.81 per cent), CoVu 358 X C 152 (19.04 per cent), V 27 X C 152 (18.05 per cent), V 322 X C 190 (17.59 per cent) and CoVu 358 X CoVu 85020 (17.06 per cent), while V 27 X C 190 had recorded negative standard heterosis of -21.33 per cent (Table 32).

4.2.2.10 Number of pods per plant

Relative heterosis was found to be positive and significant for all hybrid

Table 31. Estimate of heterosis for length of pod.

Lines	Testers											
	PTB 2			C 190			C 152			CoVu 85020		
	RH	HB	SH	RH	HB	SH	RB	HB	SH	RH	HB	SH
VCP 4	1.51	-14.03**	23.90**	-8.55**	-20.32**	14.84**	0.23	-8.24*	32.08**	-1.94	-10.65**	28.71**
CoVu 358	-12.95**	-19.54**	-5.21	0.19	-4.40	12.59*	-3.65	-4.42	14.43**	-0.95	-1.24	17.00**
DPLC 210	-10.70**	-17.17**	-3.13	-1.47	-5.65	10.34*	1.25	0.07	19.81**	-0.97	-1.62	16.60**
V 322	-3.46	-13.62**	9.38	-10.98**	-17.88**	4.01	3.67	0.84	27.67**	7.02	3.59	31.19**
V 27	-10.73**	-19.51**	0.16	-17.19**	-22.99**	-4.17	0.37	-1.53	22.53**	-2.53	-4.85	18.36**
V-271	-5.54	-14.07**	4.81	-7.18	-12.88**	6.26	0.56	-0.37	21.57**	-5.88	-7.23	13.15*

CD	5%	1%
RH	1.095	1.265
HB & SH	1.265	1.682

RH - Relative heterosis

HB - Heterobeltiosis

SH - Standard heterosis

Table 32. Estimate of heterosis for number of seeds per pod.

Lines	Testers											
	PTB 2			C 190			C 152			CoVu 85020		
	RH	HB	SH	RH	HB	SH	RH	HB	SH	RH	HB	SH
VCP 4	-5.56	-14.58*	5.64	-4.23	-16.43*	3.35	1.88	0.21	23.92**	-4.47	-5.75	16.53
CoVu 358	-25.31**	-32.93**	15.69*	3.26	-10.51	12.49	-2.90	-5.25	19.04*	-4.85	-6.87	17.06*
DPLC 210	-20.18**	-27.54**	11.12	-9.46	-20.70**	-2.74	2.73	1.45	24.37**	-1.36	-2.28	19.81*
V 322	-12.38	-16.05*	-8.38	-18.11**	-24.49**	17.59*	-0.11	-4.46	14.24	10.40	5.27	26.66**
V 27	-18.69**	-22.09**	14.93	-21.82**	-27.91**	-21.33**	3.22	-1.27	18.05*	0	-4.64	14.78
V 271	-11.27	-17.47*	-4.04	-11.08	-28.31**	-7.31	-3.12	-4.46	14.24	-8.15	-9.70	8.68

CD	5%	1%
RH	1.761	2.342
HB & SH	2.033	2.704

RH - Relative heterosis

HB - Heterobeltiosis

SH - Standard heterosis

combinations except VCP 4 X PTB 2 and CoVu 358 X PTB 2 when PTB 2 and C 190 was considered as the tester parents. When C-152 was considered as the tester parent the combinations, viz., V 322 X C 152 and V 27 X C 152 were found to be positive and significant. Among hybrid combinations with positive relative heterosis, V 322 X C 190 had recorded highest positive relative heterosis of 356.7 per cent followed by V 322 X PTB 2 (308.03 per cent) and VCP 4 X C 190 (272.39 per cent).

Heterobeltiosis was found to be positive and significant for all hybrid combinations except VCP 4 X PTB 2 and CoVu 358 X PTB 2 when PTB 2 and C 190 was considered as the tester parents. When C 152 was considered as the tester parent, the crosses V 322 X C 152 and V 27 X C 152 were found to be positive and significant. With CoVu 85020 as tester parent, the cross V 27 X CoVu 85020 was found to be positive and significant. Among hybrid combinations with positive heterobeltiosis, V 322 X C 190 had displayed highest heterobeliosis of 260.29 per cent followed by V 322 X PTB 2 (244.34 per cent) and VCP 4 X C 190 (182.68 per cent).

Positive and significant standard heterosis was recorded by all the hybrid combinations except VCP 4 X PTB 2 and CoVu 358 X PTB 2 when PTB 2 and C 190 were considered as the tester parents. When C 152 was taken as the tester parent, the crosses, viz., V 322 X C 152 and V 27 X C 152 were found to be positive and significant. With CoVu 85020 as tester parent, V 27 X CoVu 85020 was found to be positive and significant. Among hybrid combinations with positive standard heterosis, V 322 X C 190 had recorded highest positive standard heterosis of 352.78 per cent followed by VCP 4 X C 190 (255.3 per cent) and V 322 X PTB 2 (244.43 per cent) (Table 33).

4.2.2.11 Grain yield per plant

For the character grain yield per plant, relative heterosis was found to be positive and significant for all hybrid combinations except VCP 4 X PTB 2 and CoVu 358 X PTB 2 when PTB 2 and C 190 were considered as the tester parents. When C 152 was taken as the tester parent, V 322 X C 152 and V 27 X C 152 were recorded positive and significant relative heterosis. With CoVu 85020 as tester parent, none of the hybrid combinations were found to be positive and significant. Among hybrid combinations with positive relative heterosis, V 322 X C 190 had recorded highest relative heterosis of 453.04 per cent followed by V 322 X PTB 2 (326.82 per cent) and V 27 X C 152 (244.36 per cent).

Heterobeltiosis was found to be positive and significant for all hybrid combinations except VCP 4 X PTB 2, CoVu 358 X PTB 2 and V 27 X C 190 when PTB 2 and C 190 were considered as the tester parents. When C 152 was taken as the tester parent, the crosses V 322 X C 152 and V 27 X C 152 were found to be positive and significant. Among hybrid combinations with positive heterobeltiosis, V 322 X C 190 had recorded highest heterobeltiosis of 369.17 per cent followed by V 322 X PTB 2 (321.63 per cent) and V 271 X C 190 (222.76 per cent).

Positive and significant standard heterosis was displayed by all the hybrid combinations except VCP 4 X PTB 2 and CoVu 358 X PTB 2 when PTB 2 and C 190 were considered as the tester parents. When C 152 was considered as the tester, V 322

Table 33. Estimate of heterosis for number of pods per plant.

Lines	Testers											
	PTB 2			C 190			C 152			CoVu 85020		
	RH	HB	SH	RH	HB	SH	RH	HB	SH	RH	HB	SH
VCP 4	42.24	17.43	17.41	272.39**	182.68**	255.30**	37.19	36.53	-11.04	-9.02	-20.08	-31.24
CoVu 358	43.40	23.08	23.87	108.12**	63.40*	105.39**	-9.48	-14.01	-38.33	-21.05	-27.64	-37.70
DPLC 210	256.34**	217.57**	217.59**	210.67**	152.05**	216.79**	-13.34	-20.96	-38.15	-16.86	-20.62	-31.69
V 322	308.03**	244.34**	244.43**	365.70**	260.29**	352.78**	161.48**	153.33**	74.24**	46.71	32.01	13.55
V 27	87.10**	73.34*	73.34*	93.47**	62.39*	104.13**	141.04**	111.65**	80.52**	102.14**	101.29**	73.16*
V 271	166.21**	143.87**	143.90**	228.72**	173.20**	243.36**	12.91	0.21	-16.61	22.96	20.95	51.31

CD	5%	1%
RH	6.125	8.147
HB & SH	7.073	9.407

RH - Relative heterosis

HB - Heterobeltiosis

SH - Standard heterosis

X C 152 and V 27 X C 152 were found to be positive and significant. With CoVu 85020 as tester parent, V 27 X CoVu85020 was found to be positive and significant. Among hybrid combinations with positive standard heterosis, V 322 X C 190 had recorded highest standard heterosis of 557.02 per cent followed by V 271 X C 190 (351.99 per cent) and V 322 X PTB 2 (321.66 per cent) (Table 34).

4.2.2.12 Hundred seed weight

Hundred seed weight directly influence the grain yield and hence positive heterosis is important in this character. Relative heterosis for this character was found to be significant and positive for the hybrid combination V 322 X C 190 (31.54 per cent), V 27 X CoVu 85020 (12.28 per cent) V 27 X C 190 (11.36 per cent), CoVu 358 X PTB 2 (10.96 per cent), V 27 X C 190 (10.54 per cent), DPLC 210 X CoVu 85020 (8.83 per cent), V 27 X PTB 2 (8.23 per cent) and V 271 X CoVu 85020 (7.81 per cent) while VCP 4 X PTB 2 had recorded significant negative relative heterosis of -9.92 per cent.

Heterobeltiosis was found to be positive and significant for the hybrid combinations like V 322 X C 190 (31.52 per cent), V 27 X C 190 (10.40 per cent), CoVu 358 X PTB 2 (8.27 per cent) and V 271 X C 190 (6.54 per cent), while the same was significant and negative for VCP 4 X PTB 2 (-24.98 per cent), VCP 4 X CoVu 85020 (-16.13 per cent), CoVu 358 X C 190 (-14.02), VCP 4 X C 152 (-9.22 per cent), V 322 X PTB 2 (-7.5 per cent), and V 271 X PTB 2 (-6.2 per cent).

Standard heterosis was found to be positive and significant for all hybrid combinations except DPLC 210 X PTB 2, DPLC 210 X C 152 and CoVu 358 X CoVu

Table 34. Estimate of heterosis for grain yield per plant.

