GENE ACTION FOR YIELD AND RELATED TRAITS IN SOYBEAN [*Glycine max* (L.) Merrill] AND DEVELOPMENT OF INTERSPECIFIC HYBRIDS INVOLVING WILD SPECIES

THESIS

By

INDU BALA
(A-2010-40-04)

Submitted to

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CERTIFICATE – I

This is to certify that the thesis entitled **"Gene action for yield and related traits in soybean [*Glycine max* (L.) Merrill] and development of interspecific hybrids involving wild species",** submitted in partial fulfilment of the requirements for the award of the degree of **Doctor of Philosophy (Agriculture)** in the discipline of **Plant Breeding and Genetics** of CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur, is a bonafide research work carried out by **Ms. Indu Bala (A-2010-40-04)** daughter of **Smt. Amrawati Dehal** and **Sh. Munshi Ram Dehal** under my supervision and that no part of this thesis has been submitted for any other degree or diploma.

The assistance and help received during the course of this investigation have been fully acknowledged.

(Jai Dev)
Major Advisor

Place: Palampur
Dated: December, 2014

CERTIFICATE- II

This is to certify that the thesis entitled **"Gene action for yield and related traits in soybean [*Glycine max* (L.) Merrill] and development of interspecific hybrids involving wild species",** submitted by **Indu Bala (Admission No. A-2010-40-04)** daughter of **Sh. Munshi Ram Dehal** to the CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur, in partial fulfilment of the requirements for the degree of **Doctor of Philosophy (Agriculture)** in the discipline of **Plant Breeding and Genetics** has been approved by the Advisory Committee after an oral examination of the student in collaboration with an External Examiner.

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Needless to say, errors and omissions are mine!

Place : Palampur
Dated : *(Indu Bala)*

TABLE OF CONTENTS

LIST OF ABBREVIATIONS USED

Sr. No.	Abbreviation	Meaning
1	et al.	et alii (and other)
2	*i.e.*	Id est (that is)
3	*viz*.	vi delicet (namely)
4	p	Page
5	pp	particular pages
6	^{0}C	degree Celsius
7	g	Gram
8	/	Per
9	%	per cent
10	m	Meter
11	mm	Millimeter
12	ha	Hectare
13	cm	Centimeter
14	ml	Milliliter
15	l	Liter
16	µl	Microliter
17	df	degree of freedom
18	kg	Kilogram
19	vs	Against
20	amsl	Above mean sea level
21	N	North
22	E	East
23	&	And

LIST OF TABLES

LIST OF PLATES

Department of Crop Improvement,
College of Agriculture, CSKHPKV, Palampur

Title of thesis	**:**	Gene action for yield and related traits in soybean [*Glycine max* (L.) Merrill] and development of interspecific hybrids involving wild species
Name of the student	**:**	Indu Bala
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Total pages of the thesis	**:**	158
Major Advisor	**:**	Dr. Jai Dev

ABSTRACT

The present investigation entitled ñGene action for yield and related traits in soybean [*Glycine max* (L.) Merrill] and development of interspecific hybrids involving wild speciesò was carried out at the Experimental Farm of the Department of Crop Improvement, CSK HPKV, Palampur to gather information on genetic architecture for seed yield and component traits in soybean and to introgress desirable genes from wild species to cultivated ones. The experimental material comprised of 54 triple test cross progenies derived by mating 18 lines with three testers, namely, Hara Soya (L_1), Him Soya (L_2) and their F_1 (L_3). This genetic material was evaluated in a randomized complete block design with three replications during *kharif* 2013. Epistasis was found to be an integral part of genetic variation for majority of the traits. Epistatic interaction for many traits was ój+lô type except days to 50% flowering, days to 75% maturity, reproductive phase, petiole length, seed per pod, harvest index and 100 seed weight, whereas plant height, internode length, pods per plant and biological yield per plant carried óiô type epistasis alongwith ój+lô type. Additive component (D) was more pronounced than dominance component (H) for most of the traits. Both additive and dominance components were of almost equal magnitude for pod length indicating the importance of both additive and dominance type of gene action, whereas partial degree of dominance was noticed for majority of traits. The kind of genetic variance revealed from triple test cross can be exploited by intermating selected individuals in early segregating generations with delayed selection in later generations, diallel selective mating/ biparental mating or recurrent selection followed by pedigree method to exploit both additive and non-additive components alongwith epistasis. Lines Bragg, Shivalik and P9-2-2 were found to be good general combiners for most of the traits. The cross combinations, Bragg x Hara Soya, PK-472 x Him Soya, DS-1213 x Hara Soya, H-330 x Hara Soya and H-330 x Him soya showed high *per se* performance, SCA effects, heterobeltiosis and economic heterosis for seed yield per plant and were rated as potential crosses for further improvement. Cross H-330 x Him Soya showed resistance against brown spot and bacterial pustule diseases. The interspecific hybrids developed involving *Glycine max* x *G. soja*, were true to type based on confirmation at the morphological, molecular and cytological level. Sufficient variability was found for all the traits studied in wide hybrids. Seed yield per plant showed significantly positive correlation with reproductive phase, pods per plant, pod length, petiole length, harvest index and 100-seed weight.

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1. INTRODUCTION

Soybean [*Glycine max* (L.) Merrill], 2n= 40 ôKing of American Agricultureô (Kuehn 1972) and a miracle crop of the world, has its origin in North-Eastern China (Vavilov 1951 and Leppik 1971). On an average, commercial soybean contains about 40% high quality protein and 20% excellent oil. Much of the demand for soybean in the world, including India, is derived from its popularity as a source of cooking oil and, a base for margarine and other consumer products. This incredibly versatile plant serves a natural soil fertilizer too by fixing atmospheric nitrogen. Soybean is an important leguminous crop for food and feed products. It has traditionally been grown on a small scale in Himachal Pradesh, the Kumaon Hills of Uttrakhand, Eastern Bengal, the Khasi Hills, Manipur, the Naga Hills and parts of Central India covering Madhya Pradesh. It is also referred to, locally, as *bhat*, *bhatman*, *bhatmas*, *ramkulthi*, *garakalay* and *kalitur*. Besides meeting approximately 20% of the total edible oil requirement of the country, the crop is contributing approximately Rs. 7,000 crores to the foreign exchange earnings through the export of de-oiled cake (DOC).

The United States, Brazil, Argentina, China and India are currently the ýve largest producers of soybeans. In India, soybean has emerged as the major oilseed crop in a short span of time. Starting with a meager area of 0.03 mha in 1970, the crop has expanded with an unprecedented pace and touched the figure of 10.70 mha area with an estimated production of 14.14 mt with a productivity of 11.20 q/ha in 2013-14 (Anonymous 2014). In Himachal Pradesh, it occupies an area of 701 ha with a production of 917 tonnes and a productivity of 14.03 q/ha (Anonymous 2013). It is mainly grown in the mid hills under rainfed conditions and primarily used as pulse, oil as well as vegetable by the resource poor hill farmers. There exists a lot of scope for further expansion of its area and production. Himachal Pradesh provides a naturally congenial climate especially in Kangra, Mandi and Kullu districts for soybean cultivation and the crop remains free from yellow mosaic virus (YMV). The crop can tolerate mild drought and is suitable for intercrop or mixed crop with maize in northern plains and northern hills.

For increasing the production of any crop, initial and the cheapest input is the continuous availability of high yielding adapted varieties through a strong breeding programme. Such a breeding programme normally involves high volume of

hybridization. The output of such hybridization, by manipulating hybrid vigour and the generated genetic variability, would mainly depend upon the judicious use of parents based on combining ability and appropriate efficient selection method depending on gene action. In soybean, due to its floral biology and mating system, the possibility of having hybrids for exploiting hybrid vigour is remote and, therefore, under such a situation, breeder has to have an objective judgement about a particular cross likely to produce transgressive recombinants/segregants which, again, depends upon heritable hybrid vigour that may be inferred by the presence of heterosis in F_2 or successive generations. The heterotic vigour is mainly controlled through/by dominant and semidominant genes and these genes are also responsible for inbred vigour and heritability of vigour. Moreover, all the heterotic effects are constantly converted into additive and fixable effects (Fasoulas 1978).

The rational choice of the most suitable breeding method depends, to a large extent, on the nature and magnitude of the gene action involved in the control of various traits of interest to the breeder (Cockerham 1961). Therefore, it is important to partition the total genetic variance into its various components, *viz.,* additive, dominance and epistasis. A good genetic model is one which enables the breeder to have precise and unbiased estimates of all the components of genetic variation. The triple test cross (TTC) technique of Kearsey and Jinks (1968) tests the presence of epistasis and provides the estimates of additive and dominance components to a high degree of precision in the absence of epistasis. This approach is also independent of gene frequencies, gene correlations and mating systems. A relatively large number of parents can be evaluated as only three testers are used in this design compared to the diallel mating design. The work on the genetics of quantitative traits in soybean is meager; hence, the present study is proposed to assess the nature and magnitude of genetic variances operative in the inheritance of different biometrical traits.

The combining ability is an important tool for the selection of desirable parents together with the information regarding nature and magnitude of genetic variances controlling quantitative traits of economic importance. It is important to plant breeders in choosing the desirable parents for hybridization programme and to frame efficient breeding plan leading to rapid development.

The genetic base of modern soybean cultivars is narrow since most of the parents used in crossing are from soybean gene pool 1 (GP 1). To guarantee future global food security and sustainable crop production, there exists a need to broaden the genetic base of soybean cultivars. The wild relatives of soybean are a potential reservoir of diversity for this purpose. The perennial *Glycine tomentella* (Hayata) and the annual *Glycine soja* (Sieb. and Zucc.) have been hybridized successfully with the domesticated soybean to produce breeding lines suitable for yield testing (Ma and Nelson 2012; Kabelka et al. 2004; Singh et al. 1990). These wild species are an excellent source of genetic variability, agronomically useful genes, biotic and abiotic stresses. These invaluable traits could be exploited to broaden the genetic base of soybean (Chung and Singh 2008). These species also harbor some undesirable genetic traits, for example, vining, lodging susceptibility, lack of complete leaf abscission, seed shattering and small black coated seeds, however, desirable ones could be sorted out during the course of selection in successive segregating generations. Of the two, the wild progenitor of soybean, *G. soja*, is the most easily accessible to breeders and has a wealth of diversity preserved in the USDA soybean collection (Carter et al. 2004). Thus, it may be an excellent source of new agronomic genes and traits (Lee et al. 2008). This wild soybean has the same chromosome number as the cultivated soybean, crosses freely *via* insect or manual hybridization, and progeny are usually completely fertile (Singh and Hymowitz 1988; Weber 1950). Only three species (*G. argyrea*, *G. canescens*, *and G. tomentella*) have been successfully hybridized with soybean; the F_1 hybrids were rescued by embryo culture, were sterile and most researchers could not proceed beyond the amphidiploid stage, with the exception of Singh et al. (1998; R. J. Singh, unpublished results).

Keeping above in view, the present investigation was undertaken with the following objectives:

To

i) understand the nature and magnitude of gene action for yield and related traits,

ii) identify potential parents and cross combinations on the basis of combining ability and heterosis for future use, and

iii) develop hybrids between *Glycine max* and *Glycine soja* and confirm their hybridity at morphological, molecular and cytological level.

2. REVIEW OF LITERATURE

In evolving new forms of crop plants, plant breeders have to deal, mainly, with traits which are governed by polygenic system and show continuous variation. In order to devise the most appropriate breeding procedure to manipulate these genetic systems, especially in populations obtained through hybridization involving large number of parents in crosses, it is imperative for a breeder to have information on the extent of heterosis, combining ability of parents and types of gene action involved for the economic traits under improvement.

The value of wild species in plant breeding has been known since long as these are valuable gene pools, offer opportunities for enhancing genetic variability and introgressing desired traits, particularly resistance to various stresses. Although, these wild relatives have largely remained under utilized in grain legumes due to crossability barriers, however, there are some examples of successful introgression of genes into the cultivated species from their wild relatives, particularly those constituting primary and secondary gene pools. The gene pools of most of the crop plants have less variability compared to the naturally occurring genetic variation of their wild progenitors. Genetic variability of the wild species of soybean could be used for the improvement of the cultivated ones.

Studies conducted on such aspects in soybean [*Glycine max* (L.) Merrill] is limited. However, available information obtained on extent of heterosis, combining ability, gene action in soybean and some related crops and, wide hybridization in soybean is reviewed hereafter under the following sub-heads:

2.1 Triple test cross

2.2 Combining ability and gene action

2.3 Heterosis studies

2.4 Wide hybridization

2.1 Triple test cross

Choice of the most suitable breeding method, amongst several in hand, depends on the types of gene action involved in the expression of polygenic traits of breederôs interest. In the past, several biometrical models have been developed for the study of quantitative traits and estimation of the type of gene effects governing them. Most of these models have been developed ignoring the epistasis for the sake of easier derivations. Therefore, these models are not reliable for describing the nature of quantitative variation. To obtain more efficient estimates of additive, dominance and environmental components of variation for a trait, from second degree statistics, three difficulties inevitably arise:

i) It is assumed, in most of the analyses, that non-allelic interactions are absent, although, these analyses rarely provide a valid test of this assumption.

ii) The estimates of dominance components invariably have much larger standard errors than do the corresponding additive components.

iii) The additive and dominance components are differentially affected by the linkages and correlated gene distribution in the parents.

Comstock and Robinson (1952) developed North Carolina Design III to overcome the larger standard errors of dominance and epistasis. Kearsey and Jinks (1968) described an extension of North Carolina Design III as Triple Test Cross (TTC) which is applicable to any population irrespective of its mating system and, gene and genotype frequencies. The extended analysis provides test for the presence of epistatic variation in addition to unbiased estimates of additive and dominance components of variation when epistasis is absent.

Jinks et al. (1969) devised a test for detecting epistasis which is applicable only to inbred lines. This simplified version of the triple test cross retains many of the advantages of being unambiguous, statistically reliable and universal in applicability. The main limitation of this design is that if the testers do not differ at all the loci for which the lines under test differ, the test for epistasis is no longer unambiguous and the estimates of additive and dominance components of variation are biased (Virk and Jinks 1977). In order to test and allow for such biases, a modification of the simplified triple test cross analysis has been suggested by Jinks and Virk (1977). The review of work done through triple test cross on soybean is summarized hereafter.

Virk et al. (1983) investigated ten pure lines in a triple test cross and concluded that epistasis was an integral component of genetic variation for flowering time, plant height, number of nodes and seed yield per plant in pea.

Singh et al. (1986) showed that áîô (additive × additive) type epistasis was important in the control of characters in all four crosses except for seed number in two crosses where éj + lô (additive × dominance and dominance × dominance) type epistasis was also important. Both additive and dominance components of variation were significant for all the traits in all the crosses. Partial dominance and high heritability estimates were obtained for most of the traits in field pea.

Singh et al. (1987), using triple test cross analysis, observed that additive gene action was the major genetic component, however, dominance component was also found to be significant in field pea. Both components of epistasis (i and j+l type) were significant for days to flowering, plant height, pods per plant and yield per plant, though, the overall relative contribution of áîô type epistasis was more important than éj+lô type in cross óT-163 × Arkelô. On the other hand, there was great evidence of éj+lô type in the cross ó5064 × EDô. Both D and H components were significant for all the traits with the predominance of the former. The significant estimates of H and non-significant value of F indicated that dominance was ambi-directional and alleles with increasing and decreasing effects appeared to be dominant and recessive to the same extent.

Singh et al. (1988), by using triple test cross and North Carolina design III, found that additive and dominance gene effects were highly significant for all the traits except pods per plant in field pea wherein additive effects being greater than dominance effects.

Sirohi and Gupta (1993) studied genetic variance and combining ability in pea in seed protein content using triple test cross analysis and reported that only éj+lô type epistasis was significant. Both additive and dominance components were important with the predominance of additive genetic variance.

Rathore et al. (1995) detected additive genetic variance for biological yield per plant, dominance genetic variance for seeds per pod and pod length, and both additive and dominance variances for yield per plant by following triple test cross mating design in pea crop.

Sirohi and Gupta (1995) found that non-allelic interaction was an integral component for the genetic architecture of days to flowering, days to maturity, plant height, nodes per plant and internodal length. Only ój+lô (additive × dominance and dominance × dominance) type of non-allelic interactions were important for days to flowering, days to maturity, plant height and nodes per plant in pea crop.

Singh et al. (1997) demonstrated that non-allelic interactions affected days to flowering, plant height, pods per plant, seeds per pod, pod length and seed yield per plant in pea crop. Significant estimates of both additive and dominance components were observed for all these characters except pod length where only the dominance component was significant with the predominance of additive genetic component. This suggested that the selection in the early segregating generations might lead to the desired improvement in these characters. The directional element (F) was significant and positive for days to flowering, plant height, pods per plant and seed yield per plant revealing the iso-directional nature of dominance which suggested that the genes with increasing effects were predominant for these traits. The positive and non-significant values of the directional element (F) for seeds per pod and pod length indicated ambi-directional nature of dominance. The dominance ratio (average degree of dominance) was in the range of partial dominance for almost all the traits except pod length where dominance had no role to play in the expression of this character.

Rahangdale and Raut (2002) studied five generations, *viz.,* P_1, P_2, F_1, F_2 and F_3 to estimate the gene effects for oil content and other 15 quantitative traits in soybean. Additive and dominance gene effects were found important in determining the inheritance of seed oil content in all the four crosses. Complementary epistasis was found important for oil content in MACS 684 x RSC 1 and PK 472 x RSC 2. They observed that additive gene effects also determined the inheritance of days to 50% flowering, days to maturity, plant height and harvest index. Dominance gene action was critical in determining the yield and oil content. Duplicate epistasis was significantly important in the inheritance of plant height, number of branches, seeds and pods per plant, 100-seed weight and seed yield per plant.

Maloo and Nair (2005) found that estimates of means were highly significant for all the characters in all the crosses they studied. The dominance component was significant and higher in magnitude than the additive effect for pods per plant, seeds per

pod, 100-seed weight, seed yield per plant and biological yield per plant in all the crosses, it was significant for plant height in JS 80-21 x MACS 58 and PK 416 x NRC 12; for seed: pod weight ratio in Monetta x PK 472 and PK 416 x NRC 12; and for days to maturity and harvest index in Monetta x PK 472 and JS 80-21 x MACS 58. However, for days to flowering, the dominance component was significant only in JS 80-21 x MACS 58. Among the digenic interaction effects, both additive x additive and dominance x dominance interactions were significant for pods per plant in JS 80-21 x MACS 58 and PK 416 x NRC 12, and for height of pod insertion in Monetta x PK 422 and PK 416 x NRC 12. The magnitude of additive x additive and dominance x dominance interaction was more than that of additive x dominance for most of the characters in all the three crosses.

Singh et al. (2006) while using modified triple test cross design reported that the estimates of additive genetic variance (D) obtained by variances of sums of $L_{1i}+L_{2i}$, and $L_{1i}+L_{2i}+L_{3i}$ were found to be comparable for most of the characters in pea. Partial dominance was predominant for days to maturity, seed yield and protein content. Plant height exhibited complete dominance to overdominance which suggested greater role of dominant gene effect in its inheritance.

Singh et al. (2006) evaluated triple test cross progenies in pea resulting from crosses between five lines and three testers and revealed that epistasis was not an integral part of genetic variation and the additive gene effects were predominant for reproductive phase, pods per plant, yield per plant and protein content. Direction of dominance and types of genes exhibiting dominance revealed that reproductive phase and pods per plant were controlled by the increasing types of dominance genes. Positive órô values were exhibited by yield per plant and protein content.

Ganesh et al. (2008) revealed that overdominance and higher magnitude of epistatic components (h) and (l) could be the possible cause of heterosis for seed yield per plant and pods per plant whereas partial dominance was observed for days to flowering in pea crop.

Barona et al. (2009) used ôModified Triple Test Crossô (modified TTC) method in order to study the epistatic variation for grain yield in soybean**.** The experimental material

used in this work consisted of 32 lines (Pi) chosen randomly which were crossed with other two lines of the same population, contrasting for grain yield and, used as testers (L_1 and L_2). Considering the methodology of biometric analysis, the contrast of the means (L_{1i}+L_{2i}-P_i) allowed the detection of significant epistasis through óFô and ótô tests for grain yield in soybean. Therefore, in soybean, the grain yield is affected by the interaction between loci (epistasis).

Singh et al. (2010) evaluated five generations, *viz.,* P_1, P_2, F_1, F_2 and F_3 in a compact family block design to estimate gene effects for major agronomic traits in three soybean single crosses (PS 1347 x *G. soja*, JS 335 x UPSM 534 and PS 1347 x JS 335). The results showed that additive gene effects determined the inheritance of agronomic characters, *viz.,* days to 50 per cent flowering, days to maturity, plant height and harvest index. Dominance gene action was critical in determining the yield. Duplicate epistasis was found significantly important in the inheritance of most of the traits studied. On the basis of results, it was suggested that these major quantitative traits in the desirable genotypes play a major role in the improvement of high yielding varieties of soybean through exploitation of additive and non-additive variances.

Singh et al. (2011) followed TTC by using 20 lines and three testers in pea crop and revealed that total epistasis and its ój+lô type component were significant for all the traits. The additive (D) and dominance (H) components of genetic variance were highly significant for all the traits. Majority of the traits showed partial dominance except overdominance for pods per plant and seed yield per plant. The non-significant directional element (F) for all the traits indicated ambidirectional nature of dominance.

Barona et al. (2012) used 32 inbred lines, derived from a cross between two contrasting lines, which were crossed with two testers (L_1 and L_2). The experiments were carried out at two locations, in 10 x10 triple lattice designs with nine replications, consisting, 32 lines (Pi), 64 crosses (32 Pi x L_1 and 32 Pi x L_2) and controls. The variation between (L_{1i} + L_{2i} - Pi) revealed the presence of epistasis as well as an interaction of epistasis x environment. Since the predominant component of epistasis in autogamous species is additive x additive (i type), it was suggested to postpone the selection to later generations of inbreeding in order to exploit the beneficial effects of additive x additive epistasis.

2.2 Combining ability and gene action

The concept of combining ability was proposed by Sprague and Tatum in 1942 while working on maize crop. It has given great stimulus to the breeders working on other crops to direct their efforts in selecting parents possessing better combining ability. The combining ability, in general, is the ability of plants or lines to transmit their qualities to their offsprings persistently in the advanced generations. Sprague and Tatum (1942) have described general combining ability (GCA) and specific combining ability (SCA) as a measure of gene action. They defined general combining ability as the average performance of a line in hybrid combination (a measure of additive gene action) and specific combining ability designate those cases in which certain cross combinations are relatively better or worse than would be expected on the basis of GCA of parent (an estimate of non-additive gene action).

Kaw and Menon (1981), using diallel analysis, reported both GCA and SCA effects to be significant for flowering days, maturity days, height at maturity, number of nodes and number of branches per plant.

Chauhan and Singh (1983), using diallel analysis, reported that both GCA and SCA variances were highly significant for protein and oil content in soybean. Hence both additive and non additive gene action were involved and observed partial dominance for both the characters.

Saini (1983) reported predominantly additive type of gene action for all the traits studied, *viz.,* seed yield per plant, pods per plant, harvest index, 100-seed weight, percent oil content, plant height, primary branches per plant, days to flowering and days to maturity except biological yield.

Singh (1983) using diallel analysis reported that additive and additive x additive components of genetic variance were important in inheritance of all characters.

Kunta et al. (1985) analysing 4 x 4 diallel revealed the presence of additive genetic variance for seed number per pod, seed size and plant height and non- additive variance for yield and plant height; both types of variances were significant for pod number per plant and harvest index.

Sabbouh and Edwards (1985) reported that GCA effects were important for protein content, while SCA effects were important for oil content.

Tawar et al. (1989) studied gene action in soybean. Moderate estimates of heritability were obtained for seeds and pods per plant in the F_1 and F_2 generations and for days to 50% flowering, plant height, branches per plant and 100-seed weight in the F_2. Additive gene effects were important for most of the traits studied. Overdominance was observed for plant height, seed yield and pods per plant.

Sharma et al. (1993) observed that both additive ($\mathring{u}^2A$) and non-additive ($\mathring{u}^2D$) genetic variances were important in the genetic determination of seed yield and its components. However, the ratio of $\mathring{u}^2A$ to $\mathring{u}^2D$ was greater for all the traits except harvest index and 100-seed weight.

Kapila (1994) reported the presence of consistent SCA effects over locations for the nine traits of soybean varieties Cocker Stuart, Hardee and Himso 330 which were adjudged to be good general combiners for seed yield and other related traits. The best specific cross combination, Himso 400 x Lee involved parents with average GCA. Both additive and non-additive genetic variances were important for yield and other related traits.

Sharma and Phul (1994) studied combining ability analysis for yield and quality attributes in soybean. Both additive as well as non additive gene effects were present. However, the preponderance of non additive gene action was reported in the expression of all the traits under study. The better crosses for important characters like pods per plant, seed yield per plant, oil content and protein content showed that, in general, these crosses involved low x low, medium x low and high x low general combiners. The low x low crosses giving high SCA values may be due to the genetic diversity of the parents and non allelic interactions.

Sood et al. (1996), from their study involving ten lines, two testers and 20 hybrids, concluded that based on GCA and SCA variances, both additive as well as non-additive variance were equally important for seed yield per plant.

Bastawisy et al. (1997) reported high GCA effects for days to 50 per cent flowering, days to maturity, branches per plant, plant height, pods per plant and seed yield per plant.

Kunta et al. (1997) obtained significant GCA estimates for pods per plant, seeds per pod, seed weight, plant height and harvest index and SCA for seed yield per plant.

Sabbouh et al. (1998) observed that overall GCA had greater effect on protein content than SCA from data on protein and oil content of seeds of four cultivars (Essex, Forest, York and Douglas) and their F_1 and F_2 hybrids. Cultivar Douglas was identified as having the highest positive GCA effect for protein content. In contrast, SCA was more important than GCA in determining oil content.

Gadag et al. (1999) studied combining ability for yield, protein and oil contents and four other productivity-related traits in a half diallel set involving seven parents and indicated that for protein content, grain yield per plant and days to maturity, non-additive gene effects were predominant. Estimates of SCA variances were higher than GCA variances for all the traits. The high performing crosses for yield involved parents with high x low and low x low GCA effects.

Ponnusamy and Harer (1999) studied combining ability in soybean. The characters studied were governed by both additive and non-additive gene action. There was close agreement between percentage performance of parents and GCA effects for all the characters.

Sood (1999), in a line x tester analysis, reported Cocker Stuart variety as a good general combiner for per cent germination and 100 seed weight, whereas ‘Himso 330 x Lee’ and ‘Himso 459 x Punjab No. 1’ as the good specific combinations for these traits.

Cho and Scott (2000) observed that GCA effects for seed yield were significant and larger than SCA effects. Significant GCA and SCA effects were found for seed weight indicating that both additive and non additive genetic effects were involved in controlling seed weight.

Kee et al. (2000) studied gene action and heritability for different traits. Narrow-sense heritability estimate on the basis of variance components was 29.10% for maturity, which was lower than values for days to flowering and flowering period due to large error variances (σ^2E) caused by field environmental factors.

Ganeshmurthy and Seshadri (2002) observed that the variances due to GCA and SCA were significant for days to flowering, days to maturity, plant height, number of branches, number of pods, 100-seed weight, protein content, oil content, dry matter production and seed yield.

Ojo and Dashiell (2002) estimated gene action for a number of yield-related traits. Additive effects were significant for 100-seed weight, plant height, number of pods per plant and seed yield. Only 100-seed weight and yield per plant showed non-significant dominance effects. Additive effect, in general, was larger than dominance effect. However, deviation from the additive-dominance was significant for plant height only. The predominance of additive gene action in the variability for seed weight, number of pods per plant and yield per plant among the generations studied suggested that selection for these traits in early segregating generations was likely to be effective.

Agrawal et al. (2005) conducted gene action and combining ability analysis in soybean for days to flower initiation, days to flower termination, days to maturity, plant height, branches per plant, pods per plant, 100-seed weight and seed yield per plant. The additive:dominance variance ratio indicated that most of the characters were governed by additive gene action.

El-Sayad et al. (2005) observed that the variances due to GCA and SCA were significant for all the characters studied, i.e., number of days from sowing to 95% maturity of pods per plot, number of pods per plant, number of seeds per plant, 100-seed weight and seed yield per plant which revealed that both additive and non-additive effects were important for inheritance of the characters studied.

Gavioli et al. (2006) crossed eight soybean genotypes in a diallel design. The estimated GCA and SCA values were significant for the evaluated traits. The highest GCA effects were observed for all the traits, *viz.,* days to flowering, plant height and number of branches.

Maloo and Sharma (2007) studied the combining ability for oil and protein content in five lines, i.e., JS - 335, Punjab No. 1, MACS -I3, PK - 327 and Pusa - 22 crossed with three testers, PK - 472, MACS - 58 and NRC - 12 in a line x tester mating design. Based on the mean performances, combining ability and gene effects, the crosses óPK - 327 x PK ï 472ô and óJS - 335 x MACS ï 58ô showed high *per se* performance and high GCA effects.

Mebrahtu and Devine (2008) found that estimates of both GCA and SCA and, reciprocal variances were significant for plant height and 100-seed weight. The performances of the parents for green pod yield and its components were highly associated with their GCA effects.

Durai and Subbalakshni (2009) reported that GCA was greater than SCA for all the characters, indicating the preponderance of the additive gene action in the inheritances of all the characters studied except protein and oil content for which SCA was superior to GCA.

Durai and Subbalakshmi (2010) studied 15 cross combinations along with their parents for combining ability and gene action for 12 traits of vegetable importance in soybean. All the traits were found under the control of additive gene action. It was also concluded that DS 9501(P3), TNAU S 55 (P2) and TNAU S 7 (P1) were found to be good general combiners. On the basis of *per se* performance and SCA of the cross combinations and GCA of the parents involved, four cross combinations, *viz*., TNAU S 55 / DS 9501 (P2 / P3), TNAU S 55 / TS 82 (P2 / P4), DS 9501 / TS 82 (P3 / P4) and DS 9501 / CO 2 (P3 / P6) were assessed as the best material for further breeding work to obtain superior segregants.

Nassar (2013) used diallel cross, excluding reciprocals, among six parents of soybean, namely, L86-K-73, Giza111, Giza22, H88L1, H155 and DR101 to estimate combining ability for earliness traits, growth characters, yield and its components, *viz.,* number of pods per plant, number of seeds per pod, number of seeds per plant, seed yield per plant, 100-seed weight, oil percentage and protein percentage. The cross, L86-K-73 X H155 was earliest among fifteen crosses and gave the highest mean value for protein percentage. Highly significant mean squares due to both GCA and SCA were observed for all the traits except number of seeds per pod.

Oliveira et al. (2014) observed that SCA and GCA were significant for all the traits, with a predominance of additive effects. The results indicated the existence of genetic variability in the parents and progeny for all the traits. The rank of the parents based on the means was similar to the rank based on GCA for all the traits.

Wahyu et al. (2014) found that inheritance of a character has important significance in determining plant breeding strategies so that improvements in the character can be better. The population included P_1, P_2, F_1, F_1r (reciprocal F_1) and F_2. Test on the effects of female parent was done by using a mean-difference test (t-test) at 5% level of significance. The degree of dominance of genes (gene action) on the days to maturity was calculated by applying a potency ratio formula showing the gene action's effect on the crossbreeding of both parents on F_1.

2.3 Heterosis studies

Allard (1960) defined heterosis as the vigour associated with F_1 hybrids falling outside the range of parents with respect to certain traits. Plant hybrids were first described by Koelreuter in 1766. East (1909) gave genetic nature of heterosis. Bruce (1910) reported that hybrid vigour is due to the presence of dominant genes in the hybrids. Jones (1917) extended the concept of dominant favourable factors to include linkages. The concept of divergent alleles was given by East (1936). The modern concept of hybrid vigour came with the work of Shull (1948) who produced hybrid maize. The current use of hybrid in plant development was stimulated by the marked success of hybrid corn (Burton and Sprague 1961).

Tian (1981) observed 48% heterosis for seed weight per plant over mid parent in soybean. The increase in seed weight per plant depended mainly on number of seeds per plant and was relatively independent of parental values. Chen (1983) observed significant heterosis in 10 crosses of soybean for seed weight per plant (169.5%), seed number per plant (157%), pod number per plant (152.0%), plant height (131.8%) and number of internodes (126.0%).

Thseng (1983), while comparing 22 F_1 hybrids of soybean, observed that traits, *viz.,* plant height, branches number and plant weight showed the greatest heterosis. Hu et al. (1984), while comparing 12 crosses, observed that the protein content of F_1 hybrids tended towards the better parent. Mehta et al. (1984) found the range of heterosis in soybean for seed yield per plant from 3.64% to 24.90% over the better parent.

Nelson and Bernard (1984) reported that five hybrids yielded significantly more (13 to 19%) than their better parent and only one hybrid exceeded the yield of the best pure line cultivar in the test. Several hybrids significantly exceeded the height of taller

parent, but with few exceptions. Heterosis over the better parent was not observed for maturity date, harvest index, seed weight, oil percentage or protein percentage. However, significant heterosis was observed for yield.

Kunta et al. (1985) observed the range of heterosis in soybean for seed yield per plant from 2.5% to 32.5% over the better parent. Average mid parent heterosis for yield, number of pods per plant, number of seeds per pod, plant height and harvest index were 24.6, 18.0, 0.4, 19.5 and 4.9% respectively. Average better parent heterosis for yield, number of pods per plant, number of seeds per pod, seed size, plant weight, harvest index and plant height were 20.1, 6.9, -3.4, -7.5, 14.0, 1.7 and 7.6%, respectively.

Gadag and Upadhyaya (1995) evaluated 21 soybean hybrids derived from a seven-parent half-diallel set along with their parents to estimate heterosis. Heterosis was significant and positive for yield in 16 hybrids over midparent and in nine hybrids over better parent. Heterosis for yield was generally accompanied by heterosis for yield components. For protein, five hybrids and for oil, one hybrid exhibited significant positive heterosis over midparent. In view of the availability of genetic male sterility, the study revealed good scope for commercial exploitation of heterosis for yield and protein contents in soybean.

Sood et al. (1996), in a line x tester analysis, involving 10 lines, two testers and their resulting 20 F_1 hybrids, studied heterosis for morphological and physiological characters in soybean. On the basis of heterosis, crosses ôHimso 459 x Punjab No. 1ô was better for nodes on main stem and ôHimso 473 x Punjab No. 1 was better for seed yield and petiole length.

Bastawisy et al. (1997) reported highly significant heterotic effects for branches per plant, pods per plant, seeds per plant and seed weight per plant in soybean.

Dogney et al. (1998) reported that heterosis over better parent was positive and significant for seeds per plant, pods per plant, pod bearing nodes per plant, plant height and seed yield per plant. Days to maturity, 100-seed weight and internodal length showed negative and significant heterosis over better parent whereas days to flowering and number of primary branches exhibited negative heterosis over mid-parent and positive heterosis over better parent.

Maheshwari et al. (1999) derived information on heterosis from data on yield and quality traits in 13 soybean genotypes and their 22 F_1 hybrids. Significant heterosis was observed for all the characters. Three crosses, JS-80-21 x PK 472, JS 80-21 x G07 and JS-80-21 x JS 71-05 gave significantly higher yield (6.2 to 13.9 %) than the standard cultivar.

Ponnusamy and Harer (1999) studied heterosis in soybean. The highest magnitude of heterosis was observed for seed yield per plant (108.2%), followed by pods per plant (91.3%). A high degree of heterosis was found between diverse parents.

Sood (1999) evaluated 20 F_1s involving 10 diverse lines and two testers for 100-seed weight to understand the nature and magnitude of heterosis and reported -47.77 to 17.81% heterobeltiosis for 100-seed weight.

Pandini et al. (2001) carried out 10 x 10 diallel experiment at two locations for days to flowering, number of days to maturity, plant height at maturity, oil content, 100-seed weight and seed yield. Positive values of heterosis were found for most traits, especially seed yield. Heterosis for number of days to flowering was for earliness.

Priya (2001), in the study on inheritance of yield and its components in cross combinations involving vegetable and grain soybean, reported maximum heterosis of 97.93 per cent for single plant yield.

Pandini et al. (2002) observed that estimates of heterosis were significant for most traits, *viz.*, seed yield, 100- seed weight, pods per plant, harvest index and number of seed per pod. Positive values of heterosis were detected for all the traits.

Wang et al. (2002) studied F_1 seed yield heterosis in soybean, explored genetic performance of soybean heterosis and screened some highly heterotic combinations. A total of 715 elite soybean lines were used as parents to make 1326 crosses. The results showed that average high parent heterosis (HPH), mid-parent heterosis (MPH) and control variety heterosis (CKH) was 6.8, 21.0 and 11.9%, respectively. The percentage of crosses with HPH and CKH was 20% and 18.3%, respectively, in the first yield test, while the average HPH and CKH was 22.5 and 21.1%, respectively. The percentage of crosses with HPH and CKH over 20% was 22.1%, respectively, in the second yield test. Analyses for different patterns of crosses indicated that combinations made of distant

parents might have higher heterosis. Through two times yield tests, 39 highly heterotic combinations were screened and average HPH and CKH was 39.6 and 33.2%, respectively.

El-Sayad et al. (2005) observed heterosis in F_1 and F_2 diallel crosses among six soybean genotypes for different traits, *viz.,* number of pods per plant, number of seeds per plant, 100-seed weight and seed yield per plant. Significant differences among parents and crosses were detected for all the traits studied, thereby indicating genetic variability for all variables. Negative heterosis percentages relative to mid and better parents were significant in three crosses for days to maturity. Meanwhile, heterosis percentages relative to mid and better parents were significantly positive in several crosses for number of pods per plant, number of seeds per pod, 100-seed weight and seed yield per plant.

