GENETIC STUDIES IN SOYBEAN (*GLYCINE MAX* L. MERILL)

THESIS

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Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya,

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(PLANT BREEDING & GENETICS)

By

MAHESH MEENA

Department of Plant Breeding and Genetics
Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya
College of Agriculture
Gwalior (M.P.)

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CERTIFICATE – I

This is to certify that the thesis entitled “Genetic studies in Soybean (*Glycine max* L. Merill)” **submitted in partial fulfilment of the requirement of the degree of** Master of Science in Agriculture (Plant Breeding & Genetics) **of the** Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior **is a record of the bonafide research work carried out by** Shri Mahesh Meena **under my guidance and supervision. The subject of the thesis has been approved by Students Advisory Committee and the Director of Instruction.**

No part of the thesis has been submitted for any degree or diploma (Certificate/award etc.) or has been published. All the assistance and help received during the course of investigations have been duly acknowledged by him.

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Chairman	**(Sh. Sudhanshu Jain)**	__________________
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Member	**(Dr. V.S. Kandalkar)**	__________________
Member	**(Dr. V.B. Singh)**	__________________
Member	**(Dr. V.K. Shrivastav)**	__________________

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This is to certify that the thesis entitled **“Genetic studies in Soybean (*Glycine max* L. Merill)*”*** submitted by **Shri Mahesh Meena** to the **Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior** in partial fulfilment of the requirements for the degree of **M.Sc. (Ag.)** in the **Department of Plant Breeding & Genetics, College of Agriculture, Gwalior,** has after evaluation, been approved by the external examiner and by the Students Advisory Committee after an oral examination of same.

Place : Gwalior
Date :

(Sh.Sudhanshu Jain)
Chairman
Advisory Committee

Members of the students advisory committee

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Member	**(Dr. A.K. Singh)**	____________________
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Member	**(Dr. V.K. Shrivastav)**	____________________

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Dean of the collage ………………………………….

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Place: Gwalior

Date: (**Mahesh Meena)**

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CHAPTER I

INTRODUCTION

Soybean (*Glycine max* L. Merill) occupies a unique position among edible legumes.Traditional food legumes (pulse) are rich in protein but contain limited amount of oil. Soybean contains more protein (about 40-42%) than other pulse and a much higher content of edible oil (about 20%). It is also rich in lysine (5%) an essential amino acid that is deficient in most of the cereal based diets. Therefore the quality of soy protein is now recognized as being similar of meat protein. The edible oil in soybean is approximately 85% unsaturated and contains the essential fatty acids. This crop is also a good source of vitamins A, B and D. soybean is member of pepilionaceae family and believed to have originated in North Eastern China. This crop is called as “Golden Bean” or Miracle Crop” of the 20th century, because of its multiple uses. In Addition to the nutritional advantage Soybean is also recognized for its benefits to human health such as the cholesterol lowering effect of protein as approved recently by the United States food and drugs administration.

Soybean ranks first among the oilseeds in the world. In international marketed soybean oil trading is next only to palm oil. The crop contributes for nearly 25% of the world’s total oil and fats production. The USA is number one in terms of area and Argentina, China and India are the major producer of soybean accounting for 90% of world production. In India (2013-14) area under soybean production was 12.13 million ha with a production of 13.34 million tones.

Collection of germplasm and assessment of genetic variability is a basic step in any crop improvement programme. Yield being a complex character, is influenced by a number of yield contributing characters controlled by polygenes and also influenced by environment. So, the variability in the collections for these characters is the sum total of heredity effects of concerned genes plus the influence of the environment. Hence, it becomes necessary to partition the observed variability into heritable and non-heritable components measured as genotypic and phenotypic coefficients of variation (GCV and PCV), heritability and genetic advance expressed as per cent mean.

Diversity analysis provides information on deciding choice of parents from distantly related clusters to secure yield improvement in soybean. Identification of potential germplasm lines from the present collection would yield desirable genotypes which will be used for further improvement of the crop. Soybean being a potential legume crop of India has immense scope for genetic improvement for various qualitative and quantitative characters besides widening the genetic base through induced mutagenesis. Keeping the above facts in mind the present study was undertaken with objectives.

1. To find out the extent of genetic variability.
2. To assess genotypic, phenotypic and environmental coefficients of variation yield and yield contributing characters.
3. To study direct and indirect effect through path analysis.
4. To estimate genetic divergence among genotypes (D^2 analysis).

CHAPTER II
REVIEW OF LITERATURE

A thorough understanding of the genetic diversity, extent of variation, genetic architecture of the plant and heritability of characters, among the genotypes would help in developing sound plant improvement programmes. Genetic variability is the gift of nature and it’s fruitful utilization in any crop species calls for systematic collection, evaluation, description and grouping based on economic descriptors. A brief review of available information on the above aspects in soybean is presented in this section under the following headings.:

2.1. Genetic variability

2.2. Heritability and Genetic advance

2.3. Path coefficient analysis

2.4. Genetic divergence

2.1. Genetic variability

The development of an effective plant breeding programme is dependent upon the existence of genetic variability. The efficiency of selection largely depends upon the magnitude of genetic variability present in the genetic stock. Thus, the success of genetic improvement in any character depends on the nature of variability present in the gene pool.

Jagdish *et al.* (2000) found comparatively high PCV and GCV for biological yield, seed yield per plant, pods per plant and plant height.

Jain and Ramgiry (2000) recorded high phenotypic and genotypic coefficient of variability for seed yield per plant, followed by plant weight, plant height and moderate coefficient of variability for 100-seed weight, seed per pod, pod bearing nodes and days to flowering in soybean.

Rajanna *et al.* (2000) observed considerable variability for all characters at all sowing dates. The estimates of GCV and PCV were high and PCV was a good indicator of its GCV as inferred from the narrow difference between them for all the characters. This further reflected on high estimates of heritability and genetic advance as percentage of the mean suggesting the effectiveness of selection based on phenotype alone.

Singh *et al.* (2000) recorded significant differences among parents and F2s for all the studied characters in soybean. The estimates of genotypic coefficient of variation and phenotypic coefficient of variation were comparatively high for biological yield, seed yield per plant, pods per plant and plant height.

Vasline *et al.* (2000) observed maximum variability in characters such as plant height, number of branches per plant, number of capsules per plant and seed yield per plant in M2 and M3 generations.

Agrawal *et al.* (2001) recorded moderate estimates of GCV for days to flower initiations; days to flower termination, whereas low for days to maturity. High estimates of variability parameters were observed in all the three seasons. GCV was high for some of the pod characters, viz. individual pod weight, seed to pod shell ratio and pod shattering, but was moderate for seeds per pod, moisture content of pods at physiological maturity, pod length, pod thickness and pod shattering, whereas moderate for seeds per pod, moisture content of pods at physiological maturity, seed to pod shell ratio, pod width and ratio of pod thickness with pod width.

Das *et al.* (2001) observed significant variability among genotypes for all of the 11 traits studied i.e. days to 50% flowering, days to maturity, plant height, number of branches per plant, mean internodal length, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, oil content and seed yield per plant while studying 65 soybean genotypes.

Qian *et al.* (2001) observed highly significant inter-varietal differences in tofu output, quality and processing-related traits, the variation coefficient ranging from 10.58% to 38.13%. A study of dry tofu output of the P1, P2, F1, F2, F3 of the two cross combinations showed a model of mixed inheritance involving a pair of major genes and some polygenes.

Dixit *et al.* (2002) found comparatively high estimation of genetic variation for harvest index, seed yield per plant and biological yield per plant.

Sudaric *et al.* (2002) reported that among the tested cultivars, Ika had the highest mean for both yield components. Among the tested cultivars, Ika appeared to be the most suitable as a parent in future hybridizations to achieve further genetic advance in soybean grain yield.

Bandyopadhyay (2003) obtained high estimates of genotypic coefficient of variation and phenotypic coefficient of variation for most of the biological nitrogen fixation traits.

Bangar *et al.* (2003) estimated higher values of phenotypic coefficient of variation (PCV) than genotypic coefficient of variation (GCV). The GCV and PCV estimates were highest for branch number per plant and plant height among the characters. The GCV and PCV were of moderate magnitude for the pod number per plant, 100-seed weight (g) and seed yield per plant (g). Days to 50% flowering and days to maturity had very low GCV and PCV estimates. The differences between GCV and PCV magnitudes were very high for 100-seed weight (12.94) and pod number per plant (10.30).

Chamundeswari and Aher (2003) observed Significant genetic variation for number of days to maturity, plant height at maturity, number of branches per plant, number of clusters per plant, number of pods per cluster and per plant, number of seeds per pod, harvest index, mechanical damage, 100-seed weight, grain yield per plant, protein content, oil content and biological yield per plant. Genotypic coefficient of variation was highest for biological yield per plant.

Ganesamurthy and Seshadri (2004) found highly significant differences for all the 10 characters studied. Among the characters, number of pods, seed yield, plant height and dry matter production were found to be showing high genotypic coefficient of variation.

Singh *et al.* (2004) recorded the highest genetic correlation coefficient (GCV) for the number of dropped flowers, followed by the total number of flowers per plant and grain yield per plant. In general, the phenotypic correlation coefficient (PCV) was greater than the corresponding GCV.

Chettri *et al.* (2005) reported that the number of pods per plant showed a wide range of variation (50.78-80.89, general mean of 63.96+or-12.09). Days to maturity, followed by days to 50% flowering recorded the lowest phenotypic and genotypic variances and coefficients of phenotypic and genotypic variation.

Dev *et al.* (2005) found slightly higher values of phenotypic coefficient of variation than the genotypic coefficient of variation for all the traits in soybean.

Dhillon *et al.* (2005) estimated genetic variability for days to 50% flowering, plant height, pods per plant, days to maturity,100-seed weight, seed yield per plant, harvest index, and protein, oil and fatty acid content in 30 soybean strains grown during *kharif* 1999 in Ludhiana, Punjab, India. Most of the characters possessed sufficient genetic variability.

Karad *et al.* (2005) reported that the phenotypic coefficients of variation (PCV) were higher than the genotypic coefficients of variation (GCV) for all traits, indicating the effect of the environment on their expression. Estimates of GCV were high for yield per plant, plant height and pods per plant, and moderate for seeds per pod and branches per plant, indicating that these traits have scope for improvement through selection.

Sethi and Tyagi (2005) recorded high genetic coefficient of variation and heritability along with high genetic gain for biological yield per plant, 100-seed weight and plant height.

Sultana *et al.* (2005) studied thirty genotypes of soybean with a view to find out genetic variability for yield and its quantitative characters. All the tested characters were showed significant variation among the genotypes. The highest genetic variability was found in 100-seed weight followed by pod per plant, grain yield, branch per plant and plant height.

Bhushan *et al.* (2006) reported that the estimates of phenotypic coefficient of variation (PCV) for all the characters were higher than the genotypic coefficient of variation (GCV). High estimates of GCV were observed for branches per plant, pods per plant and biological yield per plant. Moderate estimates of GCV were observed for seed yield per plant, plant height and 100-seed weight. Low estimates of variability were reported for harvest index, seed protein, oil content and days to 50% flowering.

Gohil *et al.* (2006) studied the genetic variability in 55 diverse soybean (*Glycine max*) genotypes collected from different soybean growing states of India for seed yield and its component traits. The highest genotypic coefficient of variation was observed for number of pods per plant followed by seed yield per plant.

Malik *et al.* (2006) observed highly significant differences among the genotypes for leaf area, chlorophyll content, first pod height, days to 50% flowering, days to flowering completion, days to pod initiation, days to 50% maturity, plant height, number of pods per plant, number of branches per plant, number of unfilled pods, number of shattered pods, 100-seed weight, grain yield, oil content and protein content.

Mebrahtu and Mohamed (2006) assessed the amount of genetic variation that existed among vegetable soybeans for green pod yield (GPY), hundred pod weight (HPW), pod length (PL), plant height (PH), and individual sugars (glucose, fructose, sucrose, raffinose, and stachyose) and total sugar. There was substantial genetic variation for GPY, PH, and PL as indicated by relatively large genotypic variance components.

Silveira *et al.* (2006) evaluated soybean genotypes for agronomic characters. The quotient between genetic variation coefficient and the experimental (CVG/CVE) was estimated for the evaluated characters. The quotient CVG/CVE showed good conditions for a selective process, except for grain yield.

Gupta and Punetha (2007) studied twenty-three genetically diverse genotypes of soybean for genotypic and phenotypic variability in 12 quantitative traits: field emergence, days to initial flowering, days to 50% flowering, plant height, days to maturity, pods per plant, seeds per pod, 100-seed weight, seed yield per plot, seed vigour I and II, and viability. The pods per plant exhibited the highest amount of genetic variability, followed by the seed vigour-II, seed yield per plot, seed per pod, and 100-seed weight.

Sharma *et al.* (2007) estimated the coefficient of variation of 62 Indian cultivars of soybean from different regions of India to decide the selection criteria for improvement in grain yield. In general, the value of phenotypic coefficient of variation (PCV), was higher than the genotypic coefficient of variation (GCV) and ECV. Estimates of PCV ranged between 3.19% (for protein content) and 55.45% (for grain yield per plant). Maximum GCV (53.60%) was observed for grain yield per plant and minimum (2.89%) for protein content. Environmental influences were predominant for the number of nodes per plant, basal node height, flowering span, basal pod height and grain yield per plant.