Lines	Testers											
	PTB 2			C 190			C 152			CoVu 85020		
	RH	HB	SH	RH	HB	SH	RH	HB	SH	RH	HB	SH
VCP 4	57.24	44.80	71.92	215.00**	191.09**	307.63**	76.34*	45.09	72.27	1.38	-1.83	24.44
CoVu 358	43.66	41.57	45.75	130.57**	100.08**	180.24**	-10.72	-22.12	-19.76	-15.35	-23.30	-2.77
DPLC 210	223.25**	205.32**	243.33**	186.63**	158.41**	261.87**	-5.51	-20.54	-10.57	-40.44	-43.81	-28.77
V 322	326.82**	321.63**	321.66**	453.04**	369.17**	557.02**	199.09**	167.09**	160.60*	61.44	42.83	81.11
V 27	93.76*	78.18	112.31*	70.82*	58.08	121.32*	244.36**	182.99**	237.26**	64.46	59.49	102.25*
V 271	119.63**	94.98*	151.47**	236.09**	222.76**	351.99**	20.21	-4.15	23.57	8.03	7.14	38.13

CD	5%	1%
RH	4.986	6.631
HB & SH	5.767	7.657

RH - Relative heterosis

HB - Heterobeltiosis

SH - Standard heterosis

85020 when PTB 2 was taken as the standard variety. Highest standard heterosis was recorded by the hybrid combination V 322 X C 190 (73.93 per cent) followed by VCP 4 X C 190 (48.43 per cent) and V 27 X C 190 (45.96 per cent) (Table 35).

4.2.2.13 Seed protein content

Increase in the seed protein content will determine the quality of the cowpea grain. Hence positive heterosis is very important for this character. Relative heterosis estimate for this character was found to be positive and significant for VCP 4 X PTB 2 (2.33 per cent) while negative and significant for V 322 X C 190 (-6.41 per cent), V 27 X C 190 (-2.37 per cent), V 27 X CoVu 85020 (-1.91 per cent), V 271 X CoVu 85020 (-1.65 per cent), V 271 X C 190 (-1.63 per cent) , V 322 X C 152 (-1.53 per cent) and CoVu 358 X PTB 2 (-1.46 per cent).

None of the hybrid combinations had recorded positive and significant heterobeltiosis. Among hybrids with negative heterobeltiosis, V 322 X C 190 had recorded maximum negative value of -6.57 per cent followed by VCP 4 X C 152 (-4.13 per cent) and V 27 X CoVu 85020 (-3.74 per cent).

Standard heterosis was also found to be negative in all the cases in which V 322 X C 190 had recorded highest value of -11.21 per cent followed by VCP 4 X C 190 (-7.58 per cent) and V 27 X C 190 (-7.3 per cent) (Table 36).

It was seen that for many of the yield attributing characters, the crosses, V 322 X C 190 had recorded very high positive heterosis. On the contrary, this hybrid combination had exhibited very high negative heterosis value for seed protein content.

Table 35. Estimate of heterosis for hundred seed weight.

Lines	Testers											
	PTB 2			C 190			C 152			CoVu 85020		
	RH	HB	SH	RH	HB	SH	RH	HB	SH	RH	HB	SH
VCP 4	-9.92**	-24.98**	12.70**	5.11	-1.20	48.43**	5.02	-9.22**	36.48**	-1.49	-16.13**	25.96**
CoVu 358	10.96**	8.27*	13.82**	-4.20	-14.02**	13.71**	1.80	-0.24	9.21*	1.05	0.82	6.40
DPLC 210	-2.12	-3.63	-0.56	6.41*	-5.27	25.28**	-3.21	-5.99	2.92	8.83*	7.59	13.60**
V 322	5.34	-7.50*	22.36**	31.54**	31.52**	73.93**	5.92	-3.20	27.98**	4.60	-5.95	24.38**
V 27	8.23*	-4.24	24.38**	11.36**	18.48**	45.96**	4.01	-4.18	24.49**	12.28**	1.76	32.25**
V 271	3.35	-6.20*	15.86**	18.54**	6.54*	48.98**	3.58	-1.98	28.22**	7.81*	0.31	23.03**

CD	5%	1%
RH	0.663	0.882
HB & SB	0.766	1.019

RH - Relative heterosis

HB - Heterobeltiosis

SH - Standard heterosis

Table 36. Estimate of heterosis for seed protein content (per cent).

Lines	Testers											
	PTB 2			C 190			C 152			CoVu 85020		
	RH	HB	SH	RH	HB	SH	RH	HB	SH	RH	HB	SH
VCP 4	2.33**	-1.86*	-1.85*	-1.09	-2.76**	-7.58**	-0.94	-4.13**	-5.90**	0.63	-2.80**	-4.22**
CoVu 358	-1.46*	-2.24**	-2.23**	0.61	-1.12	-2.67**	0.02	-0.12	-1.68*	-0.75	-0.80	-2.26**
DPLC 210	-0.42	-0.85	-0.82	-1.02	-3.07**	-3.87**	0.51	0.001	-0.86	-1.16	-1.47	-2.30**
V 322	-0.56	-3.19**	-3.19**	-6.41**	-6.57**	-11.21**	-1.53*	-3.25**	-5.04**	-0.52	-2.45**	-3.87**
V 27	-1.26	-3.82**	-3.81**	-2.37**	-2.47**	-7.30**	-0.68	-2.27**	-4.08**	-1.91**	-3.74**	-5.14**
V 271	-0.94	-2.61**	-2.61**	-1.63*	-2.45**	-5.73**	-0.96	-1.71*	-3.53**	-1.65*	-2.58**	-4.01**

CD	5%	1%
RH	0.371	0.494
HB & SH	0.429	0.571

RH - Relative heterosis

HB - Heterobeltiosis

SH - Standard heterosis

4.3 Selection in F_2 populations

The range and mean values for the different traits such as total nodule weight, weight of effective nodules, root weight, dry weight of the plant, nitrogen content per plant at 50 per cent flowering, number of pods per plant, number of seeds per pod, length of pod, weight of hundred seeds, seed protein content and grain yield per plant of the F_2 selections in the 24 families are presented in Table 37 and It was seen that for the total nodule weight, the lowest range (1.267-1.832) was recorded by the family L2 X T2 and the highest range (0.917-2.666) by L5 X T4. The lowest mean value for the above trait (1.152) was registered by the L5 X T1 and the highest by L2 X T4 (2.367).

As regards the weight of effective nodules, the lowest range (0.911-1.503) was recorded by the family L1 X T1 and the highest range (0.812-2.552) by L5 X T4. The lowest mean value for the above trait (1.307) was registered by the family L4 X T1 and highest by L2 X T4 (2.24)

Family L1 X T1 recorded the lowest range of root weight (0.911 - 1.503) while L5 X T4 recorded the highest range (0.812 - 2.552). The lowest mean value (0.806) for the above trait was registered by the famliy L1 X T1 and highest by L1 X T2 (1.698)

It was observed that for the dry weight of the plant the lowest range (4.608-10.227) was recorded by the family L5 X T1 and the highest range (7.0-21.625) by L5 X T3. The lowest mean value for the above trait (7.171) was recorded by the family L1 X T1 and highest by L1 X T2 (15.765).

The nitrogen content per plant at 50 per cent flowering recorded the lowest range

Table 37. Range and mean value of F_2 selections.

Sl No	F_2 families	Total nodule weight (g)		Weight of effective nodules (g)		Root weight (g)		Dry weight of the plant (g)		Nitrogen content per plant (%)	
		Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean
1	L1 x T1	0.827-1.693	1.533	0.911-1.503	1.458	0.502-1.008	0.806	4.750-10.576	7.171	1.983-2.215	2.047
2	L1 x T2	0.625-1.937	1.665	0.593-1.825	1.601	0.796-1.922	1.698	8.965-22.991	15.765	2.008-2.283	2.118
3	L1 x T3	1.275-2.673	2.235	1.009-2.522	2.141	0.593-1.469	1.090	6.750-18.457	11.479	2.137-2.452	2.370
4	L1 x T4	1.009-2.732	2.255	0.930-2.511	2.156	0.611-1.502	1.101	4.622-11.430	8.784	2.008-2.295	2.262
5	L2 x T1	0.937-2.373	1.909	0.875-2.211	1.776	0.499-1.327	0.977	4.527-13.276	8.950	1.923-2.286	2.179
6	L2 x T2	1.267-1.832	1.506	1.093-1.698	1.387	0.669-1.893	1.405	7.370-21.630	14.303	1.905-2.199	2.057
7	L2 x T3	1.933-2.625	2.161	1.759-2.496	2.054	0.507-1.386	1.089	6.873-20.066	12.69	2.019-2.289	2.250
8	L2 x T4	1.715-2.730	2.367	1.526-2.519	2.240	0.553-1.227	1.041	4.334-12.473	8.778	1.995-2.291	2.215
9	L3 x T1	1.832-2.693	2.312	1.675-2.522	2.169	0.709-1.866	1.579	4.678-11.933	8.538	2.005-2.397	2.216
10	L3 x T2	0.926-2.321	1.857	0.831-2.223	1.705	0.500-1.293	0.962	4.263-13.998	9.597	1.981-2.362	2.209
11	L3 x T3	0.937-2.627	2.221	0.900-2.412	2.136	0.623-1.377	1.089	3.296-12.876	8.627	1.897-2.316	2.212
12	L3 x T4	0.731-1.933	1.599	0.665-1.805	1.501	0.702-1.375	1.155	4.476-13.224	8.994	1.972-2.352	2.233
13	L4 x T1	0.861-1.996	1.409	0.721-1.697	1.307	0.693-1.283	1.141	5.625-15.357	10.375	2.019-2.291	2.155
14	L4 x T2	0.706-1.893	1.404	0.597-1.604	1.331	0.683-1.395	1.165	6.563-20.611	13.877	2.002-2.286	2.192
15	L4 x T3	0.835-2.016	1.807	0.709-1.982	1.704	0.437-1.673	1.318	8.427-22.525	14.952	1.983-2.310	2.200

Contd....2.

Table 37. (Contd.)