Burton and Brownie (2006) found heterosis and inbreeding depression in two soybean single crosses. The average yield of F_1 of the Cross 1 was 16% greater than that of the highest-yielding parent and the average yield of the F_1 of the Cross 2 was 5% greater than the highest-yielding parent. Cross 1 showed significant inbreeding depression when regressed on percentage inbreeding which was a clear evidence of dominance for yield. Possible genetic bases for heterosis in soybean include gene complementation or interaction of duplicate favorable loci in repulsion, linked dominant alleles that are inherited as a unit, a greater number of dominant alleles in the F_1 than either parent separately, multiple dosage-dependant regulatory loci, and/or overdominance. The existence of heterosis indicated that superior gene combinations are possible. The magnitude of yield heterosis may be a useful criterion for selection among biparental crosses.

Ramana and Satyanarayana (2006) derived 16 soybean hybrids by crossing four lines (LSb 1, LSb 3, DSb 1 and JS 90-41) and 4 testers (PK 472, JS 335, PK 1029 and MACS 201) in a line x tester mating design and evaluated along with their eight parents for yield and yield component characters to estimate heterosis. Heterosis was observed for all the characters studied. The hybrids LSb 3 x PK 472, DSb 1 x PK 472, DSb 1 x PK 1029 and DSb 1 x MACS 201 recorded significant positive heterosis over mid and better-parents for grain yield per plant. Positive heterosis over better parent was recorded for oil

content in the cross LSb 3 x MACS 201 and for protein content in the cross JS 90-41 x PK-472. These heterotic cross combinations could be exploited to obtain superior segregants.

Darwish (2007) studied three crosses of soybean each with six populations for yield, yield components and some growth attributes. Negative heterosis was detected for flowering data. Significant positive heterotic effects were detected for other traits in second and third crosses.

Preeti Massey (2007) studied heterosis for yield and yield components of soybean and observed the maximum significant negative residual heterosis over the best parent and standard parent recorded for days to maturity, plant height, pods per plant and seeds per pod. The maximum significant positive residual heterosis was observed for the character seed yield per plant.

Singh et al. (2007) studied heterosis for yield and yield components in soybean in the F_2 generation of 10 crosses obtained from five parental lines (JS 335, PK 327, PK 472, PK 416 and PS 1024). The cross combinations significantly varied for all the traits except number of seeds per pod. Among the F_2 generation, the maximum significant negative residual heterosis over the best parent (BP) and standard parent (SP) for number of days to maturity was recorded for PK 472 x PS 1024 and JS 335 x PK 416, respectively. A significant increase in plant height over mid-parent (MP), BP and SP was recorded for JS 335 x PK 416. For number of pods per plant, PK 327 x PK416, JS335 x PK 416, PK 472 x PS 1024, PK 327 x PK 472 and PS 1024 x PK 416 were superior to BP and SP. For number of seeds per pod, JS 335 x PK 416 and PK 472 x PK 416 were superior to BP. The maximum heterotic response over SP was exhibited by PK 472 x PS 1024. For 100-seed weight, maximum heterosis over BP was evident in PK 472 x PK 416. The cross JS 335 x PK 416 showed the greatest significant positive residual heterosis for seed yield per plant. For harvest index and seed yield, JS 335 x PK 327, JS 335 x PK 416 and PK 472 x PS 1024 exhibited significant positive residual heterosis over BP, whereas PK 472 x PS 1024 showed significant positive residual heterosis over SP.

Patil et al. (2008) evaluated 15 crosses and observed that the magnitude and direction of heterosis, heterobeltiosis and useful heterosis varied substantially from cross

to cross and from character to character. The crosses, Bragg x IC-118013 and JS-80-21 x IC-118319 were found to have maximum useful heterosis, heterobeltiosis and average heterosis for seed yield per plant and number of pods per plant.

Perez et al. (2009) conducted an experiment on 12 F_1 hybrids and their parents at several locations for two years. They observed that during first year, mid parent heterosis (MPH) ranged from -29% to +32% and high-parent heterosis (HPH) from -23% to +1%. During 2nd year, MPH values ranged from -53% to -21%, and HPH from -66% to -35%. Seed protein content showed high-parent heterosis for some combinations. For traits related to vegetative growth such as height, positive mid parent heterosis and high-parent heterosis were observed. In general, depending on the year and parent combinations, there were hybrids that performed better than the mid-parent values suggesting that heterosis was identified in soybean.

Sudaric et al. (2009) conducted an experiment to evaluate heterosis and heterobeltiosis for four grain yield components in soybean and compared the performance of the F_1 hybrids with those of the parents involving 29 genotypes (11 parents and 18 F_1 hybrids). They observed positive heterosis and heterobeltiosis for pod number per plant (18.75%; 7.90%), seed number per plant (16.14%; 3.98%) and seed weight per plant (25.72%; 11.80%). Low positive heterosis (6.62%) and negative heterobeltiosis (-1.08%) were observed for harvest index per plant.

Yin and Yi (2009) found that heterosis for pods per plant and seeds per plant were relatively in accordance with yield heterosis. Parents-based cluster and SSR-based cluster analysis revealed that genetic relationships for eight parents were basically consistent and these were classified into two groups. Therefore, certain genetic distance is required for a cross with high heterosis and high yield, but it is not an only determinant factor for high yield heterosis.

Arya et al. (2010) studied heterosis for 27 parental lines including one control/standard parent, PS 1092 and 35 F_1 crosses for plant height, number of primary branches per plant, number of nodes per plant, number of pods per plant, number of seeds per pod, grain yield per plant, dry matter weight per plant, harvest index, days to 50% flowering, days to maturity, 100-seed weight, oil and protein contents. Some promising F_1s showed high value of heterosis in PS 1241 x PS 1330, PS 1241 x PS 1347, PS 1241 x

PS 1428, PS 1021 x AGS 129, JS 335 x DS-98-14, PK 472 x JS 71-05, PK 515 x EC 389148 and MACS 450 x Hardee for yield and its components to get better segregants in advanced generations in soybean for selection.

Mamta et al. (2010) studied 27 parental lines and 35 F_1 crosses which recorded that some promising F_1s showed high value of heterosis for yield and its components to get better segregants in advanced generation in soybean for selection.

Ghaudhary and Singh (2012) studied 17 F_1s involving eight promising soybean varieties to find out the extent and nature of heterosis. The better parent heterosis for seed yield ranged from -30.3% to 67.8% with a mean heterosis of 26.1%. The two primary yield components, *viz.,* seeds per plant and pods per plant also showed considerable heterosis over better parent, but this was negative for seeds per pod and seed size. Hybrids, Bragg × Clark-63 and Hardee × Punjab-1 exhibited maximum heterosis for seed yield, the values for which were 67.8 and 51.5%, respectively.

Nassar (2013) used diallel cross, excluding reciprocals, among six parents of soybean namely L86-K-73, Giza111, Giza22, H88L1, H155 and DR101 to estimate heterotic expression for earliness traits, growth characters, yield and its components, *viz.,* number of pods per plant, number of seeds per pod, number of seeds per plant, seed yield per plant (gm), 100-seed weight (gm), oil percentage and protein percentage. The hybrid Giza111 X H88L1 had the highest mean value for number of pods per plant, number of seeds per plant and seed yield per plant. Highly significant negative heterotic effects relative to mid-parent for flowering date were observed for two crosses whereas four crosses exhibited highly significant positive heterotic effects than the better parent for plant height. All crosses expressed highly significant positive heterotic effects for number of pods per plant and number of seeds per plant.

2.4 Wide hybridization

Exploitation of wild relatives and their genetic diversity is essential to guarantee global food security and sustainable crop production in soybean. In soybean, breeders have exploited two of its wild relatives, *Glycine tomentella* and *Glycine soja* (Siebold and Zucc.) accessions. Annual *G. soja* is of particular interest for soybean breeding because it is thought to be the wild progenitor of cultivated soybean (Harlan and deWet 1971).

Although *G. max* and *G. soja* are different species by classical taxonomy (Herman 1962), both species contain 2n=2x=40 chromosomes and hybridize readily to produce viable fertile offspring (Karasawa 1936; Singh and Hymowitz 1988; Weber 1950). Attempts to broaden the genetic base of soybean by utilizing *G. soja* were reported by Hartwig (1973), Ertl and Fehr (1985), Carpenter and Fehr (1986) and Carter et al. (2004). Molecular studies also verify that *G. max* and *G. soja* are genomically similar (Doyle and Beachy 1985; Kollipara et al. 1995). This similarity and hybridization ability has led soybean breeders to believe that the wild soybean may hold valuable genes for introgression into *G. max.*

Weber (1950) reported seed size data on F_1 and F_2 single plants from direct *G. max* x *G. soja* crosses and the calculated heterosis values were -35% MPH in the F_1 and -45% MPH in the F_2. Resulting F_1 and F_2 heterosis estimates in this type of cross were highly influenced by the poor undesirable traits of the wild soybean.

Ertl and Fehr (1985) crossed two *Glycine soja* accessions with two high yielding *Glycine max* cultivars followed by five backcrosses to the respective *G. max* parent. The F_2 plants from the backcross populations were visually examined. They observed significant variation among lines in each backcross generation for the traits, *viz.,* maturity and seed coat colour. The mean yield and lodging resistance of the populations improved from the BC_1 to the BC_4 generations. No line from the BC_1 generation performed as well as the recurrent parent for all traits. Three backcrosses to the cultivated parent were necessary to obtain a reasonable number of lines similar to the recurrent parent. The introgression of *G. soja* germplasm into the two soybean cultivars was not as effective method for increasing their yield potential.

Carpenter and Fehr (1986) concluded that under no selection, to obtain a high frequency of agronomically acceptable segregates, three backcrosses were needed, which is equivalent to about six per cent *G. soja* alleles in derived populations.

Singh and Hymowitz (1988) conducted the study with the objective of determining the genomic relationship between cultivated soybean and wild soybean (*Glycine soja*) of the subgenus s*oja*, genus *Glycine*. Observations on cross-ability rate, hybrid viability, meiotic chromosome pairing and pollen fertility in F_1 hybrids of *G. max* × *G. soja* and

reciprocals elucidated that both species hybridized readily and set mature putative hybrid pods, generated vigorous F_1 plants, had a majority of sporocytes that showed 18II + 1IV chromosome association at diakinesis and metaphase I and had a pollen fertility that ranged from 49.2% to 53.3%.

Bodanese et al. (1996) employed a different culture strategy and obtained a greatly improved frequency of embryo rescue in intersubgeneric soybean hybrids. Successful crosses were obtained in 31 different genotype combinations between 9 Brazilian soybean lines as the female parents and 12 accessions from *Glycine canescens*, *G. microphylla*, *G. tabacina* and *G. tomentella*. The hybrid pod retention rate dropped to about 10% during the first 8 days after pollination and stayed largely unchanged up to the 20th day. A total of 90 putative hybrid embryos were rescued using a highly enriched B5 medium to nourish the newly dissected embryos. The growing embryos were then placed in a high osmotic, modified B5 medium to induce maturation and dormancy.

Dogney et al. (1998) carried out interspecific crosses between *Glycine max* x *Glycine soja* and observed that estimates of heterosis over better parent were positive and significant for seeds per plant, pods per plant, pod bearing nodes per plant, plant height and seed yield per plant. Days to maturity, 100-seed weight and internodal length showed negative and significant heterosis over better parent. Days to flowering and number of primary branches exhibited negative heterosis over mid-parent and positive heterosis over better parent.

Palmer et al. (2000) studied genetics and cytology of chromosome inversions in soybean germplasm. One type of chromosome aberration, an inversion, results in the reverse orientation of genes on a chromosome. Inversions are very useful in genetic linkage tests and have been important in the evolution of certain species of animals and plants. In soybean, three accessions (PIs) with a paracentric chromosome inversion were identified. Their objective was to determine if the paracentric inversions identified in PI 597651 and PI 597652 (*Glycine max* cultivated species) and in PI 407179 (*G. soja* wild annual species) were identical. The *G. soja* inversion was backcrossed into *G. max* cultivar Hark. The two *G. max* accessions from China were intercrossed, and based on pollen staining of F_1 and F_2 plants, were considered identical in chromosome structure. However, the *G. soja* accession had a chromosome structure different from the two *G.*

max accessions. Meiotic studies confirmed the presence of the paracentric inversions. Crosses of PI 597651 with either cultivar Hark or Hark homozygous inversion gave F_1 plants with two to three times as many meiotic cells with chromosome bridges as cells with laggards and fragments. However, crosses of PI 567652 with either cultivar Hark or Hark homozygous inversion gave F_1 plants with about equal numbers of meiotic cells with bridges as cells with laggards and fragments. Therefore, cryptic structural differences between these two Chinese accessions might influence chromosome pairing, crossing over and segregation. This might explain the different meiotic behaviours in crosses of the two Chinese accessions with Hark and Hark homozygous inversion.

Yang and Wang (2000) crossed two semi-cultivated (*Glycine gracilis*) and four cultivated (*Glycine max*) cultivars and the resulting F_1 and F_2 progenies were evaluated for agro-morphological and quality characters. The relationship among these traits between intraspecific and interspecific soybean crosses was analysed. Plants derived from interspecific crosses were taller and more vigorous and had more seeds and pods per plant, a lower seed:stem ratio and a lower 100-seed weight than those from intraspecific crosses. In interspecific crosses, taller and more vigorous plants were closely associated with a lower seed:stem ratio.

Nakayama and Yamaguchi (2002) evaluated the frequency of hybridization through pollen flow from the cultivated soybean to the wild soybean to assess the ecological risk of genetically modified crops. The flowering habits of three soybean cultivars and one wild accession were monitored. The seedlings of progeny seeds gathered from individual plants of the wild accession were used for isoenzyme analysis to identify whether they were hybrids or not. In 23 plants of the wild accession, four plants produced hybrids (the incidence of hybridization=17.4%). There was no specific direction in hybridization. The hybridization rate per maternal plant varied from 0 to 5.89% with a mean of 0.73% for all maternal plants. The results indicate that natural hybrids are easily produced in a certain frequency by pollen flow from the cultivated soybean to the wild soybean under their simultaneous flowering with adequate pollinators.

Wang et al. (2004) developed five populations of BC_2F_4-derived lines using the *G. max* cultivar IA 2008 as a recurrent parent and the *G. soja* plant introduction PI 468916 as a donor parent. There were between 57 and 112 BC_2F_4-derived lines in each population and a total of 468 lines for the five populations. The lines were evaluated with

SSR markers and in field tests for yield, maturity, plant height, and lodging. Marker data were analyzed for linkage and combined with field data to identify QTLs.

Chaika et al. (2005) attempted crosses between varietal soybean accessions, interspecific hybrids (*Glycine max* x *G. soja*) and forms of wild soybean. The occurrence in the F_1 of recessive and dominant homozygous genes that do not segregate in the F_2 and further generations can be explained by the presence of two major genes responsible for the type of growth. A breeding procedure with introgressive hybridization was developed and simple hybrids were inferior to complex ones in terms of seed yield. The role of introgression of wild soybean genes into cultivated species and individual selection in increasing the seed yield of interspecific hybrids (*G. max* x *G. soja*) and ((*G. max* x *G. soja*) x *G. soja*) was reported.

Lee et al. (2005) opined that wild soybean (*Glycine soja*) is a useful genetic resource for broadening the genetic background of cultivated soybean and indicated that a single backcross is required to recover a commercially desirable seed-coat color in a population derived from an interspecific cross of *G. max* x *G. soja* when KLG10084 is used as a *G. soja* parent. Therefore, KLG10084 was considered to be a valuable gene source in overcoming the seed-coat color in interspecific crosses and was particularly useful for shortening soybean breeding program by reducing the number of backcrosses that are required.

In the Department of Crop Improvement of this University, soybean genotypes were restructured through introgression of *G. soja* chromatin x *G. max* background long ago under the leadership of Dr. O.P. Sood Senior Soybean Breeder (now retired). These genotypes were developed from two crosses, *viz.,* NRC 2 x *G. soja* and (NRC 2 x *G. soja*) x Pb I. Twenty four such restructured soybean genotypes were evaluated by Chandel et al. 2005. They were able to identify some potential genotypes for different traits. Now there is a need to make fresh wide crosses and confirm their hybridity at morphological, molecular and cytological level. The proposed study will be an attempt in this direction.

Siddhu et al. (2007) observed the effectiveness of number of pods per plant and dry matter yield per plant as independent selection criteria in early generations of two inter specific crosses of soybean, *viz.,* (PK 472 x *Glycine soja*) x PK 472 and (Bragg x

Glycine soja) x Bragg and were evaluated for yield improvement. Mean of the selected progenies for dry matter (88.45 and 82.58 g) and for pods per plant (255 and 200) were higher as compared to the bulk (77.6 and 60.59 g) and (194 and 172) in respective crosses. Proportions of significantly superior progenies over the better parents were also substantially higher in selected progenies as compared to respective bulks.

Barh et al. (2014) observed that seed yield had significant and positive correlation with number of pods per plant, number of primary branches per plant, harvest index and dry matter per plant.

Tomar et al. (2014) found that seed yield had significant and positive correlation with number of primary branches per plant, number of pods per plant, 100-seed weight, harvest index and oil content.

It may be summarized that several researchers have attempted to hybridize wild perennial *Glycine* species with the soybean but only few sterile intersubgeneric F_1 hybrid combinations have been reported (Newell et al. 1987, Singh and Hymowitz 1999). Thus far, only Singh et al. (1990, 1993) have successfully produced backcross derived fertile progenies from the soybean and a wild perennial, *Glycine tomentella* (2n=78). Monosomic alien addition lines (MAALs) and modified diploid (2n=40) lines are being isolated and identified (Singh et al. 1998). The modified diploid lines could be screened for pests and pathogens. Riggs (1998) reported the introgression of SCN resistance from *G. tomentella* into modified derived diploid soybean lines. These studies set the stage for the exploitation of perennial germplasm to broaden the genetic base of the cultivated soybean.

3. MATERIALS AND METHODS

The present study entitled ñGene action for yield and related traits in soybean [*Glycine max* (L.) Merrill] and development of interspecific hybrids involving wild speciesò was conducted during *kharif* 2011- 2013 at the Experimental Farm of the Department of Crop Improvement, CSK HPKV, Palampur (H.P.). Geographically, the farm is situated at an elevation of about 1,290 m above mean sea level with 36°6N latitude and 76°3ôE longitude representing the mid-hill zone (Zone-2) of Himachal Pradesh and is characterized by humid sub-temperate climate with high rainfall (2,500 mm per annum). The soil is acidic in nature with pH ranging from 5.0 to 5.6.

3.1 Experimental Material

The experimental materials comprised 18 fixed lines, three testers of soybean and their 54 triple test cross families. Two agronomically superior and diverse genotypes, Him soya and Hara soya (P_1 and P_2) and their F_1s were used as testers óL_1ô, óL_2ô and óL_3ô, respectively. Details of material used are given in Table 3.1.

Table 3.1 List of varieties used for developing triple test cross hybrids

S. No.	Lines	S. No.	Lines
1	SL-682	12	P2-2
2	P6-1	13	H-330
3	SL-679	14	PS-1469
4	P9-2-2	15	VLS-59
5	DS1213	16	JS-335
6	PK-472	17	P169-3
7	Hardee	18	P13-4
8	Bragg		**Testers**
9	SL-795	1	Him Soya (L_1)
10	Shivalik	2	Hara Soya (L_2)
11	PS-1466	3	Hara Soya x Him Soya (L_3)

Characteristics of two testers, i.e., Hara Soya and Him Soya

Traits	Hara Soya (Himso 1563)	Him Soya (Himso 1588)
Flower colour	White	Purple
Seed size	Bold	Small to medium
Hilum colour	Black	Dark brown
Seed colour	Green	Yellow
Maturity period	About 117 days	About 121 days
Average yield	About 18-20 q/ha	About 15-20 q/ha

3.2 Methods

3.2.1 Crossing Plan

The crosses were attempted as per triple test cross (TTC) design proposed by Kearsey and Jinks (1968). During *kharif* 2011, Hara soya was crossed with Him soya and sufficient F_1 seeds were produced. During *kharif* 2012, these three testers were used as male parents for crossing with 18 lines (females) to develop 54 triple test cross hybrids.

3.2.2 Experimental Design and Layout

The fifty four F_1 hybrids, 18 lines and 3 testers were grown in a completely randomized block design with three replications during *kharif* 2013. The experimental plot of each treatment consisted of one row of 2m length. Row to row and plant to plant distances were maintained at 50 and 20 cms, respectively.

3.2.3 Observations recorded

Observations were recorded on randomly taken five competitive plants from each entry in each replication for the following traits.

A. Morpho-metric traits:

1. **Days to 50% flowering:** It was measured as number of days from planting date to the appearance of 50 per cent flowers in each entry in each plot.

Hara Soya

Him Soya

Plate 3.1 Two testers

(a)

(b)

Plate 3.2 (a and b) General view of trial

2. **Days to 75% maturity:** It was measured as the number of days from sowing date to 75 per cent maturity in each plot.
3. **Reproductive phase:** The total number of days taken from the date of first flowering to 75 per cent maturity in each entry was recorded in each plot.
4. **Plant height (cm):** It was measured in centimeters from the base of the plant to the tip of the main shoot at maturity.
5. **Branches per plant:** The number of primary branches originating from the main shoot were counted at maturity and averaged.
6. **Nodes on main stem:** The nodes on each main stem from base to top were counted at maturity and averaged.
7. **Internode length (cm):** Internode length was obtained by dividing plant height (cm) by nodes per plant.
8. **Petiole length (cm):** Five random leaves of each plant were evaluated and their petiole length was measured in centimetres from the base of the petiole to its point of attachment with leaf and averaged.
9. **Pods per plant:** Mature pods per plant were counted at the time of maturity and averaged.
10. **Pod length (cm):** Pod length was measured for five randomly taken pods of the selected plants from the initiation point from where the pod attached to the branches or the main stem and averaged.
11. **Seeds per pod:** Seeds per pod were obtained by dividing seeds per plant by pods per plant.
12. **Biological yield per plant (g):** Sun dried plants were individually weighed before threshing. Weight of five plants was added and average was recorded in grammes.
13. **Seed yield per plant (g):** All the pods of each plant were threshed.
14. **Harvest index (%):** It was calculated as:

$$\text{Harvest index (\%)} = \frac{\text{Seed yield/plant (g)}}{\text{Biological yield/plant (g)}} \times 100$$

15. **100-seed weight (g):** One hundred randomly counted seeds were weighed on a Electrical Top Pan Balance and recorded in grammes in each entry and plot.

B. Quality traits:

1. **Crude Protein content (%):** Protein content in seed samples of each genotype for each replication was estimated with the help of InfratecÊ 1241 grain analyzer which uses near-infrared transmittance technology to test multiple parameters, *viz.,* moisture, protein, oil, starch etc. in a broad range of grain and oilseed commodities (Sudar et al. 2007). The procedure is as follows:- pour the sample into the hopper, press the analyzer key and read the result in less than a minute.
2. **Oil content (%):** Oil content (%) in seed samples of each replication for each genotype was estimated with the help of InfratecÊ 1241 grain analyzer which uses near-infrared transmittance technology to test multiple parameters, *viz.,* moisture, protein, oil, starch *etc.* in a broad range of grain and oilseed commodities (Sudar et al. 2007).

C. Reaction to diseases:

The genotypes were screened for reaction to prevailing diseases, namely, brown spot, bacterial leaf blight, bacterial pustules, target leaf spot and pod blight under field conditions on 0-9 scale (Table 3.2) given by Stonehouse (1994).

Table 3.2 Scale (0-9) used to evaluate soybean genotypes for reaction to different diseases under field conditions

Sr. No.	Grade (%)	Scale (0-9)	Reaction Category
1	0	0	Highly resistant (HR)
2	<1	1	Resistant (R)
3	1-10	3	Moderately resistant (MR)
4	11-20	5	Moderately susceptible (MS)
5	21-50	7	Susceptible (S)
6	>51	9	Highly susceptible (HS)

3.3 Statistical analyses

The data were subjected to triple test cross and line x tester analysis. The replication wise mean values of the genotypes for different traits were subjected to the following statistical analyses:

3.3.1 Analysis of variance for the randomized block design:

The data for different characters was analyzed as per Panse and Sukhatme (1984). The analysis of variance was based on the following linear model of Fisher (1954):

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

Where,

Y_{ij} = phenotypic observation of i^{th} genotype in j^{th} replication

μ = general population mean

g_i = effect of i^{th} genotype

r_j = effect of j^{th} replication

e_{ij} = random error (error associated with i^{th} genotype in the j^{th} replication)

On the basis of this model, the analysis of variance (ANOVA) was computed as follows:

ANOVA

Source of variation	Degree of freedom (df)	Sum of squares (SS)	Mean sum of squares (MS)	F ratio (F calculated)	Expected MS
Replications (r)	r-1	Sr	Mr=Sr/(r-1)	Mr/Me	$\sigma^2e+g\sigma^2r$
Genotypes (g)	g-1	Sg	Mg=Sg/(g-1)	Mg/Me	$\sigma^2e+r\sigma^2g$
Error (e)	(r-1) (g-1)	Se	Me=Se/(r-1)(g-1)	-	σ^2e
Total	rg-1	-	-	-	-

Where,

r = number of replications

g = number of genotypes

$\sigma^2 e$ = error variance = Me

$\sigma^2 g$ = variance due to genotypes = (Mg-Me)/r

$\sigma^2 r$ = variance due to replications = (Mr-Me)/g

$\sigma^2 p$ = phenotypic variance = $\sigma^2 g + \sigma^2 e$

The replication and treatment mean squares were tested against error mean squares by óFô test at P=0.05.

From this analysis, the following standard errors were calculated where the óFô test was significant:-

(i) Standard error for the treatment mean:

$$SE\ (m) = \pm \sqrt{\frac{Me}{r}}$$

(ii) Standard error for the difference of treatment mean:

$$SE\ (d) = \pm \sqrt{\frac{2Me}{r}}$$

3.3.2 Triple test cross analysis

The information on the genetic architecture of the material under investigation was gathered through triple test cross design. The analysis of this design is divided into two parts.

(i) Test for epistasis and the adequacy of the model, and

(ii) Estimation of additive and dominance components of variation.

3.3.2.1 Test for the detection of epistasis

The presence of non-allelic interaction can be determined by using the model proposed by Kearsey and Jinks (1968). This test is based on the following comparison:

Test	Comparison	Reference
$\bar{L}_{1i} + \bar{L}_{2i} - 2\bar{L}_{3i}$	1 1 -2	Kearsey and Jinks (1968)

The test $\bar{L}_{1i} + \bar{L}_{2i} - 2\bar{L}_{3i}$ is unambiguous and always tests the presence of epistasis for non-common loci between the L_1 and L_2 testers. $\bar{L}_{1i}$, $\bar{L}_{2i}$ and $\bar{L}_{3i}$ are mean of the i^{th} family with respect to the tester concerned.

The analysis of variance to detect the presence/absence of epistasis has been performed with the following partitioning.

Analysis of variance to detect the presence of epistasis and its further portioning

Source of variation	df
Epistasis	N
i type	1
(j+l) type	(nï 1)
Epistasis × replication	(rï 1)n
i type × replication	(rï 1)
(j+l) type × replication	(nï 1)(rï 1)
Error (within family)	3nr(mï 1)

where,

n = number of lines/males/TTC families

m = average number of plants, and

r = number of replications

The epistasis sum of squares for ónô degrees of freedom was further partitioned into óiô type (homozygote × homozygote) of epistatic interaction having ó1ô degree of freedom and ó(j+l)ô type of epistatic interaction, i.e. the homozygote x heterozygote and heterozygote × heterozygote interactions, having (nï 1)(r-1) degrees of

freedom. Similarly, the sum of squares due to replication × epistasis for (rï 1)n degree of freedom was divided into replication × epistasis (i-type) and replication × epistasis (j and l type) with (rï 1) and (rï 1) (nï 1) degrees of freedom, respectively. Each of the three types of epistasis was tested against their respective interaction with replications using óFô test at 5 per cent level of significance.

3.3.2.2 Estimation of additive and dominance components of variation

The genetic components are to be estimated only if epistasis is absent. In the present study, the additive (sums) and dominance (difference) components of variation have been computed irrespective of the presence or absence of epistasis for the characters under study in order to determine their relative magnitude for various interactions.

The additive (D) and dominance (H) components of genetic variation were estimated from the following orthogonal comparisons (Kearsey and Jinks 1968)

Comparison	$\bar{L}_{1i}$	$\bar{L}_{2i}$	$\bar{L}_{3i}$	Component
Sums	1	1	1	Additive
Differences	1	-1	0	Dominance

When all the three crosses are made, an alternative analysis is possible in which all comparisons among the three kinds of family means i.e. $\bar{L}_{1i}$, $\bar{L}_{2i}$ and $\bar{L}_{3i}$ are orthogonal to one another (Jinks and Perkins 1970).

Comparison	$\bar{L}_{1i}$	$\bar{L}_{2i}$	$\bar{L}_{3i}$	Component
1	1	1	1	Additive
2	1	-1	0	Dominance
3	1	1	-2	Epistasis

For testing the significance, the analysis of variance will take the following form:

(i) Analysis of variance for sums and differences

Analysis of sums

Source	d.f.	MS	Expectations of mean squares
Replication	rï 1		
Sum	nï 1	MS_3	$\frac{1}{m}\ \sigma^2e+\sigma^2sr+3r\sigma^2s$
Sum x replication	(nï 1)(rï 1)	MS_2	$\frac{1}{m}\ \sigma^2e+\sigma^2sr$
Error (within family)	3nr (mï 1)	MS_1	$\frac{1}{m}\ \sigma^2e$

Analysis of difference

Source	d.f.	MS	Expectation
Replication	rï 1		
Difference	nï 1	MS_3	$\frac{1}{m}\ \sigma^2e+\sigma^2dr+2r\sigma^2d$
Difference x replication	(nï 1)(rï 1)	MS_2	$\frac{1}{m}\ \sigma^2e+\sigma^2dr$
Error (within family)	2nr(mï 1)	MS_1	$\frac{1}{m}\ \sigma^2e$

where,

n = number of lines (males)

m = average number of plants per progeny

σ^2e = variance due to error

σ^2s = variance due to sums

σ^2d = variance due to differences

3.3.2.3 Average degree of dominance

On a simple additive-dominance model, the additive and dominance components of variation were estimated as:

$$\sigma^2 s = \frac{MS_3 - MS_2}{3r}$$

$$D = 4\sum_{i=1}^{n} uvdi^2 = 4\sigma^2 s$$

$$\sigma^2 sd = \frac{MS_3 - MS_2}{2r}$$

$$H = 4\sum_{i=1}^{n} uvhi^2 = 4\sigma^2 d$$

The average degree of dominance was computed from the estimated components of D and H as bellows:

Average degree of dominance = $(H/D)^{1/2}$

where,

H = Dominance genetic variances

D = Additive genetic variance

3.3.2.4 Covariance (sums/differences)

The covariance of $\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$ on $\bar{L}_{1i} - \bar{L}_{2i}$ for all values of i was calculated as described by Jinks et al. (1969).

In the absence of epistasis and correlated gene distribution this covariance has the expectation:

$$\text{Cov sums/differences} = \sum_{i=1}^{n} uvd_i h_i = ¼ F$$

F, therefore, has the same coefficient as D and H, but measures the sum of products of the d and h terms. Both the magnitude and the sign of covariance provide information about the magnitude and direction of dominance, which supplements that obtained from $\sigma^2 d$.

3.3.2.5 Estimation of correlation coefficient

To determine whether the covariance is significant, it can be converted into a correlation coefficient with (nï 3) degree of freedom.

$$r(\text{sums/differences}) = \frac{\text{Cov(sums/differences)}}{\sqrt{V\ (\text{sum})\ x\ V\ (\text{differences})}}$$

A number of situations can occur in practice each of which has its own interpretation. These are:

a) σ^2d is significant and r (sums/differences) is also significant

This means that there is a dominant contribution to the variation and the dominance is predominantly in one direction. By examining the sign of F (which is the opposite of the sign of co-variance), the predominant direction of the dominance effects can be determined if F is positive, then the increasing alleles are dominant more often than the decreasing alleles, if F is negative, the decreasing alleles are predominant more often than the increasing alleles.

(b) σ^2d is significant and r (sums/differences) is non-significant

This emphasizes that there is a dominance contribution to the variation but the dominance, is ambi-directional, increasing and decreasing alleles being dominant and recessive to the same extent.

(c) σ^2d is non-significant and r (sums/differences) is also non-significant

This means that there is no evidence of dominance contribution to the variation.

(d) σ^2d is non-significant and r (sums/differences) is significant

This is trivial and could arise as a result of sampling error.

3.3.3 Line x tester analysis

The data were also subjected to the line x tester analysis as per the method given by Kempthorne (1957) after excluding the L_{3i} families and the F_1 tester for obtaining information on combining ability.

3.3.3.1 Analysis of variance

Analysis of variance was carried out following model given by Panse and Sukhatme (1984):

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

(i=1, é é é é é , g)

(j=1, é é é é é , r)

where,

Y_{ij} = phenotypic observation of i^{th} entry in j^{th} replication

μ = general mean

g_i = effect of i^{th} entry

r_j = effect of j^{th} replication and

e_{ij} = the error component

The effects of the above model are assumed to be fixed unknown parameters, except e_{ij}ós which are assumed to be normally and independently distributed with mean zero and common variance σ^2. The analysis of variance based on the above model takes the following form:-

ANOVA

Source of variation	df	Sum of squares	Expected mean sum of squares
Replication	(r-1)	$1/g \sum_{j=1}^{r} y_1^2 - (\sum_{j=1}^{r} y_1)^2 / gr$	-
Progeny	(g-1)	$1/r \sum_{j=1}^{g} y_1^2 - (\sum_{j=1}^{g} y_1)^2 / gr$	$M_g=\sigma_e^2+rr_g^2$
Parent	(p-1)	$1/r \sum_{j=1}^{p} y_1^2 - (\sum_{j=1}^{p} y_1)^2 / pr$	$M_p=\sigma_e^2+rr_p^2$
Line	(f-1)	$1/r \sum_{j=1}^{t} y_1^2 - (\sum_{j=1}^{t} y_1)^2 / mr$	$M_f=\sigma_e^2+rr_f^2$
Tester	(m-1)	$1/r \sum_{j=1}^{m} y_1^2 - (\sum_{j=1}^{m} y_1)^2 / fr$	$M_m=\sigma_e^2+rr_m^2$
Line vs Testers	1	Parents SS-Lines SS-Testers SS	
Cross	(h-1)	$1/g \sum_{j=1}^{h} y_1^2 - (\sum_{j=1}^{h} y_1)^2 / hr$	$M_h=\sigma_e^2+rr_h^2$
Parent vs. Cross	1	Progenies SS-Parents SS-Cross SS	
Error	(g-1)(r-1)	Total SS-Progenies SS-Replication SS	$Me=\sigma_e^2$

where,

g = tm + t + m; p = t + m ; h = tm

m = number of testers

f = number of lines

p = number of parents

h = number of crosses

r = number of replications

g = number of genotypes

The different sum of squares were divided by their respective degree of freedom to obtain mean squares, which were tested against error mean squares using F-test at 5 per cent level of significance.

3.3.3.2 Combining ability analysis

The combining ability analysis was carried out as per the method of Kempthorne (1957).

ANOVA for combining ability

Source	df	SS	MS	Expectations of MS
Replication	rï 1	SS_R	-	-
Cross	hï 1	SS_H	-	-
Tester	mï 1	SS_M	M_1	$\sigma_e^2 + \frac{fr}{m-1}\sum_i^f g_i^2$
line	fï 1	SS_F	M_2	$\sigma_e^2 + \frac{mr}{f-1}\sum_i^m g_i^2$
Line × tester	(f-1) (m-1)	SS_{MP}	M_3	$\sigma_e^2 + \frac{fr}{m-1}\sum_i^f\sum_i^m s_{ij}^2$
Error	(mf-1) (r-1)		M_5	σ_e^2

where, r, m and f are number of replications, testers and lines, respectively.

$SS_R = \sum_{k=1}^{r} Y..k/fmï (Yé)^2/mfr$

$SS_H = \sum_{k=1}^{m} \sum_{j=1}^{f} Y_{ij}./rï ((Yé)^2/mfr$

$SS_M = \sum_{i=1}^{m} Y_i../frï (é)^2/mfr$

$SS_F = \sum_{j=1}^{f} Y.j./mrï (Yé)^2/mfr$

$SS_{MF} = \sum_{i}^{m} \sum_{j}^{f} (Y_{ij}.)^2/rï \sum_{1}^{m} Y_i../frï \sum_{j}^{f} Y.j./mr+(Yé)^2/mfr$

The different sum of squares, thus obtained were divided by their respective degrees of freedom to obtain mean squares, which were tested against respective error mean squares by F test at 5 per cent level of significance.

3.3.3.2.1 Estimation of general and specific combining ability effects

The model of Kempthorne (1957) was used for estimating the GCA and SCA effects in combining ability analysis as under:

$$Y_{ijk} = \mu + g_i + g_j + S_{ij} + e_{ijk}$$

where,

Y_{ijk} = mean value of a character measured on i × j in k^{th} replication

μ = general mean

g_i = general combining ability (GCA) effect of i^{th} line

g_j = general combining ability (GCA) effect of j^{th} tester

S_{ij} = specific combining ability (SCA) of the cross involving i^{th} line and j^{th} tester

e_{ijk} = error associated with ijk^{th} observation

i = i^{th} line (1, 2é . and 18)

j = j^{th} tester (1 and 2)

k = k^{th} replication (1, 2 and 3)

3.3.3.2.1.1 Individual effects were estimated as follows

(i) Estimation of general mean

$$\mu = \frac{Y...}{mfr}$$

where,

Y... = total of all the cross-combinations

m = number of testers

f = number of lines

r = number of replications

(ii) GCA effect of i^{th} line

$$g_i = \frac{Yi..}{mr} - \frac{Y...}{mfr}$$

where,

Yi.. = total of i^{th} female parent over all males and replications

(iii) GCA effect of j^{th} tester

$$g_j = \frac{Y.j.}{fr} - \frac{Y...}{mfr}$$

where,

Y.j. = total of j^{th} male parent over all females and replications

(iv) SCA effect of ij^{th} hybrid

$$S_{ij} = \frac{Yij.}{r} - \frac{Yi..}{mr} - \frac{Y.j.}{fr} + \frac{Y...}{mfr}$$

where,

$Y_{ij..}$ = ij^{th} combination total over all replications

(v) Standard error for combining ability effects

(a) SE ± (g_i) lines = $\pm\sqrt{Me/mr}$

(b) SE ± (g_j) testers = $\pm\sqrt{Me/fr}$

(c) SE ± (S_{ij}) crosses = $\pm\sqrt{Me/r}$

(d) SE ± (g_i-g_j) lines = $\pm\sqrt{2Me/mr}$

(e) SE ± (g_i-g_j) testers = $\pm\sqrt{2Me/fr}$

(f) SE ± (S_{ij}-S_{kj}) crosses = $\pm\sqrt{2Me/r}$

where,

Me = mean squares due to error

r = number of replications

(vi) Test of significance for GCA and SCA: There are two methods:

Method I :

GCA and SCA effects ≥[(SE_{gi}/SE_{gj}/SE_{sij}) × άô tabulated at error degree of freedom and P=0.05 were marked significantly(*).