Yadav (2007) evaluated thirty diverse genotypes of soybean during *kharif* 2003-04, in Raipur, Chhattisgarh, India to study the genetic variability for seed yield and its attributes. Seed yield per plant, number of pods per plant, number of seeds per plant, pod bearing length and plant height exhibited maximum genotypic coefficient of variation.

Costa *et al.* (2008) observed highly significant differences among families in soybean. The experimental coefficient of variation (CVe) and the CVg/CVe ratio showed wide variation among traits, being the highest values found for number of pods, number of seeds and grain yield, making evident the existence of variance to be exploited by breeding.

Ajjapplavara and Channagoudra (2009) studied genetic variability for 18 different quantitative characters in 36 genotypes of chilies. The study indicated that the moderate to high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for most of the characters except days to 50 per cent flowering.

Gangarde *et al.* (2009) studied genetic variability in 30 F4 progenies of sesame. High phenotypic and genotypic coefficient of variation were observed in the characters, number of branches per plant, seed yield per plant, number of capsules per plant and number of capsules bearing nodes which indicated large variability among the progenies for these traits.

Karnwal and Singh (2009) studied twenty elite breeding lines of soybean for genetic variability for eighteen economically important traits. Six genotypes viz. PK-1272, PK-1274, PK-1281, PK-1283, PK-1284 and PK-1286 were found significantly superior in yield and other major yield contributing characters. In general, PCV were higher than the GCV and ECV values for all the characters, suggesting that these characters were relatively much influenced by the environment.

Borate *et al.* (2010) studied population parameters such as range, mean, phenotypic and genotypic variances, PCV and GCV for 13 agronomic characters in a set of 30 chick pea genotypes. Range of variability was appreciable for days to first flowering, secondary branches, plant height, dry matter and grain yield. Values of genotypic and phenotypic variances were highest for number of pods, while lowest for seeds. PCV showed higher values than GCV for all characters.

Milatovic *et al.* (2010) studied factors affecting productivity in peach, such as flower density, initial and final fruit set by open pollination, and yield per m length of shoot in 40 cultivars during a three-year period. Significant differences among cultivars were found for all studied properties. The coefficients of variability were me lowest for initial fruit set and then for final fruit set and flower density; while they were the highest for yield.

Saraswathi *et al.* (2010) observed high phenotypic and genotypic coefficient of variation for number of primary branches per plant, plant height, total sucrose content, pod yield and kernel yield per plant in soybean. It indicates the presence of considerable amount of genetic variability for these characters.

Rajeshwar *et al.* (2010) evaluated twenty one diverse winged bean genotypes for phenotypic and genotypic variability in nine quantitative traits. Considerable amount of genetic variability was exhibited by days to 50% flowering, pod length, dry pod weight, 100 seed weight and grain yield per plant.

Patil *at al.* (2011) observed highest genotypic and phenotypic coefficient of variance for plant height followed by seed yield per plant and pods per plant and it was lowest for days to 50% flowering , days to maturity, protein content and pod length.

Bhat *at al.* (2012) reported that the characters plant height, days to flowering, days to maturity, specific leaf weight, number of pods per plant, harvest index and 100- seed weight showed very narrow difference between phenotypic and genotypic coefficient of variation in all the four leaflet type.

Mahawar et al. (2013) recorded higher value of phenotypic coefficient of variation than genotypic coefficient of variation for primary branches per plant, followed by seeds per pod, pods per plant and pod clusters per plant.

Reni and Rao (2013) evaluated forty five genotypes of soybean of diverse origin for variability. Analysis of variance revealed highly significant differences among the genotypes for the all the characters. High PCV coupled with high GCV, observed for branches per plant, pods per plant, biological yield, harvest index and yield per plant indicate the presence of wider adaptability for these traits in the genotypes studied, suggested the less influence of environment in the expression of characters.

2.2. Heritability and Genetic advance:

Selection is perhaps the most important activity in all plant breeding programmes. The efficiency of selection largely depends on the the extent of genetic variability present in the population and the heritability of the concerned character. Selection is generally more effective for characters with high heritability than those having low heritability. Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimate alone.

Jain and Ramgiry (2000) observed high estimates of heritability accompanied by high genetic advance as a percentage of mean for seed yield, plant height and pods per plant and advocated that these traits were major yield contributing traits in soybean.

Jagdish *et al.* (2000) found high estimates of heritability for all the characters studied and seed yield per plant, biological yield per plant, pods per plant and plant height showed high heritability with genetic advance as percentage of mean. They also reported high genetic advance as a percentage of mean with high heritability for seed yield per plant, biological yield per plant, pods per plant and plant height in 16 F2 generation and 14 parents of soybean.

Khan *et al.* (2000) observed heritability for yield determining components in 86 diverse maturity genotypes of soybean sown in 1989 in Pakistan. The heritability value ranged from 29.37% for seeds/pod to 98.98% for maturity.

Oliveira *et al.* (2000) observed highest heritability for characters related to vegetative growth and seed weight per plant, indicating that they were less sensitive to the environment and, therefore, easier to select. The number of pods and number of seeds per plant gave low heritability coefficients.

Rajanna *et al*. (2000) studied the extent of variability for seed yield and its components among 24 genotypes of soybean. They reported high estimates of heritability for seed yield and its components. They also reported high estimates of heritability and genetic advance as percentage of mean suggesting the effectiveness of selection based on phenotypic alone when an investigation was carried out to assess the extent of genetic variability for seed yield and its components among 24 genotypes of soybean.

Singh *et al.* (2000) recorded high estimates of heritability for all the characters in soybean. Seed yield per plant, biological yield, pods per plant and plant height showed high heritability with high genetic advance as a percentage of mean.

Vasline *et al.* (2000) observed a high heritability associated with a high genetic advance as a percentage of mean for plant height, number of branches per plant, number of capsules per plant, number of seeds per capsule and seed yield per plant in M2 and M3 generations in *Sesamum indicum* L.

Zhang and Yang (2000) reported that heritability values for plant height, number of nodes on the main stem and 100-seed weight were relatively high, as were heritability values for branch characters in soybean.

Agrawal *et al.* (2001) reported high estimates of heritability and genetic advance as percentage of mean for plant height, branches per plant, days to flower initiation, and days to flower termination. With regard to seed yield and yield attributing characters, The pod characters, viz. individual pod weight, seed to pod shell ratio, pod thickness, ratio of pod thickness with pod length and pod shattering expressed high genetic advance as percent of mean, whereas seeds per pod, moisture content of pods at physiological maturity, pod length, pod width expressed moderate genetic advance as percent of mean.

Muthuraj *et al.* (2001) studied broad sense heritability of seed quality characters namely 100-seed weight, germination (%) and electrical conductivity of seed leachate in a field experiment conducted in Delhi, India during the *kharif* season of 1998 using 27 soybean cultivars. The broad sense heritability of germination percentage and electrical conductivity of seed leachate were 41.2 and 44.0%, respectively, indicating that these seed quality characters are greatly influenced by environmental factors; the genetic component is quite low. The broad sense heritability for 100-seed weight was high (70.5%) indicating that the character is mainly controlled by additive gene effects.

Qian *et al.* (2001) estimated 87.86-99.83% heritability for dried tofu output. For the F3 generation, heritability of the major gene was 51.80-59.80% and that for the polygene was 39.18-48.03% in soybean.

Dixit *et al.* (2002) studied biometrical parameters in 38 newly developed genotypes of soybean. Harvest index, seed yield per plant and biological yield per plant showed comparatively high estimates of genetic variation and heritability;

hence, direct selection for these traits would be effective for yield improvement in soybean.

Sudaric *et al.* (2002) recorded highest heritability for seed weight and number of seeds per plant in soybean.

Bandyopadhyay (2003) recorded high heritability along with high genetic advance for number of nodules in the primary root, number of nodules in the secondary roots, total number of nodules in the primary root, number of nodules in the secondary roots, total number of nodule, weight of nodules in the primary root, weight of nodules in the secondary roots and total weight of nodules indicating the presence of additive gene action. High heritability along with low genetic advance observed in days of 50% flowering and nitrogen fixation per plant indicating non-additive gene action.

Bangar *et al.* (2003) reported that days to maturity (97.80%), branch number per plant (91.39%) and plant height (60.82%) showed the highest magnitude of heritability among all the characters. Genetic advance was high for branch number per plant, plant height and seed yield.

Chamundeswari and Aher (2003) reported that broad sense heritability was highest for plant height and number of pods per plant in soybean. Genetic advance ranged from 0.177 (harvest index) to 42.26% (plant height), whereas genetic gain ranged from 7.436 (number of days to maturity) to 63.2% (plant height). Selection based on plant height and number of pods per plant recorded genetic advance of 42.26 and 39.32, respectively.

Singh *et al.* (2004) observed high to moderate broad-sense heritability in oil percent, total flower production, number of days to flowering, number of primary branches, number of pods per plant, protein percent and number of seeds per pod.

Sudaric *et al.* (2004) reported that grain yield components were determined as more reliable criteria for selection of superior genotypes than grain yield *per se* due to higher heritability (61.87-82.31%) and better progress in selection (10.63-22.78%) in soybean. Grain quality traits had medium heritability (60.04-65.89%) and better progress in selection (6.95-8.94%) compared to grain yield that had less heritability (29.87%), and the relative genetic gain from selection was 0.43%.

Chen *et al.* (2005) analyzed the heritability of agronomic and nutritional characteristics on 15 vegetable soybean cultivars at the podding stage. The heritability of 100-seed fresh weight and protein content of fresh seeds were higher than that of the other characteristics. The genetic variation of yield per plant was high.

Chettri *et al.* (2005) reported that plant height and grain yield per unit area exhibited high estimates of heritability, genetic advance and genetic advance as percent of mean along with appropriate broad sense heritability values. The number of grains per pod and 100-grain weight showed high heritability values but low genetic advance and genetic advance as percent of mean.

Dev *et al.* (2005) recorded high estimates of heritability for all the characters in soybean except for pods per plant, whereas expected genetic gain in terms of percentage of mean was highest for clusters per plant and lowest for days to maturity. Traits with high heritability and high genetic advance also had moderate to high genotypic and phenotypic coefficients of variation and *vis-a-vis*.

Dhillon *et al.* (2005) observed high heritability coupled with high genetic advance for seed yield per plant, indicating the presence of additive gene action in the expression of this character. Non-additive heritability was observed in the expression of days to 50% flowering, protein content and palmitic acid as these traits had high heritability estimates coupled with low genetic advance.

Karad *et al.* (2005) reported high estimates of heritability and genetic advance for yield per plant, pods per plant and plant height, and moderate for days to 50% flowering, days to maturity and branches per plant, indicating the predominance of additive gene action for these traits.

Sultana *et al.* (2005) observed high estimate of heritability together with high genetic advance in percentage of mean for 100-seed weight, pods per plant, branches per plant and yield per plant.

Bhushan *et al.* (2006) observed high estimates of heritability for pods per plant, plant height and biological yield per plant. High genetic advance was observed for branches per plant, biological yield per plant and pods per plant, while seed yield per plant and plant height displayed moderate genetic advance, suggesting that all these characters were governed by additive gene effects. High heritability coupled with high genetic advance as percent of mean was observed for pods per plant and biological yield per plant. High GCV coupled with high heritability and expected genetic gain were observed for pods per plant, branches per plant and biological yield per plant, indicating that the variation in these characters was most likely due to additive gene effects, hence, simple pure line selection may be effective to improve these characters.

Cicek *et al.* (2006) reported that in soybean, maturity, seed size, and sucrose content were highly heritable, whereas plant height, canopy spread, leaflet length, leaflet width, yield, stachyose content, and raffinose content had relatively low broad-sense heritabilities. The information on heritability and interrelationships among the agronomic and seed quality traits will be helpful to breeders in constructing their breeding populations and implementing selection strategies.

Gohil *et al.* (2006) studied the broad-sense heritability and expected genetic advance for seed yield and its component traits in soybean. High heritability was observed for all the characters studied in soybean. Further, plant height, number of clusters per plant, number of pods per plant and seed yield per plant had high genetic advance coupled with high heritability, which suggested that these four traits are under the control of additive gene action and can be improved through simple selection procedures.

Karthika and Lakshmi (2006) observed high heritability and genetic advance for seed number/plant, seed yield/plant and 100-seed weight for both mutagens and cultivars. Results showed that these characters are governed by additive gene effects, which may favourably be exploited in the M2 generation.

Malik *et al.* (2006) in soybean, recorded high heritability for 100-grain weight, number of days to maturity, number of days to flowering completion, number of days to pod initiation, leaf area, number of days to 50% flowering, oil content, number of shattered pods per plants, grain yield per plant, plant height and protein contents, indicating the additive type of gene action governing the traits.

Malik *et al.* (2006) recorded high heritability in 100-grain weight, days to maturity, days to flowering completion, days to pod initiation, leaf area, days to 50% flowering, oil contents, number of shattered pods per plant and grain yield per plant, plant h eight and protein content, indicating an additive type of gene action. Selection based on heritability for these traits will provide the greatest improvement in soybean.

Mebrahtu and Mohamed (2006) observed heritability (h^2) estimates of 0.85, 0.68, 0.81, and 0.85 for green pod yield (GPY), hundred pod weight (HPW), pod length (PL), and plant height (PH), respectively. These high h^2 estimates imply that selection for improved GPY along with PL and HPW can be achieved in a breeding population.