Sl No	F_2 families	Total nodule weight (g)		Weight of effective nodules (g)		Root weight (g)		Dry weight of the plant (g)		Nitrogen content per plant (%)	
		Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean
16	L4 x T4	1.227-2.393	2.159	1.193-2.208	2.010	0.526-1.499	1.121	6.255-16.922	10.967	2.006-2.469	2.320
17	L5 x T1	0.837-1.927	1.152	0.688-1.826	1.335	0.687-1.863	1.200	4.608-10.227	7.570	1.993-2.261	2.118
18	L5 x T2	0.955-1.667	1.062	0.882-1.559	0.971	0.591-1.885	1.267	7.005-18.665	11.858	1.981-2.230	2.065
19	L5 x T3	0.832-2.086	1.795	0.628-1.993	1.739	0.665-2.076	1.603	7.000-21.625	13.043	1.912-2.282	2.177
20	L5 x T4	0.917-2.666	2.103	0.812-2.552	2.060	0.775-1.837	1.398	6.256-19.756	12.458	1.998-2.309	2.265
21	L6 x T1	0.603-1.876	1.479	0.500-1.729	1.410	0.375-1.445	0.904	5.673-12.526	8.187	1.976-2.314	2.074
22	L6 x T2	0.772-2.051	1.596	0.687-1.919	1.515	0.503-1.571	1.246	6.893-19.256	13.079	2.000-2.304	2.190
23	L6 x T3	0.622-1.927	1.651	0.507-1.827	1.479	0.315-1.287	0.927	6.697-19.227	11.607	1.965-2.371	2.207
24	L6 x T4	0.674-2.005	1.517	0.512-1.908	1.456	0.351-1.476	0.812	4.007-11.992	8.617	1.809-2.363	2.210
			**		**		**		**		**
	F value		25.47		30.57		40.69		25.53		11.86
	CD		0.218		0.194		0.109		1.449		0.068
	SE		0.075		0.066		0.037		0.495		0.023

Contd....3.

Table 37. (Contd.)

Sl No	F_2 families	Number of pods per plant		Number of seeds per pod		Length of pod (cm)		Weight of hundred seeds (g)		Seed protein content (%)		Grain yield per plant (g)	
		Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean
1	L1 x T1	4-22	13.245	6-15	12.965	7.9-16.5	14.885	10.31-11.86	11.44	25.93-27.32	26.57	4.92-16.47	10.96
2	L1 x T2	11-43	25.485	6-15	13.095	8.7-16.8	14.035	11.93-13.65	13.01	23.05-26.08	24.99	6.83-25.35	19.43
3	L1 x T3	2-18	10.495	9-16	15.35	6.9-17.3	15.76	11.05-12.67	11.71	26.21-28.93	27.07	7.99-18.25	12.25
4	L1 x T4	4-18	9.185	4-17	15.19	7.2-17.5	15.825	10.89-11.93	11.21	25.62-27.08	26.45	3.52-14.25	8.695
5	L2 x T1	7-20	12.245	5-14	12.70	6.4-14.7	12.39	9.008-10.251	9.885	26.35-29.08	27.10	8.27-20.52	13.485
6	L2 x T2	8-29	19.44	6-16	13.455	8.3-16.9	13.63	10.127-11.093	10.63	26.95-29.27	27.28	3.45-13.28	8.29
7	L2 x T3	4-18	8.811	9-17	14.96	7.8-17.3	14.015	8.96-10.25	9.5	25.62-27.24	26.24	5.21-22.87	15.96
8	L2 x T4	3-21	7.76	6-17	15.19	8.2-17.9	14.055	8.9-10.31	9.485	26.34-28.93	27.37	6.25-24.35	17.89
9	L3 x T1	10-46	24.32	5-15	12.345	6.2-15.7	12.76	8.27-9.53	8.875	25.97-29.62	27.32	2.83-10.56	6.64
10	L3 x T2	14-53	25.065	6-14	12.19	8.1-16.7	13.09	10.29-11.08	10.80	26.29-28.97	27.635	2.95-11.85	6.74
11	L3 x T3	3-20	9.445	7-17	14.975	7.9-17.2	14.11	9.088-10.47	9.81	27.261-29.322	28.135	5.73-23.20	15.515
12	L3 x T4	5-21	8.46	8-16	15.035	8.0-16.7	13.915	8.93-10.29	9.68	26.136-28.677	27.44	8.33-40.67	21.29
13	L4 x T1	9-40	21.445	4-14	12.3	6.1-15.9	12.805	9.87-10.54	10.36	23.15-25.83	24.48	6.31-24.85	16.235
14	L4 x T2	15-65	28.870	3-13	11.055	8.2-16.8	13.115	12.63-15.91	14.115	25.43-27.79	26.015	6.55-25.37	19.92
15	L4 x T3	7-30	18.415	6-16	14.315	7.9-17.6	14.92	10.95-12.45	11.38	26.18-28.92	27.595	4.35-23.55	14.29

Contd....4.

Table 37. (Contd.)

Sl No	F_2 families	Number of pods per plant		Number of seeds per pod		Length of pod (cm)		Weight of hundred seeds (g)		Seed protein content (%)		Grain yield per plant (g)	
		Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean
16	L4 x T4	4-25	10.895	7-18	15.86	6.8-16.9	15.43	10.21-11.13	10.87	26.26-28.94	27.475	4.31-16.37	9.92
17	L5 x T1	5-28	16.885	5-15	12.01	7.2-15.6	12.155	9.65-10.61	10.235	26.69-29.33	27.29	5.07-15.93	10.94
18	L5 x T2	8-43	19.44	4-15	11.96	7.0-16.2	12.12	10.12-12.36	11.635	25.56-27.33	26.24	4.08-15.11	8.945
19	L5 x T3	6-34	18.345	7-17	14.7	8.7-16.5	14.975	9.48-11.09	10.2	24.87-26.46	25.995	6.27-24.37	16.74
20	L5 x T4	5-24	15.81	6-17	14.085	9.3-14.7	13.735	10.15-11.26	10.93	25.69-29.58	27.325	8.31-19.87	12.94
21	L6 x T1	8-39	21.445	5-15	12.325	7.9-16.2	13.05	10.18-12.05	11.085	26.28-28.87	27.135	7.91-19.33	13.94
22	L6 x T2	8-49	24.095	4-16	12.44	8.6-15.2	13.115	10.97-13.13	12.25	25.79-27.48	26.585	7.11-24.83	19.96
23	L6 x T3	5-27	10.96	7-16	14.7	6.9-17.7	14.795	10.25-11.36	10.98	26.23-29.08	27.525	4.13-15.87	9.39
24	L6 x T4	4-20	14.20	6-16	14.19	8.1-17.6	13.625	9.065-10.93	9.775	26.18-28.87	27.41	4.67-15.21	10.475
			**		**		**		**				**
	F value		23.84		17.88		9.47		3.43		1.90		10.27
	CD		3.819		0.956		1.035		1.872				4.011
	SE		1.305		0.327		0.354		0.640				1.371

(2.109-2.291), and the highest range (1.809-2.363) by L4 X T1 and L6 X T4 respectively. The lowest mean value for the above trait (2.047) was registered by the family L1 X T1 and highest by L1 X T2 (2.118).

For the number of pods per plant the lowest range 7-20 was recorded by the family L2 X T1 and highest range (15-65) by L4 X T2. The lowest mean value for the above trait 7.76 was recorded by the family L2 X T4 and highest by L4 X T2 (28.87).

Families L1 X T3 and L1 X T4 registered the lowest range (9-16) and highest range (4-17) with respect to number of seeds per pod. The lowest mean value for the above trait (11.055) was registered by the family L4 X T2 and highest by L4 X T4 (15.86).

The lowest range for length of pod was recorded by L5 X T4 (9.3-14.7), and the highest range (6.9-17.7) by L6 X T3. The lowest mean value for the above trait (12.12) was recorded by the family L5 X T2 and highest by L1 X T4 (15.825).

For the character weight of hundred seeds, the lowest range was 9.87-10.54 of the family L4 X T1 and the highest range (10.12-12.36) by L5 X T2. The lowest mean value for the above trait (8.875) was recorded by the family L3 X T1 and highest by L4 X T2 (14.115).

It was observed that for the seed protein content the lowest range was 25.93-27.32 which was recorded by the family L1 X T1 and highest range (25.69-29.58) by L5 X T4. The lowest mean value for the above trait (24.485) was recorded by the family L4 X T1 and highest by L3 X T3 (28.135).

As regards grain yield the lowest range (2.83-10.56) and highest range (8.33-40.67) were observed in the families L3 X T1 and L3 X T4 respectively. The lowest mean value for the above trait (6.64) was recorded by the family L3 X T1 and highest by L3 X T4 (21.29).

DISCUSSION

DISCUSSION

Variability observed in a plant community is phenotypic which is the result of the genetic variability upon which superimposed is the variability due to the effect of environment in which the individual genotype perpetuates and survives. The variability available in a population could be partitioned into heritable and non heritable components with the aid of genetic parameters like genotypic coefficient of variation (GCV), heritability and genetic advance which serve as useful guidelines for selection.

Burton (1952) had suggested that GCV together with heritability would be a better estimate of heritable variation for excercising selection. Subsequently Johnson *et al.* (1955) opined that heritability in the broadsense alone is not enough in predicting the resultant effect of selection and that heritability along with genetic advance is more useful for this purpose.

5.1 Genotypic and phenotypic coefficients of variation, heritability and genetic advance in biological nitrogen fixation characters

5.1.1 Number of days to 50 percent flowering

The phenotypic and genotypic coefficients of variation for number of days to 50 per cent flowering did not exhibit much difference indicating a low degree of environmental influence on the character under study. A very high heritability coupled with a low genetic advance was observed. According to Panse (1957),if the heritability is mainly owing to non-additive gene effects, the expected genetic advance would be low and if there is additive gene effect, a high genetic advance may be expected. Therefore, low genetic advance noticed for days to 50 per cent flowering suggests that this character is mainly controlled by non-additive genes. This observation is in agreement with the results obtained by Ramachandran *et al.* (1980), and Singh and Mehndiratta (1969) in cowpea.

5.1.2 Number and weight of nodules in the primary root.

The phenotypic and genotypic coefficients of variation had recorded moderate difference indicating that the environmental influence is moderate in the number and weight of nodules in the primary root. A high heritability with medium to high genetic advance was recorded for these characters. The posibility of additive gene effect is evident in these characters. This observation is in conformity with the results obtained by Rosaiah *et al* (1987) and Singh and Murty (1988) in greengram.

5.1.3 Number and weight of nodules in the secondary roots.

The relative magnitude of difference between PCV and GCV for number of nodules and weight of nodules in the secondary roots indicated a moderate to low degree of environmental influence on these characters. A high heritability coupled with high genetic advance indicate the posibility of additive gene effect. This finding is in agreement with the findings of Rosaiah *et al.* (1987) and Singh and Murty (1988) in greengram.