Method II:

(a) t_i (cal) for GCA of lines = (g_i-0)/SE(g_i)

(b) t_j (cal) for GCA of testers = (g_j-0)/SE(g_j)

(c) t_{ij} (cal) for SCA of crosses = (s_{ij}-0)/SE(s_{ij})

where,

t_i (cal), t_j (cal) and t_{ij} (cal) are the calculated άôvalues,

g_i = GCA effect of i^{th} line

g_j = GCA effect of j^{th} tester and

s_{ij} = SCA effect of ij^{th} cross

The GCA effects of line and testers and SCA effects of crosses were marked (*) when the values (t_i (cal), t_j (cal) and t_{ij} (cal) ≥ t tabulated value at error degree of freedom and P=0.05.

3.3.4 Estimation of heterosis

The estimates of heterosis were calculated as the deviation of F_1 mean from the better parent (BP) and standard check (SC)

1. Heterosis over better parent (BP) % = $\frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$

2. Heterosis over the standard check (SC) % = $\frac{\overline{F_1} - \overline{SC}}{\overline{SC}} \times 100$

3.3.4.1 Calculation of standard error

SE for testing heterosis over BP *i.e.* SE (H_1) = $\pm\sqrt{2Me/r}$

SE for testing heterosis over SC *i.e.* SE (H_2) = $\pm\sqrt{2Me/r}$

3.3.4.2 Test of significance for heterosis

1. Heterosis over BP = $\frac{\overline{F_1} - \overline{BP}}{SE(H_1)} = \acute{\alpha}_1\hat{o}$ calculated

2. Heterosis over SC = $\frac{\overline{F_1} - \overline{SC}}{SE(H_2)} = \acute{\alpha}_2\hat{o}$ calculated

The ά ô calculated values (t_1 and t_2) for heterosis over better parent (BP) and standard check (SC) were compared with ά ô tabulated values at error degree of freedom and P=0.05. The ά ô calculated value ≥ ά ô tabulated values were marked significant and an asterisk (*) was put on per cent values only (Dabholkar 1992).

3.4. Wide hybridization between cultivated and wild soybeans

3.4.1 Experimental material

The experimental material for present investigation included four cultivated soybean (*Glycine max* L.) varieties, *viz.,* Bragg, SL-679, PS-1466 and PS-1469 and three wild soybean species (*Glycine soja*) lines, *viz., Glycine soja, Glycine soja* (PI 65549) and *Glycine soja* (PI 366121).

3.4.2 Development of F_1 hybrids

3.4.2.1 Sowing plan

Soybean genotypes, i.e. *Glycine max* varieties and *Glycine soja* lines were sown during *kharif* 2011 and 2012 at Experimental Farm, Department of Crop Improvement, CSK HPKV, Palampur. Staggered sowing was done at 15 days interval starting from second week of May to end of July. The accessions of wild species were sown in pots 15 days prior to each sowing date of cultivated species to achieve synchronized flowering.

3.4.2.2 Method of sowing of wild species

Seeds of wild species, *viz., Glycine soja, Glycine soja* (PI 65549) and *Glycine soja* (PI 366121) were mechanically scarified prior to sowing so as to speed up the germination and kept for germination in petriplates in incubator at 24°C for 5-6 days. The germinated seedlings were transferred to the pots.

3.4.2.3 Crossing plan

The hybridization experiments were conducted at the Experimental Farm, Department of Crop Improvement, CSK HPKV, Palampur during *kharif* 2011 and 2012 using cultivated genotypes, *viz.,* Bragg, SL-679, PS-1466 and PS-1469 as female and wild species, *viz., Glycine soja*, *Glycine soja* (PI 65549) and *Glycine soja* (PI 366121) as male. Crossing was performed from July to August.

Similarly, other wild perennial soybean species (*Glycine tomentella*) was also used in the wide hybridization studies in the foregoing fashion.

(a)

(b)

Plate 3.3 (a and b) View of crossing block

3.4.2.4 Emasculation and pollination

Emasculation was done either in the morning (08:30-10:00 h) followed by immediate pollination or in the evening (15:00-16:30 h) followed by pollination in the next morning (9:00-10:00 h). During the emasculation process, special care was taken not to touch the stigma with anthers or forcep in order to avoid selfing or damaging the stigma. Pollen from fully expanded flowers, in which anther dehiscence had already taken place, was used for pollination against the stigma of the emasculated flowers.

3.4.2.5 Data recording pertaining to development of F_1 hybrids

Data were recorded with respect to:

I. Total number of soybean flowers pollinated

II. Number of crossed pod set

III. Per cent pod set

Per cent pod set was calculated as follows:

$$\text{Per cent pod set (\%)} = \frac{\text{Total number of crossed pod set}}{\text{Number of soybean flowers pollinated}} \times 100$$

3.4.3 Characterization of interspecific F_1 hybrids

3.4.3.1 Sowing of F_1 hybrids

F_1 hybrids were evaluated during 2012 and 2013 at Experimental Farm, Department of Crop Improvement, Palampur. The F_1 hybrids along with their parents were raised in pots containing mixture of soil, sand and vermi-compost in 2:1:1 ratio in a completely randomized design (CRD) with unequal replications, as number of F_1 seeds varied for different crosses. Seeds were mechanically scarified prior to sowing so as to speed up the germination.

3.4.3.2 Recording of observations

For characterization of interspecific crosses involving cultivated and wild species data were recorded for each F_1 progeny and their parents.

3.4.4 Statistical analysis

The agronomical data obtained from each cross combinations were analysed using the Statistical Analysis System (SAS software). The analysis of variance was done as per CRD (Cochran and Cox 2006) based on the following linear model of Fisher (1954):

$$Y_{ij} = \mu + g_i + e_{ij}$$

Where,

Y_{ij} = Phenotypic effect of the i^{th} genotype of j^{th} treatment,

μ = general mean,

g_i = effect of i^{th} genotype and

e_{ij} = random error associated with i^{th} genotype of j^{th} treatment

The total variance based on this model was partitioned into different components as under :

ANOVA

Sources of variation	**Degree of freedom**	**Mean sum of square**	**F-value**	**Expected mean square**
Between treatments	g-1	Mg	Mg/Me	$\sigma^2 e + r\sigma^2 g$
Within treatments (Error)	N-g	Me		$\sigma^2 e$
Total	N-1			

Where,

g = number of genotypes

N = total number of observations

r = number of replications

$\sigma^2 g$ = variance due to genotypes

$\sigma^2 e$ = error variance

The treatment mean squares were tested against error mean square by ‘F’ test for (g-1), (N-g) degrees of freedom at 5 per cent level of significance (P = 0.05) and 1 per cent level of significance (P = 0.01).

3.4.5 Estimation of heterosis over mid parent and better parent

The magnitude of heterosis was estimated over the mid parent (MP) and better parent (BP) as follows:

$$\text{Heterosis over better parent} = \frac{\overline{F}_1 - \overline{BP}}{\overline{BP}} x\,100$$

$$\text{Heterosis over mid parent} = \frac{\overline{F}_1 - \overline{MP}}{\overline{MP}} x\,100$$

Calculation of standard error [SE (d)]

$$\text{S.E. (d) for testing heterosis over better parent} = \pm\sqrt{2\,Me/r}$$

$$\text{S.E. (d) for testing heterosis over mid parent} = \pm\sqrt{3\,Me/2r}$$

Test of significance for heterosis over better parent :

$$\text{Calculated 't'} = \frac{\overline{F}_1 - \overline{BP}}{SE}$$

Test of significance for heterosis over mid parent :

$$\text{Calculated 't'} = \frac{\overline{F}_1 - \overline{MP}}{SE}$$

Calculated value of 't' was compared with 't' tabulated at error degree of freedom at P ≤ 0.05.

3.4.6 Estimation of correlation coefficient

Correlation coefficient was worked out as given below;

$$R_{xy} = Cov_{xy} / (\mathring{u}_x \times \mathring{u}_y)$$

$$Cov_{xy} = (gMSCP - eMSCP) / r$$

Where,

gMSCP = mean sum of cross products for genotype

eMSCP = mean sum of cross products for error

r = replication

Significance of correlation coefficients was tested against ŕô values as given by Fisher and Yates (1963) at n-2 degrees of freedom at 5 per cent level of significance (P=0.05).

3.4.7 Confirmation of hybridity

Hybridity of F_1 plants was confirmed by morphological, molecular and cytological markers.

3.4.7.1 Confirmation of hybridity at morphological level

Hybridity at morphological level was confirmed through various descriptors:

S. No.	Characteristics	States				
1	Plant : Growth type	Determinate	Semi-determinate	Indeterminate		
2	Plant: Growth habit	Erect	Semi-erect			
3	Leaf : Colour	Green	Dark green			
4	Flower: Colour	White	Purple			
5	Pod: Pubescence	Absent	Present			
6	Pod: Pubescence colour	Grey	Tawny (Brown)			
7	Pod: Colour	Yellow	Brown	Black		
8	Seed: Shape	Spherical	Elliptical			
9	Seed: Colour	Yellow	Yellow green	Green	Black	
10	Seed: Lustre	Shiny	Dull			
11	Seed: Hilum colour	Yellow	Grey	Brown	Black	Variegated
12	Seed: Cotyledon colour	Yellow	Green			

3.4.7.2 Confirmation of hybridity at molecular level

3.4.7.2.1 Molecular characterization

The parents as well as their F_1s were used to confirm hybridity through SSR markers. Thirty four randomly chosen primers were screened, out of which four were found polymorphic (details of SSR primers is given in Table 3.3). The experiment was carried out in the Molecular Cytogenetics and Tissue Culture Lab of the Department of Crop Improvement, CSK HPKV, Palampur.

3.4.7.2.2 Extraction of plant genomic DNA

Genomic DNA from soybean leaf was isolated using CTAB method of Saghai-Maroof et al. (1984). Fresh excised 200-300 mg of young leaf tissue was taken and grinded in presence of liquid nitrogen to make final powder in pre-chilled pestle and mortar. The powder was transferred to a fresh autoclaved 1.5ml eppendorf tube; to this 800 µl DNA extraction buffer pre-warmed at 65^{o}C was added. The contents were mixed gently. The samples were kept for incubation at 60^{o}C for one hour. After incubation, 800 µl of C:I (Chloroform: Isoamyl alcohol) 24:1 was added and mixed gently to emulsify. The samples were centrifuged at 10000 rpm for 10 minutes. The yellow aqueous phase at the top was carefully taken out using a broad neck tip and transferred to a fresh tube. To this 500 µl of chilled Isopropanol was added and tubes were kept at -20^{o}C for one hour for precipitation of DNA. The DNA pellet was obtained by spinning the tubes at 10000 rpm for 10 minutes. The supernatant was discarded and pellet was given washings with 70% ethanol. The DNA pellet was dried till smell of ethanol was totally gone. The pellet was dissolved in 100 µl TE buffer (tris, EDTA) and kept at 4^{o}C for overnight.

3.4.7.2.3 Purification of DNA

One µl of RNase A enzyme was added and the tubes were kept in water bath at 37^{o}C for one hour for incubation. Then 100 µl of Phenol: Chloroform: Isoamyl alcohol (P:C:I) 25:24:1 was added and mixed well by inverting tubes. The tubes were centrifuged at 10000 rpm for five minutes. The upper aqueous phase was transferred to a fresh tube

and 100 µl of Chloroform: Isoamyl alcohol was added. The contents were gently mixed and centrifused at 10000 rpm at 5 minutes and transferred the aqueous phase to fresh tube. Preparation of DNA was done by adding 10 µl of 3M sodium acetate and 200 µl of chilled ethanol. The tubes were kept at -20^{o}C for 30 minutes. The DNA pellet was obtained by spinning the tubes at 10000 rpm for 10 minutes. The supernatant was discarded and pellet was retained. Washings were given to the pellets with 70% ethanol and dried till smell of ethanol disappears. The pellet was dissolved in TE buffer overnight at 4^{o}C and stored at -20^{o}C till use. Quality of DNA was checked by running the samples on 1% agarose gel.

3.4.7.2.4 PCR Amplification of DNA

Polymerase chain reaction (PCR) was performed in final reaction volume of 25µl containing 2.0µl dNTP (0.2 mM each of dATP, dGTP, dCTP and dTTP), 0.2µl *Taq* DNA *polymerase* (5U/µl), 2.5µl 10X PCR Buffer, 1.5µl $MgCl_2$, 1.0µl of primer (10uM), 2.0µl of DNA sample and 15.8µl of sterilized distilled water. DNA amplification was carried out on eppendorf thermocycler with the temperature conditions as shown in Table 3.4. Amplification products were separated by agarose gel electrophoresis. Agarose (1.2% w/v) gels were prepared in 1x TAE Buffer, 40mM Tris-acetate, 1mM EDTA (pH 8.5).

Table 3.3 List of SSR primers used in the present investigation

S. No.	Primer	Upper primer sequence (5'-->3')	Lower primer sequence (5'-->3')
1	Satt301	GCGAAACACTCCTAGTTGATTACAAA	GCGATATAATGCACAAAGAAATTAAAGA
2	Salt77	GATCTAAAGTCTGATATTTTT**A**ACTA	AAAAGGAGAAGGGAGTTGAT
3	Satt20	GAGAAAGAAATGTGTTAGTGTAA	CTTTTCCTTCTTATTCTTTGA
4	Satt5	TATCCTAGAGAAGAACTAAAAAA	GTCGATTAGGCTTGAAATA

Table 3.4 PCR conditions used for SSR analysis

Primer Type	Steps	Temperature and time	Cycles
SSR	Initial denaturation	94^0C for 5 minutes	1
	Denaturation	94^0C for 30 seconds	
	Annealing	49^0C for 30 seconds	
	Extension	72^0C for 1 minute	39
	Final extension	72^0C for 5 minutes	
	Storage	4^0C for Ð	1

3.4.7.2.5 Gel electrophoresis

After completion of PCR amplification, 3 µl of 1x loading dye was added to each PCR tube. A 4 % agarose gel in 1x TAE buffer with 10 µl ethidium bromide (10mg/ml) for 200 ml of volume was prepared. It was allowed to solidify for half an hour. The amplified PCR product was loaded in the prepared jel with 100 bp ladder. The electrophoresis was carried out at 70 V for 2.5 hours, till the bromophenol blue dye travelled more than 2/3 the length of gel. The resolved amplification products were visualized under UV-Transilluminator. The gel was photographed using a Gel Documentation System.

3.4.7.2.6 Confirmation of hybridity through SSR analysis

From the amplified DNA of soybean genotypes and their F_1s generated SSR marker profiles, the presence of SSR bands was done manually. If both the bands of two parents, *viz.*, P_1 and P_2 were present in F_1 it showed that it is true hybrid.

3.4.7.3 Confirmation of hybridity at cytological level

3.4.7.3.1 Collection and pre-treatment of roots

The roots (1-2 cm) of germinated seeds of soybean were excised and transferred into vials containing cold water. Meristematic root tips were

yellowish/brownish in colour. Drained out the water with pipette. Treated the roots with 0.002M (0.5g/L) aqueous solution of 1ml 8- Hydroxyquinoline for 3 to 5 hours at 16 to 18^{o}C in dry bath.

3.4.7.3.2 Collection of roots

For soybean chromosome analysis germinating seeds were kept at 30^{o}C for 4 hours (if germinated in dark cold room/refrigerator). This is not required when roots are collected from a sand bench/vermiculture in greenhouse. The roots (1-2 cm) of germinated seeds of soybean were excised and transferred into vials containing cold water. Care should be taken not to break the actively growing roots/meristematic roots. Meristematic root tips were yellowish/ brownish in colour.

3.4.7.3.3 Pretreatment of roots

It stops formation of spindles, increase the number of metaphase cells by arresting the chromosomes at the metaphase plate, contracts the chromosome length with distinct constrictions and increase the viscosity of cytoplasm. The procedure for this is as given below:

1. Drained out the water with pipette as taken during collection of roots.
2. Treated the roots with 0.002M (0.5g/L) aqueous solution (Dissolve in ddH_2O at room temperature) of 8- Hydroxyquinoline for 3 to 5 hours at 16 to 18^{o}C in dry bath. 1ml 8- Hydroxyquinoline is added with micro-pipette.

3.4.7.3.4 Fixation of roots

Chromosome study depends on a good fixative. The function of a fixative is to fix or stop the cells at desired stage of cell division without causing distortion, swelling or shrinkage of the chromosomes. The procedure for this is as given below:

1. Removed the 8- Hydroxyquinoline with pipette under the hood.
2. Washed with ddH_2O.
3. Put 1ml of fixative (Carnoyôs solution 1 i.e. 1 part glacial acetic acid and 3 parts ethanol) in the vials. Kept the material in the fixative at least for 24 hours at 4^{o}C.
4. Material can be stored at this stage for long duration at -20^{o}C.

3.4.7.3.3 Hydrolysis

Washed fixed root tips area with ddH_2O to remove the fixative. Hydrolyse roots in 1NHCl at 60^oC in a drybath for 10-13 minutes.

3.4.7.3.4 Staining and slide preparation

Rinsed the root tips in ddH_2O. Added 1ml of Feulgen stain. Kept at room temperature for 1-2 hours till meristematic tips have turned purple. Washed root tips in ice cold ddH_2O. Cut the stained region of the root tip. The roots are then stained by placing them in 1% acetocarmine or 1% propiono carmine for 15-20 minutes. The slide preparation was done by placing the root tip on a clean glass slide and the root tip was removed by using surgical blade. Immediately after this, the blunt side of the scalpel was used to squeeze the root so as to take out the meristematic cells. The meristematic cells were placed on the clean slide and a drop of 45 per cent acetic acid was poured on it. Tapping with fine wooden stick was exercised after placing a cover slip inclined on one side with a sterilized razor blade. Proper taping is a crucial and highly useful in separating and spreading the cells on the slide. The slide was subjected to warm treatment over a spirit lamp for few seconds and immediately squashed by placing the slides in a folded filter paper and pressing by thumb on the area of cover slip. The prepared slides were observed in the phase contrast microscope (OLYMPUS CX 31). Chromosomes were counted from good metaphase spreads.

4. RESULTS AND DISCUSSION

The objectives of the present study entitled ñGene action for yield and related traits in soybean [*Glycine max* (L.) Merrill] and development of interspecific hybrids involving wild speciesò were to get information on the nature and magnitude of gene action (additive, dominance and epistasis) in soybean using triple test cross (TTC) and line x tester analysis. The efforts were made to identify potential parents and cross combinations for the genetic improvement on the basis of combining ability and magnitude of exploitable heterosis. In addition, wide hybridization was attempted between cultivated (*Glycine max*) and wild species (*Glycine soja*) with a view to introgress desirable genes from wild species to cultivated ones. The results obtained on the above aspects have been presented and discussed for the genetic amelioration of soybean crop hereafter under following heads.

4.1 Analysis of variance for the experimental design

4.2 Triple test cross analysis

4.3 Line x tester analysis

4.4 Nature and magnitude of heterosis

4.5 Reaction to diseases

4.6 Wide hybridization between cultivated and wild species

4.1 Analysis of variance for the experimental design

Analysis of variance for the experimental design with respect to parents (18 lines and three testers) and their 54 TTC families revealed significant differences among them for all the traits, namely, days to 50% flowering, days to 75% maturity, reproductive phase, plant height, branches per plant, internode length, nodes on main stem, pods per plant, seeds per pod, pod length, biological yield per plant, seed yield per plant, harvest index, 100-seed weight, protein content and oil content except petiole length. It highlighted the presence of sufficient genetic variability in the existing genetic material (Table 4.1).

Table 4.1 Analysis of variance for different traits of the breeding material raised in RBD

Source of variation		Mean sum of squares		
		Replication	Treatment	Error
Traits	**df**	**2**	**74**	**148**
Days to 50% flowering		31.720*	50.890 *	4.630
Days to 75% maturity		149.490*	15.290*	3.470
Reproductive phase		0.003*	0.004 *	0.001
Plant height		917.520*	102.830 *	35.220
Branches/plant		3.620*	2.950*	0.560
Internode length		5.550*	0.730*	0.270
Nodes/main stem		3.240*	3.670*	0.890
Petiole length		4.660*	0.970	1.340
Pods/plant		295.050	1038.030 *	132.830
Seeds/pod		1.670*	0.040*	0.020
Pod length		0.040*	0.070*	0.009
Biological yield/plant		102.760*	215.660 *	31.430
Seed yield/plant		16.680	56.990*	6.810
Harvest index		0.009	0.008*	0.005
100 seed weight		0.730	22.320 *	1.270
Protein content		0.160	2.980*	0.190
Oil content		0.610*	2.800*	0.090

* Significant at P Ò0.05

4.2 Triple test cross analysis

According to Bernardo (2002), epistatic effects exist when the sum of the individual effects of the loci are larger or smaller than the overall effect thereof. In other words, in the absence of epistatic effects, a single additive-dominant model would fully explain the expression of a character. On the other hand, when epistasis is present, it can give biased estimates of additive and dominant genetic components resulting in inaccurate estimates of important genetic parameters such as heritability and expected response to selection.

Currently, there is a growing interest in epistasis, mainly because the epistatic effects are involved in the genetic basis of heterosis and inbreeding depression (Primomo et al. 2005). For autogamous species, the most important are possibly the additive x additive epistatic effects since inbred lines are developed by natural and artificial selection.

There are many examples of epistasis for qualitative traits, but this does not apply to the quantitative traits, where relatively complex designs are required to detect epistasis. Mather (1949) proposed a method based on the analysis of generation means, however, the additive, dominant and epistatic genetic effects that constitute the model cannot be tested independently, preventing an individual interpretation of each effect. The method of Cockerham (1954) allows testing the genetic effects of the model independently; however, for being based on variance components, the error is larger than that of the mean components. Moreover, the method involves a more complex genetic-statistical approach, limiting its applications. The Triple Test Cross (TTC) design proposed by Kearsey and Jinks (1968), which is a modification of the ñNorth Carolina IIIò design, has been widely used as it allows an accurate detection of the presence of epistasis, regardless of the allele frequency, inbreeding level and occurrence of linkage disequilibrium in the population. In TTC, each randomly selected F_2 plant is crossed to the inbred parents (P_1 and P_2) of the original cross and their F_1. In other words, the randomly selected F_2 plants are backcrossed to both the inbred parents and their F_1. Later, Jinks et al. (1969) proposed a modification, known as Modified Triple Test Cross, which is better suited for autogamous species. In this case, P_1, P_2 and their F_1s are used as testers for mating with different lines. Then these TTC families are evaluated accordingly.

Genetic architecture of any crop species has a great bearing on success of breeding procedures. Since, it is already established that estimates of genetic parameters get biased in the presence of epistasis, it is imperative to get a clearer picture by getting unbiased estimates of such parameters. In this context, triple test cross is a useful procedure to detect epistatic bias and equally applicable to segregating and non-segregating generations such as F_2, backcross and homozygous lines (Kearsey and Jinks 1968 and Chahal and Jinks 1978).

Table 4.2 Analysis of variance for triple test cross hybrids

		Mean squares due to		
Source of variation		**Replication**	**Hybrid**	**Error**
Traits	**df**	**2**	**53**	**106**
Days to 50% flowering		10.670	32.960*	5.030
Days to 75% maturity		57.020*	7.120*	2.620
Reproductive phase		0.002	0.003*	0.001
Plant height		408.730*	86.280*	35.010
Branches/plant		1.240	2.350*	0.610
Internode length		3.070*	0.770*	0.230
Nodes/main stem		4.000*	3.650*	0.910
Petiole length		6.270*	1.020	1.270
Pods/plant		147.770	1020.360*	156.160
Seeds/pod		1.300*	0.030*	0.020
Pod length		0.040*	0.080*	0.009
Biological yield/plant		62.770	206.910*	34.710
Seed yield/plant		11.740	59.040*	8.650
Harvest index		0.009	0.007*	0.005
100 seed weight		2.690	23.300*	1.500
Protein content		0.140	2.750*	0.200
Oil content		0.530*	2.620*	0.090

* Significant at P Ò0.05

The data recorded on 54 triple test cross families were subjected to triple test cross analysis to estimate different components of genetic variance. A perusal of the analysis of variance for the triple test cross (Table 4.2) indicated that mean squares due to crosses were significant for all the traits except petiole length which suggested the presence of sufficient variability in the triple test cross progenies for use in recombination breeding.

4.2.1 Test for the detection of epistasis

It has been advocated by many workers that epistasis is an integral component of genetic variation and ignorance of the presence of epistasis would lead to the biased estimates of additive and dominance components of variation. As a consequence, one may choose wrong breeding procedures. The significance of mean squares due to epistasis (Table 4.3) revealed the presence of epistasis for majority of traits, *viz.,* plant height, primary branches per plant, internode length, nodes on main stem, pods per plant, pod length, biological yield per plant, seed yield per plant, protein content and oil content except days to flowering, days to 75% maturity, reproductive phase, petiole length, seeds per pod, harvest index and 100-seed weight. The significant estimates of epistasis may be the result of the involvement of different alleles due to heterozygous state of the lines. The presence of epistasis had been detected for majority of the traits in the present set of materials underlined the importance of additive and dominance components of variance which would have been biased if procedure assuming no epistasis had been employed (Barona et al. 2012).

Further partitioning of mean squares due to epistasis revealed that mean squares due to additive x additive (i) type interaction were non-significant for all the traits except plant height, internode length, petiole length, pods per plant and biological yield per plant; whereas mean squares due to additive x dominance (j type) combined with dominance x dominance (l type) interactions were significant for all the traits except days to 50% flowering, days to 75% maturity, reproductive phase, petiole length, seeds per pod, harvest index and 100-seed weight. Therefore, it is clear from the results that epistasis is an integral component of genetic variation and should not be ignored while formulating breeding programme to improve commercially important traits. If the presence of epistasis is ignored, information of interallelic interactions may be lost and one may get biased estimates of additive and dominance components which may lead to wrong conclusions. Similar results were also observed by Singh et al. (1987), Singh et al. (1997) and many other workers.

Table 4.3 Analysis of variance for the detection of epistasis for different traits

Source of variation		Epistasis	i-type interaction	(j+l) type interaction	Epistasis x replication	i type x replication	(j+l) type x replication
Traits	**df**	**18**	**1**	**17**	**36**	**2**	**34**
Days to 50% flowering		28.720	44.460	27.790	23.440	16.460	23.850
Days to 75% maturity		11.640	8.160	11.850	14.20	23.720	13.640
Reproductive phase		0.004	0.00009	0.0043	0.004	0.007	0.004
Plant height		352.820*	569.070*	340.100*	92.340	0.940	97.720
Branches/plant		13.010*	1.040	13.710*	3.670	1.640	3.790
Internode length		3.340*	20.730*	2.310*	0.520	0.410	0.530
Nodes/main stem		21.930*	22.560	21.890*	4.210	3.780	4.230
Petiole length		4.320	16.780*	3.580	8.850	0.170	9.360
Pods/plant		3088.900*	1067.560*	3207.800*	916.720	27.390	969.03
Seeds/pod		0.140	0.120	0.140	0.090	0.030	0.100
Pod length		0.680*	0.20	0.700*	0.060	0.070	0.060
Biological yield/plant		1111.470*	586.080*	1142.370*	160.660	9.350	169.560
Seed yield/plant		214.760*	50.650	224.410*	43.400	13.990	45.130
Harvest index		0.030	0.006	0.030	0.020	0.004	0.020
100 seed weight		12.380	9.710	12.540	8.710	1.920	9.110
Protein content		6.970*	6.740	6.980*	0.980	0.390	1.010
Oil content		2.720*	1.610	2.780*	0.590	0.070	0.630

* Significant at P Ò0.05

In the breeding of autogamous species, where the objective is to obtain inbred lines, additive x additive epistasis (i type) is possibly the most important one because it is fixable in homozygous genotypes contributing to the superiority of elite lines (Cockerham 1954 and Goldringer et al. 1997).

4.2.2 Estimation of additive and dominance components

4.2.2.1 Analysis of variance

The analysis of variance for sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$) and differences ($\bar{L}_{1i} - \bar{L}_{2i}$) which provides a direct test for the detection of additive and dominance genetic components has been presented in Table 4.4. The perusal of the data revealed that the mean squares due to sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$) were significant for all the traits except petiole length and harvest index, whereas, mean squares due to differences ($\bar{L}_{1i} - \bar{L}_{2i}$) were significant for all the traits except reproductive phase, plant height, internode length, petiole length, seeds per pod, seed yield per plant and harvest index. The significance of mean squares due to the sums and differences provide a direct test of significance of additive (D) and dominance (H) components of variation.

4.2.2.2 Estimation of genetic components of variance

The genetic components additive (D), dominance (H) and related parameters were worked out for all the traits which exhibited significant mean squares due to sums and differences. Estimates of additive (D), dominance (H), covariance of sums and differences (F) and average degree of dominance $(H/D)^{1/2}$ for different groups of traits are given in Table 4.4.

The estimates of mean squares due to sums (measuring D component) and differences (measuring H component) revealed that additive genetic components were significant for all the traits except petiole length and harvest index, whereas, dominance genetic components were significant for all the traits except reproductive phase, plant height, internode length, petiole length, seeds per pod, seed yield per plant and harvest index which indicated the importance of both components in controlling these traits.

The preponderance of additive variance for most of the traits indicated the relative importance of fixable type of gene action in their inheritance. However, non-fixable type of gene action was more important for pod length due to high magnitude of dominance component (Sharma and Phul 1994).

The relative magnitude of D and H components revealed that additive genetic component was predominant for days to flowering, days to 75% maturity, reproductive phase, plant height, branches per plant, internode length, nodes on main stem, pods per plant, biological yield per plant, seed yield per plant, harvest index, 100-seed weight, protein content and oil content, whereas dominance was predominant for pod length. Use of recurrent selection has been suggested to improve the characters when both additive and non-additive gene effects are involved in expression of the traits. Singh et al. (2010) observed that additive gene effects determined the inheritance of agronomic characters, *viz.,* days to 50 per cent flowering, days to 75% maturity, plant height and harvest index. Dominance gene action was critical in determining the yield. Duplicate epistasis was significantly important in inheritance of most traits studied. It is suggested that these major quantitative traits in the desirable genotypes play a major role in the improvement of high yielding varieties of soybean through exploitation of additive and non-additive variances.

The average degree of dominance $(H/D)^{1/2}$ was in the range of partial dominance for most of the traits namely, days to flowering, days to 75% maturity, reproductive phase, plant height, branches per plant, internode length, nodes on main stem, pods per plant, biological yield per plant, seed yield per plant, harvest index, 100-seed weight, protein content and oil content highlighting the relative importance of additive gene action for these traits. The greater magnitude of additive gene action in soybean has also been reported by Tawar et al. (1989) for most of the traits; Saini (1983) for seed yield per plant, pods per plant, harvest index, percent germination, 100- seed weight, percent oil content, plant height, primary branches per plant, days to 50% flowering and days to 75% maturity except biological yield; Kunta et al. (1985) for seed number per pod, seed size and plant height and non- additive variance for yield and plant height; both types of variances were significant for pod number per plant and harvest index. Also, complete dominance was recorded for pod length indicating the importance of both additive and dominance type of gene actions. The importance of both additive and non-additive gene action was also reported by Singh (1983) and Wahyu et al. (2014).

The directional element óFô was positive but non-significant for days to 75% maturity, internode length, petiole length, pods per plant and protein content indicating ambidirectional nature of dominance thereby suggesting that alleles with increasing and decreasing effects appeared to be dominant and recessive to the same extent (Table 4.4). It was positive and significant for biological yield per plant suggesting that alleles with increasing effects appeared to be dominant. It may be argued that either epistasis or dominance does not have much of directional element. On the other hand, negative significant óFô component for days to 50 % flowering, reproductive phase, plant height, branches per plant, nodes on main stem, seeds per pod, seed yield per plant, harvest index, 100-seed weight and oil content revealed the isodirectional nature of dominance which implied that the genes with decreasing effects were predominant than those of increasing effects due to negative alleles.

It has been observed from the analysis of variance studies that sufficient genetic variability was generated in the material under investigation. The presence of epistasis implied that this component should not be overlooked as this may lead to biased, either under or over, estimates of additive and dominance components of variation. However, as of now, there is no conclusive evidence about the extent of bias and the effect of epistasis on the expression of the quantitative traits (Sofi et al. 2006). Since, additive gene action has been observed for majority of the traits including seed yield, selection in the early generations may be useful for the improvement of these traits. The results also revealed the importance of additive × dominance (j) and dominance × dominance (l) type of epistasis in the inheritance of seed yield and other related traits. Besides, importance of both D and H components was observed for pod length. Due to their non-fixable nature, the dominance component and ójô and ólô types of epistasis can be exploited through heterosis breeding by developing high yielding hybrids if commercially feasible. However, the chances of exploitation of hybrid vigour/heterosis are bleek through hybrid varieties in soybean due to autogamous nature of the crop. The other alternative approaches for utilizing such non-fixable component may be intermating of selected individuals in early segregating generations with delayed selection in the later generations, diallel selective mating/biparental mating or recurrent selection followed by pedigree method of selection which might give fruitful results by exploiting both additive

Table 4.4 Analysis of variance for sums ($\bar{L}_{1i}+\bar{L}_{2i}+\bar{L}_{3i}$) and differences ($\bar{L}_{1i}-\bar{L}_{2i}$) and the estimates of genetic parameters

		Mean squares due to				Estimates of genetic parameters				
Source of variation		**Sums**	**Sum x Rep.**	**Differences**	**Diff. x Rep.**	**D**	**H**	**$(H/D)^{1/2}$**	**r**	**F**
Traits	**df**	**17**	**34**	**17**	**34**					
Days to 50 % flowering		101.880*	9.610	37.060*	11.810	123.020*	33.670*	0.520	0.540*	-17.400*
Days to 75% maturity		21.850*	7.180	9.630*	3.520	19.560*	8.160*	0.650	-0.070	0.440
Reproductive phase		0.008*	0.001	0.002	0.001	0.009*	0.002	0.440	0.240*	-0.0004*
Plant height		329.920*	85.070	75.830	51.890	326.460*	31.920	0.310	0.270*	-13.800*
Branches/plant		5.740*	1.050	2.940*	1.020	6.250*	2.550*	0.640	0.480*	-0.960*
Internode length		2.700*	0.630	0.510	0.480	2.760*	0.040	0.110	-0.090	0.020
Nodes/main stem		11.12*	1.840	4.380*	2.070	12.370*	3.070*	0.490	0.050*	-0.160*
Petiole length		1.330	2.350	1.870	3.420	-	-	-	-0.220	0.200
Pods/plant		4183.39*	265.18	718.670*	297.450	5224.290*	561.640*	0.330	-0.450	385.440
Seeds/pod		0.150*	0.070	0.030	0.040	0.110*	-	-	0.360*	-0.004*
Pod length		0.120*	0.020	0.180*	0.020	0.130*	0.230*	1.310	-0.090	0.008
Biological yield/plant		825.180*	80.950	162.610*	56.800	992.300*	141.080*	0.380	-0.030*	5.600*
Seed yield/plant		280.560*	11.620	28.520	18.870	358.590*	12.870	0.190	0.180*	-6.120*
Harvest index		0.020	0.010	0.010	0.010	0.010	0.002	0.480	0.250*	-0.00004*
100 seed weight		88.420*	3.050	8.890*	3.170	113.82*	7.630*	0.260	0.130*	-1.880*
Protein content		9.940*	0.540	2.460*	0.280	12.540*	2.900*	0.480	-0.100	0.280
Oil content		9.030*	0.200	2.770*	0.160	11.760*	3.490*	0.540	0.490*	-0.390*

* Significant at P Ò0.05 $(H/D)^{1/2}$ = Degree of dominance
D = Additive component r = Correlation
H = Dominant component F = Directional element
- = Not calculated (because of negative value)

and non-additive components of variation along with epistasis. Moreover, the interest in soybean breeding is to improve disease resistance along with yield involving multiple parents, the random intermating in segregating generations could be effective in pooling up the useful genes of interest in advanced progenies.

Overall, the triple test cross analysis revealed the importance of additive, dominance and epistasis gene actions in the inheritance of different characters. Under these situations, biparental mating and mating of selected individual plants in early segregating generation could be done for developing potential populations having optimum levels of homozygosity and heterozygosity. Further, where all three types of gene actions are present, transgressive segregants can be exploited by alternative intermating and subsequent handling of segregating generations in order to isolate high yielding stable lines in soybean. Such a strategy will help to increase frequency of favourable alleles while maintaining genetic variation in breeding population. The results are in conformity with those of Ojo and Dashiell (2002), Rahangdale and Raut (2002), Agrawal et al. (2005), Maloo and Nair (2005), Barona et al. (2009) and Barona et al. (2012).

