

**CHARACTER ASSOCIATION AND MULTIVARIATE
ANALYSIS OF SOYBEAN (*Glycine max* (L.) Merrill)**

BY

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CERTIFICATE

This is to certify that thesis entitled, "CHARACTER ASSOCIATION AND MULTIVARIATE ANALYSIS OF 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 KAMRUN NAHAR MILI, Registration No. 08-03009 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.

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Dedicated to
My beloved parents

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CHARACTER ASSOCIATION AND MULTIVARIATE ANALYSIS OF SOYBEAN (*Glycine max* (L.) Merrill)

BY

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ABSTRACT

A field experiment was conducted at the research farm of Sheer-e-Bangla Agricultural University, Dhaka-1207 to study character association and multivariate analysis of soybean (*Glycine max* (L.) Merrill) during December 2013 to April 2014 with 27 genotypes in randomized complete block design with three replications. Analysis of variance for each trait showed significance differences among the genotypes. Phenotypic coefficient of variation was close to genotypic coefficient of variation for all the character except number of seed per pod and number of branches per pod indicating the environmental influence on the expression of these characters. High heritability associated with high genetic advance in percent of mean was observed for stover yield, seed yield per plant, hundred seed weight, and single pod weight per plant indicated that selection for these characters would be effective. Seed yield per plant had highly significant positive genotypic and phenotypic association with stover yield, number of branches per plant, number of pod per plant revealing that selection based on these traits would ultimately improve the seed yield. Path coefficient analysis revealed that number of braches per plant followed by stover yield had highest direct positive effect on seed yield. So, importance has to given for these characters in future breeding programme to improve the yield in soybean. Multivariate analysis based on 12 characters indicated that the 27 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, yield per plant and pod length. Thus, these traits may be given high emphasis while selecting the line for hybridization. The inter cluster distance was maximum between cluster I and cluster IV. The highest intra cluster distance was found in cluster II followed by cluster I. From the results it can be concluded that G24 (BS-33), G2 (P1-4174-75), G11 (AUSTRALIA), G13 (PK-327) genotype 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
σ^2_g	Genotypic Variance
g	Gram
h^2_b	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
σ^2_p	Phenotypic variance
RCBD	Randomized Complete Block Design Replication
Res.	Research
SE	Standard Error
m^2	Square meter
TSP	Triple Super Phosphate

A blue scroll graphic with a white border, featuring a vertical strip on the left side and a small circular element at the top right. The word "INTRODUCTION" is written in a bold, black, serif font across the center of the scroll.

INTRODUCTION

CHAPTER-I

INTRODUCTION

Soybean (*Glycine max* (L) Merrill) belonging to the Leguminosae family is considered as a miracle crop due to its extraordinary qualities. It is an important cash crop with unique and important traits such as the high seed protein and oil contents, and the ability to perform symbiotic nitrogen fixation. It contains 40 to 42% good quality protein and 18 to 22% oil comprising 85% unsaturated fatty acids and is free from cholesterol along with ample mineral elements, so it is highly desirable in human diet. The seeds leftover after solvent extraction are ground to make high protein meal which is used largely as a supplement to cereal seeds in feed for poultry and dairy/beef animals. Being legume it also fixes atmospheric nitrogen to available form. As the best source of protein it truly claims the title "the meat that grows on plant". In Bangladesh, it is one of the nonconventional oilseed crop that can be successfully grown during spring as well as the summer season. Although soybean as an oil crop was introduced in Bangladesh 1970's along with sunflower, but it could not make its place in the country. Probably, the main reasons are the lack of genetic and breeding work, unavailability of genotypes suitable for different cropping patterns.

The knowledge of certain genetic variability is essential for proper understanding and their manipulation in any crop improvement programme. Grain yield is the result of the expression and association of several plant growth components. Correlation coefficients, although useful in quantifying the size and direction of trait associations, can be misleading if the high correlation between two traits is a consequence of the indirect effect of the traits (Dewey and Lu, 1959). In soybean, scientists used path analysis, which partitions the genotypic correlations into direct and indirect effects of the traits (Ali *et al.*, 1989; Shivashankar and Viswanatha, 1989; Ghafoor *et al.*, (1990); Akhter and Sneller, 1996; Board *et al.*, 1997; Taware *et al.*, 1997; Shukla *et al.*, 1998; Board *et al.*, 1999; Yadav *et al.*, (2001); Iqbal *et al.*, 2003), whereas, Arshad *et al.*, (2003); Ghafoor *et al.*,

(2003) and Arshad *et al.*, (2004) have mentioned the worth of this techniques in other legumes also.

The present nutritional situation of Bangladeshis is a matter of great concern. The main nutritional problem of the country is that of protein energy malnutrition. Most of the people suffering from malnutrition. Soybean can meet up the protein deficiency problem. Soybean is regarded as an ideal food for the people of Bangladesh as it contain 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 could be good substitute for animal products because, unlike some other beans, soybean offers a complete protein profile. Soya protein products can replace animal based foods (Henkel, 2000).

Soya milk is comparable to cow's milk (Smith, 1975). 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. Several studies provide with evidence that supports the role of whole soya foods in a cancer-preventing diet (Amadou *et al.*, 2009).

Soybean is not yet popular 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 Dollar of about 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 paratha, soya milk, soya cakes, soya biscuits, soya bread etc. (Khaleque, 1985; Mondal and Wahhab, 2001).

Soybean can be grown under wide range of climatic and edaphic conditions. With well-adapted cultivars, soybean can be cultivated throughout the year of Bangladesh (Haque *et al.*, 1976; Rahman, 1982). In the northern part of the country it can also 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 due to using low yield potential varieties and poor cultivation technologies i.e. lack of application of inoculums, fertilizer etc.

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 and production in Bangladesh is fragmentary and not available in systematic form, but it is thought to be of 10,000 acres with about 5,000 tons of production (Rahman, 2002).

Genetic diversity as a major factor which can determine yield security in future (Batugal, 1999). The importance of genetic diversity in the improvement of crop has been stressed in both self and cross pollinated crop (Griffing and Lindstrom, 1954; Murty and Anand, 1966; Gaur *et al.*, 1978). 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 type of soybean contribute considerable degree of variability in respect of 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 having high genetic divergence (Upadhaya 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 assessing the relative contribution of different character to the total divergence in self-pollinated crops has been established by several workers (Golakia and Makne, 1992).

Multivariate analysis act 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 (Murty and Arunachalam, 1966; Sachan and Sharma, 1971; Jatasra and Paroda, 1978).

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. Based on these studies the quantum importance of individual character is marked to facilitated the selection program for better yield.

Keeping in view the importance of above technique, the present study was planned to quantify the genetic divergence and variability in a diverse collection of genotypes with the following objectives.

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



**REVIEW OF
LITERATURE**

CHAPTER II

REVIEW OF LITERATURE

Soybean (*Glycine max* L.) is a legume that grows in tropical, subtropical and temperate climates. Soybean is now cultivated throughout east and south east Asia where people depend on it for food, animal feed and medicine. The seeds of soybeans 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 day to maturity had very low GCV and PCV estimates. The differences between GCV and PCV tuber 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 that 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 in percent 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 in percent 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 in 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 in 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 that 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 for 100 seed weight and phenotypic co-efficient of variation y also observed plant height and grain yield in soybean. The 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. They showed 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 that 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).

Malik *et al.* (2007) reported positive Correlation coefficient for soybean yield was positive with leaf area, first pod height, days to flowering, days to maturity, plant height and number of branches per plant. Therefore, increase in these traits will ultimately increase the grain yield. Path coefficient analysis revealed that days to flowering completion had maximum direct contribution to yield followed by days to pod initiation, chlorophyll content, number of pods per plant and plant height. It is suggested that these characters can be considered as selection criteria in improving the bean yield of soybean genotypes.

Correlation studies showed that the pod yield was significant positive correlated with pods per plant and hundred seed weight (Ave 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 (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, and 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 per plant 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, Dorney *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. 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.

Rajarithnam *et al.* (1996) found that seed yield was significantly 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. Seedper 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 positive and high 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 had positively correlation 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 had 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 had 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 (Ave 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 or 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 per plant had the direct effect on seed yield followed by 100-seed weight. Pods per plant affected seed yield negatively via indirect effects of plant height, pod height and seed per 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 followed 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 for 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 eco-geographical 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 using Mahalanobis' D^2 -statistic. 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 -statistic. 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 . The clustering pattern showed that 10 clusters diversity and geographic distribution were independent of each other. Ghatge and Kadu

(1993) estimated genetic diversity using the Nthalanobis' D^2 -statistic 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.



**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, 2013 to April, 2014 to study the character association and multivariate analysis of soybean (*Glycine max*). A brief description about the location 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, economical and statistical analysis etc. Which are briefly described as follows:

3.1 Experimental site

The research work about the study of multivariate analysis of soybean was conducted at the Sher-e-Bangla Agricultural University farm, Dhaka-1207, during December, 2013 to April, 2014.

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 m 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

The research area has subtropical climate, characterized by high temperature, high relative humidity and heavy rainfall in kharif season (April to September) and little rainfall associated with moderately low temperature during the rabi season (October to March). Weather prevailed at the experimental site during the study period was presented in Appendix II.

3.4 Characteristics of soil

The soil is general soil type, shallow red brown terrace soils under Tejgaon series. Top soil was 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 it had organic matter 0.84%. The field was associated with available irrigation and drainage system and above flood level. The analysis 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 27 genotypes of soybean. The genetically pure and physically healthy seeds of these genotypes were obtained from Sher-e-Bangla agricultural University (SAU), Dhaka. 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 replications. The plot size was 200 m² and distance of 1.0 m from block to block, line to line distance 30 cm and plant to plant distance was 15 cm. The genotypes were randomly distributed to each row within each block.

3.7 Land preparation

The experimental plot was prepared by sufficient ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about proper tilth in the first week of December 2013. Stubbles and weeds were removed carefully from the research plot and leveled properly.

3.8 Manure and fertilizer application

The plot was properly fertilized with cowdung, urea, TSP and mp @ 5 ton, 60 kg, 120kg, 70 kg per hectare respectively. The full amount of cowdung, tsp ,mp, and half of the urea were applied at the time of final land preparation. The remaining urea was applied as top dressing in two installments, first after 20 days and second after 45 days of sowing.

Table 1. Sources of 27 soybean genotypes used in the present study

Sl. No.	Genotypes no.	Name	Sources
1	G1	LG-92P-1176	SAU
2	G2	P1-4174-75	SAU
3	G3	KANH-33	SAU
4	G4	AGS-79	SAU
5	G5	MTD-452	SAU
6	G6	GMOT-17	SAU
7	G7	JOYAWAZA	SAU
8	G8	F-85-11347	SAU
9	G9	YESOY-4	SAU
10	G10	SHOHAG	SAU
11	G11	AUSTRALIA	SAU
12	G12	GC-82-332411	SAU
13	G13	PK-327	SAU
14	G14	ASSET-93-19-13	SAU
15	G15	PK-327	SAU
16	G16	AGS-95	SAU
17	G17	BARI SOYBEAN-6	SAU
18	G18	NS-1	SAU
19	G19	MTD-451	SAU
20	G20	GC-830059	SAU
21	G21	86017-66-6	SAU
22	G22	MTD-16	SAU
23	G23	LG-92P-12-18	SAU
24	G24	BS-33	SAU
25	G25	ASSET-95	SAU
26	G26	BS-13	SAU
27	G27	CHINA-1	SAU

Source: Dept. of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University

3.9 Seed sowing

Seeds of 27 genotypes were sown on 24th December 2013. The seedlings appeared 6 to 13th days after sowing.

3.10 Intercultural operation

Intercultural operations were done according to necessity.