5.1.4 Total number and total weight of nodules

The relative magnitude of difference between PCV and GCV for total number and total weight of nodules indicated a moderate to low degree of environmental influence respectively. Since these characters are having high heritability estimates along with moderate to high genetic advance, posibility of additive gene efffects is evident. This finding is also in conformity with the results obtained by Rosaiah *et al.* (1987) and Singh and Murty (1988) in greengram.

5.1.5 Nitrogen content in plant at 50 pert cent flowering

The difference between PCV and GCV was low indicating a very low influence of environment over the character nitrogen content in plant. A very high heritability together with low genetic advance is indicative of the influence of non-additive gene effect for nitrogen content. This finding is in accordance with the findings of Rosaiah *et al.* (1987) in greengram.

5.1.6 Plant dry weight

Unlike the other nitrogen fixing characters, plant dry weight recorded a high value of PCV with corresponding low value of GCV, indicating the influence of environment on this character. A low heritability estimate together with low genetic advance also confirms the high influence of environment on the expression of plant dry weight in cowpea. This finding is in agreement with the findings of Miller *et al.* (1986) in cowpea, but contradictory to the findings of Rosaiah *et al.*(1987) and Singh and Murty (1988) in greengram.

5.2 Genotypic and phenotypic coefficients of variation, heritability and genetic advance of yield characters.

5.2.1 Grain yield per plant

The relative magnitude of difference between PCV and GCV were high indicating a fair amount of environmental influence in controlling the grain yield per plant. A medium magnitude of heritability was recorded with moderatly good genetic advance. Similar results were reported by Singh and Mehndiratta (1969), and Radhakrishnan and Jebaraj (1982) in cowpea and Veeraswamy *et al.* (1973) in blackgram,. Contrary to this Ramachandran, *et al.* (1980) and Savithri Amma (1992) reported high heritability and high genetic advance for grain yield in cowpea.

5.2.2 Length of pod

The PCV and GCV for length of pod had recorded a little difference indicating a low degree of environmental influence. The high heritability together with low genetic advance suggests that this character is mainly controlled by non-additive genes. This is in conformity with the results obtained by Savithri Amma (1992), Singh and Mehndiratta (1969) in cowpea. Contrary to this, Veeraswamy *et al.* (1973) and Dharmalinggam and Kadambavanasundram (1984) reported high heritability coupled with high genetic advance for length of pod in greengram and cowpea respectively.

5.2.3 Number of pods per plant

The relative magnitude of difference between PCV and GCV for number of pods per plant was low indicating a low degree of environmental influence in controlling this character. High heritability estimate with high genetic advance is indicative of the presence of additive genes in the expression of this character. This finding is in close confirmity with the findings of Ramachandran *et al.* (1980), Singh and Mehndratta (1969), Radhakrishnan and Jebaraj (1982) and Patil and Baviskar (1987) in cowpea.

5.2.4 Weight of hundred seeds

The PCV and GCV for weight of hundred seeds had recorded very little difference indicating a very low degree of environmental influence in controlling this trait. A very high heritability with a high genetic advance recorded for this character suggests the influence of additive genes in controlling this trait. This finding is in agreement with the results obtained by Thiyagarajan (1989), Apte *et al.* (1987), Savithri Amma (1992) and Patil and Baviskar (1987) in cowpea.

5.2.5 Seed protein content

The relative magnitude of PCV and GCV for seed protein content was very low indicating a low degree of environmentel influence in controlling this character. A very high heritability together with a very low genetic advance suggests the influence of non-additive genes. This finding is in accordance with the findings of Rosaiah *et al.* (1987) in greengram.

5.3 Correlation and path analysis

5.3.1 Correlation of biological nitrogen fixation characters

While considering the phenotypic and genotypic correlations of biological nitrogen fixing characters such as number of nodules in the primary root, weight of nodules in the primary root, weight of nodules of the secondary roots, total nodule weight, number of days to flower and plant dry weight with nitrogen content per plant, it was seen that the magnitude of the genotypic correlation was higher in all the cases except the correlation between number of nodules in the primary root and nitrogen content there by indicating the predominance of genetic relationship.

Total nodule weight as well as weight of effective nodules in the primary root and plant dry weight had very high positive genotypic correlation with nitrogen content in plant at the time of 50 per cent flowering. This finding is in close agreement with the findings of Singh and Murty (1988) in greengram, but contradictory to the findings of Miller *et al.* (1986) who reported that dry weight per plant at the time of flowering was not a good indicator of nitrogen fixation potential.

Number of nodules in the primary root was found to be positively correlated with nitrogen content in plant while the correlation of number of nodules in the secondary root and total number of nodules was non significant. This indicates that the total number of nodules do not contribute much to the nitrogen fixation while the efficient nodules in the primary root contribute maximum to the total biological nitrogen fixed.

It was found that number of nodules in the primary root, weight of nodules in the primary root and weight of nodules in the secondary root were positively correlated with the total nodule weight and that total nodule weight was positively correlated with the nitrogen content in the plant. Here the nodule weight was found to be more important than number. Hence a plant genotype which is able to form effective large nodules on the primary root system seems to be a better nitrogen fixer. This observation is in close conformity with the results obtained by Rosaiah *et al.* (1987) in greengram. The results however, donot agree with the findings of Miller *et al.* (1986) in cowpea.

Significant negative correlation was observed among weight of effective nodules in the primary root, weight of nodules in the secondary roots, total nodule weight and nitrogen content in plant at 50 per cent flowering with grain yield per plant. This suggests that the high nitrogen fixing genotypes may not be higher yielders because of the antagonistic relationship between grain yield and total nitrogen per plant. Hence it may not be posible to mix these two characters together. This finding is in agreement with the results obtained by Mytton (1981) in lucerne but contrary to the findings of Sudagar Singh and Gai (1984) in pea, Rosaiah *et al.* (1987) and Singh and Murty (1988) in greengram. The possible reason for negative correlation may be that all pulses are C_3 plants and for biological nitrogen fixation the host plant has to sacrifice carbon to gain nitrogen. Hence this may affect the carbohydrate synthesis to a great extent. Since negative correlation exists, simple crossing programme may not be helpful. So it is better to break this barrier by suitable breeding mothods. Hence a future line of thinking is needed in this aspect.

5.3.2 Correlation of yield and yield attributing characters

The grain yield recorded positive and significant phenotypic and genotypic correlations with number of pods per plant while its correlation with length of pod and weight of hundred seeds were positive though non-significant. This suggests that selection based on number of pods per plant will lead to an increase in the yield of seeds. This finding is in agreement with the findings of Rajendran *et al.* (1979), Dumbre *et al.* (1982), Natarajaratnam *et al.* (1985) and Patil and Bhapkar (1987) in cowpea. Positive correlation of grain yield with hundred grain weight also is in conformity with the results obtained by Patel and Telang (1976), Chikkadyavaiah (1985) and Choulwar and Borikar (1987) in cowpea.

Number of days to 50 per cent flowering had negative genotypic correlation with grain yield per plant. This finding is contrary to the results reported by Sreekumar *et al.* (1979) in cowpea. Weight of hundred seeds and seed protein content exhibited very strong negative correlations, indicating that smaller seeds will have better quality with respect to seed protein content rather than bigger seeds. At the same time seed protein content exhibited no significant correlation with seed yield suggesting that seed yield could be impoved without sacrificing the protein content of the seed. This finding is in conformity with the results reported by Rosaiah *et al.* (1987) in greengram.

5.4 Direct and indirect effects (Path analysis)

5.4.1 Biological nitrogen fixation characters

Path analysis is an efficient biometric tool throwing light on the cause-effect relationship. It enabled to identify and quantify the characters responsible for the nitrogen content and grain yield.

Total number of nodules had maximum direct effect on nitrogen content per plant followed by weight of effective nodules in the primary root. The total number of nodules exerted negative indirect effects through weight of effective nodules in the primary root which inturn had negative indirect effect through total number of nodules. Therefore for increasing nitrogen content per plant, a compromise between total number of nodules and weight of effective nodules in the primary root is necessary and due attention is to be given in this regard during selection programme.

Very high positive genotypic correlation was recorded for total nodule weight with nitrogen content per plant, but the direct effect was negative. The high positive indirect effect of this trait through weight of effective nodules in the primary root, weight of nodules in the secondary roots and total number of nodules justifies the high positive correlation. Besides, these three traits have positive direct effects with nirtogen content in plant. Hence while attempting selection for increased nitrogen content in plant, the above mentioned indirect factors are to be considered simultaneously.

Eventhough total nodule weight was showing very high genotypic correlation with nitrogen content per plant, its direct effect was negative, whereas weight of effective nodules in the primary root was showing very high positive genotypic correlation along with positive direct effect with nitrogen content per plant. Likewise weight of effective nodules in the secondary roots was significantly and positively correlated with nitrogen content along with a positive direct effect. At the same time weight of effective nodules in the primary root exerted positive indirect effect through weight of effective nodules in the secondary roots which inturn had positive indirect effect through weight of effective nodules in the primary root. Hence for increasing nitrogen content per plant, weight of effective nodules in the primary root along with weight of effectiive nodules in the secondary roots are to be considered rather than number of nodules in the primary root as well as secondary roots.

5.4.2 Yield characters

Path analysis for yield and yield attributing characters had shown that number of pods per plant had only very low negative direct effect eventhough the character recorded very high positive genotypic correlation with yield. Very high positive indirect effect of this trait through plant dry weight and weight of hundred seeds justifies the high positive correlation. This finding is contrary to the observations reported by Jagadish Murthy (1986) in cowpea.

Length of pod was having maximum positive direct effect with the grain yield, but the indirect effects *via* plant dry weight, weight of hundred seeds were negative, where as the indirect effect through number of pods per plant was positive. The reduced *non* significant correlation as compared to the direct effect was due to the significant negative indirect effect of length of pods through weight of hundred seeds and plant dry weight.

