GENETIC VARIABILITY AND CHARACTER ASSOCIATION OF SOYBEAN (*Glycine max* L. Merr.)

MAHMUDUL HASAN

DEPARTMENT OF GENETICS AND PLANT BREEDING
SHER-E-BANGLA AGRICULTURAL UNIVERSITY
DHAKA-1207

DECEMBER, 2018

GENETIC VARIABILITY AND CHARACTER ASSOCIATION OF SOYBEAN (*Glycine max* L. Merr.)

BY

MAHMUDUL HASAN

REG. NO. : 12-04793

A Thesis
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 (MS)

IN

GENETICS AND PLANT BREEDING

SEMESTER: JULY-DECEMBER, 2018

Approved by:

Prof. Dr. Naheed Zeba	**Prof. Dr. Mohammad Saiful Islam**
Supervisor	**Co-Supervisor**

Prof. Dr. Jamilur Rahman
Chairman
Examination Committee

Prof. Dr. Naheed Zeba
Department of Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Dhaka-1207, Bangladesh
Phone: +8802-9180921-167 (Office), +8802-9140770 (Res.)

CERTIFICATE

This is to certify that the thesis entitled, "**Genetic Variability and Character Association of Soybean (*Glycine max* L. Merr)**" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING**, embodies the result of a piece of bona fide research work carried out by **MAHMUDUL HASAN**, Registration number: **12-04793** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: December, 2018
Dhaka, Bangladesh

(Prof. Dr. Naheed Zeba)

Supervisor

DEDICATED TO
MY
BELOVED PARENTS

ACKNOWLEDGEMENTS

At first the author expresses his profound gratitude to Almighty Allah for his never-ending blessing to complete this work successfully. It is a great pleasure to express his reflective gratitude to his respected parents, who entiled much hardship inspiring for prosecuting his studies, thereby receiving proper education.

The author would like to express his earnest respect, sincere appreciation and enormous thankfulness to his reverend Supervisor, Prof. Dr. Naheed Zeba, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, for her scholastic supervision, continuous encouragement, constructive suggestion and unvarying inspiration throughout the research work and for taking immense care in preparing this manuscript.

The author also expresses his gratefulness to his respected Co-Supervisor Prof. Dr. Mohammad Saiful Islam, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for his scholastic guidance, helpful comments and constant inspiration, inestimatable help, valuable suggestions throughout the research work and in preparation of the thesis.

The author expresses his sincere gratitude towards the sincerity of Prof. Dr. Jamilur Rahman, Chairman, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for his valuable suggestions and cooperation during the study period. The author also expresses heartfelt thanks to Prof. Dr. Md. Shahidur Rashid Bhuiyan, Prof. Dr. Md. Sarowar Hossain, Prof. Dr. Firoz Mahmud, Prof. Dr. Md. Ashaduzzaman Siddikee, Department of Genetics and Plant Breeding, SAU, for their valuable suggestions, instructions, cordial help and encouragement during the period of the study.

The author feels proud to express his heartiest sence of gratitude, sincere appreciation and immense indebtedness to Prof. Dr. Kamal Uddin Ahamed, Vice

Chancellor, Sher-e-Bangla Agricultural University (SAU), Dhaka, for his continuous scholastic and intellectual guidance and cooperation.

The author expresses his sincere appreciation to Tanjina Rahman, Nabila Narsis, Abu Bakar Siddique, Asmaul Husna and Munni Akhtar for their inspiration, help and encouragement throughout the study period.

The author is thankful to all of the academic officers and staff of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, for their continuous cooperation throughout the study period.

The author feels proud of expressing his sincere appreciation and gratitude to the Ministry of Science and Technology, Peoples Republic of Bangladesh for selecting him National Science and Technology (NST) fellow and providing adequate funding.

The author expresses his sincere appreciation to his brother, sisters, relatives, well wishers and friends for their inspiration, help and encouragement throughout the study period.