Silveira *et al.* (2006) evaluated soybean genotypes for agronomic characters. Heritability coefficient and expected genetic gain were estimated for the evaluated characters. High heritability estimates were obtained, resulting in estimates that indicate accentuated expected genetic gain.

Thakare *et al.* (2006) recorded high heritability estimates for all the characters, days to flower initiation, plant height, number of pods per plant, number of seeds per pod, days to maturity, 100-seed weight, and seed yield per plant. Twenty-four mutant cultures on the basis of high mean performance for number of pods per plant, plant height and days to maturity with high genetic coefficient of variation and h^2 estimate were identified.

Ukkund *et al.* (2006) found high estimates of heritability for plant height (93.4%), days to first flowering (83.5%), per cent fruit set (70.7%), number of fruits per plant (81.1%), fruit length (92.4%), ten fruit weight (92.4%) and total green fruits per plant (88.4%) in chilli. Most of these characters also had moderate to high estimates of genetic advances as a per cent over mean except days to first flowering.

Darwish (2007) reported that heritability estimates, in broad sense were high to moderate in magnitude with values between 41.03 for flowering date in the second cross to 87.27% for number of pods/plant in the second cross. The predicted genetic advance was rather moderate or high for number of branches/plant and maturity date in the first and third crosses and no. of seeds/plant in the second cross and low for the remaining traits.

Gupta and Punetha (2007) advocated that pods per plant expressed the highest heritability and expected genetic advance among all the twelve quantitative traits.

Nag *et al.* (2007) noted high heritability coupled with high genetic advance as percentage of mean for plant height, pod bearing length, pod bearing nodes, pods per plant, seeds per plant and seed yield per plant, indicated the effectiveness of selection for these characters.

Sharma *et al.* (2007) recorded maximum estimates of heritability for the number of seeds per plant and minimum for flowering span. High to moderate heritability were recorded for the number of pods per plant, protein content, number of primary branches per plant, 100-seed weight, days to flower initiation, days to 50% flowering, basal pod height, number of seeds per pod and oil percentage. Low heritability was observed for basal node height and number of nodes per plant.

Siddhu *et al.* (2007) observed high estimates of broad sense heritability and high genetic advance for number of pods per plant, dry matter and for their respective yield in the selected progenies in both the crosses.

Singh *et al.* (2007) reported that number of branches, plant height, number of seeds per pod number of pods per plant, pod length and average seed yield per plot per plant exhibited high heritability and genetic gain, hence, simple selection procedure may be followed for the further improvement in these traits of French bean. The characters like days to 50% flowering and pod diameter showed low genotypic and phenotypic coefficient of variations with low to moderate heritability and genetic gain thus the selection in these traits would not be effective.

Yadav (2007) calculated high estimates of heritability coupled with high genetic advance as percentage of mean for plant height, pod bearing length, pods per plant, seeds per plant and seed yield per plant. Significant contribution of additive genetic variance was observed for all the above characters.

Costa *et al.* (2008) reported that the estimation of the heritability coefficients in the broad sense, narrow sense and by regression were close in most of the situations, showing that the largest part of genetic variance is of additive nature, in which simple selection methods can lead to satisfactory genetic gains.

Pandey *et al.* (2008) observed highest estimate for broad sense heritability for 100-seed weight (0.857), followed by germination percentage (0.840), water absorption (0.822) and dry matter weight per plant (0.812), respectively. High value of expected genetic advance was observed for germination percentage (46.30), followed by water absorption (23.04), pods per plant (22.27), dry matter weight per plant (15.19), respectively.

Singh and Yadav (2008) observed high to moderate heritability with high to moderate genetic advance for number of seeds per fruit, ascorbic acid content, number of fruits per plant, fresh fruit weight per plant, fresh fruit yield (q/ha), seed weight per plant and seed yield (q/ha) in Capsicum annuum showing dominancy of additive gene effects which suggested excellent chance of effective selection for improvement of these traits and high heritability coupled with medium genetic advance for stem diameter and total soluble solids and suggesting good chances of effective selection for these traits. While other traits showed non additive type of gene action.

Talukdar *et al.* (2008) estimated high heritability coupled with high genetic advance (as percentage of means) for important yield components offer scope for selection in grass pea.

Vekariya *et al.* (2008) reported that most of the characters like Seed yield per plant, days to flowering, days to maturity, productive phase, plant height, plant spread, number of pods per plant, number of seeds per plant, biological yield per plant were registered high estimates of heritability, but 100-seed weight, number of branches per plant harvest index had moderate estimates in chickpea. The high estimates of phenotypic and genotypic coefficient of variation, heritability and genetic advance expressed as percentage of mean were observed for number of seeds per plant, number of pods per plant and seed yield per plant.

Baskaran *et al.* (2009) obtained high heritability values for all the characters except number of sprays per plant and plant spread. In high heritability estimate coupled with high genetic advance as per cent of mean was observed for number of suckers per plant (174.91), flower disc diameter (123.23) and number of flowers per plant (114.81). It was observed that heritable variability in the breeding materials characters like number of suckers per plant, flower disc diameter, number of flowers per plant, flower weight, yield per plant and number of ray florets could be exploited for improvement through crop breeding programme.

Durai and Subbalakshmi (2009) studied the genetic parameters for yield and yield components in 6 soybean genotypes (TNAU S 7, TNAU S55, DS 9501, TS 82, Himso 1563 and CO 2) and their 15 crosses grown during the *rabi* of 2003-04 in Karnataka, India. The traits evaluated were: number of days to 50% flowering (DEE), number of days to maturity (DTM), plant height (PHT), number of branches per plant (NBP), number of clusters per plant (NCP), number of pods per cluster (NPC), number of two-seeded pods per plant (N2SP), number of three-seeded pods per plant (N3SP), total number of pods per plant (TPP), standard pod length (SPL), standard pod width (SPW), pod yield per plant (PYP), biological yield (TDMA), seed yield per plant (SYP), oil content (OCP) and protein content (PCP). Heritability estimates were high for DEE, DTM, N2SP, N3SP, SPW and PYP due to the additive gene control; moderate for PHT, NBP, NCP, NPC, TPP, SPL, TDMA and SYP due to the dominant gene control; and low for PCP and OCP due to the effect of the environment.

Gangarde *et al.* (2009) reported that the capsule length, number of capsules per plant showed high heritability estimates accompanied with high genetic advance as a per cent of mean in sesame. It suggests that most likely the heritability is due to additive gene effects and selection may be effective.

Khote *et al.* (2009) reported that characters like days to flowering, pod length, kernel length, 100-pod weight and dry matter/plant showed high heritability in groundnut. The highest genetic advance as percentage of mean was recorded for kernel yield/plant, fodder/plant, harvest index and pod yield/plant.

Karasu *et al.* (2009) reported that the estimates of heritabilities with limited phenotypic variance definition were 0.14, 0.14, 0.21, 0.004, 0.13, 0.30 and 0.26 for plant height, number of seeds per pod, 1000 seed weight, first pod height, number of seeds per plant, number of pods per plant and seed yield, respectively. The heritabilities with complete phenotypic variance definition were 0.05, 0.05, 0.04, 0.003, 0.07, 0.19 and 0.20 for the same traits, respectively. Moderate or low heritabilities estimated for all the traits showed that family selection method could be used instead of individual selection in the breeding programs for improving seed yield and its components.

Karnwal and Singh (2009) reported high estimates of heritability for pods/plant, followed by plant height, primary branches/plant and seed yield/plant whereas, pods/plant and plant height revealed high genetic advance.

Sabu *et al.* (2009) shed light the study on the genetic information of grain yield and related traits such as their heritability, genetic and environmental effects in the F1 progenies of a cross between *O. sativa* and *O. rufipogon*. A considerable amount of additive genetic variation was found in these families. The traits with high heritability, considerable phenotypic correlation and low seasonal variability can be used in further improvement of the F1 progenies. The results obtained were highly promising and can be utilized to develop new rice cultivars.

Borate *et al.* (2010) observed high heritability coupled with high genetic advance for grain yield, plant height, dry matter, days to first flowering and days to maturity indicated high additive gene effects in 30 chick pea genotypes.

Milatovic *et al.* (2010) found the relatively high values of heritability for flower density and yield.

Rajeshwar *et al.* (2010) evaluated twenty one diverse winged bean genotypes for heritability and genetic advance in nine quantitative traits Days to 50% flowering, days to maturity, number of pod per plant, 100 seed weight and grain yield per plant gave high heritability estimates with moderate genetic advance, which indicates additive gene effects to provide a rapid genetic improvement. The genetic advance and heritability estimates suggested that the characters e.g. days to 50% flowering, days to maturity, number of pod per plant, dry pod weight, 100 seed weight and grain yield per plant were under additive gene effects.

Ramteke *et al.* (2010) reported high heritability for days to maturity, days to 50 % flowering, plant height, nodes, oil and protein content, indicating the additive mode of gene action.

Saraswathi *et al.* (2010) observed high heritability and genetic advance as per cent of mean for number of primary branches per plant, plant height, total sucrose content, pod yield and kernel yield per plant. It indicates the role of additive gene action and hence, the usefulness of phenotypic selection for bringing improvement. High heritability was observed for all 13 characters. High genetic advance as per cent of mean was observed for number of primary branches per plant, plant height, number of filled pods per plant, HI, SP, SMK (%), 100-kernel weight, protein content, total sucrose content, pod yield and kernel yield along with high heritability. The characters days to maturity and oil percentage recorded moderate GAM along with high heritability.

Patil *at al.* (2011) observed high heritability and genetic advance for plant height, seed yield per plant and pods per plant.

Bhat *at al.* (2012) observed high heritability coupled with high genetic advance as per cent of mean for number of pods per plant, specific leaf weight in oval and leanceolate leaflet type.

Mahawar *et al.* (2013) obtained high heritability coupled with high genetic advance for harvest index, pod clusters per plant, pods per plant and seeds per plant, whereas high heritability coupled with low genetic advance was found for oil content, days to 50% flowering and seed filling period.

Reni and Rao (2013) observed high heritability coupled with high genetic advance as percent of mean for days to 50% flowering, plant height, branches per plant, pods per plant, pod length, seeds per pod, 100 seed weight, biological yield, harvest index and seed yield per plant indicating operation of additive gene action and the ample scope for improvement in these traits through simple selection.

2.3. Path coefficient analysis:

Khan *et al.* (2000) reported that pods per plant had the direct effect on seed yield followed by 100 seed weight. Pods/plant affected seed yield negatively *via* indirect effects of plant height, pod height and seeds/pod.

Raut *et al.* (2001) found that 100 seed weight exhibited the maximum positive direct effect on seed yield followed by number of clusters per plant, days to maturity and number of pods per plant.

Sudaric *et al.* (2002) reported that seed weight and number of seeds per plant had highest positive direct effect on grain yield in soybean. The obtained results suggest that the indirect selection for higher soybean grain yield using seed weight and number of seeds per plant was more efficient and more reliable than selection using the other yield components.

Bandyopadhyay (2003) recorded positive direct effect for all the nodular characters except the number of nodule in the secondary root with nitrogen fixation per plant. These observations indicated the interference of nodule number and nodule weight of leguminous plant in the selection of better plant type.

Chettri *et al.* (2003) reported that the number of seeds per pod, days to maturity, number of pods per plant and plant height positively affected seed yield while studying 18 genotypes of soybean.

Ganesamurthy and Seshadri (2004) studied 50 genotypes of soybean for their genetic variability, character association and path analysis. Path coefficient analysis showed that among all the traits studied, dry matter production contributed most directly to seed yield

Dev *et al.* (2005) reported that harvest index had the highest positive direct effect (0.728) on seed yield. The overall results indicated that significant positive correlations with seed yield were due to a relationship between biological yield and pods per plant and hence referred as the most cordial component of yield in soybean.

Sethi and Tyagi (2005) reported that biological yield per plant showed high and direct positive effect on seed yield in soybean.

Sultana *et al.* (2005) reported maximum contribution of branches per plant to seed yield followed by plant height, 100-seed weight and pod length in positive direction. Moreover, plant height, pod per plant, seed per pod and days to maturity contributed greatly to grain yield indirectly through branch per plant.

Malik *et al.* (2006) reported on the basis of path coefficient analysis that days to pod initiation had maximum direct contribution to yield followed. Therefore, it is suggested that these characters can be considered as selection criteria in improving the yield of different soybean genotypes.

Nag *et al.* (2007) studied path coefficient analysis among 12 quantitative traits in 30 genotypes of soybean in India. Path coefficient analysis revealed that the number of seeds per plant had the highest positive direct effect on seed yield per plant, followed by oil percent, pod bearing length and 100-seed weight.

Karnwal and Singh (2009) studied twenty elite breeding lines of soybean for path coefficient analysis for eighteen economically important traits. Path coefficient analysis indicated major role of pods/plant, total dry matter weight/plant, primary branches/plant, seed yield efficiency and 100-seed weight both directly and indirectly influenced seed yield. Therefore, main emphasis should be given on these traits during phenotypic selection for developing high yielding genotypes of soybean.

Showkat and Tyagi (2010) revealed that biological yield and harvest index were major characters influencing seed yield directly and indirectly. The results indicated that biological yield is responsible for manipulation of seed yield in soybean.

Machikowa and Laosuwan (2011) reported that pods per plant gave the highest positive direct effect on seed yield, followed by branches per plant. In addition, the indirect effects of most characters were high through pods per plant. The results obtained from genotypic correlations and path analyses showed that the efficiency in the selection for seed yield in early maturing soybean should increase through the selection of pods per plant.