Plant dry weight was found to have maximum negative direct effect with grain yield eventhough their indirect effects through length of pod and number of pods per plant were found to be positive, whereas the indirect effect through weight of hundred seed was found to be negative. This justifies the negative genotypic correlation of this character with grain yield. Hence for improving the yield, genotypes with less plant dry weight are to be considered.

The direct effect of weight of hundred seeds with grain yield was found to be negative but their genotypic correlation was positive. The indirect effects of weight of hundred seeds *via* length of pod and number of pods per plant were found to be positive, which suggests that smaller the seed size higher would be the yield through increased number of pods and length of pods. Hence small seeded genotypes are desirable for higher yield and this fact must be taken into consideration during selection programme.

5.5 Combining ability

5.5.1 Nitrogen fixation characters

5.5.1.1 Number of days to 50 per cent flowering

Number of days to 50 per cent flowering had significant mean sum of squres due to lines, testers and line x tester. Significant GCA and SCA variances were observed for this character indicating that additive and non-additive genetic components were important for the expression of this trait. But the ratio of σ^2A to σ^2D is less than unity suggesting a predominant role of non-additive gene action. This finding is in agreement with the results reported earlier by Anilkumar (1992) and Rejatha (1992) in cowpea and Deshmukh and Manjare (1980) in greengram. The above findings are, however contradictory to the results obtained by Jayarani (1993) in cowpea, Dubey and Lal (1983) in pea.

The estimate of combining ability revealed that the lines VCP 4, V 27 and V 271 and the tester PTB 2 had significant negative gca effects. Significant positive gca effects were recorded by lines CoVu 358, DPLC 210 and the testers C 152 and CoVu 85020. The cross between DPLC 210 X C 190 recorded significant sca effects. The parent DPLC 210 was also a good general combiner with the above cross. As a result it could be greatly expected to throw transgrassive segregants in the later generations and selections in the later generations would give better results. The adoption of biparental approach in this cross for still higher variability could be expected to generate transgrassive segregants.

Since the variance ratio of GCA to SCA recorded a value which is less than unity indicating the predominance of non-additive gene action. Hence there is no scope for applying selection pressure in the early stages.

5.5.1.2 Weight of nodules in the primary root

The line x tester interaction alone showed significant variance suggesting the significance of SCA variance for weight of nodules in the primary root. Hence prevalence of non-additive gene action can be expected for the expression of this trait. The ratio of σ^2A to σ^2D was also found to be less than unity indicating the prepondence of non-additive gene action. This finding is in agreement with the findings of Miller *et al.* (1986) in which sca was found to be highly significant for nodule weight. On the other hand, Singh and Murty (1988) reported the significance of both gca and sca in controlling the character nodule weight.

Among lines, VCP 4 and among testers, CoVu 85020 had significant gca effects. Out of the 24 hybrid combinations, only two hybrids, *viz.*, VCP 4 X C 152 and DPLC 210 X PTB 2 recorded significant positive sca effects. The maximum sca effect was shown by the cross VCP 4 X C 152 *ie.,*between positive x positive general combiners while for the other cross of DPLC 210 X PTB 2, negative x negative general combiners contributrd to the positive sca effect. Interestingly the negative gca effect was non-significant.

5.5.1.3 Total weight of nodules

Total weight of nodules had a significant mean sum of squares due to tester and line X tester. This indicates the significance of GCA and SCA variances and the involvement of additive and non-additive gene action for the expression of this trait, however, the ratio of σ^2A to σ^2D was less than unity indicating the predominant role of non-additive gene action. This finding is in agreement with the results obtained by Singh and Murty (1988) in greengram in which both gca and sca were found to be highly significant for this character. On contrary Miller *et al.* (1986) reported the significance of sca for this character in cowpea.

Among the lines, V 27 had significant negative gca effect whereas among testers C 152 and CoVu 85020 had significant positive gca effects. Out of all the hybrid combinations, DPLC 210 X PTB 2 had shown significant positive sca effect. Positive x negative general combiners contribute to the positive sca effect.

5.5.1.4 Weight of effective nodules

Weight of effective nodules had significant mean sum squares due to tester and line x tester. This indicated the significance of GCA and SCA variances and the involvement of additive and non-additive gene actions for the expression of this trait, however the ratio of σ^2A to σ^2D was less than unity indicating the predominance of non-additive gene action. This finding is in agreement with the results of Singh and Murty (1988) in which both gca and sca were found to be highly significant for this character. On the other hand Miller *et al.* (1986) reported significance of sca for this trait.

Among the lines, V 27 had significant negative gca effect whereas among testers C 152 and CoVu 85020 had significant positive gca effects while PTB 2 and C 190 had significant negative gca effects. Out of all the hybrid combinations, DPLC 210 X PTB 2 had shown significant positive sca effect. It was seen that positive x negative general combiners contributed to the positive sca effect.

5.5.1.5 Dry weight of plant at 50 per cent flowering

Dry weight of plant at 50 per cent flowering had a significant mean sum of squares due to tester and line x tester, indicating the significance of GCA and SCA variances and the involvement of additive and non-additive gene actions for the expression of this trait, however the ratio of σ^2A to σ^2D was less than unity indicating the predominant role of non-additive gene action. This finding is in agreement with the results of Singh and Murty (1988), Smith *et al.* (1982) and Tan (1981) in which both gca and sca were found to be highly significant for the character plant dry weight. Hely (1972) also reported significant gca and sca effects for dry weight of the plant in *Trifolium ambiguum*. Miller *et al.* (1986) reported non-additive gene action for plant dry weight in cowpea. Pinchbeck *et al.* (1980) however reported the importance of only additive gene effect in spanish clover.

Among lines, V 322 recorded positive and significant gca effect while DPLC 210 recorded negative significant gca effect. Among testers C 190 and C 152 recorded positive significant gca effects where as PTB 2 recorded significant negative effect. Among hybrid combinations, VCP 4 X C 190, DPLC 210 X PTB 2 and V 27 X CoVu 85020 recorded significant and positive sca effects. The parents involved in the crosses of VCP 4 X C 190 and V 27 X CoVu 85020 had negative and positive general combiners while parents of DPLC 210 X PTB 2 had both negative general combiners. Hence the best combinations for dry weight of plant involved positive x negative and negative x negative general combiners.

5.5.1.6 Nitrogen content in plant at 50 per cent flowering

Nitrogen content in plant at 50 per cent flowering had a significant mean sum square due to tester and line x tester indicating the significance of GCA and SCA variances and the involvement of additive and non-additive gene action for the expression of this trait. However the ratio of σ^2A to σ^2D was less than unity indicating the predominant role of non-additive gene action. This finding is in agreement with the observations of Singh and Murty (1988) in greengram, Hely (1972) in *Trifolium ambiguum*, Smith *et al* (1982) in crimson clover and Tan (1981) in alfalfa, indicating the role of both additive and non-additive gene effects for nitrogen content in plant. On the other hand , this finding doesnot agree with the findings of Pinchbeak *et al.* (1980) in spanish clover, and they proposed the importance of only additive gene effect for nitrogen content in plant.

Among lines, V 27 recorded negative and significant gca effects. C 152 and CoVu 85020 recorded significant and positive gca effects while PTB 2 and C 190 recorded significant and negative gca effects among testers. Out of all the hybrid combinations tested, none of the hybrids had recorded significant and positive sca effects however, the cross DPLC 210 X PTB 2 had shown a negative sca. It was seen that positive x negative general combiners contributed to the negative sca effect.

5.5.2 Yield characters

5.5.2.1 Length of pod

The length of pod had a significant mean sum of squares due to lines, tester and line x tester.This indicated the significance ofGCAandSCAvariances and the involvement of additive and non-additive gene actions for the expression of this trait. However, the ratio of σ^2A to σ^2D was less than unity indicating the predominant role of non-additive gene action. In agreement to the present findings Singh and Jain (1972) and Mak and Yap (1977) reported the importance of both gca and sca effects in cowpea, Patel *et al.* (1988) in greengram and Kalia *et al.* (1991) in blackgram. Contrary to this, additive gene action was reported by Jayarani (1993) in cowpea, Wilson *et al.* (1985) in greengram and Tewatia *et al.* (1988) in pea.

Significant positive gca effects were recorded by the lines VCP 4 and V 322 and testers C 152 and CoVu 85020 indicating that VCP 4 and V 322 are the best general combiners for length of pod. The hybrids, VCP 4 X PTB 2 and CoVu 358 X C 190 showed significant positive sca effects. The parents involved in the cross VCP 4 X PTB 2 had one positive and other negative general combiner while parents of cross CoVu 358 X C 190 had both negative general combiners. Hence the best combinations for length of pod involved positive x negative and negative x negative general combiners. Since the character is predominantly under the control of non-additve gene action, combination breeding would be useful for the improvement of this character.

5.5.2.2 Number of seeds per pod

A significant mean sum of squares due to tester and line x tester were found for number of seeds per pod indicating that both GCA and SCA were important for this character. The ratio of σ^2A to σ^2D was found to be less than unity suggesting the predominance of non-additive gene action. This finding is in agreement with the results reported by Jayarani (1993) in cowpea, Sreekumar (1993) and Deshmukh and Manjare (1980) in greengram, Yadavendra and Sudhirkumar (1987) and Pande *et al.* (1979) in chickpea. Contrary to the present findings, additive gene action was reported by Chauhan and Joshi (1981), Thiyagarajan et al. (1990) and Anilkumar (1992) in cowpea, Wilson *et al.* (1985) and Saxena and Sharma (1989) in greengram, Malhotra (1983) in blackgram and Katiyar *et al.* (1988) in chickpea.

Analysis of combining ability revealed that the line VCP 4 and the testesr C 152 and CoVu 85020 recorded significant positive gca effects. The varieties C 152 and CoVu 85020 are the best general combiners for number of seeds per pod. Significant and positive sca effects were recorded by the cross CoVu 358 X C 190, though the parents involved in this cross had both positive and negative general combiners. Hence the best specific combination for number of seeds per pod involved positive x negative combiners. Since the character is predominantly under the control of non-additive gene action, combination breeding will be helpful for the improvement.

