GENETIC DIVERSITY ANALYSIS IN SOYBEAN (*Glycine max* (L.) Merrill)

By

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CERTIFICATE

This is to certify that thesis entitled, **"GENETIC DIVERSITY ANALYSIS IN SOYBEAN (*Glycine max* (L.) Merrill)"** submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE** in **GENETICS AND PLANT BREEDING,** embodies the result of a piece of bonafide research work carried out by **MOST. NAJMUNNAHAR TASRIFA AKTER, Registration No. 05-01747** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: June, 2011
Dhaka, Bangladesh

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GENETIC DIVERSITY ANALYSIS IN SOYBEAN (*Glycine max* L. Merrill)

By
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ABSTRACT

A field experiment was conducted during November 2011 to March 2012 to study the genetic diversity for quantitative traits in soybean (*Glycine max* L. Merrill) with 25 genotypes in randomized block design with three replications. The genotypes were placed in a field experiment conducted at the research farm of Sher-e-Bangla Agricultural University, Dhaka- 1207. The objectives of the study were to asses the genetic diversity among the genotypes of soybean, to find out the characters influencing genetic divergence, to estimate heritability and genetic advance of yield and yield components, to screen out the parental groups which are likely to provide superior segregants on hybridization and to know the yield potentiality of genotypes. Analysis of variance for each trait showed significant differences among the genotypes. Phenotypic coefficients of variation (PCV) was also close to genotypic coefficients of variation (GCV) for all the characters except branches per plant, pod length and seeds per pod, effective node number indicating that environment had influence on the expression of these characters. High heritability associated with high genetic advance percent of mean was observed for pod length and hundred seed weight which indicated that selection for these characters would be effective. Hence, thrust has to be given for these characters in future breeding programme to improve the yield in soybean. Multivariate analysis based on 13 agronomic characters indicated that the 25 genotypes were grouped into five distant clusters. The maximum contribution of characters towards diversity was observed by days to maturity, seeds per pod and seed yield per plant. Thus, these traits may be given high emphasis while selecting the lines for hybridization. The inter cluster distance was maximum between cluster I and cluster IV. The highest intra-cluster distance was found in cluster II. From the results it can be concluded that the following genotypes *viz.*, G_{16} (BD-2339), G_{12} (BD-2335), G_{13} (BD-2336), and G_{14} (BD-2337) were identified as potential genotypes for higher seed yield in soybean.

DEDICATED

TO

MY BELOVED PARENTS

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June, 2011
SAU, Dhaka

The Author

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LIST OF ABBREVIATED TERMS

ABBREVIATION	FULL WORD
AEZ	Agro-Ecological Zone
et al.	And others
ACC	Accessions
BARI	Bangladesh Agricultural Research Institute
BBS	Bangladesh Bureau of Statistics
Cm	Centimeter
CV	Co-efficient of Variation
etc.	Etcetera
Fig.	Figure
G	Genotype
GA	Genetic Advance
GCV	Genotypic Co-efficient of Variation
δ^2_g	Genotypic Variance
G	Gram
h^2b	Heritability in broad sense
J.	Journal
Kg	Kilogram
M	Meter
MSS	Mean Sum of Square
Mm	Millimeter
MP	Muriate of Potash
No.	Number
%	Percent
PCV	Phenotypic Co-efficient of Variation

LIST OF ABBREVIATED TERMS (Cont'd.)

ABBREVIATION	FULL WORD
δ^2_p	Phenotypic variance
RCBD	Randomized Complete Block Design
R	Replication
Res.	Research
SAU	Sher-e-Bangla Agricultural University
SE	Standard Error
m^2	Square meter
TSP	Triple Super Phosphate

Chapter I

Introduction

CHAPTER I
INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is a source of both plant protein and fat and is considered to be the most important oil and legume crop in the world, in terms of total production and international trade. This alone contributes about 40-45% protein and 18-20% oil and it can be a very good source to reduce malnutrition of the people of Bangladesh. Soybean is for food, feed and industries of Bangladesh (Rahman, 2003). Also, this has become a prospective high potential crop in Bangladesh. The cultivated soybean belongs to the family Papilionaceae and the genus *Glycine*. It is originated in China with *Glycine ussuriensis* as probable progenitor (Vavilov, 1951 and Nagata, 1960). The production of this crop has increased in different regions of the world for its multipurpose uses and seems to grow well from the tropical to the mid-temperate zones. Soybean was introduced in Bangladesh around 1942; but its cultivation did not expand satisfactorily. In recent years MCC, CDP, BARC, BARI, BAU, BCSIR and other some NGOs (GKF, RDRS etc.) are trying to expand its cultivation. This crop can be cultivated throughout the year with less or even without irrigation as a cash or food crop in many ecological conditions of Bangladesh.

Soybean is becoming a potential protein and oil crop in Bangladesh because of its high protein as well as quality production capabilities (Anonymous, 1985). This is used both as pulse and oil crops. There are more than ten different crop plants grown in Bangladesh as source of edible as well as industrial oils. The incountry production of edible oil hardly exceeds 70,000 tons, which can provide about 1.5 g/capita/day, against a body requirement of 39 g/capita/day (Rahman, 1990). Over the past three decades the dramatic improvement in the yield of cereal crop was achieved

manipulation of the genetic make up of those crops. Release and cultivation of a wide array of high yielding cereal cultivars has pushed oil crops to marginal and sub marginal land of low productivity leading to poor yield. As a result there has been a continuous decrease in the area and production of oil and legume crops during the last decade. From nutritional point of view, no pulse crop like mungbean, lentil or gram is equivalent to it, rather it is very much superior to any one of these crops (Anonymous, 1985). It is a versatile crop with its multiple uses like, soya-dhal, soya-chatni, soya-khichuri, soya-milk, soya-curd, soya meat, soya-flour and roasted soybean snack in home (Mondal and Wahhab, 2001; Khaleque, 1998). In industry, soybean is used in the extraction of edible oil, preparing margarine, vegetable ghee, milk, varnishes, adhesives etc. The present small local production of soybean is being also used as the ingredients of poultry feeds and that of fish and human consumption of soya flour. Soybean as a crop improves soil fertility by fixing atmospheric nitrogen through symbiotic relationship with *Rhizobium* bacteria at root nodules of the crop. It is reported that the fixation of nitrogen by soybean is about 300 kg/ha/year in soil (Keser and Li, 1992).

The statistical information regarding soybean acreage production in Bangladesh is fragmentary and not available in the systematic form, but it is thought to be of 10,000 acres with about 5,000 tons of production (Rahman, 2002). Low production and acreage of soybean in Bangladesh results from lack of high yielding variety, competitions for a place in the existing cropping pattern and food habit. These short comings can be overcome by cultivating of high yielding variety. Development of high yielding variety requires information on variation among the breeding materials for yield and yield contributing characters.

Yield is complex entity and is the cumulative end product of many traits. It is a polygenic trait and influenced by many genetic factors as well as macro and micro environmental fluctuations. Therefore, direct selection for yield could be very difficult. For effective selection, information on the nature and magnitude of variation in the populations, association of characters with yield among themselves and extent of environmental influence on the expression of these characters are necessary. Also it becomes necessary to partition the observed variability into its heritable and non-heritable components and to have an understanding of parameters such as genotypic coefficient of variation, heritability, genetic advance etc. Correlation studies supply reliable and useful information on the nature, extent and direction of selection, with the inclusion of more variables in the correlation studies, indirect effect become complex and important (Nadan and Pandya, 1980). In crop improvement program, genetic divergence is very helpful to select the parents for future breeding program. Information about genetic diversity in available germplasm is important for the optimal design of any breeding program. This helps to choose desirable parents for establishing new breeding population. Besides, better knowledge on genetic diversity could help to sustain long term selection gain (Chowdhury *et al.* 2002). More diverse the parents, greater are the changes of obtaining high heterotic F_1 and broad-spectrum variability in segregating generations (Arunachalam, 1991).

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). The quantification of genetic diversity through biometrical procedures (Rao, 1952 and Anderson, 1957) has made it possible to choose genetically diverse parents for a successful hybridization program. Moreover, evaluation of genetic diversity is important to know the source of genes for a

particular trait within the available germplasm (Tomooka, 1991). The utility of multivariate analysis for measuring the degree of divergence and for assessing the relative contribution or of different character to the total divergence in self pollinated crops has been established by several workers (Golakia and Makne, 1992).

As yield is the main object of a breeder, so it is important to know the relationship between various characters that have direct and indirect effect on yield. According to Burton (1952), for the improvement of any character through breeding, it is essential to know the extent of variability present in that species, nature of association among the characters and the contribution of different characters towards yield. The efficiency of a plant breeding program depends on the amount of genetic variability exist in nature or how much a plant breeder can create variability in the target population so as to perform effective selection. The germplasms were received from the Plant Genetic Resource Centre (PGRC) of Bangladesh Agricultural Research Institute (BARI), Gazipur, Dhaka. Information about species as well as their identifying characters for most of the germplasm collected were unknown. So, it is an opportunity to categorize the germplasm morphologically under different species for future utilization.

A study was, therefore, conducted on the genetic diversity, analysis between yield and yield contributing characters of soybean. Therefore, the present investigation is undertaken with the following objectives:

i. To asses the genetic diversity among the genotypes of soybean,
ii. To find out the characters influencing genetic divergence,
iii. To estimate heritability and genetic advance of yield and yield components,
iv. To screen out the parental groups which are likely to provide superior segregants on hybridization and
v. To know the yield potentiality of genotypes

Chapter II
Review of literature

CHAPTER II

REVIEW OF LITERATURE

Soybean is one of the most important oil and protein crops of the world. Extensive research works have been conducted on soybean in different parts of the world. Some such works relevant to the present investigation have been reviewed in this chapter. The present research work has aimed to study the genetic divergence analysis among different yield contributing characters. In this chapter an attempt has been made to briefly review the work related to the present study.

2.1. Variability, Heritability and Genetic Advance

The improvement of a crop is dependent on the magnitude of genetic variability and the extent of heritability of desirable characters of the genotypes available. A critical review of genetic variability is therefore a prerequisite for planning and evaluation of a breeding programme.

Bangar *et al.* (2003) reported that phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV). The GCV and PCV estimates were highest for branch number per plant and plant height among the characters. The GCV and PCV were of moderate magnitude for the pod number per plant 100-seed weight (g) and seed yield per plant (g). Days to 50% flowering and days to maturity had very low GCV and PCV estimates. The differences between GCV and PCV magnitudes were very high for 1000-seed weight and pod number per plant.

Chamundeswori and Aher (2003) conducted an experiment with ninety genotypes of soybean. They observed days to maturity, plant height at maturity, number of clusters per plant, number of pods per cluster and per plant, number of seeds per pod, 100-

seed weight and grain yield per plant showed significant genetic variation. Genotypic coefficient of variation was highest for biological yield per plant. Broad sense heritability was highest for plant height and number of pods per plant.

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

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

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

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

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

maturity.

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

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

Mehetra *et al.* (1998a) 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 were 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.

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

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.

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

grain yield per plant showed high genetic advance.

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

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

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

Jagtap and Mehetra (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.

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.

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.

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.