4.3 Line x tester analysis

4.3.1 Analysis of variance

The data were subjected to line x tester analysis after excluding the $\bar{L}_{3i}$ progeny families and F_1 tester. The analysis of variance for line x tester has been presented in Table 4.5. It revealed the presence of significant differences among parents for all the traits which indicated the presence of substantial amount of genetic variability for exploitation through recombinant breeding. Further partitioning of the variances of the parents into testers, lines and lines vs testers indicated significant differences among lines for all the traits and among testers for nodes on main stem, pods per plant, seed yield per plant, 100-seed weight and protein content. The testers differed from lines for majority of the traits except reproductive phase, internode length, petiole length, seeds per pod, biological yield per plant, seed yield per plant, harvest index, 100-seed weight and pod length. The lines expressed greater magnitude of mean squares as compared to testers for almost all the traits except 100-seed weight, oil content and nodes on main

stem indicating wider genetic diversity of lines as compared to testers for these traits. The significant differences between first and second parent indicated that L_1 and L_2 testers possess the extreme high vs low relation with the population and would provide an estimate of additive and dominance variation with equal precision (Datt et al. 2011).

The crosses exhibited significant differences for most of the characters studied except petiole length and harvest index. This indicates that crosses were different from each other for these traits and hence selection is possible to identify most desirable segregants within the crosses. Similarly, the crosses also differed from the parents for almost all the traits except days to flowering, plant height, internode length, petiole length, harvest index, 100-seed weight, nodes on main stem and pod length implying that parental lines as a group differed from the crosses which may be due to heterosis resulting from dominant and complementary gene interaction. Similar results were also reported by many workers including Maloo and Nair (2005), Durai and Subbalakshmi (2010) and Nassar (2013).

4.3.2 Combining ability analysis

The success of a breeding programme depends upon the choice of suitable parents and their utilization by employing an appropriate breeding method. The combining ability analysis has been extensively used to identify potential parents and cross combination on the basis of their combining ability effects to obtain maximum genetic gain in advance generations for desirable economic traits to obtain elite purelines. This analysis facilitates the partitioning of genotypic variation of crosses into variation due to general combining ability (GCA) and specific combining ability (SCA). GCA effects are the measure of additive gene action which represents the fixable components of genetic variance and are used to classify the parents for the breeding behaviour in cross combinations. On the other hand, SCA effects are the measure of non additive gene action and are related to non-fixable component of genetic variance (Sprague 1966) which ultimately reflects hybrid vigour. It is not necessary that performance, adaptation and genetic variability are the only basis of selection of parents to obtain useful results. This is due to differential ability of the parents which, otherwise, depends upon the complex interaction among the genes and, hence, cannot be judged by *per se* performance alone (Allard 1960). The combining ability not only provides necessary information regarding the choice of

Table 4.5 Analysis of variance for parents and hybrids (line x tester)

Source of variation		Replication	Parent	Lines	Testers	Lines vs testers	Hybrid	Parents vs hybrids	Error
Traits	**df**	**2**	**19**	**17**	**1**	**1**	**35**	**1**	**110**
Days to 50% flowering		36.500*	105.680*	115.760*	0.670	39.470*	33.980*	3.780	4.640
Days to 75% maturity		147.430*	26.470*	27.450*	6.000	30.340*	8.090*	207.670*	3.640
Reproductive phase		0.004*	0.006*	0.005*	0.0004	0.003	0.003*	0.010*	0.0009
Plant height		811.090*	159.830*	171.640*	114.400	4.450*	98.620*	13.340	34.390
Branches/plant		2.460*	3.430*	2.780*	1.130	16.670*	2.280*	25.680*	0.490
Internode length		4.640*	0.660*	0.690*	0.007	0.630	0.770*	0.740	0.290
Nodes/main stem		2.180	4.030*	3.970*	4.510*	4.570*	3.760*	0.470	0.920
Petiole length		3.400	0.920	0.870	2.670	0.003	1.080	1.860	1.450
Pods/plant		254.250*	915.210*	928.430*	917.610*	688.170*	1209.040*	4092.180*	114.340
Seeds/pod		1.140*	0.060*	0.060*	0.020	0.090	0.040*	0.220*	0.020
Pod length		0.020	0.060*	0.060*	0.002	0.0006	0.070*	0.006	0.009
Biological yield/plant		83.120	191.930*	207.500*	6.000	113.250	240.160*	828.570*	31.940
Seed yield/plant		12.320	40.050*	42.470*	32.200*	6.730	75.370*	229.010*	5.680
Harvest index		0.005	0.010*	0.010*	0.020	0.010	0.007	0.0002	0.004
100 seed weight		0.380	20.680*	21.460*	26.040*	2.130	23.640*	2.250	1.270
Protein content		0.280	3.780*	3.730*	1.070*	7.420*	3.030*	1.760*	0.190
Oil content		0.410*	3.510*	2.810*	10.080*	8.890*	2.870*	0.930*	0.100

* Significant at P Ò0.05

parents but also simultaneously illustrates the nature and magnitude of gene action involved in the expression of desirable traits. In the present study, line × tester method (Kempthorne 1957) which is a useful tool for preliminary evaluation of genetic stock was employed with a view to identify good combiners which may be used to build up a population with favourable fixable genes for effective yield improvement.

4.3.2.1 Analysis of variance

The analysis of variance for combining ability indicated significant differences among hybrids (crosses) for all the traits studied except petiole length and harvest index (Table 4.6). The mean squares due to crosses were partitioned into three components, *viz.,* lines, testers and lines x testers interaction. Mean squares due to lines were significant for all the traits except days to 75% maturity, branches per plant, petiole length, pod length and harvest index. Mean squares due to testers were non-significant for all the traits except petiole length. Mean squares due to lines x testers interactions were significant for all the traits except plant height, internode length, petiole length, seeds per pod and harvest index suggesting that the experimental material possessed considerable variability and that both GCA and SCA were involved in the genetic expression of these factors thereby indicating that they are suitable for combining ability studies. The significant difference between line × tester interactions indicated that specific combining ability attributed heavily in the expression of these traits and provide the importance of non-additive variance for all the traits. The significant mean squares due to lines and testers also revealed the prevalence of additive variance for the traits studied. Maloo and Sharma (2007) found that variance due to crosses, lines and testers were significant for both protein and oil contents in F_2 generation while these were significant only for protein content in F_1. In F_3 generation, mean squares due to crosses were significant for both protein and oil content while due to lines for oil content and due to testers for protein content. Predominance of estimated component of SCA variance over GCA indicated importance of non-additive genetic effects for both the quality characters. The significant mean squares due to lines and testers also revealed the prevalence of additive variance for the traits studied.

Table 4.6 Analysis of variance for combining ability and estimates of genetic parameters

Source of variation		Replications	Crosses	Lines	Testers	Lines x Testers	Error	Estimates of genetic parameters				
Traits	**df**	**2**	**35**	**17**	**1**	**17**	**70**	**σA^2**	**σD^2**	**$(H/D)^{1/2}$**	**h^2**	**GA (5%)**
Days to 50% flowering		12.890	33.980*	50.640*	14.080	18.490*	5.260	0.380	4.620	3.460	5.890	0.310
Days to 75% maturity		46.230*	8.090*	10.930	15.560	4.820*	2.640	0.080	0.390	2.190	4.840	0.130
Reproductive phase		0.003*	0.003*	0.004*	0.0007	0.001*	0.0008	0.000	0.0002	2.150	6.880	0.003
Plant height		281.840*	98.620*	164.490*	2.770	38.390	33.720	1.500	1.330	0.940	10.500	0.820
Branches/plant		0.560	2.280*	2.870	6.210	1.470*	0.510	0.020	0.330	4.010	3.980	0.060
Internode length		1.840*	0.770*	1.350*	0.010	0.250	0.270	0.010	-	-	13.480	0.080
Nodes/main stem		1.730	3.760*	5.560*	0.007	2.190*	1.008	0.040	0.430	3.280	5.110	0.090
Petiole length		4.590*	1.090	0.660	10.890*	0.940	1.400	0.004	-	-	1.190	0.020
Pods/plant		110.130	1209.040*	2091.690*	648.760	359.340*	142.820	21.180	81.660	1.960	15.030	3.670
Seeds/pod		0.810*	0.040*	0.070*	0.008	0.020	0.030	0.0007	-	-	11.770	0.020
Pod length		0.010	0.070*	0.060	0.010	0.090*	0.009	-	0.030	-	-	-
Biological yield/plant		49.640	240.160*	412.580*	9.540	81.310*	36.710	3.960	16.450	2.040	12.750	1.460
Seed yield/plant		8.000	75.370*	140.280*	10.760	14.260*	7.710	1.520	2.860	1.370	24.270	1.250
Harvest index		0.004	0.007	0.008	0.0003	0.005	0.005	0.000	0.0002	2.370	2.200	0.002
100 seed weight		1.870	23.640*	44.210*	0.090	4.450*	1.660	0.480	1.060	1.480	24.390	0.700
Protein content		0.080	3.040*	4.970*	0.740	1.230*	0.200	0.050	0.350	2.770	9.890	0.140
Oil content		0.370*	2.870*	4.510*	0.340	1.380*	0.080	0.040	0.430	3.390	7.440	0.110

* Significant at PÒ0.05 $(H/D)^{1/2}$ = Degree of dominance

ůA^2 = Additive variance h^2 = Narrow sense heritability

ůD^2 = Dominance variance GA (5%) = Genetic advance at 5%

- = Not calculated (because of negative value)

The estimates of additive and dominance variances are also presented in Table 4.6. The relative magnitudes of additive and dominance variance components showed that non- additive variance was predominant for all the traits except plant height where preponderance of additive variance was observed. Occurrence of both additive and non-additive variance for yield and related component traits have also been reported in earlier studies by El-Sayad et al. (2005) and Agrawal et al. (2005) in variable genetic materials in soybean.

The major role of non-additive gene effects in the manifestation of almost all the traits except plant height was observed by higher value of $\mathring{u}^2D$ than $\mathring{u}^2A$ and degree of dominance $[(H/D)^{1/2}]$ being greater than one, i.e., over dominance. The role of non-additive gene action in the inheritance of different traits by following line × tester mating design has also been reported by Chauhan and Singh (1983) for protein and oil content, Kunta et al. (1985) for seed yield and plant height, Sharma and Phul (1994) for pods per plant, seed yield per plant, oil content and protein content, Gadag et al. (1999) for protein content, grain yield per plant and days to 75% maturity and Agrawal et al. (2005) for indeterminate growth habit. In this situation, where non additive component was important for the expression of characters, simple pedigree method of selection would be ineffective for its improvement. At the same time, population improvement programme like reciprocal recurrent selection which may allow to accumulate the fixable gene effect as well as to maintain considerable variability and heterozygousity for exploiting non-fixable gene effect may prove to be the most effective method. However, soybean, being the self pollinated crop, produces few seeds per pollination, thus, selection procedure is not practically economical. So, possible choice is the use of biparental progenies among selected crosses or use of selection procedure such as diallel selecting mating to exploit both additive and non additive genetic components. Furthermore, on the basis of present study, all the traits revealed low narrow sense heritability (1.19 to 24.39 per cent) which showed that non additive effects played an important role in controlling these traits.

In the presence of additive gene action, it is suggested that selection in early generations may be fruitful either following mass selection or progeny selection or hybridization and selection with pedigree breeding.

4.3.2.2 Estimates of combining ability effects

The estimates of GCA and SCA effects were worked out for all the traits exhibiting significant values for the respective variances. These estimates for individual traits are presented in Table 4.7 to Table 4.12 and described below:

4.3.2.2.1 Estimates of GCA effects

In any breeding programme, the choice of parents is the secret to success in developing high yielding varieties/hybrids. The broad principles governing the choice of parents are their *per se* performance and GCA effects in desired magnitude and direction. The parent with high mean values may not necessarily be able to transmit the superior trait into their progenies (Simmonds 1979).

The estimates of GCA effects were worked out for all the traits and are presented in Table 4.7. Earliness is a desirable trait in soybean. The days to 50% flowering, days to 75% maturity and reproductive phase are the indicators of earliness. The significant negative GCA effects were observed for six lines for days to flowering, two lines for days to 75% maturity and three lines for reproductive phase. The magnitude ranged from 6.54 to -3.95, 3.38 to -2.28 and 0.05 to -0.04 for these traits, respectively. In case of days to 50% flowering, genotype P2-2 was observed to be the best general combiner as it showed the highest significant negative GCA effect. The line P13-4 was also good general combiner for earliness followed by P6-1, H-330, PK-472 and SL-795. Female parent Shivalik was found to be the poorest general combiner exhibiting maximum positive GCA effect for the trait. In case of days to 75% maturity, genotype P6-1 was the best general combiner as it showed the highest negative GCA effects. The female H-330 was also observed a good general combiner for earliness in maturity. Reproductive phase was studied to evaluate the parents and crosses for synchronous flowering. For this trait, negative effects were considered to be favourable. For this trait, P9-2-2 and Shivalik were found to be good general combiners for longer reproductive phase and P2-2, DS-1213 and P13-4 were found to be good general combiner for shorter reproductive phase.

Table 4.7 Estimates of GCA effects of lines (females) and testers (males) for different traits

Lines	Days to 50% flowering	Days to 75% maturity	Reproductive phase	Plant height	Branches/plant	Internode length	Nodes /main stem	Petiole length	Pods/plant	Seeds/pod	Pod length	Biological yield/plant	Seed yield/plant	Harvest index	100-seed weight	Protein content	Oil content
P6-1	-2.45*	-2.28*	-0.02	- 9.22*	-0.36	-0.56 *	-0.92*	0.39	0.21	-0.06	-0.06	-4.07	-3.11*	-0.02	-1.44*	0.62*	-0.43*
SL-682	-0.28	0.05	-0.003	-0.75	-0.32	-0.32	0.53	-0.34	11.22*	-0.005	-0.02	3.96	2.09*	0.01	-0.86	-1.36*	0.02
SL-679	1.71	-1.12	0.03*	3.31	0.65*	0.58 *	-0.53	0.23	23.82*	0.05	-0.11*	2.16	2.17*	0.03	-1.53*	-0.74*	0.59*
P9-2-2	3.38*	0.05	0.05*	4.14	0.73*	0.09	0.69	-0.04	47.72*	0.11	-0.12*	20.47*	13.45*	0.07*	-0.61	0.27	-0.29*
DS-1213	-0.12	-0.78	-0.03*	-0.22	-0.56	0.04	-0.20	0.16	-3.67	0.07	-0.16*	-3.49	-1.59	0.003	0.06	0.05	-0.55*
PK-472	-1.95*	-0.45	-0.01	2.68	0.47	-0.20	1.03*	0.43	0.35	0.06	0.04	2.32	-0.36	-0.04	-0.44	-0.27	-0.21
Hardee	0.71	1.38	0.008	6.83*	1.13*	0.32	0.63	-0.11	3.91	-0.04	-0.006	7.19*	1.84	-0.04	0.06	0.31	0.33*
Bragg	2.71*	1.55	-0.02	11.2*	1.67*	0.18	1.82*	0.49	18.89*	0.21*	0.06	14.24*	5.84*	-0.02	-0.27	-0.35	0.16
SL-795	-1.95*	0.21	-0.01	-2.34	-0.58*	-0.08	-0.35	0.53	-0.36	-0.07	-0.12*	-4.65*	-2.39*	-0.005	-3.36*	1.77*	-1.56*
P2-2	-3.95*	0.88	-0.04 *	-0.77	-0.16	-0.25	0.36	-0.26	-6.46	-0.11	0.04	-0.31	-0.61	-0.02	-0.36	0.88*	-0.28*
Shivalik	6.54*	3.38*	0.05 *	6.16*	-0.36	1.03*	-0.78*	-0.44	-28.33*	0.14*	0.19*	2.410	3.81*	0.08*	9.72*	1.95*	2.36*
PS-1466	-0.62	-0.62	0.02	-4.52	-0.89*	0.91*	-2.45*	-0.02	-35.66*	-0.13*	-0.12*	-13.17*	-7.14*	-0.04	2.89*	-0.67*	1.00*
H-330	-2.12*	-2.12*	-0.008	-9.42*	-0.25	-0.55*	-0.93*	-0.14	-9.84*	-0.21*	0.04	-8.95*	-6.07*	-0.06*	-0.27	0.44*	-1.13*
PS-1469	-1.62	-0.45	-0.007	-3.90	-0.86*	-0.55*	0.43	-0.31	-10.71*	-0.15*	0.11*	-8.31*	-3.64*	0.008	-0.69	-1.19*	0.41*
VLS-59	5.21*	1.05	0.04*	0.19	-0.06	0.13	-0.28	-0.41	-9.69*	0.02	0.03	-6.96*	-3.37*	0.01	-1.63*	-0.35	0.20
JS-335	-0.78	0.21	-0.01	-0.60	0.23	-0.50*	1.02*	-0.21	-7.36	0.04	-0.006	-5.56*	-3.84*	-0.01	-0.94*	-0.17	-0.53*
P169-3	-0.78	0.05	-0.01	-1.32	-0.06	-0.16	-0.001	0.36	9.16*	0.02	0.04	3.26	3.07*	0.04	-0.86	-0.20	-0.68*
P13-4	-3.62*	-0.95	-0.03*	-1.45	-0.38	-0.11	-0.07	-0.32	-3.19	0.002	0.16*	-0.56	-0.16	0.00	0.56	-0.97*	0.57*
SE(gi) ±	0.88	0.78	0.01	2.39	0.28	0.22	0.39	0.49	4.36	0.06	0.04	2.31	0.97	0.03	0.46	0.18	0.13
SE(gi-gj) ±	1.24	1.10	0.02	3.38	0.40	0.32	0.55	0.69	6.17	0.09	0.05	3.26	1.37	0.04	0.65	0.25	0.18
Testers																	
Him Soya	-0.36	-0.38	-0.003	-0.16	-0.24*	-0.01	0.008	-0.32	2.45	-0.009	-0.01	-0.29	-0.32	-0.002	0.03	0.08	-0.06
Hara Soya	0.36	0.38	0.003	0.16	0.24*	0.01	-0.008	0.32	-2.45	0.009	0.01	0.29	0.32	0.002	-0.03	-0.08	0.06
SE (gi) ±	0.29	0.26	0.004	0.79	0.09	0.07	0.13	0.16	1.45	0.02	0.01	0.77	0.32	0.009	0.15	0.06	0.04
SE (gi-gk) ±	0.41	0.37	0.006	1.12	0.13	0.11	0.18	0.23	2.06	0.03	0.02	1.08	0.46	0.01	0.22	0.08	0.06

* Significant at P Ò0.05

In case of plant height, the highest positive GCA estimates were observed for Bragg followed by Hardee and Shivalik. The genotype H-330 exhibited the highest negative effects and, thus, was observed the poorest general combiner. In case of branches per plant which is an important yield contributing trait, the best combiner was Bragg and other female parents having positive GCA effect were Hardee, P9-2-2 and SL-679. The genotype PS-1466 was found to be a poor general combiner. Internodal length determines the height and nodes per plant. Besides having minimum internodal length, it is important to have more number of pods bearing nodes per plant. Three lines, *viz.,* Bragg, PK-472 and JS-335 were found to have desirable positive GCA effects for nodes per plant. The desirable negative GCA effects for internodal length were observed for genotype P6-1. Other female parents, namely, H-330, PS-1469 and JS-335 were also found to be the good general combiners for short internode length.

High yield is the basic objective of all crop improvement programmes. It is of immense importance to develop a genotype which has the potential to surpass commercially adopted/well adapted cultivar(s), otherwise, the genotype will be of no significance even if it has excellent performance for other traits. Number of pods per plant has a direct bearing on the total productivity of soybean. Keeping this in view, five lines were identified as the best general combiners, *viz.,* P9-2-2, SL-679, Bragg, SL-682 and P169-3. For seeds per pod, the best general combiner was Bragg followed by Shivalik. The poorest combiner among females was H-330. For pod length three lines, *viz.,* Shivalik, P13-4 and PS-1469 were adjudged as the best general combiners on the basis of their significant positive GCA effects.

For seed yield per plant, of the six lines which showed significant positive general combining ability effects, lines P9-2-2, Bragg, Shivalik, P169-3 and SL-679 were ranked among the top five. For biological yield per plant, best general combiner was P9-2-2. Other good combiners were Bragg and Hardee. Other female parents, which had positive, though, non-significant GCA effects were SL-682 followed by P169-3, Shivalik, PK-472 and SL-679 and were the average general combiner. For harvest index, best general combiner was Shivalik followed by P9-2-2. For 100-seed weight, the best general combiner among lines was Shivalik followed by PS-1466. Amongst the quality traits, five lines for protein content and six lines for oil content have shown significant positive GCA effects. Among the testers, Hara soya exhibited desirable GCA effects for branches per plant (Tables 4.7 and 4.8).

Table 4.8 List of good general combiners for different traits

Trait	Lines	Testers
Days to 50% flowering	P2-2, P13-4, P6-1, H-330, PK-472 and SL-795	None
Days to 75% maturity	P6-1 and H-330	None
Reproductive phase	P2-2, DS-1213 and P13-4	None
Plant height	Bragg, Hardee and Shivalik.	None
Branches/plant	Bragg, Hardee, P9-2-2 and SL-679	Hara Soya
Internode length	P6-1, H-330, PS-1469 and JS-335	None
Nodes/main stem	Bragg, PK-472 and JS-335	None
Pods/plant	P9-2-2, SL-679, Hardee, SL-682 and P169-3	None
Seeds/pod	Bragg and Shivalik	None
Pod length	Shivalik, P13-4 and PS-1469	None
Biological yield/plant	P9-2-2, Bragg and Hardee	None
Seed yield/plant	P9-2-2, Bragg, Shivalik, P169-3, SL-679 and SL-682	None
Harvest index	Shivalik and P9-2-2	None
100 seed weight	Shivalik and PS-1466	None
Protein content	Shivalik, SL-795, P2-2, P6-1 and H-330	None
Oil content	Shivalik, PS-1466, SL-679, P13-4 and PS-1469	None

The good general combiners with respect to different traits indicated that no single parent was proved to be a good general combiner for all the traits (Table 4.8). Line ôBraggô was found to be a good general combiner for plant height, branches per plant, seeds per pod, biological yield per plant, seed yield per plant and nodes on main stem (Table 4.9). Likewise line P9-2-2 was found to be good general combiner for most of the traits, *viz*., branches per plant, pods per plant, biological yield per plant, seed yield per plant and harvest index. On the basis of the parents with good GCA to different traits, it can be concluded that line Shivalik was found to be good general combiner for eight traits followed by Bragg for six traits followed by P9-2-2 for five traits and P13-4, P6-1, H-330, Hardee and SL-679 for four traits each (Table 4.9). Various workers have recorded good general combiners for various traits in soybean with their different genetic materials (Kaw and Menon 1981; Chauhan and Singh 1983; Sabbouh and Edwards 1985;

Sharma and Phul 1994; Kapila et al. 1994; Gadag et al. 1999; Cho and Scott 2000; Kee et al. 2000; El-Sayad et al. 2005; Gavioli et al. 2006; Mebrahtu and Devine 2008; Ojo and Ayuba 2013 and Oliveira et al. 2014).

Table 4.9 List of lines exhibiting desirable general combining effects for seed yield and related traits

Lines	Traits
P2-2	Days to 50% flowering, reproductive phase and protein content
P13-4	Days to 50% flowering, reproductive phase, oil content and pod length
P6-1	Days to 50% flowering, Days to 75% maturity, internode length and protein content
H-330	Days to 50% flowering, Days to 75% maturity, internode length and protein content
PK-472	Days to 50% flowering and nodes/main stem
SL-795	Days to 50% flowering and protein content
DS-1213	Reproductive phase
Bragg	Plant height, branches/plant, seeds/pod, biological yield/plant, seed yield/plant and nodes/main stem
Hardee	Plant height, branches/plant, pods/plant and biological yield/plant
Shivalik	Plant height, seeds/pod, seed yield/plant, harvest index, 100-seed weight, protein content, oil content and pod length
P9-2-2	Branches/plant, pods/plant, biological yield/plant, seed yield/plant and harvest index
SL-679	Branches/plant, pods/plant, seed yield/plant and oil content
PS-1469	Internode length, oil content and pod length
JS-335	Internode length and nodes/main stem
SL-682	Pods/plant and seed yield/plant
P169-3	Pods/plant and seed yield/plant
PS-1466	100-seed weight and oil content
Tester	
Hara Soya	Branches/plant

4.3.2.2.2 Estimates of SCA effects

SCA is the deviation in performance of a cross combination which is estimated on the basis of GCA of the parents involved in cross combination. These effects represent dominance and epistasis components of variation which are non-fixable and related to hybrid vigour. This means that SCA effects could contribute more towards improvement of self pollinated crops where commercial exploitation of hybrids is feasible. However, the interest of the breeders in the production of homozygous lines usually rests upon the transgressive segregants which can be obtained from the segregating population of cross combinations. The choice of the cross combinations is effected based on the *per se* performance, heterosis and SCA of the cross combinations and also the GCA effects of parents involved.

The estimates of SCA effects (Table 4.10) revealed that all the cross combinations were average combiners for different traits. In case of days to flowering, cross combination, Hardee x Him Soya showed the highest significantly negative SCA effects followed by DS-1213 x Him Soya. For days to 75% maturity, SL-682 x Him Soya showed the highest significantly negative SCA effect and was the best combination for early maturity. For reproductive phase, the highest significant positive SCA effects was obtained from the cross Hardee x Hara Soya. For shorter reproductive phase, the best specific combination was Hardee x Him Soya. Rest of the cross combinations were either having negative or positive non-significant SCA effects. For branches per plant, the highest positive SCA effects were obtained for PS-1469 x Hara Soya. For nodes on main stem, only one cross combination (Shivalik x Him Soya) showed significant positive SCA effects.

For pods per plant, two cross combinations showed significant positive SCA effects. The highest significant SCA effects were observed for PK-472 x Him Soya followed by Shivalik x Him Soya. For pod length, the highest positive SCA effects were obtained for the cross combination Hardee x Hara Soya. The other cross combinations which also exhibited highly significant positive SCA effects for the trait were SL-682 x Him Soya, P6-1 x Hara Soya, DS-1213 x Him Soya, SL-679 x Him Soya, P169-3 x Him Soya and H-330 x Him Soya. For biological yield per plant, the highest positive SCA effect was obtained for the cross combination H-330 x Him Soya. The other cross

Table 4.10 Estimates of SCA effects of different cross combinations for different traits

Crosses	Days to 50% flowering	Days to 75% maturity	Reproductive phase	Plant height	Branches/ plant	Internode length	Nodes/ stem	Petiole length	Pods/plant	Seeds/pod	Pod length	Biological yield/plant	Seed yield/plant	Harvest index	100 seed weight	Protein content	Oil content
P9-2-2 x Him Soya	0.69	-1.12	0.003	-3.69	0.41	-0.17	-0.47	0.08	-8.82	0.02	-0.04	-2.25	-0.57	0.02	-0.36	1.29*	-0.32
P9-2-2 x Hara Soya	-0.69	1.12	-0.003	3.69	-0.41	0.17	0.47	-0.08	8.82	-0.02	0.04	2.25	0.57	-0.02	0.36	-1.29*	0.32
PS1466 x Him Soya	-0.47	-0.78	0.01	1.87	-0.11	-0.21	0.94	0.42	6.46	0.02	-0.006	2.51	0.83	-0.002	-0.11	0.04	-0.02
PS1466 x Hara Soya	0.47	0.78	-0.01	-1.87	0.11	0.21	-0.94	-0.42	-6.46	-0.02	0.006	-2.51	-0.83	0.002	0.11	-0.04	0.02
P6-1 x Him Soya	0.53	-0.62	-0.003	2.34	0.65	0.02	0.41	0.35	1.96	-0.01	-0.19*	0.38	-1.18	-0.04	-1.28	-0.26	-0.03
P6-1 x Hara Soya	-0.53	0.62	0.003	-2.34	-0.65	-0.02	-0.41	-0.35	-1.96	0.01	0.19*	-0.38	1.18	0.04	1.28	0.26	0.03
PK-472 x Him Soya	-1.47	0.21	-0.007	1.41	0.17	0.42	-0.59	-0.02	19.66*	0.02	-0.006	3.39	-0.03	-0.03	0.14	-0.86*	0.67*
PK-472 x Hara Soya	1.47	-0.21	0.007	-1.41	-0.17	-0.42	0.59	0.02	-19.66*	-0.02	0.006	-3.39	0.03	0.03	-0.14	0.86*	-0.67*
VLS-59 x Him Soya	1.03	-0.62	0.01	0.21	-0.39	0.17	-0.32	-0.35	0.19	0.04	-0.04	2.03	0.98	-0.002	0.97	0.09	0.13
VLS-59 x Hara Soya	-1.03	0.62	-0.01	-0.21	0.39	-0.17	0.32	0.35	-0.19	-0.04	0.04	-2.03	-0.98	0.002	-0.97	-0.09	-0.13
P13-4 x Him Soya	1.52	0.71	0.009	-5.42	-0.43	-0.27	-0.56	0.12	-7.57	-0.03	-0.04	-3.72	-1.28	0.005	-0.69	-0.34	-0.002
P13-4 x Hara Soya	-1.52	-0.71	-0.009	5.42	0.43	0.27	0.56	-0.12	7.57	0.03	0.04	3.72	1.28	-0.005	0.69	0.34	0.002
PS1469 x Him Soya	0.19	-0.12	0.007	-2.24	-1.23*	-0.15	-0.26	0.25	-8.78	-0.01	0.01	-4.55	-2.52*	-0.01	-0.53	0.12	-0.07
PS1469 x Hara Soya	-0.19	0.12	-0.007	2.24	1.23*	0.15	0.26	-0.25	8.78	0.01	-0.01	4.55	2.52*	0.01	0.53	-0.12	0.07
DS1213 x Him Soya	-4.14*	0.71	-0.02	-1.69	-0.29	0.18	-0.81	-0.02	2.69	-0.04	0.18*	-3.30	-1.42	0.00	0.14	0.56*	-0.18
DS1213 x Hara Soya	4.14*	-0.71	0.02	1.69	0.29	-0.18	0.81	0.02	-2.69	0.04	-0.18*	3.30	1.42	0.00	-0.14	-0.56*	0.18
SL-679 x Him Soya	-0.80	0.05	0.006	0.33	0.62	0.01	-0.008	0.55	1.15	-0.04	0.13*	0.76	1.25	0.03	0.38	-0.34	0.74*
SL-679 x Hara Soya	0.80	-0.05	-0.006	-0.33	-0.62	-0.01	0.008	-0.55	-1.15	0.04	-0.13*	-0.76	-1.25	-0.03	-0.38	0.34	-0.74*
SL-682 x Him Soya	1.19	-2.28*	-0.006	-0.21	-0.09	0.08	-0.23	0.13	-9.82	0.03	0.26*	-4.68	-2.30*	-0.005	-0.28	-0.15	-0.03
SL-682 x Hara Soya	-1.19	2.28*	0.006	0.21	0.09	-0.08	0.23	-0.13	9.82	-0.03	-0.26*	4.68	2.30*	0.005	0.28	0.15	0.03
H-330 x Him Soya	1.36	0.55	0.01	-0.57	0.47	-0.16	0.19	-0.08	3.52	-0.04	0.11*	7.19*	2.32*	-0.04	-1.19	0.33	0.13
H-330 x Hara Soya	-1.36	-0.55	-0.01	0.57	-0.47	0.16	-0.19	0.08	-3.52	0.04	-0.11*	-7.19*	-2.32*	0.04	1.19	-0.33	-0.13
P169-3 x Him Soya	0.53	1.21	0.01	-0.52	0.34	0.17	-0.34	-0.33	-4.75	0.002	0.13*	-0.72	-0.30	0.002	2.14*	0.21	-1.45*
P169-3 x Hara Soya	-0.53	-1.21	-0.01	0.52	-0.34	-0.17	0.34	0.33	4.75	-0.002	-0.13*	0.72	0.30	-0.002	-2.14*	-0.21	1.45*
P2-2 x Him Soya	0.69	0.38	0.001	3.61	0.29	0.34	0.07	-0.78	5.16	0.04	-0.04	5.63*	1.99	-0.02	1.14	0.13	0.18
P2-2 x Hara Soya	-0.69	-0.38	-0.001	-3.61	-0.29	-0.34	-0.07	0.78	-5.16	-0.04	0.04	-5.63*	-1.99	0.02	-1.14	-0.13	-0.18
Shivalik x Him Soya	0.19	0.71	-0.01	4.09	0.61	-0.21	1.54*	0.18	10.76*	0.10	-0.006	3.28	3.09*	0.04	0.05	0.06	-0.33
Shivalik x Hara Soya	-0.19	-0.71	0.01	-4.09	-0.61	0.21	-1.54*	-0.18	-10.76*	-0.10	0.006	-3.28	-3.09*	-0.04	-0.05	-0.06	0.33
Hardee x Him Soya	-4.31*	-0.78	-0.05*	-3.27	-0.56	-0.14	-0.44	0.35	-9.25	-0.09	-0.26*	-6.24*	-0.87	0.07	-0.34	-0.23	0.22
Hardee x Hara Soya	4.31*	0.78	0.05*	3.27	0.56	0.14	0.44	-0.35	9.25	0.09	0.26*	6.24*	0.87	-0.07	0.34	0.23	-0.22
JS-335 x Him Soya	0.69	0.38	0.02	0.53	-0.26	0.005	0.06	-0.92	-4.12	0.03	-0.09	-0.64	-0.40	-0.01	0.47	-0.29	0.27
JS-335 x Hara Soya	-0.69	-0.38	-0.02	-0.53	0.26	-0.005	-0.06	0.92	4.12	-0.03	0.09	0.64	0.40	0.01	-0.47	0.29	-0.27
SL-795 x Him Soya	0.36	1.21	-0.004	1.37	-0.16	0.12	0.008	0.25	-0.70	0.04	-0.04	-0.12	-0.05	-0.002	0.38	-0.27	0.49*
SL-795 x Hara Soya	-0.36	-1.21	0.004	-1.37	0.16	-0.12	-0.008	-0.25	0.70	-0.04	0.04	0.12	0.05	0.002	-0.38	0.27	-0.49*
Bragg x Him Soya	2.19	0.21	0.01	1.84	-0.04	-0.21	0.81	-0.19	2.72	0.02	-0.06	1.03	0.45	-0.005	-1.03	-0.11	-0.39*
Bragg x Hara Soya	-2.19	-0.21	-0.01	-1.84	0.04	0.21	-0.81	0.19	-2.72	-0.02	0.06	-1.03	-0.45	0.005	1.03	0.11	0.39*
SE (Sij) ±	1.24	1.10	0.02	3.38	0.40	0.32	0.55	0.69	6.17	0.09	0.05	3.26	1.37	0.04	0.65	0.25	0.18
SE (Sij-Skl) ±	1.76	1.56	0.02	4.78	0.57	0.45	0.78	0.98	8.73	0.13	0.07	4.61	1.95	0.06	0.92	0.36	0.26

* Significant at P Ò0.05

combinations which also exhibited highly significant positive SCA effects for the trait were Hardee x Him Soya and P2-2 x Him Soya. For seed yield per plant, the highest positive SCA effects were obtained for Shivalik x Him Soya, PS-1469 x Hara Soya, H-330 x Him Soya and SL-682 x Hara Soya. For harvest index, no cross combination showed significant SCA effects.

For 100-seed weight, only one combination (P169-3 x Him Soya) showed significant positive SCA effect. For protein content, only three cross combinations, *viz.,* P9-2-2 x Him Soya, PK-472 x Hara Soya and DS-1213 x Him Soya exhibited positive significant SCA effects. For oil content, the highest positive SCA effect was obtained for the cross combination P169-3 x Hara Soya. The other cross combinations which also exhibited highly significant positive SCA effects for this trait were SL-679 x Him Soya, PK-472 x Him Soya, SL-795 x Him Soya and Bragg x Hara Soya.

The trait wise good cross combinations have been summarized in Table 4.11. It was observed that no single cross could reveal significant SCA effects for all the traits. Earlier workers have also reported significant SCA effects in their respective studies under different environmental conditions for different traits, *viz*., oil content by Sabbouh and Edwards (1985); protein content, grain yield per plant and days to 75% maturity by Gadag et al. (1999); seed weight by Cho and Scott (2000), and number of pods per plant, number of seeds per plant, 100-seed weight and seed yield per plant by El-Sayad et al. (2005).

On the basis of SCA effects, it can be concluded that desirable SCA effects were not revealed by any of cross combinations for all the traits (Table 4.10). Three cross combinations namely, PS-1469 x Hara Soya, Shivalik x Him Soya and H-330 x Him Soya were found to be good specific combiners for seed yield per plant (Table 4.12). The cross combinations involving one good and other poor or average combiner may give desirable transgressive segregants if the additive effect of one parent and complementary epistatic effect (if present in the cross) act in the same direction and maximize desirable plant character. But in the present study, high SCA effects were also shown by some cross combinations involving poor × poor and average × poor general combiners which might be due to diverse genetic background of the parental lines involved in the crosses. The specific interaction effects of poor × poor crosses may perform better than good ×

good and good × poor combinations because of the prevalence of high magnitude of non-additive component for the superiority of the pertinent cross combination. However, Singh et al. (1985) were of the view that the best crosses involving atleast one parent with good combining ability may produce transgressive segregants which are also possible in many of the crosses of the present study.