5.5.2.3 Number of pods per plant

Number of pods per plant recorded significant mean sum of squares due to lines, testers and line x testers, exhibiting significance of bothGCAandSCAvariances. The ratio of σ^2A to σ^2D was less than unity indicating the importance of non-additive gene action. Significance of both gca and sca for number of pods per plant reported by Jayarani (1993), Anilkumar (1992) and Thiyagarajan *et al.* (1990) in cowpea, Sreekumar (1993) and Deshmukh and Manjare (1980) in green gram and Pande *et al.* (1979) and Yadavendra and Sudhirkumar (1987) in Chickpea which are in close agreement to the present findings. However, predominance of additive gene action contradicting to the present results was reported by Chauhan and Joshi (1981) in cowpea, Patel *et al.* (1987) in pigeonpea, Dubey and Lal (1983) in pea, Wilson *et al.* (1985) and Saxena and Sharma (1989) in greengram and Katiyar *et al.* (1988) in chickpea.

Estimate of combining ability revealed that the line V 322 and testers C 190 and PTB 2 showed significant positive gca effects indicating that V 322, C 190 and PTB 2 are the best general combiners for the number of pods per plant. Significant positive sca effects were recorded by the crosses, DPLC 210 X PTB 2, VCP 4 X C 910, V 322 X C 910, V 27 X C 152 and V 27 X CoVu 85020 in which first three crosses had parents with positive gca effects while the last two with positive x negative general combiners. Hence the best specific combination for more number of pods per plant involved positive x positive and positive x negative general combiners. Hence number of pods per plant was found to be under the control of both additive and non-additive genes with the preponderance of non-additive gene action. For the improvement of this character, combination breeding is suggested.

5.5.2.4 Grain yield per plant

Grain yield per plant had a significant mean sum of squares due to lines, testers and line x tester. This indicated the significance of GCA and SCA variances and the involvement of additive and non-additive gene action for the expression of this trait, though the ratio of σ^2A to σ^2D was less than unity indicating the predominance of non-additive gene action. In agrement to the present findings, Anilkumar (1992) and Thiyagarajan et al. (1990) reported non-additive gene action in cowpea, Pande *et al.* (1979) and Yadavendra and Sudhirkumar (1987) in chickpea, Sreekumar (1993) and Deshmukh and Manjare (1980) in greengram and Singh *et al.* (1987) in blackgram. Contrary to this, additive gene action was reported by Chauhan and Joshi (1981) and

Thiyagarajan and Rajasekaran (1989) in cowpea, Wilson *et al.* (1985) and Saxena and Sharma (1989) in greengram, Malhotra (1983) in blackgram and Kaityar *et al.* (1988) in chickpea. The significance of sca alone was reported by Jayarani (1993) in cowpea.

Significant positive gca effect was recorded by the line V 322 and tester C 190 in the combining ability analysis indicating that V 322 and C 190 are the best general combiners for grain yield per plant. The hybrid, DPLC 210 X PTB 2, V 322 X C 190 and V 27 X C 152 had significant positive sca effects. The parents involved in the cross V 322 X C 190 were significant positive general combiners for yield while parents of DPLC 210 X PTB 2 and V 27 X C 152 had positive and negative general combiners. Hence the best combinations for high yield involved positive x positive and Positive x negative and negative x positive general combiners.

Since the character is predominantly under the control of non-additive gene action,combination breeding would be useful for the improvement of yield.

5.5.2.5 Hundred seed weight

Hundred seed weight had significant mean sum of squres due to lines, tester and line x testers. SignificantGCAandSCAvariances were observed for this character indicating that additive and non-additive genetic component were important for the expression of this trait. However the ratio of σ^2A to σ^2D was less than unity suggesting a predominant role of non-additive gene action. This finding is in agreement with the results reported by Jayarani (1993) and Thiyagarajan *et al.* (1990) in cowpea, and Malhotra (1983) in blackgram. Sreekumar (1993) reported the significance of sca variance alone suggesting the expression of non-additive gene action in greengram. But contrary to this finding, Chauhan and Joshi (1981) and Anilkumar (1992) had reported additive gene action for hundred seed weight in cowpea.

The estimation of combining ability revealed that the line V 322, V 27 and VCP 4 had significant positive gca effects while CoVu 358 and DPLC 210 had significant and negative gca effects. Among testers, C 190 had positive gca effect while all other testers had significant negative effect. Hence V 322, V 27, VCP 4 and C 190 are the best general combiners for this character. The cross involving CoVu 358 X PTB 2, V 322 X C 190, VCP 4 X C 152 and DPLC 210 X CoVu 85020 had showed significant positive sca effects, while VCP 4 X PTB 2, CoVu 358 X C 190 and V 322 X CoVu 85020 had shown significant negative sca effects.

It can be seen that the best specific combiners for hundred seed weight involved positive x positive, positive x negative and negative x negative general combiners as parents. Since the character is predominantly under the control of non-additive gene action, combination breeding will be helpful for the improvement.

5.5.2.6 Seed protein content

Seed protein content had a significant mean sum of squares due to lines, tester and line x tester. This indicated the significance of GCA and SCA variances and the involvement of additive and non-additive gene action for the expression of this character, however the ratio of σ^2A to σ^2D was less than unity indicating the predominant role of non- additive gene action.

Significant positive gca effects were recorded by the lines VCP 4, V 322 and V 27 and tester C 190 in the combining ability analysis indicating that VCP 4, V 322, V 27 and C 190 are the best general combiners for seed protein content. The hybrid CoVu 358 X PTB 2 and DPLC 210 X CoVu 85020 recorded significant positive sca effect however both the parents of these cross combinations had significant negative gca effects. The hybrid combination V 322 X C 190 recorded highest positive sca effect wherein both the partents had positive gca effects. The cross, VCP 4 X C 152 showed significant positive sca effect, in which the parent VCP 4 had positive and C 152 had negative gca effects. Hence the best hybrid combination for seed protein content involved positive x positive, positive x negative and negative x negative general combiners. Since the character is predominantly under the control of non-additive gene action, combination breeding would be useful for the improvement of seed protein content.

5.6 Heterosis

Marked heterosis was observed in many cross combinations for most of the characters studied and pronounced heterotic expression was obtained for weight of nodules in the primary root, total weight of nodules, weight of effective nodules, dry weight of plant at 50 per cent flowering, dry weight of the root, number of pods per plant and grain yield. However, in commercial practice, the expression of heterosis in a given hybrid will have no real meaning unless it is significantly superior than the standard check available. Taking this view into consideration, the performance of all hybrids was compared with a standard check parent, PTB 2.

Negative heterosis is desirable for days to flowering (earliness). Maximum negative heterosis of -10.92 per cent (V 322 X PTB 2) over mid parent and -8.06 per cent (V 27 X C 152 and V 271 X CoVu 85020) over better parent were recorded for this character while none of the hybrid combinations had recorded negative standard heterosis.

Negative heterosis indicating early flowering was expressed by twelve hybrids over mid parent, six hybrids over better parent and no hybrid over standard parent. Heterosis for early flowering was reported in cowpea by Rejatha (1992) and Hofman (1962), which are in agreement with the present findings.

Positive heterosis is important for weight of nodules in the primary root. Highest positive relative heterosis was recorded by the hybrid combination V 27 X CoVu 85020 (89.25 per cent) while V 322 X CoVu 85020 recorded highest positive heterobeltiosis of 56.52 per cent. Highest positive standard heterosis was recorded by VCP 4 X C 152 (429.55 per cent).

Total weight of nodules and weight of effective nodules are the key characters which determine the nitrogen fixation efficiency of a cowpea cultivar, hence positive heterosis is important in this regard. Among the hybrids tested, V 27 X CoVu 85020 displayed highest positive relative heterosis of 71.93 and 72.38 per cent for total weight of nodules and weight of effective nodules, while V 322 X CoVu 85020 recorded highest heterobeltiosis of 43.48 and 44.41 per cent respectively. VCP 4 X C 152 had displayed the highest standard heterosis of 324.6 and 362.6 per cent.

Positive heterosis is desirable for dry weight of the plant at 50 per cent flowering. Highest positive heterosis of 85.55 per cent (DPLC 210 X PTB 2) over mid parent and 91.13 per cent (V 27 X C 152) over better parent were recorded for this character. VCP 4 X C 190 had displayed highest standard heterosis of 265.3 per cent.

Nitrogen content in plant at 50 per cent flowering determines the nitrogen fixation efficiency of a cowpea genotype. Hence positive heterosis assumes importance in this trait. V 27 X CoVu 85020 recorded the highest relative heterosis of 8.08 per cent while V 322 X CoVu 85020 displayed highest positive heterobeltiosis of 6.62 per ecnt.

Nitrogen fixation characters like weight of nodules in the primary root, total weight of nodules, weight of effective nodules, dry weight of the plant and nitrogen content in plant at 50 per cent flowering are predominantly governed by the non-additive type of gene action. Hence the heterotic vigour expressed by the hybrid combination with respect to these characters are justified. Since the biological feasibility for the exploitation of heterosis is not economical as a plant improvement programme in this crop, genetic improvement of these trait can be brought about more effectively through combination breeding involving genetically diverse and high combining parents.

While discussing the character length of pod, it was revealed that none of the hybrid combination had displayed positive and significant relative heterosis and heterobeltiosis. This finding does not agree with the results reported by Rejatha (1992) and Singh and Jain (1972) in cowpea. But Singh and Jain (1971) reported negative heterosis for this character in greengram. Many of the hybrids had displayed positive and significant standard heterosis for this character in which VCP 4 X C 152 had recorded the highest value of 32.08 per cent.

None of the hybrid combination had recorded positive and significant relative heterosis or heterobeltiosis for this character while standard heterosis was found to be positive and significant. Hybrid combination V 322 X CoVu 85020 displayed the highest standard heterosis of 26.66 per cent.

Marked heterosis was observed for the character number of pods per plant in which V 322 X C 190 had recorded the highest positive relative heterosis,heterobeltiosis and standard heterosis of 356.7, 260.29 and 352.78 per cent respectively. Positive and significant heterosis was reported by Rejatha (1992) in cowpea, Rao and Chopra (1988) in chickpea, Reddy *et al.* (1979) in pigeon pea while Singh and Jain (1971) reported negative heterosis for this character in greengram.

