GENETIC DIVERSITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS IN SOYBEAN

(*Glycine max* (L.) Merrill)

By

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CERTIFICATE

This is to certify that thesis entitled, ***"Genetic Diversity, Correlation and Path Co-efficient Analysis in Soybean (Glycine max (L.) Merrill)"*** *submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of* ***MASTER OF SCIENCE*** *in* ***GENETICS AND PLANT BREEDING,*** *embodies the result of a piece of bona fide research work carried out by* ***Md. Mostofa Mahbub,*** *Registration No.* ***05-01550*** *under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

I further certify that such help or source of information, as has been availed of during the course of this investigation has duly been acknowledged.

.....

Dated: June 2013
Place: Dhaka, Bangladesh

(Prof. Dr. Md. Sarowar Hossain)
Supervisor

DEDICATED TO

MY

BELOVED PARENTS

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June, 2013 **The Author**

SAU, Dhaka

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ABSTRACT

A field experiment was conducted during December, 2011 to April, 2012 to study the genetic variability, correlation, path coefficient analysis and genetic diversity for quantitative traits in soybean (*Glycine max* (L.) Merrill) with 28 genotypes in randomized complete block design with three replications. The genotypes were placed in a field experiment conducted at the research farm of Sher-e-Bangla Agricultural University, Dhaka- 1207. Analysis of variance for each trait showed significant differences among the genotypes. Phenotypic coefficients of variation (PCV) was close to genotypic coefficients of variation (GCV) for all the characters except pod length and seeds per pod indicating that environment had influence on the expression of these characters. High heritability associated with high genetic advance percent of mean was observed for plant height, number of branches per plant, pods per plant, seeds per plant and hundred seed weight which indicated that selection for these characters would be effective. Seed yield per plant had highly significant positive genotypic and phenotypic association with plant height, branches per plant, pods per plant, pod length, seeds per pod, seeds per plant and hundred seed weight revealing that selection based on these traits would ultimately improve the seed yield. Path coefficient analysis revealed that seeds per plant and hundred seed weight had the highest positive direct effect on seed. Hence, thrust has to be given for these characters in future breeding programme to improve the yield in soybean. Multivariate analysis based on 11 characters indicated that the 28 genotypes were grouped into five distant clusters. The maximum contribution of characters towards diversity was observed by days to first flowering, number of pods per plant and seeds per pod. Thus, these traits may be given high emphasis while selecting the lines for hybridization. The inter cluster distance was maximum between cluster II and cluster IV. The highest intra cluster distance was found in cluster V. From the results it can be concluded that the following genotypes *viz.*, F-85-11347 (G4), LG-92P-12-18 (G8), PI-4174-75 (G23) and MTD-451 (G28) were identified as potential genotypes for higher seed yield in soybean.

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LIST OF ABBREVIATED TERMS

ABBREVIATION	FULL WORD
AEZ	Agro-Ecological Zone
et al.	And others
ACC	Accessions
BARI	Bangladesh Agricultural Research Institute
BBS	Bangladesh Bureau of Statistics
cm	Centimeter
CV	Co-efficient of Variation
etc.	Etcetera
Fig.	Figure
G	Genotype
GA	Genetic Advance
GCV	Genotypic Co-efficient of Variation
δ^2_g	Genotypic Variance
G	Gram
h^2b	Heritability in broad sense
J.	Journal
Kg	Kilogram
M	Meter
MSS	Mean Sum of Square
Mm	Millimeter
MP	Muriate of Potash
No.	Number
%	Percent
PCV	Phenotypic Co-efficient of Variation
δ^2_p	Phenotypic variance
RCBD	Randomized Complete Block Design
R	Replication
Res.	Research
SAU	Sher-e-Bangla Agricultural University
SE	Standard Error
m^2	Square meter
TSP	Triple Super Phosphate

Chapter I

Introduction

CHAPTER I

INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is a wonderful crop gifted by the god to mankind which is one of the richest sources of oil as well as protein. It is an oil crop as well as a pulse crop. From the viewpoint of nutrient no pulse crop is equivalent to it, rather it is very much superior to any one of the pulse crops. Soybean seed contains about 40-45% protein and 18-20% oil and provides around 60% of the world supply of vegetable protein and 30% of the oil (Fehr, 1989). Though the oil content of soybean is less than those of two major oilseeds, viz. mustard and groundnut, its protein content is quite high, against 20-25% and 24-26% of mustard and groundnut, respectively. As a good source of protein, unsaturated fatty acids, minerals like Ca and P including vitamin A, B, C, and D, soybean can meet up different nutritional needs (Rahman, 1982).

The present nutritional situation of Bangladesh is a matter of great concern. The prime nutritional problem of the country is that of protein-energy malnutrition. Most of our people are suffering from malnutrition. Soybean can play an important role to meet up the protein deficiency problem. Soybean is regarded as an ideal food for the people of Bangladesh as it contains high quality of protein and reasonable quantity of oil as a source of energy (Khaleque, 1985). The poor people of our country cannot afford to take high priced animal protein like meat, fish, egg, milk, etc. Soya protein products can be good substitutes for animal products because, unlike some other beans, soybean offers a 'complete' protein profile. Soya protein products can replace animal-based foods (Henkel, 2000).

The protein of soybean is called complete protein, because it supplies sufficient amount of various kinds of amino acids required for building and repairing the body tissues. Its food value in heart disease and diabetes is well known. The area of cancer

prevention is perhaps the most controversial area of health research on soybean. Many studies provide with evidence that supports the role of whole soya foods in a cancer-preventing diet (Amadou *et al.*, 2009). Consumption of soya may reduce the risk of colon cancer (Symolon *et al.*, 2004).

Soybean is not yet popular as a crop but its oil is very popular as cooking oil. From our internal production of the total oil crop, one third of the oil requirement can be met-up. The shortfall is imported at the cost of about US$ 160 million per year. The major import is soybean and palm oil. Extraction of oil from soybean seed is not yet possible in our country. Soybean produced in our country is mostly used for making nutritious food items like soya dal, soya khechuri, soya pollao, soya bori, soya chatni, soya parata, soya milk, soya cakes, soya biscuits, soya bread etc. (Mondal and Wahhab, 2001; Khaleque, 1985). Soya milk is comparable to cow's milk (Smith, 1975).

Soybean belongs to the family Leguminosae under sub-family Papilionaceae. It is originated in China with *Glycine ussuriensis* as probable progenitor (Vavilov, 1951 and Nagata, 1960). Being a leguminous crop it improves the soil by fixing the atmospheric nitrogen through *Rhizobium* bacteria that lives in root nodules. Steward (1966) stated that in a season the plants can fix 94 kg/ha nitrogen in the soil. As a result it is very suitable crop to fit into the cropping systems of Bangladesh. According to Keyser and Li (1992) the *Bradyrhizobium japonicum* can fix atmospheric nitrogen about 300 $kgha^{-1}year^{-1}$ in symbiosis with soybean.

Soybean can be grown under a wide range of climatic and edaphic conditions. With well-adapted cultivars, soybean can be cultivated throughout the year in Bangladesh (Rahman, 1982; Haque *et al.*, 1976). In the northern part, it can also be grown in summer without affecting the production of transplant aman rice. Even, it can be grown in char and haor areas after receding flood water with no tillage and minimum inputs. But still the yield of soybean is very discouraging compared to other soybean producing countries. This is mainly due to use of low yield potential varieties and

poor cultivation technologies i.e. lack of application of inoculums, fertilizer etc. Seeds yield and protein content of soybean are both heritable traits (Imsande, 1992).

Soybean can play a vital role in balancing the protein-calorie malnutrition in Bangladeshi diet. Generally protein and oil contents are negatively correlated, so it is difficult to find a high oil containing crop with high protein content. But total protein plus oil content is higher in soybean and can be selected for improvement. The statistical information regarding soybean acreage production in Bangladesh is fragmentary and not available in the systematic form, but it is thought to be of 10,000 acres with about 5,000 tons of production (Rahman, 2002).

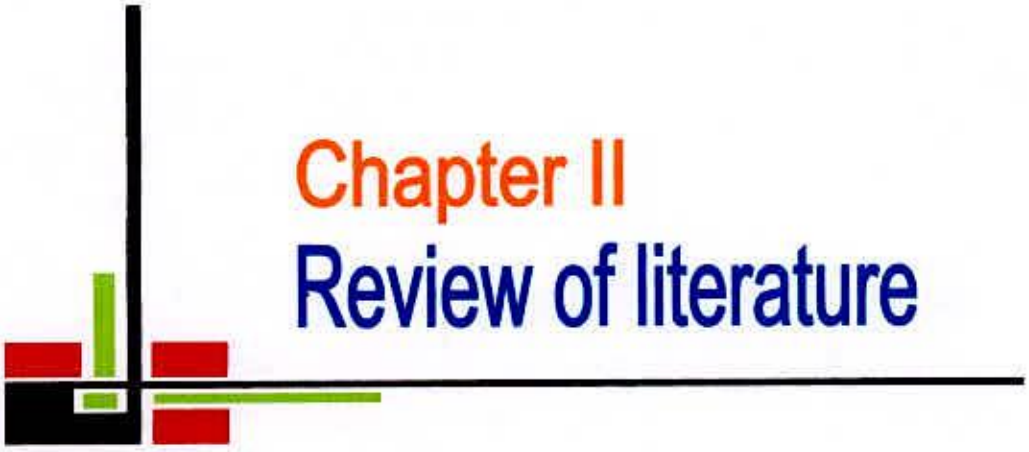
Batugal (1999) stated genetic diversity as a major factor that determines yield security in future. The importance of genetic diversity in the improvement of crop has been stressed in both self and cross pollinated crop (Gaur *et al.*, 1978; Murty and Anand, 1966; Griffing and Lindstrom, 1954). Knowledge of genetic diversity within a crop and correlation among the yield contributing characters is essential for the long-term success of a breeding program and maximizes the exploration of germplasm resources. These indigenous types of soybean contribute considerable degree of variability in respect to qualitative and quantitative characters. The quantification of genetic diversity through biometrical procedures (Rao, 1952 and Anderson, 1957) has made it possible to choose genetically diverse parents for a successful hybridization program. A successful hybridization program for varietal improvement depends mainly on the selection of the parents having high genetic divergence (Upadhyay and Mehta, 2010). Moreover, evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomooka, 1991). The utility of multivariate analysis for measuring the degree of divergence and for assessing the relative contribution or of different character to the total divergence in self-pollinated crops has been established by several workers (Golakia and Makne, 1992).

Multivariate analysis acts as a useful tool to quantify the degree of divergence between the biological populations at genotypic level and to assess the relative contribution of different components to the total divergence both inter and intra cluster levels (Jatasra and Paroda, 1978; Sachan and Sharma, 1971; Murty and Arunachalam, 1966).

Yield is a complex character controlled by a large number of contributing characters and their interactions. A study of correlation between different quantitative characters provides an idea of association that could be effectively exploited to formulate selection strategies for improving yield components. For any effective selection program, it would be desirable to consider the relative magnitude of association of various characters with yield. The path coefficient technique developed by Wright (1921) helps in estimating direct and indirect contribution of various components in building up the total correlation towards yield. On the basis of these studies the quantum importance of individual characters is marked to facilitate the selection program for better yield.

Keeping in view the above facts, the present investigation was therefore undertaken to quantify the genetic divergence and variability in a diverse collection of genotypes with the following objectives:

- To assess the genetic diversity among the genotypes,
- To know the association of traits with yield and its contributing traits
- To know the yield potentiality of genotypes and
- To screen out the suitable parental groups which are likely to provide superior segregates on hybridization.



Chapter II
Review of literature

CHAPTER II

REVIEW OF LITERATURE

Soybean is one of the most important crops in Bangladesh. The seeds of this soybean have high nutritive value and are good source of protein and oil. Some studies on the variability, interrelationship, path co-efficient analysis, heritability and genetic advance have been carried out in many countries of the world. The available literature on the variability, interrelationship, path co-efficient analysis, heritability and genetic advance of country bean has been briefly reviewed under the following headings.

2.1 Variability, heritability and genetic advance

2.2 Correlation co-efficient

2.3 Path co-efficient

2.4 Genetic diversity

2.1. Variability, heritability and genetic advance

A thorough understanding of the genetic variation for different traits and their heritability is important for successful crop improvement program. In soybean, a wide variability has been noticed for various traits. A summary of literature available on this aspect is presented below.

Bangar *et al.* (2003) reported that phenotypic coefficient of variation (PCV) was higher 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 1000-seed weight and pod number per plant.

Chamundeswori and Aher (2003) conducted an experiment with ninety genotypes of soybean. They observed days to maturity, plant height at maturity, number of clusters per plant, number of pods per cluster and per plant, number of seeds per pod, 100-seed weight and grain yield per plant showed significant genetic variation. Genotypic coefficient of variation was highest for biological yield per plant. Broad sense heritability was highest for plant height and number of pods per plant.

Genetic variability was studied by Agrawal *et al.* (2001) using 196 soybean germplasm. They found that GCV were moderate for days to flower initiation, days to flower termination, whereas low for days to maturity. Heritability and genetic advance as percentage of mean were high for all the plant growth characters (except moderate GAM for days to maturity).

Jain and Ramgiry (2000) showed significant variation for yield per plant. High heritability values accompanied by high genetic advance as a percentage of mean were noticed for seed yield, plant height and pods per plant.

Mehetre *et al.* (2000) studied variability for 11 characters with 60 diverse genotypes of soybean. They reported that pods per plant and seed yield per plant had high genotypic and phenotypic co-efficient of variation. They also reported that plant height and pods per plant had high genotypic and phenotypic co-efficient of variation and high heritability associated with high genetic advance as percentage of mean.

Singh *et al.* (2000) reported that genotypic coefficient of variation and phenotypic coefficient of variation was comparatively high, for seed yield per plant, pods per plant and plant height. Seed yield per plant, pods per plant and plant height showed high heritability with high genetic advance as a percentage of mean.

Archana *et al.* (1999) reported that plant height and 100 seed weight had high genotypic co-efficient of variation and high heritability accompanied with high genetic advance as percent of mean in soybean.

Bhandarkar (1999) observed high co-efficient of variation and moderate heritability for pods per plant and seed yield per plant in soybean. He also observed high heritability and genetic advance as percent of mean for plant height and days to maturity.

Nehru *et al.* (1999) conducted an experiment to estimate genetic advance and heritability for 16 yield and quality components in 49 genotypes of soybean. They found days to maturity and 100 seed weight had high heritability but low genetic advance.

Gupta *et al.* (1998) estimated heritability and genetic advance is derived from data on seven yield related traits in 40 pea genotypes. Result show that the phenotypic correlation was lower than its genotypic counterpart for most of the characters. Days to 50% flowering, pod weight per plant, 100-seed weight and protein content exhibited high estimates of heritability.

Mehetre *et al.* (1998) reported that genotypic co-efficient of variation was high for plant height, 100 seed weight and yield per plant in soybean. High heritability accompanied with high genetic advance was also observed for plant height, 100 seed weight and yield per plant.

Shrivastava and Shukla (1998) revealed a significant amount of variability for plant height, seed yield per plant and pods per plant in soybean. These characters had high heritability coupled with high expected genetic advance.

Mehetre *et al.* (1997) estimated high heritability accompanied by high genotypic co-efficient of variation for pods per plant, 100 seed weight and yield per plant in soybean.

Major *et al.* (1996) observed high genotypic and phenotypic co-efficient of variation for 100 seed weight and grain yield in soybean. They also observed plant height and grain yield per plant showed high genetic advance.

Rajarathinam *et al.* (1996) conducted an experiment to estimate genetic advance, heritability and genetic variability in 35 genotypes of soybean. They reported that high heritability and genetic advance were for plant height, pod per plant, 100 seed weight and seed yield per plant.

Dobhal and Gautam (1995) observed a wide range of variability for plant height, days to maturity, pod per plant and yield per plant in soybean germplasm. High broad sense heritability coupled with high genetic advance was observed for plant height, pods per plant and yield per plant.

Singh *et al.* (1995) observed pods per plant and yield per plant showed maximum genotypic co-efficient of variation in soybean. Pods per plant also showed highest heritability.

Jagtap and Mehetre (1994) revealed that plant height and number of pods per plant showed highest genotypic co-efficient of variation in soybean.

Jangale *et al.* (1994) conducted an experiment with 34 genotypes of soybean. High heritability was observed for days to 50% flowering, days to maturity, pods per plant and seeds per pod.

Mahajan *et al.* (1994) reported that pods per plant and yield per plant showed high genotypic co-efficient of variation in soybean. High heritability was recorded for pods per plant.

Malhotra (1973) observed that seed yield had the highest co-efficient of genetic variation and predicted genetic advance as a percentage of mean in soybean.

2.2 Correlation co-efficient

The interrelationship of different characters with yield determines the efficiency of selection in breeding programs. It merely indicates the intensity of association. Phenotypic correlation reflects the observed relationship, while genotypic correlation underline the true relationship among characters. Selection procedures could be varied depending on the relative contribution of each. The following paragraphs give review of literature on correlation between different characters in soybean.

Association studies indicated that pods per plant, clusters per plant, seeds per pod and days to 50% flowering were significantly correlated with grain yield (Inderjit *et al.* 2007).

Correlation studies showed that the pod yield was significant positive correlated with pods per plant and hundred seed weight (Avc and Ceyhan, 2006).

Seed yield per plant had significant and positive association with number of pods per plant, plant height, harvest index, and number of grains per pod (Singh and Singh, 2006).

Chamnundeswari and Aher (2003) conducted an experiment with ninety genotypes of soybean. They reported that seed yield showed positive correlation with number of pods per cluster, number of clusters per plant, number of pods per plant and biological yield per plant.

Character association studies conducted by Sharma *et al.* (2003) and indicated that positive and significant association of seed yield per plant with biological yield per plant, pods per plant and pod length. Significant negative correlation of harvest index was observed with plant height. It can be predicted that selection for pods per plant, pod length and biological yield per plant would improve seed yield per plant. Recombination breeding may be suggested for simultaneous improvement of biological yield per plant and harvest index.

Onemli (2003) reported that the number of pods positively correlated with plant height, number of branches, pod length, seed length, number of pods per plant and 1000-seed weight, but was negatively correlated and significant correlations with number of seeds per pod, seed length and pod length in soybean. Number of pods and 1000-seed had negative effect on seed yield via the number of pods.

The genotypic correlation coefficients were higher than the phenotypic correlation coefficients. Pod yield per plant showed positive phenotypic correlation with pod length, number of grains per pod, number of pods per plant and shelling percentage described by Chaudhary and Sharma (2003).

Seed yield per plant exhibited a significant and positive correlation with plant height, number of pods per plant, 1000-seed weight, number of grains per pod and harvest index (Tiwari *et al.* 2001).

Chand (1999) reported that the genotypic correlation coefficients higher than the phenotypic and environmental correlation coefficients in soybean. Seed yield was positively correlated with days to flowering and maturity, plant height and branches seeds and pods per plant in terms of genotype and phenotypic correlation coefficients. No correlation between 100-seed weight and seed yield per plant was established. Plant height was negatively correlated with 100-seed weight. The characters which showed significant positive correlation with yield were also positively associated among themselves, except days to maturity with seeds per plant.

In another experiment Dogney *et al.* (1998) investigated that the number of seeds per pod and 100 seed weight had a high positive direct effect on yield in soybean. The characters number of seeds per pod, days to maturity had medium to low direct effect on seed yield.

Peluzio *et al.* (1998) revealed that the negative correlation between days to maturity and pods per plant in soybean.

Saurabh *et al.* (1998) conducted an experiment and estimated significant and positive correlations between plant height and pods per plant in soybean.

Significant positive correlations of seed yield with plant height, pod length, number of pods per plant and straw yield per plant were reported Devendra *et al.* (1998).

Sridhara *et al.* (1998) reported that number of pods per plant and number of seeds per plant directly contributed the most to yield in soybean. Pod length seed number, plant height and number of branches through number of pods per plant seemed to be significant contributors of seed yield.

Praneetha and Thamuraj (1997) observed that pods per plant and yield per plant had high genotypic co-efficient of variation and heritability in vegetable soybean.

Ramgiry and Raha (1997) observed that genotypic correlation coefficients were higher than phenotypic correlation coefficients in soybean. Seed yield per plant showed positive correlations with seeds per plant and nods per plant.

Rahman *et al.* (1996) revealed a significant and positives correlation between pods per plant and 100 seed weight with seed yield in soybean. Plant height and days to maturity showed the significant and positive correlation with pods per plant. The number of pods per plant and seeds per pod had higher direct effect on yield.

Rajarathinam *et al.* (1996) found that seed yield was significant correlated with plant height, number of primary branches per plant and pod number in soybean.

Shinde *et al.* (1996) reported that the genotypic correlations were higher than the phenotypic ones in soybean. Seed yield per plant showed highly significant and positive correlations with plant height pods per plant and seeds per pod. Seeds per pod were significantly correlated with yield and its direct effect was very strong.

Jadhav *et al.* (1995) observed that number of branches, pods and seeds per plant pod length and pod weight per plant were positively and highly significantly correlated with seed yield in soybean. Yield is higher correlated with yield and yield contributing characters.

Wu *et al.* (1995) revealed that seed yield was positively correlated with pods per plant, plant height in summer soybean. Seed yield was influenced by 100 seed weight, pods per plant and nodes per main stem among these high yielding genotypes.

Mahajan *et al.* (1993) informed that grain yield per plant was positively correlated with pods per plant (0.75), branches per plant (0.52) in soybean. Days to maturity (0.47) and plant height were the most important yield contributing characters.

Das *et al.* (1984) reported a highly significant positive correlation between seed yield and pods per plant and a significant positive correlation between seed yield and seeds per pod in soybean. Pods per plant and 100 seed weight showed very high direct effects on seed yield.

Ahmed *et al.* (1971) observed that seed yield per plant was significantly and positively correlated with plant height, days to maturity, number of pods per plant and seeds per pod in soybean.

Juneje and Sharma (1971) studied the correlation of 11 characters in 30 varieties of soybean and observed that seed yield was positively correlated with number of branches and pods per plant, days to flowering and days to pod formation.

2.3 Path co-efficient

Assuming yield is a contribution of several characters which are correlated among themselves and to the yield, path coefficient analysis was developed (Wright, 1921, Dewey and Lu, 1959). Unlike the correlation coefficient which measures the extent

of relationship, path coefficient measures the magnitude of direct and indirect contribution of a component characters to a complex character and it has been defined as a standardized regression coefficient which splits the correlation coefficient into direct and indirect effects.