Table 4.11 List of cross combinations showing good specific combining ability (SCA) effects for different traits

Trait	Cross combination (s)
Days to 50% flowering	Hardee x Him Soya and DS-1213 x Him Soya
Days to 75% maturity	SL-682 x Him Soya
Reproductive phase	Hardee x Him Soya
Plant height	None
Branches/plant	PS-1469 x Hara Soya
Internode length	None
Nodes/main stem	Shivalik x Him Soya
Pods/plant	PK-472 x Him Soya and Shivalik x Him Soya
Seeds/pod	None
Pod length	Hardee x Hara Soya, SL-682 x Him Soya, P6-1 x Hara Soya, DS- 1213 x Him Soya, SL-679 x Him Soya, P169-3 x Him Soya and H-330 x Him Soya
Biological yield/plant	H-330 x Him Soya
Seed yield/plant	Shivalik x Him Soya, PS-1469 x Hara Soya, H-330 x Him Soya and SL-682 x Hara Soya
Harvest index	None
100 seed weight	P169-3 x Him Soya
Protein content	P9-2-2 x Him Soya, PK-472 x Hara Soya and DS-1213 x Him Soya
Oil content	P169-3 x Hara Soya, SL-679 x Him Soya, PK 472 x Him Soya, SL-795 x Him Soya and Bragg x Hara Soya

Table 4.12 List of cross combinations exhibiting desirable specific combining ability effects for seed yield and related traits

Crosses	Traits
Hardee x Him Soya	Days to 50% flowering and reproductive phase
DS-1213 x Him Soya	Days to 50% flowering, protein content and pod length
SL-682 x Him Soya	Days to 75% maturity and pod length
PS-1469 x Hara Soya	Branches/plant and seed yield/plant
PK-472 x Him Soya	Pods/plant and oil content,
Shivalik x Him Soya	Pods/plant, seed yield/plant and nodes/main stem
H-330 x Him Soya	Biological yield/plant, seed yield/plant and pod length
SL-682 x Hara Soya	Seed yield/plant
P169-3 x Him Soya	100-seed weight and pod length
P9-2-2 x Him Soya	Protein content
PK-472 x Hara Soya	Protein content
P169-3 x Hara Soya	Oil content
SL-679 x Him Soya	Oil content and pod length
Hardee x Hara Soya	Pod length
SL-795 x Him Soya	Oil content
Bragg x Hara Soya	Oil content
P6-1 x Hara Soya	Pod length

4.3.2.3 Percent contribution of different components towards hybrid sum of squares

The relative contribution of lines, testers and lines x testers interaction towards the total sum of squares of the hybrids are presented in Table 4.13.

The proportional per cent contribution of lines ranged from 29.60 (petiole length) to 90.85 (100-seed weight). The contribution of lines was higher for 100-seed weight (90.85) followed by seed yield per plant (90.40), internode length (84.21), pods per plant

(84.03), biological yield per plant (83.44), seeds per pod (82.01), plant height (81.01), protein content (79.62), oil content (76.24), reproductive phase (74.87), days to 50% flowering (72.38), nodes on main stem (71.74), days to 75% maturity (65.60), harvest index (62.53), branches per plant (61.00), pod length (39.27) and petiole length (29.60). The proportional per cent contribution of testers ranged from 0.006 (nodes per main stem) to 28.60 per cent (petiole length). The proportional lines x testers contribution (per cent) of testers ranged from 9.13 (100-seed weight) to 60.29 per cent (pod length). The lines x testers components contributed maximum for pod length (60.29), followed by petiole length (41.79), harvest index (37.32), branches per plant (31.24), days to 75% maturity (28.90), nodes on main stem (28.25), days to flowering (26.43), reproductive phase (24.43), oil content (23.41), protein content (19.67), plant height (18.90), seeds per pod (17.44), biological yield per plant (16.44), internode length (15.74), pods per plant (14.43), seed yield per plant (9.19) and 100-seed weight (9.13).

Table 4.13 Estimates of proportional contribution of lines, testers and their interactions

Traits	Contribution (%) due to		
	Lines	Testers	Line x tester
Days to 50% flowering	72.38	1.18	26.43
Days to 75% maturity	65.60	5.49	28.90
Reproductive phase	74.87	0.69	24.43
Plant height	81.01	0.08	18.90
Branches/plant	61.00	7.76	31.24
Internode length	84.21	0.03	15.74
Nodes/main stem	71.74	0.006	28.25
Petiole length	29.60	28.60	41.79
Pods/plant	84.03	1.53	14.43
Seeds/pod	82.01	0.53	17.44
Pod length	39.27	0.42	60.29
Biological yield/plant	83.44	0.11	16.44
Seed yield/plant	90.40	0.40	9.19
Harvest index	62.53	0.13	37.32
100 seed weight	90.85	0.01	9.13
Protein content	79.62	0.70	19.67
Oil content	76.24	0.33	23.41

Further, it was observed that the per cent contribution of lines was higher than the corresponding testers and their interaction for all the traits. Therefore, it can be concluded that lines played a significant role in the expression of different characters in various cross combinations.

4.4 Nature and magnitude of heterosis

Discovery of hybrid vigour by Shull (1908) has given birth to heterosis breeding. The phenomenon of heterosis has provided the most important genetic tool in improving yield of self as well as cross pollinated species. In contrast to the consistency of evidence of heterozygote superiority in out breeding species, the evidence for inbreeding species has been conflicting. Commercial exploitation of heterosis in grain sorghum (Rao 1968), experiment with *Arabidopsis thaliana* (Griffing and Langridge 1963) and lima bean (Allard and Workman 1963), and possibility of developing hybrid wheat (Athwal and Borlaug 1967) suggest that self and cross fertilized plants are essentially similar in their heterotic response and use of heterosis should carefully be considered in all crop plants irrespective of the breeding system. In soybean, a self pollinated crop, heterosis has been reported by Wentz and Stewart as early as 1924 (Wentz and Stewart 1924) but subsequently limited number of workers have studied it (Leffel and Weiss 1958; Weber et al. 1970; Chaudhari and Singh 1974; Paschal and Wilcox 1975; Kaw and Menon 1979 and Mehta et al. 1984.

Another important aspect from practical point of view, which needs consideration, is the identification of potential cross combinations with respect to seed yield and its related traits. Recently, a considerable attention has been paid to increase the yield potential by the possible use of heterosis from intervarietal hybrids of soybean.

In present study, the crosses have exhibited a high magnitude of heterosis for yield and other traits. Heterosis over the mid parent and the better parent was calculated for all the 36 F_1s involving eighteen lines and two testers. The results obtained for different traits are presented in Table 4.14 and described as under:

Days to 50% flowering

For this trait, negative heterosis is of main interest to the breeder because it is always desirable to incorporate earliness, hence more attention was given towards negative heterosis for this trait. Heterosis over the mid parent ranged from -11.86 to 20.92 per cent, and eight crosses exhibited negative heterosis. The highest negative

heterosis was observed for P2-2 x Hara Soya followed by P2-2 x Him Soya, P13-4 x Hara Soya, P13-4 x Him Soya, P9-2-2 x Hara Soya, P9-2-2 x Him Soya, SL-679 x Him Soya and PS-1469 x Him Soya. On the other hand, heterosis over the better parent ranged from -21.21 to 17.74 per cent, and eleven crosses, *viz.,* P2-2 x Hara Soya followed by P2-2 x Him Soya, P13-4 x Hara Soya, P13-4 x Him Soya, PS-1469 x Him Soya, PS-1469 x Hara Soya, P9-2-2 x Hara Soya, P9-2-2 x Him Soya, VLS-59 x Hara Soya, SL-679 x Him Soya and VLS-59 x Him Soya exhibited significant negative heterosis.

Days to 75% maturity

As already mentioned in days to flowering, one is always interested to have early maturing strains, hence for this trait also negative heterosis is of interest. None of the crosses exhibited significant negative heterosis over mid parent, whereas one cross, namely, P169-3 x Him Soya exhibited significant negative heterosis over the better parent. Heterosis over the better parent ranged from -2.83 to 5.65.

Reproductive phase

This trait was studied to score the hybrids and parents for their synchronous habit of flowering and maturity. Over the mid parent, six crosses showed significant negative heterosis, *viz.,* VLS-59 x Hara Soya followed by Bragg x Hara Soya, P13-4 x Hara Soya, VLS-59 x Him Soya, P9-2-2 x Hara Soya and PS-1469 x Hara Soya. Over the better parent 13 crosses, namely, VLS-59 x Hara Soya followed by Bragg x Hara Soya, VLS-59 x Him Soya, P13-4 x Hara Soya, PS-1469 x Hara Soya, Bragg x Him Soya, PS-1469 x Him Soya, P13-4 x Him Soya, P9-2-2 x Him Soya, P9-2-2 x Hara Soya, P2-2 x Him Soya, P2-2 x Hara Soya and JS-335 x Hara Soya.

The range of heterosis to the extent of -11.27 to 13.62 per cent over mid parent and -16.29 to 12.76 per cent over better parent was observed for the trait. The cross combination of Hardee x Hara Soya, PK-472 x Hara Soya, H-330 x Him Soya, PK-472 x Him Soya and P6-1 x Hara Soya exhibited significant positive heterosis over the respective mid parent. The highest and positive heterotic response over the better parent was observed for Hardee x Hara Soya followed by PK-472 x Hara Soya, H-330 x Him Soya and PK-472 x Him Soya.

Table 4.14 Estimates of heterosis for different traits in soybean

Crosses	Days to 50% flowering				Days to 75% maturity				Reproductive phase			
	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)
P9-2-2 x Him Soya	-5.91*	-10.73*	-0.54	-0.54	-0.40	-2.11	1.37	1.37	-5.97	-10.43*	-1.05	-1.05
P9-2-2 x Hara Soya	-6.46*	-11.71*	-1.63	-0.55	1.20	0.26	3.83*	2.15	-7.13*	-10.43*	-1.05	-3.57
PS-1466 x Him Soya	5.98*	1.09	1.09	1.09	2.02	0.53	3.55*	3.55*	4.79	3.14	3.14	3.14
PS-1466 x Hara Soya	9.46*	4.95	3.80	4.95	3.07*	2.39	5.46*	3.76*	0.26	-2.55	0.00	-2.55
P6-1 x Him Soya	6.27*	5.98*	5.98*	5.98*	2.04	1.35	2.73*	2.73*	6.60	5.76	5.76	5.76
P6-1 x Hara Soya	6.30*	6.01*	5.43	6.59*	2.83*	2.69*	4.37*	2.69*	6.77*	4.59	7.33	4.59
PK-472 x Him Soya	8.08*	5.43	5.43	5.43	5.09*	4.37*	4.37*	4.37*	9.57*	7.85*	7.85*	7.85*
PK-472 x Hara Soya	14.85*	12.64*	11.41*	12.64*	4.50*	2.96*	4.64*	2.96*	11.29*	8.16*	10.99*	8.16*
VLS-59 x Him Soya	-2.80	-8.61*	3.80	3.80	0.27	-2.33	3.01*	3.01*	-7.77*	-14.03*	-0.52	-0.52
VLS-59 x Hara Soya	-4.35	-10.53*	1.63	2.75	1.06	-0.78	4.64*	2.96*	-11.27*	-16.29*	-3.14	-5.61
P13-4 x Him Soya	-6.73*	-13.82*	1.63	1.63	2.00	-0.26	4.37*	4.37*	-5.62	-11.47*	1.05	1.05
P13-4 x Hara Soya	-9.77*	-17.05*	-2.17	-1.10	0.66	-0.78	3.83*	2.15	-8.70*	-13.30*	-1.05	-3.57
PS-1469 x Him Soya	-4.98*	-12.39*	3.80	3.80	2.12	-0.77	5.19*	5.19*	-4.56	-11.95*	4.19	4.19
PS-1469 x Hara Soya	-4.00	-11.93*	4.35	5.49	2.11	0.00	6.01*	4.30*	-7.11*	-13.27*	2.62	0.00
DS-1213 x Him Soya	4.84	0.00	0.00	0.00	5.58*	5.15*	6.01*	6.01*	-2.92	-4.19	-4.19	-4.19
DS-1213 x Hara Soya	20.92*	15.93*	14.67*	15.93*	4.18*	3.76*	5.46*	3.76*	3.66	1.02	3.66	1.02
SL-679 x Him Soya	-5.51*	-8.63*	-2.17	-2.17	2.55*	0.79	4.37*	4.37*	-1.03	-2.54	0.52	0.52
SL-679 x Hara Soya	-1.32	-5.08	1.63	2.75	2.26*	1.32	4.92*	3.23*	-3.31	-3.55	-0.52	-3.06
SL-682 x Him Soya	1.69	-2.17	-2.17	-2.17	3.57*	3.01*	3.01*	3.01*	-5.26	-5.76	-5.76	-5.76
SL-682 x Hara Soya	-0.57	-3.85	-4.89	-3.85	7.08*	5.65*	7.38*	5.65*	-3.90	-5.61	-3.14	-5.61

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Crosses	Days to 50% flowering				Days to 75% maturity				Reproductive phase			
	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)
H-330 x Him Soya	15.85*	15.22*	15.22*	15.22*	5.50*	3.69*	7.38*	7.38*	9.79*	8.12*	11.52*	11.52*
H-330 x Hara Soya	13.19*	13.19*	11.96*	13.19*	4.39*	3.43*	7.10*	5.38*	5.85	5.58	8.90*	6.12
P169-3 x Him Soya	-0.53	-3.09	2.17	2.17	1.46	-1.54	4.64*	4.64*	4.62	2.51	6.81	6.81
P169-3 x Hara Soya	-0.53	-3.61	1.63	2.75	-0.66	-2.83*	3.28*	1.61	0.25	-0.50	3.66	1.02
P2-2 x Him Soya	-11.33*	-20.35*	0.00	0.00	0.13	-2.34	2.73*	2.73*	-4.48	-9.00*	0.52	0.52
P2-2 x Hara Soya	-11.86*	-21.21*	-1.09	0.00	-0.66	-2.34	2.73*	1.08	-5.16	-8.53*	1.05	-1.53
Shivalik x Him Soya	-1.08	-2.13	0.00	0.00	1.60	-1.04	4.37*	4.37*	-1.05	-1.05	-1.05	-1.05
Shivalik x Hara Soya	0.00	-1.60	0.54	1.65	0.26	-1.55	3.83*	2.15	1.81	0.51	3.14	0.51
Hardee x Him Soya	3.24	2.69	3.80	3.80	4.23*	4.09*	4.37*	4.37*	0.00	-0.52	0.52	0.52
Hardee x Hara Soya	19.02*	17.74*	19.02*	20.33*	5.28*	4.57*	6.28*	4.57*	13.62*	12.76*	15.71*	12.76*
JS-335 x Him Soya	0.00	-2.08	2.17	2.17	3.79*	2.96*	4.64*	4.64*	-1.01	-4.39	2.62	2.62
JS-335 x Hara Soya	-0.53	-3.13	1.09	2.20	2.96*	2.96*	4.64*	2.96*	-6.23	-8.29*	-1.57	-4.08
SL-795 x Him Soya	1.63	1.63	1.63	1.63	4.34*	3.49*	5.19*	5.19*	-2.06	-3.55	-0.52	-0.52
SL-795 x Hara Soya	2.19	1.63	1.63	2.75	2.15	2.15	3.83*	2.15	-1.27	-1.52	1.57	-1.02
Bragg x Him Soya	2.51	0.00	0.00	0.00	3.69*	3.55*	3.55*	3.55*	-7.35*	-12.90*	-1.05	-1.05
Bragg x Hara Soya	-3.08	-4.95	-5.98*	-4.95	3.12*	2.15	3.83*	2.15	-10.90*	-15.21*	-3.66	-6.12

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Crosses	Plant height				Branches/plant				Internode length			
	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)
P9-2-2 x Him Soya	-17.63	-18.38	-16.87	-16.87	-1.66	-19.13*	25.42	25.42	-16.66*	-17.78	-17.78	-17.78
P9-2-2 x Hara Soya	-9.09	-16.03	0.92	-16.03	-15.60	-24.59*	16.95	-4.17	-9.86	-11.69	-10.44	-11.69
PS-1466 x Him Soya	-3.47	-17.13*	15.56	15.56	-9.46	-24.72*	13.56	13.56	-18.49*	-22.85*	-13.60	-13.60
PS-1466 x Hara Soya	-17.09*	-22.82*	7.63	-10.45	-3.73	-12.92	31.36*	7.64	-10.89	-15.09	-4.92	-6.24
P6-1 x Him Soya	13.53	3.28	26.04*	26.04*	30.07*	10.71	57.63*	57.63*	11.46	9.09	9.09	9.09
P6-1 x Hara Soya	-4.26	-4.99	15.95	-3.53	3.21	-4.71	36.44*	11.81	10.38	7.30	8.82	7.30
PK-472 x Him Soya	27.78*	25.81*	25.81*	25.81*	12.26	-9.38	47.46*	47.46*	10.26	7.47	7.47	7.47
PK-472 x Hara Soya	10.57	-0.13	20.03	-0.13	5.95	-7.29	50.85*	23.61	-7.41	-10.36	-9.09	-10.36
VLS-59 x Him Soya	-5.66	-19.01*	12.94	12.94	-34.44*	-51.24*	0.00	0.00	0.77	0.20	1.35	1.35
VLS-59 x Hara Soya	-13.18	-19.17*	12.71	-6.22	-19.17*	-35.54*	32.20*	8.33	-6.25	-6.37	-5.05	-6.37
P13-4 x Him Soya	-1.28	-8.10	6.63	6.63	-5.13	-23.71*	25.42	25.42	-7.77	-12.46	-12.46	-12.46
P13-4 x Hara Soya	12.13	10.19	32.43*	10.19	11.24	-3.09	59.32*	30.56*	3.45	-2.46	-1.08	-2.46
PS-1469 x Him Soya	12.40	3.08	23.57*	23.57*	-8.28	-26.53*	22.03	22.03	2.54	0.54	0.54	0.54
PS-1469 x Hara Soya	12.20	12.05	34.67*	12.05	36.47*	18.37*	96.61*	61.11*	8.22	5.38	6.87	5.38
DS-1213 x Him Soya	19.26*	6.83	34.98*	34.98*	30.56*	10.59	59.32*	59.32*	1.04	-2.21	4.51	4.51
DS-1213 x Hara Soya	16.44*	13.60	43.53*	19.42*	40.13*	29.41*	86.44*	52.78*	-6.37	-8.76	-2.49	-3.85
SL-679 x Him Soya	4.85	1.59	8.32	8.32	-18.23*	-39.34*	25.42	25.42	6.63	-4.18	-4.18	-4.18
SL-679 x Hara Soya	-5.16	-10.51	7.55	-10.51	-35.57*	-48.77*	5.93	-13.19	5.58	-5.71	-4.38	-5.71
SL-682 x Him Soya	14.59	10.71	10.71	10.71	0.00	-13.12	17.80	17.80	3.65	-6.20	-6.20	-6.20
SL-682 x Hara Soya	5.34	-6.47	12.40	-6.47	4.61	-0.62	34.75*	10.42	-0.63	-10.62	-9.36	-10.62

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	Plant height				Branches/plant				Internode length			
Crosses	**Heterosis over mid parent (%)**	**Heterosis over better parent (%)**	**Economic heterosis I (%)**	**Economic heterosis II (%)**	**Heterosis over mid parent (%)**	**Heterosis over better parent (%)**	**Economic heterosis I (%)**	**Economic heterosis II (%)**	**Heterosis over mid parent (%)**	**Heterosis over better parent (%)**	**Economic heterosis I (%)**	**Economic heterosis II (%)**
H-330 x Him Soya	23.32*	20.86	25.89*	25.89*	4.90	-10.71	27.12	27.12	18.65*	14.61	14.61	14.61
H-330 x Hara Soya	15.25	7.56	29.28*	7.56	-12.82	-19.05	15.25	-5.56	24.98*	19.92 *	21.62	19.92 *
P169-3 x Him Soya	-1.50	-4.15	1.31	1.31	-9.41	-23.08*	10.17	10.17	29.45*	18.99 *	18.99	18.99 *
P169-3 x Hara Soya	-7.50	-13.08	4.47	-13.08	-20.77*	-26.63*	5.08	-13.89	21.19*	10.69	12.26	10.69
P2-2 x Him Soya	5.47	-0.46	-0.46	-0.46	21.31	17.46	25.42	25.42	-2.03	-7.21	-7.21	-7.21
P2-2 x Hara Soya	-19.99*	-30.45*	-16.41	-30.45*	7.41	0.69	22.88	0.69	-16.80*	-21.71 *	-20.61	-21.71 *
Shivalik x Him Soya	-6.78	-20.86*	13.41	13.41	-10.32	-27.60*	17.80	17.80	-21.26*	-24.00 *	-18.32	-18.32 *
Shivalik x Hara Soya	-27.72*	-33.55*	-4.78	-20.77*	-30.36*	-39.06*	-0.85	-18.75	-13.15	-15.60	-9.29	-10.56
Hardee x Him Soya	2.69	-0.29	5.86	5.86	-9.22	-21.95*	8.47	8.47	-2.64	-3.23	-3.23	-3.23
Hardee x Hara Soya	7.56	1.28	21.73	1.28	14.29	7.32	49.15*	22.22	2.93	1.59	3.03	1.59
JS-335 x Him Soya	5.40	-1.08	12.79	12.79	-12.05	-31.78*	23.73	23.73	-4.22	-12.93	-12.93	-12.93
JS-335 x Hara Soya	-5.13	-7.56	11.09	-7.56	-1.68	-17.76*	49.15*	22.22	-4.74	-13.94	-12.73	-13.94
SL-795 x Him Soya	5.69	-0.81	13.10	13.10	1.08	-11.95	18.64	18.64	-2.69	-3.70	-3.70	-3.70
SL-795 x Hara Soya	-8.22	-10.58	7.47	-10.58	8.25	3.14	38.98*	13.89	-7.70	-9.30	-8.01	-9.30
Bragg x Him Soya	25.47*	13.87	13.87	13.87	-12.42	-28.72*	13.56	13.56	0.15	-9.29	-9.29	-9.29
Bragg x Hara Soya	5.19	-11.73	6.09	-11.73	-9.04	-19.68*	27.97	4.86	9.11	-1.79	-0.40	-1.79

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Crosses	Nodes/main stem				Petiole length				Pods/plant			
	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)
P9-2-2 x Him Soya	0.00	-2.21	2.31	2.31	-1.59	-2.11	-2.11	-2.11	4.59	2.95	2.95	2.95
P9-2-2 x Hara Soya	0.68	-5.77	13.08	-5.77	7.82	2.66	1.58	13.53	53.77*	26.34	22.36	96.41*
PS-1466 x Him Soya	19.73*	7.32	35.38*	35.38*	0.84	-5.26	-5.26	-5.26	39.22*	35.60*	43.04*	43.04*
PS-1466 x Hara Soya	-7.81	-10.06	13.46	-5.45	5.04	4.12	-6.84	4.12	38.10*	9.83	15.85	85.97*
P6-1 x Him Soya	2.70	-8.43	16.92	16.92	1.35	-1.32	-1.32	-1.32	48.16*	41.57*	55.39*	55.39*
P6-1 x Hara Soya	-13.35*	-15.96*	7.31	-10.58	6.57	3.61	-1.84	9.71	64.97*	29.31*	41.92*	127.81*
PK-472 x Him Soya	17.80*	16.04	19.62*	19.62*	-0.28	-6.32	-6.32	-6.32	118.54*	118.04*	118.04*	118.04*
PK-472 x Hara Soya	19.31*	10.90	33.08*	10.90	11.57	10.59	-1.05	10.59	88.01*	52.83*	52.13*	144.21*
VLS-59 x Him Soya	-6.11	-19.34*	12.31	12.31	-3.16	-7.37	-7.37	-7.37	-17.84*	-34.71*	10.77	10.77
VLS-59 x Hara Soya	-7.72	-14.09*	19.62*	-0.32	14.12	12.97	3.16	15.29	-11.46	-39.47*	2.69	64.85*
P13-4 x Him Soya	8.05	-4.17	23.85*	23.85*	0.81	-1.58	-1.58	-1.58	-7.06	-16.68	5.08	5.08
P13-4 x Hara Soya	9.57	5.65	36.54*	13.78	9.97	6.63	1.58	13.53	28.10*	-4.31	20.68	93.72*
PS-1469 x Him Soya	8.50	-2.74	22.69*	22.69*	1.97	-4.74	-4.74	-4.74	6.63	4.70	8.64	8.64
PS-1469 x Hara Soya	4.37	1.83	28.46*	7.05	9.25	7.65	-3.68	7.65	54.10*	23.31	27.95*	105.38*
DS-1213 x Him Soya	18.60*	9.03	30.00*	30.00*	0.54	-2.11	-2.11	-2.11	62.71*	48.98*	48.98*	48.98*
DS-1213 x Hara Soya	24.12*	23.72*	48.46*	23.72*	12.00	8.89	3.16	15.29	83.30*	60.33*	33.28*	113.95*
SL-679 x Him Soya	-2.62	-15.14*	14.23	14.23	3.17	2.63	2.63	2.63	21.03	17.28	17.28	17.28
SL-679 x Hara Soya	-10.27	-15.14*	14.23	-4.81	5.03	0.00	-1.05	10.59	36.20*	13.33	6.30	70.64*
SL-682 x Him Soya	10.64	2.63	20.00*	20.00*	-5.09	-6.84	-6.84	-6.84	10.86	-8.74	-8.74	-8.74
SL-682 x Hara Soya	5.52	4.17	25.00*	4.17	3.40	-0.27	-3.95	7.35	79.18*	75.94*	13.72	82.54*

Contdé /-

Crosses	Nodes/main stem				Petiole length				Pods/plant			
	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)
H-330 x Him Soya	4.32	-2.03	11.54	11.54	-8.56	-10.00	-10.00	-10.00	-21.35	-21.75	-21.75	-21.75
H-330 x Hara Soya	-8.55	-10.90	6.92	-10.90	3.39	-0.54	-3.68	7.65	-25.52	-39.32*	-39.94*	-3.59
P169-3 x Him Soya	-24.58*	-32.93*	-13.85	-13.85	-8.68	-8.68	-8.68	-8.68	-51.16*	-55.74*	-45.53*	-45.53*
P169-3 x Hara Soya	-24.46*	-26.95*	-6.15	-21.79*	7.22	1.58	1.58	13.53	-33.66*	-50.04*	-38.52*	-1.31
P2-2 x Him Soya	8.46	8.46	8.46	8.46	-12.23	-13.16	-13.16	-13.16	53.86*	8.94	8.94	8.94
P2-2 x Hara Soya	-3.15	-11.22	6.54	-11.22	11.24	6.45	4.21	16.47	64.99*	37.60	-14.28	37.60
Shivalik x Him Soya	20.33*	4.86	41.15*	41.15*	-3.80	-6.84	-6.84	-6.84	15.51	14.87	16.16	16.16
Shivalik x Hara Soya	-17.22*	-21.71*	5.38	-12.18	4.02	1.69	-4.74	6.47	-7.15	-24.97	-24.14	21.78
Hardee x Him Soya	5.54	1.42	10.00	10.00	-2.20	-6.32	-6.32	-6.32	-14.54	-16.21	-12.80	-12.80
Hardee x Hara Soya	5.05	0.00	20.00*	0.00	2.91	1.72	-6.84	4.12	29.75*	3.71	7.93	73.25*
JS-335 x Him Soya	8.63	-7.10	30.77*	30.77*	-13.37	-14.74	-14.74	-14.74	2.70	-1.42	-1.42	-1.42
JS-335 x Hara Soya	-0.88	-8.20	29.23*	7.69	12.43	8.15	4.74	17.06	34.39*	12.71	3.66	66.39*
SL-795 x Him Soya	9.03	0.98	18.46*	18.46*	-1.18	-1.31	-1.05	-1.05	49.16*	28.96*	28.96*	28.96*
SL-795 x Hara Soya	-0.49	-1.60	18.08*	-1.60	5.41	-0.26	0.00	11.76	82.86*	69.55*	23.63	98.45*
Bragg x Him Soya	26.44*	25.95*	26.92*	26.92*	-9.28	-10.00	-10.00	-10.00	25.41*	15.35	15.35	15.35
Bragg x Hara Soya	-2.09	-9.94	8.08	-9.94	4.48	-0.27	-1.84	9.71	36.21*	18.64	-0.41	59.87*

Contdé /-

Crosses	Seeds/pod				Pod length				Biological yield/plant			
	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)
P9-2-2 x Him Soya	0.96	-1.56	-1.56	-1.56	-5.41*	-8.70*	-1.87	-1.87	15.95	4.24	4.24	4.24
P9-2-2 x Hara Soya	-2.80	-7.69	-2.50	-7.69	-3.14	-6.09*	0.93	0.00	43.13*	33.29	23.32	33.29
PS-1466 x Him Soya	-1.22	-3.57	1.25	1.25	0.00	0.00	0.00	0.00	25.39*	6.64	52.12*	52.12*
PS-1466 x Hara Soya	-5.34	-5.62	-0.31	-5.62	0.47	0.00	0.93	0.00	15.27	-4.98	35.54*	46.50*
P6-1 x Him Soya	6.75	3.75	3.75	3.75	-6.60*	-7.48*	-7.48*	-7.48*	32.29*	27.55	37.41*	37.41*
P6-1 x Hara Soya	5.63	0.00	5.62	0.00	4.23*	2.78	3.74	2.78	36.61*	26.97	36.78*	47.84*
PK-472 x Him Soya	10.36	6.56	6.56	6.56	-3.26	-3.70	-2.80	-2.80	140.28*	117.21*	117.21*	117.21*
PK-472 x Hara Soya	6.29	0.00	5.63	0.00	-2.78	-2.78	-1.87	-2.78	123.88*	109.70*	94.01*	109.70*
VLS-59 x Him Soya	3.03	0.00	6.25	6.25	-3.32	-4.67*	-4.67*	-4.67*	-20.93*	-41.62*	22.44	22.44
VLS-59 x Hara Soya	-2.95	-3.24	2.81	-2.66	-0.94	-2.78	-1.87	-2.78	-27.56*	-47.80*	9.48	18.33
P13-4 x Him Soya	3.49	1.88	1.87	1.87	0.47	0.00	0.93	0.93	8.25	-3.15	22.69	22.69
P13-4 x Hara Soya	4.63	0.30	5.94	0.30	2.78	2.78	3.74	2.78	39.36*	20.57	52.74*	65.09*
PS-1469 x Him Soya	-4.14	-5.94	-5.94	-5.94	2.86	0.93	0.93	0.93	41.49*	37.78*	37.78*	37.78*
PS-1469 x Hara Soya	3.41	-1.18	4.37	-1.18	2.37	0.00	0.93	0.00	85.89*	83.68*	74.06*	88.14*
DS-1213 x Him Soya	8.46	8.12	8.12	8.12	5.99*	4.55*	7.48*	7.48*	57.81*	48.14*	68.83*	68.83*
DS-1213 x Hara Soya	10.37*	7.10	13.12	7.10	-3.67	-4.55*	-1.87	-2.78	89.61*	71.77*	95.76*	111.59*
SL-679 x Him Soya	-4.10	-5.00	-5.00	-5.00	-3.57	-7.69*	0.93	0.93	10.85	8.47	13.34	13.34
SL-679 x Hara Soya	-1.84	-5.33	0.00	-5.33	-10.22*	-13.68*	-5.61*	-6.48*	11.52	5.13	9.85	18.73
SL-682 x Him Soya	-1.28	-3.75	-3.75	-3.75	7.34*	5.41*	9.35*	9.35*	20.99	9.23	9.23	9.23
SL-682 x Hara Soya	-5.92	-10.65	-5.63	-10.65	-6.85*	-8.11*	-4.67*	-5.56*	69.31 *	58.36*	46.51*	58.36*

Contdé /-

Crosses	Seeds/pod				Pod length				Biological yield/plant			
	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)
H-330 x Him Soya	4.32	3.05	5.62	5.62	9.35*	9.35*	9.35*	9.35*	59.27*	54.95*	63.84*	63.84*
H-330 x Hara Soya	5.71	4.14	10.00	4.14	3.26	2.78	3.74	2.78	13.21	6.13	12.22	21.29
P169-3 x Him Soya	-0.33	-5.63	-5.63	-5.63	1.89	0.93	0.93	0.93	-31.96*	-38.36*	-24.06	-24.06
P169-3 x Hara Soya	-2.56	-10.06	-5.00	-10.06	-5.16*	-6.48*	-5.61*	-6.48*	-22.54	-32.19*	-16.46	-9.70
P2-2 x Him Soya	-3.43	-7.50	-7.50	-7.50	0.93	0.93	0.93	0.93	8.62	2.55	15.46	15.46
P2-2 x Hara Soya	-9.03	-15.09*	-10.31	-15.09*	3.26	2.78	3.74	2.78	-26.32	-32.89*	-24.44	-18.33
Shivalik x Him Soya	-7.12	-11.58*	-2.19	-2.19	3.26	2.78	3.74	3.74	-11.62	-25.72*	9.10	9.10
Shivalik x Hara Soya	-17.63*	-19.49*	-10.94	-15.68*	3.70	3.70	4.67*	3.70	-27.50*	-40.92*	-13.22	-6.20
Hardee x Him Soya	-3.11	-3.70	-2.50	-2.50	-3.35	-5.61*	-5.61*	-5.61*	-30.23*	-37.25*	-21.45	-21.45
Hardee x Hara Soya	3.32	1.18	6.87	1.18	11.43*	8.33*	9.35*	8.33*	17.07	1.79	27.43	37.74*
JS-335 x Him Soya	11.78*	3.75	3.75	3.75	-4.11*	-6.25*	-1.87	-1.87	5.13	4.74	4.74	4.74
JS-335 x Hara Soya	6.54	-3.55	1.87	-3.55	0.91	-0.89	3.74	2.78	16.51	12.56	11.72	20.75
SL-795 x Him Soya	6.92	3.75	3.75	3.75	3.85	0.93	0.93	0.93	43.04*	39.65*	39.65*	39.65*
SL-795 x Hara Soya	0.78	-4.73	0.62	-4.73	6.22*	2.78	3.74	2.78	52.06*	49.87*	42.77*	54.31*
Bragg x Him Soya	8.72	1.25	1.25	1.25	1.83	0.00	3.74	3.74	35.24*	29.68	29.68	29.68
Bragg x Hara Soya	4.89	-4.73	0.62	-4.73	5.02*	3.60	7.48*	6.48*	34.78*	34.23	24.19	34.23

Contdé /-

Crosses	Seed yield/plant				Harvest index				100 seed weight			
	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)
P9-2-2 x Him Soya	-1.69	-18.49	-18.49	-18.49	-11.59	-17.14	-17.14	-17.14	9.52	-4.17	-4.17	-4.17
P9-2-2 x Hara Soya	36.71*	32.52	-7.10	32.52	-12.08	-14.38	-25.14*	-9.66	-3.31	-24.74*	1.39	-24.74 *
PS-1466 x Him Soya	18.85	14.03	24.09	24.09	-4.85	-16.00	-16.00	-16.00	-15.43*	-28.16*	2.78	2.78
PS-1466 x Hara Soya	31.25*	7.91	17.42	67.48*	6.81	2.76	-14.86	2.76	-25.00*	-27.18*	4.17	-22.68*
P6-1 x Him Soya	18.76	11.61	11.61	11.61	-10.13	-18.86	-18.86	-18.86	-4.55	-12.50	-12.50	-12.50
P6-1 x Hara Soya	65.71*	48.90*	30.97*	86.81*	18.18	16.55	-3.43	16.55	-0.64	-19.59*	8.33	-19.59*
PK-472 x Him Soya	118.63*	91.83*	91.83*	91.83*	-9.36	-11.43	-11.43	-11.43	13.24	6.94	6.94	6.94
PK-472 x Hara Soya	169.72*	160.11*	96.34*	180.06*	12.82	5.39	0.57	21.38	-6.83	-22.68*	4.17	-22.68*
VLS-59 x Him Soya	-20.91*	-35.12*	1.29	1.29	-4.92	-17.14	-17.14	-17.14	21.13*	19.44*	19.44	19.44*
VLS-59 x Hara Soya	-18.06	-40.63*	-7.31	32.21	6.91	1.38	-16.00	1.38	-11.38	-23.71*	2.78	-23.71*
P13-4 x Him Soya	-10.20	-14.56	-5.38	-5.38	-18.04*	-23.43*	-23.43*	-23.43*	-1.35	-3.95	1.39	1.39
P13-4 x Hara Soya	27.47*	4.08	15.27	64.42*	-11.11	-13.16	-24.57*	-8.97	-6.36	-16.49*	12.50	-16.49*
PS-1469 x Him Soya	7.94	0.86	0.86	0.86	-24.63*	-27.43*	-27.43*	-27.43*	3.36	0.00	6.94	6.94
PS-1469 x Hara Soya	75.07*	58.17*	37.42*	96.01*	-10.75	-15.43	-21.71*	-5.52	-4.60	-14.43*	15.28	-14.43*
DS-1213 x Him Soya	44.48*	33.76*	33.76*	33.76*	-9.21	-21.14*	-21.14*	-21.14*	-13.66*	-28.83*	9.72	9.72
DS-1213 x Hara Soya	101.11*	83.33*	56.13*	122.70*	1.46	-4.14	-20.57*	-4.14	-25.96*	-30.63*	6.94	-20.62*
SL-679 x Him Soya	8.72	-2.15	-2.15	-2.15	-1.95	-13.71	-13.71	-13.71	-13.29	-13.89	-13.89	-13.89
SL-679 x Hara Soya	14.33	7.26	-14.19	22.39	-2.16	-6.21	-22.29*	-6.21	-32.14*	-41.24*	-20.83	-41.24*
SL-682 x Him Soya	-1.59	-13.55	-13.55	-13.55	-20.00*	-22.29*	-22.29*	-22.29*	2.70	0.00	5.56	5.56
SL-682 x Hara Soya	64.90*	58.81*	20.22	71.47*	-9.68	-15.15	-20.00*	-3.45	-8.67	-18.56*	9.72	-18.56*