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

Khan *et al.* (2000) observed correlation among yield determining components in 86 diverse maturity genotypes of soybean. Path coefficient analysis revealed that pods/plant had the direct effect on seed yield followed by 100 seed weight. Pods/plant affected seed yield negatively via indirect effects of plant height, pod height and seed/pod.

Singh *et al.* (2000) reported that leaf area had positive direct effect on biological yield but it showed negative effect on seed yield in soybean.

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.

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

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

on seed yield.

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

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.

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

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.

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

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.

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

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

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

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.

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

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

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.

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

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

Ahmed *et al.* (1971) observed that seed yield per plant was significantly and

positively correlated with plant height, days to maturity, number of pods per plant and seeds per pod in soybean.

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

2.2. Genetic divergence among soybean germplasm

Genetic diversity analysis is used to identify specific parents for realizing heterosis and recombination in breeding programme. Several workers have followed the technique of Mahalanobis' D^2-statistics on a wide range of crop species to measure the genetic distance among the breeding materials and to identify the characters responsible for such type of divergence.

Several statistical methods are usually used for discriminating among the genotypes viz. Mahalanobis' generalized distance (Mahalanobis' 1936), the algorithm methods of Williams and Lambert (1960), Coopers (Cooper, 1963). Of them Mahalanobis' D^2 statistics was extensively used by the researchers the Mahalanobis techniques has been followed by several workers on wide range of crop species.

Sihag *et al.* (2004) studied genetic diversity among 160 soybean genotypes using Malhalanobis' D^2 statistic and grouped the genotype into 8 clusters. The clustering pattern revealed that no definite relationship existed between genetic diversity and geographic diversity. The genotypes from the same eco-geographic region were classified in different clusters, and genotypes from different eco-geographic regions were classified into one cluster.

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

Das *et al.* (2000) studied genetic divergence of 65 soybean genotypes using Mahalanobis D^2 statistic and grouped the genotypes into 13 clusters. Grouping pattern of the genotypes suggested no parallelism between genetic divergence and geographical distribution of the genotypes. Variance of cluster means revealed that pods per plant and plant height had the maximum contribution towards divergence.

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

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

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

Mehetre *et al.* (1997a) 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.

Chowdhury *et al.* (1996) 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.

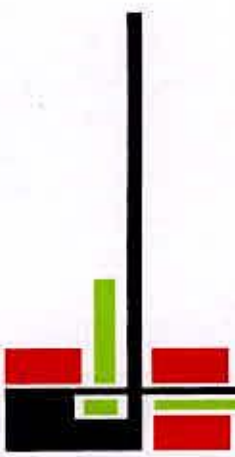
Praneetha and Thamburaj (1996) observed that fifteen and 22 genotypes of soybean were grouped into 6 and 3 clusters, respectively, on the basis of D^2 analysis of 14 clusters.

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

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

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

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



Chapter III

Materials and Methods

CHAPTER III

MATERIALS AND METHODS

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

3.1. Experimental site

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

3.2. Geographical Location

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

3.3. Climate

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

3.4. Characteristics of soil

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

3.5. Planting materials

Twenty five (25) genotypes of soybean were used for the present research work. The purity and germination percentage were leveled as around 100 and 80, respectively. The genetically pure and physically healthy seeds of these genotypes were collected from Plant Genetic Resources Centre (PGRC) of Bangladesh Agricultural Research Institute (BARI), Gazipur, Dhaka. The name and origin of these genotypes are presented in Table 1.

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

Sl. No.	Genotypes No.	Name/Acc No. (BD)	Origin
1	G_1	BD-2324	PGRC, BARI
2	G_2	BD-2325	PGRC, BARI
3	G_3	BD-2326	PGRC, BARI
4	G_4	BD-2327	PGRC, BARI
5	G_5	BD-2328	PGRC, BARI
6	G_6	BD-2329	PGRC, BARI
7	G_7	BD-2330	PGRC, BARI
8	G_8	BD-2331	PGRC, BARI
9	G_9	BD-2332	PGRC, BARI
10	G_{10}	BD-2333	PGRC, BARI
11	G_{11}	BD-2334	PGRC, BARI
12	G_{12}	BD-2335	PGRC, BARI
13	G_{13}	BD-2336	PGRC, BARI
14	G_{14}	BD-2337	PGRC, BARI
15	G_{15}	BD-2338	PGRC, BARI
16	G_{16}	BD-2339	PGRC, BARI
17	G_{17}	BD-2340	PGRC, BARI
18	G_{18}	BD-2341	PGRC, BARI
19	G_{19}	BD-2342	PGRC, BARI
20	G_{20}	BD-2349	PGRC, BARI
21	G_{21}	BD-2352	PGRC, BARI
22	G_{22}	BARI SOYBEAN-5	PGRC, BARI
23	G_{23}	BARI SOYBEAN-6	PGRC, BARI
24	G_{24}	BANGLADESH SOYBEAN-4	PGRC, BARI
25	G_{25}	SHOHAG	PGRC, BARI

3.6. Design of the experiment

The study was laid out in Randomized Complete Block Design (RCBD) with three (3) replications. The plot size was 260 m^2. A distance of 1.0 m from block to block, 50 cm from each row within each line. Each plot has a single row of 3 m length. Plant to plant distance was 7 cm. The genotypes were randomly distributed to each row within each block.

3.7. Land preparation

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

3.8. Manure and fertilizers application

Total cowdung and triple super phosphate (TSP) and muriate of potash (MOP) and half urea were applied in the field during final land preparation. Half urea was applied in the plot after two weeks of planting. Remaining urea and muriate of potash (MOP) were applied after five weeks of planting. Doses of manure and fertilizers used in the study are showing in Table 2.

Table 2. Doses of manures and fertilizers used in the study

Sl. No.	Fertilizers/ Manures	Dose
		Quantity/ha
1.	Urea	60 kg
2.	TSP	120 kg
3.	MOP	60 kg
4.	Cow dung	4000 kg

3.9. Intercultural operations

When the plants were well established, 1st mulching and weeding were done uniformly in all the plots. Second weeding was done after 20 days of the first one.

3.9.1. Thinning and gap filling

When the plants were well established, the soil around the base of each seedling was pulverized. A few gaps filling was done by healthy seedlings of the same stock where initial planted seedlings failed to survive. Thinning was done 15 days after sowing for the proper development and avoid crowd environment.

3.9.2. Weeding and mulching

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

3.9.3. Irrigation and after-care

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

3.9.4. Pesticide application

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

3.10. Harvesting

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

Photograph showing one replication view of the experimental field in Plate 1 A, Single row of the soybean plant in the experimental field in Plate 1 B, Single soybean plant in the experimental field in Plate 2 C, A soybean plant with flower in Plate 2 D, and A soybean plant with pod in Plate 3 and 4.

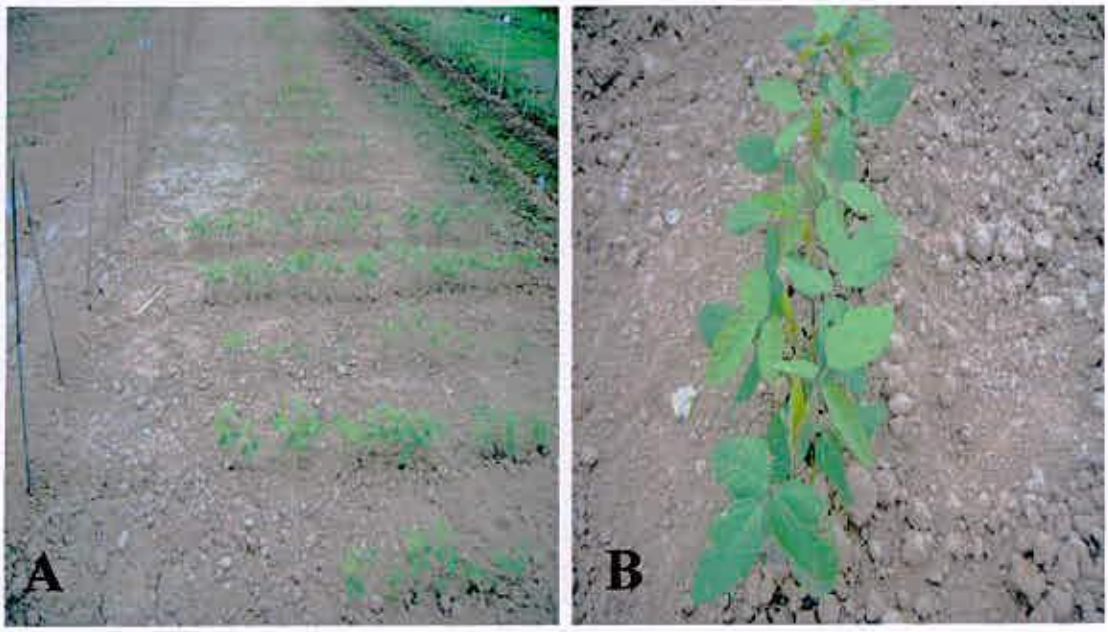


Plate 1: A. One replication view of the experimental field and B. Single row of soybean plant in the experimental field

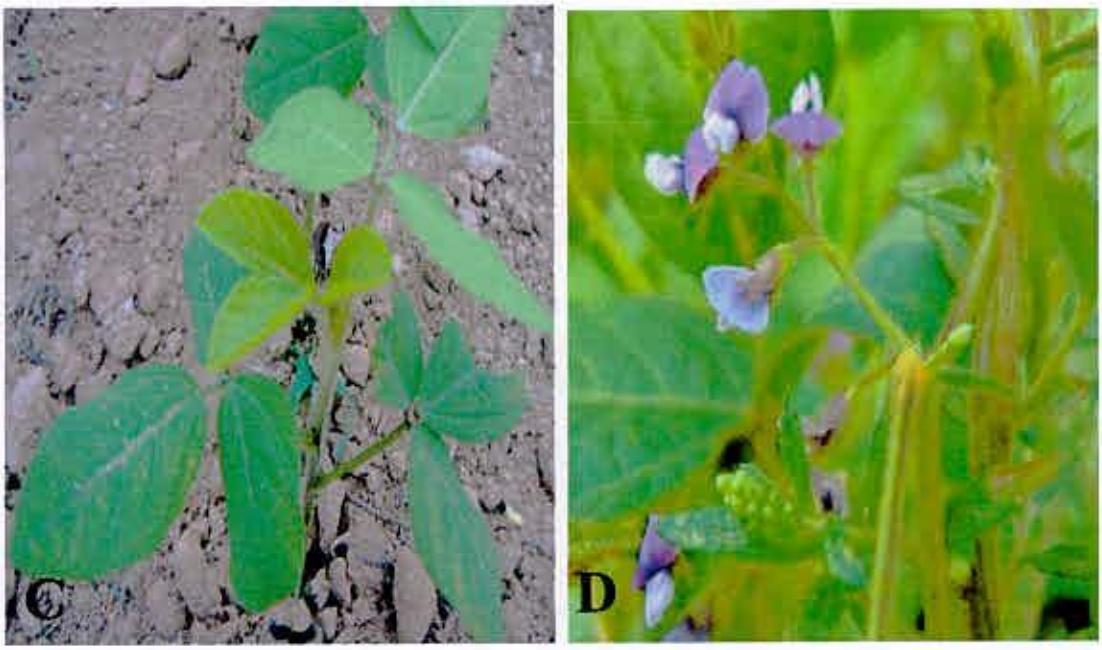


Plate 2. C. Single soybean plant in the experimental field. and D. Single soybean plant with flower

Plate 3: A soybean plant with pods

Plate 4: A Soybean plant with pods

3.11. 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.