3.10.1 Thinning

After well establishment of the plants, the base soil around each seedlings was pulverized. After 15 days of sowing thinning was done for proper development and avoid crowd environment.

3.10.2 Weeding and mulching

As per requirement several weeding and mulching were done. For ease of aeration and less competition of seedling growth weeding was done at the very first stage. mulch was provided after an irrigation to prevent crust formation and also for good aeration.

3.10.3 Irrigation and after-care

The plants were properly irrigated for four consecutive days. The 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 the disease insecticide sprayed in the field.

3.11 Harvesting

At full maturity the plants were harvested. Maturity characterized with yellowish of leaves completion of leaf shedding and pod color mostly become dark brown. Different varieties were harvested at different date according to their full maturity.

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

Determined as the days required, from sowing to first anthesis.

3.12.2 Days to 50% flowering

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

3.12.3 Days to 80% 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.



Plate 1. The experimental field



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12.10.15.

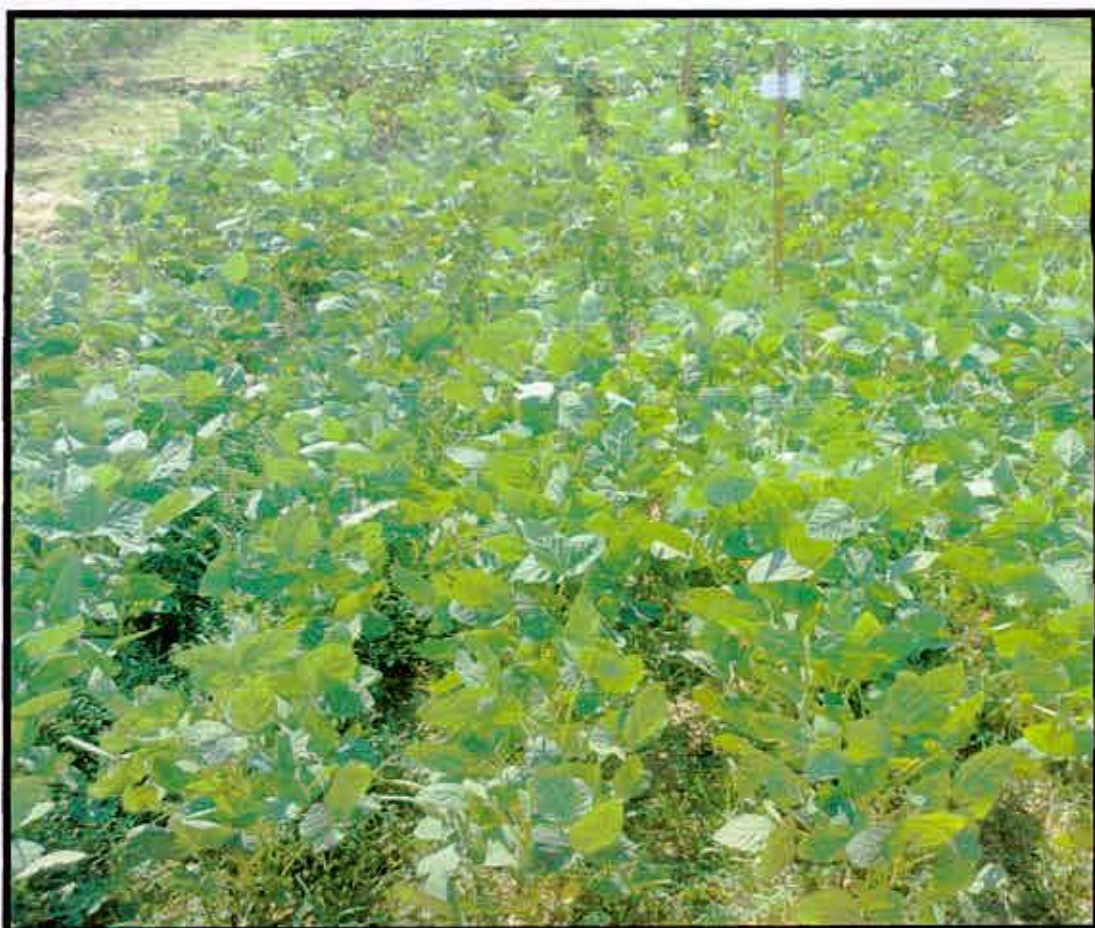


Plate 2. Field view of the experimental



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

3.12.8 Number of seeds per pod

Average number of seeds from ten randomly selected pods.

3.12.9 Stover yield.

Mean number of Stover 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 Single pod weight per plant

Weight of single pod selected at random from each plant was expressed in grams.

3.12.12 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).

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

Where, GMS = Genotypic mean sum of squares

EMS = Error mean sum of square

r = number of replications

Phenotypic variance, $\sigma_{ph}^2 = \sigma_g^2 + EMS$

Where,

σ_g^2 = 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)

Genotypic co-efficient of variation, $GCV \% = \frac{\sqrt{\sigma_g^2}}{\bar{x}} \times 10$

Where,

σ_g^2 = Genotypic variance

\bar{x} = Population mean

Similarly,

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

Phenotypic co-efficient variation, $PCV = \frac{\sqrt{\sigma_{ph}^2}}{\bar{x}} \times 100$

Where,

σ_{ph}^2 = 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).

$$\text{Heritability, } h^2_b (\%) = \frac{\sigma^2_g}{\sigma^2_{ph}} \times 100$$

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).

$$\text{Genetic advance, GA} = K \cdot h^2 \cdot \sigma_p$$

$$\text{Or Genetic advance, GA} = K \cdot \frac{\sigma^2_g}{\sigma^2_{ph}} \cdot \sigma_{ph}$$

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 in 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).

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

Where,

\sum = Summation

x and y are the two variables correlated

N = Number of observation

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:

$$\text{Genotypic correlation, } r_{gxy} = \frac{GCOV_{xy}}{\sqrt{GV_x GV_y}} = \frac{\sigma_{gxy}}{\sqrt{(\sigma_{g_x}^2 \cdot \sigma_{g_y}^2)}}$$

Where,

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

$\sigma_{g_x}^2$ = Genotypic variance of the trait x

$\sigma_{g_y}^2$ = Genotypic variance of the trait y

$$\text{Phenotypic correlation (} r_{pxy} \text{)} = \frac{PCOV_{xy}}{\sqrt{PV_x PV_y}}$$

Where,

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

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

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

3.13.8 Estimation of path coefficient analysis

It was done according to the procedure employed by Dewey and Lu (1959) 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 on yield per hectare. In order to estimate direct and indirect effects of the correlated characters, i. e. 1, 2, 3....and 12 on yield y, a set of simultaneous equations (twelve equations in this example) is required to be formulated as shown below:

$$r_{1,y} = P_{1,y} + r_{1,2} P_{2,y} + r_{1,3} P_{3,y} + r_{1,4} P_{4,y} + r_{1,5} P_{5,y} + r_{1,6} P_{6,y} + r_{1,7} P_{7,y} + r_{1,8} P_{8,y} + r_{1,9} P_{9,y} + r_{1,10} P_{10,y} + r_{1,11} P_{11,y} + r_{1,12} P_{12,y}$$

$$r_{2,y} = r_{1,2} P_{1,y} + P_{2,y} + r_{2,3} P_{3,y} + r_{2,4} P_{4,y} + r_{2,5} P_{5,y} + r_{2,6} P_{6,y} + r_{2,7} P_{7,y} + r_{2,8} P_{8,y} + r_{2,9} P_{9,y} + r_{2,10} P_{10,y} + r_{2,11} P_{11,y} + r_{2,12} P_{12,y}$$

$$r_{3,y} = r_{1,3} P_{1,y} + r_{2,3} P_{2,y} + P_{3,y} + r_{3,4} P_{4,y} + r_{3,5} P_{5,y} + r_{3,6} P_{6,y} + r_{3,7} P_{7,y} + r_{3,8} P_{8,y} + r_{3,9} P_{9,y} + r_{3,10} P_{10,y} + r_{3,11} P_{11,y} + r_{3,12} P_{12,y}$$

$$r_{4,y} = r_{1,4} P_{1,y} + r_{2,4} P_{2,y} + r_{3,4} P_{3,y} + P_{4,y} + r_{4,5} P_{5,y} + r_{4,6} P_{6,y} + r_{4,7} P_{7,y} + r_{4,8} P_{8,y} + r_{4,9} P_{9,y} + r_{4,10} P_{10,y} + r_{4,11} P_{11,y} + r_{4,12} P_{12,y}$$

$$r_{5,y} = r_{1,5} P_{1,y} + r_{2,5} P_{2,y} + r_{3,5} P_{3,y} + r_{4,5} P_{4,y} + P_{5,y} + r_{5,6} P_{6,y} + r_{5,7} P_{7,y} + r_{5,8} P_{8,y} + r_{5,9} P_{9,y} + r_{5,10} P_{10,y} + r_{5,11} P_{11,y} + r_{5,12} P_{12,y}$$

$$r_{6,y} = r_{1,6} P_{1,y} + r_{2,6} P_{2,y} + r_{3,6} P_{3,y} + r_{4,6} P_{4,y} + r_{5,6} P_{5,y} + P_{6,y} + r_{6,7} P_{7,y} + r_{6,8} P_{8,y} + r_{6,9} P_{9,y} + r_{6,10} P_{10,y} + r_{6,11} P_{11,y} + r_{6,12} P_{12,y}$$

$$r_{7,y} = r_{1,7} P_{1,y} + r_{2,7} P_{2,y} + r_{3,7} P_{3,y} + r_{4,7} P_{4,y} + r_{5,7} P_{5,y} + r_{6,7} P_{6,y} + P_{7,y} + r_{7,8} P_{8,y} + r_{7,9} P_{9,y} + r_{7,10} P_{10,y} + r_{7,11} P_{11,y} + r_{7,12} P_{12,y}$$

$$r_{8,y} = r_{1,8} P_{1,y} + r_{2,8} P_{2,y} + r_{3,8} P_{3,y} + r_{4,8} P_{4,y} + r_{5,8} P_{5,y} + r_{6,8} P_{6,y} + r_{7,8} P_{7,y} + P_{8,y} + r_{8,9} P_{9,y} + r_{8,10} P_{10,y} + r_{8,11} P_{11,y} + r_{8,12} P_{12,y} +$$

$$r_{9,y} = r_{1,9} P_{1,y} + r_{2,9} P_{2,y} + r_{3,9} P_{3,y} + r_{4,9} P_{4,y} + r_{5,9} P_{5,y} + r_{6,9} P_{6,y} + r_{7,9} P_{7,y} + r_{8,9} P_{8,y} + P_{9,y} + r_{9,10} P_{10,y} + r_{9,11} P_{11,y} + r_{9,12} P_{12,y} +$$

$$r_{10,y} = r_{1,10} P_{1,y} + r_{2,10} P_{2,y} + r_{3,10} P_{3,y} + r_{4,10} P_{4,y} + r_{5,10} P_{5,y} + r_{6,10} P_{6,y} + r_{7,10} P_{7,y} + r_{8,10} P_{8,y} + r_{9,10} P_{9,y} + P_{10,y} + r_{10,11} P_{11,y} + r_{10,12} P_{12,y}$$

$$r_{11,y} = r_{1,11} P_{1,y} + r_{2,11} P_{2,y} + r_{3,11} P_{3,y} + r_{4,11} P_{4,y} + r_{5,11} P_{5,y} + r_{6,11} P_{6,y} + r_{7,11} P_{7,y} + r_{8,11} P_{8,y} + r_{9,11} P_{9,y} + r_{10,11} P_{10,y} + P_{11,y} + r_{11,12} P_{12,y} + r_{11,13} P_{13,y}$$

$$r_{12,y} = r_{1,12} P_{1,y} + r_{2,12} P_{2,y} + r_{3,12} P_{3,y} + r_{4,12} P_{4,y} + r_{5,12} P_{5,y} + r_{6,12} P_{6,y} + r_{7,12} P_{7,y} + r_{8,12} P_{8,y} + r_{9,12} P_{9,y} + r_{10,12} P_{10,y} + r_{11,12} P_{11,y} + P_{12,y}$$

Where,

r_{1y} = Genotypic correlation coefficients between y and I th character (y = Fruit yield)

P_{iy} = Path coefficient due to i th character (i= 1, 2, 3,....12)

1 = Plant height

2 = Days to first flowering

3 = Days to 50% flowering

4 = Days to 80% maturity

5 = Number of branches per plant

6 = Number of pod per plant

7 = Number of seed per pod

8 = Pod length (cm)

9 = Thousand seed weight (gm)

10 = Stover yield (g)

11 = Single pod weight per plant (g)

12 = Yield (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
- $r_{1,12} P_{12,y}$ = indirect effect of 1 via 12 on y

Where,

$P_{1,y}, P_{2,y}, P_{3,y}, \dots, P_{8,y}$ = Path coefficient of the independent variables 1, 2, 3, ..., 12 on the dependent variable y, respectively.