Pods per plant, 100-seed weight, seeds per pod and days to maturity had positive direct effect on grain yield, while plant height, pods per cluster and pod length had negative direct effect on grain yield (Inderjit *et al.* 2007).

The results of path analysis revealed that direct effects were highest for number of pods per plant, node at which first fertile pod develops, number of branches, number of seeds per pod and pod length which can serve as reliable variable for selection (Harpreet *et al.* 2007).

The highest direct effect was exhibited by pods per plant, indirect effects, especially through the seeds per pod in pea (Avc and Ceyhan, 2006).

Pods per plant, 100-seed weight, seeds per pod and days to maturity had positive direct effect on grain yield, while plant height, pods per cluster and pod length had negative direct effect on grain yield (Singh and Singh, 2006).

Path coefficient analysis revealed that number of pods per plant and shelling percentage had the maximum direct effect on green pod yield. Thus, due importance should be given to these characters for improvement of yield (Mohan *et al.* 2005).

Chettri *et al.* (2003) reported that grain yield was significantly correlated with days to maturity and number of grain per pod in soybean at the genotypic level. Days to maturity and number of grains per pod were also correlated. Days to maturity were significantly correlated with plant height and days to 50% flowering at the phenotypic levels. The number of days to 50% flowering was positively and significantly correlated with days to maturity but negatively with number of seeds per pod and 100

grain weight at the genotypic level. Path coefficient estimates showed that the number of grain per pod, days to maturity, number of pods per plant and plant height positively affected grain yield.

A path coefficient analysis of yield-contributing traits in soybean was conducted by Shrivastava *et al.* (2001). They observed highest positive direct effects on seed yield for the number of branches per plant, followed by days to 50% flowering and days to maturity, plant height, 100-seed weight, biological yield and harvest index. Plant height, on the other hand, had a negative effect on yield.

Khan *et al.* (2000) observed correlation among yield determining components in 86 diverse maturity genotypes of soybean. Path coefficient analysis revealed that pods/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 seed/pod.

Rajanna *et al.* (2000) estimated significant and positive correlation of number of pods per plant, number of clusters per plant and 100-seed weight with seed yield in soybean. Days to maturity, plant height and number of branches per plant exhibited significant and positive correlation with number of clusters per plant and number of pods per plant. Path analysis indicated effect on seed yield per plant.

Mehetre *et al.* (1997) conducted an experiment with 4 soybean genotypes. Yield per plant was highly significant and positively correlated with 100-seed weight but non-significant and positively correlated with leaf area. Path coefficient analysis indicated that the number of branches per plant exerted the highest positive direct effect fallowed by contribution of 100-seed weight, number of pods per plant. The highest indirect positive effect was found for number of pods per plant.

Praneetha and Thamburaj (1997) revealed that pods per plant and single pod weight in soybean were the most important yield determinants because of their high direct and indirect effects.

Major *et al.* (1996) reported that the grain yield showed significant and positive correlation with branches per plant, pods per plant and 100-seed weight in soybean. Path analysis revealed that pods per plant and 100-seed weight had high direct and positive effects on grain yield.

Dobhal and Gautam (1995) showed that yield per plant was positively and significant associated with pods per plant and days to maturity both at phenotypic and genotypic levels in soybean. Path analysis revealed that pod per plant was the strongest forces influencing yield.

Saad (1995) observed that the path analysis showed direct contribution of yield components to seed yield for cultivars was in the descending order number of pods per plant, 100-seed weight, number of seeds per pod and plant height, while highest indirect effects were exerted by number of seeds per pod via number of pods per plant in soybean.

Mishra *et al.* (1994) reported that the number of seeds and pods per plant had a substantial contribution towards the seed yield in soybean. Path coefficient analysis showed the positive direct effect of 100-seed weight, number of seeds per plant and number of pods per plant on seed yield.

Singh *et al.* (1994) revealed that grain yield per plant showed high positive association with number of pods per plant and days to maturity in soybean. Plant height showed high positive correlation with days to maturity. Plant height days to maturity, number of pods per plant had a low positive direct effect on grain yield.

2.4 Genetic diversity

The assessment of genetic diversity using quantitative traits has been of prime importance in many contexts particularly in differentiating well defined populations. The germplasm in a self pollinated crop can be considered as heterogeneous sets of groups, since each group being homozygous within itself. Selecting the parents for breeding program in such crops is critical because, the success of such program depends upon the segregants of hybrid derivatives between the parents, particularly when the aim is to improve the quantitative characters like yield. To help the breeder in the process to identify the parents that nick better, several methods of divergence analysis based on quantitative traits have been proposed to suit various objectives. Among them, Mahalanobis' generalized distance occupies a unique place and an efficient method to gauge the extent of diversity among genotypes, which quantify the difference among several quantitative traits. A summary of literature available on this aspect in soybean is presented below.

One hundred twenty genotypes were evaluated for 10 characters to study genetic diversity and association between yield and its components. The study indicated presence of considerable genetic divergence among the genotypes. The genotypes were grouped into six clusters. To get the desirable segregants the hybridization among the genotypes of cluster III and VI, cluster V and VI and cluster I and VI as the inter cluster distance was greater between these clusters (Inderjit *et al.* 2007).

Singh *et al.* (2007) evaluated one hundred twenty genotypes for 10 characters to study genetic diversity and association between yield and its components. The study indicated presence of considerable genetic divergence among the genotypes. The genotypes were grouped into six clusters. To get the desirable segregants the hybridization among the genotypes of cluster III and VI, Cluster V and VI and cluster I and VI as the inter cluster distance was greater between these clusters.

Sihag *et al.* (2004) studied genetic diversity among 160 soybean genotypes using Malhalanobis' D^2 statistic and grouped the genotype into 8 clusters. 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 regions were classified into one cluster.

Vart *et al.* (2002) estimated genetic diversity in 56 genotypes of soybean by using D^2 statistic and grouped them into 11 clusters. The clustering pattern was not significantly influenced by the ecogeographical distribution of the genotypes.

Das *et al.* (2000) studied genetic divergence of 65 soybean genotypes using Mahalanobis D^2 statistic and grouped the genotypes into 13 clusters. 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.

Shrivastava *et al.* (2000) studied the genetic divergence among 50 soybean genotypes for nine yield component characters and the genotypes were grouped into five clusters, based on D^2 values. The highest inter cluster divergence was observed between cluster III and IV.

Chowdhury *et al.* (1998) conducted an experiment to assess genetic diversity among 55 soybean Mahalanohis' D^2. The genotypes fell in seven clusters of different sizes. Genetic divergence and geographic distribution were not necessarily related of the ten different characters, pods per plant, yield per plant and effective nodes per plant contributed maximum on the total divergence. The highest inter-cluster distance was observed between I and V followed by I and VI indicates that highly divergent types existed in these clusters.

Rahman (1998) estimated genetic divergence among sixteen genotypes of soybean using Mahalanobis' D^2 statistics. The genotypes were grouped into seven clusters. The inter cluster average D^2 values should maximum distance between cluster I and

VI followed by that between I and III. The genetically diverse genotypes from these groups could be used as parents in hybridization programme for getting desirable segregants. Germplasms much in use of these characters of respective cluster would offer a good scope of improvement of the crop through rational selection.

Sanjay *et al.* (1998) reported genetic divergence of 30 advanced breeding lines of soybean and were grouped into 7 clusters, of which cluster I and II contained the most important genotypes. Cluster I was characterized by high yield per plant (23.72 g), 100-120 pods per plant, a reproductive phase high harvest index and high seed weight, cluster II contained genotypes almost similar to those in cluster I.

Chowdhury *et al.* (1997) observed 30 genotypes of soybean (*Glycine max*) for genetic divergence using Mahalanobis' D^2 statistics and reported that genotypes were clustered in six diverse groups. They demonstrated that geographical isolation may not be the only factor causing genetic diversity but also the 100 seed weight and yield per plant were the main contributors of total divergence.

Mehetre *et al.* (1997) observed 41 genotypes of soybean were grouped into 12 different clusters. Genetic diversity was independent of geographic region. From the cluster mean values donor for different character are suggested.

Praneetha and Thamburaj (1996) observed that fifteen and 22 genotypes of soybean were grouped into 6 and 3 clusters, respectively, on the basis of D^2 analysis of 14 clusters.

Dobhal (1995) observed significant variability among 65 soybean genotypes for 12 yield components, allowing genotypes to be grouped into 17 clusters. D^2 analysis revealed that yield per plant, number of pods per plant, pod length and seed per pod made a high contribution towards total genetic distance.

Kumar and Nadarajan (1994) studied eleven yield components in 64 genotypes of soybean for genetic divergence and reported that genotypes were clustered in 11 diverse groups.

Mehetre *et al.* (1994) estimated genetic divergence among 51 genotypes of soybean and the genotypes were grouped into 10 clusters. The clustering pattern showed that diversity and geographic distribution were independent of each other.

Ghatge and Kadu (1993) estimated genetic diversity using the Mhalanobis' D^2 statistics in soybean. The genotypes were grouped into 7 clusters. The clustering pattern revealed that genetic diversity did not have a strong association with geographical origin.

Chapter III

Materials and Methods

CHAPTER III

MATERIALS AND METHODS

An experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh during the period from December, 2011 to April, 2012 to study on the genetic diversity, correlation and path coefficient analysis in Soybean (*Glycine max* (L.) Merrill). A brief description about the locations of the experimental site, characteristics of soil, climate, materials, layout and design of the experiment, land preparation, manuring and fertilizing, intercultural operations, harvesting, data recording procedure, economic and statistical analysis etc. which are presented as follows:

3.1 Experimental site

The research work relating to determine the genetic diversity of soybean was conducted at the Sher-e-Bangla Agricultural University Farm, Dhaka-1207, during December, 2011 to April, 2012.

3.2 Geographical location

The experimental area was situated at 23°77'N latitude and 90°33'E longitude at an altitude of 8.6 meter above the sea level (Anon., 2004).The experimental field belongs to the Agro-ecological zone of "The Modhupur Tract", AEZ-28 (Anon., 1988a). This was a region of complex relief and soils developed over the Modhupur clay, where floodplain sediments buried the dissected edges of the Modhupur Tract leaving small hillocks of red soils as 'islands' surrounded by floodplain (Anon., 1988b). The experimental site was shown in the map of AEZ of Bangladesh in Appendix I.

3.3 Climate

Area has subtropical climate, characterized by high temperature, high relative humidity and heavy rainfall in Kharif season (April-September) and scanty rainfall associated with moderately low temperature during the Rabi season (October-March). Weather information regarding temperature, relative humidity, rainfall and sunshine hours prevailed at the experimental site during the study period was presented in Appendix II.

3.4 Characteristics of soil

Soil of the experimental site belongs to the general soil type, Shallow Red Brown Terrace Soils under Tejgaon Series. Top soils were clay loam in texture, olive-gray with common fine to medium distinct dark yellowish brown mottles. Soil pH ranged from 6.0-6.6 and had organic matter 0.84%. Experimental area was flat having available irrigation and drainage system and above flood level. Soil samples from 0-15 cm depths were collected from experimental field. The analyses were done by Soil Resource and Development Institute (SRDI), Dhaka. Physicochemical properties of the soil are presented in Appendix III.

3.5 Planting Materials

The material comprised of 28 genotypes of soybean. The genetically pure and physically healthy seeds of these genotypes were obtained from the Oil Seed Research Center (OSRC) of Bangladesh Agricultural Research Institute (BARI), Gazipur. List of the genotypes are given in Table 1.

3.6 Design and layout of the experiment

The study was laid out in Randomized Complete Block Design (RCBD) with three (3) replications. The plot size was 180 m^2 and distance of 1.0 m from block to block, 50 cm from each row within each line. Each plot has a single row of 3 m length. Plant to plant distance was 10 cm. The genotypes were randomly distributed to each row within each block.

Table 1. Name and origin of twenty eight soybean genotypes used in the present study

Sl. No.	Genotypes No.	Name	Origin
1	G_1	AGS-79	OSRC, BARI
2	G_2	BS-13	OSRC, BARI
3	G_3	JOYAWAZA	OSRC, BARI
4	G_4	F-85-11347	OSRC, BARI
5	G_5	AGS-95	OSRC, BARI
6	G_6	GC-82-332411	OSRC, BARI
7	G_7	BOAS-5	OSRC, BARI
8	G_8	LG-92P-12-18	OSRC, BARI
9	G_9	BS-33	OSRC, BARI
10	G_{10}	GC-830059	OSRC, BARI
11	G_{11}	ASSET-95	OSRC, BARI
12	G_{12}	BARI SOYBEAN-6	OSRC, BARI
13	G_{13}	KANH-33	OSRC, BARI
14	G_{14}	NS-1	OSRC, BARI
15	G_{15}	GMOT-17	PGRC, BARI
16	G_{16}	LG-92P-1176	OSRC, BARI
17	G_{17}	CHINA-1	OSRC, BARI
18	G_{18}	MTD-16	OSRC, BARI
19	G_{19}	SHOHAG	OSRC, BARI
20	G_{20}	PK-327	OSRC, BARI
21	G_{21}	AUSTRALIA	OSRC, BARI
22	G_{22}	YESOY-4	OSRC, BARI
23	G_{23}	PI-4174-75	OSRC, BARI
24	G_{24}	MTD-452	OSRC, BARI
25	G_{25}	86017-66-6	OSRC, BARI
26	G_{26}	ASSET-93-19-13	OSRC, BARI
27	G_{27}	BARI SOYBEAN-5	OSRC, BARI
28	G_{28}	MTD-451	OSRC, BARI

Source: Bangladesh Agricultural Research Institute (BARI)

3.7 Land preparation

The experimental plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about to good tilth in the last week of November 2011. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly.

3.8 Manure and fertilizer application

The plots were fertilized with cow dung, urea, TSP and MP @ 5 ton, 60 kg, 120 kg, 70 kg per ha, respectively. The entire cow dung, TSP, MP and half of the urea were applied at the time of final land preparation. The remaining half of urea was applied as top dressing in two installments, first after 20 days and second after 45 days of sowing.

3.9 Seed sowing

Seeds of the 28 genotypes were sown on 12 December, 2011. The seedlings were emerged six to eleven days after sowing.

3.10 Intercultural operation

Intercultural operations were done as and when necessary.

3.10.1 Thinning

When the plants were well established, the soil around the base of each seedling was pulverized. Thinning was done 15 days after sowing for the proper development and avoid crowd environment.

3.10.2 Weeding and mulching

Several weeding and mulching were done as per requirement. At the very first stage weeding was done for ease of aeration and less competition seedling growth and mulch was provided after an irrigation to prevent crust formation and facilitate good aeration.

3.10.3 Irrigation and after-care

The plants were properly irrigated for 4 consecutive days. Then flood irrigation was given to the plants after flowering. Final irrigation was given during pod setting stage.

3.10.4. Pesticide application

During the cropping period, there was mosaic virus infestation in the field, In order to prevent this disease insecticide sprayed in the field. There were different types of weeds which were controlled effectively by hand weeding.

3.11 Harvesting

The plants were harvested at full maturity. Such maturity came with yellowing of leaves with completion of leaf shedding and the pod color mostly become dark brown. Different varieties were harvested at different dates as they reach maturity converting variable periods.

Photograph showing the experimental field in Plate 1, one replication view of the experimental field in Plate 2, soybean plant in the experimental field in Plate 3, A soybean plant with flower in Plate 4, A soybean plant with pod in Plate 5 and pod of soybean in Plate 6.

3.12 Data recording

Ten plants in each entry were selected randomly and were tagged. These tagged plants were used for recording observations for the following characters.

3.12.1 Days to first flowering

Determine as the days required from sowing to first anthesis.

3.12.2 Days to 50% flowering

Determine as the days required from sowing to 50% anthesis.

Plate 1: The experimental field

Plate 2: One replication view of the experimental field

Plate 3: Soybean plant in the experimental field

Plate 4: A soybean plant with flower

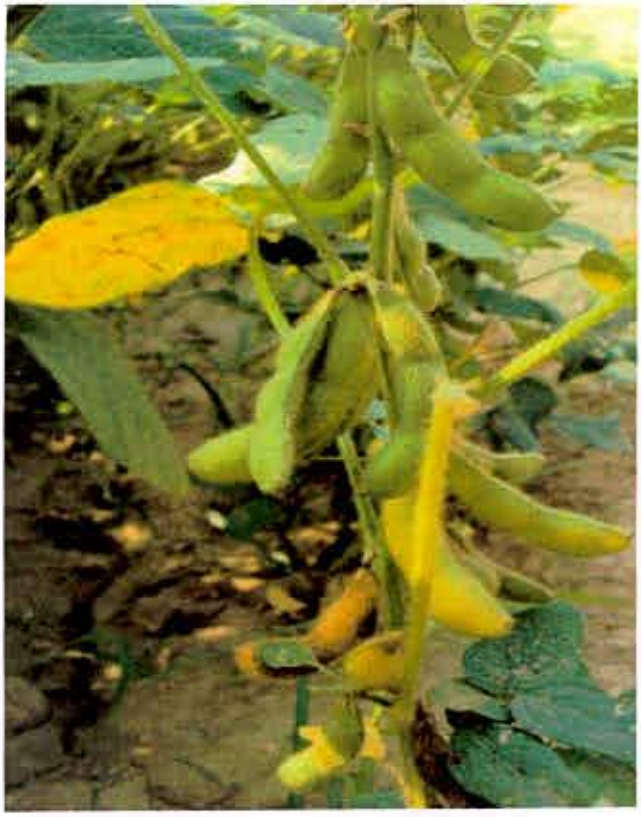


Plate 5: A soybean plant with pod

Plate 6: A pod of soybean

3.12.3 Days to maturity

The number of days was counted from the date of sowing to first harvesting.

3.12.4 Plant height (cm)

The average height of the main stem from the ground level to the tip measured at time of harvesting.

3.12.5 Number of branches per plant

Mean number of branches per plant counted from ten sample plant after harvest.

3.12.6 Pods per plant

Mean number of pods from ten randomly selected plants.

3.12.7 Pod length (cm)

Mean length of pods excluding peduncle from ten randomly selected plants.

3.12.8 Number of seeds per pod

Average number of seeds from ten randomly selected pods.

3.12.9 Seeds per plant

Mean number of seeds from ten randomly selected plants.

3. 12.10 Hundred seed weight (g)

Weight of 100 seeds selected at random from each plant was expressed in grams.

3.12.11 Seed yield per plant

Average seed yield from ten randomly selected plants was recorded in grams.

3.13 Statistical analysis:

Mean data of the characters were subjected to multivariate analysis. Univariate analysis of the individual character was done for all characters under study using the

mean values (Singh and Chaudhury, 1985) and was estimated using MSTAT-C computer programme. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV%) were also estimated using MSTAT-C. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2000 software through four techniques viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA).

3.13.1 Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.* (1955).

$$\text{Genotypic variance } (\sigma^2_g) = \frac{GMS - EMS}{r}$$

Where,

GMS = Genotypic mean sum of squares

EMS = Error mean sum of square

r = number of replications

$$\text{Phenotypic variance } (\sigma^2_{ph}) = \sigma^2_g + EMS$$

Where,

σ^2_g = Genotypic variance

EMS = Error mean sum of square

3.13.2 Estimation of genotypic and phenotypic co-efficient of variation

Genotypic and phenotypic co-efficient of variation were calculated by the formula suggested by Burton (1952)

$$\text{Genotypic co-efficient of variation (GCV \%)} = \frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100$$

Where,

σ^2_g = Genotypic variance

$\bar{x}$ = Population mean

Similarly,

The phenotypic co-efficient of variation was calculated from the following formula.

$$\text{Phenotypic co-efficient variation (PCV)} = \frac{\sqrt{\sigma^2 ph}}{\bar{x}} \times 100$$

Where,

σ^2_{ph} = Phenotypic variance

$\bar{x}$ = Population mean

3.13.3 Estimation of heritability

Broad sense heritability was estimated (Lush, 1943) by the following formula, suggested by Johnson *et al.* (1955).

$$h^2_b\% = \frac{\sigma^2_g}{\sigma^2_{ph}} \times 100$$

Where,

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.13.4 Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1943) and Johnson *et al.* (1955).

Genetic advance (GA) = K. h^2. σ_{ph}

$$GA = K.\frac{\sigma^2_g}{\sigma^2_{ph}}.\sigma_{ph}$$

Where,

K = Selection intensity, the value which is 2.06 at 5% selection intensity

σ_{ph}= Phenotypic standard deviation

h^2_b= Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.13.5 Estimation of genetic advance mean's percentage

Genetic advance as percentage of mean was calculated from the following formula as proposed by Comstock and Robinson (1952):

$$\text{Genetic advance (\% of mean)} = \frac{\text{Genetic Advance (GA)}}{\text{Population mean } (\bar{x})} \times 100$$

3.13.6 Estimation of simple correlation co-efficient:

Simple correlation co-efficients (r) was estimated with the following formula (Clarke, 1973; Singh and Chaudhary, 1985).

$$r = \frac{\sum xy - \frac{\sum x . \sum y}{N}}{\sqrt{\left\{\sum x^2 - \frac{(\sum x)^2}{N}\right\}\left\{\sum y^2 - \frac{(\sum y)^2}{N}\right\}}}$$

Where,

$\sum$ = Summation

x and y are the two variables correlated

N = Number of observations

3.13.7 Estimation of genotypic and phenotypic correlation co-efficient

For calculating the genotypic and phenotypic correlation co-efficient for all possible combinations the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956) were adopted.

The genotypic co-variance component between two traits and have the phenotypic co-variance component were derived in the same way as for the corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows:

$$\text{Genotypic correlation } (r_{gxy}) = \frac{GCOVxy}{\sqrt{GVx.GVy}} = \frac{\sigma_{gxy}}{\sqrt{(\sigma^2_{gx}.\sigma^2_{gy})}}$$

Where,

σ_{gxy} = Genotypic co-variance between the traits x and y

σ^2_{gx} = Genotypic variance of the trait x

σ^2_{gy} = Genotypic variance of the trait y

$$\text{Phenotypic correlation } (r_{pxy}) = \frac{PCOVxy}{\sqrt{PVx.PVy}} = \frac{\sigma_{pxy}}{\sqrt{(\sigma^2_{px}.\sigma^2_{py})}}$$

Where,

σ_{pxy} = Phenotypic covariance between the traits x and y

σ^2_{px} = Phenotypic variance of the trait x

σ^2_{py} = Phenotypic variance of the trait y

3.13.8 Estimation of path coefficient analysis

Path coefficient is a standardized partial regression coefficient and as such it is a measure of direct and indirect effect of set variables (component characters) as a dependent variable such as fruit yield. Direct and indirect effect of component characters on fruit yield were computed using appropriate correlation coefficient of different component characters as suggested by Wright (1921) and elaborated by Deway and Lu (1959).