3.11.1. Days to germination

Days to germination were determined from the date of sowing to the date when 80% of the seeds of the plot germinated.

3.11.2. Days to 50 percent flowering

The number of days was counted from the date of sowing to days to 50% flowering.

3.11.3. Days to 100 percent flowering

The number of days was counted from the date of sowing to 100 percent of plants flowered.

3.11.4. Days to maturity

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

3.11.5. Plant height (cm)

The plant height was measured from ground level to tip of the plant expressed in centimeters and mean was computed.

3.11.6. Number of branches per plant

The number of branches arising from the main stem above the ground was recorded at 60 days after planting.

3.11.7. Number of pods per plant

The total number of pod harvested from the five plants was counted and the average number of pods per plant was calculated.

3.11.8. Number of seeds per pod

Number of seeds per pod was counted from 5 pods taken from 3 randomly selected plant of each genotype and was counted and averaged.

3.11.9. 100 seed weight (g)

100 seed weight and seed weight per plant was worked out and expressed in grams (g).

3.11.10. Effective nodes number

Mean number of effective nodes per plant counted from five sample plant after harvest.

3.11.11. Pod Length (cm)

It was measured by measured from stalk end to tip by using centimeter scale.

3.11.12. Biological Yields (g)

Seed yield and Stover yield were altogether regarded as biological yield.

Biological yield = Seed yield (g) + Stover yield (g)

3.11.13. Harvest Index (%)

Harvest index was calculated on the ratio of grain to biological yield and expressed as percentage. It was calculated by using the following formula (Gardner *et al.*, 1985).

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

Where, Biological yield (g) = Seed yield (g) + Stover yield (g)

3.11.14. Yield per plant (g)

Weight of the total seed of individual plant in grams was taken as yield of plant.

3.12.1. Statistical analysis

The data were recorded for each character and averaged to obtain mean data. 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).

3.12.1.1. Estimation of genotypic and phenotypic variances

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

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

Where,

GMS = Genotypic mean sum of squares

EMS = Error mean sum of square

r = number of replications

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

Where,

σ^2_g = Genotypic variance

EMS= Error mean sum of square

3.12.1.2. Estimation of genotypic and phenotypic co-efficient of variation

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

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

Where,

σ^2_g = Genotypic variance

$\bar{x}$ = Population mean

Similarly,

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

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

Where,

σ^2_{ph}= Phenotypic variance

$\bar{x}$ = Population mean

3.12.1.3. Estimation of heritability

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

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

Where,

$h^2{}_b$ = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.12.1.4. Estimation of genetic advance

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

Genetic advance (GA) = K. h^2. σ_{ph}

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

Where,

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

σ_{ph} = Phenotypic standard deviation

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.12.1.5. Estimation of genetic advance mean's percentage

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

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

3.12.2. Multivariate analysis

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

3.12.2.1. 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.

3.12.2.2. 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).

3.12.2.3. 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.

3.12.2.4. Canonical Vector analysis (CVA)

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

3.12.2.5. Calculation of D^2 values

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

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

Where,

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

x = Number of characters.

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

3.12.2.6. 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.

3.12.2.7. 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.

ni = Number of populations in cluster i.

nj = Number of populations in cluster j.

3.12.2.8. 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.

3.12.2.9. 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 Chaudhury (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 parent(s)
- Selection of particular genotype(s) from the selected cluster(s)
- Relative contribution of the characters to the total divergence
- Other important characters of the genotypes.

Chapter IV

Results and Discussion

CHAPTER IV

RESULT AND DISCUSSION

Results of univariate and multivariate analysis based on days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of seeds per plant, number of pods per plant, 100 seed weight (g), pod length (cm), seed yield per plant (Kg) etc. are discussed under the following subheadings.

4.1. Genetic parameters

The analysis of variance indicated the existence of highly significant variability for all the characters studied. viz., days to first flowering, days to 50% flowering, plant height, branches per plant, effective nodes number, pod length, hundred seed weight, pods per plant, number of seeds per pod, seeds per plant, days to maturity, seed yield per plant. The mean sum of square, mean, range, variance components, coefficients of genotypic and phenotypic variations, heritability estimates, genetic advance and genetic advance in percent of mean (GAPM) are presented in Table 3. The results are discussed character wise as follows:

Table 3. Estimation of genetic parameters in thirteen characters of twenty five genotypes in soybean

Parameters	Range	Mean	MS	σ^2_p	σ^2_g	σ^2_e	PCV	GCV	ECV	h^2_b	GA (5%)	GAPM
D50%F	58.67-74.00	64.49	37.05**	13.15	11.96	1.19	5.62	5.36	1.69	90.93	6.79	10.53
BP	1.67-4.56	2.99	1.39*	0.53	0.43	0.10	24.32	22.02	10.33	81.97	1.23	41.14
PH	34.56-59.33	44.96	109.99**	38.43	35.78	2.64	13.79	13.31	3.62	93.12	11.89	26.45
DM	120.00-126.00	122.83	9.80**	3.29	3.26	0.03	1.48	1.47	0.13	99.17	3.70	3.01
PP	21.44-88.33	37.28	798.73**	268.78	264.98	3.80	43.97	43.66	5.23	98.59	33.30	89.32
SPP	60.00-237.78	100.75	5633.05**	1893.10	1869.98	23.12	43.19	42.92	4.77	98.78	88.54	87.88
SP	2.44-2.78	2.68	0.015*	0.01	0.00	0.01	4.51	0.89	4.42	3.85	0.01	0.37
HSW	35.71-88.78	63.68	528.98**	179.10	174.94	4.15	21.02	20.77	3.20	97.68	26.93	42.29
ENN	7.44-24.44	14.77	70.54**	26.12	22.22	3.90	34.60	31.91	13.38	85.05	8.95	60.60
PL	3.28-4.47	3.83	0.21*	0.09	0.06	0.02	7.75	6.56	4.13	71.66	0.44	11.49
BY	42.72-178.77	75.33	2065.76**	694.39	685.69	8.71	34.98	34.76	3.92	98.75	53.60	71.15
HI	66.98-95.00	81.78	131.70**	47.53	42.08	5.45	8.43	7.93	2.85	88.53	12.57	15.37
SYP	32.42-160.23	62.08	1862.00**	628.14	616.93	11.22	40.37	40.01	5.40	98.21	50.71	81.68

Here, **, * Correlation is significant at the 0.01 and 0.05 level respectively. D50%F = Days of 50% flowering, BP = Branches per plant, PH = Plant height (cm), DM = Days to maturity, PP = Pod per plant, SPP = Seed per plant, SP = Seed per pod, HSW = 100 seed weight (g), ENN = Effective node number, PL = Pod length (cm), BY = Biological yield (g), HI = Harvest index, SYP = Seed yield per plant (g), MS = Mean sum of square, σ^2_p = Phenotypic variance, σ^2_g = Genotypic variance and σ^2_e = Environmental variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation, h^2b= Heritability, GA= Genetic advance and GAPM= Genetic advance in percent of mean.

4.1.1. Genetic variability, heritability and genetic advance

The success of crop improvement programme depends on the extent of genetic variability existing in the population or germplasm. The magnitude of genetic variability can determine the pace and quantum of genetic improvement through selection or through hybridization followed by selection. 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.

The presence of narrow gap between PCV and GCV for all the characters under 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 advances as per cent 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 character were studied and the results are presented in Table1 and depicted in Fig. 1 and Fig. 2. The mean performance of soybean genotypes for various growth characters and yield components are presented in Appendix IV.

4.1.2. Days to 50% flowering

Significant differences were recorded among the entries with respect to days to 50% flowering. The value ranged from 58.67 to 74.00 days, in the genotype BD-2335 and

BD-2352, respectively. The Genotypic, phenotypic and environmental variances observed were 11.96, 13.15 and 1.19, respectively. 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 (5.36) and phenotypic co-efficient of variation (5.62) were close to each other (Table 3). There was a very little difference between phenotypic and genotypic co-efficient of variation, indicating minor environmental influence on this character. The heritability (90.93%) estimates for this trait was very high, genetic advance (6.79) and genetic advance over percentage of mean (10.53) were found moderately low (Table 3), 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). Days to 50% flowering and days to maturity had very low GCV and PCV estimates.