$r_{1,y}, r_{2,y}, r_{3,y}, \dots, r_{12,y}$ = Correlation coefficient of 1, 2, 3, ..., 12 with y, respectively.

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

$$P^2_{RY} = 1 - (r_{1,y}P_{1,y} + r_{2,y}P_{2,y} + \dots + r_{12,y}P_{12,y})$$

Where,

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

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

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

$r_{i,y}$ = 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, 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 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

$$D^2 = \sum_i d_i^2 = \sum_i (Y_i^j - Y_i^k) \quad (j \neq k)$$

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:

- ❖ Choice of cluster from which genotypes are selected for use as parents,
- ❖ Selection of particular genotype(s) from the selected cluster(s),
- ❖ Relative contribution of the characters to the total divergence and
- ❖ Other important characters of the genotypes performance



**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 seven soybean genotypes as well as yield and its contributing characters were computed and statistically analyzed and the result of the present investigation of correlation co-efficient and path analysis genetic diversity in Soybean (*Glycine max* (L.) Merrill) carried out during Rabi season 2013-14 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 plant height, branches per plant, number of pods per plant, 50% flowering, days to maturity, seeds per plant, pod length, hundred seed weight, number of seed per pod, 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 12 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 Plant height (cm)

The grand mean plant height recorded was 55.34 cm. It ranged from 34.57 cm to 75.85 cm (Table 2). The analysis of variance revealed highly significant differences among the genotypes with respect to plant height. The maximum plant height (75.85 cm) was recorded by the genotype 'PK-327' and the lowest plant height (34.57cm) was recorded by 'AUSTRALIA' (Appendix IV). The genotypic and phenotypic variance was observed 71.08 and 97.31, respectively for plant height with low environmental influence. The phenotypic co-efficient of variation (17.82) was higher than the genotypic co-efficient of variation (15.23), which indicated presence of considerable variability among the

genotypes for this trait. The heritability (73.05%) estimates for this trait was not high, genetic advance (14.84) was low and genetic advance in per cent of mean (26.82) was found also low, revealed that this trait was governed by 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).

4.2.2 Days to first flowering

The mean number of days to first flowering was 82.1. It had a range of 74 to 90.33 days. The accession 'BS-33' was the earliest to flower while F-85-11347 was late to flower (Appendix IV). The Genotypic, phenotypic and environmental variances observed were 12.43, 13.76 and 1.33 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 (4.29) and phenotypic co-efficient of variation (4.52) 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 (90.32%) estimates for this trait was high, genetic advance (6.90) was moderately low and genetic advance over percentage of mean (8.41) was found at medium level, 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.

Table 2. Estimation of genetic parameters in 12 characters of 27 soybean genotypes

Parameters	Range	Mean	MS	CV (%)	σ^2P	σ^2g	σ^2e	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
PH	34.57-75.85	55.34	239.46**	9.25	97.31	71.08	26.23	17.82	15.23	9.25	73.05	14.84	26.82
DFF	74.00-90.33	82.10	38.61**	1.41	13.76	12.43	1.33	4.52	4.29	1.41	90.32	6.90	8.41
D50F	76.33-93.67	84.78	42.05**	1.43	15.00	13.53	1.47	4.57	4.34	1.43	90.18	7.19	8.49
D80M	116.33-157.00	127.32	218.42**	0.85	73.59	72.42	1.16	6.74	6.68	0.85	98.40	17.39	13.66
NBP	3.47-11.57	6.22	10.68**	16.63	4.27	3.20	1.07	33.23	28.77	16.63	74.96	3.19	51.32
NPP	28.33-95.00	49.51	931.31**	18.36	365.52	282.89	82.63	38.62	33.97	18.36	77.39	30.48	61.57
NSP	2.00-3.33	2.89	0.21**	8.33	0.11	0.05	0.06	11.48	7.90	8.33	47.40	0.32	11.21
PL	2.82-4.95	3.64	0.66**	6.87	0.26	0.20	0.06	14.06	12.26	6.87	76.09	0.80	22.04
HSW	5.13-14.70	9.06	23.52**	5.62	8.01	7.75	0.26	31.24	30.73	5.62	96.76	5.64	62.27
SY	2.90-19.83	7.84	47.89**	11.95	16.55	15.67	0.88	51.89	50.49	11.95	94.69	7.94	101.22
SPWP	1.47-9.74	4.37	9.03**	14.94	3.30	2.87	0.43	41.54	38.76	14.94	87.07	3.26	74.51
YIELD	8.37-49.81	18.54	314.23**	12.19	108.15	103.04	5.11	56.09	54.75	12.19	95.28	20.41	110.09

** Correlation is significant at the 0.01 level. DFF= Days to first flowering, PH= Plant height (cm), D50F= Days to 50% flowering, D80M= Days to 80% maturity, NBP= Number of branches per plant, NPP= Number of pod per plant, NSP=Number of seeds per pod, PL= Pod length, HSW= Hundred seed weight (g), SY= Stover yield, SPWP= Single pod weight per plant, YIELD=Yield per plant, MS= Mean sum of square, CV(%)= Coefficient of variation, σ^2P = Phenotypic variance, σ^2g = Genotypic variance, σ^2e = Environmental variance, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, ECV= Environmental coefficient of variation.

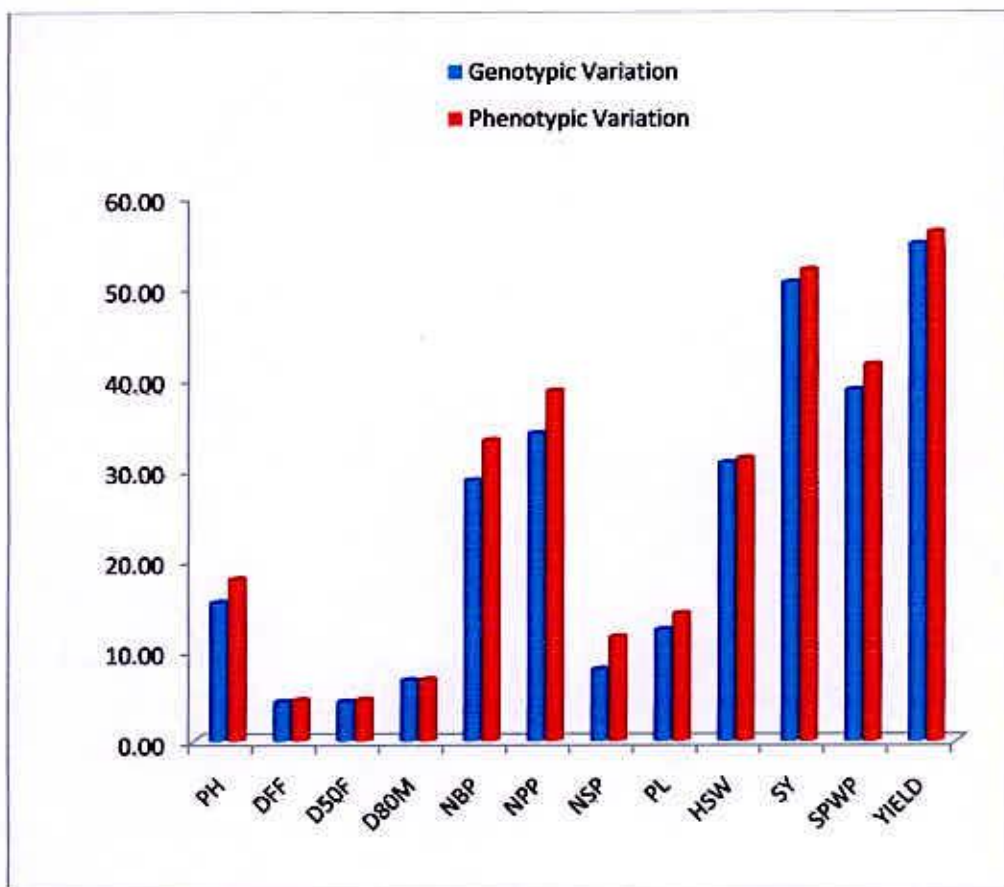


Fig. 1. Genotypic and Phenotypic variations in Soybean

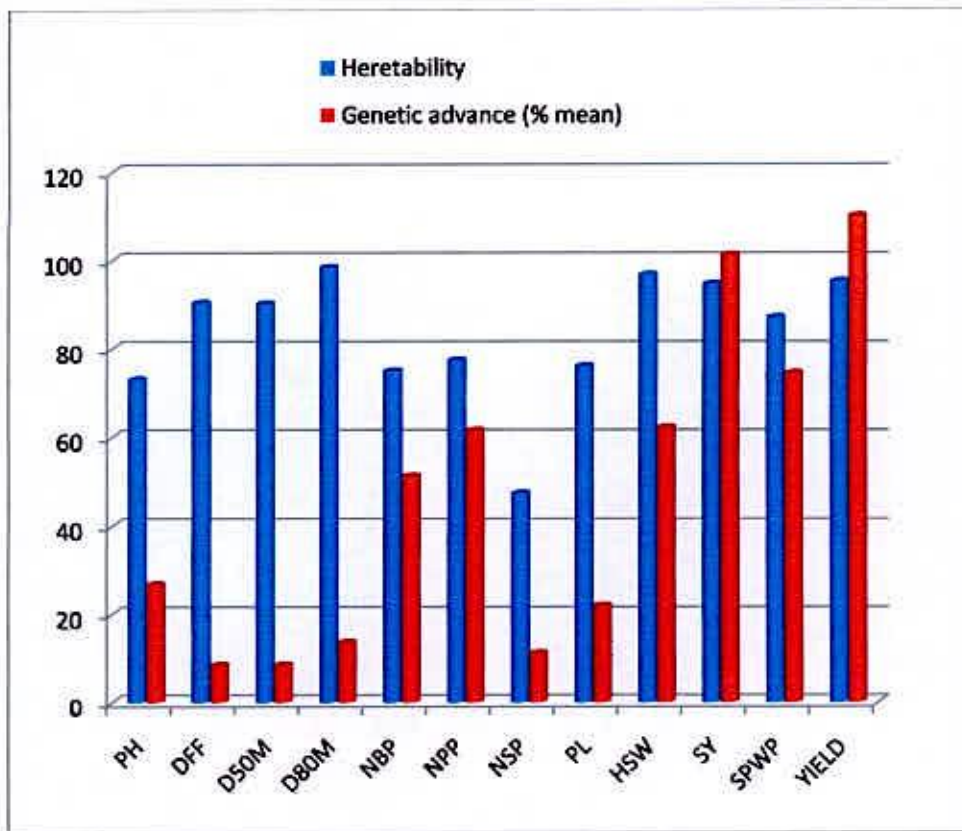


Fig. 2. Heritability and genetic advance over mean in soybean

4.2.3 Days to 50% flowering

Significant differences were recorded among the entries with respect to days to 50% flowering. The value ranged from 76.33 to 93.67 days, in the genotype 'BS-33' and F-85-11347 respectively (Appendix IV). The Genotypic, phenotypic and environmental, variances observed were 13.53, 15.00 and 1.47, 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 (4.34) and phenotypic co-efficient of variation (4.57) were close to each other (Table 2 and Fig 1) indicating minor environmental influence on this character. The heritability (90.18%) estimates for this trait was high, genetic advance (7.19) was at moderate level and genetic advance over percentage of mean (8.49) 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).