Patil *at al.* (2011) reported that pods per plant had highest positive direct effect on seed yield per plant followed by plant height. The studies suggest that selection for pods per plant, seed yield and plant height to evolve high yielding varieties of soybean.

Mahawar *et al.* (2013) reported that plant height, number of primary branches per plant, seeds per pod, pods per plant and number of pod clusters per plant are useful components for improving seed yield.

2.4. Genetic divergence

Mahalanobis (1936) developed the D^2 statistic, which actually provides a measure of magnitude of divergence between two groups under consideration. Mahalanobis (1936) first used this technique in the form of generalized distance, which considers the variation produced by any character and their co-joint effect that it bears on other characters. Mahalonobis also pointed out that D^2 would remain constant when samples were drawn from two different populations irrespective of size of the representative samples which indicated that D^2 supplied measure of actual magnitude of divergence between two groups under comparison.

Jain and Ramgiry (2000) assessed the genetic diversity of 56 soybean genotypes of Indian and exotic origins using D^2 statistics. The genotypes were grouped into 4 clusters viz. I, II, III and IV, with 41, 9, 5 and 1 genotypes respectively. They observed the highest inter cluster distance between cluster II and IV followed by that between cluster III and IV, which may serve as potential parents for hybridization programmes. The genotypes included in the cluster with the highest inter cluster distance were genetically more divergent irrespective of their place of origin. Geographical distribution was not the sole factor for genetic diversity. Cluster mean of different characters indicated the difference for characters like plant height, pods per plant, plant weight, seeds per plant, yield per plant and harvest index.

Cluster III had the highest mean values for seed yield per plant. The highest mean seeds per plant and plant height were observed for cluster III and II, respectively. Cluster II had the highest mean for harvest index.

Shrivastava *et al.* (2001) studied the genetic divergence among 50 genotypes of soybean for nine yield component characters. Based on D^2 values, the genotypes were grouped into cluster I (10 genotypes), II (6), III (9), IV (14), and V (11). They observed the highest inter cluster divergence between cluster II and III while the lowest between cluster III and IV. They found significant variations between cluster means for all characters except harvest index.

Das *et al* (2001) studied genetic divergence among 65 soybean genotypes. Based on D^2 values, they grouped the genotypes into 13 clusters of which 6 were monogenotype. Grouping pattern of the genotypes suggested no parallelism between genetic divergence and geographical distribution of the genotypes. Variance of cluster means revealed that pods per plant and plant height had the maximum contribution towards divergence.

Vart *et al.* (2002) evaluated 56 soybean genotypes for genetic divergence. The lines were grouped into 11 clusters, and the clustering pattern was not significantly influenced by the ecogeographical distribution of the genotypes. The intra cluster values of 0 to 240.5 showed considerable diversity among clusters while the intra cluster distances for cluster I to VII suggested close relationship and almost parallel diversity among the genotypes included in these clusters. The inter cluster divergence values varied from 273.1(between II and V) to 3548.2(between I and IX). The results revealed that geographic diversity might not be an important factor in determining genetic divergence.

Chandankar *et al.* (2002) evaluated the genetic divergence among 25 genotypes of soybean using Mahalanobis D^2 statistics. They grouped the 25 genotypes into 9 clusters and found the grouping of the genotypes into the various clusters was not related to their geographic origin. The diversity among the genotypes measured by inter cluster distances was adequate for improvement by hybridization. Canonical analysis indicated genetic divergence for number of days to 50% flowering, number of branches per plant, numbers of pods per plant, biological yield per plant and oil content.

Azevedo *et al.* (2004) studied the genetic divergence among soyabean lines and cultivars without lipoxygenase. The genotypes were grouped according to the Tocher optimization method based on Mahalanobis distance and Euclidean distance. The grouping varied with the dissimilarity measure used. The Tocher method and the Euclidean distance allowed the formation of 3 groups, compared to the Tocher method and Mahalanobis distance which formed only 2 groups. Plant height contributed the most to genetic divergence.

Sethi and Tyagi *et al.* (2004) studied the genetic diversity of soybean genotypes using multivariate analysis. They grouped the genotypes into 6 clusters, with each cluster having 2-9 genotypes. Clusters IV and VI were the most diverse and hence were the most promising for use in soybean breeding programmes.

Sihag *et al.* (2004) used Mahalanobis D^2 analysis to study the genetic diversity among 160 soybean genotypes using data on 8 yield components. Data were subjected to multivariate analysis and the genotypes were grouped into 8 clusters. The most divergent clusters were V and VIII followed by VI and VIII. The clustering pattern revealed that no definite relationship existed between genetic diversity and geographic diversity. The genotypes from the same eco geographic region were classified in different clusters and genotypes from different eco geographic region were classified into one cluster.

Malik *et al.* (2009) assayed the genetic variation of seed protein by SDS-PAGE for ninety-two accessions of soybean (*Glycinemax*). The germplasm represented five different origins/sources (Pakistan, USA, AVRDC, North Korea and Japan). Ten major bands were recorded out of total 26 bands detected, while 50% of total were polymorphic. Dendrogram constructed using Ward’s method divided the accessions in two main groups consisting of four clusters. The results of cluster analysis indicated that genetic diversity between Pakistani and US or AVRDC accessions is much larger that the genetic diversity between Pakistani and North Korean or Japanese accessions. Although cluster analysis completely separated most of the Pakistani accessions from USA and AVRDC accessions, but could not distinguish between the accessions from Japan and North Korea. As the accessions from various sources differed considerably, it was difficult to establish any relationship between origin and clustering pattern.

Iqbal *et al.* (2010) reported significant differences among genotypes at multivariate level in terms of days to maturity, plant height at maturity, number of branches per plant, number of pods per plant, 100-seed weight (g), oil content, grain yield per plant (g), biological yield per plant (g) and harvest index, which indicate the existence of genetic variation.

Husain and Srivastav (2011) reported that genetic diversity studied in the past is best applied to the future when germplasm collection and breeding programme operate in cohesion. Soybean has great diversity, its global germplasm collection being 1,70,000, out of which as many as 45,000 accessions may be unique. Despite such diversity fewer than 1000 accessions have been used in breeding. The reasons for this are is agronomic inferiority of germplasm, difficulty in assessing the value of alleles for yield and other complexity inherited traits.

CHAPTER III

MATERIALS AND METHODS

The present experiment was conducted during *kharif* 2013. The details of the materials used and techniques adopted during the course of investigation are described in this chapter.

3.1. Experimental site

The experiment was conducted in the experimental area of College of Agriculture, Gwalior; M.P. Field was fairly uniform with gentle slope, adequate drainage and normal fertility status

3.2. Experimental material

The experimental material consisted of 40 genotypes of soybean collected from College of Agriculture, Gwalior. Details of genotypes used in present investigation are given in Table 3.2.

3.3. Experimental details

The experiment was done in Randomized Complete Block Design (RCBD) with three replications and seeds were sown on 2nd July 2013. The row length was 4m and the number of rows per plot was 3 with row to row spacing of 30 cm. Space between plant to plant was maintained at 7.5 cm.

A random selection of five plants in each plot was made and the observations were recorded on each selected plant. The mean values of each character under study were computed on the basis of five plants for each genotype in each replication.

Table 3.1: Detail of experimental material used for present investigation

Genotype No.	Name of genotype	Genotype No.	Name of genotype
V1	KDS 726	V21	RVS 2002-22
V2	PS 1539	V22	RKS 111
V3	DS 3050	V23	BAUS 27
V4	SL 983	V24	DSb 25
V5	DS 2961	V25	RSC 10-17
V6	RKS 109	V26	NRC 96
V7	SL 995	V27	RVS 2002-19
V8	DS 3047	V28	MAUS 613
V9	AMS1001	V29	NRC 97
V10	JS 20-79	V30	DSb 23-2
V11	MACS 1419	V31	JS 20-89
V12	NRC 98	V32	KBS 100-2012
V13	RVS 2002-4	V33	VLS 87
V14	KDS 722	V34	KDS 743
V15	NRC 111	V35	BAUS 96
V16	NRC 107	V36	MACS 1410
V17	MACS 1410	V37	MACS 1370
V18	JS 20-53	V38	VLS 86
V19	PS 1543	V39	PS 1540
V20	Himso 1685	V40	RSC 10-04

3.4. Observation recorded

The following observations were recorded on 5 plants for each entry:

1. Days to 50% flowering:

Number of days taken from the date of sowing to the day on which 50% of the plants in a genotype initiate first flower was recorded as days to flowering.

2. Days to maturity

Number of days taken from date of sowing to physiological maturity of the plant was recorded as days to maturity.

3. Plant height (cm)

Height of the main stem from the ground level to the top of the main stem was measured in centimeters at the time of harvesting.

4. Number of primary branches per plant

The number of primary branches per plant was recorded as total number of primary branches on the main stem.

5. Number of pods per plant

This was recorded by counting the number of pods present on main stem and branches in each of the five selected plants.

6. Number of seeds per pod

Number of seeds per pod was counted from fifty randomly selected pods in each of the five selected plants.

7. Number of three and two seeded pods per plant

The number of three and two seeded pods of five randomly selected plants were counted separately and average were workout as number of three and two seeded pods per plant.

8. 100 grain weight (g)

100 seed weight was computed by weighing 100 seeds which are randomly chosen filled seeds from a complete sample made by mixing the seeds of all the five plants in each replication and recorded in grams.

9. Seed yield per plant (g)

The seed yield per plant was recorded from each selected individual after harvest.

10. Harvest index:

The harvest index is considered as the yield of economic part expressed as the percentage of the total biological yield in the term of dry matter.

$$\text{Harvest index} = \frac{\text{Economic yield (seed yield)}}{\text{Biological yield}} \times 100$$

3.5 Statistical analysis:

1. Analysis of variance:

Data were analysed by method outlined by Panse and Sukhatme (1954) using the mean values of five randomly selected plants in each treatment for each replication. The model of analysis of variance table is given below:

ANOVA table for the design of experiment:

Source	Degree of freedom	Mean sum of squares	Variance ratio
Replication	(r-1)	M_r	M_r/M_e
Treatment	(t-1)	M_t	M_t/M_e
Error	(r-1) (t-1)	M_e	-
Total	rt-1	-	-

where, r = Number of replications

t = Number of treatments

2. Estimation of phenotypic and genotypic coefficients of variation:

The phenotypic and genotypic coefficients of variation in per cent were computed by the following formulae given by Burton (1952).

$$\text{Phenotypic Coefficient of Variation (PCV)} = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

$$\text{Genotypic Coefficient of Variation (GCV)} = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

The coefficient of variation were categorized as proposed by Sivasubramanian and Madhava Menon (1973)

0-10% - Low
10-20% - Moderate
>20% - High

3. Estimation of heritability and genetic advance:

Heritability in per cent in broad sense was estimated by the following formula given by Singh and Choudhary (1977):

$$\text{Heritability } (h^2) = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

Heritability values are catagorised as low, moderate and high (Robinson *et al.,* 1949) and are given below,

0-30% - Low

30-60% - Moderate

60% and above - High

The estimates of expected genetic advance from selection, G(s), was obtained by the formula suggested by Robinson *et al.* (1949).

$$G(s) = k \times h^2 \times \sigma p$$

where,

k = Selection differential in standard deviation units which is 2.06 for 5% selection intensity,

h^2 = Heritability in broad sense, and

σ_p = Phenotypic standard deviation

Genetic advance was expressed as percentage of mean by using the formula suggested by Johnson *et al.*(1955).

$$\text{Genetic advance as percentage of mean} = \frac{\text{Genetic advance}}{\text{Grand mean}} \times 100$$

Genetic advance as percent of mean was classified as low, moderate and high (Johnson *et al*., 1955) and values are given below:

0-10% - Low

10-20% - Moderate

20% and above - High

4. Path coefficient analysis:

The proportion of direct and indirect contributions of various characteristics to the total correlation coefficients with grain yield per plant, was estimated through path coefficient analysis as suggested by Wright (1921, 1934) and elaborated by Dewey and Lu (1959).

Path coefficient is a standardized partial regression, which measures the direct influence of one variable upon another and allows partition of correlation coefficient into components of direct and indirect effects.

To estimate various direct and indirect effects, the following set of simultaneous equations were formed and solved.

$r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \ldots + r_{1l}P_{ly}$

$r_{2y} = r_{2y}P_{1y} + P_{2y} + r_{23}P_{3y} + \ldots + r_{2l}P_{ly}$

.

.

$r_{ly} = r_{l1}P_{1y} + r_{l2}P_{2y} + r_{l3}P_{3y} + \ldots + P_{ly}$

where,

r_{1y} to r_{ly} = Coefficient of correlation between causal factor 1 to l and dependent character y,

r_{12} to $r_{l-1,l}$ = Coefficient of correlation among causal factors themselves, and

P_{1y} to P_{ly} = Direct effects of characters 1 to l on character y.

Residual effect, which measures the contribution of the characters not considered in the causal scheme, was obtained as:

Residual effect (P_{RY}) = $\sqrt{1 - R^2}$

where,

$$R^2 = \sum_{iy} P_{iy}^2 + 2\sum_{\substack{i \neq j \\ i > j}} P_{iy}\, P_{jy}\, r_{ij}$$

5. Multivariate analysis:

(a) Estimation of Wilk's (Λ) criterion:

To test the significance of difference between lines, taking all the characters simultaneously, 'V' statistic was calculated which was based on Wilk's (Λ) criterion (Wilk, 1932). The sum of squares and sum of products of error and error + variety were utilized for estimation of "Λ".