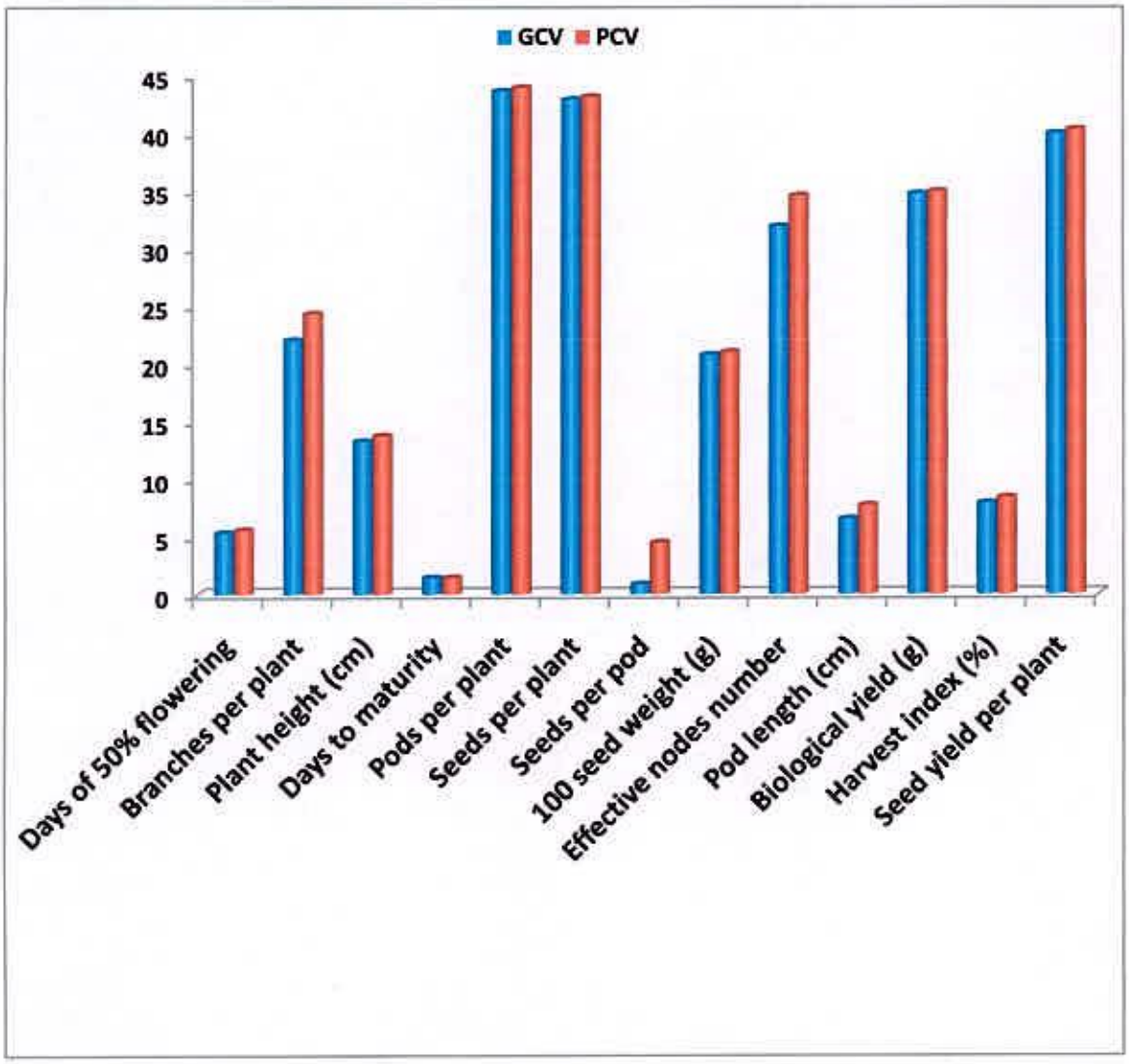


Figure 1. Genotypic and phenotypic variability in soybean

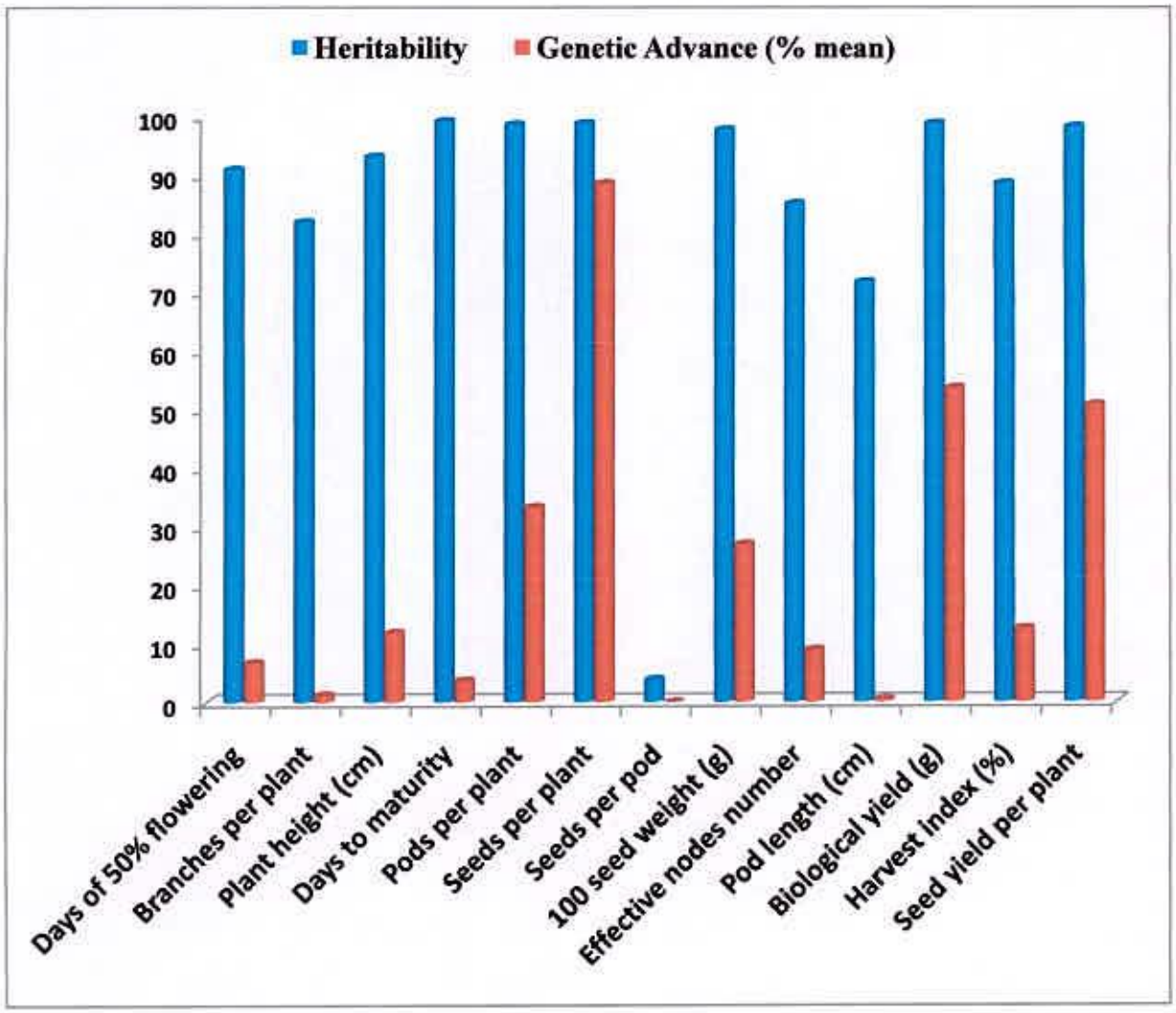


Figure 2. Heritability and genetic advance over mean in soybean

4.1.3. Branches per plant

Significant mean sum of square for number of branches per plant (1.39) in soybean indicated considerable difference among the genotypes studied (Table 3). It ranged from 1.67 to 4.56 with a mean value of 2.99. Maximum number of branches were recorded in G_{13} (BD-2336) and G_{12} (BD-2335) genotype showed the minimum number of branches. The phenotypic variance (0.53) appeared to be higher than the genotypic variance (0.43) 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 22.02 and 24.32, respectively (Table 3) which indicated presence of considerable variability among the genotypes. The heritability (81.97) estimates for this trait was high, genetic advance (1.23) was low and genetic advance in per cent of mean (41.14) were found moderately high (Table 3), revealed that this trait was governed by non-additive gene.

Bangar *et al.* (2003) reported that phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV). The GCV and PCV estimates were highest for branch number per plant.

4.1.4. Plant height (cm)

The grand mean plant height recorded was 44.96 cm. It ranged from 34.56 cm to 59.33 cm (Table 3). The analysis of variance revealed highly significant differences among the genotypes with respect to plant height. The maximum plant height (59.33 cm) was recorded by the G_5 (BD-2328) and the lowest plant height (34.56 cm) was recorded by G_{19} (BD-2342) (Appendix IV). The PCV and GCV were 13.79 and 13.31 percent respectively (Table 3). There was little difference between phenotypic and genotypic co-efficient of variation indicating little environmental influence in the

expression of this character. In the present study, the genotypic and phenotypic co efficient of variability were moderate for plant height. The estimates of heritability was high at 93.12 per cent with an expected genetic advance (11.89%) (Table 3). Plant height exhibited high heritability and genetic advance as per cent mean which is similar to the earlier findings by Archana *et al.* (1999) and Jain and Ramgiry (2000).

4.1.5. Days to maturity

Significant differences were recorded among the entries with respect to days to maturity. The value ranged from 120 to 126 DAS. The accession G_1 (BD-2324), G_2 (BD-2325) and G_3 (BD-2326) showed minimum (120 DAS) and the accession G_{18} (BD-2341) showed maximum (126 DAS) days to maturity, respectively (Appendix IV). The PCV and GCV were 1.48 and 1.47 percent with a overall mean of 122.83 days. The heritability estimates were very high (99.17) with an expected genetic advance over mean of 3.70 percent. Very high heritability and low genetic advance for days to maturity was indicated that this trait controlled by non additive gene. Jangale *et al.* (1994) observed that high heritability was observed for days to 50% flowering, days to maturity.

4.1.6. Pods per plant

Significant mean sum of square for pods per plant (798.73) in Soybean indicated considerable difference among the genotypes studied (Table 3). The number of pods per plant was ranged from 21.44 to 88.33 with mean of 37.28. The minimum numbers of pods per plant were observed in accession G_{17} (BD-2340) while maximum numbers of pods per plant were found in the genotype G_{16} (BD-2339). The phenotypic variance (268.78) appeared to be higher than the genotypic variance (264.98) 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 43.66 and 43.97, respectively (Table 3) which indicated presence of considerable variability among the genotypes. The heritability (98.59%) estimates for this trait was very high, genetic advance (33.30) was moderately high and genetic advance in per cent of mean (89.32) was found high (Table 3), revealed that this trait was governed by additive gene. Mahajan *et al.* (1994) reported that pods per plant and yield per plant showed high genotypic co-efficient of variation. High heritability was recorded for pods per plant.

4.1.7. Seeds per plant

Significant mean sum of square for seeds per plant (5633.05) in Soybean indicated considerable difference among the genotypes studied (Table 3). It ranged from 60 to 237.78 with a mean of 100.75. Highest seeds per plant were recorded by the accession G_{16} (BD-2339) while accession G_{22} (BARI SOYBEAN-5) showed the lowest seeds per plant. The phenotypic variance (1893.10) appeared to be higher than the genotypic variance (1869.98) 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 42.92 and 43.19, respectively (Table 3) which indicated presence of considerable variability among the genotypes. The heritability (98.78%) estimates for this trait was very high, genetic advance (88.54) was very high and genetic advance in per cent of mean (87.88) was found very high (Table 3), revealed that this trait was governed by additive gene.

4.1.8. Number of seeds per pod

Significant mean sum of square for number of seeds per pod (0.015) in Soybean indicated considerable difference among the genotypes studied (Table 3). The

germplasm accessions differed significantly for this character. The values ranged from 2.44 to 2.78 with a mean of 2.68. The genotype G_{12} and G_{13} (BD-2335 and BD-2336) had highest number of seeds per pod while it was lowest in the genotype G_1 (BD-2324). The phenotypic variance (0.01) appeared to be higher than the genotypic variance (0.00) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 0.89 and 4.51 respectively (Table 3) which indicated presence of considerable variability among the genotypes. The heritability (3.85%) estimates for this trait was low, genetic advance (0.01) and genetic advance in per cent of mean (0.37) was found very low (Table 3), revealed that this trait was governed by non additive gene. Jangale *et al.* (1994) reported that high heritability was observed for seeds per pod.

4.1.9. Hundred seed weight (g)

Mean sum of square for hundred seed weight (528.98) in Soybean is highly significant indicated considerable difference among the genotypes studied (Table 3). The mean hundred seed weight noticed was 63.68 g with a range of 35.71 g to 88.78 g. The line G_{14} (BD-2337) showed the minimum hundred seed weight and the maximum hundred seed weight was recorded in the accession G_{23} (BANGLADESH SOYBEAN-6). The phenotypic variance (179.10) appeared to be higher than the genotypic variance (174.94) 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 20.77 and 21.02, respectively which were close to each other (Table 3). There was a very little difference between phenotypic and genotypic co-efficient of variation, indicating minor environmental

influence on this character. The heritability (97.68%) estimates for this trait was very high, genetic advance (26.93) was moderately high and genetic advance in per cent of mean (42.29) was found high (Table 3), revealed that this trait was governed by additive gene. Major *et al.* (1996) observed high genotypic and phenotypic co-efficient of variation for 100 seed weight and grain yield.