4.2.4 Days to 80% maturity

Significant mean sum of square for plant maturity (218.42) in soybean indicated considerable difference among the genotypes studied (Table 2). The value ranged from 116.33 to 157.00 with a mean of 127.32. The genotype 'AUSTRALIA' had highest and lowest in the genotype 'LG-92P-1176' (Appendix IV). The phenotypic variance (73.59) appeared to be higher than the genotypic variance (72.42) 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 6.68 and 6.74, 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 (98.40%) estimates for this trait was high, genetic advance (17.39) moderately high and genetic advance in per cent of mean (13.66) was found low, revealed that this trait was governed by additive gene (Plate 7 and Plate 8).



Plate 7. Showing phenotypic variation in flower Between G1 and G16 Genotype of soybean



Plate 8. Showing phenotypic variation in leaf and stem between G-9 and G-13 genotype of soybean

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.

4.2.5 Number of branches per plant

In case of number of branches per plant mean sum of square significant (10.68) in soybean indicated considerable difference among the genotypes studied (Table 2). It ranged from 3.47 to 11.57 with a mean value of 6.22. Maximum number of branches recorded in ASSET-93-19-13 and AGS-79 genotype showed the minimum number of branches (Appendix IV). The phenotypic variance (4.27) appeared to be higher than the genotypic variance (3.20) 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 28.77 and 33.23, respectively which indicated presence of considerable variability among the genotypes. The heritability (74.96%) estimates for this trait was moderately high, genetic advance (3.19) was low and genetic advance in per cent of mean (51.32) 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. Phenotypic variation is showed in Plate 8.

4.2.6 Number of pods per plant

Significant mean sum of square for pods per plant (931.31) in soybean indicated if considerable variation for this trait (Table 2). The number of pods per plant was ranged from 28.33 to 95.00 with mean of 49.51. The minimum number of pods per plant was observed in accession SHOHAG while maximum number of pods per plant was found in the genotype F-85-11347 (Appendix IV). The phenotypic variance (365.52) appeared to be higher than the genotypic variance (282.89) 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 33.97 and 38.62,

respectively which indicated presence of considerable variability among the genotypes. The heritability (77.39%) estimates for this trait was high, genetic advance (30.48) was moderately high and genetic advance in per cent of mean (61.57) was found moderately high, revealed that this trait was governed by 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).

4.2.7 Number of seeds per pod

Significant mean sum of square for number of seeds per pod (0.21) in soybean indicated existence of considerable variation for this trait (Table 2). The germplasm accessions differed significantly for this character. The values ranged from 2.00 to 3.33 with a mean of 2.89. The genotype AUSTRALIA had highest number of seeds per pod while it was lowest in the genotype SHOHAG (Appendix IV). The phenotypic variance (0.11) appeared to be higher than the genotypic variance (0.05) suggested considerable influence of environment on the expression of the of variation genes controlling this trait. The genotypic co-efficient and phenotypic co-efficient of variation were 7.90 and 11.48, respectively indicating presence of considerable variability among the genotypes. The heritability (47.40%) estimates for this trait was low, genetic advance (0.32) and genetic advance in per cent of mean (11.21) was found very low. (Table.2) revealed that this trait was governed by non additive gene.

4.2.8 Pod length (cm)

Mean sum of square for pod length (0.66) in soybean highly significant indicated considerable difference among the genotypes studied (Table 2). It ranged from 2.82 to 4.95 cm with a mean of 3.64 cm. The minimum pod length was recorded by the accession SHOHAG and accession 4.95 showed the maximum pod length (Appendix IV). The phenotypic variance (0.26) and genotypic variance (0.20) 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 12.26 and 14.06, respectively which indicated presence of considerable variability among the genotypes. The heritability (76.09%) estimates for this trait was high, genetic advance (0.80) was very low and genetic advance in per cent of mean (22.04) was found

moderately high, revealed that this trait was governed by additive gene. Dobhal (1995) observed total genetic distance was highest for pod length.

4.2.9. Hundred seed weight (g)

The mean sum of square for hundred seed weight (23.52) in soybean significantly indicated considerable differences among the genotypes studied (Table.2). The mean hundred seed weight noticed was 9.06 with a range of 5.13-14.70 g. The line GMOT-17 showed the minimum hundred seed weight and the maximum hundred seed weight was recorded in the accession LG-92P-12-18. The phenotypic variance appeared 8.01 to be higher than the genotypic variance 7.75 suggested no considerable influence of environment on the expression of the genes controlling this trait. There was a very little difference between phenotypic 31.24 and genotypic co-efficient of variation 30.73, indicating minor environmental influence on this character. Heritability (96.76%) estimates for this trait was very high, genetic advance (5.64) was low and genetic advance in per cent of mean (62.27) was found high, revealed that this trait was governed by additive gene.

4.2.10. Stover yield (g)

Significant mean sum of square for stover yield per plant (47.89) in soybean indicated existence of considerable variation for this trait. The mean stover yield per plant was 7.84 g with a range of 2.90-19.83 g in the genotype 'MTD-451' and 'F-85-11347' respectively. The phenotypic variance (16.55) appeared to be higher than the genotypic variance (15.67) 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 50.49 and 51.89, respectively which indicated presence of considerable variability among the genotypes. The heritability (94.69%) estimates for this trait was high, genetic advance (7.94) low and genetic advance in per cent of mean (101.22) was found very high, revealed that this trait was governed by additive gene.

4.2.11. Single pod weight per plant (g)

In case of single pod weight per plant, mean sum of square (9.03) in soybean significant indicated existence of considerable variation for this trait (Table 2). The mean single pod weight per plant was 4.37 g with a range of 1.47-9.74 g in the genotype 'GC-82-332411' and 'F-85-11347' respectively. The phenotypic variance (3.30) appeared to be higher than the genotypic variance (2.87) 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 38.76 and 41.54, respectively which indicated presence of considerable variability among the genotypes. The heritability (87.07%) estimates for this trait was high, genetic advance (3.26) low and genetic advance in per cent of mean (74.51) was found very high, revealed that this trait was governed by additive gene.

4.2.12. Yield per plant (g)

In case of yield per plant, mean sum of square (314.23) in soybean significant indicated existence of considerable variation for this trait (Table 2). The mean yield per plant was 18.54g with a range of 8.37-49.81 g in the genotype MTD-16and F-85-11347, respectively. The phenotypic variance (108.15) appeared to be higher than the genotypic variance (103.04) 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 54.75 and 56.09 respectively which indicated presence of considerable variability among the genotypes. The heritability (95.28%) estimates for this trait was high, genetic advance (20.41) low and genetic advance in per cent of mean (110.09) was found very high, revealed that this trait was governed by additive gene. Malhotra (1973) observed that 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). Phenotypic variation of pod showed in Plate 9, 10, 11, and Plate 12.



Plate 9. Phenotypic variation in pods from G1 to G 8 genotypes

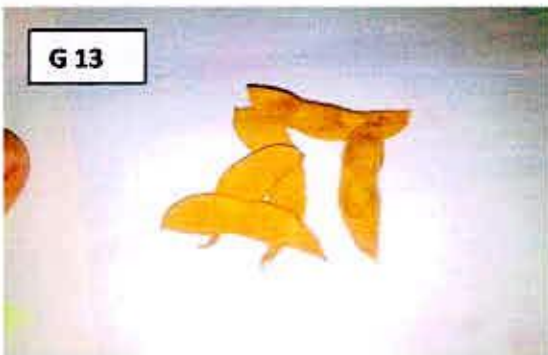
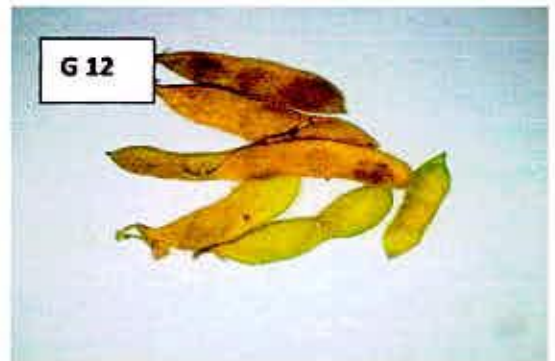


Plate 10. Phenotypic variation in pods from G9 to G16 genotypes



Plate 11. Phenotypic variation in pods from G 18 to G-24 genotypes



Plate 12. Phenotypic variation in pods from G 25 to G 27 genotypes

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 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 Plant height (cm)

Plant height had significant and positive correlation with day to first flowering (0.418 and 0.400), day to 50% flowering (0.410 and 0.395), number of branches per plant (0.554 and 0.482) and number of pod per plant (0.672 and 0.627) at both the genotypic and phenotypic levels (Table 4). A negative correlation of Days to 80% maturity (-0.083 and -0.086) showed at both the levels.

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

Character	DFE	D50F	D80M	NBP	NPP	NSP	PL	HSW	SY	SPWP	YIELD
PH	0.40*	0.39*	-0.09	0.48*	0.63**	0.05	0.03	-0.15	0.32	0.19	0.36
DFF		0.98**	0.06	0.34	0.41*	0.12	0.21	-0.08	0.34	0.28	0.43*
D50F			0.06	0.28	0.44*	0.15	0.19	-0.09	0.31	0.31	0.42*
D80M				-0.07	0.16	0.25	0.18	0.49**	0.20	0.33	0.21
NBP					0.50**	0.15	0.11	-0.18	0.29	0.11	0.65**
NPP						0.25	0.09	-0.03	0.66**	0.52**	0.57**
NSP							0.56**	0.11	0.19	0.35	0.23
PL								0.38*	0.38	0.41*	0.30
HSW									0.00	0.48*	-0.04
SY										0.52**	0.63**
SPWP											0.43*

** Significant at 1%

* Significant at 5%

DFF= Days to first flowering, PH= Plant height (cm), D50F= Days to 50% flowering, D80M= Days to 80% maturity, NBP= Number of branches per plant, NPP= Number of pod per plant, NSP=Number of seeds per pod, PL= Pod length, HSW= Hundred seed weight (g), SY= Stover yield, SPWP= Single pod weight per plant, YIELD=Yield per plant