Contdé /-

Crosses	Seed yield/plant				Harvest index				100 seed weight			
	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)
H-330 x Him Soya	55.43*	44.73*	44.73*	44.73*	-1.58	-10.86	-10.86	-10.86	83.22*	81.94*	81.94	81.94*
H-330 x Hara Soya	52.13*	37.91*	18.92	69.63*	27.53*	26.21*	4.57	26.21*	72.62*	49.48*	101.39	49.48*
P169-3 x Him Soya	-43.46*	-44.12*	-42.80*	-42.80*	-16.77	-23.43*	-23.43*	-23.43*	56.25*	52.78*	52.78	52.78*
P169-3 x Hara Soya	-24.44	-36.34*	-34.84*	-7.06	-8.22	-8.84	-23.43*	-7.59	1.33	-13.40*	16.67	-13.40*
P2-2 x Him Soya	-1.34	-21.08	-21.08	-21.08	-10.45	-31.43*	-31.43*	-31.43*	3.91	-7.21	18.06	18.06*
P2-2 x Hara Soya	-12.07	-18.40	-42.80*	-18.40	12.61	-7.59	-23.43*	-7.59	-24.71*	-26.80*	-1.39	-26.80*
Shivalik x Him Soya	-10.25	-19.69	1.72	1.72	-0.62	-8.00	-8.00	-8.00	-7.77	-18.10*	5.56	5.56
Shivalik x Hara Soya	-33.11*	-48.05*	-34.19*	-6.13	-8.84	-10.07	-23.43*	-7.59	-20.97*	-22.68*	4.17	-22.68*
Hardee x Him Soya	-29.02*	-34.77*	-22.15	-22.15	-0.29	-2.29	-2.29	-2.29	-12.26	-18.07*	-5.56	-5.56
Hardee x Hara Soya	-1.70	-21.98*	-6.88	32.82	-18.85*	-24.40*	-27.43*	-12.41	-20.22*	-25.98*	-0.28	-25.98*
JS-335 x Him Soya	-15.91	-22.15	-22.15	-22.15	-15.60	-21.14*	-21.14*	-21.14*	-12.99*	-26.67*	6.94	6.94
JS-335 x Hara Soya	12.19	2.27	-12.90	24.23	-2.36	-4.61	-17.14	0.00	-29.70*	-32.38*	-1.39	-26.80*
SL-795 x Him Soya	41.46*	24.73	24.73	24.73	-0.95	-10.29	-10.29	-10.29	-2.53	-10.47	6.94	6.94
SL-795 x Hara Soya	76.80*	69.58*	29.46*	84.66*	10.80	9.66	-9.14	9.66	-21.31*	-25.77*	0.00	-25.77*
Bragg x Him Soya	24.66	7.10	7.10	7.10	-8.33	-18.29	-18.29	-18.29	-6.67	-17.20*	6.94	6.94
Bragg x Hara Soya	48.48*	46.71*	5.38	50.31*	4.26	1.38	-16.00	1.38	-6.32	-8.25	23.61*	-8.25

Contdé /-

Crosses	Protein content				Oil content			
	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)
P9-2-2 x Him Soya	7.13*	6.67*	7.61*	7.61*	-2.47	-4.65*	-4.65*	-4.65*
P9-2-2 x Hara Soya	0.93	-0.65	0.23	2.56*	-5.24*	-13.18*	-0.36	-13.18*
PS-1466 x Him Soya	-6.06*	-10.57*	-1.06	-1.06	1.66	-0.42	-0.42	-0.42
PS-1466 x Hara Soya	-5.65*	-11.15*	-1.70	0.57	-4.64*	-12.47*	0.46	-12.47*
P6-1 x Him Soya	-2.38*	-4.48*	-0.19	-0.19	7.83*	2.81	2.81	2.81
P6-1 x Hara Soya	-0.35	-3.58*	0.76	3.09*	1.03	-9.58*	3.78*	-9.58*
PK-472 x Him Soya	0.00	-0.90	0.92	0.92	2.29	1.75	1.75	1.75
PK-472 x Hara Soya	5.29*	3.17*	5.07*	7.50*	-11.30*	-17.42*	-5.22*	-17.42*
VLS-59 x Him Soya	3.20*	2.89*	2.89*	2.89*	-1.07	-2.79	-2.79	-2.79
VLS-59 x Hara Soya	3.40*	2.53*	1.92*	4.28*	-8.74*	-15.99*	-3.59*	-15.99*
P13-4 x Him Soya	0.65	0.45	0.84	0.84	0.64	-1.61	-1.61	-1.61
P13-4 x Hara Soya	3.17*	1.81	2.20*	4.57*	-5.80*	-13.70*	-0.95	-13.70*
PS-1469 x Him Soya	3.58*	3.53*	3.63*	3.63*	1.27	1.12	1.12	1.12
PS-1469 x Hara Soya	3.67*	2.44*	2.54*	4.92*	-4.39*	-10.67*	2.52	-10.67*
DS-1213 x Him Soya	2.01*	0.98	3.06*	3.06*	-3.83*	-6.90*	-0.55	-0.55
DS-1213 x Hara Soya	-0.29	-2.40*	-0.39	1.92	-7.75*	-10.95*	2.20	-10.95*
SL-679 x Him Soya	5.23*	4.14*	6.33*	6.33*	-1.11	-5.09*	-5.09*	-5.09*
SL-679 x Hara Soya	7.77*	5.47*	7.69*	10.18*	-15.68*	-24.07*	-12.85*	-24.07*
SL-682 x Him Soya	2.32*	0.29	4.42*	4.42*	-3.32*	-4.45*	-2.16	-2.16
SL-682 x Hara Soya	3.84*	0.65	4.80*	7.23*	-8.97*	-13.88*	-1.16	-13.88*

Contdé /-

Crosses	Protein content				Oil content			
	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)	Heterosis over mid parent (%)	Heterosis over better parent (%)	Economic heterosis I (%)	Economic heterosis II (%)
H-330 x Him Soya	8.65*	8.58*	8.58*	8.58*	12.44*	11.12*	13.80*	13.80*
H-330 x Hara Soya	7.65*	6.49*	6.36*	8.82*	4.06*	-1.54	13.00*	-1.54
P169-3 x Him Soya	1.96*	1.25	1.25	1.25	-2.78*	-2.94	-2.94	-2.94
P169-3 x Hara Soya	1.51	1.06	-0.35	1.96*	6.50*	-0.51	14.18*	-0.51
P2-2 x Him Soya	3.68*	3.35*	4.02*	4.02*	-7.64*	-9.39*	-5.83*	-5.83*
P2-2 x Hara Soya	3.70*	2.20*	2.86*	5.25*	-15.18*	-19.19*	-7.25*	-19.19*
Shivalik x Him Soya	-1.58	-2.59*	-0.55	-0.55	-2.63*	-5.18*	0.06	0.06
Shivalik x Hara Soya	-1.24	-3.35*	-1.33	0.96	-5.14*	-8.96*	4.48*	-8.96*
Hardee x Him Soya	-0.51	-1.88*	0.91	0.91	-0.01	-1.95	2.01	2.01
Hardee x Hara Soya	1.43	-1.09	1.72	4.08*	-8.48*	-12.75*	0.13	-12.75*
JS-335 x Him Soya	0.32	-0.56	1.22	1.22	-0.97	-1.84	-1.84	-1.84
JS-335 x Hara Soya	2.61*	0.57	2.37*	4.75*	-10.15*	-16.62*	-4.31*	-16.62*
SL-795 x Him Soya	2 24*	1.22	1.22	1.22	-7.48*	-12.81*	-1.44	-1.44
SL-795 x Hara Soya	4.45*	4.30*	2.22*	4.59*	-17.89*	-18.51 *	-6.47*	-18.51*
Bragg x Him Soya	-3.39*	-6.20*	-0.41	-0.41	0.36	0.06	0.66	0.66
Bragg x Hara Soya	-2.18*	-6.07*	-0.27	2.04*	-1.80	-7.86*	5.75*	-7.86*

* Significant at P Ò0.05

Economic heterosis I = Heterosis over standard check-1

Economic heterosis II = Heterosis over standard check-2

Plant height

The range of heterosis over mid parent was from -27.72 to 27.78 per cent and over better parent it was from -33.55 to 25.81 per cent. The combination PK-472 x Him Soya exhibited the highest significant heterosis over mid parent as well as over better parent. Over mid parent, there were five crosses, *viz.,* PK-472 x Him Soya, Bragg x Him Soya, H-330 x Him Soya, DS-1213 x Him Soya and DS-1213 x Hara Soya which exhibited significant positive heterosis. The results were agreement with those previously obtained by El-Hosary et al (2001), Mansour et al (2002) and Fayiz (2009).

Branches per plant

There were 15 hybrids which showed positive heterosis over mid parent and eight hybrids exhibited positive heterosis over better parent. Though, there were four combinations, *viz.,* DS-1213 x Hara Soya, PS-1469 x Hara Soya, DS-1213 x Him Soya and P6-1 x Him Soya which showed significant positive heterosis over mid parent yet only one combination DS-1213 x Hara Soya had the significant positive heterosis over better parent. The range of heterosis over mid parent was from -35.57 to 40.13 per cent and over better parent, it was from -51.24 to 29.41 per cent. The hybrid DS-1213 x Hara Soya exhibited the highest significant positive heterosis over mid parent as well as better parent.

Internode length

For this trait, negative heterosis is of main interest to the plant breeder because it is always desirable to incorporate stronger stem, hence more attention was given towards negative heterosis for shorter internode length. The range of heterosis over mid parent was from -21.26 to 29.45 per cent and over better parent, it was from -24.00 to 19.92 per cent. Over mid parent, there were 19 crosses which exhibited negative heterosis and 25 crosses had negative heterosis over better parent. There were four crosses *viz.,* Shivalik x Him Soya, PS-1466 x Him Soya, P2-2 x Hara Soya and P9-2-2 x Him Soya which showed significant negative heterosis over mid parent whereas three crosses *viz.,* Shivalik x Him Soya, PS-1466 x Him Soya and P2-2 x Hara Soya showed significant negative heterosis over better parent. The highest positive heterosis over mid parent was obtained from P169-3 x Him Soya and over better parent it was recorded for H-330 x Hara Soya.

Nodes on main stem

The range of heterosis over mid parent was from -24.58 to 26.44 per cent and over better parent it was from -32.93 to 25.95 per cent for this trait. Cross Bragg x Him Soya followed by DS-1213 x Hara Soya exhibited the highest significant heterosis over mid parent as well as better parent. When heterosis was measured over mid parent, there were 21 crosses exhibiting positive heterosis and out of these, seven crosses exhibited significant heterosis. When heterosis was measured over better parent, there were 14 crosses exhibiting positive heterosis and out of these two crosses *viz.,* Bragg x Him Soya and DS-1213 x Hara Soya exhibited significant heterosis.

Pods per plant

There were 27 hybrids which showed positive heterosis over mid parent and 24 hybrids indicated positive heterosis over better parent. Twenty one crosses over mid parent and ten crosses over better parent had significant heterosis. The range observed for the heterosis over mid parent was from -51.16 to 118.54 per cent and over better parent it was from -55.74 to 118.04 per cent. The hybrid PK-472 x Him Soya was found to have the highest heterosis both over mid parent as well as better parent.

Seeds per pod

There were 20 hybrids which showed positive heterosis over mid parent and none of the hybrids indicated positive heterosis over better parent. The range of heterosis over mid parent was from -17.63 to 11.78 per cent. Two crosses, *viz.,* JS-335 x Him Soya and DS-1213 x Hara Soya exhibited significant positive heterosis over mid parent.

Pod length

The range of heterosis over mid parent was from -10.22 to 11.43 per cent and over better parent it was from -13.68 to 9.35 per cent. There were 21 hybrids which showed positive heterosis over mid parent and 16 hybrids indicated positive heterosis over better parent. Seven crosses over mid parent and four crosses over better parent had significant heterosis. Cross Hardee x Hara Soya showed the highest significant heterosis over mid parent and cross H-330 x Him Soya showed the highest significant heterosis over better parent.

In some cases, more than 50 per cent of the crosses have shown negative heterosis. Absence of heterosis is possible due to cancellation of positive and negative effects exhibited by the parents involved in the cross combination and can also happen when the dominance is not of unidirectional nature (Mather and Jinks 1971). Breederôs interest lies in hybrids only if they are superior than the standard varieties. Crosses exhibiting standard heterosis are of great utility.

Biological yield per plant

Out of 36 crosses, 28 cross combinations exhibited positive heterosis over mid parental value. Out of these 28 cross combinations, 17 crosses showed significant positive heterosis. The range observed for the heterosis over mid parent was from -31.96 to 140.28 per cent. When heterosis was estimated over better parent, 26 crosses exhibited positive effect and out of these only 10 crosses showed significant heterosis. The range observed for the heterosis over better parent was from -47.80 to 117.21 per cent. The highest significant positive heterosis over mid parent and better parent was recorded for the cross PK-472 x Him Soya.

Seed yield per plant

For seed yield per plant, out of 36 crosses, 22 hybrids showed positive heterosis over mid parent while 21 crosses exhibited positive heterosis over better parent. The range of heterosis over mid parent was from -43.46 to 169.72 per cent and over better parent it was from -48.05 to 160.11 per cent. The cross PK-472 x Hara Soya showed significant positive heterosis over mid parent as well as better parent. Out of 22 crosses, 15 hybrids showed significant positive heterosis over mid parent and out of 21 crosses, 11 hybrids showed significant positive heterosis over better parent. Shang et al. (1992), Ibrahime et al. (1996), Bastawisy et al. (1997), Mansour et al. (2002) and El-Garhy et al. (2008) also reported heterosis for yield and its components traits.

Harvest index (%)

There were 10 hybrids which showed positive heterosis over mid parent and seven hybrids exhibited positive heterosis over better parent, though, there was only one hybrid H-330 x Hara Soya which showed significant positive heterosis over mid parent and better parent. The range of heterosis over mid parent was from -24.63 to 27.53 per cent and over better parent it was from -31.43 to 26.21 per cent.

100-seed weight

The range of heterosis over mid parent recorded for this trait was -32.14 to 83.22 per cent and over better parent, it was from ï 41.24 to 81.94 per cent. Cross H-330 x Him Soya was found to have the highest heterosis over mid parent as well as better parent. When heterosis was measured over mid parent, there were 10 crosses exhibiting positive heterosis and out of these, only four crosses *viz.,* H-330 x Him Soya, H-330 x Hara Soya, P169-3 x Him Soya and VLS-59 x Him Soya had significant heterosis. Out of five crosses exhibiting positive heterosis over better parent, there were four crosses *viz.,* H-330 x Him Soya, P169-3 x Him Soya, H-330 x Hara Soya and VLS-59 x Him Soya which had significant heterosis.

Protein content

The highest positive heterosis over both mid parent and better parent was recorded for H-330 x Him Soya. Out of 36 hybrids, 25 exhibited positive heterosis over mid parent and 22 exhibited positive heterosis over better parent. Out of these crosses exhibiting positive heterosis, there were 20 and 13 crosses exhibiting significant heterosis over mid and better parent, respectively. The range of heterosis over mid parent was from -6.06 to 8.65 per cent and over better parent it was from -11.15 to 8.58 per cent.

Oil content

The range of heterosis over mid parent was from -17.89 to 12.44 per cent and over better parent it was from -24.07 to 11.12 per cent for this trait. Cross H-330 x Him Soya exhibited the highest significant heterosis over mid parent and better parent. There were 10 hybrids which showed positive heterosis over mid parent and five hybrids indicated positive heterosis over better parent. Four crosses, *viz.,* H-330 x Him Soya, P6-1 x Him Soya, P169-3 x Him Soya and H-330 x Hara Soya over mid parent and only one cross H-330 x Him Soya over better parent had significant heterosis. Similar results have been reported by Chen (1983), Wehrmann et al. (1987), Fahmi et al. (1999) and several other workers.

On the basis of heterosis, it can be concluded that heterosis was displayed for almost all the characters. Seed yield is the sum total of contribution made by individual component and hence a complex character itself. The breeder has to simplify complex

situation to breed for high yield by handling number of related traits simultaneously. A good number of crosses showed the presence of desirable heterotic response for the different characters over the standard cultivars.

4.5 Reaction to diseases

The reactions of parents and hybrids to different diseases under natural conditions are shown in Table 4.15.

Frogeye Leaf Spot (FLS)

Frogeye leaf spot is fungal disease is caused by *Cercospora sojina* and its symptoms appear as small spots with dark reddish-brown margin. Old lesions have papery tan to white centre. Spots usually develop in mid-season in young, upper leaves of plant.

Ten genotypes, *viz.,* P169-3, P6-1 x Him Soya, VLS-59 x Him Soya, P13-4 x Him Soya, P169-3 x Him Soya, P2-2 x Hara Soya, Shivalik x Him Soya, P13-4 x (Hara Soya x Him Soya), Shivalik x (Hara Soya x Him Soya) and Bragg x (Hara Soya x Him Soya) were found to be resistant to this disease.

Pod Blight (PB)

This fungal disease is caused by *Colletotrichum truncatum* and its symptoms appear as brown lesions develop on stems, pods and leaves. Infected tissues turn brown and senesce early.

Five genotypes, *viz.,* PS-1469, SL-679 x Him Soya, JS-335 x Him Soya, VLS-59 x (Hara Soya x Him Soya) and Shivalik x (Hara Soya x Him Soya) were found to be resistant to this disease.

Brown Spot (BS)

Brown spot is caused by *Septoria glycines* and its symptoms appear as small spots that are somewhat angular to irregular and light to dark brown. The spots develop on both surfaces of the lower leaves. Heavily infected leaves quickly turn yellow and drop off and may cause extensive defoliation and yield reduction. Brown lesions of an irregular size and shape with indefinite margins may also develop on the stem, branches, petiole and pods.

Three genotypes, *viz.,* PS-1469, P9-2-2 x Him Soya and DS-1213 x (Hara Soya x Him Soya) were found to be highly resistant to this disease. Six genotypes *viz.,* H-330, P169-3 x Hara Soya, H-330 x Him Soya, H-330 x Hara Soya, H-330 x (Hara Soya x Him Soya) and Hardee x (Hara Soya x Him Soya) were found to be resistant.

Bacterial Pustule (BP)

Bacterial pustule is caused by *Xanthomonas campestris* pv *glycines* and its symptoms appear as small, pale, yellowish green spots (lesions) with dark reddish brown centers are most conspicuous on the upper leaf surface with minute, raised, light colored pustule at the central part of each lesion. The leaves become ragged when parts of the brown, dead areas tear away.

Nine genotypes, *viz.,* P9-2-2, P13-4, P9-2-2 x Him Soya, H-330 x Him Soya, P6-1 x Hara Soya, PS-1469 x Him Soya, Hardee x Him Soya, PS-1469 x (Hara Soya x Him Soya) and PS-1466 x (Hara Soya x Him Soya) were found to be resistant.

Overall, on the basis of results and foregoing discussion, it may concluded that on the basis of GCA effects different lines, *viz.,* Bragg, P9-2-2, Shivalik, P13-4, P6-1, H-330, Hardee and SL-679 were found to be good general combiners for different traits. Among these lines Bragg, Shivalik, P6-1 and Hardee were found moderately resistant to frogeye leaf spot. Lines P9-2-2 and P13-4 were found resistant to bacterial pustule. Line H-330 was observed resistant to brown spot and moderately resistant to frogeye leaf spot. Thus, these lines may be used in further future hybridization programme as source of resistance after thorough testing. On the basis of SCA effects, three cross combinations, namely, PS-1469 x Hara Soya, Shivalik x Him Soya and H-330 x Him Soya were found to be good specific combiners for seed yield per plant. The cross PS-1469 x Hara Soya was found moderately resistant to frogeye leaf spot. The crosses Shivalik x Him Soya and H-330 x Him Soya were found resistant to frogeye leaf spot and brown spot, respectively. Thus, these cross combinations may be carried forward and evaluated further. On the basis of heterosis for seed yield per plant, PK-472 x Hara Soya, PK-472 x Him Soya, H-330 x Him Soya and PS-1469 x Hara Soya were the top four hybrid combinations showing heterosis over both the standard checks Hara Soya and Him Soya. Among these four crosses, the cross H-330 x Him Soya was resistant to brown spot and bacterial pustule, whereas, cross PS-1469 x Hara Soya was found moderately resistant

Table 4.15 Reaction of parents and hybrids to different diseases

Reaction	HR	R	MR	MS	S	HS
Grade (%)	**0**	**<1**	**1-10**	**11-20**	**21-50**	**>51**
Scale (0-9)	**0**	**1**	**3**	**5**	**7**	**9**
Frogeye leaf spot		P169-3, P6-1 x Him Soya, VLS-59 x Him Soya, P13-4 x Him Soya, P169-3 x Him Soya, P2-2 x Hara Soya, Shivalik x Him Soya, P13-4 x (Hara Soya x Him Soya), Shivalik x (Hara Soya x Him Soya), Bragg x (Hara Soya x Him Soya)	P6-1, DS-1213, Hardee, Bragg, Shivalik, PS-1466, H-330, PS-1469, Him Soya, Hara Soya x Him Soya, P9-2-2 x Him Soya, PS-1469 x Hara Soya, PS-1469 x (Hara Soya x Him Soya), DS-1213 x Him Soya, H-330 x Hara Soya, H-330 x (Hara Soya x Him Soya), P2-2 x (Hara Soya x Him Soya)	P9-2-2, PK-472, SL-795, PS-1466 x Him Soya, DS-1213 x (Hara Soya x Him Soya), P169-3 x (Hara Soya x Him Soya)	SL-679	
Pod blight		PS-1469, SL-679 x Him Soya, JS-335 x Him Soya, VLS-59 x (Hara Soya x Him Soya), Shivalik x (Hara Soya x Him Soya)	Shivalik, VLS-59, Hara Soya, Hara Soya x Him Soya, P9-2-2 x Hara Soya, VLS-59 x Hara Soya, SL-682 x Him Soya, P2-2 x Him Soya, Shivalik x Hara Soya, JS-335 x Hara Soya, Bragg x Hara Soya, P6-1 x (Hara Soya x Him Soya), P169-3 x (Hara Soya x Him Soya)	SL-682, P2-2, Him Soya, P2-2 x Hara Soya, P9-2-2 x (Hara Soya x Him Soya)	SL-679, P9-2-2 x Him Soya	
Brown spot	PS 1469, P9-2-2 x Him Soya, DS-1213 x (Hara Soya x Him Soya)	H-330, P169-3 x Hara Soya, H-330 x Him Soya, H-330 x Hara Soya, H-330 x (Hara Soya x Him Soya), Hardee x (Hara Soya x Him Soya)	PK-472, PS-1466, VLS-59, JS-335, Hara Soya x Him Soya, P6-1 x Hara Soya, DS-1213 x Hara Soya, Shivalik x Hara Soya, SL-679 x (Hara Soya x Him Soya), Shivalik x (Hara Soya x Him Soya),	Him Soya, Hardee, SL-795, Shivalik, P6-1, SL-682, P6-1 x Him Soya, VLS-59 x Hara Soya, PS-1469 x Him Soya, Bragg x Hara Soya	Bragg, P2-2, P9-2-2 x (Hara Soya x Him Soya)	
Bacterial pustule		P9-2-2, P13-4, P9-2-2 x Him Soya, H-330 x Him Soya, P6-1 x Hara Soya, PS-1469 x Him Soya, Hardee x Him Soya, PS-1469 x (Hara Soya x Him Soya), PS-1466 x (Hara Soya x Him Soya)	P6-1 x Him Soya, P2-2 x Hara Soya, P9-2-2 x (Hara Soya x Him Soya)	P2-2		

Table 4.16 List of top ranking cross combinations based on *per se* performance, SCA effects, heterobeltiosis, economic heterosis I and economic heterosis II

Trait	*Per se* performance	SCA effects	Heterobeltiosis	Economic heterosis I	Economic heterosis II	Common
Days to 50% flowering	Bragg x Hara Soya, SL-682 x Hara Soya, P13-4 x Hara Soya, SL-679 x Him Soya, SL-682 x Him Soya	Hardee x Him Soya and DS-1213 x Him Soya	P2-2 x Hara Soya, P2-2 x Him Soya, P13-4 x Hara Soya, P13-4 x Him Soya, PS-1469 x Him Soya, PS-1469 x Hara Soya, P9-2-2 x Hara Soya, P9-2-2 x Him Soya, VLS-59 x Hara Soya, SL-679 x Him Soya	Bragg x Hara Soya	-	Bragg x Hara Soya
Days to 75% maturity	P9-2-2 x Him Soya, P6-1 x Him Soya, P2-2 x Him Soya, P2-2 x Hara Soya, VLS-59 x Him Soya	SL-682 x Him Soya	P169-3 x Hara Soya	-	-	-
Reproductive phase	Hardee x Hara Soya, H-330 x Him Soya, PK-472 x Hara Soya, H-330 x Hara Soya, P6-1 x Hara Soya, P169-3 x Him Soya	Hardee x Him Soya	Hardee x Hara Soya, PK-472 x Hara Soya, H-330 x Him Soya, PK-472 x Him Soya	Hardee x Hara Soya, H-330 x Him Soya, PK-472 x Hara Soya, H-330 x Hara Soya, PK-472 x Him Soya	Hardee x Hara Soya, H-330 x Him Soya, PK-472 x Hara Soya, PK-472 x Him Soya	Hardee x Hara Soya
Plant height	P9-2-2 x Him Soya, P2-2 x Hara Soya, Shivalik x Hara Soya, P2-2 x Him Soya, P9-2-2 x Hara Soya, P169-3 x Him Soya	-	PK-472 x Him Soya	PS-1469 x Him Soya, PK-472 x Him Soya, H-330 x Him Soya, P6-1 x Him Soya, H-330 x Hara Soya	DS-1213 x Hara Soya, PS-1469 x Him Soya, PK-472 x Him Soya, H-330 x Him Soya, P6-1 x Him Soya	PK-472 x Him Soya
Branches/plant	PS-1469 x Hara Soya, DS-1213 x Hara Soya, P13-4 x Hara Soya, DS-1213 x Him Soya, P6-1 x Him Soya	PS 1469 x Hara Soya	DS-1213 x Hara Soya, PS-1469 x Hara Soya	PS-1469 x Hara Soya, DS-1213 x Hara Soya, P13-4 x Hara Soya, DS-1213 x Him Soya, P6-1 x Him Soya	PS-1469 x Hara Soya, DS-1213 x Him Soya, P6-1 x Him Soya, DS-1213 x Hara Soya, PK-472 x Him Soya	PS-1469 x Hara Soya and DS-1213 x Hara Soya

Contd...

Trait	*Per se* performance	SCA effects	Heterobeltiosis	Economic heterosis I	Economic heterosis II	Common
Nodes on main stem	DS-1213 x Hara Soya, Shivalik x Him Soya, P13-4 x Hara Soya, PS-1466 x Him Soya, PK-472 x Hara Soya	Shivalik x Him Soya	Bragg x Him Soya, DS-1213 x Hara Soya	DS-1213 x Hara Soya, Shivalik x Him Soya, P13-4 x Hara Soya, PS-1466 x Him Soya, PK-472 x Hara Soya	Shivalik x Him Soya, PS-1466 x Him Soya, JS-335 x Him Soya, DS-1213 x Him Soya, Bragg x Him Soya	DS-1213 x Hara Soya, Shivalik x Him Soya
Internode length	H-330 x Hara Soya, P169-3 x Him Soya, H-330 x Him Soya, P169-3 x Hara Soya, P6-1 x Him Soya	-	H-330 x Hara Soya, P169-3 x Him Soya		H-330 x Hara Soya,P169-3 x Him Soya	H-330 x Hara Soya, P169-3 x Him Soya
Pods/plant	PK-472 x Him Soya, P6-1 x Him Soya, PK-472 x Hara Soya, DS-1213 x Him Soya, PS-1466 x Him Soya	PK 472 x Him Soya and Shivalik x Him Soya	PK-472 x Him Soya, SL-682 x Hara Soya, SL-795 x Hara Soya, DS-1213 x Hara Soya, PK-472 x Hara Soya	PK-472 x Him Soya, P6-1 x Him Soya, PK-472 x Hara Soya, DS-1213 x Him Soya, PS-1466 x Him Soya	PK-472 x Hara Soya, P6-1 x Hara Soya, PK-472 x Him Soya, DS-1213 x Hara Soya, PS-1469 x Hara Soya	PK-472 x Him Soya
Pod length	SL-682 x Him Soya, H-330 x Him Soya, Hardee x Hara Soya, DS-1213 x Him Soya, Bragg x Hara Soya	Hardee x Hara Soya, SL 682 x Him Soya, P6-1 x Hara Soya, DS-1213 x Him Soya, SL 679 x Him Soya, P169-3 x Him Soya, H-330 x Him Soya	H-330 x Him Soya, Hardee x Hara Soya, SL-682 x Him Soya, DS-1213 x Him Soya	SL-682 x Him Soya, H-330 x Him Soya, Hardee x Hara Soya, DS-1213 x Him Soya, Bragg x Hara Soya	SL-682 x Him Soya, H-330 x Him Soya, Hardee x Hara Soya, DS-1213 x Him Soya, Bragg x Hara Soya	SL-682 x Him Soya, H-330 x Him Soya, DS-1213 x Him Soya
Seeds/pod	DS-1213 x Hara Soya, H-330 x Hara Soya, DS-1213 x Him Soya, PK-472 x Him Soya, VLS-59 x Him Soya	-	-	-	-	-

Contd...

Trait	*Per se* performance	SCA effects	Heterobeltiosis	Economic heterosis I	Economic heterosis II	Common
Biological yield/plant	PK-472 x Him Soya, DS-1213 x Hara Soya, PK-472 x Hara Soya, PS-1469 x Hara Soya, DS-1213 x Him Soya	H-330 x Him Soya	PK-472 x Him Soya, PK-472 x Hara Soya, PS-1469 x Hara Soya, DS-1213 x Hara Soya, SL-682 x Hara Soya	PK-472 x Him Soya, DS-1213 x Hara Soya, PK-472 x Hara Soya, PS-1469 x Hara Soya, DS-1213 x Him Soya	PK-472 x Him Soya, DS-1213 x Hara Soya, PK-472 x Hara Soya, PS-1469 x Hara Soya, DS-1213 x Him Soya	PK-472 x Him Soya, DS-1213 x Hara Soya, PK-472 x Hara Soya
Seed yield/plant	PK-472 x Hara Soya, PK-472 x Him Soya, DS-1213 x Hara Soya, H-330 x Him Soya, PS-1469 x Hara Soya	Shivalik x Him Soya, PS 1469 x Hara Soya, H-330 x Him Soya, SL 682 x Hara Soya	PK-472 x Hara Soya, PK-472 x Him Soya, DS-1213 x Hara Soya, SL-795 x Hara Soya, SL-682 x Hara Soya	PK-472 x Hara Soya, PK-472 x Him Soya, DS-1213 x Hara Soya, H-330 x Him Soya, PS-1469 x Hara Soya	PK-472 x Hara Soya, DS-1213 x Hara Soya, PS-1469 x Hara Soya, PK-472 x Him Soya, P6-1 x Hara Soya	PK-472 x Hara Soya, PK-472 x Him Soya, H-330 x Him Soya, PS-1469 x Hara Soya
Harvest index	H-330 x Hara Soya, PK-472 x Hara Soya, Hardee x Him Soya, P6-1 x Hara Soya, Shivalik x Him Soya	-	H-330 x Hara Soya	-	H-330 x Hara Soya	H-330 x Hara Soya
100-seed weight	H-330 x Hara Soya, H-330 x Him Soya, P169-3 x Him Soya, Bragg x Hara Soya, VLS-59 x Him Soya	P169-3 x Him Soya	H-330 x Him Soya, P169-3 x Him Soya, H-330 x Hara Soya, VLS-59 x Him Soya	Bragg x Hara Soya	H-330 x Him Soya, P169-3 x Him Soya, H-330 x Hara Soya, P2-2 x Him Soya	P169-3 x Him Soya, Bragg x Hara Soya
Protein content	H-330 x Him Soya, SL-679 x Hara Soya, P9-2-2 x Him Soya, H-330 x Hara Soya, SL-679 x Him Soya	P9-2-2 x Him Soya, PK-472 x Hara Soya, DS-1213 x Him Soya	H-330 x Him Soya, P9-2-2 x Him Soya, H-330 x Hara Soya, SL-679 x Hara Soya, SL-795 x Hara Soya	H-330 x Him Soya, SL-679 x Hara Soya, P9-2-2 x Him Soya, H-330 x Hara Soya, SL-679 x Him Soya	SL-679 x Hara Soya, H-330 x Hara Soya, H-330 x Him Soya, P9-2-2 x Him Soya, PK-472 x Hara Soya	H-330 x Him Soya, SL-679 x Hara Soya, P9-2-2 x Him Soya, H-330 x Hara Soya
Oil content	P169-3 x Him Soya, H-330 x Him Soya, H-330 x Hara Soya, Bragg x Hara Soya, P6-1 x Hara Soya	P169-3 x Hara Soya, SL-679 x Him Soya, PK 472 x Him Soya, SL-795 x Him Soya, Bragg x Hara Soya	H-330 x Him Soya	P169-3 x Him Soya, H-330 x Him Soya, H-330 x Hara Soya, Bragg x Hara Soya, Shivalik x Hara Soya	H-330 x Him Soya	H-330 x Him Soya, Bragg x Hara Soya

Heterobeltiosis = Heterosis over better parent; Economic heterosis I = Heterosis over standard check -1

Economic heterosis II = Heterosis over standard check -2

to frogeye leaf spot. Further evaluation of hybrids based on *per se* performance, SCA effects and heterosis would be more useful than individual parameters (Table 4.16). These cross combinations also exhibited significant SCA effects coupled with high GCA of both or one of the parents. Therefore, additive component seemed to have influenced seed yield in these crosses. These crosses also showed heterosis for component traits which might have resulted into better hybrid vigour. Hence, in such crosses heterosis for yield may be due to predominance of additive gene action and better selection response may be expected in advance generations. It may, therefore, be possible to take advantage of such heterotic effects in subsequent generations.

4.6 Wide hybridization between cultivated and wild species

The results on various aspects of the present study have been presented and discussed under the following headings:

4.6.1 Crossability of cultivated soybean with wild species

4.6.2 Confirmation of hybridity of interspecific crosses

4.6.3 Evaluation of interspecific crosses

4.6.3.1 Analysis of variance

4.6.3.2 Mean performance of parents and their interspecific crosses

4.6.3.3 Simple correlation for yield with its related traits

4.6.3.4 Heterosis of F_1ôs over mid parent and better parent

4.6.4 Mode of inheritance of diseases

4.6.1 Crossability of cultivated soybean with wild species

Data on number of buds pollinated, pod set and pod set percentage during *kharif* 2011 and 2012 at Palampur are presented in Tables 4.17 and 4.18. In all, 1282 pollinations were attempted between *Glycine max* and *Glycine soja*. These pollinations resulted in the production of 53 F_1 pods. Similary, 2271 pollinations were attempted between *Glycine max* and *Glycine tomentella.* But the pod set percentage was zero. Difference among the soybean genotypes for crossability has also been reported by Nakayama and Yamaguchi (2002) indicating thereby the presence of genotypic differences for crossability within cultivated soybean.

Table 4.17 Number of buds pollinated and pod set (%) during *kharif* 2011 and 2012 in *Glycine max* and *Glycine soja* crosses

Cross combinations	Number of buds pollinated		Number of pod set		Pod set (%)	
	2011	2012	2011	2012	2011	2012
Bragg x *G. soja*	298	132	12	7	4.02	5.30
PS 1466 x *G. soja* (PI 366121)	223	104	9	3	4.03	2.88
SL-679 x *G. soja* (PI 65549)	153	110	8	2	5.22	1.81
PS 1469 x *G. soja*	184	78	8	4	4.34	5.12
Total	**858**	**424**	**37**	**16**	**4.31**	**3.77**

Table 4.18 Number of buds pollinated and pod set during *kharif* 2011 and 2012 in *Glycine max* and *Glycine tomentella* crosses

Cross combinations	Number of buds pollinated		Number of pod set	
	2011	2012	2011	2012
Hardee x *Glycine tomentella* (PI 505235)	194	164	0	0
PK-472 x *Glycine tomentella* (PI 505235)	181	156	0	0
H-330 x *Glycine tomentella* (PI 505235)	196	183	0	0
P6-1 x *Glycine tomentella* (PI 483224)	110	97	0	0
Bragg x *Glycine tomentella* (PI 483224)	189	127	0	0
DS-1213 x *Glycine tomentella* (PI 483224)	202	151	0	0
JS-335 x *Glycine tomentella* (PI 483224)	196	125	0	0
Total	**1268**	**1003**	**0**	**0**

Plate 4.1 *Glycine tomentella* species used in present study

4.6.2 Confirmation of hybridity of interspecific crosses

Establishing the true hybrid nature of crosses in the beginning of an experiment is important to develop reliable segregating populations for mapping of genes controlling desirable traits. The F_1 hybrids showed vigour which was established by their morphological expression. The hybridity was confirmed at the morphological, molecular and cytological level.

4.6.2.1 Confirmation of hybridity of interspecific crosses at morphological level

True nature of crosses under study was confirmed in F_1's for the following traits at morphological level as given in Table 4.19.

Leaf and plant morphology of parents and interspecific crosses are shown in Plate 4.2 (a and b), Plate 4.3 (a, b, c and d) and Plate 4.4 (a and b), respectively.