4.1.10. Effective nodes number

Significant mean sum of square for number of nodes per plant (70.54) in Soybean indicated considerable difference among the genotypes studied (Table 3). The number of node per plant was ranged from 7.44 to 24.44 with a mean of 14.77. Maximum number of node per plant was recorded in the genotype G_{16} (BD-2339) and minimum days in the genotype G_{17} (BD-2340). The phenotypic variance (26.12) appeared to be higher than the genotypic variance (22.22) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 31.91 and 34.60 respectively (Table 3) which indicated presence of considerable variability among the genotypes. The heritability (85.05%) estimates for this trait was high, genetic advance (8.95) and genetic advance in per cent of mean (60.60) were found high (Table 3), revealed that this trait was governed by additive gene. Chowdhury *et al.* (1998) observed genetic divergence and geographic distribution were not necessarily related to effective nodes per plant but its contribution is maximum on the total divergence.

4.1.11. Pod length (cm)

Mean sum of square for pod length (0.21) in Soybean is significant indicated considerable difference among the genotypes studied (Table 3). It ranged from 3.28 to 4.47 cm with a mean of 3.83 cm. The minimum pod length was recorded by the

accession G_1 (BD- 2324) and accession G_{11} (BD-2334) showed the maximum pod length. The phenotypic variance (0.09) appeared to be higher than the genotypic variance (0.06) 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 6.56 and 7.75, respectively (Table 3) which indicated presence of considerable variability among the genotypes. The heritability (71.66%) estimates for this trait was high, genetic advance (0.44) was low and genetic advance in per cent of mean (11.49) was found moderately low (Table 3), revealed that this trait was governed by non-additive gene. Dobhal (1995) observed total genetic distance was highest for pod length per plant.

G1 G2 G3

G4 G5 G6

G7 G8 G9

Plate 5a. Showing phenotypic variation in pods among different genotypes of soybean (G_1-G_9)

G10 G11 G12

G13 G14 G15

G16 G17 G18

Plate 5b. Showing phenotypic variation in pods among different genotypes of soybean (G_{10}-G_{18})

G19 G20 G21

G22 G23 G24

G25

Plate 5c. Showing phenotypic variation in pods among different genotypes of soybean (G_{19}-G_{25})

4.1.12. Biological yield (g)

Significant mean sum of square for biological yield per plant (2065.76) in Soybean indicated considerable difference among the genotypes studied (Table 3). The mean biological yield per plant noticed was 75.33 g with a range of 42.72 g to 178.77 g in the genotype G_1 (BD-2324) and G_{16} (BD-2339), respectively. The phenotypic variance (694.39) appeared to be higher than the genotypic variance (685.69) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 34.76 and 34.98, respectively (Table 3) which indicated presence of considerable variability among the genotypes. The heritability (98.75%) estimates for this trait was very high, genetic advance (53.60) and genetic advance in per cent of mean (71.15) was found high (Table 3), revealed that this trait was governed by additive gene. Chamundeswori and Aher (2003) observed genotypic coefficient of variation was highest for biological yield per plant.

4.1.13. Harvest index (%)

Significant mean sum of square for harvest index (131.70) in soybean indicated considerable difference among the genotypes studied (Table 3). It ranged from 66.98 to 95.00 with a mean value of 81.78. Maximum harvest index were recorded in G_{12} (BD-2335) and G_{18} (BD-2341) genotype showed the minimum harvest index. The phenotypic variance (47.53) appeared to be higher than the genotypic variance (42.08) 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 7.93 and 8.43, respectively (Table 3) which indicated presence of considerable variability among the genotypes. The heritability (88.53)

estimates for this trait was high, genetic advance (12.57) was moderately low and genetic advance in per cent of mean (15.37) were found moderately low (Table 3), revealed that this trait was governed by non additive gene.

4.1.14. Seed yield per plant (g)

Significant mean sum of square for seed yield per plant (1862) in Soybean indicated considerable difference among the genotypes studied (Table 3). The mean seed yield per plant noticed was 62.08 g with a range of 32.42 g to 160.23 g in the genotype G_1 (BD-2324) and G_{16} (BD-2339), respectively. The phenotypic variance (628.14) appeared to be higher than the genotypic variance (616.93) 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 40.01 and 40.37, respectively (Table 3) which indicated presence of considerable variability among the genotypes. The heritability (98.21%) estimates for this trait was very high, genetic advance (50.71) and genetic advance in per cent of mean (81.68) was found very high (Table 3), revealed that this trait was governed by additive gene. Malhotra (1973) observed that seed yield had the highest co-efficient of genetic variation and predicted genetic advance as a percentage of mean.

4.2. Multivariate Analysis

4.2.1. Principal component analysis (PCA)

Principal component analysis was carried out with 25 genotypes of soybean. First four Eigen values for four principal coordination axes of genotypes accounted for 74.93% variation (Table 4). A two dimensional scattered diagram (Fig. 3 and Fig. 4) was developed on the basis of the principal component score, Z_1 and Z_2 score (Appendices VI).

4.2.2. Principal coordinate analysis (PCO)

The results obtained from principal coordinate analysis showed that the highest inter genotypic distance was observed between genotypes G_1 and G_{16} (258.792) followed by G_{16} and G_{22} (258.308) (Table 5) and the lowest distance was observed (2.514) between genotypes G_6 and G_{18} followed by the distance (4.235) between genotypes G_4 and G_8 (Table 6). The difference between the highest and the lowest inter genotypic distance indicated the moderate variability among the 25 genotypes of soybean. The highest intra-cluster distance was recorded in cluster II (0.062) (Table 8) containing seven genotypes viz. BD-2328, BD-2332, BD-2336, BD-2338, BD-2349, BD-2352 and BANGLADESH SOYABEAN-4 (Table 7). The lowest intra-cluster distance was observed in cluster I and IV (0.00) having one genotypes for both cluster I and IV viz. 2339 and BD-2337, respectively (Table 7). It favored to decide that intra-group diversity was the highest in cluster II and the lowest both in cluster I and IV. Cluster III having eight genotypes viz. BD-2324, BD-2325, BD-2326, BD-2329, BD-2334, BD-2335, BD-2341 and BARI SOYABEAN-5 (Table 7) and had an intra-cluster distance 0.045 (Table 9). Cluster V having eight genotype viz. BD-2327, BD-2330, BD-2331, BD-2333, BD-2340, BD-2342, BARI SOYABEAN-6 and SHOHAG and had an intra-cluster distance 0.024 (Table 7 and 9).

Table 4. Eigen values and yield percent contribution of thirteen characters of tweenty five soybean germplasm

Characters	Eigen values	% contribution	Cumulative variation (%)
Days of 50% flowering	4.944	38.03	38.03
Branches per plant	2.184	16.80	54.83
Plant height (cm)	1.358	10.45	65.28
Days to maturity	1.255	9.65	74.93
Pods per plant	0.959	7.38	82.31
Seeds per plant	0.710	5.46	87.77
Seeds per pod	0.580	4.46	92.23
100 seed weight (g)	0.503	3.87	96.1
Effective node number	0.334	2.57	98.67
Pod length (cm)	0.126	0.94	99.61
Biological yield	0.042	0.33	99.94
Harvest index (%)	0.003	0.04	99.98
Seed yield per plant	0.002	0.02	100.00

Table 5. Ten highest inter genotypic distance among the twenty five soybean genotypes

Sl No.	Genotypic combination	Distances
	A. Ten highest inter genotypic distance	
01	$G_1 - G_{16}$	258.792
02	$G_{16} - G_{22}$	258.308
03	$G_{16} - G_{18}$	253.74
04	$G_6 - G_{16}$	253.098
05	$G_{16} - G_{17}$	243.472
06	$G_{11} - G_{16}$	241.538
07	$G_2 - G_{16}$	241.168
08	$G_7 - G_{16}$	238.043
09	$G_3 - G_{16}$	237.251
10	$G_{16} - G_{23}$	235.887

Table 6. Ten lowest inter genotypic distance among the twenty five soybean genotypes

Sl No.	Genotypic combination	Distances
	A. Ten lowest inter genotypic distance	
01	$G_6 - G_{18}$	2.514
02	$G_4 - G_8$	4.235
03	$G_3 - G_{11}$	4.293
04	$G_2 - G_{11}$	4.900
05	$G_{18} - G_{22}$	4.976
06	$G_6 - G_{22}$	5.230
07	$G_9 - G_{20}$	5.496
08	$G_2 - G_3$	6.404
09	$G_{17} - G_{23}$	7.991
10	$G_{15} - G_{20}$	8.118

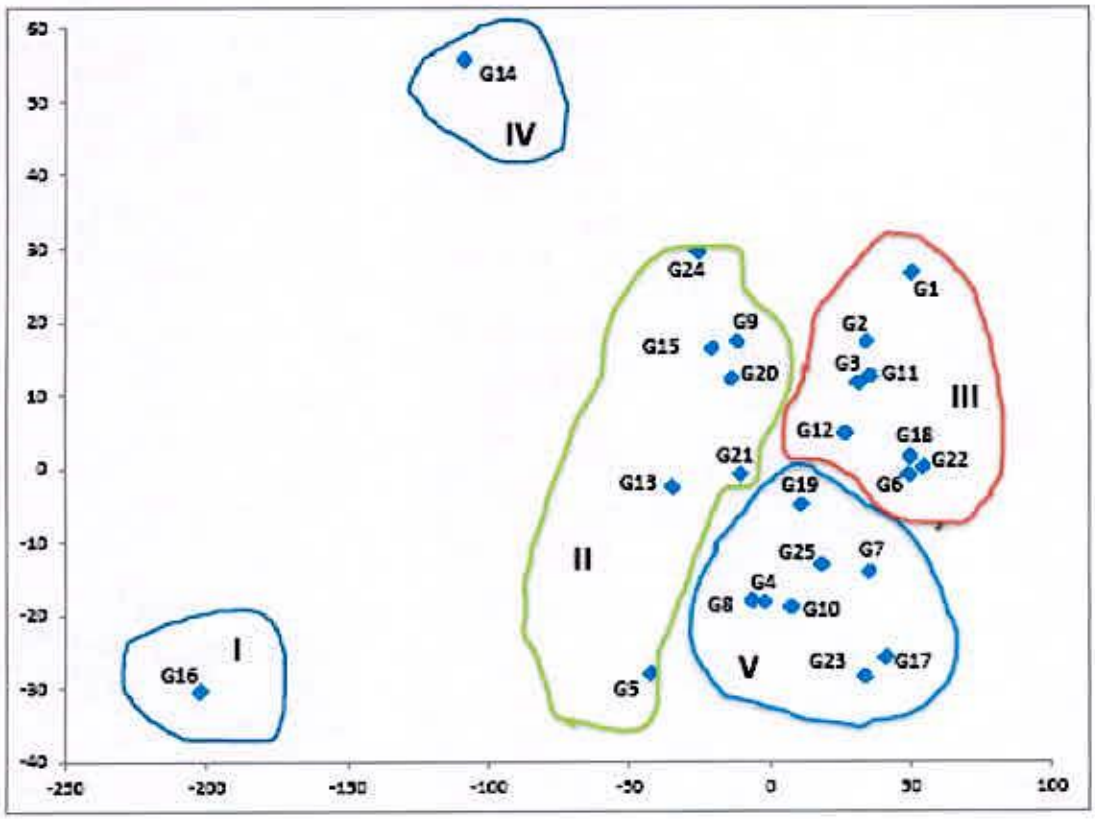


Figure 3. Scatter distribution of 25 soybean genotypes based on their principal component scores super imposed with clustering