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

Character		DFE	D50F	D80M	NBP	NPP	NSP	PL	HSW	SY	SPWP	YIELD
PH	G	0.418*	0.410*	-0.083	0.554*	0.672**	0.087	0.060	-0.153	0.331	0.201	0.388
	P	0.400*	0.395*	-0.086	0.482*	0.627**	0.049	0.029	-0.150	0.315	0.194	0.359
DFE	G		0.988**	0.071	0.350	0.425*	0.155	0.224	-0.086	0.348	0.296	0.436*
	P		0.978**	0.055	0.341	0.406*	0.124	0.211	-0.084	0.340	0.282	0.430*
D50F	G			0.068	0.291	0.465*	0.166	0.201	-0.084	0.312	0.320	0.433*
	P			0.063	0.277	0.441*	0.147	0.192	-0.086	0.307	0.307	0.424*
D80M	G				-0.075	0.162	0.286	0.190	0.496**	0.200	0.337	0.211
	P				-0.070	0.155	0.247	0.181	0.493**	0.197	0.325	0.210
NBP	G					0.546**	0.179	0.107	-0.189	0.311	0.130	0.683**
	P					0.501**	0.153	0.105	-0.176	0.291	0.112	0.648**
NPP	G						0.356	0.137	-0.033	0.701**	0.544**	0.614**
	P						0.246	0.093	-0.034	0.663**	0.518**	0.575**
NSP	G							0.658**	0.110	0.218	0.428	0.258
	P							0.564**	0.106	0.185	0.349	0.228
PL	G								0.413*	0.404	0.452*	0.306
	P								0.384*	0.376	0.412*	0.299
HSW	G									0.003	0.494*	-0.035
	P									0.004	0.484*	-0.036
SY	G										0.527**	0.641**
	P										0.519**	0.630**
SPWP	G											0.454*
	P											0.431*

** Significant at 1% * Significant at 5%

DFE= Days To first flowering, PH= Plant height (cm), D50F= Days to 50% flowering, D80M= Days to 80% maturity, NBP= Number of branches per plant, NPP= Number of pod per plant, NSP=Number of seeds per pod, PL= Pod length, HSW= Hundred seed weight (g), SY= Stover yield, SPWP= Single pod weight per plant, YIELD=Yield per plant,

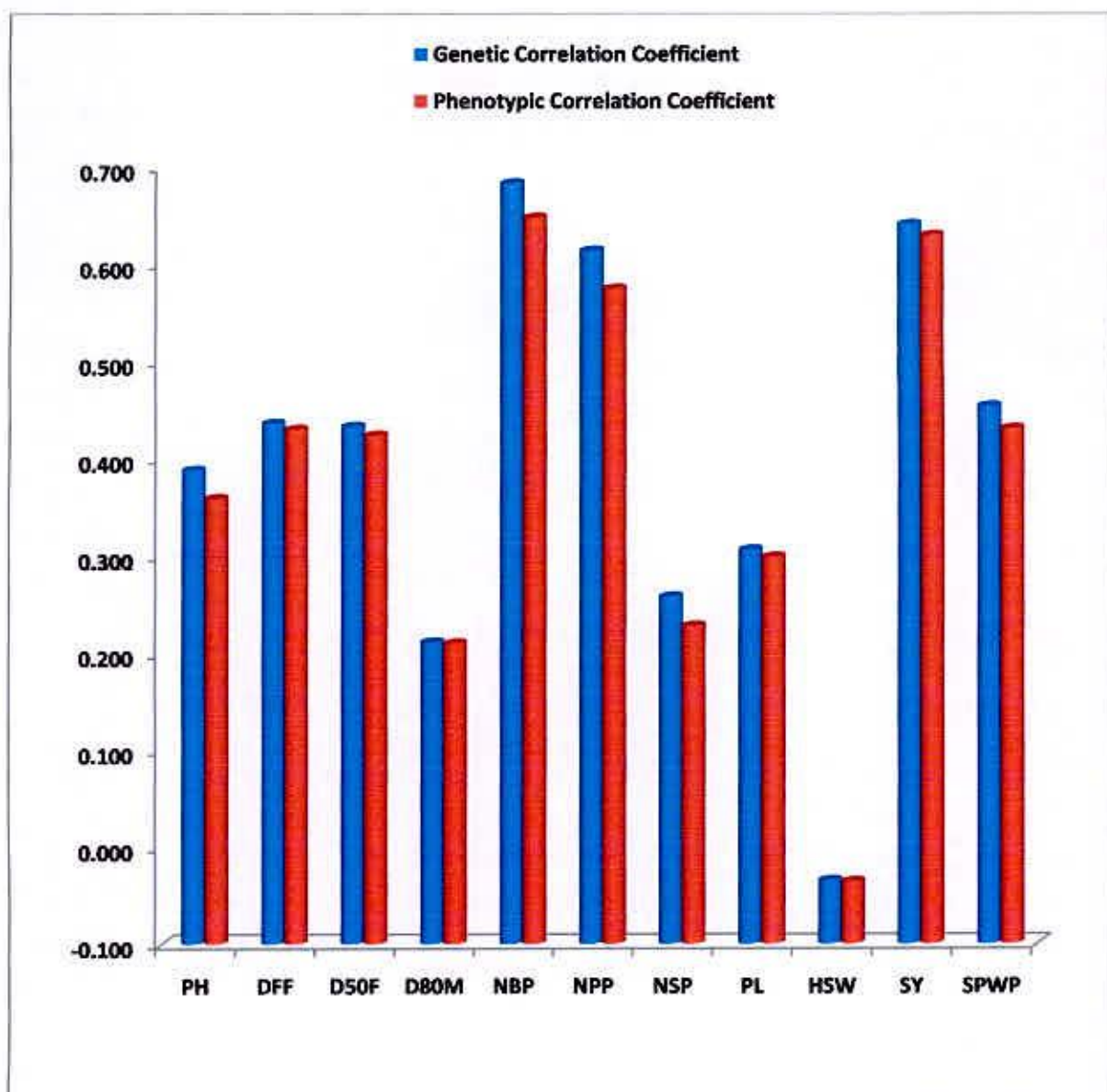


Fig. 3. Genotypic and phenotypic correlation coefficient for different characters with yield

4.3.2 Days to first flowering

Days to first flowering showed significant and positive correlation with days to 50% flowering, (0.988 and 0.978) and number of pod per plant (0.425 and 0.406) and yield per plant (0.436 and 0.430) both at genotypic and phenotypic levels (Table 4).

4.3.3 Days to 50% flowering

The correlation of days to 50% flowering with number of pod per plant (0.465 and 0.905), yield per plant (0.433 and 0.424) was positive and significant at both the genotypic and phenotypic levels (Table 4). Inderjit *et al.* (2007) reported that days to 50% flowering were significantly correlated with grain yield.

4.3.4. Days to 80% maturity

Days to 80% maturity had a highly significant positive association with hundred seed weight (0.496 and 0.493) at both the genotypic and phenotypic levels (Table 4). Chand (1999) observed that maturity of soybean was positively correlated with seed yield.

4.3.5 Number of branches per plant

The number of branches per plant had positive and highly significant correlation with pods per plant (0.546 and 0.501) and yield per plant (0.683 and 0.648) 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 Number of pod per plant

Number of pods per plant had highly significant and positive association with stover yield (0.701 and 0.663), single pod weight per plant (0.544 and 0.518) and yield per plant (0.614 and 0.575) (Table 4). Saurabh *et al.* (1998) observed that significant and positive correlations between plant height and pods per plant

4.3.7 Number of seeds per pod

Number of seeds per pod showed a highly positive association with pod length (4.3.6 and 0.564) at both the genotypic and phenotypic levels (Table 4). This character also showed positive correlation with yield. Inderjit *et al.* (2007) reported that seeds per pod significantly correlated with seed yield.

4.3.8 Pod length (cm)

Pod length had significant and positive association with number of hundred seed weight (0.413 and 0.384), single pod weight per plant (0.452 and 0.412) at both the genotypic and phenotypic levels (Table 4). But a non significant positive correlation with yield. Sridhara *et al.* (1998) reported that pod length significant contributors of seed yield.

4.3.9 Hundred seed weight (g)

Hundred seed weight had significantly positive association with single pod weight per plant (0.494 and 0.484) at both the genotypic and phenotypic levels (Table 4). Hundred seed weight showed non-significant negative correlation with yield. Avc and Ceyhan, (2006) find that hundred seed weight significantly correlated with pod yield.

4.3.10 Stover yield (g)

Stover yield had highly significant positive association with single pod weight per plant (0.527 and 0.519) and yield (0.641 and 0.630) at both the genotypic and phenotypic levels (Table 4). Stover yield correlated with seed yield which was early findings by Chand (1999).

4.3.11 Single pod weight per plant (g)

A highly significant and positive association of single pod weight plant at both the genotypic and phenotypic levels was observed with yield per plant (0.454 and 0.431).

4.3.12 Yield per plant (g)

A highly significant and positive association of yield per plant at both the genotypic and phenotypic levels was observed with days to first flowering (0.436 and 0.430), days to

50% flowering (0.433 and 0.424), number of branches per plant (0.683 and 0.648) pods per plant (0.614 and 0.575), Stover yield (0.641 and 0.630) 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, 100-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 Dewey 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 yield of plant and its indirect effect through other characters were computed and the results are presented in Table 5.

4.4.1 Plant height (cm)

Plant height had negative direct effect (-0.024) on yield per plant. Days to first flowering influenced the yield per plant indirectly through day to 50% flowering days to 80% maturity and number of branch per plant, pod length, stover yield and single pod weight per plant (0.528, 0.380, 0.319, 0.085, 0.178 and 0.022, respectively (Table 5). It had a negative indirect effect through day to first flowering -0.489, pods per plant (-0.169) number of seed per pod (-0.001) and hundred seed weight (-0.005).

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
		PH	DFE	D50F	D80M	NBP	NPP	NSP	PL	HSW	SY	SPWP	
PH	-0.024	-0.024	-0.489	0.528	0.380	0.319	-0.169	-0.001	0.085	-0.005	0.178	0.022	0.36
DFE	-0.122	-0.009	-0.122	0.132	-0.011	0.226	-0.110	-0.001	0.057	-0.002	0.189	0.033	0.43*
D50F	0.135	-0.009	-1.197	0.135	0.011	0.186	-0.118	-0.001	0.051	-0.003	0.172	0.037	0.42*
D80M	0.186	-0.001	0.076	0.083	0.186	-0.048	-0.049	-0.011	0.049	-0.029	0.010	0.049	0.21
NBP	0.665	-0.011	-0.415	0.379	-0.013	0.665	-0.134	-0.001	0.029	-0.006	0.161	0.013	0.65**
NPP	-0.268	-0.015	-0.501	0.595	0.029	0.332	-0.268	-0.002	0.024	-0.001	0.367	0.006	0.57**
NSP	-0.009	-0.001	-0.146	0.203	-0.046	0.099	-0.067	-0.009	0.152	0.003	0.105	0.042	0.23
PL	0.270	0.006	-0.010	0.018	0.049	0.062	0.005	-0.106	0.270	-0.110	0.004	0.127	0.3
HSW	0.035	0.003	0.097	-0.121	0.091	-0.119	0.008	-0.001	0.103	0.035	0.000	0.057	-0.04
SY	0.557	-0.007	-0.415	0.419	0.037	0.193	-0.177	-0.001	0.073	0.000	0.557	0.062	0.63**
SPWP	0.120	-0.004	-0.342	0.419	0.061	0.073	-0.139	-0.003	0.111	0.017	0.289	0.120	0.43*

Residual effect= 0.287

** Significant at 1%

* Significant at 5%

DFE= Days to first flowering, PH= Plant height (cm), D50F= Days to 50% flowering, D80M= Days to 80% maturity, NBP= Number of branches per plant, NPP= Number of pod per plant, NSP=Number of seeds per pod, PL= Pod length, HSW= Hundred seed weight (g), SY= Stover yield, SPWP= Single pod weight per plant, YIELD=Yield per plant

4.4.2. Days to first flowering

Days to first flowering had negative direct effect (-0.122) on yield per plant. This character influenced the yield per plant indirectly through day to 50 % flowering, number of branch per plant, pod length, stover yield and single pod weight per plant 0.132, 0.226, 0.057, 0.057 and 0.033 respectively (Table 5). It had a negative indirect effect through day to days to 80% maturity (-0.011), pods per plant (-0.110) number of seed per pod (-0.001) and hundred seed weight (-0.002).