Path coefficient analysis was done according to the procedure employed by Deway and Lu (1955) also quoted in Singh and Chaudhary (1985), using phenotypic correlation coefficient values. In path analysis, correlation coefficients between yield and yield contributing characters were partitioned into direct and indirect effects of yield contributing characters on seed yield per hectare. In order to estimate direct and indirect effects of the correlated characters, i. e. 1, 2, 3.....and 11 on yield y, a set of simultaneous equations (eight equations in this example) is required to be formulated as shown below:

$$r_{1.y} = P_{1.y} + r_{1.2}P_{2.y} + r_{1.3}P_{3.y} + r_{1.4}P_{4.y} + r_{1.5}P_{5.y} + r_{1.6}P_{6.y} + r_{1.7}P_{7.y} + r_{1.8}P_{8.y} + r_{1.9}P_{9.y} + r_{1.10}P_{10.y} + r_{1.11}P_{11.y}$$

$$r_{2.y} = r_{1.2}P_{1.y} + P_{2.y} + r_{2.3}P_{3.y} + r_{2.4}P_{4.y} + r_{2.5}P_{5.y} + r_{2.6}P_{6.y} + r_{2.7}P_{7.y} + r_{2.8}P_{8.y} + r_{2.9}P_{9.y} + r_{2.10}P_{10.y} + r_{2.11}P_{11.y}$$

$$r_{3.y} = r_{1.3}P_{1.y} + r_{2.3}P_{2.y} + P_{3.y} + r_{3.4}P_{4.y} + r_{3.5}P_{5.y} + r_{3.6}P_{6.y} + r_{3.7}P_{7.y} + r_{3.8}P_{8.y} + r_{3.9}P_{9.y} + r_{3.10}P_{10.y} + r_{3.11}P_{11.y}$$

$r_{4.y} = r_{1.4} P_{1.y} + r_{2.4} P_{2.y} + r_{3.4} P_{3.y} + P_{4.y} + r4_{1.5} P_{5.y} + r_{4.6} P_{6.y} + r_{4.7} P_{7.y} + r_{4.8} P_{8.y} + r_{4.9} P_{9.y} + r_{4.10} P_{10.y} + r_{4.11} P_{11.y}$

$r_{5.y} = r_{1.5} P_{1.y} + r_{2.5} P_{2.y} + r_{3.5} P_{3.y} + r_{4.5} P_{4.y} + P_{5.y} + r_{5.6} P_{6.y} + r_{5.7} P_{7.y} + r_{5.8} P_{8.y} + r_{5.9} P_{9.y} + r_{5.10} P_{10.y} + r_{5.11} P_{11.y}$

$r_{6.y} = r_{1.6} P_{1.y} + r_{2.6} P_{2.y} + r_{3.6} P_{3.y} + r_{4.6} P_{4.y} + r_{5.6} P_{5.y} + P_{6.y} + r_{6.7} P_{7.y} + r_{6.8} P_{8.y} + r_{6.9} P_{9.y} + r_{6.10} P_{10.y} + r_{6.11} P_{11.y}$

$r_{7.y} = r_{1.7} P1.y + r_{2.7} P_{2.y} + r_{3.7} P_{3.y} + r_{4.7} P_{4.y} + r_{5.7} P_{5.y} + r_{6.7} P_{6.y} + P_{7.y} + r_{7.8} P_{8.y} + r_{7.9} P_{9.y} + r_{7.10} P_{10.y} + r_{7.11} P_{11.y}$

$r_{8.y} = r_{1.8} P_{1.y} + r_{2.8} P_{2.y} + r_{3.8} P_{3.y} + r_{4.8} P_{4.y} + r_{5.8} P_{5.y} + r_{6.8} P_{6.y} + r_{7.8} P_{7.y} + P_{8.y} + r_{8.9} P_{9.y} + r_{8.10} P_{10.y} + r_{8.11} P_{11.y}$

$r_{9.y} = r_{1.9} P_{1.y} + r_{2.9} P_{2.y} + r_{3.9} P_{3.y} + r_{4.9} P_{4.y} + r_{5.9} P_{5.y} + r_{6.9} P_{6.y} + r_{7.9} P_{7.y} + r_{8.9} P_{8.y} + P_{9.y} + r_{9.10} P_{10.y} + r_{9.11} P_{11.y}$

$r_{10.y} = r_{1.10} P_{1.y} + r_{2.10} P_{2.y} + r_{3.10} P_{3.y} + r_{4.10} P_{4.y} + r_{5.10} P_{5.y} + r_{6.10} P_{6.y} + r_{7.10} P_{7.y} + r_{8.10} P_{8.y} + r_{9.10} P_{9.y} + P_{10.y} + r_{10.11} P_{11.y}$

$r_{11.y} = r_{1.11} P_{1.y} + r_{2.11} P_{2.y} + r_{3.11} P_{3.y} + r_{4.11} P_{4.y} + r_{5.11} P_{5.y} + r_{6.11} P_{6.y} + r_{7.11} P_{7.y} + r_{8.11} P_{8.y} + r_{9.11} P_{9.y} + r_{10.11} P_{10.y} + P_{11.y}$

Where,

r_{1y} = Genotypic correlation coefficients between y and I th character

(y= Grain yield)

P_{iy} = Path coefficient due to i th character (i= 1, 2, 3,……,11)

1 = Days to First Flowering

2 = Days to 50% Flowering

3 = Days to maturity

4 = Plant Height

5= Number of branches per plant

6 = Pods per plant

7 = Pod length (cm)

8 = Number of Seeds per Pod

9 = Seeds per Plant

10 = Hundred seed weight (g)

11 = Seed Yield per Plant (g)

Total correlation, say between 1 and y i. e., r_{1y} is thus partitioned as follows:

$P_{1.y}$ = the direct effect of 1 on y

$r_{1.2} P_{2.y}$ = indirect effect of 1 via 2 on y

$r_{1.3} P_{3.y}$ = indirect effect of 1 via 3 on y

$r_{1.4} P_{4.y}$ = indirect effect of 1 via 4 on y

$r_{1.5} P_{5.y}$ = indirect effect of 1 via 5 on y

$r_{1.6} P_{6.y}$ = indirect effect of 1 via 6 on y

$r_{1.7} P_{7.y}$ = indirect effect of 1 via 7 on y

$r_{1.8} P_{8.y}$ = indirect effect of 1 via 8 on y

$r_{1.9} P_{9.y}$ = indirect effect of 1 via 9 on y

$r_{1.10} P_{10.y}$ = indirect effect of 1 via 10 on y

$r_{1.11} P_{11.y}$ = indirect effect of 1 via 11 on y

Where,

$P_{1.y}, P_{2.y}, P_{3.y}$ ..... $P_{11.y}$ = Path coefficient of the independent variables 1, 2, 3,.....,11 on the dependent variable y, respectively.

$r_{1.y}, r_{2.y}, r_{3.y}$, ..., $r_{11.y}$ = Correlation coefficient of 1, 2, 3, ..., 11 with y, respectively.

After calculating the direct and indirect effect of the characters, residual effect (R) was calculated by using the formula given below (Singh and Chaudhary, 1985)

$$P^2_{RY} = 1 - (r_{1.y}P_{1.y} + r_{2.y}P_{2.y} + \ldots\ldots\ldots\ldots\ldots + r_{11.y}P_{11.y})$$

Where,

$P^2_{RY} = R^2$

And hence residual effect, $R = (P^2_{RY})^{1/2}$

$P_{1.y}$ = Direct effect of the i th character on yield y.

$r_{1.y}$ = Correlation of the i th character with yield y.

3.14 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance (D^2) statistic and its auxiliary analyses. The parents selection in hybridization programme based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) suggested that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a hybridization programme. Multivariate analysis viz. Principal Component analysis, Principal Coordinate analysis, Cluster analysis and Canonical Vector analysis (CVA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

3.14.1 Principal Component analysis (PCA)

Principal Component analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, Principles components were computed from the correlation matrix and genotypes

scores obtained for first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity. Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.14.2 Principal Coordinate analysis (PCO)

Principal Coordinate analysis is equivalent to PCA but it is used to calculate inter unit distances. Through the use of all dimension of p it gives the minimum distance between each pair of the n points using similarity matrix (Digby *et al.*, 1989).

3.14.3 Cluster analysis (CA)

Cluster analysis divides the genotypes of a data set into some number of mutually exclusive groups. Clustering was done using non-hierarchical classification. In Genstat, the algorithm is used to search for optimal values of chosen criterion proceeds as follows. Starting from some initial classification of the genotypes into required number of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

3.14.4 Canonical Vector analysis (CVA)

Canonical vector analysis (CVA) finds linear combination of original variabilities that maximize the ratio of between group to within group variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing of the ratio of among groups to the within group variations. The canonical vector are based upon the roots and vectors of WB, where W is the pooled within groups covariance matrix and B is the among groups covariance matrix.

3.14.5 Calculation of D^2 values

The Mahalanobis's distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952), and Singh and Chaudhury (1985). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statistic is defined by the formula

$$D^2 = \sum_{i}^{x} d_i^2 = \sum_{i}^{x} (Y_i^j - Y_j^k) \qquad (j \neq k)$$

Where,

Y = Uncorrelated variable (character) which varies from i = 1 ------to x

x = Number of characters.

Superscript j and k to Y = A pair of any two genotypes.

3.14.6 Computation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

$$\text{Average intra-cluster distance} = \frac{\sum D_i^2}{n}$$

Where,

D_i^2 = the sum of distances between all possible combinations (n) of genotypes included in a cluster.

n= Number of all possible combinations between the populations in cluster.

3.14.7 Computation of average inter-cluster distances

Average inter-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

$$\text{Average inter-cluster distance} = \frac{\sum D_{ij}^2}{n_i \times n_j}$$

Where,

$\sum D_{ij}^2$ = The sum of distances between all possible combinations of the populations in cluster i and j.

n_i= Number of populations in cluster i.

n_j= Number of populations in cluster j.

3.14.8 Cluster diagram

Using the values of intra and inter-cluster distances ($D = \sqrt{D^2}$), a cluster diagram was drawn as suggested by Singh and Chuadhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

3.14.9 Selection of varieties for future hybridization programme

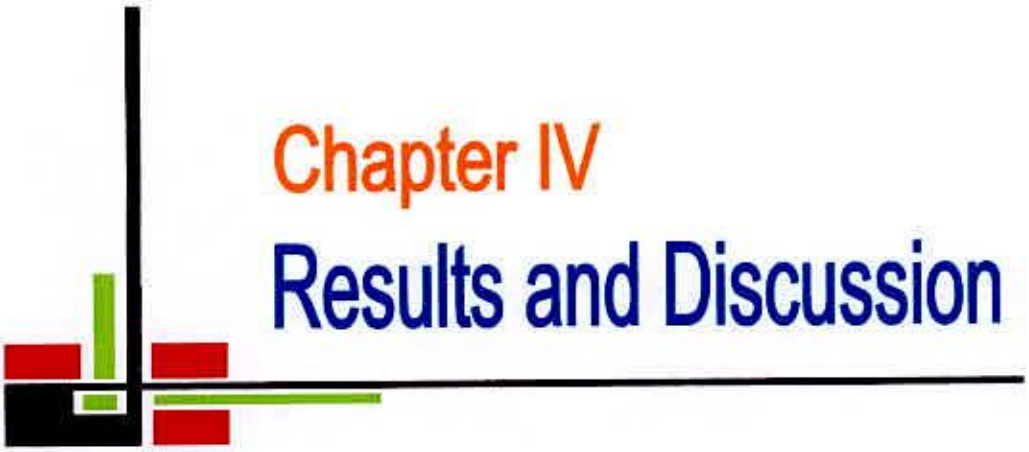
Divergence analysis is usually performed to identify the diverse genotypes for hybridization purposes. The genotypes grouped together are less divergent among themselves than those, which fall into different clusters. Clusters separated by largest statistical distance (D^2) express the maximum divergence among the genotypes included into these different clusters. Variety (s) or line(s) were selected for efficient hybridization programme according to Singh and Chuadhury (1985). According to them the following points should be considered while selecting genotypes for hybridization programme:

i. Choice of cluster from which genotypes are selected for use as parent(s)

ii. Selection of particular genotype(s) from the selected cluster(s)

iii. Relative contribution of the characters to the total divergence

iv. Other important characters of the genotypes



Chapter IV

Results and Discussion

CHAPTER IV

RESULTS AND DISCUSSION

The results obtained from the study are presented and discussed in this chapter. The data pertaining to twenty eight soybean genotypes as well as yield and its contributing characters were computed and statistically analyzed and the result of the present investigation of genetic diversity, correlation co-efficient and path analysis in Soybean (*Glycine max* (L.) Merrill) carried out during Rabi 2011-12 are presented in the following sections:

4.1 Genetic parameters

4.2 Genetic variability, heritability and genetic advance

4.3 Correlation co-efficient

4.4 Path co-efficient analysis

4.5 Multivariate analysis

4.1 Genetic parameters

The analysis of variance indicated significantly higher amount of variability present among the genotypes for all the characters studied *viz*., days to first flowering, days to 50% flowering, days to maturity, plant height, branches per plant, number of pods per plant, pod length, hundred seed weight, number of seeds per pod, seeds per plant, seed yield per plant (Appendix VI). The results clearly indicated that there exists high variability for yield and yield components among the genotypes studied. Therefore there is a lot of scope for selection for majority of the traits in the genotypes. The mean sum of squares of all the 11 characters is presented in Appendix VI.

4.2 Genetic variability, heritability and genetic advance

The magnitude of genetic variability can determine the pace and quantum of genetic improvement through selection or through hybridization followed by selection. The success of crop improvement program depends on the extent of genetic variability existing in the population or germplasm. Phenotypic variance measures the magnitude of variation arising out of differences in phenotypic values while the genotypic variance measures the magnitude of variation due to difference within the genotypic values. Heritability estimates aim in determining the relative amount of heritable portion of variation.

Narrow gap between PCV and GCV for all the characters presence under these study, suggested that these traits studied has low environmental influence. The estimates of heritability alone fail to indicate the response to selection (Johnson *et al.,* 1955). Therefore, the heritability estimates appears to be more meaningful when accompanied by estimates of genetic advance. The genetic advance as per cent of mean (GAM) was also estimated.

The estimates of mean, range, genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic advance as per cent mean for all the characters were studied and the results are presented in Table 2 and depicted in Fig. 1 and 2. The mean performance of soybean genotypes for various growth characters and yield components are presented in Appendix IV.

4.2.1 Days to first flowering

The mean number of days to first flowering was 66.15. It had a range of 51.67 to 76.33 days. The accession 'AUSTRALIA' was the earliest to flower while 'F-85-11347' was late to flower (Appendix IV). The Genotypic, phenotypic and environmental variances observed were 37.97, 38.26 and 0.29, respectively (Table 2). The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait. The difference between the genotypic co-efficient of variation

(9.31) and phenotypic co-efficient of variation (9.35) were close to each other. There was a very little difference between phenotypic and genotypic co-efficient of variation, indicating minor environmental influence on this character. The heritability (99.25%) estimates for this trait was high, genetic advance (12.65) was moderately high and genetic advance over percentage of mean (19.12) was found high, indicated that this trait was controlled by non-additive gene. Agrawal *et al.* (2001) found that GCV were moderate for days to flower initiation, days to flower termination, whereas low for days to maturity. Phenotypic appearance of flower is presented in Plate 7 and Plate 8.

4.2.2 Days to 50% flowering

Significant differences were recorded among the entries with respect to days to 50% flowering. The value ranged from 55.33 to 79.00 days, in the genotype 'AUSTRALIA' and 'F-85-11347' respectively (Appendix IV). The Genotypic, phenotypic and environmental, variances observed were 36.15, 37.02 and 0.87, respectively (Table 2). The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait. The difference between the genotypic co-efficient of variation (8.64) and phenotypic co-efficient of variation (8.74) were close to each other (Table 2 and Fig 1) indicating minor environmental influence on this character. The heritability (97.65%) estimates for this trait was high, genetic advance (12.24) was moderately high and genetic advance over percentage of mean (17.59) were found moderately high, indicated that this trait was controlled by non-additive gene. Bangar *et al.* (2003) reported that phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV).

4.2.3 Days to maturity

Significant mean sum of square for plant maturity (4,101.14) in soybean indicated considerable difference among the genotypes studied (Table 2). The value ranged from 105.33 to 132.00 with a mean of 124.29. The genotype 'BS-13' had highest and

Table 2. Estimation of genetic parameters in eleven characters of 28 genotypes in soybean

Parameters	Range	Mean	MS	CV (%)	σ^2p	σ^2g	σ^2e	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
DFF	51.67-76.33	66.15	395.46**	0.81	38.26	37.97	0.29	9.35	9.31	0.81	99.25	12.65	19.12
D50%F	55.33-79.00	69.6	125.79**	1.34	37.02	36.15	0.87	8.74	8.64	1.34	97.65	12.24	17.59
DM	105.33-132.00	124.29	4,101.14**	0.15	50.66	50.62	0.04	5.73	5.72	0.15	99.93	14.65	11.79
PH	21.90-79.87	56.89	153.98**	3.84	248.03	243.26	4.77	27.68	27.42	3.84	98.08	31.82	55.93
BPP	1.80-5.87	4.12	40.76**	8.21	1.63	1.52	0.11	31.01	29.9	8.21	92.98	2.45	59.4
NPP	24.62-59.57	38.83	48.76**	6.09	94.46	88.88	5.58	25.03	24.28	6.09	94.09	18.84	48.52
PL	2.53-4.19	3.03	150.46**	1.69	0.13	0.13	0	12.08	11.96	1.69	98.03	0.74	24.4
NSP	2.37-2.66	2.51	7.88**	1.8	0.01	0	0	3.27	2.73	1.8	69.63	0.12	4.69
SPP	60.70-158.37	97.55	66.76**	5.42	639.6	611.69	27.91	25.93	25.35	5.42	95.64	49.82	51.08
HSW	6.27-16.57	10.49	224.84**	2.48	5.12	5.05	0.07	21.56	21.42	2.48	98.68	4.6	43.83
SYP	5.73-17.40	10.16	78.98**	6.17	10.6	10.21	0.39	32.05	31.45	6.17	96.3	6.46	63.57

** Correlation is significant at the 0.01 level.

DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), BPP = Branches per plant, NPP = Number of pods per plant, PL = Pod length (cm), NSP = Number of seeds per pod, SPP = Seeds per plant, HSW = Hundred seed weight (g), SYP = Seed yield per plant (g), MS = mean sum of square, CV (%) = Coefficient of variation, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance,σ^2 e = Environmental variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation

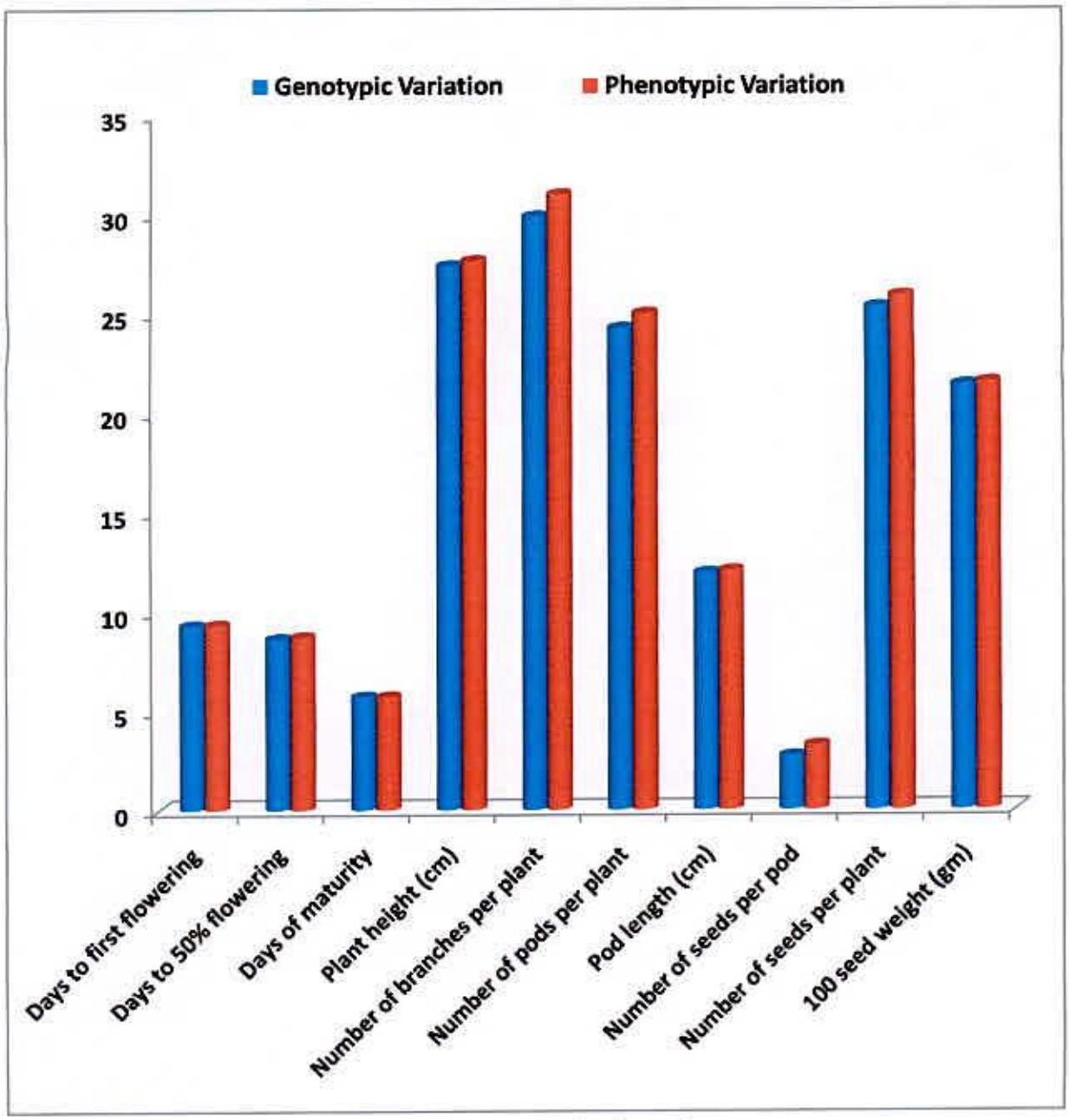


Fig 1: Genotypic and phenotypic variability in soybean

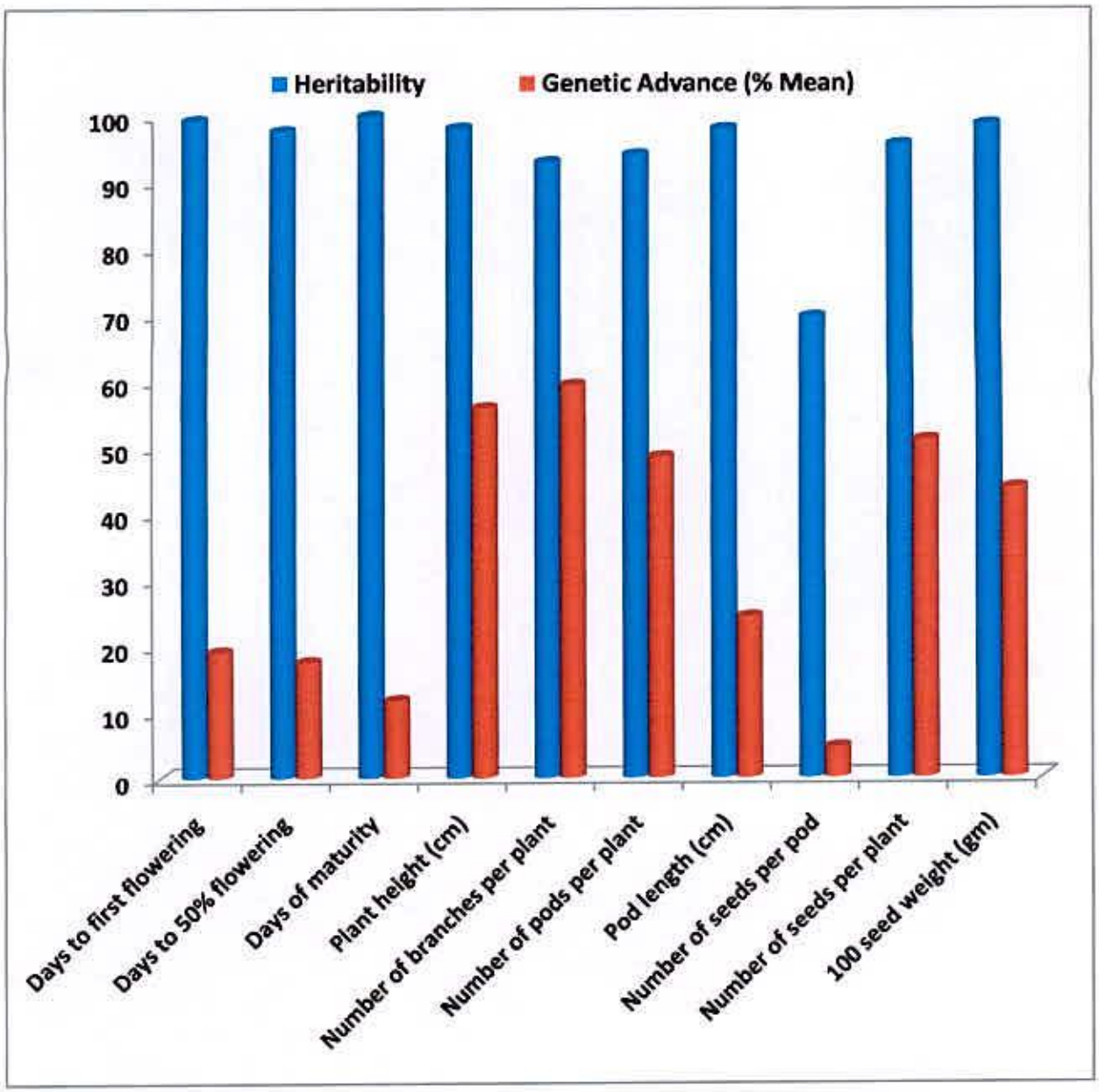


Fig 2: Heritability and genetic advance over mean in soybean

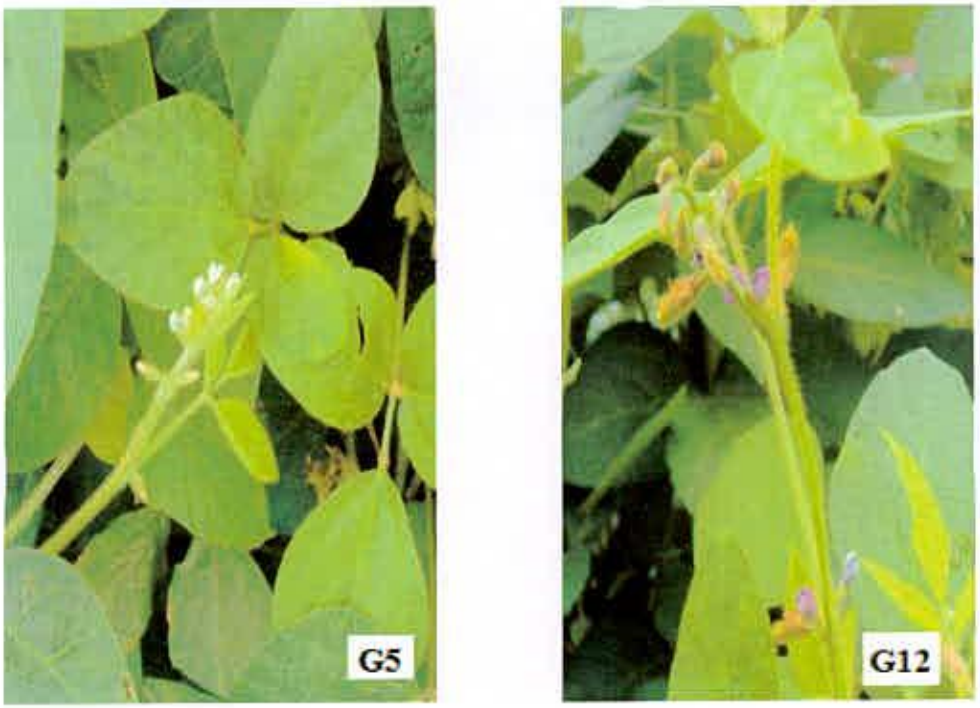


Plate 7: Showing phenotypic variation in flower between G5 and G12 genotype of soybean

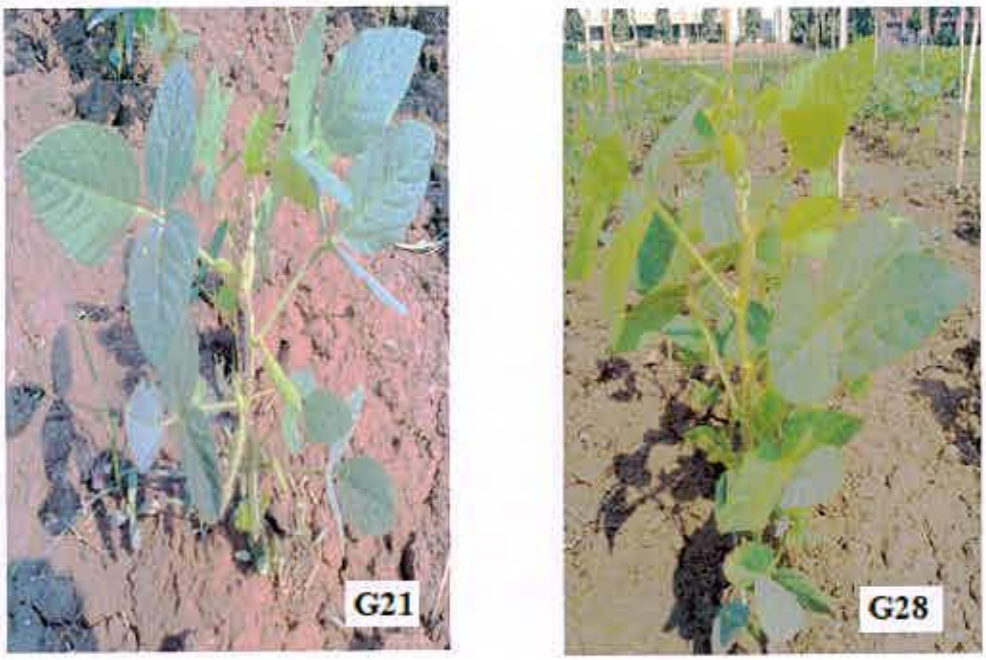


Plate 8: Showing phenotypic variation in leaf and stem between G21 and G28 genotype of soybean

lowest in the genotype 'AUSTRALIA' (Appendix IV). The phenotypic variance (50.66) appeared to be higher than the genotypic variance (50.62) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 5.72 and 5.73, respectively which were close to each other (Table 2). There was a very little difference between phenotypic and genotypic co-efficient of variation, indicating minor environmental influence on this character. The heritability (99.93%) estimates for this trait was high, genetic advance (14.65) moderately high and genetic advance in per cent of mean (11.79) was found low, revealed that this trait was governed by additive gene. Jangale *et al.* (1994) observed that high heritability was observed for days to maturity. Bhandarkar (1999) reported that high heritability and genetic advance for days to maturity in soybean.

4.2.4 Plant height (cm)

The grand mean plant height recorded was 56.89 cm. It ranged from 21.90 cm to 79.87 cm (Table 2). The analysis of variance revealed highly significant differences among the genotypes with respect to plant height. The maximum plant height (79.87 cm) was recorded by the genotype 'MTD-451' and the lowest plant height (21.90 cm) was recorded by 'AUSTRALIA' (Appendix IV). The highest genotypic and phenotypic variance was observed 243.26 and 248.03, respectively for plant height with large environmental influence. The phenotypic co-efficient of variation (27.68) was higher than the genotypic co-efficient of variation (27.42), which indicated presence of considerable variability among the genotypes for this trait. The heritability (98.08%) estimates for this trait was moderately high, genetic advance (31.82) was high and genetic advance in per cent of mean (55.93) was found also high, revealed that this trait was governed by non-additive gene. Plant height exhibited high heritability and high genetic advance as per cent mean in case of soybean which is similar to the earlier findings by Archana *et al.* (1999); Jain and Ramgiry(2000).

4.2.5 Number of branches per plant

In case of number of branches per plant mean sum of square significant (40.76) in soybean indicated considerable difference among the genotypes studied (Table 2). It ranged from 1.80 to 5.87 with a mean value of 4.12. Maximum number of branches recorded in 'MTD-451' and 'SHOHAG' genotype showed the minimum number of branches (Appendix IV). The phenotypic variance (1.63) appeared to be higher than the genotypic variance (1.52) suggested considerable influence of environment on the expression of the genes controlling this trait (Fig 1). The genotypic co-efficient of variation and phenotypic co-efficient of variation were 29.90 and 31.01 respectively which indicated presence of considerable variability among the genotypes. The heritability (92.98%) estimates for this trait was moderately high, genetic advance (2.45) was low and genetic advance in per cent of mean (59.40) were found very high, revealed that this trait was governed by additive gene. Bangar *et al.* (2003) reported that phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV). The GCV and PCV estimates were highest for branch number per plant.

4.2.6 Pods per plant

Significant mean sum of square for pods per plant (48.76) in soybean indicated existence of considerable variation for this trait (Table 2). The number of pods per plant was ranged from 24.62 to 59.57 with mean of 38.83. The minimum number of pods per plant was observed in accession '86017-66-6' while maximum number of pods per plant was found in the genotype 'F-85-11347' (Appendix IV). The phenotypic variance (94.46) appeared to be higher than the genotypic variance (88.88) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 24.28 and 25.03, respectively which indicated presence of considerable variability among the genotypes. The heritability (94.09%) estimates for this trait was high, genetic advance (18.84) was moderately high and genetic advance in per cent of mean (48.52) was found high, revealed that this trait was governed by non-additive gene. Pods per plant showed high heritability with high

genetic advance in soybean which is similar to the earlier findings by Singh *et al.* (2000); Dobhal and Gautam (1995); Jangle *et al.* (1994); Jagtap and Mehetre (1994).

4.2.7 Pod length (cm)

Mean sum of square for pod length (150.46) in soybean highly significant indicated considerable difference among the genotypes studied (Table 2). It ranged from 2.53 to 4.19 cm with a mean of 3.03 cm. The minimum pod length was recorded by the accession 'MTD-16' and accession 'PI-4174-75' showed the maximum pod length (Appendix IV). The phenotypic variance (0.13) and genotypic variance (0.13) suggested that there was no influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 11.96 and 12.08, respectively which indicated presence of considerable variability among the genotypes. The heritability (98.03%) estimates for this trait was high, genetic advance (0.74) was very low and genetic advance in per cent of mean (24.40) was found moderately high, revealed that this trait was governed by additive gene. Dobhal (1995) observed total genetic distance was highest for pod length. Phenotypic appearance in pod presented in Plate 9.

4.2.8 Number of seeds per pod

Significant mean sum of square for number of seeds per pod (7.88) in soybean indicated existence of considerable variation for this trait (Table 2). The germplasm accessions differed significantly for this character. The values ranged from 2.37 to 2.66 with a mean of 2.51. The genotype 'GC-82-332411' had highest number of seeds per pod while it was lowest in the genotype 'BS-13' (Appendix IV).The phenotypic variance (0.01) appeared to be higher than the genotypic variance (0.00) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 2.73 and 3.27, respectively which indicated presence of considerable variability among the genotypes. The heritability (69.63%) estimates for this trait was low, genetic advance (0.12) and genetic advance in per cent of mean

Plate 9: Showing phenotypic variation in pod and stem between G12 and G21 genotype of soybean

(4.69) was found very low (Table 2), revealed that this trait was governed by non-additive gene. Jangale *et al.* (1994) reported that high heritability was observed for seeds per pod. Chamundeswori and Aher (2003) revealed that number of seeds per pod showed significant genetic variation in case of genotypes of soybean.

4.2.9 Seeds per plant

The value of mean sum of square for seeds per plant (66.76) in soybean significant indicated existence of considerable variation for this trait (Table 2). It ranged from 60.70 to 158.37 with a mean of 97.55. Highest seeds per plant were recorded by the accession 'F-85-11347' while accession '86017-66-6' showed the lowest seeds per plant (Appendix IV). The phenotypic variance (639.60) appeared to be higher than the genotypic variance (611.69) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 25.35 and 25.93, respectively which indicated presence of considerable variability among the genotypes. The heritability (95.64%) estimates for this trait was high, genetic advance (49.82) was very high and genetic advance in per cent of mean (51.08) was found high, revealed that this trait was governed by non-additive gene. Phenotypic variation in seeds is presented in Plate 10.

4.2.10 Hundred seed weight (g)

The mean sum of square for hundred seed weight (224.84) in soybean significant indicated considerable difference among the genotypes studied (Table 2). The mean hundred seed weight noticed was 10.49 g with a range of 6.27g to 16.57g. The line 'GC-830059' showed the minimum hundred seed weight and the maximum hundred seed weight was recorded in the accession 'PI-4174-75' (Appendix IV). The phenotypic variance (5.12) appeared to be lower than the genotypic variance (5.05) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 21.42 and 21.56, respectively which were close to each

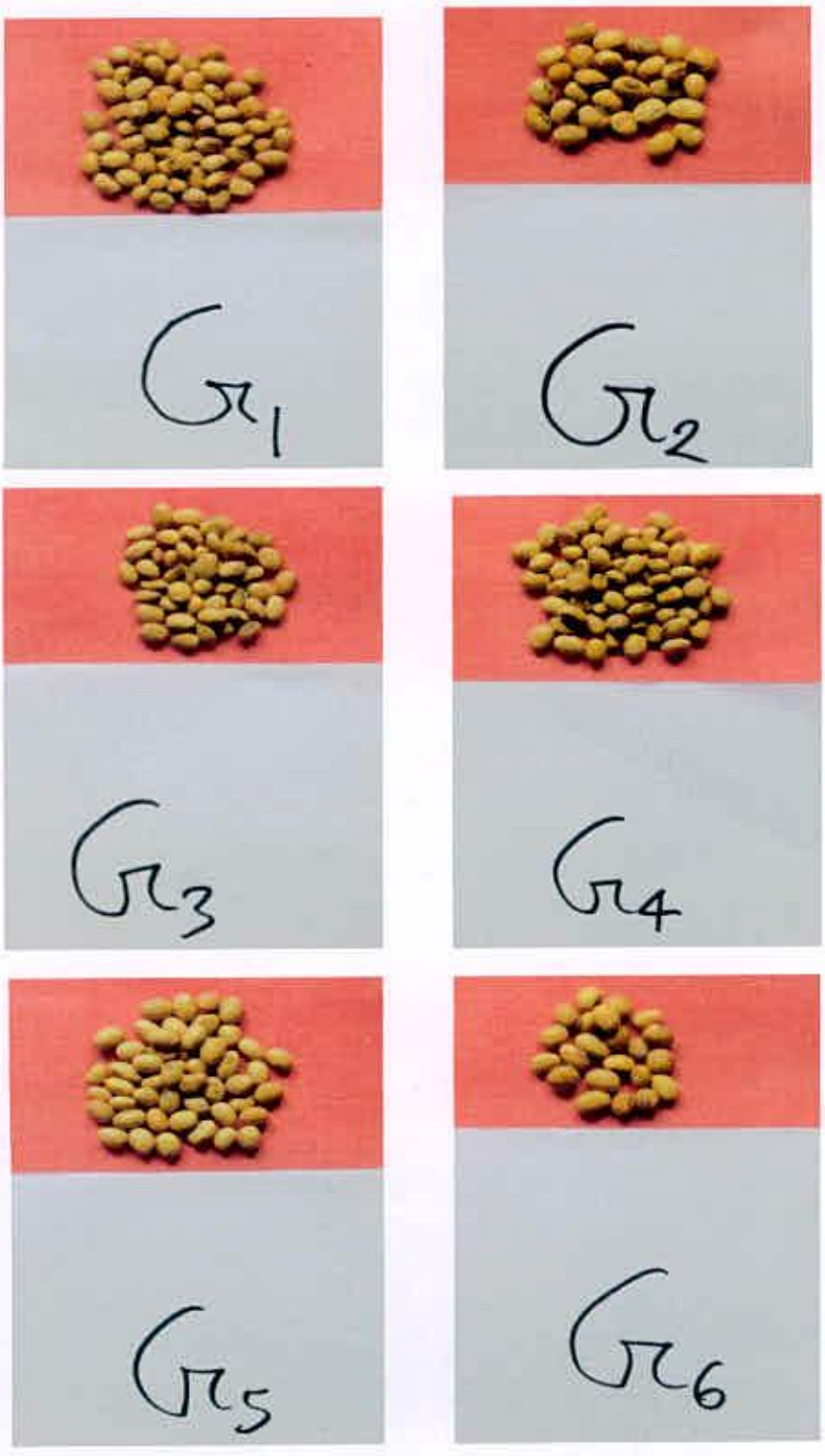


Plate 10 a: Showing phenotypic variation in seeds among different genotypes of soybean (G_1-G_6)

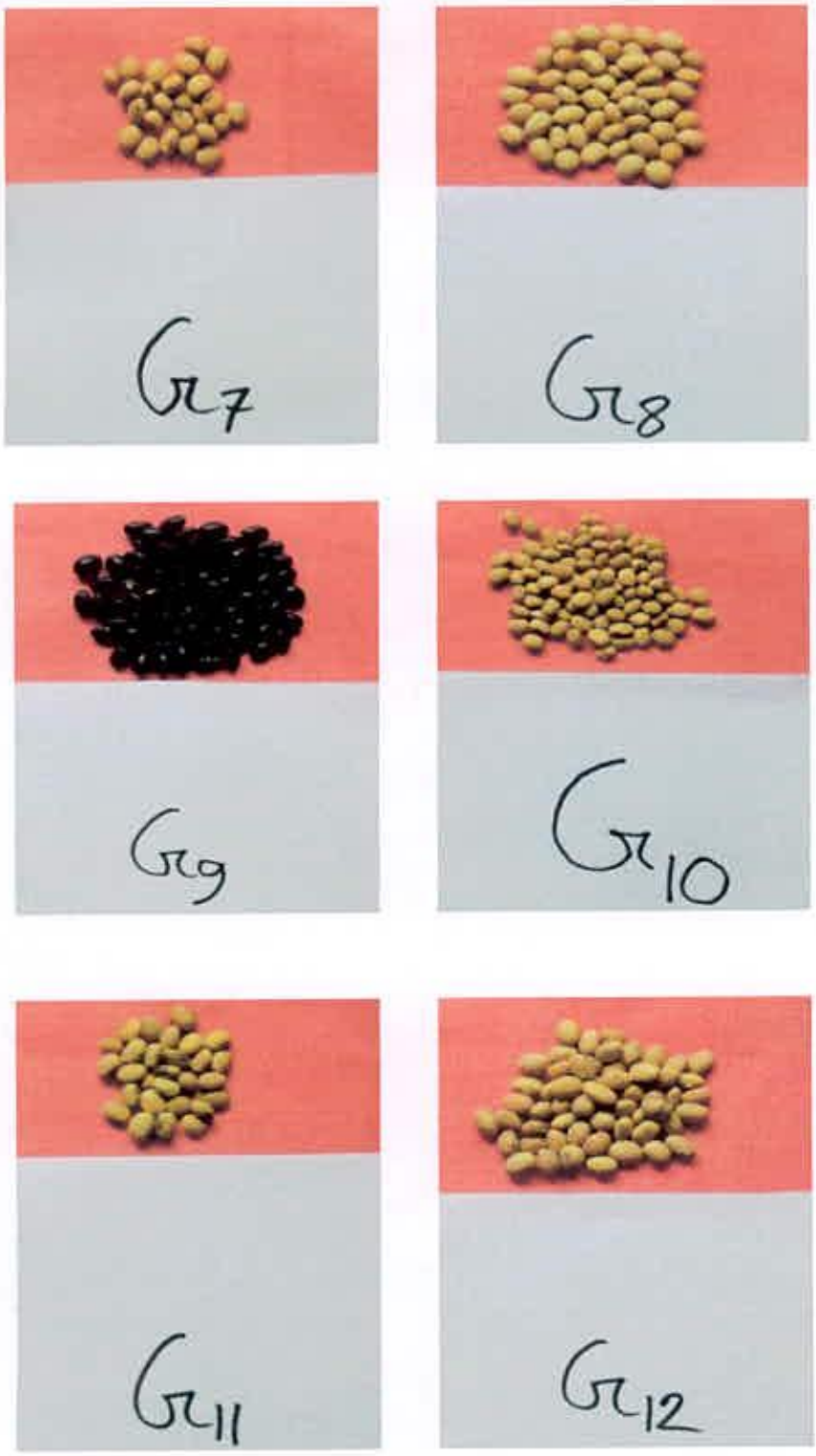


Plate 10 b: Showing phenotypic variation in seeds among different genotypes of soybean (G_7-G_{12})