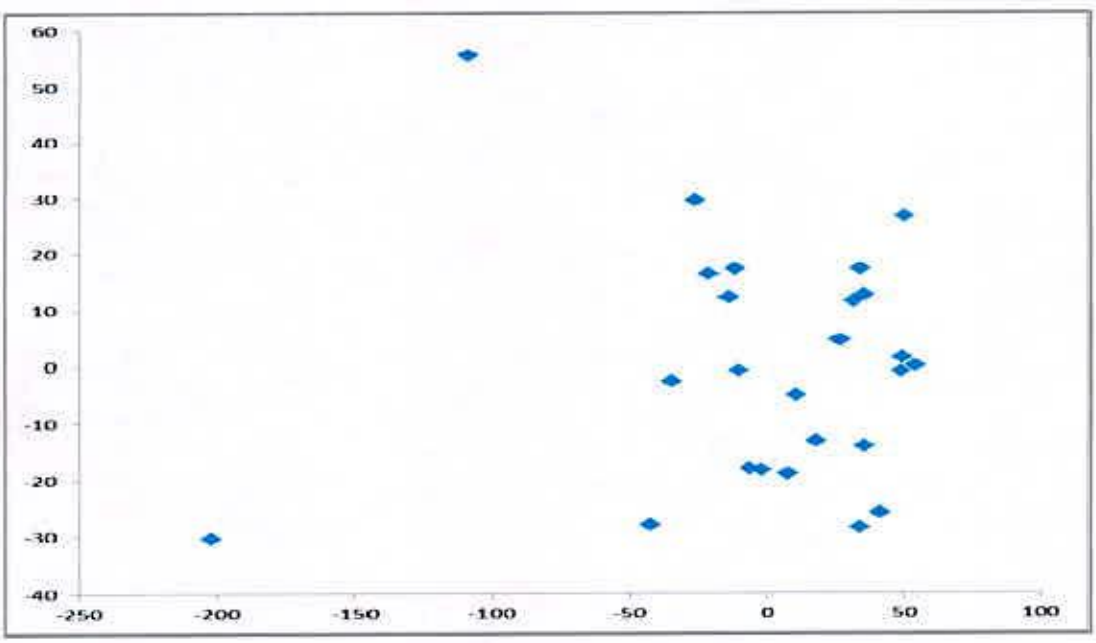


Figure 4. Scatter diagram of 25 soybean genotypes of based on their principal component scores

Table 7. Distribution of twenty five soybean genotypes in five clusters

Cluster no.	No. of Genotypes	Designation
I	1	BD-2339
II	7	BD-2328, BD-2332, BD-2336, BD-2338, BD-2349, BD-2352, BANGLADESH SOYABEAN-4
III	8	BD-2324, BD-2325, BD-2326, BD-2329, BD-2334, BD-2335, BD-2341, BARI SOYABEAN-5
IV	1	BD-2337
V	8	BD-2327, BD-2330, BD-2331, BD-2333, BD-2340, BD-2342, BARI SOYABEAN-6, SHOHAG

4.4.3. Non-hierarchical clustering

The computations from covariance matrix gave non-hierarchical clustering among 25 genotypes of soybean and grouped them into five clusters. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. So the results obtained through PCA were confirmed by non-hierarchical clustering. Table 7 represents the clusters occupied by 25 genotypes of soybean. It explains that both cluster III and V was contained the highest number of genotypes eight, cluster II constitute by seven genotypes and both cluster I and IV constitute by single genotype. Cluster III and V were composed of BD-2324, BD-2325, BD-2326, BD-2329, BD-2334, BD-2335, BD-2341 and BARI SOYABEAN-5 and BD-2327, BD-2330, BD-2331, BD-2333, BD-2340, BD-2342, BARI SOYABEAN-6 and SHOHAG, respectively. All the genotypes of cluster III and V are collected from Plant Genetic Resource Centre, BARI, Gazipur. Intra cluster mean for 13 traits are presented in Table 9. Cluster I was formed by one genotypes viz. BD-2339 was collected from Plant Genetic Resource Centre, BARI, Gazipur (Table 7). The highest cluster mean value was achieved for seven characters viz. days to maturity (124.0 days), pods per plant (88.33), seeds per plant (237.78), seed yield per plant (160.23), harvest index (88.95) and biological yield (178.77 g) (Table 8). Cluster IV was formed by one genotype BD-2337. The highest cluster mean value was achieved for two characters viz. branches per plant (3.27) and days to maturity (124.0 days). Cluster II was formed by seven genotypes viz. BD-2328, BD-2332, BD-2336, BD-2338, BD-2349, BD-2352, and BANGLADESH SOYABEAN-4 were collected from Plant Genetic Resource Centre, BARI, Gazipur. The highest cluster mean value was achieved for two character viz. plant height (46.51) and seed per pod (2.73). Cluster V was formed by eight genotypes viz. BD-2327, BD-2330, BD-2331, BD-2333, BD-

2340, BD-2342, BARI SOYABEAN-6 and SHOHAG were collected from Plant Genetic Resource Centre, BARI, Gazipur. The highest cluster mean value was achieved for one character viz. 100 seed weight (77.68 g). Cluster III was formed by eight genotype viz. BD-2324, BD-2325, BD-2326, BD-2329, BD-2334, BD-2335, BD-2341 and BARI SOYABEAN-5 were collected from Plant Genetic Resource Centre, BARI, Gazipur. The highest cluster mean value was achieved for one characters viz. pod length (3.87). Among 13 characters cluster I stood first for seven characters viz. days to maturity (124.0 days), pod per plant (88.33), seed per plant (237.78), seed yield per plant, biological yield (178.77 g) and harvest index (88.95).

Table 8. Cluster mean of thirteen different characters of twenty five soybean genotypes

Characters	I	II	III	IV	V
Days of 50% flowering	66.00	66.52	63.38	66.67	63.38
Branches per plant	3.56	3.21	2.78	3.67	2.85
Plant height (cm)	45.00	46.51	45.65	44.89	42.92
Days to maturity	124.00	123.14	122.29	124.00	122.79
Pods per plant	88.33	44.37	26.61	79.11	30.15
Seeds per plant	237.78	119.82	72.63	210.11	81.39
Seeds per pod	2.71	2.73	2.64	2.67	2.69
100 seed weight (g)	67.40	57.55	58.07	35.71	77.68
Effective node number	24.44	17.16	12.79	23.56	12.35
Pod length (cm)	3.73	3.80	3.87	3.80	3.82
Biological yield	178.77	82.98	54.30	92.65	74.56
Harvest index (%)	88.95	82.13	77.83	81.31	84.59
Seed yield per plant	160.23	68.65	41.90	74.98	62.63

4.4.4. Canonical variate analysis

The highest inter-cluster distance was observed (Table 9 or Fig. 5) between cluster I and IV (36.93) followed by cluster II and IV (35.14). The lowest inter-cluster distance was observed between cluster III and V (5.78) followed by cluster III and IV (7.18). Moderate or intermediate distance was found between cluster I and II (16.96). On the other hand, the highest intra cluster distance was found in cluster II (0.062) followed by cluster III (0.045).The lowest intra cluster distance was observed in cluster V (0.024). The inter cluster distances were found much higher than the intra cluster distances suggesting wider genetic diversity among the genotype of different groups. Results of different multivariate analysis were superimposed in figure 5 from which it may be concluded from the above results that different multivariate techniques supplemented and confirmed one another.

As per scatter diagram the genotypes were apparently distributed into five clusters. It was also revealed that the genotypes of cluster I was more diverse from the genotypes of cluster III. It is assumed that maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to maximum divergent clusters. However, for a practical plant breeding, the objective is not only high heterosis but also to achieved high-level production. Mohanty and Prusti (2001) reported that genetic diversity was not associated with geographic distribution. In the present study the maximum distance existence between cluster I and IV. But considering the yield and duration crossing involving cluster I and IV may be exhibit high heterosis for yield. Rahman (1998) estimated genetic divergence among sixteen genotypes of soybean using Mahalanobis' D^2 statistics.

Table 9. Average Intra (Bold) and inter-cluster distances (D^2) of twenty five soybean genotypes

Cluster	I	II	III	IV	V
I	**0.00**	16.96	30.03	36.93	24.25
II		**0.062**	28.18	35.14	23.45
III			**0.045**	7.18	5.78
IV				**0.00**	12.84
V					**0.024**