4.4.3 Days to 50% flowering

Days to 50% flowering had positive direct effect (0.135) on yield per plant. Days to 50% flowering showed positive indirect effect with days to 80% maturity (0.011), branches per plant (0.186), pod length (0.051) and stover yield (0.172) single pod weight per plant (0.037) (Table 5). It had a negative indirect effect through plant height (-0.009), days to first flowering (-1.197) and pod per plant (-0.118) number of seed per pod (-0.001) and hundred seed weight (-0.003).

4.4.4 Days to 80% maturity

Path analysis revealed that days to 80% maturity had positive direct effect (0.186) on yield per plant. Days to 80% maturity showed indirectly positive influenced for days to first flowering (0.076), days to 50% flowering (0.083) and pod length (0.049), stover yield (0.010) single pod weight per plant (0.049). It influenced the seed yield per plant in negative direction through plant height (-0.001) and branches per plant (-0.048) pod per plant (-0.049) number of seed per pod (-0.011) hundred seed weight (-0.029) (Table 5). Days to maturity showed positive direct effect on grain yield which is similar to the earlier findings by Inderjit *et al.* (2007).

4.4.5 Number of branches per plant

Branches per plant had the direct positive effect on yield per plant (0.665) whereas It had negative indirect effect through), plant height (-0.011), days to first flowering (-0.415), Days to 80% maturity (-0.013), pods per plant (-0.134), seeds per pod (-0.001), hundred seed weight (-0.006) (Table5). However, its indirect effects through days to 50%

flowering (0.379), pod length (0.029) and stover yield (0.161) single pod weight per plant (0.013) leading to positive association.

4.4.6 Number of pods per plant

Pods per plant had the negative direct effect on yield per plant (-0.268). It showed positive indirect effect through days to 50% flowering (0.595), days to 80% maturity (0.029) branches per plant (0.332), pod length (0.024), stover yield (0.105) single pod weight per plant (0.042). This trait showed the negative indirect effect with plant height (-0.015), days to first flowering (-0.501) and seeds per pod (-0.002) hundred seed weight (-0.001) (Table 5).

4.4.7 Number of seeds per pod

Number of seeds per pod had the negative direct effect on yield per plant (-0.009) and it had positive and indirect influence on seed yield per plant through pod length (0.152), hundred seed weight (0.003) stover yield (0.105) single pod weight per plant (0.042) (Table 5).

4.4.8 Pod length (cm):

Path analysis revealed that pod length had positive direct effect (0.270) on yield per plant whereas, it showed indirect positive effects on seed yield per plant by plant height (0.006) days to 50% flowering (0.018), days to 80% maturity (0.049) branches per plant (0.062) pods per plant (0.005) stover yield (0.004) single pod weight per plant (0.127) (Table 5). It showed indirect negative effect on seed yield per plant through days to first flowering (-0.010) seeds per pod (-0.106) hundred seed weight (-0.110). Harpreet *et al.* (2007) observed that pod length can serve as reliable variable for selection.

4.4.9 Hundred seed weight (g)

Hundred seed weight had positive direct effect on yield (0.035) and it showed indirect positive effects through plant height (0.003), days to first flowering (0.097), days to 80% maturity (0.091), pod per plant (0.008), pod length (0.103), single pod weight per plant (0.057) (Table 5). Hundred seed weight had positive direct effect on grain yield which is similar to the earlier findings by Inderjit *et al.* (2007).

4.4.10 Stover yield (g)

Stover yield had positive direct effect on yield (0.557) and it showed indirect positive effects through days to 50% flowering (0.419), days to 80% maturity (0.037), branch per plant (0.193), pod length (0.073), single pod weight per plant (0.062) (Table 5).

4.4.11 Single pod weight per plant

Single pod weight per plant had positive direct effect on yield (0.120) and it showed indirect positive effects through days to 50% flowering (0.419), days to 80% maturity (0.061), branch per plant (0.073), pod length (0.111), hundred seed weight (0.017) stover yield (0.289) (Table 5). 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 branches per plant and stover yield.

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 36.45% of the total variation among the genotypes, while 6 of these with eigen values above unity accounted for 91.92% 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 (Z1-Z2) 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



Table 6. Eigen values and yield percent contribution of 12 characters of 27 germplasm

Characters	Eigen values	Percent variation	Cumulative % of percent variation
Plant height	4.37	36.45	36.45
Days to first flowering	2.24	18.69	55.14
Days to 50% flowering	1.22	10.2	65.34
Days to 80% maturity	1.07	8.92	74.26
Number of branches per plant	0.75	6.22	80.48
Number of pod per plant	0.72	5.98	86.46
Number of seeds per pod	0.66	5.46	91.92
Pod length	0.45	3.73	95.65
100 seed weight	0.24	2.03	97.68
Stover yield	0.15	1.27	98.95
Single pod weight per plant	0.11	0.96	99.91
Yield per plant	0.01	0.09	100

were apparently distributed into five groups, which indicated that considerable diversity existed among the genotypes.

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 (15.10) between the cluster I and cluster IV, followed by I and V (12.89) and IV and V (12.24). 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 I and IV indicated the genotypes in these clusters were diverse than other clusters. Cluster I was the most diverse as many other clusters showed maximum inter cluster distance with it. The minimum distance observed between clusters II and V (2.93) indicated close relationship among the genotypes.

The intra cluster D^2 values are given in Table 7. The intra cluster distance was measured in the clusters I, II, III and IV. The intra cluster distance was higher in cluster II (1.64) followed by cluster I (1.55) and lowest in cluster IV (1.41). 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 as (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 8 and 10 (Table 9). The lowest distance was observed between the genotype 6 and genotype 3. The difference between the highest and the lowest inter genotypic distance indicated the prevalence of variability among the 27 genotypes of soybean studied.

Table 7. Intra (bold) and inter cluster distances (D^2) for 27 genotypes of soybean

Cluster	I	II	III	IV	V
I	1.55	10.07	5.32	15.10	12.89
II		1.64	6.34	11.07	2.93
III			1.40	10.01	9.24
IV				1.41	12.24
V					0.00

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

Sl	Cluster	Nearest cluster with D^2 values	Farthest cluster with D^2 values
1	I	III (5.32)	IV (15.10)
2	II	V (2.93)	IV (11.07)
3	III	I (5.32)	IV (10.01)
4	IV	III (10.01)	I (15.10)
5	V	II (2.93)	I (12.89)

Table 9. Ten highest and ten lowest inter genotypic distance among 27 genotypes of soybean

Highest distance				Lowest distance			
Sl No.	Genotype		Distance	Sl No.	Genotype		Distance
1	G8	G10	10.51	1	G3	G6	1.74
2	G10	G8	10.51	2	G6	G3	1.74
3	G4	G8	10.17	3	G21	G23	1.81
4	G24	G8	9.47	4	G23	G21	1.81
5	G17	G8	9.06	5	G27	G23	1.93
6	G16	G8	9.01	6	G5	G18	2.13
7	G11	G8	8.83	7	G22	G21	2.14
8	G12	G8	8.76	8	G9	G22	2.19
9	G19	G8	8.69	9	G18	G5	2.23
10	G24	G18	8.59	10	G13	G9	2.26

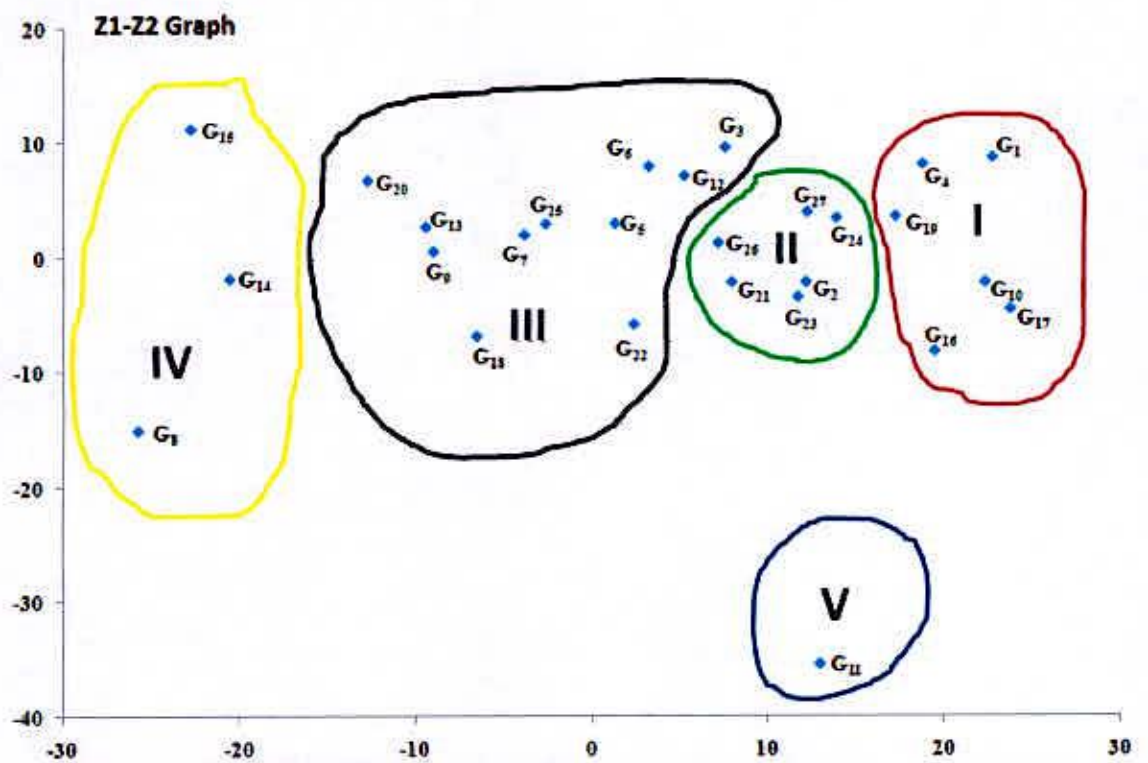


Fig. 4. Scatter diagram of 27 genotypes of soybean based on their principle component scores super imposed with clustering

4.5.4 Nonhierarchical clustering

With the application of co variance matrix for non-hierarchical clustering, 27 soybean genotypes were grouped into five different clusters. From Table 10, cluster III had the maximum 11 genotypes (KANH-33, MTD-452, GMOT-17, JOYAWAZA, YESOY-4, GC-82-332411, PK-327, NS-1, GC-830059, MTD-16, ASSET-95) followed by cluster I (LG-92P-1176, AGS-79, SHOHAG, AGS-95, BARI SOYBEAN-6, MTD-451), cluster II (P1-4174-75, 86017-66-6, LG-92P-12-18, BS-33, BS-13, CHINA-1) and cluster IV (F-85-11347, ASSET-93-19-13, PK-327). Cluster V comprised with one genotype 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 27 genotypes of soybean is presented in Fig. 4.