4.6.2.2 Confirmation of hybridity of interspecific crosses at molecular level

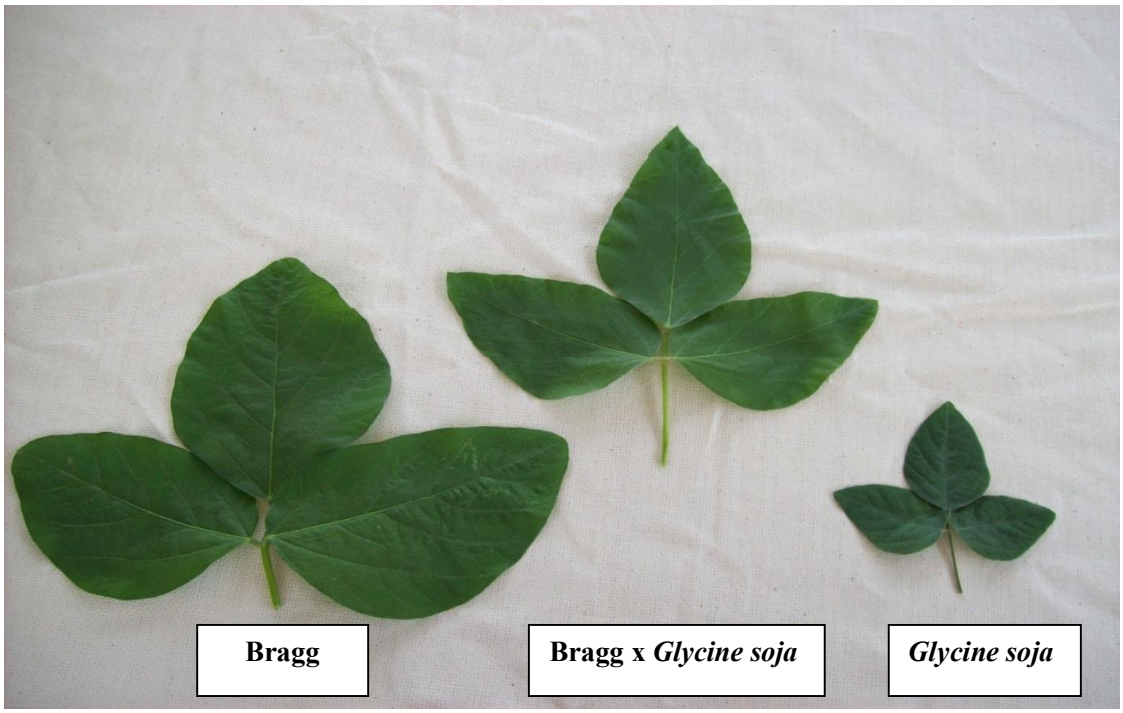
The hybridity of four interspecific crosses, *viz.,* Bragg x *Glycine soja*, SL-679 x *Glycine soja* (PI-65549), PS-1466 x *Glycine soja* (PI-366121) and PS-1469 x *Glycine soja* was confirmed at molecular level through four SSR markers. A total of 34 SSR markers were screened to confirm the hybridity of interspecific crosses. Of these only four markers, *viz.,* Satt301, Salt77, Satt20 and Satt5 were found polymorphic between parents and hybrids and showed robust and reproducible bands as shown in Plate 4.4 (a, b and c).

4.6.2.2 Confirmation of hybridity of interspecific crosses at cytological level

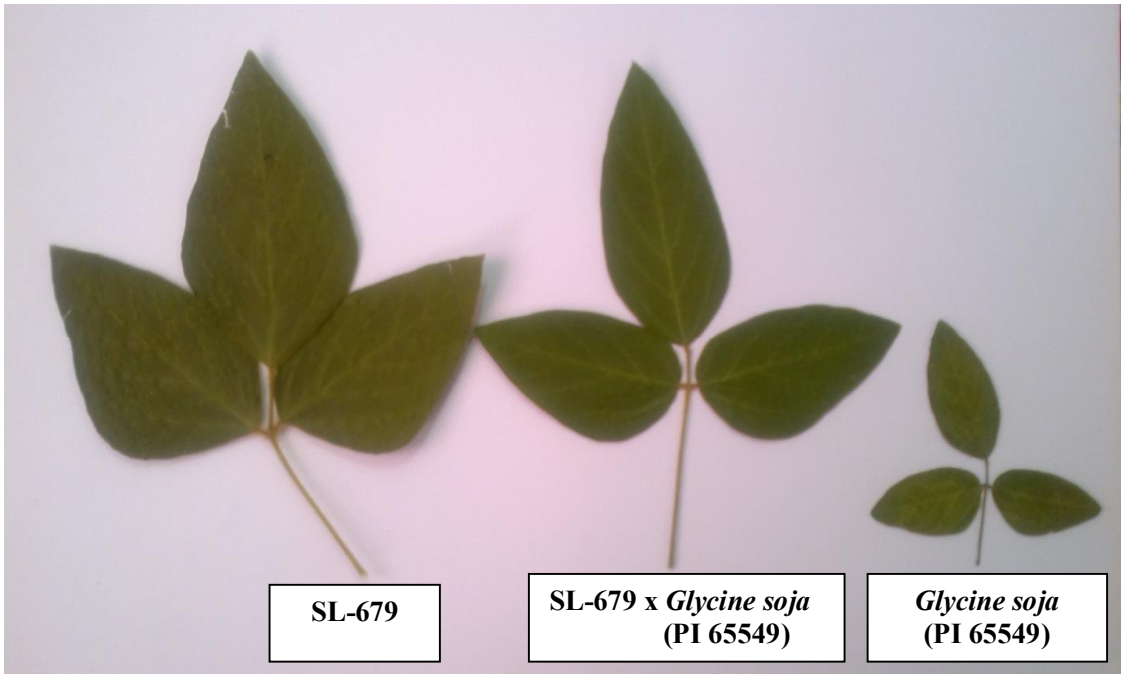
A number of slides were attempted, however, not many good spreads could be achieved. A representative slide is shown below in Plate 4.5.

Table 4.19 Morphological characterization of parents and their F_1s

Traits	Cross Combinations											
	Bragg X *Glycine soja*			SL-679 X *Glycine soja* (PI 65549)			PS-1469 X *Glycine soja*			PS-1466 X *Glycine soja* (PI 366121)		
	P_1	P_2	F_1	P_1	P_2	F_1	P_1	P_2	F_1	P_1	P_2	F_1
Days to 50% flowering	Late	Medium	Late	Late	Medium	Late	Late	Medium	Late	Late	Medium	Late
Plant Growth type	Determinate	Indeterminate	Indeterminate	Determinate	Indeterminate	Indeterminate	Determinate	Indeterminate	Indeterminate	Determinate	Indeterminate	Indeterminate
Plant Growth habit	Erect	Semi-erect	Semi-erect	Erect	Semi-erect	Semi-erect	Erect	Semi-erect	Semi-erect	Erect	Semi-erect	Semi-erect
Plant height	Medium	Tall	Tall	Medium	Tall	Tall	Medium	Tall	Tall	Medium	Tall	Tall
Leaf Colour	Green	Dark green	Green	Green	Dark green	Green	Green	Dark green	Green	Green	Dark green	Green
Flower Colour	White	Purple	Purple	White	Purple	Purple	White	Purple	Purple	White	Purple	Purple
Pod Pubescence	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
Pod Pubescence colour	Tawny (Brown)	Tawny (Brown)	Tawny (Brown)	Tawny (Brown)	Tawny (Brown)	Tawny (Brown)	Tawny (Brown)	Tawny (Brown)	Tawny (Brown)	Tawny (Brown)	Tawny (Brown)	Tawny (Brown)
Pod Colour	Yellow	Black	Brown	Yellow	Black	Brown	Yellow	Black	Brown	Yellow	Black	Brown
Seed Shape	Spherical	Elliptical	Spherical	Spherical	Elliptical	Spherical	Spherical	Elliptical	Spherical	Spherical	Elliptical	Spherical
Seed Colour	Yellow	Black	Yellow	Yellow	Black	Yellow	Yellow	Black	Yellow	Yellow	Black	Yellow
Seed Lustre	Shiny	Dull	Dull	Shiny	Dull	Dull	Shiny	Dull	Dull	Shiny	Dull	Dull
Seed Hilum colour	Black	Grey	Brown	Black	Grey	Brown	Black	Grey	Brown	Black	Grey	Brown
Seed Cotyledon colour	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow



(a)



(b)

Plate 4.2 (a and b) Leaf morphology of parents and interspecific crosses

Bragg

Bragg x *Glycine soja*

Glycine soja

(a)

SL-679

SL-679 x *Glycine soja* (PI 65549)

***Glycine soja* (PI 65549)**

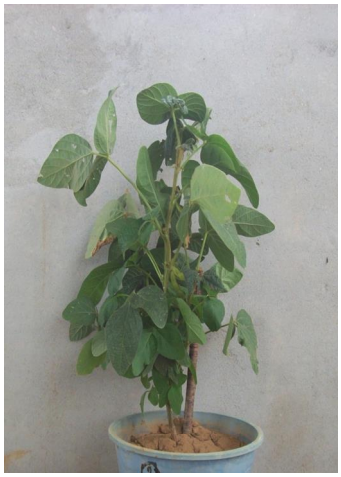
(b)

PS-1466

PS-1466 x *Glycine soja* (PI366121)

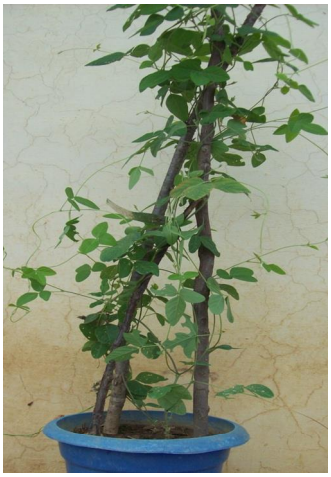
***G.soja* (PI366121)**

(c)



PS-1469

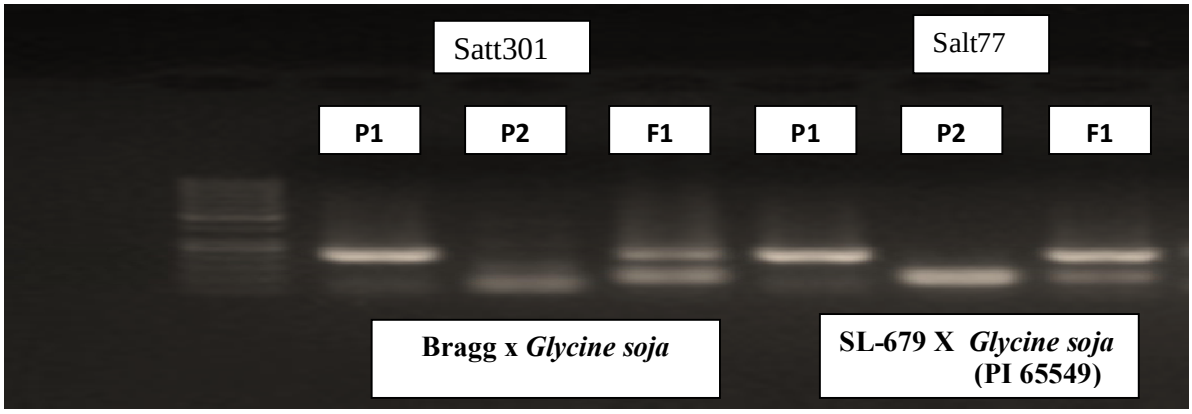
PS-1469 x *Glycine soja*



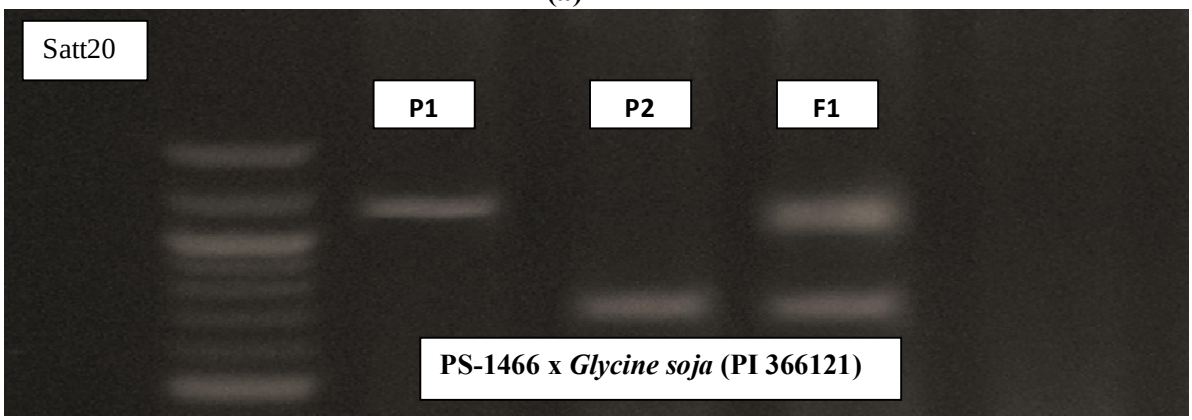
Glycine soja

(d)

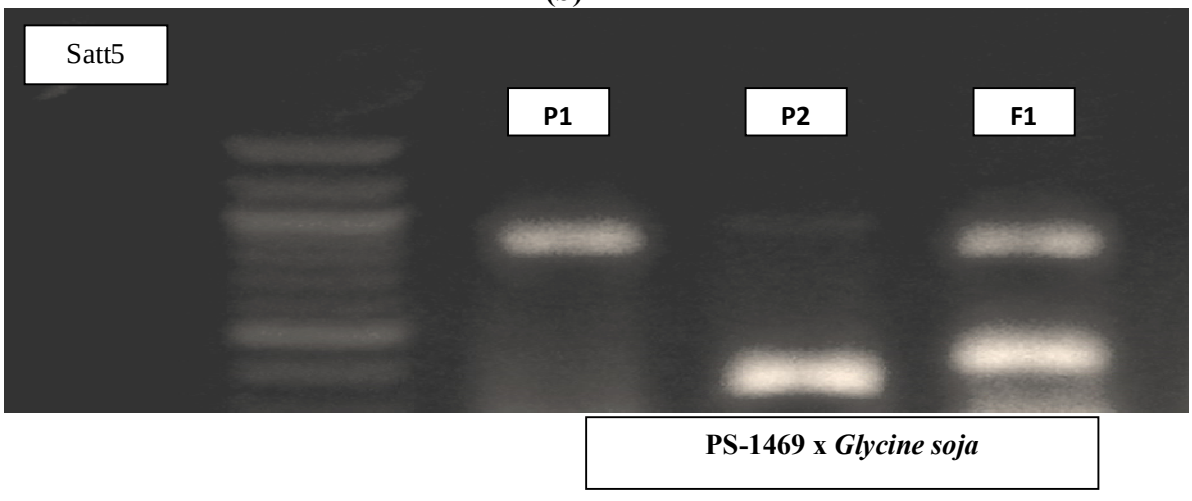
Plate 4.3 (a, b, c and d) Plant morphology of parents and interspecific crosses at morphological level



(a)

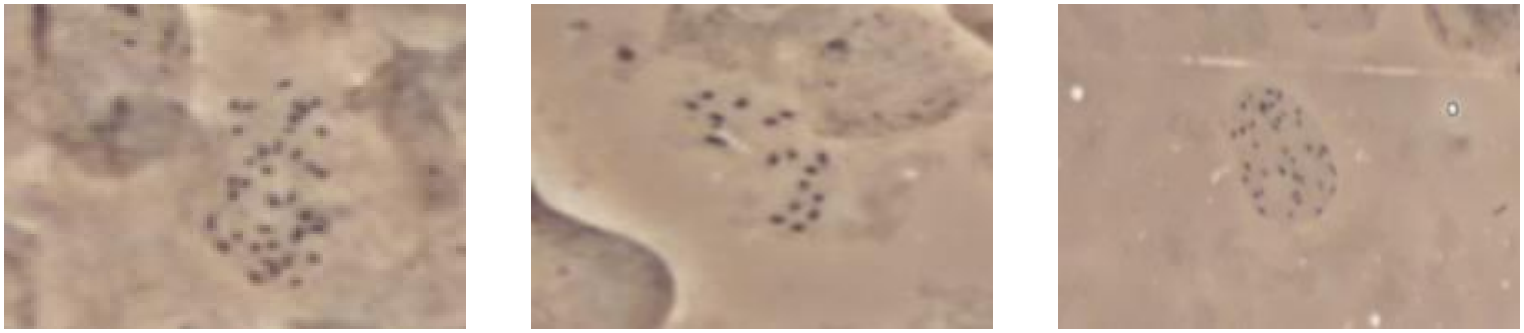


(b)



(c)

Plate 4.4 (a, b and c) Hybridity of parents and interspecific crosses at molecular level



Bragg

Bragg x *Glycine soja*

Glycine soja

Plate 4.5 Hybridity of parents and interspecific crosses at cytological level

4.6.3 Evaluation of interspecific crosses

Four interspecific crosses along with their parents were evaluated under field conditions to investigate their actual performance for different agronomic traits and results obtained are discussed as under.

4.6.4.1 Analysis of variance

Analysis of variance (Table 4.20) revealed significant differences among genotypes for all the traits studied, *viz.,* days to 50% flowering, days to 75% maturity, reproductive phase, plant height, branches per plant, internode length, nodes per main stem, petiole length, pods per plant, seeds per pod, pod length, biological yield per plant, seed yield per plant, harvest index and 100-seed weight indicating thereby presence of sufficient variability and scope of selection for these traits.

Table 4.20 Analysis of variance for different traits in soybean

S. No.	Traits	Mean sum of squares		
		df	Genotypes	Error
1	Days to 50% flowering		26.39*	5.25
2	Days to 75% maturity		73.63*	9.05
3	Reproductive phase		0.01*	.001
4	Plant height		3511.53*	49.90
5	Branches/plant		8.23*	0.92
6	Nodes/main stem		4.55*	1.53
7	Internode length		31.60*	1.24
8	Petiole length		69.13*	0.43
9	Pods/plant		1556.29*	20.74
10	Seeds/pod		0.06*	0.03
11	Pod length		0.92*	0.03
12	Biological yield/plant		35.95*	12.12
13	Seed yield/plant		18.32 *	0.74
14	Harvest index		170.35*	20.14
15	100-seed wt		64.01*	1.50

* Significant at P Ò0.05

4.6.4.2 Mean performance of parents and their interspecific crosses

Range and mean values of parents and their interspecific crosses for different characters are presented in Table 4.21.

Days to 50% flowering

Among genotypes of soybean and wild species, the range for days to 50% flowering varied from 55.67-64.67 days with an average of 60.58 days and from 56.67-61.67 days with an average of 58.83 days, respectively. However, in F_1ôs the range for days to 50% flowering varied from 61.67-64.67 days with an average of 62.87 days.

Days to 75% maturity

Days to 75% maturity varied from 122.00-129.67 days with a mean of 124.58 days and 115.33-131.67 days with a mean of 126.42 days for soybean and wild genotypes, respectively. Whereas, in F_1ôs, it ranged from 127.00-132.33 days with a mean of 128.80 days.

Reproductive phase

Reproductive phase varied from 0.62-0.66 days with a mean of 0.64 days and 0.45-0.60 days with a mean of 0.52 days for soybean and wild genotypes, respectively. Whereas, in F_1ôs, it ranged from 0.57-0.59 days with a mean of 0.58 days.

Plant height

Plant height varied from 43.27-54.67 cm with a mean of 49.12 and 83.33-122.33 cm with a mean of 101.75 cm for soybean and wild genotypes, respectively. Whereas, in F_1ôs, it ranged from 111.67-132.00 cm with a mean of 123.47 cm.

Branches per plant

Branches/plant varied from 3.93-5.67 with a mean of 5.21 and 6.00-9.67 with a mean of 7.50 for soybean and wild genotypes, respectively. Whereas, in F_1ôs, it ranged from 5.33-7.33 with a mean of 6.53.

Internode length

Internode length varied from 4.15-5.29 cm with a mean of 4.78 cm and 7.64-12.02 cm with a mean of 9.49 cm for soybean and wild genotypes, respectively. Whereas, in F_1ôs, it ranged from 10.65-13.32 cm with a mean of 11.68 cm.

Table 4.21 Overall range and mean performance of parents and their interspecific crosses for different traits in soybean

Traits	P_1		P_2		F_1		BC_1	
	Range	Mean ± SE	Range	Mean ± SE	Range	Mean ± SE	Range	Mean ± SE
Days to 50% flowering	55.67-64.67	60.58±0.94	56.67-61.67	58.83±1.81	61.67-64.67	62.87±1.13	63.00-66.00	64.67± 0.88
Days to 75% maturity	122.00- 129.67	124.58±2.03	115.33-131.67	126.42±1.87	127.00-132.33	128.80 ±1.48	127.00-132.00	129.33± 1.45
Reproductive phase	0.62-0.66	0.64±0.02	0.45-0.60	0.52±0.01	0.57-0.59	0.58 ± 0.009	0.57-0.59	0.58± 0.01
Plant height	43.27-54.67	49.12±5.64	83.33-122.33	101.75±1.76	111.67-132.00	123.47± 3.62	120.00-127.00	123.33± 2.03
Branches/plant	3.93-5.67	5.21±0.42	6.00-9.67	7.50±0.68	5.33-7.33	6.53±0.61	7.00-8.00	7.33± 0.33
Nodes/main stem	8.67-11.13	10.30±0.58	9.33-13.33	11.00± 0.64	9.67-11.67	10.73±0.88	11.00-13.00	11.67± 0.67
Internode length	4.15-5.29	4.78±0.48	7.64-12.02	9.49± 0.67	10.65-13.32	11.68±0.82	9.23-11.55	10.65± 0.72
Petiole length	12.00-12.67	12.33±0.63	1.83-3.27	2.27±0.11	2.77-3.27	3.06 ±0.13	2.80-3.00	2.90± 0.06
Pods/plant	54.53-80.73	67.38±4.05	17.00-24.33	22.17±2.98	23.00-25.00	23.67±1.92	21.00-27.00	23.33± 1.86
Seeds/pod	1.91-2.23	2.08±0.06	1.93-2.37	2.06± 0.16	1.87-2.37	2.06±0.15	2.00-2.12	2.04± 0.04
Pod length	3.50-3.67	3.56±0.06	2.13-3.00	2.46±0.12	2.63-3.47	3.13±0.11	3.00-3.60	3.37± 0.19
Biological yield/plant	28.80-32.93	30.38±2.33	25.00-31.00	27.08±2.18	31.00-36.33	33.13±1.46	35.00-38.00	36.33± 0.88
Seed yield/plant	10.00-15.87	12.68±0.60	6.65-9.23	8.15±0.41	8.52-9.85	9.11±0.51	6.89-7.60	7.33± 0.43
Harvest index	35.24-49.00	41.92±3.03	26.37-34.85	30.59±2.97	23.46-30.24	27.72±2.09	21.33-25.03	23.46± 1.11
100 seed weight	11.47-18.50	14.78±1.07	3.75-6.18	5.13±0.52	6.18-8.07	7.15 ±0.36	7.68-9.13	8.96± 0.22

Nodes on main stem

Nodes on main stem varied from 8.67-11.13 with a mean of 10.30 and 9.33-13.33 with a mean of 11.00 for soybean and wild genotypes, respectively. Whereas, in F_1ôs, it ranged from 9.67-11.67 with a mean of 10.73.

Petiole length

Petiole length varied from 12.00-12.67 cm with a mean of 12.33 cm and 1.83-3.27 cm with a mean of 2.27 cm for soybean and wild genotypes, respectively. Whereas, in F_1ôs, it ranged from 127-2.77-3.27 cm with a mean of 3.06 cm.

Pods per plant

Pods per plant varied from 54.53-80.73 with a mean of 67.38 and 17.00-24.33 with a mean of 22.17 for soybean and wild genotypes, respectively. Whereas, in F_1ôs, it ranged from 23.00-25.00 with a mean of 23.67.

Seeds per pod

Seeds per pod varied from 1.91-2.23 with a mean of 2.08 and 1.93-2.37 with a mean of 2.06 for soybean and wild genotypes, respectively. Whereas, in F_1ôs, it ranged from 1.87-2.37 with a mean of 2.06.

Pod length

Pod length varied from 3.50-3.67 cm with a mean of 3.56 cm and 2.13-3.00 cm with a mean of 2.46 cm for soybean and wild genotypes, respectively. Whereas, in F_1ôs, it ranged from 2.63-3.47 cm with a mean of 3.13 cm.

Biological yield per plant

Biological yield per plant varied from 28.80-32.93 g with a mean of 30.38 g and 25.00-31.00 g with a mean of 27.08 g for soybean and wild genotypes, respectively. Whereas, in F_1ôs, it ranged from 31.00-36.33 g with a mean of 33.13 g.

Seed yield per plant

Seed yield per plant varied from 10-15.87 g with a mean of 12.68 g and 6.65-9.23 g with a mean of 8.15 g for soybean and wild genotypes, respectively. Whereas, in F_1ôs, it ranged from 8.52-9.85 g with a mean of 9.11 g.

Harvest index

Harvest index varied from 35.24-49.00 per cent with a mean of 41.92 per cent and 26.37-34.85 per cent with a mean of 30.59 per cent for soybean and wild genotypes, respectively. Whereas, in F_1ôs, it ranged from 23.46-30.24 per cent with a mean of 27.72 per cent.

100-seed weight

100-seed weight varied from 11.47-18.50 g with a mean of 14.78 g and 3.75-6.18 g with a mean of 5.13g for soybean and wild genotypes, respectively. Whereas, in F_1ôs, it ranged from 6.18-8.07 g with a mean of 7.15 g.

4.6.4.3 Simple correlation for yield and related traits

Yield is a complex character and a function of several component characters. Direct selection based on yield alone will not be very effective in crop improvement programmes. Grafius (1956) had also opined that the improvement of complex characters such as seed yield might be accomplished better through component breeding. Therefore, it is also important to gather information on association of yield with other characters and among themselves so as to form the basis to identify characters for increasing the efficiency of both direct and indirect selection and thereby defining an ideal plant type. Based on the estimates of correlation, the breeder will be able to decide the method of breeding to be followed to exploit the useful correlation. In order to understand the nature and magnitude of correlations among seed yield per plant and other traits, estimates of simple correlation coefficients were computed for parents (cultivated and wild) and their interspecific crosses and results obtained are discussed here after. The estimates of simple correlations are presented in Table 4.22.

Seed yield per plant exhibited significant and positive correlation with reproductive phase, pods per plant, harvest index, 100-seed weight, pod length and petiole length. Significant and positive correlation of seed yield with number of pods per plant and harvest index was observed by Barh et al. (2014) and for 100-seed weight by Tomar et al. (2014). It was significantly negatively correlated with plant height and internode length. Significant positive correlation was observed for days to 50% flowering and biological yield per plant. Reproductive phase has significant positive correlation with pods per plant, 100-seed weight, petiole length and pod length. Plant height has positive correlation with internode length, whereas, negative correlation with pods per

Table 4.22 Simple correlation coefficients among different agro-morphological traits in soybean

	Days to 50% flowering	Days to 75% maturity	Reproductive phase	Plant height	Branches/ plant	Pods/ plant	Biological yield/plant	Harvest index	100-seed weight	Seeds/ pod	Nodes/main stem	Internode length	Petiole length	Pod length
Seed yield/plant	0.1679	0.0596	0.7144*	-0.6720*	-0.3453	0.7841*	0.2809	0.8205*	0.6863*	-0.0020	-0.2160	-0.5919*	0.7975*	0.5259*
Days to 50% flowering		0.4436	0.3926	0.1984	-0.0678	0.0856	0.5678*	-0.1421	-0.0963	-0.0298	0.0910	0.1597	0.0178	0.2729
Days to75% maturity			0.1278	0.2312	0.4578	-0.2261	0.3014	-0.0825	-0.2583	-0.1541	-0.1911	0.3139	-0.2750	-0.2319
Reproductive phase				-0.4558	-0.3837	0.5994*	0.4351	0.4864	0.6554*	0.1950	-0.1338	-0.4226	0.6672*	0.6820*
Plant height					0.3355	-0.8334*	0.2281	-0.7893*	-0.7089*	-0.0536	0.2217	0.9232*	-0.8698*	-0.3188
Branches/plant						-0.4936	-0.1607	-0.2439	-0.5324*	-0.3575	0.1188	0.3201	-0.5660*	-0.5731*
Pods/plant							0.0837	0.7189*	0.7761*	0.0874	-0.1028	-0.7889*	0.9494*	0.6072*
Biological yield/plant								-0.3023	0.1584	0.1498	0.1471	0.1596	0.0704	0.4888
Harvest index									0.5928*	-0.0597	-0.3081	-0.6734*	0.7485*	0.2638
100 seed weight										0.1598	-0.2188	-0.6430*	0.8880*	0.7135*
Seeds/pod											-0.0040	-0.0933	0.1752	0.2750
Nodes/main stem												-0.1521	-0.1962	-0.0542
Internode length													-0.8062*	-0.3237
Petiole length														0.6823*

* Significant at P Ò0.05

plant, harvest index, 100-seed weight and petiole length. Branches per plant have negative correlation with 100-seed weight, petiole length and pod length. Pods per plant have positive correlation with harvest index, 100-seed weight, petiole length and pod length and negative correlation with internode length. Harvest index has positive correlation with 100-seed weight and petiole length, whereas negative correlation with internode length. 100-seed weight has positive correlation with petiole length and pod length, whereas negative correlation with internode length.

Based on simple correlation studies, it can be concluded that seed yield per plant is positively correlated with reproductive phase, pods per plant, harvest index, 100-seed weight, pod length and petiole length and selection through these traits would be effective.

4.6.4.4 Heterosis in interspecific crosses over mid parent and better parent

Heterosis is the superiority of F_1 over the mean of the parents or over the better parent or over the standard check (Hayes et al. 1955). The primary objective of heterosis breeding is to achieve substantial enhancement in yield and quality aspects of crop plants. But in case of self pollinated crops including soybean, heterosis *per se* cannot be exploited by way of heterotic hybrids due to biological infeasibility. However, the heterotic hybrids are used as the source populations for deriving superior progenies. The superiority of the F_1ös was estimated over mid parent and better parent for all the 15 characters studied (Table 4.23) and results obtained are discussed here after.

Days to 50% flowering

The extent of heterosis over mid parent and better parent ranged from 2.45 (PS-1466 x *G. soja* (PI 366121)) to 7.25 per cent (Bragg x *G. soja*) and from 5.06 (PS-1469 x *G. soja*) to 11.17 per cent (SL-679 x *G. soja* (PI 65549)), respectively. Out of four crosses, none showed significantly negative heterosis over mid parent and better parent.

Days to 75% maturity

Per cent heterosis of F_1ös over their respective mid parent and better parent ranged from 0.00 (Bragg x *G. soja*) to 8.03 per cent (PS-1466 x *G. soja* (PI 366121)) and from 3.50 (SL-679 x *G. soja* (PI 65549)) to 14.74 per cent (PS-1466 x *G. soja* (PI 366121)), respectively.

Reproductive phase

The extent of heterosis over mid parent and better parent ranged from -4.98 (PS-1469 x *G. soja*) to 9.51 per cent (SL-679 x *G. soja* (PI 65549)) and from -2.22 (Bragg x *G. soja*) to 30.37 per cent (SL-679 x *G. soja* (PI 65549)), respectively.

Plant height

For plant height the range of heterosis over mid parent and better parent was from 49.15 (PS-1466 x *G. soja* (PI 366121)) to 102.21 per cent (PS-1469 x *G. soja*) and from 123.77 (Bragg x *G. soja*) to 195.82 per cent (PS-1469 x *G. soja*), respectively.

Branches per plant

The extent of heterosis over mid parent and better parent ranged from -30.43 (Bragg x *G. soja*) to 9.59 (SL-679 x *G. soja* (PI 65549)) and from -44.85 (Bragg x *G. soja*) to 0.00 per cent (PS-1466 x *G. soja* (PI 366121)), respectively.

Internode length

The extent of heterosis over mid parent and better parent ranged from 51.67 (SL-679 x *G. soja* (PI 65549)) to 111.73 per cent (PS-1469 x *G. soja*) and from 10.18 (SL-679 x *G. soja* (PI 65549)) to 74.43 per cent (PS-1469 x *G. soja*), respectively.

Nodes on main stem

For nodes on main stem, the range of heterosis over mid parent and better parent was from -15.53 (PS-1466 x *G. soja* (PI 366121)) to 14.38 per cent (SL-679 x *G. soja* (PI 65549)) and from -22.48 (PS-1466 x *G. soja* (PI 366121)) to 5.39 per cent (SL-679 x *G. soja* (PI 65549)), respectively.

Petiole length

For petiole length per cent heterosis of F_1ôs over their respective mid parent and better parent ranged from -62.44 (PS-1469 x *G. soja*) to -53.55 per cent (Bragg x *G. soja*) and from -78.16 (PS-1469 x *G. soja*) to -72.78 per cent (Bragg x *G. soja*), respectively.

Pods per plant

Per cent heterosis of F_1ôs over their respective mid parent and better parent ranged from -52.25 (SL-679 x *G. soja* (PI 65549)) to -33.83 per cent (Bragg x *G. soja*) and from -69.03 (PS-1466 x *G. soja* (PI 366121)) to -56.60 per cent (Bragg x *G. soja*), respectively.

Table 4.23 Observed heterosis (%) in interspecific crosses of soybean over mid parent and better parent

Crosses	Over mid parent	Over better parent	Over mid parent	Over better parent	Over mid parent	Over better parent	Over mid parent	Over better parent
	Days to 50% flowering		Days to 75% maturity		Reproductive phase		Plant height	
Bragg x *G. soja*	7.25*	10.77*	0.00	3.52*	-3.51	-2.22	77.29*	123.77*
PS 1466 x *G. soja* (PI 366121)	2.45	8.66	8.03*	14.74*	1.96	24.64*	49.15*	144.19*
SL-679 x *G. soja* (PI 65549)	7.08*	11.17*	0.39	3.50	9.51*	30.37*	75.84*	150.00*
PS 1469 x *G. soja*	3.60	5.06	0.13	4.10*	-4.98	-2.21	102.21*	195.82*
	Branches/plant		Nodes/ main stem		Internode length		Petiole length	
Bragg x *G. soja*	-30.43*	-44.85*	-3.13	-6.06	85.98*	57.33*	-53.55	-72.78*
PS 1466 x *G. soja* (PI 366121)	3.15	0.00	-15.53*	-22.48*	81.38*	38.65*	-55.25*	-74.22*
SL-679 x *G. soja* (PI 65549)	9.59*	-11.11*	14.38*	5.39	51.67*	10.18*	-55.18	-74.17*
PS 1469 x *G. soja*	-11.76*	-37.95*	-1.69	-12.12*	111.73*	74.43*	-62.44	-78.16*
	Pods/plant		Seeds/pod		Pod length		Biological yield/plant	
Bragg x *G. soja*	-33.83*	-56.60*	15.21*	11.95*	2.27	-18.26*	7.89	1.74
PS 1466 x *G. soja* (PI 366121)	-52.11*	-69.03*	-2.78	-3.28	-12.22*	-24.76*	12.13*	-0.80
SL-679 x *G. soja* (PI 65549)	-52.25*	-68.06*	0.17	-2.44	23.08*	-0.95	26.39*	18.06*
PS 1469 x *G. soja*	-41.13*	-62.53*	-5.36	-10.31*	10.98*	-10.36*	12.49*	8.08*
	Seed yield/plant		Harvest index		100 seed weight			
Bragg x *G. soja*	-21.32*	-32.35*	-26.17*	-32.55*	-49.30*	-66.61*		
PS 1466 x *G. soja* (PI 366121)	-12.50*	-37.93*	-19.76*	-38.29*	-0.23	-29.64*		
SL-679 x *G. soja* (PI 65549)	4.06	-6.07	-18.36*	-21.29*	-18.66*	-48.13*		
PS 1469 x *G. soja*	-14.21*	-24.11*	-24.47*	-30.37*	-32.11*	-53.20*		

* Significant at P Ò0.05

Seeds per pod

The extent of heterosis over mid parent and better parent ranged from -5.36 (PS-1469 x *G. soja*) to 15.21 per cent (Bragg x *G. soja*) and from -10.31 (PS-1469 x *G. soja*) to 11.95 per cent (Bragg x *G. soja*), respectively.

Pod Length

The extent of heterosis over mid parent and better parent ranged from -12.22 (PS-1466 x *G. soja* (PI 366121)) to 23.08 per cent (SL-679 x *G. soja* (PI 65549)) and from -24.76 (PS-1466 x *G. soja* (PI 366121)) to -0.95 per cent (SL-679 x *G. soja* (PI 65549)), respectively.

Biological yield per plant

The range of heterosis over mid parent and better parent was from 7.89 (Bragg x *G. soja*) to 26.39 per cent (SL-679 x *G. soja* (PI 65549)) and from -0.80 (PS-1466 x *G. soja* (PI 366121)) to 18.06 per cent (SL-679 x *G. soja* (PI 65549)), respectively.

Seed yield per plant

The extent of heterosis over mid parent and better parent ranged from -21.32 (Bragg x *G. soja*) to 4.06 per cent (SL-679 x *G. soja* (PI 65549)) and from -37.93 (PS-1466 x *G. soja* (PI 366121)) to -6.07 per cent (SL-679 x *G. soja* (PI 65549)), respectively.

Harvest index

The range of heterosis over mid parent and better parent varied from -26.17 (Bragg x *G. soja*) to -18.36 per cent (SL-679 x *G. soja* (PI 65549)) and from -38.29 (PS-1466 x *G. soja* (PI 366121)) to -21.29 per cent (SL-679 x *G. soja* (PI 65549)), respectively.

100-seed weight

Per cent heterosis of F_1ôs over their respective mid parent and better parent ranged from -49.30 (Bragg x *G. soja*) to -0.23 per cent (PS-1466 x *G. soja* (PI 366121)) and from -66.61 (Bragg x *G. soja*) to -29.64 per cent (PS-1466 x *G. soja* (PI 366121)), respectively.

Overall on the basis of heterosis, it was found that significant heterosis over mid parent and better parent was observed for plant height and internode length. Similar results were also obtained by Dogney et al. 1998. Weber (1950) also reported mid parent heterosis in *G. max* x *G. soja* crosses and found that resulting F_1 and F_2 heterosis estimates in this type of cross were highly influenced by the poor undesirable traits of the wild soybean.

4.6.4 Mode of inheritance of diseases

On the basis of mode of inheritance (Table 4.24), it was observed that resistance to both the diseases, i.e., frogeye leaf spot and brown spot was controlled by single dominant gene (monogenic resistance).

Table 4.24 Reaction of F_1, F_2 and BC_1 plants to frogeye leaf spot and brown spot diseases under field conditions

	Frogeye leaf spot				Brown spot			
Generation	**Number of plants**		**Ratio fit**	**χ^2 value**	**Number of plants**		**Ratio fit**	**χ^2 value**
	Resistant	**Susceptible**			**Resistant**	**Susceptible**		
Glycine max* x *G. soja								
F_1	5				5			
F_2	214	60	3:1	1.40	198	76	3:1	1.09
BC_1	21	14	1:1	1.40	18	17	1:1	0.03

5. SUMMARY AND CONCLUSIONS

The present study entitled ñGene action for yield and related traits in soybean [*Glycine max* (L.) Merrill] and development of interspecific hybrids involving wild speciesò was carried out to gather information on genetic architecture, combining ability and heterosis.