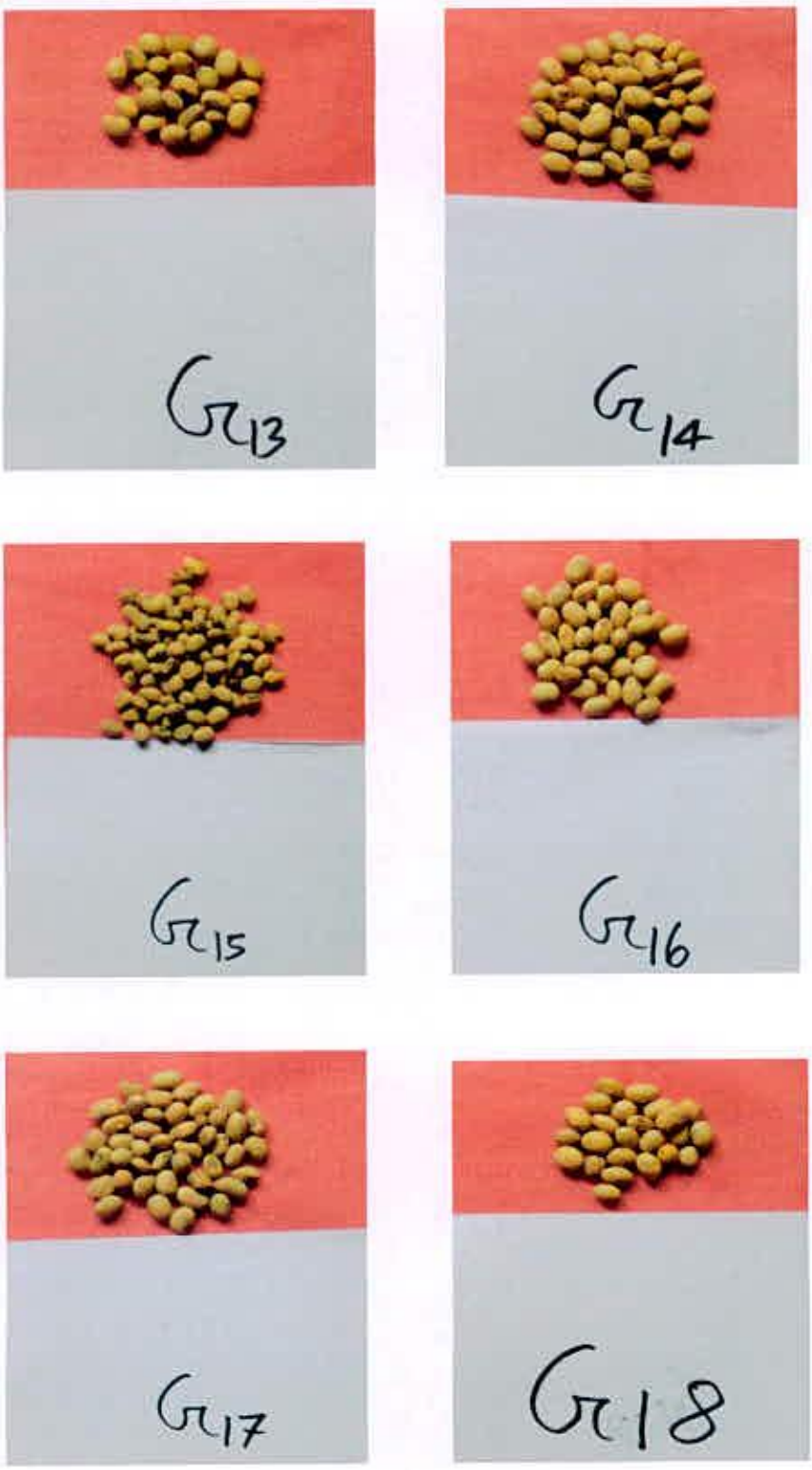


Plate 10 c: Showing phenotypic variation in seeds among different genotypes of soybean (G_{13}-G_{18})

Plate 10 d: Showing phenotypic variation in seeds among different genotypes of soybean (G_{19}-G_{24})

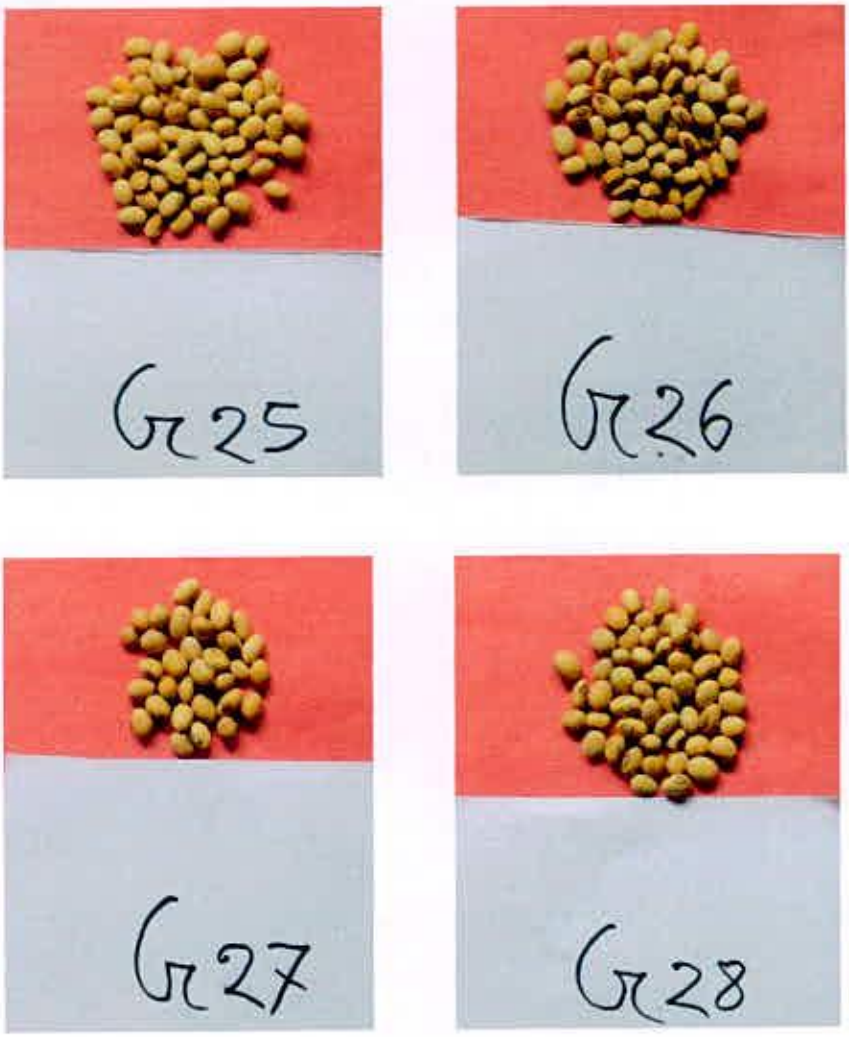


Plate 10 e: Showing phenotypic variation in seeds among different genotypes of soybean (G_{25}-G_{28})

other. There was a very little difference between phenotypic and genotypic co-efficient of variation, indicating minor environmental influence on this character. The heritability (98.68%) estimates for this trait was very high, genetic advance (4.60) was low and genetic advance in per cent of mean (43.83) was found high, revealed that this trait was governed by additive gene. Major *et al.* (1996) observed high genotypic and phenotypic co-efficient of variation for 100 seed weight and grain yield. Nehru *et al.* (1999) reported that 100 seed weight had high heritability but low genetic advance in case of soybean.

4.2.11 Seed yield per plant (g)

In case of seed yield per plant, mean sum of square (78.98) in soybean significant indicated existence of considerable variation for this trait (Table 2). The mean seed yield per plant was 10.16 g with a range of 5.73 g to 17.40 g in the genotype '86017-66-6 and 'PI-4174-75', respectively. The phenotypic variance (10.60) appeared to be higher than the genotypic variance (10.21) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 31.45 and 32.05 respectively which indicated presence of considerable variability among the genotypes. The heritability (96.30%) estimates for this trait was high, genetic advance (6.46) low and genetic advance in per cent of mean (63.57) was found very high, revealed that this trait was governed by additive gene. Malhotra (1973) observed that seed yield had the highest co-efficient of genetic variation and predicted genetic advance as a percentage of mean. Shrivastava and Shukla (1998) revealed that seed yield per plant had high heritability coupled with high expected genetic advance. The genotypic co-efficient of variation and phenotypic co-efficient of variation is high which is similar to the earlier findings by Singh *et al.* (2000).

4.3 Correlation co-efficient

We know yield is the resultant of combined effect of several component characters and environment. Understanding the interaction of characters among themselves and with environment has been of great use in the plant breeding. Through correlation studies provide information on the nature and extent of association between only two pairs of metric characters. From this it would be possible to bring about genetic up gradation in one character by selection of the other of a pair. Hence, an attempt has been made to study the character association in the soybean accessions at both the levels.

Pearson correlation analysis among seed yield and its contributing characters are shown in Table 3. For clear understanding correlation coefficients are separated into genotypic and phenotypic level in Table 4. The genotypic correlation coefficients in most cases were higher than their phenotypic correlation coefficients indicating the genetic reason of association. While phenotypic correlation coefficient were higher than genotypic correlation coefficient indicating suppressing effect of the environment which modified the expression of the characters at phenotypic level. The depicted of genotypic and phenotypic correlation coefficient among yield and yield contributing characters of soybean are shown in Fig 3.

4.3.1 Days to first flowering:

Days to first flowering showed highly significant and positive correlation with days to 50% flowering (0.999 and 0.985), days to maturity (0.917 and 0.913) and branches per plant (0.527 and 0.509) both at genotypic and phenotypic levels (Table 4). It had also highly significant and positively correlated with plant height (0.464 and 0.460) and pod length (0.268 and 0.265) at both the genotypic and phenotypic level. Chand (1999) reported that days to flowering positively correlated with seed yield in soybean.

Table 3. Pearson correlation coefficients among different pairs of yield and yield contributing characters for different genotypes of soybean

	D50%F	DM	PH	BPP	NPP	PL	NSP	SPP	HSW	SYP
DFF	0.98**	0.91**	0.45**	0.50**	0.18	0.26**	0.02	0.20	-0.03	0.17
D50%F		0.90**	0.46**	0.51**	0.19	0.28**	-0.01	0.21*	-0.02	0.18
DM			0.40**	0.43**	0.146	0.19	-0.03	0.15	-0.07	0.11
PH				0.83**	0.63**	0.32**	0.01	0.66**	-0.28**	0.37**
BPP					0.53**	0.46**	0.06	0.55**	-0.11	0.39**
NPP						0.25*	0.29**	0.98**	-0.22	0.66**
PL							0.25**	0.32**	0.62**	0.72**
NSP								0.34**	0.07	0.33**
SPP									-0.16	0.72**
HSW										0.55**

** = Significant at 1%.
* = Significant at 5%.

DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), BPP = Branches per plant, NPP = Number of pods per plant, PL = Pod length (cm), NSP = Number of seeds per pod, SPP = Seeds per plant, HSW = Hundred seed weight (g), SYP = Seed yield per plant (g).

Table 4. Genotypic (G) and phenotypic (P) correlation coefficient among different pairs of yield and yield contributing characters for different genotypes of soybean

		D50%F	DM	PH	BPP	NPP	PL	NSP	SPP	HSW	SYP
DFF	G	0.999**	0.917**	0.464**	0.527**	0.185	0.268**	0.015	0.206	-0.033	0.174
	P	0.985**	0.913**	0.460**	0.509**	0.003	0.265**	0.016	0.202	-0.033	0.170
D50%F	G		0.916**	0.480**	0.543**	0.207	0.294**	0.034	0.224*	-0.026	0.194
	P		0.905**	0.467**	0.518**	0.200	0.285**	-0.009	0.203	-0.025	0.186
DM	G			0.411**	0.451**	0.149	0.200	-0.042	0.161	-0.070	0.119
	P			0.408**	0.435**	0.146	0.198	-0.036	0.159	-0.070	0.117
PH	G				0.865**	0.666**	0.326**	0.023	0.684**	-0.284**	0.389**
	P				0.838**	0.640**	0.326**	0.017	0.662**	-0.282**	0.380**
BPP	G					0.556**	0.490**	0.109	0.585**	-0.121	0.413**
	P					0.530**	0.465**	0.067	0.558**	-0.113	0.397**
NPP	G						0.266**	0.347**	0.991**	-0.232*	0.664**
	P						0.255**	0.291**	0.984**	-0.226*	0.662**
PL	G							0.300**	0.336**	0.635**	0.749**
	P							0.256**	0.325**	0.626**	0.727**
NSP	G								0.388**	0.100	0.380**
	P								0.340**	0.078	0.332**
SPP	G									-0.165	0.719**
	P									-0.163	0.722**
HSW	G										0.558**
	P										0.551**

** = Significant at 1%.
* = Significant at 5%.

DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), BPP = Branches per plant, NPP = Number of pods per plant, PL = Pod length (cm), NSP = Number of seeds per pod, SPP = Seeds per plant, HSW = Hundred seed weight (g), SYP = Seed yield per plant(g).

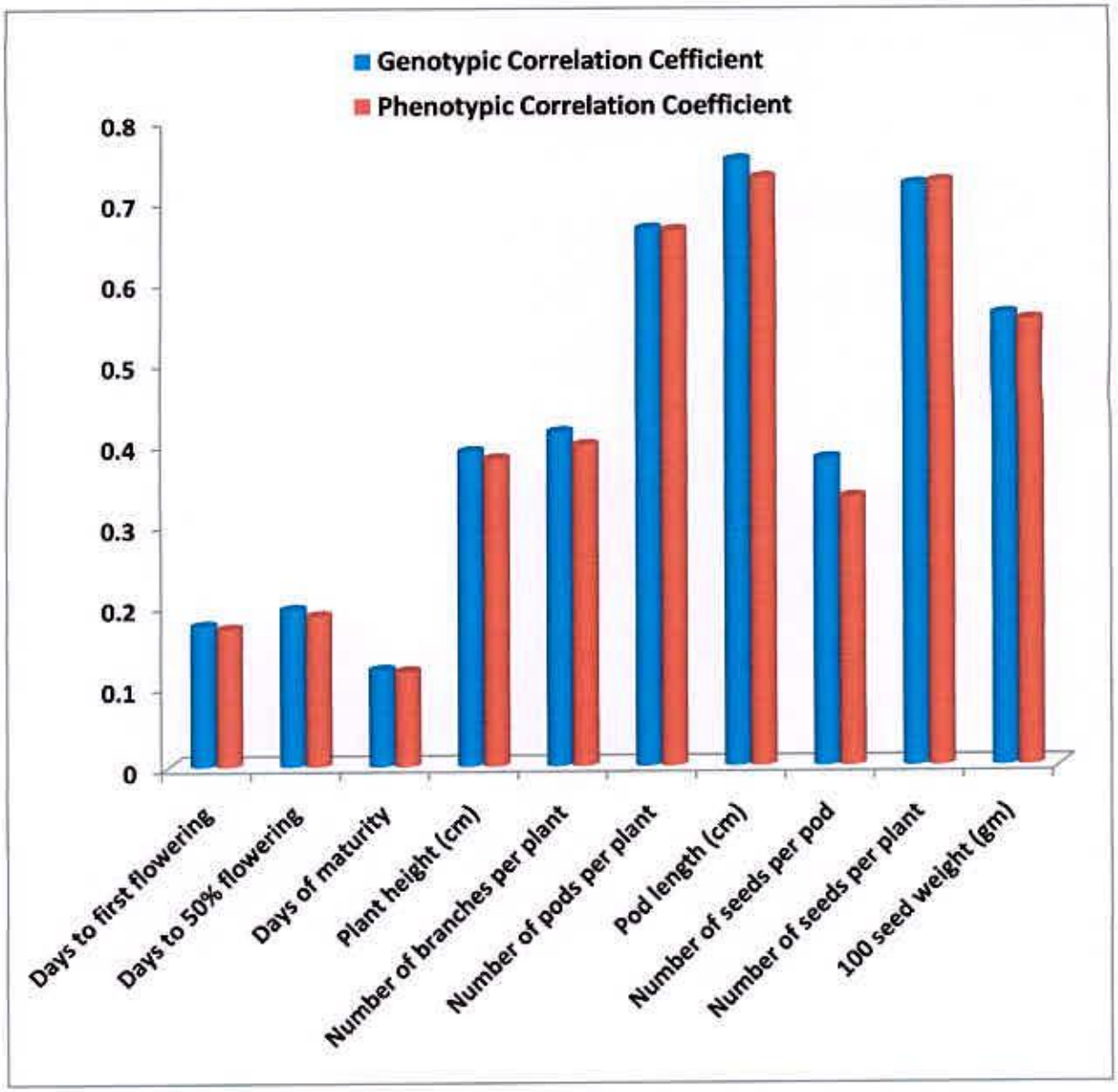


Fig 3: Genotypic and phenotypic correlation coefficient of different character with yield

4.3.2 Days to 50% flowering:

The correlation of days to 50% flowering with number days of maturity (0.916 and 0.905), plant height (0.480 and 0.467), branches per plant (0.543 and 0.518) and pod length (0.294 and 0.285) was positive and highly significant at both the genotypic and phenotypic levels (Table 4). However, it had significant and positively correlation with seeds per plant (0.224) at the genotypic level. Inderjit *et al.* (2007) reported that days to 50% flowering were significantly correlated with grain yield.

4.3.3 Days to maturity:

Days to maturity had significant positive association with plant height (0.411 and 0.408) and branches per plant (0.451 and 0.435) at both the genotypic and phenotypic levels (Table 4). Chand (1999) observed that maturity of soybean was positively correlated with seed yield.

4.3.4 Plant height (cm):

Plant height had highly significant and positive correlation with branches per plant (0.865 and 0.838), pods per plant (0.666 and 0.640), pod length (0.326) and seeds per plant (0.684 and 0.662) at both the genotypic and phenotypic levels (Table 4). A significant negative correlation of hundred seed weight (-0.284 and -0.282) showed at both the levels. Plant height exhibited negatively correlated with 100-seed weight in soybean which is similar to the earlier findings by Chand (1999).

4.3.5 Number of branches per plant:

The number of branches per plant had positive and highly significant correlation with pods per plant (0.556 and 0.530), pod length (0.490 and 0.465) and seeds per plant (0.585 and 0.558) both at genotypic and phenotypic levels (Table 4). Branches per plant positively correlated with seed yield which was early findings by Chand (1999).

4.3.6 Pods per plant:

Pods per plant had highly significant and positive association with pod length (0.266 and 0.255), seeds per pod (0.347 and 0.291), seeds per plant (0.991 and 0.984) and it

showed significant and negative correlation with hundred seed weight (-0.232 and -0.226) at both the genotypic and phenotypic levels (Table 4). Saurabh *et al.* (1998) observed that significant and positive correlations between plant height and pods per plant.

4.3.7 Pod length (cm):

Pod length had significant and positive association with number of seeds per pod (0.300 and 0.256), number of seeds per plant (0.336 and 0.325) and hundred seed weight (0.635 and 0.625) at both the genotypic and phenotypic levels (Table 4). Sridhara *et al.* (1998) reported that pod length significant contributors of seed yield.

4.3.8 Number of seeds per pod:

Number of seeds per pod showed positive association with seeds per plant (0.388 and 0.340) at both the genotypic and phenotypic levels (Table 4). Inderjit *et al.* (2007) reported that seeds per pod significantly correlated with seed yield.

4.3.9 Seeds per plant:

Seeds per plant had highly significant positive association with seed yield per plant (0.719 and 0.722) at both the genotypic and phenotypic levels (Table 4). Seeds per plant correlated with seed yield which was early findings by Chand (1999).

4.3.10 Hundred seed weight (g):

Hundred seed weight had significant positive association with seed yield per plant (0.558 and 0.551) at both the genotypic and phenotypic levels (Table 4). Avc and Ceyhan, (2006) find that hundred seed weight significantly correlated with pod yield

4.3.11 Seed yield per plant:

A highly significant and positive association of seed yield per plant at both the genotypic and phenotypic levels was observed with plant height (0.389 and 0.380), branches per plant (0.0413 and 0.397), pods per plant (0.664 and 0.662), pod length (0.749 and 0.727), seeds per pod (0.380 and 0.332), seeds per plant (0.719 and 0.722)

and hundred seed weight (0.558 and 0.551). Days to first flowering (0.174 and 0.170), days to 50% flowering (0.194 and 0.186) and days to maturity (0.119 and 0.117) had shown insignificant positive association with seed yield per plant at both the levels (Table 4). Here, seed yield per plant exhibited a significant and positive correlation with plant height, number of pods per plant, 1000-seed weight, number of seeds per pod which is similar to the earlier findings by Tiwari *et al.* (2001) and Ahmed *et al.* (1971).

4.4 Path coefficient analysis

Though correlation analysis indicates the association pattern of components traits with yield, they simply represent the overall influence of a particular trait on yield rather than providing cause and effect relationship. The path coefficient analysis technique was developed by Wright (1921) and demonstrated by Deway and Lu (1959) facilitates the portioning of correlation coefficients into direct and indirect contribution of various characters on yield. It is standardized partial regression coefficient analysis. As such, it measures the direct influence of one variable upon other. Such information would be of great value in enabling the breeder to specifically identify the important component traits of yield and utilize the genetic stock for improvement in a planned way.

In path coefficient analysis the direct effect of a trait on seeds per plant and its indirect effect through other characters were computed and the results are presented in Table 5.

4.4.1 Days to first flowering:

Days to first flowering had negative direct effect (-0.010) on yield per plant. Days to first flowering influenced the seed yield per plant indirectly through days to maturity (0.057), plant height (0.019), pod length (0.019) and seeds per plant (0.180) (Table 5). It had a negative indirect effect through branches per plant (-0.031), pods per plant (-0.017) and hundred seed weight (-0.019).