Table 10. Distribution of genotypes of soybean in different clusters

Cluster no.	No. of Genotypes	Number of populations	Name of genotypes
I	G1, G4, G10, G16, G17, G19	6	LG-92P-1176, AGS-79, SHOHAG, AGS-79, BARI SOYBEAN-6, MTD-451
II	G2, G21, G23, G24, G26, G27	6	P1-4174-75, 86017-66-6, LG-92P-12-18, BS-33, BS-13, CHINA-1
III	G3, G5, G6, G7, G9, G12, G13, G18, G20, G22, G25	11	KANH-33, MTD-452, GMOT-17, JOYAWAZA, YESOY-4, GC-82-332411, PK-327, NS-1, GC-830059, MTD-16, ASSET-95
IV	G8, G14, G15	3	F-85-11347, ASSET-93-19-13, PK-327,
V	G11	1	AUSTRALIA

Table 11. Cluster mean values of 12 different characters of 27 genotypes of soybean

Characters	I	II	III	IV	V
Plant height (cm)	48.78	54.36	57.38	69.9	34.57
Days to first flowering	81.44	81.34	82.03	86.67	77.67
Days to 50% flowering	84.16	84	84.45	90	81
Days to 80% maturity	124.28	128.67	123.88	133.44	157
Number of branches per plant	5.35	5.61	6.42	9.05	4.47
Number of pod per plant	38.7	43.1	48.28	92.2	38.27
Number of seeds per pod	2.54	3	2.96	3	3.33
Pod length (cm)	3.19	3.99	3.62	3.79	3.95
100 seed weight (g)	8.13	13.02	7.14	8.93	12.37
stover yield (g)	4.74	6.75	8.31	14.36	8.21
Single pod weight per plant (g)	2.96	5.49	3.78	6.99	4.72
Yield per plant (g)	12	14.21	19.4	35.73	22.59

4.5.5 Cluster mean analysis

The cluster means of 12 different characters (Table 11) were compared and indicated considerable differences between clusters for all the characters studied. Maximum plant height were observed in cluster IV (69.9), whereas minimum plant height in cluster V (34.57). Then maximum days to first flowering were observed in IV (86.67) whereas minimum days to first flowering were observed in cluster V (77.67). Maximum (90) and minimum (81) days to 50 per cent flowering were observed in cluster IV and V, respectively. Cluster V, composed of genotypes showing highest days of 80% maturity (157) in cluster lowest in the cluster III (123.88). Maximum (9.05) and minimum (4.47) number of branches were observed in cluster IV and V, respectively. Maximum number of pods per plant was observed in cluster IV (92.2), whereas minimum number of pods per plant was observed in cluster V (38.27). Maximum (3.33) and minimum (2.54) seed per pod were observed in cluster V and I, respectively. The maximum pod length (3.99) was observed in the cluster II, whereas minimum pod length (3.19) was observed in cluster I. Hundred seed weight was the highest in cluster II with a mean value of (13.02) and it was least in genotypes belongs to the cluster III (7.14). The maximum number of stover yield was observed in cluster IV (14.36), whereas minimum number of seeds per pod was observed in cluster I (4.74). Highest single pod weight per plant was recorded by the genotype making up cluster IV (6.99) while cluster V showed the least single pod weight I (2.96) per plant. The maximum yield per plant (35.73g) was observed in the cluster IV; whereas minimum (12 g) was in the cluster I. Cluster V mainly an early flowering genotype where as it produce the lowest mean values for first flowering. Cluster IV has late flowering and late days of maturity. Again cluster I has the early days of maturity, lowest single pod weight, minimum yield, and minimum pod length, seeds per pod. The genotypes belonging to the cluster IV were maximum of yield per plant , single pod weight per plant, stover yield, pod per plant, branches 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 I and where the genotypes belonging to II and V were the least diverse. Genotypes of cluster I-V and V-IV were moderately diverse from each other. The similar diverse genotypes were included between the cluster III-IV and III-V.

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 2 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 (Z1) obtained from PCA, the important characters responsible for genetic divergence in the axis of differentiation were days to first flowering (2.195), number of pod per plant (0.0708), pod length (0.499), and yield (0.112). In vector 2 (Z2), the second axis of differentiation plant height (0.0054), days to first flowering (0.7711), days to 80% maturity (0.0178), number of pod per plant (0.137), pod length (0.9861), single pod weight per plant (0.2357) and yield (0.047) were important because all these characters had positive signs.

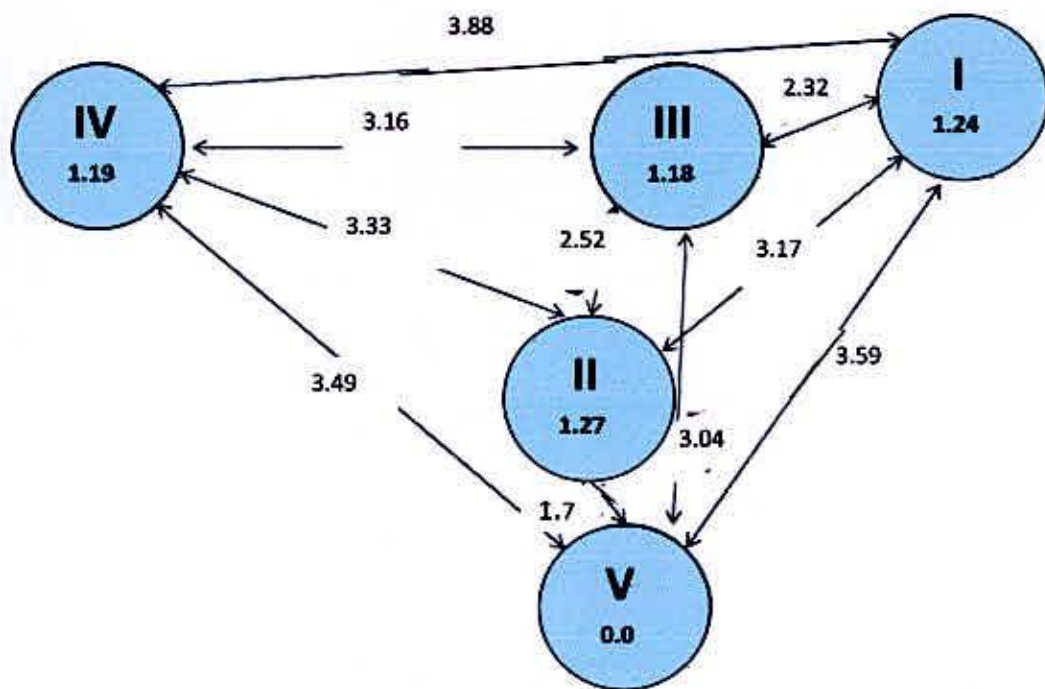


Fig.5. Intra and inter cluster distances (D^2) of 27 genotypes in soybean

Table 12. Relative contributions of the 12 characters of 27 varieties to the total divergence

Characters	Vector -1	Vector- 2
Plant height (cm)	-0.1883	0.0054
Days to first flowering	2.195	0.7711
Days to 50% flowering	-2.0313	-0.6766
Days to 80% maturity	-0.1178	0.0178
Number branches per plant	-1.1267	-0.1455
Number of pod per plant	0.0708	0.137
Number of seed per pod	-6.7284	-5.0663
Pod length (cm)	0.499	0.9861
Hundred seed weight (g)	-0.4394	-0.8838
Stover yield (g)	-0.5726	-0.2168
Single pod weight per plant (g)	-0.6258	0.2357
Yield per plant (g)	0.112	0.047

On the other hand, plant height, days to 50% flowering, days to 80% maturity, number branches per plant, number of seed per pod, hundred seed weight, stover yield, and single pod weight per plant possessed the negative sign in the first axis of differentiation and days to 50% flowering, number branches per plant, number of seed per pod, stover yield, hundred 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, yield, pod length, number of pod per plant, were positive in both the axis, which indicated that they were the important component characters having higher contribution to genetic divergence among the materials studied.

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 G24 (BS-33) for minimum days to first flowering from cluster II; G2 (P1-4174-75) for maximum pod length from cluster II; G11 (AUSTRALIA) for maximum number of seeds per pod from cluster V, G13 (PK-327) for maximum plant height from cluster III were found promising. Therefore considering group distance and other agronomic performance G-8 (F-85-11347), G-10 (SHOHAG), G24 (BS-33), G2 (P1-4174-75), G11 (AUSTRALIA) and G13 (PK-327) might suggested for future hybridization program.



**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, assess 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 27 genotypes of soybean (*Glycine max* (L). Merrill), at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, during December, 2013 to April, 2014. 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 BS-33 was the earliest to first flower of 74 days while F-85-11347 was late to first flower for 90.33 days. The minimum and maximum duration for 50% flowering were required by the genotypes BS-33 (76.33 days) and F-85-11347 (93.67 days), respectively. The maximum plant height (75.85 cm) was recorded by the genotype 'PK-327' and the lowest plant height (34.57cm) was recorded by 'AUSTRALIA'. Maximum number of branches recorded in 'ASSET-93-19-13' and 'AGS-79' genotype showed the minimum number of branches. The minimum pod length was recorded by the accession 'SHOHAG' and accession 4.95 showed the maximum pod length. The line GMOT-17 showed the minimum hundred seed weight and the maximum hundred seed weight was recorded in the accession LG-92P-12-18. The minimum number of pods per plant was observed in accession SHOHAG while maximum number of Pods per plant was found in the genotype F-85-11347. The genotype AUSTRALIA had highest number of seeds per pod while it was lowest in the genotype SHOHAG. The genotypes AUSTRALIA, BS-13, 86017-66-6, YESOY-4, AGS-95 had the highest days to maturity and lowest in the genotype LG-92P-1176. A range of 8.37-49.81 g yield in the genotype MTD-16 and F-85-11347, 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 plant height, days to first flowering, days to 50% flowering, days to 80% maturity, number of braches per plant, number of pod per plant, pod length, hundred seed weight, stover yield, single pod weight per plant and yield. suggested that effective selection may be done for these characters. High genetic advance found in case of hundred seed weight, stover yield, single pod weight per plant and yield per plant. Low heritability coupled with low genetic advance in percent of mean was observed number of seeds per pod.

Days to 50% flowering, days to 80% maturity, number of braches per plant, number of pod per plant and stover yield, single pod weight per plant showed significant and positive correlation with seed yield per plant at both genotypic and phenotypic levels. Days to 80% maturity was significantly and positively correlated with hundred seed weight at both levels. Branches per plant were positively and significantly correlated with pod per plant and yield at both levels. Pods per plant correlated with Stover yield, single pod weight per plant at both levels. Pod length was positively and significantly correlated with single pod weight per plant and hundred seed weight at both levels. Days to 80% maturity showed the highest positive direct effect (0.186) with seed yield per plant.

Days to 50% flowering, days to 80% maturity, braches per plant, pod length and hundred seed weight, stover yield, single pod weight per plant also showed positive direct effect on seed yield. The highest indirect effect of stover yield observed with 50% flowering. Brach 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 seven soybean genotypes based on twelve characters was measured through multivariate analysis. The 27 genotypes fell into five distant clusters. The cluster III comprised the maximum number (11) of genotypes. The cluster I, II, IV

and V comprised 6, 6, 3 and 1 genotypes, respectively. The highest inter-cluster distance (15.10) was observed between the cluster II and IV and the highest distant genotypes were G2 (P1-4174-75) and G8(F-85-11347). The lowest inter-cluster distance (2.93) was observed between the cluster II and V. 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 days to first flowering, pod length 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:

- Wide range of genetic diversity existed among the soybean genotypes. Wide genetic diversity was observed in 27 genotypes of soybean, which were grouped into five clusters and most diverse genotypes were G2 and G8. That variability could be used for future breeding program of soybean in Bangladesh.
- High heritability coupled with high genetic advance in percent of mean was observed in plant height, hundred seed weight, stover yield single pod weight per plant, branches per plant, single pod weight per plant and yield per plant. Hence, yield improvement in soybean would be achieved through selection of these characters.
- Days to first flowering, days to 50% flowering, number of branches per plant, number of pod per plant, stover yield and single pod weight per plant showed significant and positive correlation at both genotypic and phenotypic levels. This result suggested that seed yield per plant can be increased by improving these characters.