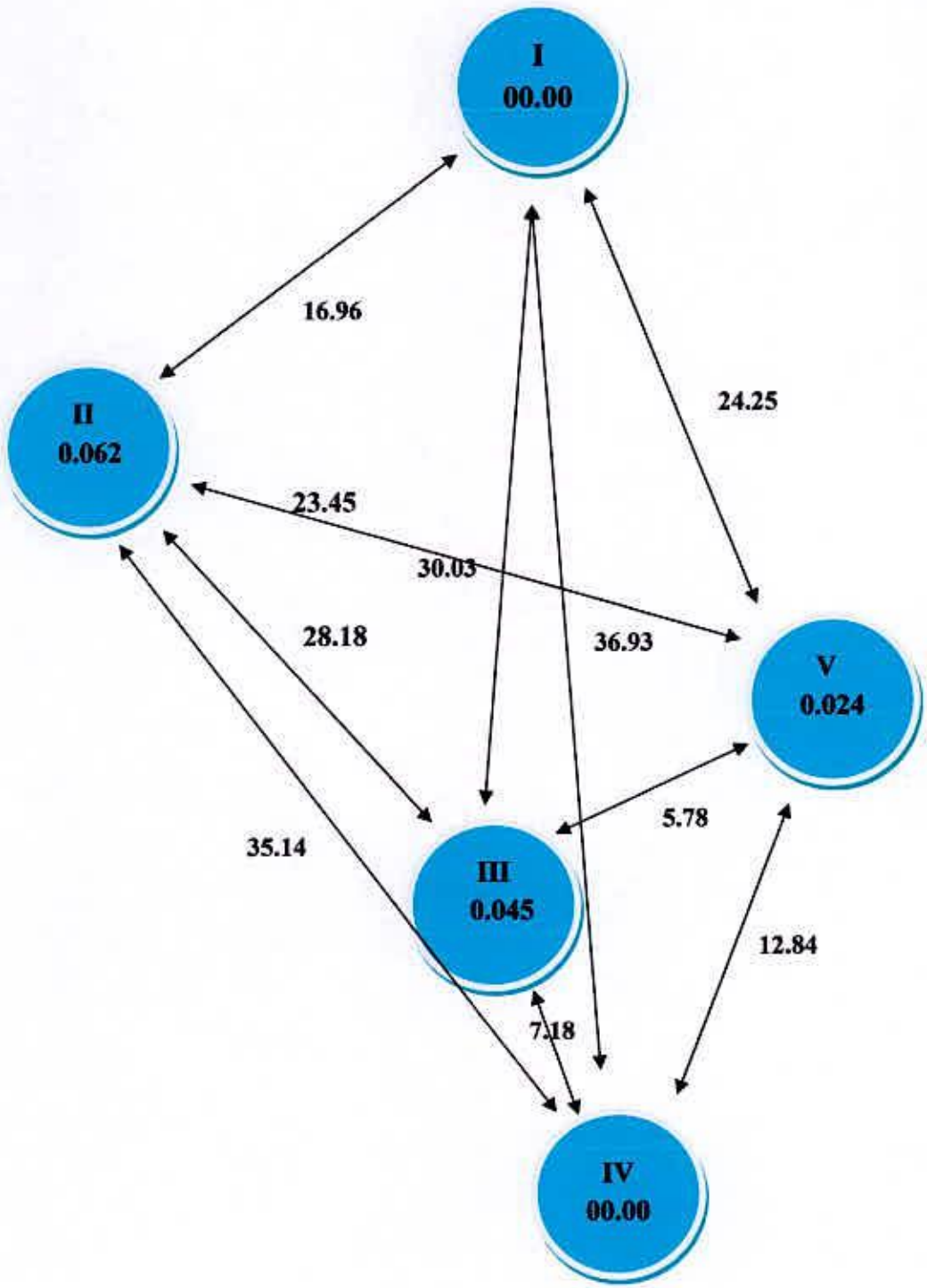


Figure 5. Diagram showing intra and inter -cluster distances (D^2) of twenty five genotypes in soybean

The genotypes were grouped into five 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 diversed 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.

4.4.5. Contribution of characters towards divergence of the genotypes

The values of Vector I and Vector II are presented in Table 10. Vector I obtained from PCA expressed that days to maturity (0.606), pods per plant (3.432), seeds per plant (15.291), seeds per pod (25.813), 100 seed weight (19.204 g) and seed yield per plant (19.660 g) were major characters that contribute to the genetic divergence. It was the reflection of first axis of differentiation. In vector II days to days to maturity (4.377), seed per pod (14.344), effective nodes number per plant (0.304) and seed yield per plant (24.151) showed their important role toward genetic divergence. The value of Vector I and Vector II revealed that both Vectors had positive values for days to maturity, seed per pod and seed yield per plant indicating the highest contribution of these traits towards the divergence among 25 genotypes of soybean. Negative values in both vectors for days of 50% flowering, branches per plant, plant height (cm), pod length (cm), biological yield (g) and harvest index had lower contribution towards the divergence.

Table 10. Latent vectors for thirteen principal component characters of twenty five soybean genotypes

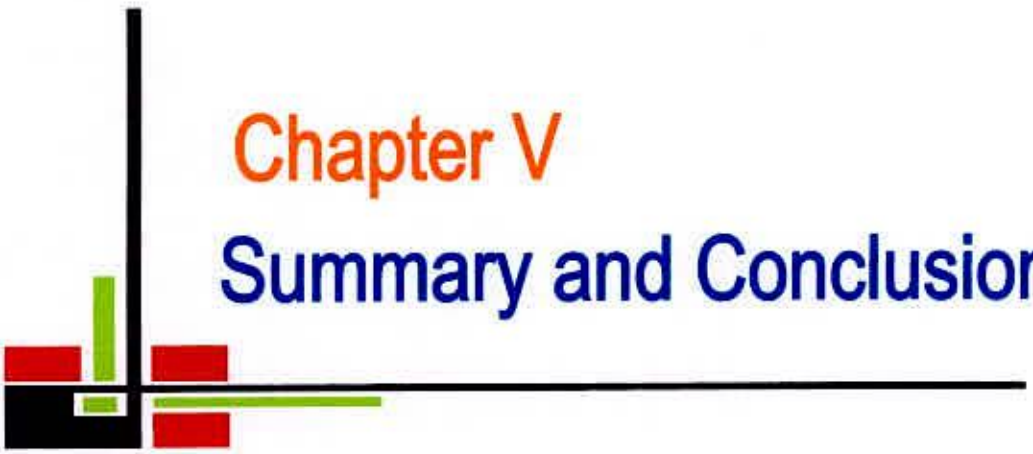
Characters	Vector-1	Vector-2
Days of 50% flowering	-1.817	-0.254
Branches per plant	-6.948	-0.380
Plant height (cm)	-0.257	-0.641
Days to maturity	0.606	4.377
Pods per plant	3.432	-2.523
Seeds per plant	15.291	-5.953
Seeds per pod	25.813	14.344
100 seed weight (g)	19.204	-8.683
Effective node number	-0.281	0.304
Pod length (cm)	-10.741	-7.535
Biological yield (g)	-33.296	-13.247
Harvest index (%)	-27.628	-11.241
Seed yield per plant (g)	19.660	24.151

4.4.6. Comparison of different multivariate techniques

The clustering pattern of D^2 analysis through non-hierarchical clustering had taken care of simultaneous variation in all the characters under study. However, the distribution of genotypes in different clusters of the D^2 analysis had followed more or less similar trend of the Z_1 and Z_2 vector of the principal component analysis. The D^2 and principal component analysis were found to be alternative methods in giving the information regarding the clustering pattern of genotypes. However, the principal component analysis provides the information regarding the contribution of characters, towards divergence of soybean.

4.4.7. Selection of genotypes as parent for hybridization programme

Genotypically distant parents are able to produce higher heterosis. 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 (Falconer, 1960; Moll *et al.*, 1962; Ramanujan *et al.*, 1974; Ghaderi *et al.*, 1984; Major *et al.*, 1996 and Mehetra *et al.*, 2000). Considering the magnitude of cluster mean and agronomic performance the genotype G_{12} (BD-2335) for minimum days to first flowering and maximum harvest index from cluster III; G_{16} (BD-2339) for maximum number of pods per plant, effective nodes number, seed yield per plant and biological yield per plant from cluster I; G_{23} (BARI SOYBEAN-6) for maximum 100 seed weight and from cluster V; G_4 (BD-2337) for maximum pod length from cluster-v were found promising. Therefore considering group distance and other agronomic performance the inter genotypic crosses between G_{12} (BD-2335) and G_{16} (BD-2339); G_{12} (BD-2335) and G_{23} (BARI SOYBEAN-6); G_{12} (BD-2335) and G_4 (BD-2337); G_{16} (BD-2339) and G_{23} (BARI SOYBEAN-6); G_{16} (BD-2339) and G_4 (BD-2337); G_{23} (BARI SOYBEAN-6) and G_4 (BD-2337); may be suggested for future hybridization programme.



Chapter V

Summary and Conclusion

CHAPTERR V

SUMMARY AND CONCLUSION

The experiment was conducted with a view to identify divergent parents for hybridization programme, identify the characters contributing to genetic diversity, asses the magnitude of genetic divergence in genotypes and determine the variability in respect of yield and some yield contributing characters of 25 genotypes of soybean (*Glycine max* L. Merrill) at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, during November 2011 to March 2011. 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 minimum and maximum duration for 50% flowering were required by the genotypes BD-2335 (58.67 days) and BD-2352 (74.00 days), respectively. The maximum plant height (59.33 cm) was recorded by the genotype BD-2328 and the lowest plant height (34.56cm) was recorded by BD-2342. Maximum number of branches per plant was recorded in BD-2336 and BD-2335 genotype showed the minimum number of branches per plant. Maximum number of nodes per plant was recorded in the genotype BD-2339 and minimum days in the genotype BD-2340.

The minimum pod length was recorded by the genotype BD- 2324 and genotype BD-2334 showed the maximum pod length. The line BD-2337 showed the minimum hundred seed weight and the maximum hundred seed weight was recorded in the genotype BANGLADESH SOYBEAN-6. The minimum number of pods per plant was observed in genotype BD-2340 while maximum number of pods per plant was

found in the genotype BD-2339. The genotype BD-2335, BD-2336 had highest number of seeds per pod while it was lowest in the genotype BD-2324. Highest seeds per plant were recorded by the genotype BD-2339 while genotype BARI SOYBEAN-5 showed the lowest seeds per plant. The genotype BD-2341 had highest plant maturity and lowest in the genotype BD-2325, BD-2326. Genotype BD-2324 and BD-2339 were the lowest and the highest for seed yield per plant, respectively.

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

Genetic diversity of 25 soybean genotypes based on thirteen characters were measured through multivariate analysis. The 25 genotypes fell into five distant clusters. The cluster III and V comprised the maximum number (8) of genotypes followed by cluster II (7). The cluster I and IV comprised one genotype. The highest inter-cluster distance (36.93) was between the cluster I and IV and the highest distant genotypes were G_1 (BD-2324) and G_{16} (BD-2339). The lowest inter-cluster distance

(5.78) was observed between the cluster III and V and the lowest distance genotypes were G_6 (BD-2329) and G_{18} (BD-2341).

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. Days to maturity, seeds per pod and seeds yield per plant were the important component characters having higher contribution to the genetic divergence.

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

1. Wide range of genetic diversity existed among the soybean genotypes. Wide genetic diversity was observed in 25 genotypes of soybean, which were grouped into five clusters and most diverse genotypes were G_1 and G_{16}. That variability could be used for future breeding programme of soybean in Bangladesh.

2. High heritability coupled with high genetic advance in percent of mean were observed in pod length and hundred seed weight. Hence, yield improvement in soybean would be achieved though selection of these characters.

3. The genotypes of clusters I were more diversed from the genotypes of cluster IV.

4. Days to maturity, seeds per pod and seeds yield per plant were found responsible for the maximum diversity. On the other hand, days of 50% flowering, branches per plant, plant height (cm), pod length (cm), biological yield (g) and harvest

index have the least responsibility of both the primary and secondary differentiation of genotypes.

5. Further collection of soybean germplasm would be continued for getting more variability and desired traits in soybean.

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

1. Genotypes G_{16} (BD-2339), G_{12} (BD-2335), G_{13} (BD-2336), and G_{14} (BD-2337) could be included in the further study in view of seed yield for releasing as soybean varieties.

2. The maximum variability found for pod length and hundred seed weight. So selection based on these characters could be effective for the improvement of soybean yield.

3. Relatively higher value and lower differences between genotypic co-efficient of variation and phenotypic coefficient of variation of different yield contributing characters were observed which indicates high potentiality to select these traits in future which were less affected by environmental influence.

4. The genotypes of cluster I and IV could be used as parents for future breeding programme to developed soybean variety.