Table 5. Path coefficient analysis showing direct and indirect effects of different characters on yield of soybean

Characters	Direct effect	Indirect effect										Pearson Correlation with yield
		DFF	D50%F	DM	PH	BPP	NPP	PL	NSP	SPP	HSW	
DFF	-0.010	-	-0.008	0.057	0.019	-0.031	-0.017	0.019	0.000	0.180	-0.019	0.17
D50%F	-0.001	-0.030	-	0.056	0.020	-0.031	-0.018	0.020	0.000	0.189	-0.013	0.18
DM	0.062	-0.028	-0.008	-	0.017	-0.026	-0.014	0.014	0.000	0.135	-0.045	0.11
PH	0.043	-0.014	-0.004	0.025	-	-0.051	-0.058	0.023	0.000	0.595	-0.179	0.37**
BPP	-0.031	-0.015	-0.004	0.027	0.036	-	-0.049	0.033	-0.001	0.496	-0.070	0.39**
NPP	-0.040	-0.006	-0.002	0.009	0.027	-0.033	-	0.018	-0.002	0.883	-0.141	0.66**
PL	0.072	-0.008	-0.002	0.012	0.014	-0.028	-0.023	-	-0.002	0.288	0.397	0.72**
NSP	-0.004	-0.001	0.000	-0.002	0.000	-0.004	-0.027	0.018	-	0.306	0.045	0.33**
SPP	1.200	-0.006	-0.002	0.009	0.028	-0.034	-0.091	0.023	-0.003	-	-0.102	0.72**
HSW	0.739	0.001	0.000	-0.004	-0.012	0.007	0.020	0.045	-0.001	-0.144	-	0.55**

Residual effect: 0.395

** = Significant at 1%.
* = Significant at 5%.

DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), BPP = Branches per plant, NPP = Number of pods per plant, PL = Pod length (cm), NSP = Number of seeds per pod, SPP = Seeds per plant, HSW = Hundred seed weight (g), SYP = Seed yield per plant (g).

4.4.2 Days to 50% flowering:

Days to 50% flowering had negative direct effect (-0.001) on yield per plant. Days to 50% flowering showed positive indirect effect to seed yield per plant via days to maturity (0.056), plant height (0.020), pod length (0.020) and seeds per plant (0.189) (Table 5). It had a negative indirect effect through branches per plant (-0.031), pods per plant (-0.018) and hundred seed weight (-0.013).

4.4.3 Days to maturity:

Path analysis revealed that days to maturity had positive direct effect (0.062) on yield per plant. Days to maturity showed indirectly positive influenced for plant height (0.017), pod length (0.014) and seeds per plant (0.135), it influenced the seed yield per plant in negative direction through hundred seed weight (-0.045) and branches per plant (-0.026) (Table 5).Days to maturity showed positive direct effect on grain yield which is similar to the earlier findings by Inderjit *et al.* (2007).

4.4.4 Plant height (cm):

Path analysis revealed that plant height had positive direct effect (0.043) on yield per plant. The indirect and positive effect on seed yield per plant exhibited by plant height via days to maturity (0.025), pod length (0.023) and seeds per plant (0.595), whereas, through other traits it had negligible indirect effects (Table 5). Chettri *et al.* (2003) found that plant height positively affected grain yield.

4.4.5 Number of branches per plant:

Branches per plant had the negative direct effect on yield per plant (-0.031) whereas, it had negative indirect effect through hundred seed weight (-0.070), pods per plant (-0.049) and seeds per pod (-0.001) (Table 5). However, its indirect effects through days to maturity (0.027), plant height (0.036), pod length (0.033) and seeds per plant (0.496) leading to positive association.

4.4.6 Pods per plant:

Pods per plant had the negative direct effect on yield per plant (-0.040). It showed positive indirect effect through days to maturity (0.009), plant height (0.027), pod length (0.018) and seeds per plant (0.883) (Table 5). This trait showed the negative indirect effect with hundred seed weight (-0.141) and branches per plant (-0.033) to the seed yield.

4.4.7 Pod length (cm):

Path analysis revealed that pod length had positive direct effect (0.072) on yield per plant whereas, it showed indirect positive effects on seed yield per plant by hundred seed weight (0.397), days to maturity (0.012), plant height (0.014) and seeds per plant (0.288) (Table 5). It showed indirect negative effect on seed yield per plant through branches per plant (-0.028), pods per plant (-0.023) and seeds per pod (-0.002). Harpreet *et al.* (2007) observed that pod length can serve as reliable variable for selection.

4.4.8 Number of seeds per pod:

Number of seeds per pod had the negative direct effect on yield per plant (-0.004) and it had positive and indirect influence on seed yield per plant through pod length (0.018), seeds per plant (0.306) and hundred seed weight (0.045) (Table 5). However, this trait showed the negative indirect effect for pods per plant (-0.027) and branches per plant (-0.004).

4.4.9 Seeds per plant:

Seeds per plant had positive and indirect influence via days to maturity (0.009), plant height (0.028) and pod length (0.023) (Table 5). It influenced the seed yield per plant negatively through hundred seed weight (-0.102) and pods per plant (-0.091).Seeds per plant had the positive direct effect on yield per plant (1.200)

4.4.10 Hundred seed weight (g):

Hundred seed weight had positive indirect effect through branches per plant (0.007), pods per plant (0.020) and pod length (0.045) to seed yield (Table 5). This trait showed negative indirect effect via seeds per plant (-0.144) and plant height (-0.012). Path analysis revealed that hundred seed weight had positive direct effect (0.739) on yield per plant. Hundred seed weight had positive direct effect on grain yield which is similar to the earlier findings by Inderjit *et al.* (2007).

From the present path analysis study in soybean, it may be concluded that improvement in seed yield per plant could be brought by selection for component characters like seeds per plant and pod length.

4.5 Multivariate Analysis

4.5.1 Principal component analysis (PCA)

Analysis yielded eigen values of each principal component axes of coordination of genotypes in which the first axes accounted 43.72% of the total variation among the genotypes, while 8 of these with eigen values above unity accounted for 99.81% presented in Table 6. Based on principal component scores I and II obtained from the principal component analysis (Appendix V), a two-dimensional scatter diagram (Z_1-Z_2) using component score 1 as X axis and component score 2 as Y axis was constructed, which has been presented in Fig 4. The positions of the genotypes in the scatter diagram were apparently distributed into five groups, which indicated that considerable diversity existed among the genotypes.

Table 6. Eigen values and yield percent contribution of 11 characters of 28 germplasm

Characters	Eigen values	Percent variation	Cumulative % of Percent variation
Days to first flowering	4.8096	43.72	43.72
Days to 50% flowering	2.4439	22.22	65.94
Days of maturity	1.9023	17.29	83.23
Plant height (cm)	0.9155	8.32	91.55
Number of branches per plant	0.5491	4.99	96.54
Number of pods per plant	0.1455	1.32	97.86
Pod length (cm)	0.1123	1.02	98.88
Number of seeds per pod	0.1025	0.93	99.81
Number of seeds per plant	0.0122	0.11	99.92
100 seed weight (gm)	0.0048	0.05	99.97
Seeds yield per plant (gm)	0.0023	0.03	100.00

Z1-Z2 Graph

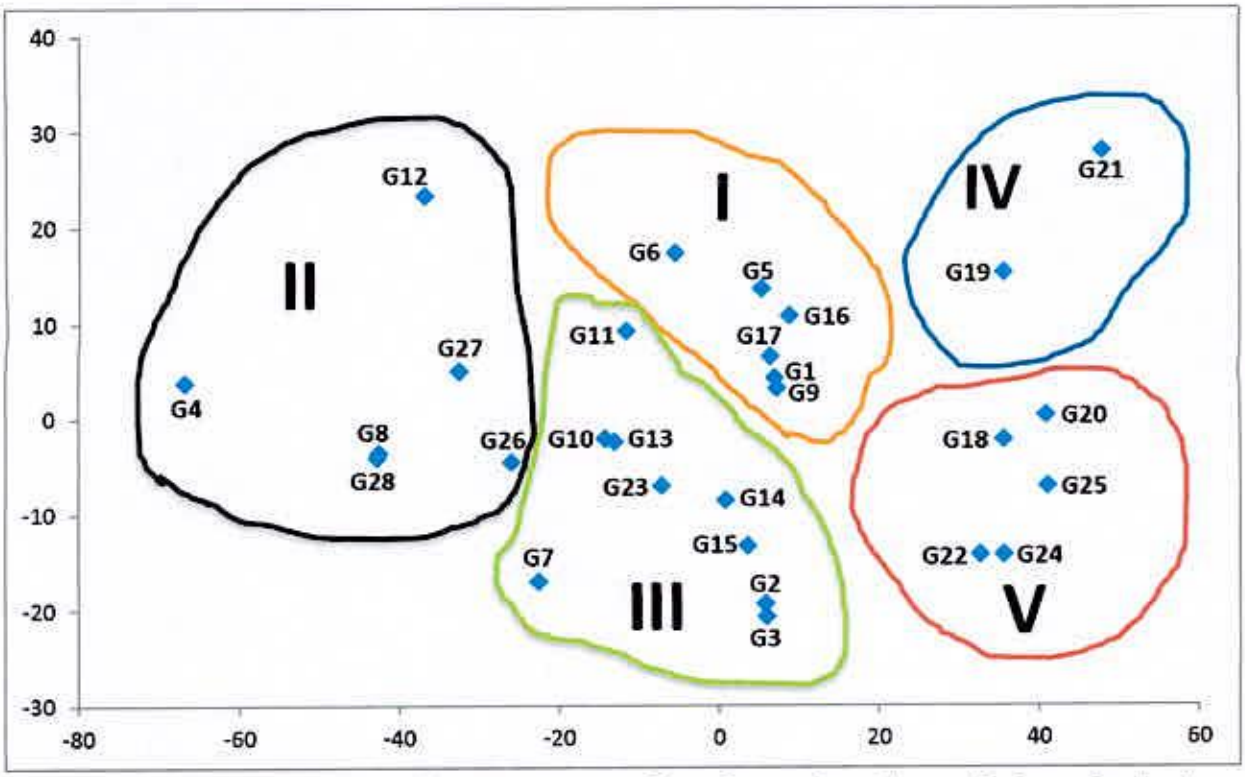


Fig4: Scatter diagram of 28 genotypes of soybean based on their principal component scores super imposed with clustering

4.5.2 Canonical variate analysis

The inter cluster D^2 values are given in Table 7 and the nearest and farthest cluster from each cluster based on D^2 value is given in Table 8. The inter cluster D^2 values were maximum (11.19) between the cluster II and cluster IV, flowed by II and V (9.36) and III and IV (8.74). The higher inter-cluster distances between these clusters indicate to obtain wide spectrum variability of population. However, the highest inter cluster distance was observed between clusters II and IV indicated the genotypes in these clusters were diverse than those clusters. Cluster II was the most diverse as many other clusters showed maximum inter cluster distance with it. The minimum distance observed between clusters II and III (4.04) indicated close relationship among the genotypes.

The intra cluster D^2 values are given in Table 7. The intra cluster distance was observed in the clusters I, II, III and V whereas, rests cluster IV comprised only two genotypes. The intra cluster distance was higher in cluster V (0.113) followed by cluster II (0.087) and lowest in cluster III (0.037). The intra cluster distances in all the five clusters were lower than the inter cluster distances and which indicated that genotypes within the same cluster were closely related. The inter cluster distances were larger than the intra cluster distances which indicated wider genetic diversity among the genotypes of different groups.

4.5.3 Principal coordinate analysis (PCO)

Inter genotypic distances (D^2) as obtained by principal coordinate analysis (PCO) for all possible combinations between the pairs of genotypes. Inter genotypic distances as obtained from principal coordinate analysis showed that the highest distance was observed between the genotype 4 and 21 (Table 9). The lowest distance was observed between genotypes 8 and 28. The difference between the highest and the lowest inter genotypic distance indicated the prevalence of variability among the 28 genotypes of soybean studied.

Table 7. Intra (Bold) and inter cluster distances (D^2) for 28 genotypes of soybean

Cluster	I	II	III	IV	V
I	**0.056**	6.20	4.32	6.56	4.73
II		**0.087**	4.04	11.19	9.36
III			**0.037**	8.74	5.95
IV				**0.012**	5.04
V					**0.113**

Table 8. The nearest and farthest clusters from each cluster between D^2 values in soybean

Sl No.	Cluster	Nearest Cluster with D^2values	Farthest Cluster with D^2 values
1	I	III (4.32)	IV (6.56)
2	II	III (4.04)	IV (11.19)
3	III	II (4.04)	IV (8.74)
4	IV	V (5.04)	II (11.19)
5	V	I (4.73)	II (9.36)

Table 9. Ten highest and ten lowest inter genotypic distance among the 28 genotypes of soybean

Highest distance				Lowest distance			
Sl No.	**Genotype**		**Distance**	**Sl No.**	**Genotype**		**Distance**
01	G4	G21	117.27	01	G8	G28	0.532
02	G4	G25	108.31	02	G1	G9	1.074
03	G4	G20	107.62	03	G10	G13	1.140
04	G4	G24	103.93	04	G2	G3	1.298
05	G4	G19	103.06	05	G1	G17	2.362
06	G4	G18	102.48	06	G22	G24	2.970
07	G4	G22	101.01	07	G9	G17	3.436
08	G21	G28	96.35	08	G5	G16	4.480
09	G8	G21	95.98	09	G16	G17	4.899
10	G12	G21	84.97	10	G14	G15	5.546

4.5.4 Nonhierarchical clustering

With the application of co variance matrix for non-hierarchical clustering, 28 soybean genotypes were grouped into five different clusters. From Table 9, cluster III had the maximum 9 genotypes (BS-13, JOYAWAZA, BOAS-5, GC-830059, ASSET-95, KANH-33, NS-1, GMOT-17, PI-4174-75) followed by cluster I (AGS-79, AGS-95, GC-82-332411, BS-33, LG-92P-1176, CHINA-1), cluster II (F-85-11347, LG-92P-12-18, BARI SOYBEAN-6, ASSET-93-19-13, BARI SOYBEAN-5, MTD-451) and cluster V (MTD-16, PK-327, YESOY-4, MTD-452, 86017-66-6). Cluster IV comprised with two genotypes SHOHAG and AUSTRALIA.

The results confirmed the clustering pattern of the genotype according to the principal component analysis. Composition of different clusters with their corresponding genotypes in each cluster is presented in Table 10. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. For that reason it can be said that the results obtained through PCA were established by nonhierarchical clustering. Clustering pattern of 28 genotypes of soybean is presented in Fig 4.

4.5.5 Cluster mean analysis

The cluster means of 11 different characters (Table 11) were compared and indicated considerable differences between clusters for all the characters studied. Maximum days to first flowering were observed in cluster III (68.55), whereas minimum days to first flowering were observed in cluster IV (55.17). Maximum (71.93) and minimum (58.83) days to 50 per cent flowering were observed in cluster III and IV respectively. Cluster III composed of genotypes showing highest days of maturity (126.44) and lowest in the cluster IV (107.67). Genotypes in cluster IV showed the lowest plant height (28.25) and that in cluster II had the highest mean (72.67) plant height. Maximum (5.15) and minimum (2.05) number of branches were observed in cluster II and IV respectively. Maximum number of pods per plant was observed in cluster II (51.99), whereas minimum number of pods per plant was observed in cluster IV (27.97). The maximum pod Length (3.23) was observed in the cluster II, whereas minimum pod length (2.83) was observed in cluster V.

Table 10. Distribution of genotypes of soybean in different clusters

Cluster no.	No. of Genotypes	Number of populations	Name of genotypes
I	G1, G5, G6, G9, G16, G17	6	AGS-79, AGS-95, GC-82-332411, BS-33, LG-92P-1176, CHINA-1
II	G4, G8, G12, G26, G27, G28	6	F-85-11347, LG-92P-12-18, BARI SOYBEAN-6, ASSET-93-19-13, BARI SOYBEAN-5, MTD-451
III	G2, G3, G7, G10, G11, G13, G14, G15, G23	9	BS-13, JOYAWAZA, BOAS-5, GC-830059, ASSET-95, KANH-33, NS-1, GMOT-17, PI-4174-75
IV	G19, G21	2	SHOHAG, AUSTRALIA
V	G18, G20, G22, G24, G25	5	MTD-16, PK-327, YESOY-4, MTD-452, 86017-66-6

Table 11. Cluster mean values of 11 different characters of 28 genotypes of soybean

Characters	I	II	III	IV	V
Days to first flowering	64.28	67.67	68.55	55.17	66.67
Days to 50% flowering	67.89	71.22	71.93	58.83	69.80
Days to maturity	124.17	125.11	126.44	107.67	126.20
Plant height (cm)	44.56	72.67	67.59	28.25	44.93
Number of branches per plant	3.42	5.15	4.80	2.05	3.33
Number of pods per plant	39.68	51.99	39.16	27.97	25.74
Pod length (cm)	2.97	3.23	3.06	2.90	2.83
Number of seeds per pod	2.52	2.53	2.50	2.51	2.47
Number of seeds per plant	97.96	133.11	98.38	69.39	64.13
100 seed weight (gm)	10.27	10.63	9.52	12.75	11.44
Seeds yield per plant (gm)	10.06	14.08	9.40	8.86	7.48

The maximum number of seeds per pod was observed in cluster II (2.53), whereas minimum number of seeds per pod was observed in cluster V (2.47). A highest seeds per plant was recorded by the genotype making up cluster II (133.11) while cluster V showed the least seeds (64.13) per plant. 100 Seed Weight was the highest in cluster IV with a mean value of (12.75) and it was least in genotypes belongs to the cluster III (9.52). The maximum seed yield per plant (14.08 g) was observed in the cluster II, whereas minimum (7.48 g) was in the cluster V.

Cluster IV mainly an early flowering genotype where as it produce the lowest mean values for first flowering. Cluster III has late flowering and late days of maturity. Again cluster IV has the early days of maturity, lowest plant height, branches per plant, pods per plant and maximum 100 seed weight. The genotypes belonging to the cluster III were lowest 100 seed weight. The genotypes belong to the cluster II were maximum plant height, branches per plant, pods per plant, pod length, seeds per pod, seeds per plant and seed yield per plant. The genotypes of the cluster V were low yielder because of least pod length, seeds per pod, seeds per plant and seed yield per plant. To develop high yielding varieties these groups can be used in hybridization program.

4.5.6 Cluster diagram

With the help of D^2 values within and between clusters, an arbitrary cluster diagram (Fig 5) was constructed, which showed the relationship between different genotypes. However, the diagram was not following exact scale. It was apparent from the Fig 5 that the genotypes included in the cluster IV was far diverse from the genotypes of the cluster II and where the genotypes belonging to II and III were the least diverse. Genotypes of cluster II-V and III-IV were moderately diverse from each other. The similar diverse genotypes were included between the cluster I-IV and I-II.

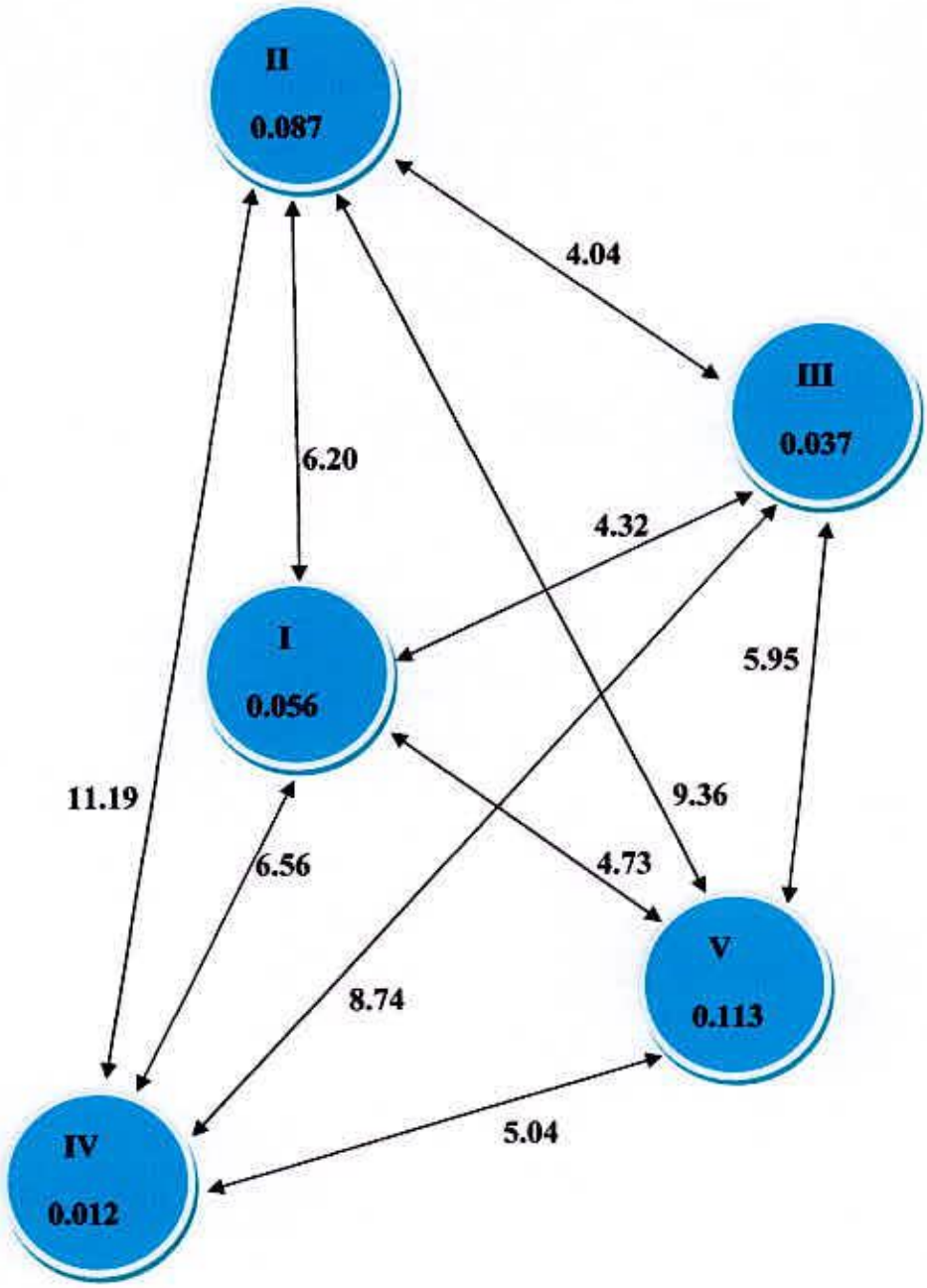


Fig 5: Intra and inter cluster distances (D^2) of 28 genotypes in Soybean

4.5.7 Contribution of characters towards divergence of the genotypes

Contribution of characters towards the divergence obtained from canonical variate analysis is presented in Table 12. In this method vectors was calculated to represent the varieties in the graphical form (Rao, 1952). This is helpful in cluster analysis as it facilitated the study of group constellation and also serves as a pictorial representation of the configuration of various groups. The absolute magnitude of the coefficients in the first two canonical vectors also reflected to a great extent, the importance of the characters for primary and secondary differentiation. The character, which gave high absolute magnitude for vector 1, was considered to be responsible for primary differentiation. Likewise, the characters, which gave higher absolute magnitude for vector 1 was considered to be responsible for secondary differentiation. If same character given equal magnitude for both the vectors than the characters considered responsible for primary as well as secondary differentiation.