Hundred seed weight directly influence the grain yield, hence positive heterosis is desirable for this character. The hybrid combination V 322 X C 190 had displayed high degree of relative heterosis, heterobeltiosis and standard heterosis of 31.54, 31.52 and 73.93 per cent respectively. For hundred seed weight, nine hybrids showed positive and significant heterosis over mid parent, four hybrids over better parent and twenty one hybrids over standard parent. Singh and Jain (1972) reported significant positive heterosis for this chartacter over mid parent in cowpea.

Enhanced seed protein content will determine the quality of cowpea grain. Hence positive heterosis is of much importance. Only one hybrid combination VCP 4 X PTB

2 had displayed positive and significant relative heterosis of 2.33 per cent while none of the hybrid combination had recorded positive and significant heterobeltiosis and standard heterosis. Similar results were reported by Furedi (1970) and Kurnik *et al.* (1970) in pea.

For grain yield per plant, thirteen hybrids showed positive and significant heterosis over mid parent, ten hybrids over better parent and thirteen hybrids over standard parent. Among the hybrid combinations with positive heterosis, V 322 X C 190 had recorded very high relative heterosis, heterobeltiosis and standard heterosis of 453.04, 369.17 and 557.02 respectively. Singh and Jain (1971) in greengram and Rejatha (1992) in cowpea also reported considerable relative heterosis in grain yield.

Since yield is a complex entity depending up on the multivariate interaction of its various components, it would be interesting to compare the hybrids with respect to the components of yield also. Sivan Pillai (1980), while reviewing the exploitation of heterosis in blackgram and Rejatha (1992) in cowpea stated that heterosis for yield component was observed for pod number, cluster number and 100 seed weight. In this study, heterosis in seed yield was due to heterosis in yield components especially number of pods per plant and hundred seed weight. These findings have important bearing in planning future breeding programme in cowpea. It is apparent that hybrid vigour was manifested by the hybrids with respect to all the characters in general and three important traits, viz. number of pods per plant, hundred seed weight and seed yield in particular.

Heterosis in seed yield is reflected through heterosis in yield components mainly pod number and 100 seed weight. Interestingly gene action studies revealed that these characters are governed by non-additive genes. Hence an important approach for yield improvement in this crop would be to develop hybrid strains. At first sight, the development of hybrid varieties may appear to be discouraging because cleistogamy is prevalent to a great extent in cowpea and this ensures self fertilization. The production of hybrid seed by hand pollination is very tedious. Besides, the flowers of cowpea are very sensitive and may shed after emasculation and even after pollination. A search for cytoplasmic male sterile lines which would obviate the necessity of emasculation, would be worth while. At present, however there is little scope for the exploitation of heterosis in this crop, a more effective method of improvement for biological nitrogen fixation and yield components would be through combination breeding.

5.7 Evaluation of parents

It has been found that nonadditive gene action is involved in most of the characters studied. Hence recombination breeding can be suggested for the improvement of these characters. Choice of parents assumes great importance in a recombination breeding programme for crop improvement. In the evaluation of parents, their general combining ability effects for the different traits were considered first.

In the case of number of days to flowering, lines V 27, V 271 and VCP 4 recorded significant negative gca effects indicating their good combining ability for early flowering.

Characters like weight of nodules in the primary root, total weight of nodules, weight of effective nodules, dry weight of the plant at 50 per cent flowering and nitrogen content per plant were considered for the selection of nitrogen fixing parent. Among lines, VCP 4 was found to be the best line because it recorded very high gca effect for all the nitrogen fixing characters except for dry weight of the plant. For the character dry weight of the plant, line V 322 recorded the highest gca effect.

For the yield and yield attributing characters, V 322 was found to be the best line which had registered high gca effect for number of pods per plant, hundred seed weight and grain yield per plant while VCP 4 had recorded high gca effect for length of pod and number of seeds per pod. As regards seed protein content DPLC 210 had recorded heighest gca effect. In general, V 322 was the best line for the yield characters.

Among testers, PTB 2 was found to be the best tester for number of days to flowering since it had registered significant negative gca effect. For nitrogen content per plant and weight of nodules in the primary root, CoVu 85020 was found to be the best tester with high gca effects. The tester C 152 had recorded very high positive gca effect for the character total weight of nodules and weight of effective nodules and C 190 for dry weight of the plant. In general, by considering the key nitrogen fixing characters, CoVu 85020 and C 152 can be considered as best testers.

Characters like number of pods per plant and hundred seed weight are found to be most important contributing for grain yield per plant. Tester C 190 had registered positive and significant gca effect for the above characters, on the other hand C 152 had recorded high gca effect for length of pod and number of seeds per pod. By considering the importance of yield attributing characters, tester C 190 can be considered as the best tester for the yield attributing character. Seed protein content determines the quality of a variety. PTB 2 with very small seeds had registered high gca for seed protein content.

In a nutshell, VCP 4 can be considered as the best line for the biological nitrogen fixation characters and V 322 as the best line for yield whereas CoVu 85020 as the best tester for biological nitrogen fixation characters and C 190 as the best tester for yield character.

5.8 Evaluation of cross combination

The nature of the specific combining ability (sca) effects in the different cross combinations was used for evaluation of hybrid combinations. As regards days to flowering, none of the cross combination had recorded significant negative sca effect which was found to be desirable. However, among crosses V 27 X C 152 and V 271 X CoVu 85020 recorded high sca effects. The parents involved for both the cross combinations had negative and positive gca effects. The cross combinations involving high sca effects are expected to segregate for desirable transgressive segregants, as the desirable additive gene effect of the high promising parent and the complementary epistatic effects of the crosses are coupled in the direction to maximise the expression of the character.

As regards nitrogen fixation traits such as total weight of nodules and weight of effective nodules, the best cross combinations were produced by a high x low general combiners which resulted in to a high sca effect in the hybrid combination. This indicated the importance of both additive and non-additive genic system in the control of these traits as in the case of days to flowering. The predominance of sca variance over gca variance for these traits indicated the preponderance of non-additive gene action over additive genes in the control of the traits.

In the case of dry weight of the plant DPLC 210 X PTB 2 recorded highly significant sca effect but cross with low x low general combiners contributed to high sca effect in this hybrid combination. Hybrid combination VCP 4 X C 152 was found to be the best hybrid for nitrogen content in plant with high sca effect. The parents involved in this combination were high x high general combiners.

To sum up, VCP 4 X C 152 was the best hybrid combination for biological nitrogen fixation because they had high sca effect for nitrogen content per plant and weight of nodules in the primary root while, DPLC 210 X PTB 2 had registered high sca values for the characters such as total weight of nodules, weight of effective nodules and dry weight of the plant.

In the case of grain yield per plant, V 27 X C 152 had registered high sca effect and parents involved were high x low general combiners. Hybrid combination CoVu 358 X C 190 had recorded heighest sca effects for length of pod, number of seeds per pod and seed protein content. With respect to number of seeds per pod and seed protein content, the parent involved were high x low general combiners while for length of pod, low x low general combiners contributed to high sca effect.

DPLC 210 X PTB 2 recorded highest sca effect with high x high general combiners V 322 X C 190 had recorded highest sca effect for hundred seed weight. High x high general combiners contributed to the highest sca effect for hundred seed weight.

For yield contributing characters, the predominance of SCA variance over GCA variance for the trait revealed the importance of non-additive genes over additive genes in the control of the trait and the superior cross combinations with high sca effects are expected to segregate for desirable transgrassive segregants, as the desirable additive gene effect of the high performing parent and the complementary epistatic effects of the cross are coupled in the direction to maximise the expression of the yield character under consideration.

SUMMARY

SUMMARY

Grain legumes supply major portion of the world's dietary protein needs. They are popular in agriculture on account of their potential for reducing gaseous nitrogen into a biologically usable form. Cowpea forms an important component in the tropical cropping system of India, especially Kerala. Much work has been reported relating to the aspects of genetic improvement on yield components in cowpea. However practically very little study has been done with respect to genetic basis of nitrogen fixation traits.

The present study was undertaken with the main objective of providing basic information on the genetic variability for biological nitrogen fixation and yield component traits in cowpea and to analyse the genetic basis of those traits as a prelude to breeding for improved nitrogen fixation and for better yield. The salient features of the study are summarised here under.

Preliminary evaluation trial was conducted with 53 grain type cowpea genotypes during summer 1991 at the College of Agriculture, Vellayani, Thiruvananthapuram for the estimation of genetic variability for biological nitrogen fixation traits such as number of days to 50 per cent flowering, number of nodules in the primary root, number of nodules in the secondary roots, total number of nodules, weight of effective nodules in the primary root, weight of nodules in the secondary roots, total nodule weight, plant dry weight and

nitrogen content in plant at 50 per cent flowering and yield characters such as length of pods, number of pods per plant, weight of 100 seeds, seed protein content and grain yield.

The relative magnitude of difference of phenotypic and genotypic coefficient of variation was found to be narrow for characters like number of days to flower, total nodule weight and nitrogen content per plant, weight of 100 seeds and seed protein content, while moderate magnitude of difference were recorded for number of nodules in the primary root, number of nodules in the secondary roots, total number of nodules, weight of effective nodules in the primary root, weight of nodules in the secondary root, length of pod and number of pods per plant. Hence these characters are being greatly influenced by the genetic factors rather than environmental factors. Plant dry weight and grain yield per plant registered a wider relative magnitude of PCV and GCV indicating the greater influence of environment over these two characters.

Heritability was found to be high for the characters such as number of days to 50 per cent flowering, total nodule weight, nitrogen content in plant, weight of 100 seeds and seed protein content and medium for number of nodules in the primary root, number of nodules in the secondary root, total number of nodules, weight of effective nodules in the primary root, weight of nodules in the secondary roots, length of pods and number of pods per plant and low for plant dry weight and grain yield.

Genetic advance as per cent of mean was found to be high for the characters like number of nodules in the secondary roots, weight of effective nodules in the primary root, weight of nodules in the secondary roots, total nodule weight, number of pods per plant and weight of 100 seeds and moderate for number of nodules in the primary root, total number of nodules and grain yield. Low genetic advance was recorded by number of days to flower, plant dry weight, nitrogen content per plant, length of pod and seed protein content. Hence characters such as number and weight of nodules in the primary root, number and weight of nodules in the secondary roots, total number and weight of nodules, number of pods per plant and weight of 100 seeds may be controlled by additive genes whereas days to 50 per cent flowering, nitrogen content in plant, length of pod and seed protein content may be controlled by non-additive genes. Low heritability together with low genetic advance recorded by plant dry weight and grain yield per plant confirms the high influence of environment on the expression of these characters.