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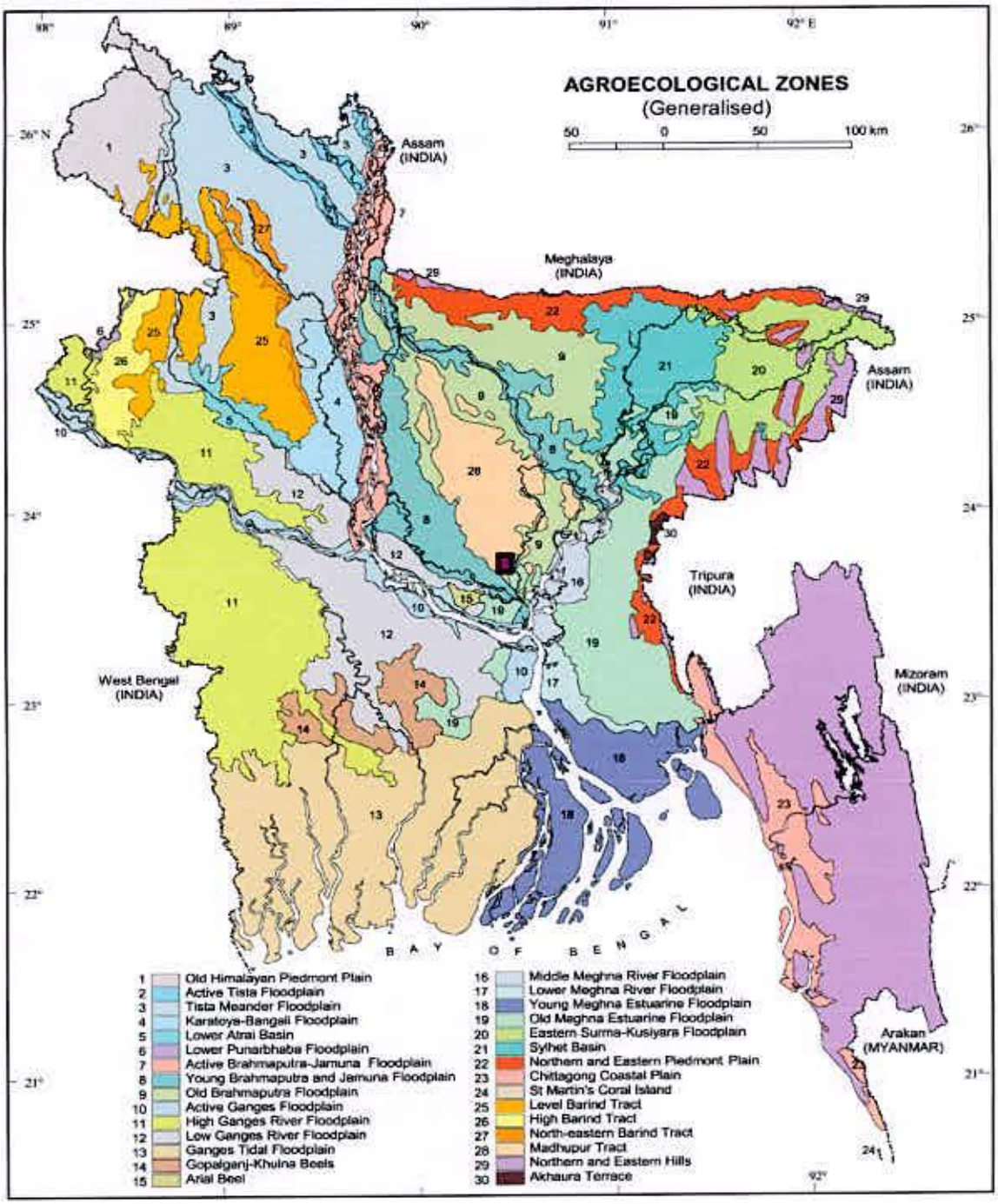
Appendices

APPENDICES

Appendix I. Map showing the experimental site under the study



The experimental site under study

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

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
November, 2011	32.3	16.3	69	0	7.9
December, 2011	29.0	13.0	79	0	3.9
January, 2012	28.1	11.1	72	1	5.7
February, 2012	33.9	12.2	55	1	8.7
March, 2012	34.6	16.5	67	45	7.3

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

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

Soil characteristics	Analytical results
Agrological Zone	Madhupur Tract
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 thirteen different yield and yield contributing characters of soybean

Genotype	D50%F	BP	PH	DM	PP	SPP	SP	HSW	ENN	PL	BY	HI	SYP
1	64.00	2.00	40.89	120.00	28.00	71.44	2.44	45.30	12.44	3.28	42.72	75.84	32.42
2	66.00	3.33	47.22	120.00	29.78	81.00	2.60	52.35	15.44	3.90	52.25	81.15	42.37
3	63.67	3.22	49.33	120.00	29.67	80.56	2.62	55.85	19.33	3.79	57.42	79.51	44.94
4	62.33	3.11	51.78	124.33	34.78	95.44	2.76	76.69	21.00	3.97	79.62	92.69	73.19
5	63.00	3.11	59.33	122.00	43.00	120.44	2.76	76.13	18.44	4.32	108.56	83.38	91.65
6	65.00	2.78	58.44	122.33	21.78	62.89	2.69	64.02	9.22	3.60	59.51	68.71	40.33
7	59.00	3.33	42.78	122.00	27.00	70.00	2.64	77.90	10.78	4.34	62.62	87.42	54.46
8	66.00	2.56	39.00	120.00	37.78	97.89	2.67	76.11	17.11	3.71	83.07	89.93	74.50
9	61.67	2.89	36.33	121.00	40.78	117.00	2.69	50.78	11.56	3.69	73.97	79.90	59.42
10	64.67	2.11	45.89	122.00	31.78	88.00	2.76	76.21	10.00	3.62	80.43	85.88	67.11
11	62.00	2.78	40.78	124.00	28.00	78.56	2.69	55.32	12.00	4.47	55.09	78.49	43.45
12	58.67	1.67	42.78	122.00	30.11	83.78	2.78	62.53	11.67	4.14	56.10	95.00	52.51
13	66.67	4.56	52.22	122.00	46.11	124.89	2.78	62.13	20.00	3.80	91.97	83.43	77.61
14	66.67	3.67	44.89	124.00	79.11	210.11	2.67	35.71	23.56	3.80	92.65	81.31	74.98
15	66.33	3.67	50.44	126.00	42.56	123.89	2.71	51.36	14.11	3.78	76.74	82.27	63.54
16	66.00	3.56	45.00	124.00	88.33	237.78	2.71	67.40	24.44	3.73	178.77	88.95	160.23
17	63.00	2.22	41.22	124.00	21.44	61.78	2.62	86.33	7.44	3.78	70.25	76.69	53.39

Appendix IV: (Cont'd.)

Genotype	D50%F	BP	PH	DM	PP	SPP	SP	HSW	ENN	PL	BY	HI	SYP
18	65.33	3.11	41.67	126.00	23.44	62.78	2.64	62.67	9.67	3.81	59.15	66.98	39.27
19	67.33	3.78	34.56	124.00	34.33	90.22	2.64	67.81	12.11	3.66	71.46	85.68	61.13
20	72.33	2.00	41.89	122.00	41.78	115.11	2.73	53.69	17.56	3.86	78.31	78.37	61.76
21	74.00	2.44	39.22	125.00	48.33	104.44	2.69	63.67	18.11	3.53	80.99	82.04	66.49
22	62.33	3.33	44.11	124.00	22.11	60.00	2.62	66.52	12.56	4.00	52.15	77.00	39.91
23	64.00	3.00	45.56	124.00	24.33	66.56	2.71	88.78	9.78	3.86	71.27	83.66	59.05
24	61.67	3.78	46.11	124.00	48.00	133.00	2.73	45.10	20.33	3.62	70.30	85.49	60.06
25	60.67	2.67	42.56	122.00	29.78	81.22	2.76	71.65	10.56	3.64	77.76	74.75	58.19
Mean	64.49	2.99	44.96	122.83	37.28	100.75	2.68	63.68	14.77	3.83	75.33	81.78	62.08
Min	58.67	1.67	34.56	120.00	21.44	60.00	2.44	35.71	7.44	3.28	42.72	66.98	32.42
Max	74.00	4.56	59.33	126.00	88.33	237.78	2.78	88.78	24.44	4.47	178.77	95.00	160.23

D50%F = Days of 50% flowering, BP = Branches per plant, PH = Plant height, DM = Days to maturity, PP = Pods per plant, SPP = Seeds per plant, SP = Seeds per pod, HSW = 100 seed weight (g), ENN = Effective nodes number, PL = Pod length (cm), BY = Biological yield, HI = Harvest index (%), SYP = Seed yield per plant.

Appendix V. Analysis of variances of thirteen yield and yield related characters of soybean

Source of variation	df	Mean sum of squares												
		D50%F	BP	PH	DM	PP	SPP	SP	HSW	ENN	PL	BY	HI	SYP
Replication	2	4.05*	0.27	8.82*	0.01	3.80	17.94	0.09**	11.81	5.27	0.06	25.77	13.05	19.75
Genotype	24	37.05**	1.39**	109.99**	9.80**	798.74**	5,633.09**	0.01	528.98**	70.54**	0.21**	2,065.77**	131.70**	1,862.13**
Error	48	1.19	0.09	2.64	0.02	3.80	23.12	0.01	4.15	3.90	0.02	8.70	5.45	11.21

Here, * = significant at P < 0.05 level, ** = significant at P < 0.01,df =Degrees of freedom, D50%F = Days of 50% flowering, BP = Branches per plant, PH = Plant height, DM = Days to maturity, PP = Pods per plant, SPP = Seeds per plant, SP = Seeds per pod, HSW = 100 seed weight (g), ENN = Effective nodes number, PL = Pod length (cm), BY = Biological yield, HI = Harvest index (%), SYP = Seed yield per plant.

Appendix VI. Principal component score of twenty five genotypes of soybean

SL. NO.	Z_1	Z_2
G_1	50.25	26.63
G_2	34.24	17.22
G_3	31.34	11.51
G_4	-1.99	-18.32
G_5	-42.48	-28.01
G_6	49.2	-0.96
G_7	35.31	-14.18
G_8	-6.22	-18.1
G_9	-11.68	17.2
G_{10}	7.61	-18.99
G_{11}	35.52	12.49
G_{12}	26.56	4.69
G_{13}	-34.65	-2.6
G_{14}	-108.48	55.69
G_{15}	-20.74	16.3
G_{16}	-202.18	-30.4
G_{17}	41.25	-25.88
G_{18}	49.55	1.53
G_{19}	11.03	-5.06
G_{20}	-13.78	12.12
G_{21}	-10.42	-0.85
G_{22}	54.32	0.11
G_{23}	33.7	-28.5
G_{24}	-25.65	29.52
G_{25}	18.38	-13.17

Appendix VII . Mean performance of different parameters of twenty five genotypes in soybean

Parameters	Minimum	Mean	Maximum
Days to 50% flowering	58.67	64.49	74.00
Branches per plant	1.67	2.99	4.56
Plant height (cm)	34.56	44.96	59.33
Days to maturity	120.00	122.83	126.00
Pods per plant	21.44	37.28	88.33
Seeds per plant	60.00	100.75	237.78
Seeds per pod	2.44	2.68	2.78
100 seed weight (g)	35.71	63.68	88.78
Effective node number	7.44	14.77	24.44
Pod length (cm)	3.28	3.83	4.47
Biological yield (g)	42.72	75.33	178.77
Harvest index (%)	66.98	81.78	95.00
Seed yield per plant (g)	32.42	62.08	160.23