The materials for the investigation comprised 18 fixed lines of soybean, *viz.,* SL-682, P6-1, SL-679, P9-2-2, DS-1213, PK-472, Hardee, Bragg, SL-795, Shivalik, PS-1466, P2-2, H-330, PS-1469, VLS-59, JS-335, P169-3 and P13-4 whereas, Him Soya, Hara Soya and their F_1 (Hara Soya x Him Soya) were used as L_1, L_2 and L_3 testers, respectively. The F_1 was produced during *kharif* 2011. All the 18 lines were crossed to each of the three testers to produce 54 triple test cross (TTC) progenies during *kharif* 2012. These progenies and their parents were grown in a randomized complete block design with three replications during *kharif* 2013 at the Experimental Farm of the Department of Crop Improvement, CSK HPKV, Palampur (H.P.).

The observations were recorded on randomly taken five competitive plants from each entry in each replication for the traits, *viz.,* days to 50% flowering, days to maturity, reproductive phase, plant height, branches per plant, nodes on main stem, internode length, petiole length, pods per plant, pod length, seeds per pod, biological yield per plant, seed yield per plant, harvest index, 100-seed weight, protein content and oil content.

The data were subjected to the biometrical analysis by following triple test cross method of Kearsey and Jinks (1968) comprising 54 progenies involving 18 lines and three testers to detect epistasis and estimates of additive and dominance components of genetic variance. The data were also subjected to Line × Tester analysis (Kempthorne 1957) to estimate the general and specific combining ability effects alongwith heterosis by excluding the triple test cross progenies and F_1 tester (L_3) thus, comprising of 36 cross combinations derived from 18 lines and two testers.

Analysis of variance indicated the presence of sufficient genetic variability among crosses for all the traits which indicated the presence of sufficient genetic variability in the existing genetic material. Triple test cross analysis revealed the presence of significant epistasis for majority of the traits namely, plant height, branches per plant, internode length, nodes on main stem, pods per plant, pod length, biological yield per plant, seed yield per plant, protein content and oil content. Further, partitioning of epistasis revealed the importance of ój+lô type (additive × dominance and dominance × dominance) of epistasis for almost all the traits except days to flowering, days to maturity, reproductive phase, petiole length, seeds per pod, harvest index and 100-seed weight whereas, mean squares due to additive x additive (i) type interaction were non-significant for all the traits except plant height, internode length, petiole length, pods per plant and biological yield per plant.

Mean sum of squares due to sums (additive) were significant for all the traits except petiole length and harvest index whereas, mean sum of squares due to differences (dominance) were significant for all the traits except reproductive phase, plant height, internode length, petiole length, seeds per pod, seed yield per plant and harvest index. The significance of mean squares due to the sums and differences provide a direct test of significance of additive (D) and dominance (H) components of variation. However, the relative magnitude of additive component (D) was predominant over dominance component (H) for most of the traits indicating the relative importance of fixable type of gene action in their inheritance. The average degree of dominance $(H/D)^{1/2}$ was in the range of partial dominance for most of the traits, namely, days to flowering, days to maturity, reproductive phase, plant height, branches per plant, internode length, nodes on main stem, pods per plant, biological yield per plant, seed yield per plant, harvest index, 100-seed weight, protein content and oil content highlighting the relative importance of additive gene action for these traits.

The gene action studies based on triple test cross revealed that epistasis should not be overlooked as it may, otherwise, lead to biased estimates of additive and dominance components. The triple test cross analysis indicated the importance of additive, dominance and epistasis gene actions in the inheritance of different traits which can be exploited by employing alternative intermating in the early segregating generations, biparental mating or diallel selective mating to isolate transgressive segregants.

The line × tester analysis revealed significant differences for lines, testers and line × tester for majority of the traits studied. Further, non-additive gene action ($\mathring{u}_D^2$) played a major role in the manifestation of almost all the traits which suggested the use of breeding approaches such as single seed descent method, single pod descent method, reciprocal recurrent selection with one or two intermatings and diallel selective mating for the improvement of seed yield and related traits.

The estimates of GCA effects revealed that line Shivalik was found to be good general combiner for eight traits followed by Bragg for six traits, P9-2-2 for five traits and P13-4, P6-1, H-330, Hardee and SL-679 for four traits each. Lines P2-2, P13-4, P6-1, H-330, PK-472 and SL-795 were good general combiners for earliness. For pods per plant, P9-2-2, SL-679, Hardee, SL-682 and P169-3 were the top ranking five general combiners. For seed yield per plant, P9-2-2, Bragg, Shivalik, P169-3, SL-679 and SL-682 were the top ranking general combiners. For quality traits, Shivalik, SL-795, P2-2, P6-1, H-330, PS-1466, SL-679, P13-4 and PS-1469 were observed good general combiners.

On the basis of SCA effects, it was observed that none of the crosses could reveal significant specific combining ability effects for all the traits. For seed yield per plant, Shivalik x Him Soya (good x poor), PS-1469 x Hara Soya (poor x average), H-330 x Him Soya (poor x poor) and SL-682 x Hara Soya (good x average) were the best specific combiners which may give desirable transgressive segregants if the additive effect of one parent and complementary epistatic effect act in the same direction and maximize desirable plant characters.

Heterosis was observed for almost all the characters. For seed yield per plant, PK-472 x Hara Soya, PK-472 x Him Soya, DS-1213 x Hara Soya, H-330 x Him Soya, PS-1469 x Hara Soya were the best cross combinations showing economic heterosis. Overall, the cross combinations, PK-472 x Hara Soya, PK-472 x Him Soya, H-330 x Him Soya and PS-1469 X Hara Soya exhibited high SCA, heterosis and *per se* performance for seed yield per plant and therefore, rated as a potential parent of the crosses for further improvement.

In case of wide hybridization, successful interspecific hybrids were obtained when we crossed the cultivated soybean with wild annual *G. soja* although the success rate was low, whereas, the success rate was zero in case of wild perennial *G. tomentella*. Probably we need to improve our crossability skills. Alternately, embryo rescue technique may be employed to recover the hybrids between cultivated soybean and wild

perennial species. The hybridity of hybrids between cultivated and wild annual soybean (*G. soja*) was confirmed at morphological, molecular and cytological level. However there is a need to refine the protocol and skill to obtain better spreads for cytological investigations.

Conclusions

Triple test cross analysis

- Sufficient variability was observed in the triple test cross progenies for all the traits except petiole length.
- Epistasis was found to be an integral part of genetic variation for all the traits except days to 50% flowering, days to 75% maturity, reproductive phase, petiole length, seed per pod, harvest index and 100 seed weight.
- Epistatic interaction for most of traits was ój+lô type except days to 50% flowering, days to 75% maturity, reproductive phase, petiole length, seed per pod, harvest index and 100 seed weight, whereas plant height, internode length, pods per plant and biological yield per plant carried óiô type epistasis alongwith ój+lô type.
- Additive component (D) was more pronounced than dominance component (H) for most of the traits indicating the relative importance of fixable type of gene action in their inheritance.
- Both additive and dominance components were of almost equal magnitude for pod length indicating the importance of both additive and dominance type of gene action, whereas partial degree of dominance was noticed for majority of traits.

Line x tester analysis

- Line Bragg showed high general combining ability followed by Shivalik and P2-2.
- Lines Bragg, Shivalik and P9-2-2 were found to be good general combiners for most of the traits.

- Cross combinations - Shivalik x Him Soya, H-330 x Him Soya, DS-1213 x Him Soya, SL-682 x Him Soya, PS-1469 x Hara Soya, P169-3 x Him Soya and SL-679 x Him Soya were found to have good SCA effects for most of the traits.
- Cross combinations - PK-472 x Hara Soya, PK-472 x Him Soya, H-330 x Him Soya, PS-1469 x Hara Soya showed high *per se* performance, SCA effects, heterobeltiosis and economic heterosis.
- Cross H-330 x Him Soya showed resistance against brown spot and bacterial pustule diseases.

Wide hybridization

- The interspecific hybrids developed were true to type based on confirmation at the morphological, molecular and cytological level.
- Sufficient variability was found for all the traits studied.
- None of the cross combinations were found heterotic for seed yield.
- Interspecific crosses showed significant positive heterosis for plant height and internode length over better parent and mid parent.
- Seed yield per plant showed significantly positive correlation with reproductive phase, pods per plant, pod length, petiole length, harvest index and 100-seed weight. Significantly negative correlation was observed with plant height and internode length.

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APPENDIX-I

Mean performance of parents and their hybrids for different traits

Traits	Days to 50% flowering	Days to 75% maturity	Reproductive Phase	Plant Height	Branches/Plant	Internode length	Nodes on main stem	Petiole Length	Pods/ plant	Seeds /pod	Pod length	Biological yield /plant	Seed yield/plant	Harvest Index	100 seed weight	Protein content	Oil content
Lines																	
P6-1	68.34	126.34	70.33	44.06	6.10	4.81	9.06	12.53	63.53	2.03	3.83	21.34	10.20	51.00	9.00	37.70	16.77
SL-682	55.67	125.67	61.67	60.34	5.93	5.54	10.93	11.13	69.20	2.24	3.56	38.13	16.86	44.67	17.16	41.34	16.84
SL-679	61.00	123.67	62.67	52.80	5.60	4.74	11.06	12.00	72.00	2.01	3.50	28.00	13.63	47.00	10.00	39.05	15.92
P9-2-2	58.34	120.34	61.67	41.93	6.40	4.70	8.93	11.13	65.30	1.98	3.60	21.60	11.70	55.67	10.67	38.06	17.37
DS-1213	69.67	128.67	73.67	60.34	8.06	5.00	12.06	11.56	111.30	2.26	3.46	56.06	24.20	43.33	11.67	37.15	16.95
PK-472	72.34	127.67	72.67	50.20	6.46	4.44	11.20	12.06	82.73	2.06	3.60	33.86	17.16	50.67	12.67	37.52	16.77
Hardee	72.67	129.34	75.33	51.40	6.53	4.71	10.93	11.00	68.06	2.05	3.43	25.34	13.46	54.00	12.83	37.41	17.51
Bragg	55.67	123.00	62.00	54.67	5.67	5.29	10.34	12.00	54.53	2.12	3.67	30.46	13.20	43.00	18.50	38.14	18.75
SL-795	65.67	126.34	65.67	46.13	8.13	3.94	11.67	12.53	61.53	2.09	3.90	27.93	12.40	44.33	11.83	38.16	16.15
P2-2	56.67	120.67	63.00	40.34	5.34	4.01	10.13	12.20	42.40	2.03	3.70	21.53	11.73	55.00	12.67	38.91	17.98
Shivalik	60.67	126.33	65.67	45.06	5.60	4.61	9.86	12.26	64.93	2.18	3.56	28.26	13.36	47.33	11.83	37.32	17.98
P-1466	64.67	129.67	66.33	45.73	5.63	4.15	11.13	12.66	80.73	1.90	3.50	32.93	15.86	49.00	11.46	36.85	17.50
H-330	77.00	128.34	70.33	38.40	4.20	4.42	8.67	12.40	27.30	1.95	3.56	30.10	9.30	31.00	15.26	37.62	18.25
PS-1469	62.67	128.67	63.67	62.00	6.40	5.32	11.67	11.86	66.33	2.36	3.60	39.26	19.63	49.67	15.46	38.15	18.53
VLS-59	62.00	122.34	64.33	45.93	5.46	4.89	9.40	11.60	68.26	2.16	3.40	33.46	18.50	56.00	13.83	38.44	18.27
JS-335	64.00	124.00	68.33	49.34	7.13	4.05	12.20	12.26	60.33	1.83	3.73	26.53	13.20	50.67	17.50	38.04	17.25
P169-3	61.34	124.00	65.67	49.34	5.30	4.84	10.16	12.70	47.83	2.01	3.36	25.46	11.83	47.33	14.34	36.63	19.85
P13-4	58.34	121.67	72.33	35.26	6.26	4.02	8.73	12.46	55.06	1.84	3.70	24.53	11.13	45.67	15.50	39.68	17.66
Testers																	
Him Soya	61.34	122.00	63.67	43.26	3.93	4.95	8.67	12.66	65.60	2.13	3.57	26.74	15.50	58.33	12.00	37.37	17.56
Hara Soya	60.67	124.00	65.33	52.00	4.80	5.02	10.40	11.34	40.86	2.25	3.60	24.74	10.86	48.33	16.16	36.52	20.15
Hara Soya x Him Soya	63.00	126.00	67.33	50.16	4.70	5.19	9.70	12.43	73.20	2.14	3.40	41.20	19.36	47.33	15.83	37.32	18.30

Contd....

Traits	Days to 50% flowering	Days to 75% maturity	Reproductive Phase	Plant height	Branches/plant	Internode length	Nodes/main stem	Petiole length	Pods/ plant	Seeds/ pod	Pod length	Biological yield/plant	Seed yield/ plant	Harvest Index	100 seed weight	Protein content	Oil content
Hybrids																	
P9-2-2 x Him Soya	61.00	123.67	63.00	35.96	4.93	4.07	8.86	12.40	67.54	2.10	3.50	27.86	12.64	48.33	11.50	40.22	16.74
P9-2-2 x Hara Soya	60.34	126.67	63.00	43.67	4.60	4.43	9.80	12.87	80.26	2.08	3.60	32.96	14.40	43.67	12.16	37.46	17.49
P9-2-2 x (Hara Soya x Him Soya)	56.34	127.00	64.67	37.60	5.53	3.75	9.96	11.40	83.13	2.00	3.83	35.40	15.30	43.00	12.83	40.20	16.61
PS-1466 x Him Soya	62.00	126.34	65.67	50.00	4.46	4.27	11.73	12.00	93.84	2.16	3.56	40.67	19.23	49.00	12.34	36.97	17.48
PS-1466 x Hara Soya	63.67	128.67	63.67	46.56	5.16	4.71	9.83	11.80	76.00	2.13	3.60	36.23	18.20	49.67	12.50	36.74	17.64
PS-1466 x (Hara Soya x Him Soya)	62.34	127.00	65.00	51.26	4.83	4.56	11.23	11.93	101.76	2.22	3.40	43.06	22.70	52.67	11.83	37.38	17.60
P6-1 x Him Soya	65.00	125.34	67.33	54.53	6.20	5.40	10.13	12.50	101.93	2.21	3.30	36.73	17.30	47.33	10.50	37.30	18.05
P6-1 x Hara Soya	64.67	127.34	68.33	50.16	5.36	5.38	9.30	12.43	93.10	2.25	3.70	36.57	20.30	56.33	13.00	37.65	18.22
P6-1 x (Hara Soya x Him Soya)	66.00	126.34	69.33	46.36	6.00	5.26	8.80	12.93	99.90	2.14	3.63	36.40	16.00	44.00	12.16	38.43	17.70
PK-472 x Him Soya	64.67	127.34	68.67	54.43	5.80	5.32	10.36	11.86	143.03	2.27	3.46	58.06	29.73	51.67	12.83	37.72	17.86
PK-472 x Hara Soya	68.34	127.67	70.67	51.93	5.93	4.50	11.53	12.53	99.80	2.25	3.50	51.87	30.43	58.67	12.50	39.27	16.64
PK-472 x (Hara Soya x Him Soya)	64.00	126.00	66.00	48.26	4.73	4.16	11.56	11.73	88.03	2.16	3.90	39.60	22.60	57.33	11.83	37.44	17.91
VLS-59 x Him Soya	63.67	125.67	63.33	48.86	3.93	5.02	9.73	11.73	72.67	2.26	3.40	32.74	15.70	48.33	14.34	38.45	17.07
VLS-59 x Hara Soya	62.34	127.67	61.67	48.76	5.20	4.70	10.36	13.06	67.36	2.19	3.50	29.26	14.36	49.00	12.34	38.09	16.93
VLS-59 x (Hara Soya x Him Soya)	63.67	128.00	64.33	48.03	7.34	4.09	11.63	11.06	83.34	2.24	3.83	39.93	17.56	43.67	12.83	37.78	17.13
P13-4 x Him Soya	62.34	127.34	64.33	46.13	4.93	4.34	10.73	12.46	68.94	2.17	3.60	32.80	14.67	44.67	12.16	37.68	17.27
P13-4 x Hara Soya	60.00	126.67	63.00	57.30	6.26	4.89	11.83	12.86	79.16	2.26	3.70	40.83	17.86	44.00	13.50	38.19	17.39
P13-4 x (Hara Soya x Him Soya)	61.00	127.34	61.67	51.36	5.00	4.49	11.53	12.00	87.63	2.15	3.43	38.83	19.26	49.33	12.34	37.67	18.02
PS1469 x Him Soya	63.67	128.34	66.33	53.47	4.80	4.97	10.63	12.06	71.26	2.01	3.60	36.83	15.63	42.33	12.83	38.73	17.75
PS1469 x Hara Soya	64.00	129.34	65.33	58.27	7.73	5.29	11.13	12.20	83.93	2.23	3.60	46.53	21.30	45.67	13.83	38.32	18.00
PS1469 x (Hara Soya x Him Soya)	63.00	127.34	66.00	47.47	5.86	4.85	9.73	12.06	66.93	2.09	3.36	35.80	16.43	45.67	12.67	38.42	17.98
DS-1213 x Him Soya	61.34	129.34	61.00	58.40	6.26	5.17	11.26	12.40	97.73	2.31	3.83	45.13	20.73	46.00	13.16	38.52	17.46
DS-1213 x Hara Soya	70.34	128.67	66.00	62.10	7.34	4.82	12.86	13.06	87.43	2.41	3.50	52.34	24.20	46.33	12.83	37.23	17.94
DS-1213 x (Hara Soya x Him Soya)	66.34	128.00	67.33	49.50	5.80	4.18	11.86	12.73	97.80	2.19	3.73	45.70	20.70	45.33	12.16	36.88	18.07
SL-679 x Him Soya	60.00	127.34	64.00	46.86	4.94	4.74	9.90	13.00	76.93	2.03	3.60	30.30	15.16	50.33	10.34	39.74	16.67
SL-679 x Hara Soya	62.34	128.00	63.33	46.53	4.16	4.73	9.90	12.53	69.73	2.13	3.36	29.36	13.30	45.33	9.50	40.25	15.30
SL-679 x (Hara Soya x Him Soya)	61.34	128.34	62.33	42.73	3.86	4.48	9.53	12.34	65.23	2.03	3.70	27.00	15.34	59.67	10.00	38.92	16.21
SL-682 x Him Soya	60.00	125.67	60.00	47.90	4.63	4.64	10.40	11.80	59.86	2.05	3.90	29.20	13.40	45.33	12.67	39.03	17.18
SL-682 x Hara Soya	58.34	131.00	61.67	48.63	5.30	4.48	10.83	12.16	74.60	2.01	3.40	39.16	18.63	46.67	13.16	39.16	17.35
SL-682 x (Hara Soya x Him Soya)	57.34	129.67	60.00	50.80	5.60	5.16	9.86	11.40	53.60	2.12	3.46	38.46	15.86	41.33	15.50	39.19	17.24

Contd....

Traits	Days to 50% flowering	Days to 75% maturity	Reproductive Phase	Plant height	Branches/plant	Internode length	Nodes/main stem	Petiole length	Pods/ plant	Seeds/ pod	Pod length	Biological yield/plant	Seed yield/ plant	Harvest Index	100 seed weight	Protein content	Oil content
H-330 x Him Soya	70.67	131.00	71.00	54.46	5.00	5.67	9.67	11.40	51.33	2.25	3.90	43.80	22.43	52.00	21.83	40.58	19.98
H-330 x Hara Soya	68.67	130.67	69.33	55.93	4.53	6.02	9.26	12.20	39.40	2.35	3.70	30.00	18.43	61.00	24.16	39.75	19.84
H-330 x (Hara Soya x Him Soya)	67.67	130.67	71.33	53.07	5.00	5.52	9.53	12.06	58.06	2.23	3.60	38.46	18.90	49.33	23.16	38.61	20.05
P169-3 x Him Soya	62.67	127.67	68.00	43.83	4.34	5.89	7.46	11.56	35.73	2.01	3.60	20.30	8.86	44.67	18.34	37.84	17.04
P169-3 x Hara Soya	62.34	126.00	66.00	45.20	4.13	5.55	8.13	12.86	40.34	2.03	3.37	22.34	10.10	44.67	14.00	37.24	20.05
P169-3 x (Hara Soya x Him Soya)	61.00	127.34	65.00	55.87	6.53	4.61	12.13	12.36	78.76	2.26	3.83	51.73	21.30	40.67	15.34	36.87	18.73
P2-2 x Him Soya	61.34	125.34	64.00	43.06	4.93	4.59	9.40	11.00	71.46	1.97	3.60	30.87	12.23	40.00	14.16	38.87	16.53
P2-2 x Hara Soya	60.67	125.34	64.33	36.16	4.83	3.93	9.23	13.20	56.23	1.91	3.70	20.20	8.86	44.67	11.83	38.44	16.28
P2-2 x (Hara Soya x Him Soya)	62.34	126.00	63.67	45.60	5.23	4.42	10.34	11.40	72.13	2.05	3.40	32.03	14.34	44.67	11.34	38.58	17.07
Shivalik x Him Soya	61.00	127.34	63.00	48.73	4.63	4.01	12.23	11.80	76.20	2.08	3.70	29.16	15.76	53.67	12.67	37.16	17.57
Shivalik x Hara Soya	61.67	126.67	65.67	41.20	3.90	4.49	9.13	12.06	49.76	1.90	3.73	23.20	10.20	44.67	12.50	36.87	18.35
Shivalik x (Hara Soya x Him Soya)	60.67	127.34	61.67	46.46	3.93	4.32	10.87	11.53	67.13	2.09	3.60	30.26	15.13	49.00	12.34	37.89	17.47
Hardee x Him Soya	63.67	127.34	64.00	45.80	4.26	4.79	9.53	11.86	57.20	2.08	3.36	21.00	12.06	57.00	11.34	37.71	17.91
Hardee x Hara Soya	73.00	129.67	73.67	52.67	5.86	5.10	10.40	11.80	70.80	2.28	3.90	34.06	14.43	42.33	11.96	38.02	17.58
Hardee x (Hara Soya x Him Soya)	68.67	130.00	69.00	48.60	5.46	4.09	11.93	11.73	72.00	2.12	3.90	35.00	15.70	45.33	12.67	37.82	16.72
JS-335 x Him Soya	62.67	127.67	65.33	48.80	4.86	4.31	11.34	10.80	64.67	2.21	3.50	28.00	12.06	46.00	12.83	37.83	17.24
JS-335 x Hara Soya	62.00	127.67	62.67	48.06	5.86	4.32	11.20	13.26	68.00	2.17	3.70	29.86	13.50	48.33	11.83	38.26	16.80
JS-335 x (Hara Soya x Him Soya)	64.00	128.34	65.33	46.13	4.83	4.46	10.34	12.13	66.06	2.14	3.70	30.06	14.10	47.33	12.50	38.05	17.76
SL-795 x Him Soya	62.34	128.34	63.33	48.93	4.67	4.76	10.27	12.53	84.60	2.21	3.60	37.34	19.34	52.33	12.83	37.83	17.31
SL-795 x Hara Soya	62.00	126.67	64.67	46.50	5.46	4.55	10.23	12.67	81.10	2.15	3.70	38.16	20.07	53.00	12.00	38.20	16.42
SL-795 x (Hara Soya x Him Soya)	62.67	126.67	66.00	44.06	4.20	4.15	10.60	11.86	71.53	2.09	3.40	30.13	13.93	46.00	11.34	37.69	17.21
Bragg x Him Soya	61.34	126.34	63.00	49.26	4.46	4.49	11.00	11.40	75.67	2.16	3.70	34.67	16.60	47.67	12.84	37.22	17.67
Bragg x Hara Soya	57.67	126.67	61.33	45.90	5.03	4.93	9.36	12.43	65.34	2.14	3.83	33.20	16.34	49.00	14.84	37.27	18.57
Bragg x (Hara Soya x Him Soya)	59.34	126.4	62.33	40.10	3.86	4.51	8.86	12.60	53.43	1.94	3.73	22.56	12.80	56.00	12.34	36.89	17.88
CD (5%)	3.47	3.01	0.05	9.57	1.21	0.84	1.53	NS	18.59	0.25	0.16	9.05	4.21	0.11	1.82	0.71	0.51
CV (%)	3.41	1.47	4.57	12.24	13.98	11.04	9.14	9.57	16.13	7.23	2.64	16.62	16.18	13.86	8.46	1.16	1.79

APPENDIX-II

Reaction of parents and their hybrids to different diseases under field conditions

Lines	Frogeye leaf spot	Pod blight	Brown spot	Bacterial pustule
P6-1	MR	MR	MS	MR
SL-682	MR	MS	MS	MR
SL-679	S	S	MR	M
P9-2-2	MS	MR	MR	MR
DS-1213	MR	R	MR	M
PK-472	MS	MR	MR	M
Hardee	MR	MR	MS	MS
Bragg	S	MS	S	MR
SL-795	MS	MS	MS	MS
P2-2	MR	MS	S	MS
Shivalik	MR	MR	MS	MS
P-1466	MR	MR	MR	MR
H-330	MR	MR	R	MR
PS-1469	MR	R	R	MS
VLS-59	MR	MR	MR	MR
JS-335	MR	R	MR	MR
P169-3	R	MR	MS	MS
P13-4	MS	MS	MS	R
Testers				
Him Soya	MR	MS	MS	MS
Hara Soya	MR	MR	MR	MR
Hara Soya x Him Soya	MR	MR	MR	MR

Contd….

Hybrids	Frogeye leaf spot	Pod blight	Brown spot	Bacterial pustule
P9-2-2 x Him Soya	MR	S	R	R
P9-2-2 x Hara Soya	MR	MR	MR	MR
P9-2-2 x (Hara Soya x Him Soya)	MS	MS	S	MR
PS-1466 x Him Soya	MS	MR	MS	MS
PS-1466 x Hara Soya	MS	MS	MS	MR
PS-1466 x (Hara Soya x Him Soya)	MS	MR	MS	R
P6-1 x Him Soya	R	MR	MS	MR
P6-1 x Hara Soya	MR	MS	MR	R
P6-1 x (Hara Soya x Him Soya)	MR	MR	MR	MS
PK-472 x Him Soya	MR	MS	MS	MR
PK-472 x Hara Soya	MR	MS	MS	MR
PK-472 x (Hara Soya x Him Soya)	MS	S	MS	MS
VLS-59 x Him Soya	R	R	MR	MS
VLS-59 x Hara Soya	MR	MR	MS	MR
VLS-59 x (Hara Soya x Him Soya)	MR	R	MR	MS
P13-4 x Him Soya	R	S	MS	MR
P13-4 x Hara Soya	M	MS	S	MS
P13-4 x (Hara Soya x Him Soya)	R	MR	MS	MR
PS1469 x Him Soya	MS	MR	MS	R
PS1469 x Hara Soya	MR	MS	MS	MS
PS1469 x (Hara Soya x Him Soya)	MR	MS	MR	R
DS-1213 x Him Soya	MR	MR	MS	S
DS-1213 x Hara Soya	MS	MS	MR	MS
DS-1213 x (Hara Soya x Him Soya)	MS	S	R	MR
SL-679 x Him Soya	MR	R	MS	MS
SL-679 x Hara Soya	MS	MS	MS	S
SL-679 x (Hara Soya x Him Soya)	MS	MS	MR	MR
SL-682 x Him Soya	MR	MR	MS	S
SL-682 x Hara Soya	MS	MR	MS	MS
SL-682 x (Hara Soya x Him Soya)	MR	MS	MR	MR
H-330 x Him Soya	MR	MS	R	R
H-330 x Hara Soya	MR	MS	R	MS

Contd….

Hybrids	Frogeye leaf spot	Pod blight	Brown spot	Bacterial pustule
H-330 x (Hara Soya x Him Soya)	MR	MR	R	MS
P169-3 x Him Soya	R	MS	S	MR
P169-3 x Hara Soya	S	MR	R	MS
P169-3 x (Hara Soya x Him Soya)	MS	MR	MS	MR
P2-2 x Him Soya	MS	MR	S	MS
P2-2 x Hara Soya	R	MS	MS	MR
P2-2 x (Hara Soya x Him Soya)	MR	MR	S	S
Shivalik x Him Soya	R	MS	MR	MS
Shivalik x Hara Soya	MR	MR	MR	MS
Shivalik x (Hara Soya x Him Soya)	R	R	MR	MR
Hardee x Him Soya	S	MS	MR	R
Hardee x Hara Soya	MS	MS	MS	MS
Hardee x (Hara Soya x Him Soya)	MS	MR	R	MS
JS-335 x Him Soya	MS	MS	MS	MR
JS-335 x Hara Soya	MR	MR	MR	MS
JS-335 x (Hara Soya x Him Soya)	MR	MR	MS	MR
SL-795 x Him Soya	MS	MS	MR	MSS
SL-795 x Hara Soya	MS	MS	MS	MS
SL-795 x (Hara Soya x Him Soya)	MR	MR	MR	MS
Bragg x Him Soya	MR	MS	MR	MS
Bragg x Hara Soya	MS	MR	MS	MR
Bragg x (Hara Soya x Him Soya)	R	MR	MR	MR

APPENDIX-III

Mean weekly weather data for the year 2011 (*kharif*) at CSK HPKV, Palampur

Week No. (Dates)	Temp. (°C)		RH (%)	Sun-shine hrs	Rainfall (mm)	Rainy days
	Max.	Min.				
22 (28May-03Jun)	29.0	17.5	65.5	9.1	42.8	3
23 (04Jun-10Jun)	30.3	18.3	70.5	7.5	39.2	4
24 (11Jun-17Jun)	28.5	20.4	83.5	6.6	117.8	4
25 (18Jun-24Jun)	29.2	19.4	79.0	6.6	34.6	5
26 (25Jun-01Jul)	25.9	20.1	92.5	1.8	167.0	6
27 (02Jul-08Jul)	27.1	19.1	84.5	5.4	117.4	6
28 (09Jul-15Jul)	27.2	19.8	91.0	4.9	87.8	5
29 (16Jul-22Jul)	27.2	20.6	89.0	3.9	61.8	7
30 (23Jul-29Jul)	24.4	20.1	92.5	0.9	196.8	6
31 (30Jul-05Aug)	26.8	20.0	90.5	4.4	106.0	5
32 (06Aug-12Aug)	25.5	20.4	94.5	2.0	191.4	7
33 (13Aug-19Aug)	24.0	17.7	92.5	2.9	335.0	7
34 (20Aug-26Aug)	25.4	19.7	93.0	2.8	209.2	7
35 (27Aug-02Sep)	26.9	19.5	86.0	3.1	68.8	5
36 (03Sep-09Sep)	27.8	18.5	89.5	6.3	39.8	2
37 (10Sep-16Sep)	25.4	18.8	91.0	3.3	83.6	5
38 (17Sep-23Sep)	26.8	16.1	84.0	9.0	12.2	1
39 (24Sep-30Sep)	25.9	15.4	85.5	5.9	32.4	4
40 (01Oct-07Oct)	25.6	15.8	85.0	8.2	32.2	2
41 (08Oct-14Oct)	27.2	14.4	70.5	8.5	0.0	0
42 (15Oct-21Oct)	25.7	12.5	64.5	9.6	0.0	0
43 (22Oct-28Oct)	23.9	11.7	63.0	8.2	2.6	1
44 (29Oct-04Nov)	23.4	12.6	76.5	7.7	1.8	1
45 (05Nov-11Nov)	23.6	11.5	77.5	7.5	0.0	0
Total	-	-	-	-	1980.2	93
Mean	26.4	17.5	83.0	5.7	-	-

APPENDIX-IV

Mean weekly weather data for the year 2012 (*kharif*) at CSK HPKV, Palampur

Week No. (Dates)	Temp. (°C)		RH (%)	Sun-shine hrs	Rainfall (mm)	Rainy days
	Max.	Min.				
22 (28May-03Jun)	35.6	21.6	28.0	8.8	0.4	1
23 (04Jun-10Jun)	31.9	19.7	41.0	5.4	0.1	0
24 (11Jun-17Jun)	34.8	20.9	37.0	9.7	1.8	1
25 (18Jun-24Jun)	35.0	23.7	47.5	7.5	25.6	2
26 (25Jun-01Jul)	32.4	20.3	55.5	8.4	31.4	2
27 (02Jul-08Jul)	28.6	20.7	84.0	4.1	222.2	5
28 (09Jul-15Jul)	27.8	19.2	85.0	6.0	103.8	5
29 (16Jul-22Jul)	28.2	20.0	81.0	6.9	71.8	4
30 (23Jul-29Jul)	27.1	19.9	90.5	3.6	317.8	7
31 (30Jul-05Aug)	23.8	19.5	96.0	1.2	376.0	7
32 (06Aug- 12Aug)	26.8	19.8	89.0	3.4	104.6	4
33 (13Aug-19Aug)	26.9	19.9	92.5	3.1	107.7	6
34 (20Aug-26Aug)	23.2	19.0	95.5	1.0	330.2	7
35 (27Aug-02Sep)	26.4	18.5	91.0	3.9	33.0	3
36 (03Sep-09Sep)	26.9	19.9	87.5	3.7	114.8	5
37 (10Sep-16Sep)	26.1	19.3	91.0	3.5	120.6	6
38 (17Sep-23Sep)	25.1	15.9	87.0	5.5	134.0	4
39 (24Sep-30Sep)	27.1	15.4	75.0	9.1	7.4	1
40 (01Oct-07Oct)	27.6	15.0	68.0	9.9	3.4	1
41 (08Oct-14Oct)	26.3	13.2	55.5	9.6	4.2	1
42 (15Oct-21Oct)	25.3	13.4	55.0	8.9	0.0	0
43 (22Oct-28Oct)	22.6	9.5	62.5	9.2	14.6	1
44 (29Oct-04Nov)	23.9	10.3	61.5	9.6	0.0	0
45 (05Nov-11Nov)	22.0	9.2	59.5	9.1	0.0	0
Total	-	-	-	-	2125.4	73
Mean	27.6	17.7	71.5	6.0	-	-

APPENDIX-V

Mean weekly weather data for the year 2013 (*kharif*) at CSK HPKV, Palampur

Week No. (Dates)	Temp. (°C)		RH (%)	Sun-shine hrs	Rainfall (mm)	Rainy Days
	Max.	Min.				
22 (28May-03Jun)	31.5	18.8	50.1	8.2	62.6	2
23 (04Jun-10Jun)	31.0	21.3	61.7	7.0	59.2	3
24 (11Jun-17Jun)	25.6	17.4	90.0	2.6	220.4	7
25 (18Jun-24Jun)	28.5	19.1	78.1	7.4	84.8	4
26 (25Jun-01Jul)	26.9	19.5	87.4	3.9	71.2	7
27 (02Jul-08Jul)	26.3	19.8	91.4	3.0	284.2	6
28 (09Jul-15Jul)	27.1	19.1	86.6	5.0	57.2	6
29 (16Jul-22Jul)	25.8	19.8	95.3	1.9	193.6	7
30 (23Jul-29Jul)	26.2	19.4	91.3	4.2	199.0	7
31 (30Jul-05Aug)	26.7	20.1	90.3	2.7	205.6	6
32 (06Aug-12Aug)	26.7	20.1	90.3	2.7	205.6	6
33 (13Aug-19Aug)	24.6	18.7	92.4	0.8	132.6	7
34 (20Aug-26Aug)	27.0	19.0	88.5	4.0	149.6	7
35 (27Aug-02Sep)	26.9	18.3	88.6	4.6	125.7	6
36 (03Sep-09Sep)	26.2	16.9	82.5	5.6	71.0	5
37 (10Sep-16Sep)	26.3	16.3	84.3	5.7	32.8	5
38 (17Sep-23Sep)	27.4	15.2	70.5	8.5	117.2	2
39 (24Sep-30Sep)	26.9	16.2	82.8	6.5	103.0	4
40 (01Oct-07Oct)	24.6	15.9	87.9	4.4	84.8	5
41 (08Oct-14Oct)	24.2	16.7	88.4	1.2	49.8	3
42 (15Oct-21Oct)	25.3	12.6	69.5	8.4	16.6	1
43 (22Oct-28Oct)	23.6	11.4	77.5	8.0	0.0	0
44 (29Oct-04Nov)	22.8	9.7	58.3	8.0	0.0	0
45 (05Nov-11Nov)	19.6	7.5	62.4	5.9	30.6	3
Total	-	-	-	-	2557.1	109
Mean	26.2	17.0	81.1	5.0	-	-

Brief Biodata of student

Name : Indu Bala

Father's Name : Sh. Munshi Ram Dehal

Mother's Name : Smt. Amravati Dehal

Date of Birth : 10-06-1987

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Academic Qualifications:

Qualification	Year	School/Board/University	Marks (%)	Division	Major subject
Matric	2002	HP Board of School Education, Dharamshala	79.14	First	English, Maths, Hindi, Social Science, Science, Sanskrit, I.T.
10+2	2004	HP Board of School Education, Dharamshala	72.00	First	English, Biology, Physics, Chemistry, I.T.
B. Sc. (Ag.)	2008	CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur	77.70	First	Agriculture
M. Sc. (Ag.)	2010	CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur	80.00	First	Plant Breeding & Genetics
Ph. D. (Ag.)	2015	CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur	85.00	First	Plant Breeding & Genetics

Title of M.Sc. Thesis : Genetic differentiation and correlation studies in chickpea (*Cicer arietinum* L.)

Fellowships/ Scholarships/ Gold Medals/ Awards/ Any other Distinction:

1	2004-2011	University merit scholarship holder during B.Sc., M.Sc. and Ph.D.
2	2011-2014	**DST INSPIRE FELLOW** for Doctoral programme from 2011-2014
3	2013 & 2014	Qualified **National Eligibility Test**- 2013 & 2014 for Professorship organized by Agricultural Scientists Recruitment Board recognized by UGC/CSIR

Publications:

- Papers: 4
- Abstracts: 10

Visits abroad : Nil