Based on the genetic correlation of characters studied, it was understood that high nitrogen fixing genotypes may not be higher yielders because of the antagonistic relationship between grain yield and total nitrogen per plant. It was found that number of nodules in the primary root, weight of nodules in the primary root and weight of nodules in the secondary root were positively correlated with the nodule weight and that total weight was positively correlated with the nitrogen content in plant. Hence genotype which was able to form effective large nodules on the primary root system seems to be a better nitrogen fixer.

Number of days to 50 per cent flowering had negative genotypic correlation with grain yield. Hence an early flowering genotype may be better yielder than a late flowering genotype. Weight of hundred seed and seed protein content exhibited very strong negative correlation. At the same time no correlation existed between seed yield per plant and protein content indicating that small seeded genotypes are better with respect to protein content and seed yield could be improved with out sacrificing the protein content of the seed. The grain yield recorded positive and significant phenotypic and genotypic correlation with number of pods per plant indicating that selection based on number of pods per plant will lead to an increase in the yield of seeds.

Based on the selection index worked out with nitrogen fixing characters such as total nodule weight, plant dry weight and nitrogen content per plant, top ranking three genotypes such as VCP 4, CoVu 358 and DPLC 210 were selected as lines and bottom ranking two genotypes such as PTB 2 and C 190 were selected as testers. Selections were made based on grain yield per plant for the yield character. Top yielders such as V 322, V 27 and V 271 were selected as lines and two low yielders such as C 152 and CoVu 85020 were selected as testers. Indepent selection criteria were followed due to the negative correlation of nitrogen content per plant and grain yield per plant.

A line x tester analysis was carried out and variance found to be significant for the characters such as number of days to 50 per cent flowering, weight of nodules in the primary root, total weight of nodules, weight of effective nodules, dry weight of the plant, nitrogen content per plant, length of pod, number of seeds per pod, number of pods per plant, hundred seed weight, seed protein content and yield per plant. The data were further analysed for combining ability. The variance due to lines were significant for number of days to flower, length of pod, number of pods per plant, hundred seed weight, seed protein content and yield per plant and variance for testers were significant for number of days to flower, total weight of nodules, weight of effective nodules, dry weight of the plant, nitrogen content per plant, length of pod, number of seeds per pod, number of pods per plant, hundred seed weight, seed protein content and yield per plant. However the variance due to line x tester interaction was significant for all the characters under study, which indicated that both additive and non-additive gene actions might be involved in their inheritance. The predominance ofSCAvariance overGCAvariance for all the traits indicated the preponderance of non-additive genes over additive genes in the control of the trait. VCP 4 was found to be the best general combiner for most of the nitrogen fixing characters and V 322 was the best general combiner for the grain yield.

The cross combinations of V 27 X C 152 and V 271 X CoVu 85020 showed the best performance with respect to specific combining ability for the character number of days to 50 per cent flowering while VCP 4 X C 152 for weight of nodules in the primary root and nitrogen content in plant. DPLC 210 X PTB 2 recorded high sca for total weight of nodules, weight of effective nodules, dry weight of the plant and number of pods per plant, on the other hand CoVu 358 X C 190 recorded high sca for length of pod, number of seeds per pod and seed protein content. The cross combination V 322 X C 190 exhibited high sca for hundred seed weight and V-27 X C 152 for grain yield per plant. Such superior cross combinations involving high and low performing parents and exhibiting high sca effects are expected to segregate for desirable transgrassive segregants. The GCA and SCA variance ratio which was less than unity for all the traits under study indicated predominance of non-additive gene action in the inheritance of these traits.

For all the characters under study, the SCA variances were more important indicating the predominance of non-additive genetic variances. The combining ability of these characters can possibly be exploited through heterosis breeding. In the absence of biological feasibility, exploitation of heterosis, however, is not economical as a plant improvement programme in this crop, though hybrid vigour was exhibited by majority of the hybrids for most of the characters.Therefore, the genetic improvement of these traits can be brought about more effectively through combination breeding involving genetically diverse and high combining parents. Hence F_2 generation was raised from the 24 cross combinations and out of which ten recombinants were selected from VCP 4 X PTB 2, VCP 4 X C 152, V 322 X PTB 2, V 27 X PTB 2 and V 271 X PTB 2 crosses for further testing and selection.

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GENETIC ANALYSIS OF BIOLOGICAL NITROGEN FIXATION TRAITS AND YIELD COMPONENTS IN COWPEA
(*Vigna unguiculata* (Linn). Walp).

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ABSTRACT OF A THESIS
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ABSTRACT

A study on the parameters of variability, correlations, path-coefficients, combining ability, gene action and heterosis in cowpea was undertaken at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during 1991 to 1993. Fifty three genotypes of cowpea collected from different sources were planted in a field experimennt for the estimation of variability, correlation and path coefficient. Eleven biological nitrogen fixation characters, *viz.*, number of days to flower, length of primary root, number of secondary roots, number of nodules in the primary root, number of nodules in the secondary roots, total number of nodules, weight of effective nodules in the primary root, weight of nodules in the secondary roots, total weight of nodules, nitrogen content in the plant at 50 per cent flowering and plant dry weight and six yield characters, viz., grain yield per plant, length of pods, number of pods per plant, number of seeds per pod, weight of 100 seeds and seed protein content were considered for this study.

The ten selected varieties/types from the initial evaluation trial were crossed in a line x tester model, keeping the three high nitrogen fixing types and three high yielding types as lines (total six lines) and two low nitrogen fixing and two low yielding types as testers (total four testers). The F_1's along with their parents were compared in a field experiment and combining ability, gene action and heterosis were estimated. The study of combining ability and gene action were confined to six biological nitrogen fixation

characters, viz., number of days to 50 per cent flowering, weight of nodules in the primary root, total weight of nodules, weight of effective nodules, dry weight of the plant and nitrogen content per plant and six yield characters, viz., length of pod, number of seeds per pod, number of pods per plant, hundred seed weight, seed protein content and grain yield per plant.

The analysis of variance revealed that a considerable amount of variation among the varieties was present with respect to the characters under study. Characters like number of days to flower, total nodule weight, nitrogen content per plant, weight of 100 seeds and seed protein content had recorded narrow relative magnitude of difference of phenotypic and genotypic coefficient of variation along with high heritability estimate. Moderate magnitude of difference of PCV and GCV along with moderate heritability was recorded for the characters viz., number of nodules in the primary root, number of nodules in the secondary roots, total number of nodules, weight of effective nodules in the primary root, weight of nodules in the secondary root, length of pods and number of pods per plant. Plant dry weight and grain yield registered a wider difference of PCV and GCV along with low heritability indicating the greater influence of environment over these two characters.

Genetic advance as percentage of mean was found to be high for the characters like number of nodules in the secondary roots, weight of effective nodules in the primary root, weight of nodules in the secondary roots, total nodule weight, number of pods per plant and 100 seed weight and moderate for number of nodules in the primary root, total number of nodules and grain yield. Low genetic advance was recorded by number of days to flower, plant dry weight, nitrogen content per plant, length of pod and seed protein content. Hence characters such as number and weight of nodules in the primary root, number and weight of nodules in the secodary roots, total number annd weight of nodules, number of pods per plant and weight of 100 seeds may be controlled by additive genes whereas days to 50 per cent flowering, nitrogen content in plant, length of pod and seed protein content may be controlled by non-additive genes.

Correlation coefficients were workedout at the genotypic and phenotypic levels. Based on the genetic correlation of characters studied, it was understood that high nitrogen fixing genotypes may not be high yielders because of the antagonistic relationship between grain yield and total nitrogen per plant. Weight of nodules in the primary root and total nodule weight were positively correlated with the nitrogen content in plant. Hence genotypes which was able to form effective large nodules on the primary root system seems to be a better nitrogen fixer.

Number of days to 50 per cent flowering had negative genotypic correlation with grain yield. Hence an early flowering genotype may be better yielder than a late flowering type. Weight of hundred seeds and seed protein content exhibited very strong negative correlation indicating that small seeded genotypes may be better with respect to protein content. Grain yield recorded positive phenotypic and genotypic correlation with number of pods per plant.

Path coefficient analysis at the genotypic level revealed that total number of nodules had the highest positive direct effect on nitrogen content per plant followed by weight of effective nodules in the primary root and weight of effective nodules in the secodary root. Highest positive direct effect was recorded for length of pod with grain yield.

The combining ability analysis revealed that both additive and non-additive gene actions were important for all the characters under study. However GCA and SCA variance ratio which was less than unity for all the traits under study indicated the predominance of non-additive gene action in the inheritance of these traits. Considering the combining ability effects, VCP 4 was found to be the best general combiner for most of the biological nitrogen fixing characters and V 322 was the best general combiner for the grain yield.

The cross combination of V 27 X C 152 and V 271 X CoVu 85020 showed the best performance with respect to sca for the character number of days to 50 per cent flowering while VCP 4 X C 152 for weight of nodules in the primary root and nitrogen content in plant. DPLC 210 X PTB 2 recorded high sca for total weight of nodules, weight of effective nodules, dry weight of the plant and number of pods per plant, on the other hand CoVu 358 X C 190 recorded high sca for length of pod, number of seeds per pod and seed protein content. The cross combination V 322 X C 190 exhibited high sca for hundred seed weight and V 27 X C 152 for grain yield per plant.

Marked heterosis was observed in many cross combinations for most of the characters studied and pronounced heterotic expression was obtained for weight of nodules in the primary root, total weight of nodules, weight of effective nodules, dry weight of the plant at 50 per cent flowering, number of pods per plant and grain yield. It was already established that these characters are being predominantly governed by the non-additive gene action. Hence the heterotic vigour experssed by the hybrid combination with respect to these characters are justified. Since the biological feasibility for the exploitation of heterosis is not economical as a plant improvement programme in this crop, genetic improvement of these trait can be brought about more effectively through combination breeding involving genetically diverse and high combining parents.