- Days to 50% flowering, days to 80% maturity, number of branches per plant, pod length, plant height, days to maturity, stover yield and hundred seed weight showed positive direct effect on yield. So yield improvement was associated with these characters.
- The genotypes of clusters I was more diverse from the genotypes of cluster IV.
- Days to first flowering, pods per plant, and 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.
- Further collection of soybean germplasms would be continued for getting more variability and desired traits in soybean.

RECOMMENDATION

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

- Genotypes G24 (BS-33) G2 (P1-4174-75) G11 (AUSTRALIA), G13 (PK-327) could be included in the furthest study in view of seed yield for releasing as soybean varieties.
- The maximum variability was found for pod length, seeds per pod and hundred seed weight. So selection based on these characters could be effective for the improvement of soybean yield.
- The genotypes of cluster I and IV could be used as parents for future breeding program to developed soybean variety.



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CHAPTER- VI

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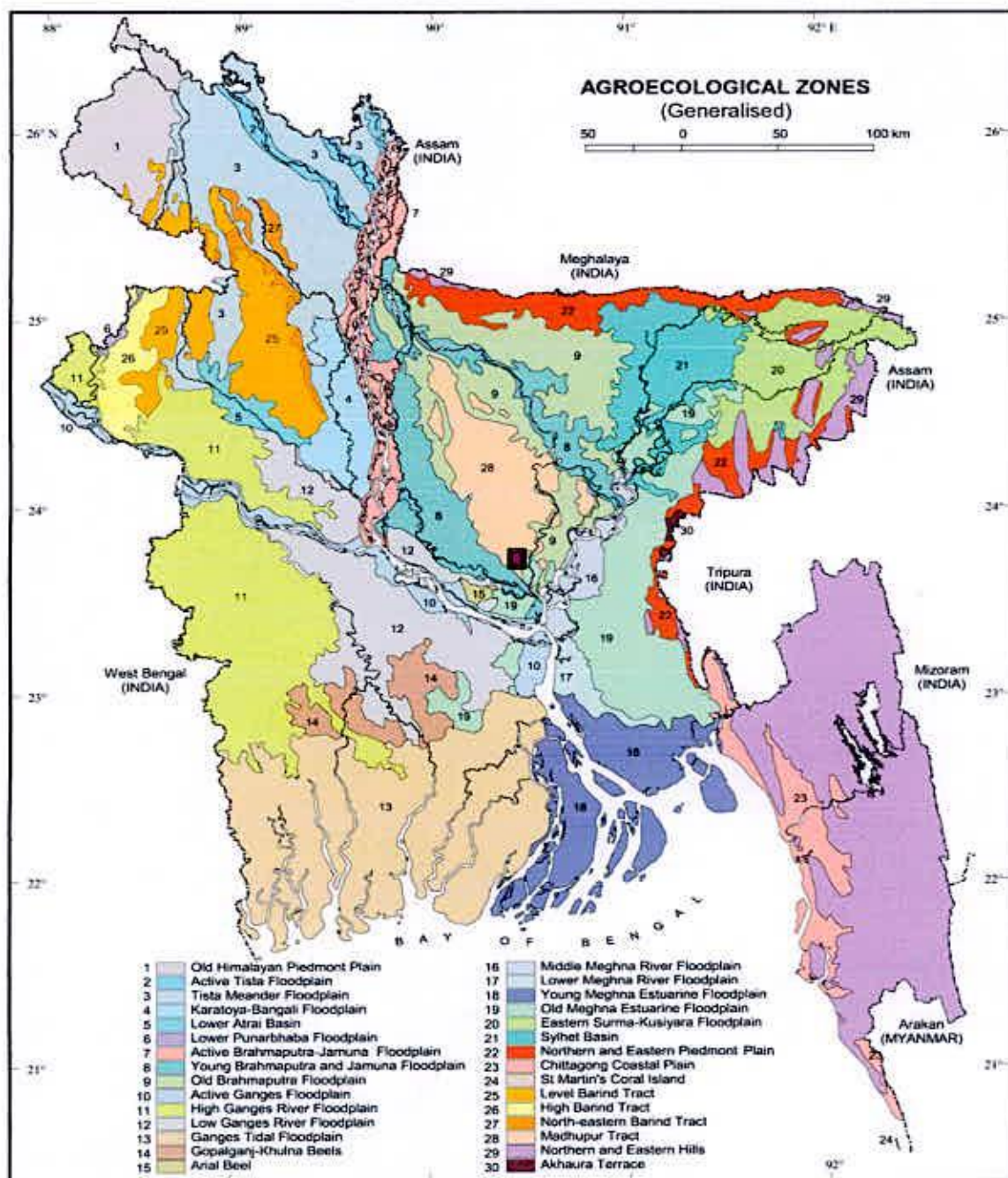
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APPENDICES

Appendix I. Map showing the experimental site under the study



 The experimental site under study

Appendix II. Monthly average temperature, relative humidity, total rainfall and sunshine of the experimental site during the period of December, 2013 to April, 2014

Month	Air temperature (°C)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (h)
	Maximum	Minimum			
November, 2012	34.8	18.0	77	227	5.8
December, 2012	32.3	16.3	69	0	7.9
January, 2013	29.0	13.0	79	0	3.9
February, 2013	28.1	11.1	72	1	5.7
March, 2013	33.9	12.2	55	1	8.7
April, 2013	34.6	16.5	67	45	7.3

Source: Bangladesh Meteorological Department (Climate and 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
p ^H	6.00 – 6.63
Organic matter	0.84
Total N (%)	0.46
Available phosphorous	21 ppm
Exchangeable K	0.41 meq / 100 g soil

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

Appendix IV. Mean performance of various growth parameter and yield components

Genotype	PH	DFP	D50F	D80F	NBP	NPP	NSP	PL	HSW	SY	SPWP	YIEL
LG-92P-1176	50.4	85	87.33	116.33	5	48.67	2.33	3.35	11	8.07	4.37	12.35
P1-4174-75	54.11	82.67	85.33	127.33	4.07	30.47	3	4.95	11.67	12.6	4.87	15.13
KANH-33	64.11	84	87	120.67	4.87	39.27	3	3.57	5.2	6.73	4.81	15.15
AGS-79	47.25	77.33	81.33	118.33	3.47	48.53	2.8	3.03	7.1	3.99	1.98	9.22
MTD-452	50.07	81.33	84.33	120.33	5.73	50	3.07	4.22	8.23	8.23	4.9	19.67
GMOT-17	55.31	81.33	83.67	119	5.43	37.4	3	3.65	5.13	5.78	3.61	13.57
JOYAWAZA	60.48	82.33	86.33	117.33	7.83	44.73	2.8	3.11	6.47	5.85	3.47	38.48
F-85-11347	59.65	90.33	93.67	137	8.27	95	3	4.19	10.1	19.83	9.74	49.81
YESOY-4	60.69	82.67	84.33	131.67	5.67	58.33	3	3.09	8.23	10.19	4.51	16.07
SHOHAG	54.05	77.67	80.33	131	5.6	28.33	2	2.82	8.37	4.2	2.97	10.67
AUSTRALIA	34.57	77.67	81	157	4.47	38.27	3.33	3.95	12.37	8.21	4.72	22.59
GC-82-332411	58.97	81.33	82.67	120.33	10.53	43.2	3	3.53	6.13	6.1	1.47	18.28
PK-327	66.42	82	84.33	131.33	5.4	55.87	3	3.95	8.13	7.27	3.16	19.79
ASSET-93-19-13	74.21	85	87	131.33	11.57	88.93	3	3.75	8.63	14.97	6.47	43.36
PK-327	75.85	84.67	89.33	132	7.3	92.67	3	3.43	8.07	8.29	4.75	14.01
AGS-95	52.35	79	80.67	130.67	6.7	40.93	2.47	3.47	10.13	4.93	2.45	17.34
BARI SOYBEAN-6	46.22	84	86.33	130.33	4.33	28.4	2.63	3.01	6.87	4.33	3.23	10.34
NS-1	52.3	83.67	85.67	128	7.67	38.67	3	4.23	9.03	7.53	3	28.3
MTD-451	42.43	85.67	89	119	7	37.33	3	3.47	5.3	2.9	2.77	12.07
GC-830059	55.53	81.33	83.33	119.67	8	63.33	3	3.83	5.5	12.07	3.77	21.13
86017-66-6	54.41	77.67	80.67	131.67	4.67	53.67	3	3.57	13.13	6.33	5.85	14.08
MTD-16	52.47	81	83.67	129	4.8	46.64	3	3.43	8.83	6.37	6.17	8.37
LG-92P-12-18	55.59	81	83	131.33	6.2	37.73	3	3.7	14.7	4.83	5.71	14.57
BS-33	43.97	74	76.33	119.67	6.13	43.13	3	3.78	12.1	6.87	6.35	10.51
ASSET-95	54.8	81.33	83.67	125.33	4.67	53.67	2.67	3.23	7.63	15.33	2.68	14.63
BS-13	55.45	89.67	92.33	135.67	6.47	46.33	3	3.79	13.4	4.71	4.65	14.79
CHINA-1	62.61	83	86.33	126.33	6.13	47.27	3	4.17	13.13	5.13	5.5	16.21
Mean	55.34	82.1	84.78	127.32	6.22	49.51	2.89	3.64	9.06	7.84	4.37	18.54
Min.	34.57	74	76.33	116.33	3.47	28.33	2	2.82	5.13	2.9	1.47	8.37
Max.	75.85	90.33	93.67	157	11.57	95	3.33	4.95	14.7	19.83	9.74	49.81

Appendix V. Z1-Z2 score of 27 genotypes of soybean

Genotypes	PCA 1	PCA 2
LG-92P-1176	22.85	8.81
P1-4174-75	12.22	-2.09
KANH-33	7.61	9.67
AGS-79	18.86	8.22
MTD-452	1.38	3.04
GMOT-17	3.3	8.02
JOYAWAZA	-3.78	2.06
F-85-11347	-25.71	-15.02
YESOY-4	-8.96	0.59
SHOHAG	22.44	-2.1
AUSTRALIA	13.02	-35.4
GC-82-332411	5.31	7.2
PK-327	-9.37	2.75
ASSET-93-19-13	-20.52	-1.81
PK-327	-22.75	11.3
AGS-95	19.55	-8.11
BARI SOYBEAN-6	23.88	-4.45
NS-1	-6.48	-6.79
MTD-451	17.33	3.67
GC-830059	-12.69	6.79
86017-66-6	8.01	-2.1
MTD-16	2.45	-5.77
LG-92P-12-18	11.76	-3.37
BS-33	13.96	3.53
ASSET-95	-2.56	3.01
BS-13	7.23	1.33
CHINA-1	12.3	4.03

Appendix VI. Analysis of variance of 12 yield and yield related character of soybean

Source	DF	Mean sum of square											
		PH	DFE	D50F	D80M	NBP	NPP	NSP	PL	TSW	SY	SPWP	YIELD
Replication	2	64.01	3.05	4.037	4.79*	4.23*	70.47	0.1	0.15	0.57	3.21*	0.1	5.16
Treatment	26	239.46**	38.61**	42.05**	72.42**	10.68**	931.30**	0.21**	0.66**	23.52**	47.89**	9.03**	314.23**
Error	52	26.23	1.33	1.47	1.17	1.07	82.63	0.06	0.06	0.26	0.88	0.43	5.11

** Significant at 1%

* Significant at 5%

DFE= Days to first flowering, PH= Plant height (cm), D50F= Days to 50% flowering, D80M= Days to 80% maturity, NBP= Number of branches per Plant, NPP= Number of pod per plant, NSP=Number of seeds per pod, PL= Pod length, HSW= Hundred seed weight (g), SY= Stover yield, SPWP= Single pod weight per plant, YIELD=Yield per plant.

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