To calculate the value of "Λ" following relationship was used:

$$\text{"}\Lambda\text{"} \quad = \quad \frac{|E|}{|E + V|}$$

where,

$|E|$ was the determinant of error sum of squares and sum of products matrix and $|E + V|$ was the determinant of the "error + variety' sum of squares and sum of products matrix.

χ^2 was used to test the significance of "Λ" as

$$\chi^2_{pq} = V = -\, m \log_e \Lambda$$

where,

m = n - $\frac{p + q + 1}{2}$ with pq degree of freedom.

where,

n = total number of observations –1,

p = number of characters,

q = k – 1, and

k = number of lines

(b) Estimation of D^2-statistic:

To estimate divergence between two lines Mahalanobis (1936) D^2-statistic was used. He defined generalized distance between two lines as:

$$\Delta^2 = \sum\sum \lambda^{ij}\delta_i\delta_j$$

where,

λ^{ij} = Reciprocal matrix of the common dispersion matrix λ_{ij},

δ_i = Difference between mean values of two lines for the i^{th} character, and

δ_j = Difference between mean values of two lines for the j^{th} character.

D^2-statistic is the sample estimate of the generalized distance which is estimated as:

$$D^2 = \sum_{i,j=1}^{P} s^{ij} d_i d_j$$

where, s^{ij} and d_i are the sample estimates of λ^{ij} and δ_i, respectively. For calculating D^2 values inversion of matrix was required which is quite cumbersome. To overcome this difficulty original correlated, unstandardized character means (X_i) were transformed to uncorrelated, standardized variables (Y_i) by Pivotel condensation method (Rao, 1952). D^2 between any pairs of populations, for example population 1 and 2, was then estimated as:

$$D_p^2 = \sum_{i=1}^{p} (Y_{i1} - Y_{i2})^2$$

where, p = number of characters used for estimation of divergence.

(c) Determination of population constellations:

Population constellations were determined by Tocher's method described by Rao (1952). A cluster or constellation may be explained as a group of populations or genotypes such that any two populations belonging to the same cluster showed, on the average, a smaller D^2 value than those belonging to different clusters.

Tocher suggested that two closely related populations of low D^2 value be pooled together and then a third population of similar D^2 value be added to this group such that it did not increase the average D^2 value appreciably. This process is continued. Any population, which sharply increases the average D^2 value should not be included in that group.

After formation of first cluster, the process is repeated to form second, third clusters, using remaining populations until all populations are included in one or the other cluster. After cluster formation average intra and inter-cluster distances were calculated. The square root of corresponding average D^2 values represents the distance within and between groups.

(d) Canonical analysis:

To visualize multidimensional picture of variability among genotypes canonical analysis was done. Canonical roots were estimated by transformation of correlated, unstandardized means into uncorrelated, standardized variables (Rao, 1952). From these uncorrelated standardized variables, matrix of variance and covariance (matrix A) was obtained by computing sums of squares and sums of products. From matrix A, matrix $(A)^p$ was derived, where p is the number of characters. The column totals of matrix $(A)^p$ were obtained and each total was divided by the highest value among them to obtain the first approximation trial vector. The canonical variates were determined by iteration. The vectors were then standardized by dividing them with correlated sum of squares of these vectors. The first root, λ_1, was calculated as the p^{th} root of the highest column total of the last approximation.

The second root, λ_2, was obtained by transforming the original $(A)^p$ matrix to reduced matrix $(B)^p$. Each i × j^{th} element of $(B)^p$ was calculated as: (i, j)th element of $(A)^p = \lambda_1 \times i^{th}$ element × j^{th} element of the vector.

Estimation of second and third canonical root was done following the same procedure as in the case of 'A' was followed. The utility of estimation of other roots depends on the proportions of the sum of squares accounted for by the first three roots.

CHAPTER-IV
RESULTS

A field experiment comprising of 40 soybean genotypes was laid out in a randomised block design with all recommended agronomic practices during *kharif* 2013. The extent of genetic variability, direct and indirect effect of yield attributing characters on seed yield through path analysis and genetic diversity was studied. The results of the present investigation are presented under the following headings.

4.1 Genetic variability, heritability and genetic advance

4.2 Genetic diversity

4.3 Path analysis

4.1 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

The analysis of variance for 11 characters was carried out to partition the total variance due to genotypes and other sources. Analysis of variance revealed highly significant differences among genotypes in respect of all the characters studied. The mean sum of squares of all the 11 characters studied is presented in Table 4.1. The mean performance of these genotypes for various characters is presented in Appendix I. Range, mean, phenotypic and genotypic coefficient of variation, heritability estimates and predicted genetic advance as per cent of mean for characters studied are presented in Table 4.2.

4.1.1 Days to 50 per cent flowering

The variability observed for days to 50 per cent flowering was high, as reflected by its wide range from 31.67 days (NRC 107) to 59.00 days (RSC 10-17) with an average value of 50.35 days. PCV and GCV were moderate being 10.42 per cent and 10.20 per cent, respectively. The magnitude of heritability estimated was very high (95.9%) with high expected genetic advance of 20.58 as per cent of mean.

4.1.2 Days to maturity

Days to maturity ranged from 92.33 days (NRC 107) to 121.00 days (BAUS 96). The average value for the trait was 110.82 days. The PCV and GCV values were low (7.17% and 7.12%, respectively). High heritability estimate of 98.7 per cent was recorded with moderate (14.56%) expected genetic advance as percent of mean.

4.1.3 Plant height

The mean plant height was 65.41 cm with a range of 34.80 cm (VLS 87) to 91.67 cm (MACS 1419). This trait exhibited high PCV and moderate GCV value (20.14% and 19.66%, respectively).. The trait had a high heritability of 95.3 per cent and high expected genetic advance as percent of mean (39.54%).

4.1.4 Number of primary branches

The number of primary branches exhibited a considerable variation, which ranged from 2.33 (KDS 722) to 5.67 (RSC 10-17) with overall mean of 3.41. The trait revealed high PCV (26.96%) and GCV (20.68%) values. The heritability recorded was moderate (58.8%) with high genetic advance as percent of mean (32.55%).

4.1.5 Number of pods per plant

Number of pods per plant showed a wide variation, which ranged from 18.67 (BAUS 27) to 111.67 (JS 20-89) and mean value for this trait was 42.85. The PCV (45.65%) and GCV (44.46%) were high for this trait. The heritability estimate was high (94.9%) with high genetic advance as percent of mean (89.22%).

4.1.6 Number of seeds per pod

Number of seeds per od ranged from 2.00 (DSb 23-2) to 2.78 (JS 20-89) with a mean of 2.40. This trait exhibited moderate PCV and low GCV value (10.26% and 8.24%, respectively). It had high heritability of 64.6 per cent with moderate genetic advance as percent of mean (13.75%). Genotypes KDS 726, DS 3050, AMS 1001, JS 20-79, MACS 1419, KDS 722, NRC 107, RSC 10-17, MACS 1370 and PS 1540 were at par to JS 20-89.

4.1.7 Number of three seeded pods per plant:

A very wide range of 0.00 (DSb 23-2) to 95.33 (JS 20-89) was observed for number of three seeded pods per plant with the mean value of 17.18. The high PCV and GCV values of 96.22 per cent and 96.61 per cent, respectively were exhibited for this trait. The heritability observed was 96.7 per cent with high genetic advance of 191.73 as per cent of mean.

4.1.8 Number of two seeded pods per plant

Number of two seeded pods per plant ranged from 5.00 (BAUS 27) to 53.00 (NRC 97) with a mean of 24.03. High PCV (51.01%) and GCV (48.60%) values were recorded for this trait with high heritability value of (90.8%). Genetic advance as per cent mean was also high (95.34%) for this trait. Genotype, NRC 97 was at par to NRC 96.

4.1.9 100 seed weight:

Seed index (100 seed weight) ranged from 10.37 g (SL 955) to 14.21 g (PS 1540) with a mean of 11.99 g. This trait exhibited moderate PCV and low GCV value (10.02% and 6.56%, respectively). It had moderate heritability of 42.9 per cent with low genetic advance as percent of mean (8.84%). Genotypes PS 1539, KDS 722, MACS 1410, JS 20-53, NRC 96 and NRC 97 were at par to PS 1540.

4.1.10 harvest index:

The harvest index was 18.47% and it ranged from 10.70% (SL 983) to 35.21% (JS 20-89). The PCV and GCV values for this trait were high (30.20% and 28.12%, respectively). Heritability was high (86.7%) with high expected genetic advance as percent of mean (53.93%).

4.1.11 Seed yield per plant

The mean seed yield per plant ranged from 4.21 g (SL 983) to 17.05 g (JS 20-89) with a mean value of 8.51 g. High estimate of PCV (36.31%) and GCV (35.16%), heritability (93.8%) and genetic advance as per cent of mean (70.15%) was observed.

Table 4.1: Analysis of variance for eleven quantitative characters in soybean

S. No.	Characters	Mean sum of squares		
		Replication	Genotypes	error
1.	Days to 50% flowering	0.5312	80.2388**	1.14021.
2.	Days to maturity	1.5000	187.5627**	0.8419
3.	Plant height (cm)	1.9687	504.3288**	8.1501
4.	Number of primary branches	1.1083	1.8374**	0.3476
5.	Number of pods/plant	44.4219	1108.6658**	19.6473
6.	Number of seeds/pod	0.3745	0.1394**	0.02154
7.	Number of three seeded pods/plant	51.9882	802.7817**	9.1115
8.	Number of two seeded pods/plant	33.0234	422.7758**	1.3854
9.	100 seed weight (g)	0.6924	2.6839**	0.8257
10.	Harvest index	4.1640	85.0500**	4.1234
11.	Seed yield/plant (g)	0.3638	27.4284**	0.5927

** Significant at p=0.01

Table 4.2: Estimation of range, mean and different genetic parameters for different characters in 40 genotypes of soybean

S. No	Characters	Mean	Range	PCV (%)	GCV (%)	Broad sense Heritability (%)	Genetic advance	Genetic advance as % of mean
1.	Days to 50% flowering	50.35	31.67-59.00	10.42	10.20	95.9	10.36	20.58
2.	Days to maturity	110.82	92.33-121.00	7.17	7.12	98.7	16.14	14.56
3.	Plant height (cm)	65.41	34.80-91.67	20.14	19.66	95.3	25.86	39.54
4.	Number of primary branches	3.41	2.33-5.67	26.96	20.68	58.8	1.11	32.55
5.	Number of pods/plant	42.85	18.67-111.67	45.65	44.46	94.9	38.23	89.22
6.	Number of seeds/pod	2.40	2.00-2.78	10.26	8.24	64.6	0.33	13.75
7.	Number of three seeded pods/plant	17.18	0.00-95.33	96.22	94.61	96.7	32.94	191.73
8.	Number of two seeded pods/plant	24.03	5.00-53.00	51.01	48.60	90.8	22.91	95.34
9.	100 seed weight (g)	11.99	10.37-14.21	10.02	6.56	42.9	1.06	8.84
10.	Harvest index	18.47	10.70-35.21	30.20	28.12	86.7	9.96	53.93
11.	Seed yield/plant (g)	8.51	4.21-17.05	36.31	35.16	93.8	5.97	70.15

4.2 GENETIC DIVERSITY:

The pooled divergence for all the characters within genotypes, tested by the Wilk's criterion, was significant. Hence the analysis of genetic divergence among genotypes used in the study was considered relevant.

4.2.1 D^2 analysis:

The mean values of the forty genotypes were converted into standardized uncorrelated mean values and D^2 values were computed for all possible 780 pairs of genotypes. The highest D^2 value of 2191.28 was observed between the genotype JS 20-79 and DSb 25 and the lowest D^2 value of 27.49 between genotype DS 3047 and MAUS 613.

4.2.1.1 Group constellation

Six clusters were formed by grouping all the 40 genotypes in such a way that genotypes within each cluster had smaller D^2 value than those in other clusters (Table 4.3). Cluster pattern revealed that, cluster III was largest consisting of 13 genotypes, followed by cluster I with 10 genotypes, while the clusters II and V had eight and six genotypes, respectively. The cluster VI was solitary. Cluster IV had 2 genotypes.

4.2.1.2 Intra and inter-cluster average distance:

Average D^2 values of intra and inter cluster distance are given in Table 4.4. Maximum differences among the genotypes within the same cluster (intra cluster) was shown by cluster II (5.368) followed by cluster I (4.991) and cluster III (4.507), while cluster VI had the no i.e. zero intra cluster distance followed by cluster IV (3.119) and cluster V (3.960). Inter cluster distances varied from 7.274 to 77.159. Cluster I and VI showed maximum inter cluster distance (77.159) followed by cluster V and VI (75.186), cluster III and VI (71.403), cluster IV and VI (41.719), cluster II and VI (40.641), cluster I and IV (28.270) and cluster III and IV (22.677). The lowest inter cluster distance was calculated between cluster I and III (7.274) followed by cluster I and II (8.323). Cluster VI was farthest to other clusters.

4.2.1.3 Cluster means

The cluster means in respect of 11 characters are presented in Table 4.5

1. Days to 50% flowering:

The cluster mean was lowest (43.78 days) for cluster V.

2. Days to maturity:

Cluster mean was lowest (97.78 days) for cluster V.

3. Plant height:

Cluster mean was lowest (54.83 cm) for cluster V and highest (83.73 cm) for cluster IV.