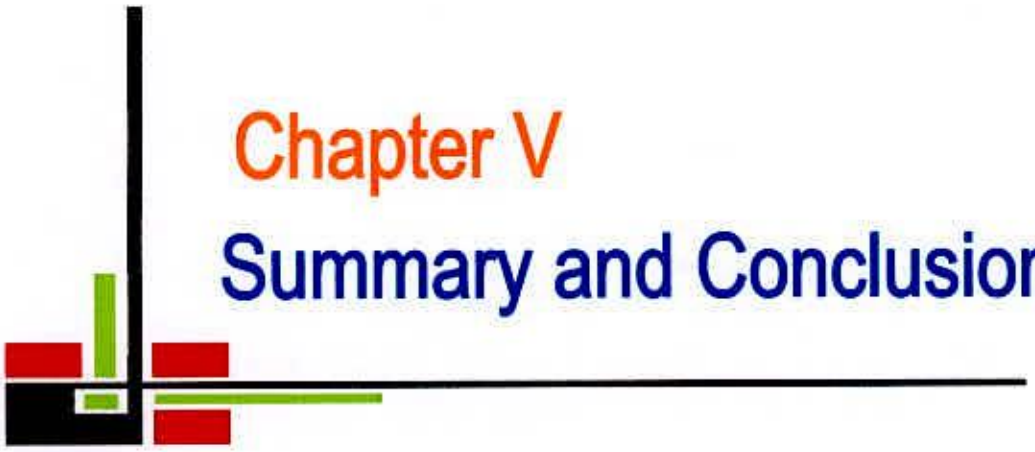
In vector (Z_1) obtained from PCA, the important characters responsible for genetic divergence in the axis of differentiation were days to first flowering (0.1177), days to maturity (0.0034), plant height (0.1120), number of pods per plant (0.1469), pod length (1.4211) and seed yield per plant (0.7018). In vector 2 (Z_2), the second axis of differentiation days to first flowering (0.4451), days to maturity (0.0317), plant height (0.1570), number of pods per plant (0.0435), number of seeds per pod (5.2176) and seeds yield per plant (0.1904) were important because all these characters had positive signs. On the other hand days of 50% flowering, number of branches per plant, number of seeds per pod, number of seeds per plant and 100-seed weight possessed the negative sign in the first axis of differentiation and days of50% flowering, number of branches per plant, pod length, number of seeds per plant and 100-seed weight possessed negative signs in the second axis of differentiation that means it had minor role in the genetic diverse. Days to first flowering, number of pods per plant and seed yield per plant had positive signs in both the vectors and on the other hand, seeds per pod had highest value in both the axis, which indicated that they were the important component characters having higher contribution to the genetic divergence among the materials studied.

Table 12. Relative contributions of the eleven characters of 28 varieties to the total divergence

Characters	Vector-1	Vector-2
Days to first flowering	0.1177	0.4451
Days to 50% flowering	-0.1075	-0.4480
Days to maturity	0.0034	0.0317
Plant height (cm)	0.1120	0.1570
Number of branches per plant	-0.2540	-0.1808
Number of pods per plant	0.1469	0.0435
Pod length (cm)	1.4211	-1.1421
Number of seeds per pod	-1.4670	5.2176
Number of seeds per plant	-0.0466	-0.1211
100 seed weight (gm)	-0.8678	-0.0428
Seeds yield per plant (gm)	0.7018	0.1904

4.5.8 Selection of genotypes as parent for hybridization programme:

Selection of genetically diverse parents is an important step for hybridization program. So the genotypes were to be selected on the basis of specific objectives. A high heterosis could be produced from the crosses between genetically distance parents. Considering the magnitude of cluster mean and agronomic performance the genotype G21 (AUSTRALIA) for minimum days to first flowering from cluster IV; G23 (PI-4174-75) for maximum pod length from cluster III; G4 (F-85-11347) for maximum number of seeds per pod from cluster II, G28 (MTD-451) for maximum plant height from cluster II were found promising. Therefore considering group distance and other agronomic performance G21 (AUSTRALIA), G4 (F-85-11347), G8 (LG-92P-12-18), G17 (CHINA-1), G12 (BARI SOYBEAN-6), G23 (PI-4174-75) and G28 (MTD-451) may be suggested for future hybridization program.



Chapter V

Summary and Conclusion

CHAPTER V

SUMMARY AND CONCLUSION

The experiment was conducted with a view to identify divergent parents for hybridization program, identify the characters contributing to genetic diversity, asses the magnitude of genetic divergence in genotypes and determine the variability in respect of yield and some yield contributing characters, the degrees of association among the characters and their direct and indirect effects of 28 genotypes of soybean (*Glycine max* (L). Merrill) at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, during December, 2011 to April, 2012. The salient findings of the present study have been summarized on the basis of the characters studied.

The analysis of variance showed significant differences among the genotypes for all the characters. The accession AUSTRALIA was the earliest to first flower of 51.67 days while F-85-11347 was late to first flower for 76.33 days. The minimum and maximum duration for 50% flowering were required by the genotypes AUSTRALIA (55.33 days) and F-85-11347 (79.00 days), respectively. The maximum plant height (79.87 cm) was recorded by the genotype MTD-451 and the lowest plant height (21.9 cm) was recorded by AUSTRALIA. Maximum number of branches per plant was recorded in MTD-451 and SHOHAG genotype showed the minimum number of branches per plant. The maximum pod length was recorded by the accessions PI-4174-75 and MTD-16 showed the minimum pod length. The line GC-830059 showed the minimum hundred seed weight and the maximum hundred seed weight was recorded in the accession PI-4174-75. The minimum number of pods per plant was observed in accession 86017-66-6 while maximum number of pods per plant was found in the genotype F-85-11347. The genotype F-85-11347 and GC-82-332411 had the highest number of seeds per pod while it was lowest in the genotype BS-13. Highest seeds per plant were recorded by the accession F-85-11347 while accession 86017-66-6 showed the lowest seeds per plant. The genotypes BOAS-5, BS-13,

JOYAWAZA, F-85-11347 and LG-92P-12-18 had the highest days to maturity and lowest in the genotype AUSTRALIA. The genotype 86017-66-6 and PI-4174-75 were the lowest and the highest for seed yield per plant, respectively.

The phenotypic variance was higher than genotypic variance in all the characters studied. The genotypic coefficients of variation were higher than phenotypic coefficients of variation in all the characters studied. Phenotypic coefficients of variation were also close to genotypic coefficients of variation for most of the characters. High heritability (>60%) was observed for the characters like days to first flowering, days to 50% flowering, days to maturity, pod length and hundred seed weight. The high heritability coupled with high genetic advance in percent of mean observed in plant height, number of branches per plant, number of pods per plant and number of seeds per plant suggested that effective selection may be done for these characters. Low heritability coupled with low genetic advance in percent of mean was observed number of seeds per pod.

Plant height, branches per plant, pods per plant, pod length, seeds per pod, seeds per plant and hundred seed weight showed significant and positive correlation with seed yield per plant at both genotypic and phenotypic levels. Significant and positive genotypic and phenotypic correlation was observed between days to first flowering and days to 50% flowering. Plant height positively and significantly correlated with branches per plant, pods per plant, pod length and seeds per plant at both levels. Days to maturity was significantly and positively correlated with plant height and branches per plant at both levels. Branches per plant were positively and significantly correlated with pods per plant, pod length and seeds per plant at both levels. Pods per plant were positively and significantly correlated with pod length, seeds per pod and seeds per plant at both levels. Pod length was positively and significantly correlated with seeds per pod, seeds per plant and hundred seed weight at both levels. Significant and positive correlation was observed between seeds per pod and seeds per plant.

Seeds per plant showed the highest positive direct effect (1.200) with seed yield per plant. On the other hand negative direct effect on seed yield per plant showed by days to first and 50% flowering, branches per plant, pods per plant and seeds per pod. Plant height, days to maturity, pod length and hundred seed weight also showed positive direct effect on seed yield. The highest indirect effect of pods per plant observed with seeds per plant. Seeds per plant showed high direct effect on seed yield indicated that direct selection for this trait might be effective and there is a possibility of improving seed yield per plant through selection based on those characters.

Genetic diversity of twenty eight soybean genotypes based on eleven characters was measured through multivariate analysis. The 28 genotypes fell into five distant clusters. The cluster III comprised the maximum number (9) of genotypes. The cluster I, II, IV and V comprised 6, 6, 2 and 5 genotypes respectively. The highest inter-cluster distance (11.19) was observed between the cluster II and IV and the highest distant genotypes were G4 (F-85-11347) and G21 (AUSTRALIA). The lowest inter-cluster distance (4.04) was observed between the cluster II and III and the lowest distance genotypes were G8 (LG-92P-12-18) and G28 (MTD-451).

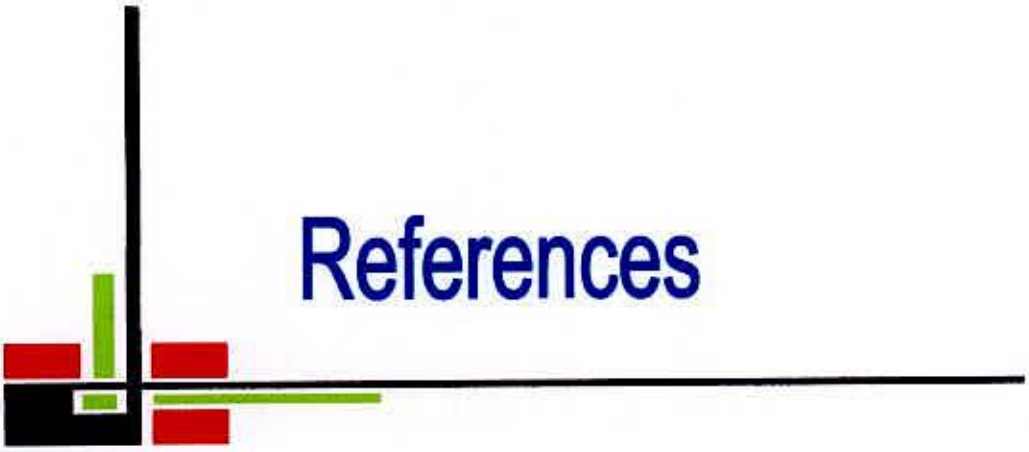
The inter-cluster distances were larger than the intra-cluster distances. The intra-cluster distance in the entire five clusters was more or less low indicating that the genotypes within the same cluster were closely related. Pods per plant and seed yield per plant were the important component characters having higher contribution to the genetic divergence.

The result of the present study revealed that a wide variability exists among the collected soybean genotypes. In addition, there was also genotype of different yield contributing characters with yield of soybean. From the findings of the present study, the following conclusions could be drawn:

1. Wide range of genetic diversity existed among the soybean genotypes. Wide genetic diversity was observed in 28 genotypes of soybean, which were grouped into five clusters and most diverse genotypes were G4 and G21. That variability could be used for future breeding program of soybean in Bangladesh.
2. High heritability coupled with high genetic advance in percent of mean was observed in plant height and branches per plant. Hence, yield improvement in soybean would be achieved though selection of these characters.
3. Pods per plant, pod length, seeds per plant and hundred seed weight showed significant and positive correlation with seed yield per plant at both genotypic and phenotypic levels. This results suggested that seed yield per plant can be increased by improving these characters.
4. Pod length, plant height, days to maturity, seeds per plant and hundred seed weight showed positive direct effect on yield. So yield improvement was associated with these characters.
5. The genotypes of clusters II were more diverse from the genotypes of cluster IV.
6. Days to first flowering, pods per plant, seeds per pod and seed yield per plant were found responsible for the maximum diversity. On the other hand, seeds per plant and branches per plant have the least responsibility of both the primary and secondary differentiation of genotypes.
7. Further collection of soybean germplasms would be continued for getting more variability and desired traits in soybean.

Based on the results of the study, the following recommendations may be drawn:

1. Genotypes G4 (F-85-11347), G8 (LG-92P-12-18), G17 (CHINA-1), G23 (PI-4174-75), G28 (MTD-451) and G7 (BOAS-5) could be included in the furthest study in view of seed yield for releasing as soybean verities.
2. The maximum variability was found for pod length, seeds per plant and hundred seed weight. So selection based on these characters could be effective for the improvement of soybean yield.
3. The genotypes of cluster II and IV could be used as parents for future breeding program to developed soybean variety.



References

REFERENCES

Agrawal, A. P., Patil, S. A. and Math, P. S. (2001).Variability, heritability and genetic advance of some quantitative character over the seasons in soybean. *Madras Agril. J.* **88** (1-3): 36- 40.

Ahmed, M., Baluch, A. and Khan, K. (1971). Correlation studies in soybean. *Agric. Pakistan PI. Breed.* Abst. **43** (8): 22-24.

Amadou, I., Yong-Hui, S. and Sun, J. (2009). Fermented Soybean Products: Some Methods, Antioxidants Compound Extraction and their Scavenging Activity. *Asian J. Biochem.* 4 (3) Pp: 68-76.

Anderson, E. (1957). A semi geographical method for the analysis of complex problems. *Proc. Nat. Acad. Sci. Wash.*, **43**: 923-927.

Anonymous, (1988a). Review of vegetable crop programme Mennonite Central Committee (MCC), Bangladesh. Pp: 26-35.

Anonymous, (1988b). Crop Status Report. Christian Reformed Worlds Relief Committee, Bogra. Pp: 124-127.

Anonymous, (2004). FAO Irrigation and Drainage Paper. Food and Agriculture Organization of the United Nations, Rome, Italy. **3**: 80-82.

Archana, T., Khorgade, P. W., Ghorade, R. B., Manjusha, G., Thorat, A. and Ghodke, M. (1999). Variability, heritability and genetic advance in soybean. *J. Soils and Crops.* **9** (2): 198-200.

Avc, M. A. and Ceyhan, E. (2006). Correlations and genetic analysis of pod characteristics in pea (*Pisumsativum* L.). *Asian J. Pl. Sci.*, **5** (1): 1-4.

Bangar, N. D., Mukher, G. D., Lad, D. B. and Mukhar, D. G. (2003). Genetic variability, correlation and regression studies in soybean. *J. Maharastra Agril. Univ.* **28** (3):320-321.

Batugal, P. A. (1999). The Role of International Cooperation in the Development of Biotechnology in Coconut. Current Advances in Coconut Biotechnology. pp: 19-30.

Bhandarkar, S. (1999). Studies on genetic variability and correlation analysis in soybean *(Glycine max* L. Merrill). *Mysore J. Agril. Sci.* **33** (3): 130-132.

Burton, G. W. (1952). Quantitative interaction in grasses. In: *Proc.* 6th Inter Grassland Congr., **1** : 277-283.

Chamundeswori, N. and Aher, R. P. (2003). Character association and component analysis in soybean *(Glycine max* L. Merril). *Annals Biology*. **19** (2): 199-203.

Chand, P. (1999). Association analysis of yield and its component in soybean *(Glycine max* L. Merrill). *Madras Agril. J.*, **86** (7-9): 378-381.

Chaudhary, D. K. and Sharma, R. R. (2003). Genetic variability, correlation and path analysis for green pod yield and its components in garden pea. *Indian J. Hort.,* **60** (3): 251-256.

Chettri, M., Mondal, S. and Nath, R. (2003). Studies on correlation and path analysis in soybean in the Darjeeling hills. *J. Hill Res.***16** (2): 101-103.

Chowdhury, N. A. Z., Alam, M. S., Rahim, M. A. and Mirza, S. H. (1997). Genetic divergence for yield and its morphological components of soyben (*Glycine max* L. Merrill). *J. Asiatic Soci. Bangladesh Sci.* **22** (2): 125-130.

Chowdhury, N. A. Z., Mia, M. F. U., Mirza, S. H., Alam, M. S. and Chaudhury, E. H. (1998). Genetic diversity in soybean (*Glycine max* L. Merrill). *Bangladesh J. Pl. Breed Genet.* **11** (1 & 2): 55-58.

Clarke, G. M. (1973). Statistics and Experimental Design. Edward Arnold. London.

Comstock, R. E., Robinson, H. F. and Harvey, V. H. (1952), Estimates of heritability and degree of dominance in corn. *Agron. J.* **41** : 353-359.

Das, M. L., Rahman, A., Khan, M. H. R. and Miah, M. J. (1984). Correlation and path coefficient studies in soybean. *Bangladesh J. Bot.* **13** (1): 1-5.

Das, S. P., Harer, P. N. and Biradat, A. B. (2000).Genetic divergence and selection of genotypes in soybean. *J. Maharastra Agril. Univ.* **25** (3): 250-252.

Devendra, K., Malik, B. P. S., Lekh, R., Kumar, D. and Raj, L. (1998). Genetic variability and correlation studies in field pea (*Pisum sativum* L.). *Legume Res.*, **21** (1): 23-29.

Deway, D. R. and Lu, K. N. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.*, **51** : 515-518.

Digby, P. N., Galway and Lane, P. (1989). Genstat 5, A second course. *Oxford Sci. Publ., Oxford.* pp: 103-108.

Dobhal, V. K. (1995). Genetic divergence in soybean. *Legume Res.*, **18** (10): 29-34.

Dobhal, V. K. and Gautam, N. K. (1995). Genetic variability and association analysis in soybean germplasm. *J. Hill Res.* **8** (2): 203-208.

Dogney, M. L., Gour, V. K. and Mehta, A. K. (1998). Path coefficient analysis yield attributing characters in back cross population of soybean in back cross population of soybean (*Glycine max* X *Glycine soja*) *Glycine max* L. Merrill. *Crop Res. Hisar.* **16** (3): 352-357.

Fehr, W. R. (1989). Soybean. In oil crops of the world. Graw Hill Publishing Comp. London.

Gaur, P. C., Gupta, P. K. and Kishore, H. (1978). Studies on genetic divergence in potato. *Euphytica.* **27**: 361-368.

Ghatge, R. D. and Kadu, R. N. (1993). Genetic diversity in soybean. *Annals Agril. Res.* **14** (2): 143-148.

Golakia, P. R. and Makne, V. G. (1992). D^2 analysis in Virginia runner groundnut genotypes. *Indian. J. Genet.* **55** (3): 252-256.

Griffing, B. and Lindstorm, E. W. (1954). A study of combining abilities of corn inbred having varying properties of corn belt and non-corn belt germplasm. *Agron. J.* **46**: 545-552.

Gupta, M. K., Singh, J. P. and Mishra, V. K. (1998). Heritability, genetic advance and correlation analysis in pea (*Pisum sativum* L.). *Hisar. Crop Res.* **16** (2): 202-204.

Hanson, C. H., Robinson, H. F. and Comstock, R. E. (1956). Biometric studies of yield segregating population in Korean lespedeza. *Agron. J.* **48**: 268-272.

Haque, M. S., Sikder, B. H., Ali, M. and Mannan, M. A. (1976). Effect of different doses of P application on the growth and yield performance of soybean. Ann. Report. Bangladesh Coordinated Soybean Res. Pro. (BARC), Dhaka, Bangladesh. pp: 36-37.

Harpreet, K., Mohan, S. and Brar, P. S. (2007). Correlation and path analysis in garden pea (*Pisumsativum*L.). *Crop Improv.*, **34** (2): 186-191.

Henkel, J. (2000). Soy: Health Claims for Soy Protein, Question About Other Components. *FDA Consumer* (Food and Drug Administration). **34** (3): 18–20.

Imsande, J. and Agron, J. (1992). Agronomic characteristics that identify high yield, high protein soybean genotypes. 84 (3): 409-414.

Inderjit S., Pritpal, S. and Sandhu, J. S. (2007). Genetic divergence and association studies in field pea (*Pisumsativum* L.). *Crop Improv.*, **34** (2): 179-182.

Jadhav, A. S., Jadhav, P. J. and Bachchhav, S. M. (1995). Correlation coefficient analysis of soybean . *J. Maharastra Agril. Univ.* **20** (1): 150-151.

Jagtap, D. R. and Mehetre, S. S. (1994). Genetic variability in some quantitative characters of soybean. *Annals Agril. Res.* **15** (1): 45-49.

Jain, P. K. and Ramgiry, S. R. (2000). Genetic variability of metric traits in Indian germplasm of soybean [(*Glycine max* (L.) Merril]. *Advances Sci.* **13** (1):127-131.

Jangale, C. B., Birari, S. P. and Apte, U. B. (1994). Genetic variability and heritability in soybean. *Agril. Sci. Digest Karnel.* **14** (2): 117-120.

Jatasra, D. S. and Paroda, R. S. (1978). Genetic divergence in wheat under different environmental conditions. Central Res. Comn. 6: 307-317.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. (1955), Estimation of genetic and environmental variability in soybean. *Agron. J.*, **47** : 477-483.

Juneje, S. L. and Sharma, S. L. (1971). Correlation studies for yield and other characters in soybean (*Glycine max* L. Merrill). *Himachal J. agril. Res.* **1**(1): 40-45.

Keyser, H. H. and Li, F. (1992). Potential for increasing biological nitrogen fixation in soybean. *Plant and Soil.* 141: 119-135.

Khaleque, M. A. (1985). A guide Book on Production of Oil crops in Bangladesh, DAE, Ministry of Agric. Govt. of Bangladesh, and FAO/UNDP Project, Strengthening the Agricultural Extension Service, Khamarbari, Dhaka. pp: 101-110.

Khan, A., Hatam, M. and Khan, A. (2000). Heritability and interrelationship among yield determining components of soybean varieties. *Pakistan J. Agril. Res.* **16**(1): 5-8.

Kumar, M. and Nadarajan, N. (1994). Genetic divergence studies in soybean (*Glycine max* L. Merrill). *Indian J. Genet.* **54** (3): 242-246.

Lush, J. L. (1943). Heritability of qualitative characters in farm animals. Proceedings of 8th Congress Genetics and Heriditas Supplement. pp: 356-375.