4. Number of primary branches:

Cluster mean was highest (5.67) for cluster IV.

5. Number of pods per plant:

Cluster mean was highest (111.67) for cluster VI.

6. Number of seeds per pod:

Cluster mean was highest (2.78) for cluster VI.

7. Number of three seeded pods per plant:

Cluster mean was highest (95.33) for cluster VI.

8. Number of two seeded pods per plant:

Cluster mean was highest (37.92) for cluster II.

9. 100 seed weight:

Cluster mean was highest (13.17 g) for cluster IV.

10. Harvest index:

Cluster mean was highest (35.21%) for cluster VI.

11. Seed yield per plant:

Cluster mean was highest (17.05 g) for cluster VI.

4.2.1.4 Cluster characteristics

When observed for early flowering habit, NRC 107 in the cluster V was early flowering with mean number of days to 50 per cent flowering being 31.67 days, with minimum number of days to maturity of 92.33 days, and with minimum plant height of 44.00 cm, indicating genotypes of this cluster have characteristic early flowering and early maturing habit and dwarf type plants.

Solitary cluster VI with genotype JS 20-89 had highest seed yield per plant (17.05 g) with highest pod per plant (111.67), seeds per pod (2.78), number of three seeded pods per plant (95.33) and harvest index (35.21%).

Cluster I with genotype VLS 87 showed minimum height of the plant (34.80 cm), while cluster II with genotype NRC 97 showed highest number of two seeded pods per plant (53.00).

Highest value for number of primary branches (5.67) and 100 seed weight (14.21 g) was observed in cluster IV with genotypes RSC 10-17 and PS 1540, respectively.

4.2.1.5. Percent contribution of each character:

The percent contribution of 11 characters towards total genetic divergence is listed in Table 4.6. The selection and choice of parents mainly depends upon contribution of characters towards divergence. In the present investigation the highest contribution in manifestation of genetic divergence was exhibited by days to maturity (44.87%) followed by plant height (16.92%), number of three seeded pods per plant (11.41%), days to 50% flowering (9.36%), number of pods per plant (7.44%) and seed yield per plant (5.51%).

Table 4.3: Distribution of 40 genotypes into different clusters

S. No.	Cluster No.	No. of genotypes	Name of genotype
1	**I**	**10**	SL 955, NRC 111, MACS 1410, JS 20-53, Himso 1685, DSb 23-2, KBS 100-2012, VLS 87, BAUS 96 and RSC 10-04
2	**II**	**8**	PS 1539, DS 3047, JS 20-79, NRC 98, PS 1543, NRC 96, NRC 97 and MACS 1410
3	**III**	**13**	KDS 726, DS 3050, SL 983, DS 2961, RKS 109, AMS 1001, MACS 1419, RKS 111, BAUS 27, DSb 25, MAUS 613, KDS 743 and MACS 1370
4	**IV**	**2**	RSC 10-17 and PS 1540
5	**V**	**6**	RVS 2002-4, KDS 72, NRC 107, RVS 2002-22, RVS 2002-19 and MAUS 613
6	**VI**	**1**	JS 20-89

Table 4.4: Average intra and inter cluster D^2 values of 40 genotypes of soybean

Cluster	**I**	**II**	**III**	**IV**	**V**	**VI**
I	4.991	8.323	7.274	28.270	10.068	77.159
II		5.368	14.055	15.148	12.759	40.641
III			4.507	22.677	10.285	71.403
IV				3.119	34.610	41.719
V					3.960	75.186
VI						0.000

Table 4.5: The mean values of eleven characters for 6 clusters in 40 genotypes of soybean

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches	No. of pods/ plant	No. of seeds/ pod	No. of 3 seeded pods/ plant	No. of 2 seeded pods/ plant	100 seed weight (g)	Harvest index	Seed yield/plant (g)
I	52.97	112.80	58.59	3.30	35.83	2.14	5.17	29.30	11.83	18.53	8.15
II	48.79	110.08	68.98	3.62	58.67	2.38	22.38	37.92	12.87	21.48	11.57
III	51.49	115.41	69.23	3.21	33.67	2.54	16.28	14.28	11.25	15.58	6.55
IV	55.33	113.67	83.73	5.67	69.33	2.65	37.33	21.33	13.17	17.54	9.58
V	43.78	97.78	54.83	2.94	33.06	2.42	12.56	18.06	12.19	18.13	7.48
VI	51.33	109.67	82.13	3.67	111.67	2.78	95.33	28.00	12.79	35.21	17.05

Table 4.6: Per cent contribution of different traits towards total diversity

S. No.	Characters	Times ranked first	Per cent contribution
1	Days to 50% flowering	73	9.36
2	Days to maturity	350	44.87
3	Plant height (cm)	132	16.92
4	Number of primary branches	1	0.13
5	Number of pods/plant	58	7.44
6	Number of seeds/pod	0	0.00
7	Number of three seeded pods/plant	89	11.41
8	Number of two seeded pods/plant	26	3.33
9	100 seed weight (g)	1	0.13
10	Harvest index	7	0.90
11	Seed yield/plant (g)	43	5.51

4.2.2 Canonical analysis:

How far divergence between the genotypes determined through D^2 values agree with those determined by canonical analysis was also examined. Canonical analysis deals with the replacement of the measurements of a number of mutually correlated characters by a relatively few measurements obtained as linear combinations of large number of such measurements. The divergence was determined by canonical analysis following the procedure given by Rao (1952). The standardized best linear functions (canonical vectors) were obtained and the first four canonical vectors and percentage of variation absorbed by them are presented in Table 4.7. The sum of all canonical roots was 8752.22, which the $Root_1$ = 4392.78, $Root_2$ = 2109.92, $Root_3$ = 778.60 and $Root_4$ = 520.22. The first canonical root absorbed 50.19 per cent of total variability and second one accounted for 24.11 per cent of variability. Further, first two roots together accounted for 74.30% of the diversity indicating that the difference for these traits in these genotypes was nearly complete in the two phases.

The relative contribution of characters towards genetic divergence was found out from the canonical coefficients of first two canonical vectors. Days to maturity recorded the highest coefficient of 0.8054 followed by plant height, days to 50% flowering, number of pods per plant, number of three seeded pods per plant and seed yield per plant recording 0.3928, 0.3374, -0.1921, 0.1456 and 0.1395, respectively, as reflected by the first vector. In the second vector, the maximum coefficient of 0.6433 was recorded by number of three seeded pods per plant followed by number of pods per plant, seed yield per plant and plant height recording 0.5952, 0.3255 and 0.2622, respectively.

Table 4.7: Values of first four canonical vector, which supply best linear function of genotypes

Characters	**Canonical root**			
	CR1	**CR2**	**CR3**	**CR4**
Days to 50% flowering	0.3374	-0.0573	-0.4762	0.4360
Days to maturity	0.8054	-0.1287	0.1999	-0.4675
Plant height (cm)	0.3928	0.2622	0.3482	0.5104
Number of primary branches	-0.0309	0.0928	0.1057	0.0693
Number of pods/plant	-0.1921	0.5952	0.2368	-0.1174
Number of seeds/pod	-0.0152	0.1075	-0.2689	-0.1667
Number of three seeded pods/plant	0.1456	0.6433	-0.3764	-0.3427
Number of two seeded pods/plant	-0.0658	0.0124	0.5261	-0.1255
100 seed weight (g)	0.0085	0.1021	0.1741	0.1755
Harvest index	-0.0035	0.0815	0.1513	0.0979
Seed yield/plant (g)	0.1395	0.3255	-0.0281	0.3330
Percentage of variation absorbed	**50.19**	**24.11**	**8.90**	**5.94**

4.3 Path analysis:

The direct and indirect effects of the studied characters on the seed yield per plant at genotypic and phenotypic levels are presented in Table 4.8 and 4.9.

4.3.1. Direct effects:

Path coefficient analysis based of genotypic correlation indicate that harvest index registered the maximum positive direct effect of 0.853 followed by number of two seeded pods per plant, number of three seeded pods per plant, number of primary branches and number of seeds per pod registering 0.709, 0.604, 0.571 and 0.305, respectively (Table 4.8). Number of pods per plant recorded the highest negative direct effect of –0.970 followed by plant height (-0.216). The trait like days to maturity exhibited low positive direct effect (0.017) on seed yield per plant, while the traits like 100 seed weight and days to 50% flowering registered negative direct effects of -0.126 and -0.045 but the values being low in magnitude.

4.3.2. Indirect effects:

4.3.2.1 Days to 50% flowering:

Days to 50% flowering recorded the maximum positive indirect effect of 0.103 *via* number of primary branches followed by number of pods per plant (0.101). The maximum negative indirect effect of –0.132 was seen *via* harvest index followed by number of two seeded pods per plant (-0.104).

4.3.2.2 Days to maturity:

The highest positive indirect effect of 0.154 was recorded *via* number of primary branches while maximum maximum negative indirect effect of –0.235 was observed through harvest index.

4.3.2.3 Plant height:

Plant height recorded the maximum positive indirect effect of 0.270 *via* number of primary branches followed by number of three seeded pods per plant (0.226), harvest index (0.144) and number of seeds per pod (0.101). Maximum Negative indirect effects of –0.388 was observed through number of pods per plant.

4.3.2.4 Number of primary branches:

The indirect effects of number of primary branches *via* days to maturity, number of seeds per pod, number of three seeded pods per plant and number of two seeded pods per plant were positive and the maximum positive indirect effect of 0.212 was seen through number of two seeded pods per plant followed by number of three seeded pods per plant (0.177). Its indirect effects *via* days to 50% flowering, plant height, number of pods per plant, 100 seed weight and harvest index were negative and the maximum negative indirect effect of –0.522 was observed through number of pods per plant.

4.3.2.5 Number of pods per plant:

Number of pods per plant recorded the maximum positive indirect effect of 0.475 *via* number of three seeded pods per plant followed by harvest index (0.453), number of two seeded pods per plant (0.432) and number of primary branches (0.307). The indirect effects *via* plant height and 100 seed weight were negative and the maximum negative indirect effects of –0.086 was observed through plant height.

4.3.2.6 Number of seeds per pod:

Number of seeds per pod exhibited maximum positive indirect effects of 0.427 *via* number of three seeded pods per plant. The maximum negative indirect effect of -0.393 was observed through number of two seeded pods per plant followed by number of pods per plant (-0.224).

4.3.2.7 Number of three seeded pods per plant:

Number of three seeded pods per plant recorded the maximum positive indirect effect of 0.385 *via* harvest index followed by number of seeds per pod (0.216) and number of primary branches (0.168). The indirect effects *via* days to 50% flowering, plant height, number of pods per plant and 100 seed weight were negative and the maximum negative indirect effects of –0.764 was observed through number of pods per plant.

4.3.2.8 Number of two seeded pods per plant:

Number of two seeded pods per plant exhibited maximum positive indirect effects of 0.365 *via* harvest index followed by number of primary branches (0.171). The maximum negative indirect effect of -0.592 was observed through number of pods per plant followed by number of seeds per pod (-0.170).

4.3.2.9 100 seed weight:

The correlation of 100 seed weight was positive and highly significant (0.334). This is due to indirect positive effects through number of two seeded pods per plant (0.378), number of primary branches (0.246), harvest index (0.197) and number of three seeded pods per plant (0.191). Its indirect effects *via* days to maturity, plant height and number of pods per plant were negative and the maximum negative indirect effect of -0.565 was observed through number of pods per plant.

4.3.2.10 Harvest index:

Harvest index recorded the maximum positive indirect effect of 0.303 *via* number of two seeded pods per plant followed by number of three seeded pods per plant (0.273). The maximum negative indirect effect of harvest index on seed yield per plant was seen *via* number of pods per plant.

Table 4.8: Genotypic path

Characters	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches	No. of pods/ plant	No. of seeds/ pod	No. of 3 seeded pods/plant	No. of 2 seeded pods/ Plant	100 seed weight	Harvest index	Corre-lation with seed yield
Days to 50% flowering	**-0.045**	0.010	-0.064	0.103	0.101	0.013	0.023	-0.104	0.032	-0.132	-0.062
Days to maturity	-0.027	**0.017**	-0.092	0.154	0.021	0.013	0.005	-0.043	0.034	-0.235	-0.154
Plant height	-0.013	0.007	**-0.216**	0.270	-0.388	0.101	0.226	0.058	-0.001	0.144	0.187
Number of primary branches	-0.008	0.004	-0.102	**0.571**	-0.522	0.018	0.177	0.212	-0.054	-0.033	0.264
Number of pods/plant	0.005	0.000	-0.086	0.307	**-0.970**	0.071	0.475	0.432	-0.074	0.453	0.613
Number of seeds/pod	-0.002	0.001	-0.071	0.034	-0.224	**0.305**	0.427	-0.393	-0.003	-0.069	0.003
Number of three seeded pods/plant	-0.002	0.000	-0.081	0.168	-0.764	0.216	**0.604**	0.043	-0.040	0.385	0.530
Number of two seeded pods/plant	0.007	-0.001	-0.018	0.171	-0.592	-0.170	0.036	**0.709**	-0.068	0.365	0.440
100 seed weight	0.011	-0.005	-0.002	0.246	-0.565	0.008	0.191	0.378	**-0.126**	0.197	0.334

Harvest index	0.007	-0.005	-0.036	-0.022	-0.515	-0.025	0.273	0.303	-0.029	**0.853**	0.804

Residual = 0.2079

Table 4.9: Phenotypic path

Characters	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches	No. of pods/ plant	No. of seeds / pod	No. of 3 seeded pods/ plant	No. of 2 seeded pods/ plant	100 seed weight	Harvest index	Correlation with seed yield
Days to 50% flowering	**0.027**	-0.008	-0.018	0.020	0.001	-0.001	0.010	-0.018	0.004	-0.077	-0.059
Days to maturity	0.016	**-0.013**	-0.026	0.029	0.000	-0.002	0.002	-0.009	0.003	-0.152	-0.151
Plant height	0.008	-0.005	**-0.064**	0.049	-0.006	-0.015	0.105	0.011	0.001	0.092	0.173
Number of primary branches	0.004	-0.003	-0.022	**0.141**	-0.007	-0.001	0.067	0.032	-0.003	-0.024	0.183*
Number of pods/plant	-0.003	0.000	-0.024	0.060	**-0.016**	-0.008	0.215	0.087	-0.008	0.279	0.583**

Number of seeds/pod	0.000	0.000	-0.019	0.002	-0.002	**-0.052**	0.170	-0.070	0.002	-0.031	0.001
Number of three seeded pods/plant	0.001	0.000	-0.024	0.033	-0.012	-0.031	**0.286**	0.008	-0.004	0.248	0.505**
Number of two seeded pods/plant	-0.003	0.001	-0.005	0.030	-0.009	0.025	0.015	**0.148**	-0.006	0.231	0.427**
100 seed weight	-0.005	0.002	0.002	0.024	-0.006	0.004	0.056	0.042	**-0.021**	0.087	0.186*
Harvest index	-0.004	0.003	-0.010	-0.006	-0.008	0.003	0.122	0.059	-0.003	**0.583**	0.739**

Residual = 0.3595

CHAPTER-V
DISCUSSION

The investigation entitled "**Genetic studies in Soybean (*Glycine max* L. Merill)**" was carried out during *kharif* 2013 at Research Farm, College of Agriculture, Gwalior. The improvement that can be brought out for a character, in a genotype character depends entirely on the magnitude of the genetic variability for that character and heritability. The knowledge of the estimates of variability in the source population in respect of yield and its heritable components is a pre-requisite for any breeding programme aimed at improving the yield and other characters. Attempts to improve a character by selection would be futile unless a major portion of the variation is heritable. Thus it is imperative to have information on both phenotypic and genotypic coefficient of variation to get an idea regarding the heritability of the character. The information on phenotypic coefficient of variation and heritability will be handy for prediction of the genetic advance possible by selection for the character. The genetic parameters such as genotypic and phenotypic coefficient of variation and genetic advance help to split the total variability into heritable and non-heritable components. The knowledge on path coefficient analysis for direct and indirect effects of yield attributing characters on yield is also necessary. Measure of genetic divergence reveals the differences in gene frequencies. Mahalanobis generalized distance estimated by D^2 statistic Tocher (Rao, 1952) is a unique tool for discriminating populations by considering a set of parameters together.

Results of the present investigation are discussed in the light of available literature and explanation wherever possible is provided for the trends revealed by these observations under following heads viz., variability, heritability and genetic advance, genetic divergence and path analysis.

5.1 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

In the present investigation, 40 diverse genotypes of soybean were studied to assess their genetic potential. All the genotypes exhibited significant differences for all the traits. Many early workers Singh *et al.* (2000), Das *et al.* (2001), Chamundeswari and Aher (2003), Ganesamurthy and Seshadri (2004), Dhillon *et al.* (2005), Sultana *et al.* (2005), Malik *et al.* (2006), Mebrahtu and Mohamed (2006), Gupta and Punetha (2007), Costa *et al.* (2008), Borate *et al.* (2010), Milatovic *et al.* (2010) and Reni and Rao (2013) reported high variability for different traits in soybean. Thus, it is implied that there was reasonably sufficient variability in the material used for their study, which provides ample scope for selecting superior and desired genotypes by the plant breeders for further improvement.

The assessment of heritable and non-heritable components in the total variability observed is indispensable in adapting suitable breeding procedure. The heritable portion of the over all observed variation can be ascertained by studying the components of variation such as GCV, PCV, heritability and predicted genetic advance. In the present study the phenotypic coefficient of variation was found to be high for plant height, number of primary branches, number of pods per plant, number of three seeded pods per plant, number of two seeded pods per plant, harvest index and seed yield per plant. For all these traits except plant height, genotypic coefficient of variation was also found to be moderate. High PCV and GCV estimated values for these traits indicating selecting genotypes through these characters will be effective. It is interesting to note that the differences between GCV and PCV values were minimum for most of the characters implying least influence of environment and additive gene effects indicating genotypes can be improved and selected for these characters. Similar observations were also reported by Jagdish *et al.* (2000), Singh *et al.* (2000), Karad *et al.* (2005), Gohil *et al.* (2006), Yadav (2007), Patil *at al.* (2011) and Reni and Rao (2013) for grain yield per plant; Bangar *et al.* (2003), Bhushan *et al.* (2006), Gohil *et al.* (2006), Saraswathi *et al.* (2010), Mahawar et al. (2013) and Reni and Rao (2013) for number of primary branches; Jagdish *et al.* (2000), Singh *et al.* (2000), Karad *et al.* (2005), Bhushan *et al.* (2006), Gohil *et al.* (2006), Yadav (2007), Borate *et al.* (2010), Patil *at al.* (2011), Mahawar et al. (2013) and Reni and Rao (2013) for number of pods per plant; and by Reni and Rao (2013) for harvest index.

Results obtained from present investigation has revealed moderate GCV and PCV for days to 50% flowering indicating still there is possibility of improvement of genotypes through this character. The days to maturity exhibited low GCV and PCV values.

The coefficient of variation indicated only the extent of variability present in these characters and does not indicate the heritable portion. This could be ascertained from heritability estimates which in broad sense include both additive and non-additive gene effects and in narrow sense include the proportion of heritable variation which is due to additive component (Lush, 1949). The knowledge of heritability is helpful in assessing merits and demerits of a particular trait as it enables the plant breeder to decide the course of selection procedures to be followed under a given situation.

In the present study, heritability values for all the characters except number of primary branches and 100 seed weight was found to be high. High heritability values for these traits indicated that the variation observed was mainly under genetic control and was less influenced by environment.

Heritability estimates are useful in deciding the characters to be considered while making selection, but selection based on this factor alone may limit the progress, as it is prone for changes with environment, material etc (Johanson *et al.,* 1955). In other words, estimates of heritability have a role to play in determining the effectiveness of selection of a character, provided they are considered in conjugation with the predicted genetic advance as suggested by Johnson *et al*. (1955). In the present study for the characters *viz*., days to 50% flowering, plant height, number of pods per plant, number of three seeded pods per plant, number of two seeded pods per plant, harvest index and seed yield per plant, had shown high heritability and genetic advance as per cent mean, however, the same characters exhibited moderate to high GCV and PCV hence direct selection of genotypes can be done through these characters for further improvement of genotypes. In these characters where high heritability was associated with high genetic advance, the variation was mostly due to additive gene effects. The results are in accordance with reports of earlier work done by Jain and Ramgiry (2000), Jagdish *et al.* (2000), Singh *et al.* (2000), Vasline *et al.* (2000), Agrawal *et al.* (2001), Dixit *et al.* (2002), Chettri *et al.* (2005), Dhillon *et al.* (2005), Karad *et al.* (2005), Bhushan *et al.* (2006), Gohil *et al.* (2006), Karthika and Lakshmi (2006), Gupta and Punetha (2007), Nag *et al.* (2007), Siddhu *et al.* (2007), Yadav (2007), Vekariya *et al.* (2008), Gangarde *et al.* (2009), Karnwal and Singh (2009), Borate *et al.* (2010), Patil *at al.* (2011), Bhat *at al.* (2012), Mahawar *et al.* (2013) and Reni and Rao (2013).

In the present study high heritability coupled with moderate genetic advances was observed for days to maturity and number of seeds per pod suggesting further improvement of genotypes for these characters for further selection and subsequent use in breeding programme.

POTENTIAL GENOTYPES IDENTIFIED BASED ON VARIABILITY STUDIES

The following potential genotypes are identified for the different traits:

S.No.	Traits	Potential genotypes
1.	Days to 50% flowering	NRC 107
2.	Days to maturity	NRC 107
3.	Plant height	VLS 87 (for dwarfness) MACS 1419, DSb 25 (for tallness)
4.	Number of primary branches	RSC 10-17
5.	Number of pods per plant	JS 20-89
6.	Number of seeds per pod	JS 20-89, KDS 726, DS 3050, AMS 1001, JS 20-79, MACS 1419, KDS 722, NRC 107, RSC 10-17, MACS1370, PS 1540
7.	Number of three seeded pods per plant	JS 20-89
8.	Number of two seeded pods per plant	NRC 97, NRC 96
9.	100 seed weight	PS 1540, PS 1539, KDS 722, MACS 1410, JS 20-53, NRC 96, NRC 97, JS 20-89
10.	Harvest index	JS 20-89
11.	Seed yield per plant	JS 20-89

5.2 GENETIC DIVERSITY

Genetic divergence studies are the vital tools for the evaluation of genotypes and selection of parents for the breeding programme. So, present study was mainly aimed at analysis of genetic divergence among the 40 genotypes and to identify the superior and divergent genotypes for formulating the crossing programme.

Wilk's lambda criterion was used for simultaneous test of significance of the differences in the mean values of the eleven characters and the pooled effect was found significant indicating a wide spectrum of diversity among the genotypes.

Genetic differences among genotypes were quantified by estimating D^2 statistic. The estimates of D^2 values varied substantially from 27.49 to 2191.28. The maximum divergence (D^2 = 2191.28) was recorded between genotype NRC 107 and DSb 25. These two genotypes also showed significant differences between them in respect of all the characters except number of pods per plant, number of seeds per pod and 100 seed weight (Appendix I). A cross between these two genotypes is expected to give a heterotic hybrid and wide spectrum of variability. Therefore, these genotypes may be used as parents for hybridization. On the other hand minimum divergence (D^2=27.49) was observed between genotypes V8 and V28 which did not differ significantly from each other for more than half of the studied characters therefore, these may be related in their evolution.

The inter-cluster distances were greater than intra-cluster distances, revealing that considerable amount of genetic diversity existed among the genotypes. Average intra-cluster distance revealed that clusters IV, V and VI, which contained 2, 6 and 1 genotypes, had little intra-cluster distance. It indicated these genotypes could be closely related in their evolutionary process and passed through similar evolutionary factors.

Inter-cluster distance is the main criterion for selection of genotypes using D^2 analysis. Genotypes belonging to the clusters with maximum inter-cluster distance are genetically more divergent and hybridization between genotypes of divergent clusters is likely to produce wide variability with desirable segregants. The maximum inter-cluster distance was recorded between cluster I and cluster VI (77.159) followed by cluster V and VI (75.186), III and VI (71.403), IV and VI (41.719) and cluster II and VI (40.641). In general cluster VI was situated maximum apart from all the clusters. Therefore, it is suggested that if the diverse genotypes from these groups are used in breeding programme, it is expected to throw a wide range of segregants. The minimum inter-cluster distance between cluster I and III and cluster I and II indicates that the genotypes of these clusters are genetically less diverse and were almost with same genetic makeup.

In regards to per cent contribution of characters towards divergence it was observed that days to maturity attributed maximum per cent towards divergence followed by plant height, number of three seeded pods per plant and days to 50% flowering. Azevedo *et al.* (2004) and Iqbal *et al.* (2010) indicated that these characters were the major contributors towards genetic divergence.

In the present study, D^2 values, cluster means and inter-cluster divergence were utilized for the choice of parents and deciding the cross combinations which are likely to produce the highest possible variability and high heterotic effects for various economic characters. The cluster VI exhibited maximum mean values for seed yield per plant with number of pods per plant, number of seeds per pod, number of three seeded pods per plant and harvest index and was highly divergent from cluster IV, which showed dwarf plants and from cluster V, which showed earliness in days to 50% flowering and days to maturity along with dwarf plants. Thus, by crossing programme involving the genotypes from these clusters, selections for early, dwarf and high yielding varieties and a wide spectrum of variability for the number of pods per plant, number of seeds per pod, number of three seeded pods per plant and harvest index. The cluster IV recorded the maximum mean value for number of primary branches and 100 seed weight and was highly divergent from cluster VI. Thus it is indicated that crossing programme involving the genotypes from these two clusters heterosis and broad spectrum variability for number of primary branches, number of pods per plant, number of seeds per pod, number of three seeded pods per plant, 100 seed weight, harvest index and seed yield per plant and selection for early and dwarf and high yielding varieties along with increased number of primary branches, number of pods per plant, number of seeds per pod, number of three seeded pods per plant, 100 seed weight and harvest index in the subsequent segregating generations could be obtained. Similarly, II had higher number of two seeded pods per and this cluster was also highly divergent from cluster VI. Hence, to improve any particular trait donor for hybridization could be chosen from an appropriate cluster.

Practical utility:

Based on the study of genetic divergence the following genotypes were identified which can be used in breeding programme.