Mahajan, C. R., Mehetre, S. S. and Patil, P. A. (1993). Association of morphological traits with yield in soybean *(Glycine max* L. Merrill). *Annals Pl. Physiol.* 7 (1): 131-133.

Mahajan, C. R., Patil, P. A., Mehetre, S. S. and Ghatge, B. D. (1994). Genotypic and phenotypic variability of some quantitative characters in soybean (*Glycine max* L. Merrill). *Annals Agril. Res.* **15** (1): 41-44.

Mahalanobis, P. C. (1936). On the generalized distance in statistics. *Proceedings of National academic Sci. (India),* **2** : 79-85.

Major, S., Gyanendra, S. and Singh, G. (1996). Assessment of genetic variability, correlation and path analysis in soybean *(Glycine max* L. Merril) under mid hills of Sikkim. *J. Hill Res.* **9**(1): 150-152.

Malhotra, R. S. (1973). Genetic variability and discriminate function in soybean (*Glycine max* L. Merrilll). *Madras Agric. J.* **60** (4): 225-228.

Mehetre, S. S., Mahajan, C. R., Patil, P. A. and Hajare, D. N. (1994). Genetic divergence in soybean *(Glycine max* L. Merrill). *Indian J. Genet.* **54** (1): 83-88.

Mehetre, S. S., Shinde, R. B. and Desai, N. S. (1997). Variation and heritability, correlation, path analysis and genetic divergence studies on assimilate partitioning in leaves, leaf growth and yield characters of soybean. *Crop Res. Hisar.* **13** (2): 373-390.

Mehetre, N., Bohar, A. B. L., Rawat, G. S. and Mishra, Y. (2000). Variability and character association in soybean. *Bangladesh. J. Agril. Res.* **25** (1): 1-7.

Mehetre, S. S., Shinde, R. B., Borle. U. M. and Surana, P. P. (1997). Correlation and path analysis studies of partitioning in root growth and yield characters in soybean *(Glycine max* L. Merrill). *Crop Res. Hisar.* **13**(2): 415-422.

Mehetre, S. S., Shinde, R. B., Borle, U. M. and Surana, P. P. (1998). Studies on variability, heritability and genetic advance for some morphological traits in soybean *(Glycine max* L. Merrill). *Adv. Pl. Sci.* **11**(1): 205-208.

Millar, P. A., Williams, J. C., Robinson, H. F. and Comstock, R. E. (1958). Estimates of genotypic and environmental variance and covariance and their implication in selection. *Agron. J.* **50**:126-131.

Mishra, A. K., Ali, S. A., Tiwari, R. C. and Raghuwanshi, R. S. (1994). Correlation and path analysis in segregation populations of soybean. *International J. Tropic. Agric.* **12** (3-4): 278-281.

Mohan, S., Yuvinder, K., Harinder, S. and Brar, P. S. (2005). Correlation and path coefficient analysis in garden pea (*Pisum sativum* L.). *Environ. Eco.*, **23** (2): 315-318.

Mondal, M. R. I. and Wahhab, M. A. (2001). Production Technology of Oil crops. Oilseed Research center, Bangladesh Argil. Res. Inst., Joydebpur, Gazipur. pp: 1-10.

Murty, B. R. and Arunachalam, V. (1966). The nature of genetic divergence in relation to breeding system in crop plants. Indian J. Genet. 26 A: 188-198.

Murty, B. R. and Anand, I. J. (1966). Combining ability and genetic diversity in some varieties of *Linumusitatissium. Indian J. Genet.* 26: 21-36.

Nagata, T. (1960). Studies on the differentiation soybean in Japan and the world. *Mom. Hyogo. Univ.* **3** (2): 63-102.

Nehru, S. D., Rangaiah, S., Basavarajaiah, D. and Kulkarni, R. S. (1999). Studies on genetic variability in soybean. *Surrent Res. Univ. Agril. Sci. Bangalore.* **28**(1-2): 3-4.

Onemli, F. (2003). Association and path co-efficient analysis for components of soybean. *Bulgarian J. Agril. Sci.* **9** (1): 339-342.

Peluzio, J. M., Sediyama, C. S., Sediyama, T. and Reis, M. S. (1998). Phenotypic, genotypic and environmental correlations between some traits of soybean in Pefro. Afonso, Tocantins State. Revista-Ceres. **45** (259): 303-308.

Pranteetha, S. and Thamburaj, S. (1997). Variability, heritability, genetic advance and path analysis in vegetable soybean (*Glycine max* L. Merrill). *South Indian Hort.* **45** (3-4): 115-119.

Rahman, L. (2002). Studies on the development of varieties, production technology, food and fish feed uses of soybean in Bangladesh (BAU-USDA soybean project BG-ARS 107). p: 6.

Rahman, L. (1982). Cultivation of Soybean and Its Uses. The city press, Dhaka. pp: 5-7.

Rahman, M. M. (1998). Genetic divergence in soybean. *Progress Agric.* **9** (1-2): 185-187.

Rahman, M. M., Kader, M. and Debi, B. K. (1996). Study of variation for yield and yield contributing characters and relation between them in soybean. *Progress. Agric.* 7(2): 61-64.

Rajanna, M. P., Viswanatha, S. R., Kulkarni, R. S. and Ramesh, S. (2000). Correlation and path analysis in soybean *[Glycine max* (L.) Merrill]. *Crop Res. Hisar*. **20** (2): 244-247.

Rajarathinam, S., Muppidathi, N. and Pandian, R. S. (1996). Variability and character association in soybean during Rabi season. *Madras Agric. J.* **83**(12): 776-777.

Ramgiry, S.R.and Raha, P. (1997). Correlation and path analysis for yield and quality attributes in soybean (*Glycine max* L. Merrill). *Crop res. Hisar*. **13**(1): 137-142.

Rao, C. R. (1952). Advanced statistical methods in Biometrical Research. John willy and sons. New York.

Saad, A. M. M. (1995). Statistical studies of some economic characters in certain soybean varieties. *Annals Agril. Sci. Moshtohor*. **32** (2): 551-557.

Sachan, K. S. and Sharma, J. R. (1971). Multivariate analysis of genetic divergence in tomato. Indian J. Genet. 31: 86-93.

Sanjay, C., Pushpendra and Singh, K. (1998). Metrolyph and index score analysis in advance breeding lines of soybean. *Soybean Genet.News*. **25**: 77-79.

Saurabh, S., Kamendra, S. and Pushpendra. (1998). Correlation and path coefficient analysis of yield and its components in soybean (*Glycine max* L. Merrill). *Soybean Genet.News*. **25**: 67-70.

Sharma, A. K., Singh, S. P. and Sharma, M. K. (2003). Genetic variability, heritability and character association in pea (*Pisum sativum* L.). *Crop. Res. Hisar.*, **26** (1): 135-139.

Shinde, A. K., Birari, S. P., Bhave, S. G. and Joshi, R. M. (1996). Correlation and path coefficient analysis in soybean (*Glycine max* L. Merrill). *Annals Agril. Res.* **17** (1): 28-32.

Shrivastava, M. K. and Shukla, R. S. (1998). Genetic analysis for yield and its components in soybean under different environments. *Crop. Res. Hisar.* **16**(2): 196-201.

Shrivastava, M. K., Shukla, R. S. and Singh, C. B. (2000). Genetic divergence in soybean, *JNKVV Res. J.* **34** (1-2): 25-28.

Shrivastava, M. K., Shukla, R. S. and Jam, P. K. (2001). Path co-efficient analysis in diverse genotype of soybean (*Glycine max* L. Merrill). *Adv. Pl. Sci.* **14** (1): 47-51.

Sihag, R., Hooda, J. S., Vashishtha, R. D. and Malik, B. P. S. (2004). Genetic divergence in soybean (*Glycine max* L. Merrill). *Annals Biology.* **20**(1): 17-21.

Singh, A. P., Sumit, S., Bargale, M., Sharma, H. K. and Sharma, S. (1994). Association analysis for yield and its components in soybean (*Glycine max* L. Merrill). *Crop Res. Hisar.* **7** (2): 247-251.

Singh, I., Singh, P. and Sandhu, J. S. (2007). Genetic divergence and association studies in field pea (*Pisum sativum* L.). crop Improv., **34** (2): 179-182.

Singh, J., Parmar, R. P. and Yadav, H. S. (2000). Assessment of genetic variability and selection parameters in early generation of soybean. *Adv. Pl. Sci.* **13**(1): 227-232.

Singh, I., PhuL, P. S., Singh, T. P., Gupta, R. P. and Sharrna, S. R. (1995). Genetic variability and response of soybean genotypes to *Bradyrhizobium japonicum* inoculation. *J. Res. Panjab Agril.* Univ. **32** (2): 245-252.

Singh, J. D. and Singh, I. P. (2006). Genetic variability, heritability, expected genetic advance and character association in field pea (*Pisum sativum* L.). *Legume Res.* **29** (1): 65-67.

Singh, J. D. and Singh, I. P. (2006). Genetic divergence in advanced genotypes for grain yield in field pea (*Pisum sativum* L.). *Legume Res.* **29** (4): 301-303.

Singh, R. K. and Chaudhury, B. D. (1985). Biometrical methods of quantitative genetic analysis. *Haryana J. Hort. Sci.*, **12** (2): 151-156.

Smith. (1975). Consumptions of foods- raw, Processed, prepared. Agriculture Hand book no. 8, Agril. Res. Service. Washington, D.C.

Sridhara, S., Thimmegowda, S. and Chalapathi, M. V. (1998), yield structure analysis in soybean (*Glycine max* L. Merrill). *Indian Agriculturist*. **42** (2): 81-87.

Steward, W. D. P. (1966). Nitrogen fixation in plants. Athloc Press, Univ. London. pp: 85-90.

Symolon, H., Schmelz, E., Dillehay, D. and Merrill, A. (May 2004). Dietary Soy Sphingolipids Suppress Tumorigenesis and Gene Expression in 1,2-dimethylhydrazine-treated CF1 Mice and ApcMin Mice. *Journal of Nutrition.* **134** (5): 1157–1161.

Tiwari, S. K., Singh, H. L., Kumar, R. and Nigam, H. K. (2001). A postmortem of selection parameters in pea (*Pisum sativum* L.). *Crop Res.*, **2** (2): 237-242.

Tomooka, N. (1991). Genetic diversity and landrace differentiation of mungbean, *Vigna radiate* (L.) wilczek and evaluation of its wild relatives (The subgenus ceratotrophics) as breeding materials. Tech. Bull. Trop. Res. Centre, Japan no. 28. Ministry of Agr., Forestry and Fisheries, Japan. p:1.

Upadhayay, D. and Mehta, N. (2010). Biometrical Studies in Dolches Bean (*Dolchos lablab* L.) for Chhattisgarh plains. Research Journal of Agricultural Sciences 2010, 1 (4): 441-447.

Vart, D., Hooda, J. S., Malik, B. P. S. and Khtri, R. S. (2002). Genetic divergence in soybean (*Glycine max* L. Merrill). *Env. Ecol.* **20** (2): 708-711.

Vavilov, N. I. (1951). The origin, variation immunity and breeding of cultivated plants (Transkstarr, Chester), Chron, Bot. 13. The Ronald Press Co. New York. USA.

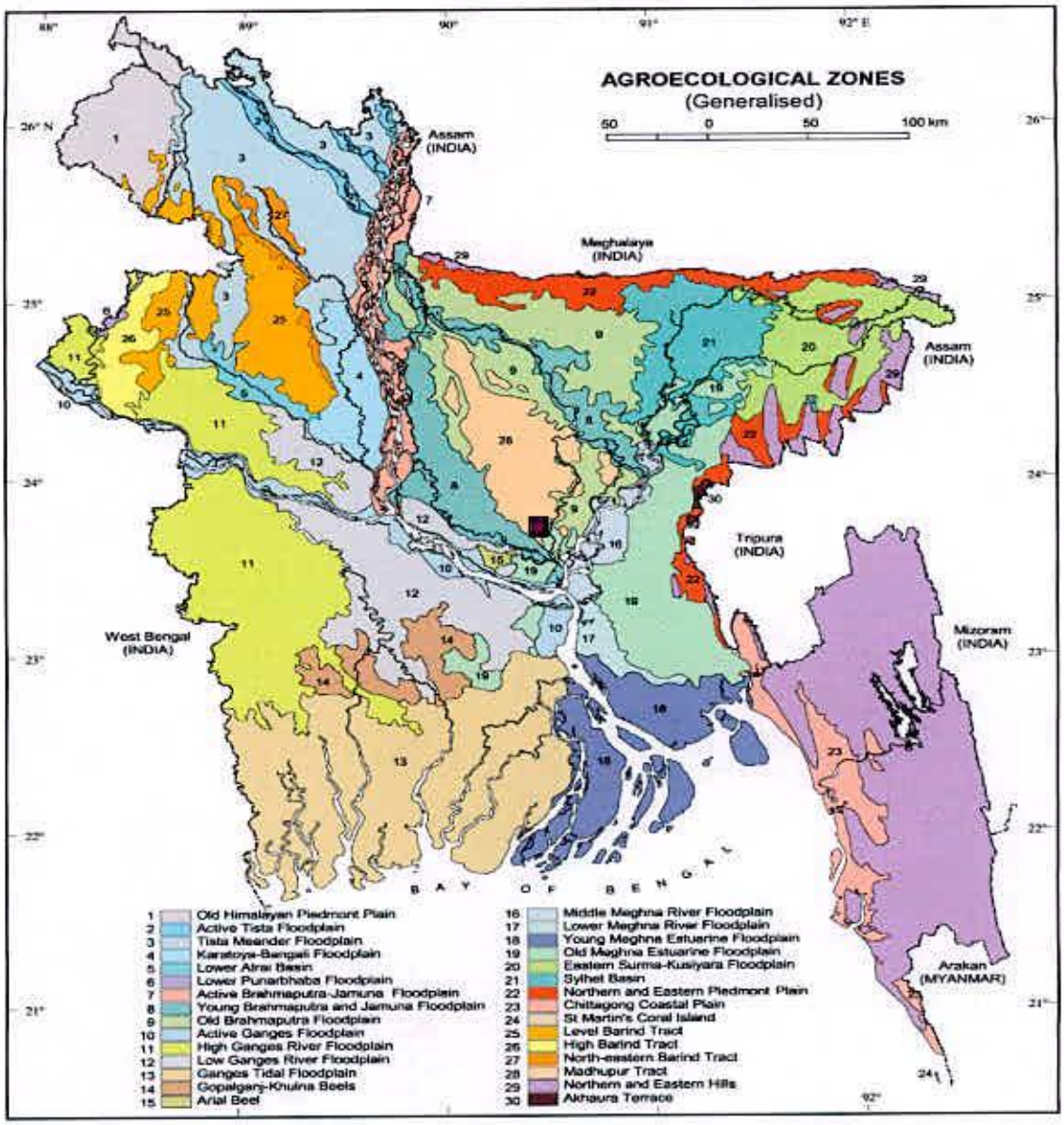
Wright, S. (1921). Correlation and Causation. *J. Agric. Res.*, **20** : 202-209.

Wu, J. J., Hao, X. X. and Jiang, J. W. (1995). Analysis of high yielding genotype features in summer soybean. *Soybean Sci.* **14** (1): 1-6.

Appendices

APPENDICES

Appendix I. Map showing the experimental site under the study



The experimental site under study

Appendix II. Monthly average Temperature, Relative Humidity and Total Rainfall and sunshine of the experimental site during the period from December, 2011 to April, 2012

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
December, 2011	29.0	13.0	79	0	3.9
January, 2012	28.1	11.1	72	1	5.7
February, 2012	33.9	12.2	55	1	8.7
March, 2012	34.6	16.5	67	45	7.3
April, 2012	34.9	20.3	69	54	7.6

Source: Bangladesh Meteorological Department (Climate & Weather Division), Agargoan, Dhaka - 1212

Appendix III: Physical characteristics and chemical composition of soil of the experimental plot

Soil Characteristics	Analytical Results
Agrological Zone	Madhupur Tract
pH	6.00 – 6.63
Organic Matter	0.84
Total N (%)	0.46
Available phosphorous	21 ppm
Exchangeable K	0.41meq / 100g soil

Source: Soil Resource and Development Institute (SRDI), Dhaka

Appendix IV: Mean performance of various growth parameter and yield components of 11 characters of 28 genotypes of soybean

Genotype	DFF	D50%F	DM	PH	BPP	NPP	PL	NSP	SPP	HSW	SYP
AGS-79	67.67	70.67	128.00	44.37	2.77	39.20	2.78	2.39	95.07	8.70	8.57
BS-13	75.67	78.67	132.00	64.20	4.70	35.33	3.00	2.37	86.07	11.47	9.80
JOYAWAZA	75.33	78.67	132.00	65.67	5.20	34.70	2.92	2.47	85.60	7.77	6.73
F-85-11347	76.33	79.00	132.00	73.27	5.67	59.57	3.06	2.66	158.37	10.17	16.13
AGS-95	60.67	64.67	120.00	44.80	3.53	39.97	2.73	2.48	98.07	10.23	10.03
GC-82-332411	62.33	65.67	120.00	44.43	4.07	44.33	2.96	2.66	109.20	9.83	10.60
BOAS-5	72.33	76.00	132.00	79.43	5.17	44.57	2.99	2.45	109.10	10.40	11.23
LG-92P-12-18	72.33	76.00	132.00	73.17	5.67	52.40	3.20	2.56	133.13	9.70	12.77
BS-33	67.33	72.67	128.00	44.80	3.40	40.87	3.13	2.60	93.73	10.30	9.57
GC-830059	66.67	70.33	120.00	68.73	4.43	43.07	2.68	2.51	107.33	6.27	6.77
ASSET-95	57.33	61.33	119.00	63.20	3.47	44.07	2.65	2.47	108.17	6.77	7.23
BARI SOYBEAN-6	59.67	63.33	116.00	58.70	3.83	54.10	3.27	2.52	136.07	11.53	15.60
KANH-33	61.33	63.67	121.00	74.13	5.77	41.70	3.08	2.51	104.40	9.17	9.67
NS-1	69.33	72.67	121.00	65.77	5.53	36.20	3.44	2.55	92.73	10.73	9.90
GMOT-17	67.33	70.67	129.00	67.57	4.53	34.70	2.59	2.54	89.07	6.53	5.83
LG-92P-1176	66.33	69.00	128.00	36.77	2.47	39.67	2.67	2.48	96.80	9.63	9.27
CHINA-1	61.33	64.67	121.00	52.20	4.30	34.07	3.54	2.51	94.91	12.90	12.30
MTD-16	66.33	69.00	125.00	40.47	2.40	27.27	2.53	2.44	67.90	11.57	7.87
SHOHAG	58.67	62.33	110.00	34.60	1.80	29.03	3.06	2.49	72.37	12.17	8.83
PK-327	60.00	63.67	119.00	43.97	1.87	24.70	2.54	2.51	62.20	11.87	8.00
AUSTRALIA	51.67	55.33	105.33	21.90	2.30	26.90	2.75	2.54	66.40	13.33	8.90
YESOY-4	70.67	73.67	131.00	49.03	4.47	26.50	3.13	2.46	66.00	13.17	8.70
PI-4174-75	71.67	75.33	132.00	59.63	4.40	38.10	4.19	2.61	102.97	16.57	17.40
MTD-452	70.67	74.33	131.00	47.00	4.63	25.60	3.10	2.43	63.87	11.17	7.10
86017-66-6	65.67	68.33	125.00	44.17	3.27	24.62	2.86	2.49	60.70	9.40	5.73
ASSET-93-19-13	69.33	72.00	127.33	71.83	4.10	45.67	3.13	2.58	117.60	9.53	11.00
BARI SOYBEAN-5	59.00	63.67	116.33	79.17	5.77	49.43	3.15	2.41	122.40	9.87	12.07
MTD-451	69.33	73.33	127.00	79.87	5.87	50.80	3.57	2.47	131.10	13.00	16.90
Mean	66.15	69.60	124.29	56.89	4.12	38.83	3.03	2.51	97.55	10.49	10.16
Min.	51.67	55.33	105.33	21.90	1.80	24.62	2.53	2.37	60.70	6.27	5.73
Max.	76.33	79.00	132.00	79.87	5.87	59.57	4.19	2.66	158.37	16.57	17.40

DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), BPP = Branches per plant, NPP = Number of pods per plant, PL = Pod length (cm), NSP = Number of seeds per pod, SPP = Seeds per plant, HSW = Hundred seed weight (g), SYP = Seed yield per plant (g).

Appendix V. Z1-Z2 score of 28 genotypes of soybean

Genotype	PCA 1	PCA 2
AGS-79	7.02	4.22
BS-13	5.84	-19.42
JOYAWAZA	5.99	-20.71
F-85-11347	-66.66	3.78
AGS-95	5.37	13.58
GC-82-332411	-5.39	17.33
BOAS-5	-22.56	-17.03
LG-92P-12-18	-42.56	-3.58
BS-33	7.25	3.17
GC-830059	-14.2	-2.1
ASSET-95	-11.56	9.19
BARI SOYBEAN-6	-36.76	23.36
KANH-33	-13.1	-2.4
NS-1	0.83	-8.54
GMOT-17	3.61	-13.34
LG-92P-1176	8.86	10.77
CHINA-1	6.44	6.51
MTD-16	35.65	-2.18
SHOHAG	35.76	15.26
PK-327	40.91	0.35
AUSTRALIA	48.09	27.97
YESOY-4	32.73	-14.25
PI-4174-75	-7.19	-7.01
MTD-452	35.7	-14.25
86017-66-6	41.11	-7.06
ASSET-93-19-13	-25.95	-4.54
BARI SOYBEAN-5	-32.44	5.0
MTD-451	-42.79	-4.06

Appendix VI: Analysis of variances of eleven yield and yield related characters of soybean

Analysis of variance

Source	df	Mean sum of square										
		DFF	D50%F	DM	PH	BPP	NPP	PL	NSP	SPP	HSW	SYP
Replication	2	1.87**	1.87	00.0	5.57	0.34	21.01*	0.002	0.005	63.42	0.04	0.77
Treatment	27	114.21**	109.32**	151.89**	734.54**	4.67**	272.21**	0.396**	0.016**	1862.98**	15.21**	31.03**
Error	54	0.29	0.87	0.04	4.77	0.11	5.58	0.003	0.002	27.91	0.07	0.39

** = Significant at 1%.
* = Significant at 5%.

DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), BPP = Branches per plant, NPP = Number of pods per plant, PL = Pod length (cm), NSP = Number of seeds per pod, SPP = Seeds per plant, HSW = Hundred seed weight (g), SYP = Seed yield per plant (g).