Cluster number	Genotypes	Desirable characteristics
I	**VLS 87**	**Dwarf**
II	**NRC 97**	**Higher number of two seeded pods per plant**
IV	**RSC 10-17**	**More number of primary branches**

	PS 1540	**Bold seed**
V	**NRC 107**	**Early in days to 50% flowering and days to maturity and dwarf**
VI	**JS 20-89**	**High yielded with more number of pods per plant, number of seeds per pod, number of three seeded pods per plant and harvest index**

Canonical analysis:

The relative contribution of characters towards genetic divergence was assessed by the canonical coefficient of first two vectors. The vector (I) confirm the important role of days to maturity, plant height, days to 50% flowering, number of pods per plant and number of three seeded pods per plant. The additional information we got from vector (II) that number of three seeded pods per plant, number of pods per plant, seed yield per plant and plant height played an important role after the variability explained by the first root was excluded.

Path analysis:

Correlation measures only mutual relationship without concerning to cause and effect. Path coefficient provides a method for separating direct and indirect effects and measures the relative importance of casual factors, which ultimately affect the seed yield. The perusal of results on path coefficient analysis based on genotypic correlation revealed appreciable amount of direct positive effect of harvest index, number of two seeded pods per plant, number of three seeded pods per plant and number of primary branches on seed yield per plant, indicating the dependability of seed yield per plant on these traits. Among other traits, number of pods per plant and plant height exhibited negative direct effect on seed yield per plant, and indicates that these characters had inverse relationship with seed yield per plant and have least significance in selection programme. However, plant height, which is indicator of dwarfness, suggest that dwarfnes and high seed yield do go together in selection programme.

Out of these 6 traits, harvest index, number of two seeded pods per plant, number of three seeded pods per plant and number of primary branches, which showed strong positive correlations with seed yield per plant also had high magnitude of direct effects indicating that these characters were of great importance for improvement in seed yield. These results were in agreement with the findings of Dev *et al.* (2005) and Showkat and Tyagi (2010) for harvest index; and of Sultana *et al.* (2005), Karnwal and Singh (2009), Machikowa and Laosuwan (2011) and Mahawar *et al.* (2013) for number of primary branches.

Though plant height and number of pods per plant showed negative direct effect but its genotypic as well as phenotypic correlation with seed yield per plant was converted into positive and significant correlation due to substantial positive indirect effect *via* number of primary branches, number of three seeded pods per plant, harvest index, number of two seeded pods per plant and number of seeds per pod.

The direct effect of 100 seed weight were negative and low but had positive significant correlation with seed yield per plant which implied that 100 seed weight might probably contributed for yield through indirect effects.

Days to 50% flowering and days to maturity showed very low direct effect on seed yield per plant. Its indirect effects through most of the traits were also negligible and ultimately resulted in non-significant correlation with seed yield per plant.

Residual effect was found to be 20.79% in case of genotypic and 35.95% in case of phenotypic path. Therefore, the characters which included in present study are not quite sufficient i.e. some other growth, yield and quality characters may be included in further st

CHAPTER VI

SUMMARY, CONCLUSION AND SUGGESTION

The present investigation was carried out to evaluate a set of soybean genotypes for variability in morphological characters, extent of genetic variability, direct and indirect effects and genetic divergence. The material for the study comprised of 40 soybean genotypes. These were evaluated in randomised block design with three replications during *kharif* 2013, at Research Farm, College of Agriculture, Gwalior. The experimental results are summarized below.

1. Analysis of variance revealed highly significant differences among the genotypes for all the quantitative characters.
2. Environmental influence was very meagre on expression of most of these characters as it was evident by narrow gap between genotypic and phenotypic coefficients of variation.
3. The genotypes exhibited high variability for the characters like number of primary branches, number of pods per plant, number of three seeded pods per plant, number of two seeded pods per plant, harvest index and seed yield per plant and moderate as well as moderate to high variability for days to 50% flowering, plant height and number of seeds per pod.
4. The characters viz., days to 50% flowering, plant height, number of pods per plant, number of three seeded pods per plant, number of two seeded pods per plant, harvest index and seed yield per plant exhibited high heritability coupled with a high genetic advance indicating that simple selection scheme would be sufficient for these traits to bring genetic improvement in desired direction.
5. Using Mahalanobis D^2 statistics, 40 genotypes were grouped into 6 divergent clusters. Cluster III had the maximum number of 13 genotypes followed by I with 10 genotypes, clusters II, V and IV had 8, 6 and 2 genotypes, respectively and the cluster VI was solitary with single genotype.
6. Days to maturity contributed maximum to genetic divergence (44.87%) followed by plant height (16.92%), number of three seeded pods per plant (11.41%) and days to 50% flowering (9.36%).

7. Intra cluster distance was highest (5.368) in cluster II followed by cluster I (4.991). Inter cluster D^2 values ranged from 7.274 between clusters I and III to 77.159 between clusters I and VI, indicating wide genetic variability. It is desirable to select genotypes from clusters having high inter cluster distance and also with high seed yield as parents in the recombination breeding programmes.

8. Canonical analysis revealed that days to maturity, plant height, days to 50% flowering, number of pods per plant and number of three seeded pods per plant relatively contributed more to the divergence as seen in the primary axis of differentiation. In the secondary axis of differentiation, number of three seeded pods per plant was the most important followed by number of pods per plant, seed yield per plant and plant height.

9. Path analysis revealed that harvest index, which showed strong positive association with seed yield per plant, also exhibited positive direct effect on seed yield per plant. The other characters which exhibited positive association with seed yield per plant and also had positive direct effects on seed yield per plant were number of two seeded pods per plant, number of three seeded pods per plant and number of primary branches.

Suggestions:

- The traits viz., days to 50% flowering, plant height, number of pods per plant, number of three seeded pods per plant, number of two seeded pods per plant, harvest index and seed yield per plant possessing high genetic advance as per cent of mean coupled with high heritability may be further improved through simple selection.
- Path analysis revealed that harvest index had high magnitude of positive direct effects followed by number of two seeded pods per plant, number of three seeded pods per plant and number of primary branches. These traits, thus, may be used for selecting high yielding genotypes.
- Cluster VI had high yielding along with more number of pods per plant, number of seeds per pod, number of three seeded pods per plant and harvest index genotypes while cluster V had earliest and dwarf genotypes. Cluster II had highest number of two seeded pods per plant entries while cluster IV had

highest number of primary branches and 100 seed weight genotypes. Cluster VI was farthest to other clusters. Hybridization among the genotypes from these highly diverged clusters might produce high yielding genotypes having broad genetic base.

- On the basis of genetic divergence and mean performance the genotypes JS 20-89, NRC 107, RSC 10-17, PS 1540, NRC 97 and VLS 87 have been suggested for further use in breeding programme.

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APPENDIX-I

Mean performance of selected 40 genotypes of soybean for eleven characters

Genotype	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches	No. of pods/ Plant	No. of seeds/ pod	No. of 3 seeded pods/ plant	No. of 2 seeded pods/ plant	100 seed weight (g)	Harvest index	Seed yield/ plant (g)
KDS 726	51.00	111.67	59.73	2.67	30.00	2.58	17.33	12.00	11.20	18.40	8.77
PS 1539	47.67	105.67	85.53	3.67	42.00	2.53	18.00	20.33	13.90	20.62	12.43
DS 3050	53.67	117.33	58.13	3.33	21.33	2.59	11.33	8.00	11.14	11.16	4.63
SL 983	50.00	117.67	67.13	3.00	26.00	2.43	8.67	13.33	11.24	10.70	4.21
DS 2961	45.33	116.67	61.93	3.67	24.67	2.27	5.33	16.00	11.06	12.17	5.52
RKS 109	46.33	117.33	72.73	3.67	46.33	2.53	22.33	21.33	11.18	17.43	8.41
SL 955	53.00	116.67	68.07	3.33	48.67	2.25	12.00	36.00	10.37	15.44	6.69
DS 3047	50.67	117.67	68.47	3.67	40.33	2.31	11.67	26.67	12.62	25.92	10.94
AMS 1001	53.67	109.33	78.40	2.67	51.33	2.58	28.00	19.00	11.23	26.05	8.66

JS 20-79	54.00	113.67	64.47	3.00	51.67	2.56	39.33	30.33	12.44	21.96	12.19
MACS 1419	53.67	114.67	91.67	3.33	36.67	2.62	21.33	14.00	10.75	20.21	7.24
NRC 98	49.33	116.00	75.67	4.33	70.33	2.29	19.67	50.33	12.59	23.36	12.86
RVS 2002-4	44.33	95.67	58.40	3.67	37.00	2.34	12.67	24.33	12.13	20.37	9.43
KDS 722	49.33	104.33	52.93	2.33	28.33	2.68	16.67	8.33	12.94	13.74	5.92
NRC 111	50.33	103.33	64.93	3.33	41.33	2.14	5.00	30.33	11.35	15.73	5.82

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Mean performance of selected 40 genotypes of soybean for eleven characters

Genotype	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches	No. of pods/ Plant	No. of seeds/ pod	No. of 3 seeded pods/ plant	No. of 2 seeded pods/ plant	100 seed weight (g)	Harvest index	Seed yield/ plant (g)
NRC 107	31.67	92.33	44.00	3.33	47.00	2.55	23.00	20.00	11.78	23.61	8.36
MACS 1410	52.67	112.33	57.13	3.33	32.67	2.17	4.33	23.67	12.84	15.56	6.36
JS 20-53	51.67	112.00	46.53	3.33	42.00	2.10	4.00	35.67	12.92	19.97	7.46
PS 1543	56.00	116.67	66.33	3.33	59.67	2.38	25.33	41.67	12.68	20.18	9.96
Himso 1685	48.33	117.67	63.53	3.33	50.67	2.20	9.67	38.33	12.72	17.07	7.17
RVS 2002-22	45.33	95.33	56.47	2.67	22.33	2.53	11.00	10.33	11.41	16.47	8.30
RKS 111	54.67	107.33	54.93	3.33	19.00	2.48	6.67	7.67	12.05	12.04	4.80
BAUS 27	51.33	121.00	76.67	2.33	18.67	2.71	12.33	5.00	10.75	12.78	5.33
DSb 25	56.00	120.00	90.53	4.33	50.67	2.43	15.33	31.67	11.38	14.54	6.84
RSC 10-17	59.00	107.33	84.13	5.67	64.67	2.61	33.00	23.00	12.13	22.13	10.07

NRC 96	41.67	109.33	70.00	4.67	69.33	2.28	19.33	49.67	13.87	19.89	9.92
RVS 2002-19	44.00	100.33	57.33	2.33	32.33	2.16	4.67	24.67	12.72	18.77	6.18
MAUS 613	49.67	117.33	71.40	2.67	32.00	2.39	10.67	14.67	10.56	22.13	10.39
NRC 97	41.33	97.33	65.00	2.67	74.00	2.22	15.00	53.00	13.30	23.13	9.17
DSb 23-2	49.33	106.67	42.13	3.33	31.67	2.00	0.00	26.33	11.40	26.80	14.89

APPENDIX-I

Mean performance of selected 40 genotypes of soybean for eleven characters

Genotype	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches	No. of pods/ Plant	No. of seeds/ pod	No. of 3 seeded pods/ plant	No. of 2 seeded pods/ plant	100 seed weight (g)	Harvest index	Seed yield/ plant (g)
JS 20-89	51.33	109.67	82.13	3.67	111.67	2.78	95.33	28.00	12.79	35.21	17.05
KBS 100-2012	55.00	110.33	73.47	2.67	19.00	2.19	4.67	29.67	11.29	26.18	10.46
VLS 87	55.33	107.67	34.80	2.33	25.00	2.30	10.00	24.33	12.25	18.18	7.10

KDS 743	50.33	110.67	51.07	3.33	44.33	2.65	26.00	14.67	12.37	12.29	5.31
BAUS 96	58.67	121.00	63.67	4.67	30.33	2.06	1.67	25.00	11.10	11.82	7.48
MACS 1410	49.67	104.33	56.40	3.67	62.00	2.50	30.67	31.33	11.58	16.74	15.10
MACS 1370	53.67	119.33	65.60	3.33	36.67	2.75	26.33	8.33	11.32	12.67	5.00
VLS 86	48.00	98.67	59.87	3.33	31.33	2.30	7.33	20.67	12.18	15.80	6.70
PS 1540	51.67	120.00	83.33	5.67	74.00	2.69	41.67	19.67	14.21	12.95	9.10
RSC 10-04	55.33	120.33	71.60	3.33	37.00	2.02	0.0	23.67	12.04	18.53	8.01
C.D. 5%	1.709	1.468	4.569	0.944	7.093	0.235	4.829	5.956	1.454	3.249	1.232

VITA

Name of Author : **Mr. Mahesh Meena**

Mother's Name : Smt. Ganpati bai

Father's Name : Shri Narmada prasad

Date of Birth : 05/09 /1987

E-mail : maheshmeena811@gmail.com

Mobile No. : +09754223481

Permanent Address : Village – Sukarwas,
Post – Vasudev, Teh-Nasrullaganj,
Dist – Sehore (M.P.) , Pin –466001

Educational Qualification:

Name of examination	Board/University	Year of passing	Mark Obtained	Division
High School	M.P., Board Bhopal	2003	253/500	second
Higher Secondary	M.P., Board Bhopal	2005	294/450	First
B.Sc. (Ag.)	RVSKVV, Indore (M.P.)	2012	1091/1600	First
M.Sc. (Ag.)	RVSKVV, Gwalior (M.P.)	2015		First

I

I have submitted my thesis in 2014, during his course work in partial fulfilment of the requirement for the degree of M.Sc. in Plant Breeding & Genetics

Place: Gwalior

Date : **(Mahesh Meena)**