The author expresses his immense gratefulness to all of them who assisted and inspired him to achieve higher education and regret for his inability for not to mention every one by name.

The Author

TABLE OF CONTENTS

TABLE OF CONTENTS (Cont'd)

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

Some commonly used abbreviations

Full Word	Abbreviation
Agricultural	*Agril.*
Agro-Ecological Zone	AEZ
and others	*et al.*
and others (at elli)	*et al.*
Bangladesh Bureau of Statistics	BBS
Biology	*Biol.*
Biotechnology	*Biotechnol.*
Botany	*Bot.*
Centimeter	cm
Cultivar	cv.
Date After Seeding	DAS
Degree Celsius	^{0}C
Etcetera	Etc
Etcetera	etc.
exempli gratia (for example)	e.g.
Food and Agriculture Organization	FAO
Gram per liter	g/L
Hectare	ha
International	*Intl.*
Journal	*J.*
Muriate of Potash	MP
Newsletter	*Newsl.*
Pages	pp.
Physiology	*Physiol.*
Randomized Complete Block Design	RCBD
Research	*Res.*
Science	*Sci.*
Sher-e-Bangla Agricultural University	SAU
Species (Plural)	spp.
Square meter	m^2

GENETIC VARIABILITY AND CHARACTER ASSOCIATION OF SOYBEAN (*Glycine max* L. Merr.)

ABSTRACT

The present research work was conducted to study the genetic diversity analysis of soybean during the period from December 2017 to May 2018 in rabi season in the experimental field of Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka. In this experiment, 22 soybean genotypes were used as experimental materials. Mean performance, variability, correlation, path analysis and genetic diversity analysis on different yield attributes and yield of soybean genotypes was estimated. Analysis of variance for each trait showed significant differences among the genotypes except pod wide, seed per pod, seed yield per plot and seed yield per hectare. In correlation study, highly significant positive association was recorded for seed yield of soybean genotypes with first flowering, days to 50% flowering, days to physiological, days to harvest maturity, plant height, number of branch per plant, number of pod per plant, seed yield per plant and yield per plot. Path coefficient analysis evidenced that 50% flowering, day to physiological maturity, plant height, number of branch per plant, pod per plant, 100 seed weight and yield per plot had the positive direct effect on yield per plant. Therefore, importance has to be given for these characters in the further breeding program to improve soybean yield. Multivariate analysis based on fifteen characters of twenty-two soybean genotypes was divided into three distant clusters. The maximum contribution of traits towards diversity was observed by first flowering, days to 50% flowering, days to physical maturity, days to harvest maturity, plant height, number of main branches per plant and pod length. As a result, these traits could be emphasized during the selection of parents for hybridization. The highest inter-cluster distance was observed between cluster I and II and the maximum intra cluster distance was found in cluster I. Considering group distance and other agro-morphogenic performance, genotypes G2 (GM0009) and G13 (GM0014) found the potential for future hybridization program in the response of increase soybean yield.

CHAPTER I

INTRODUCTION

Among the all oilseeds soybean is an important oilseed and first ranks in the world. The cultivated soybean belongs to the family Leguminosae under sub-family papilionaceae and genus *Glycine* comprises 1200 species. It is a self-pollinated crop and selfing >99% (Juan *et al.*, 2010). The cultivated species of soybean is *Glycine max* L. Merr. and the total number of chromosome 2n=2x=40 (Kawakami, 1930; Karpechenko, 1925). The form and structure of a soybean plant vastly vary (Sing, 2010) and height varying from one to six feet (Cooper, 1975). The plants are erect, bushy, herbaceous and annual growth habit.

Soybean contains 40-42% protein and 20-22% of edible oil (Gopalan *et al.*, 1994). The edible oil in soybean is approximately 85 percent unsaturated and contains the essential fatty acids. The balanced combination of protein, oil and carbohydrate of soybean products serve as a valuable food, feed and bio-feedstocks besides nutritional quality. Regularly eating soy-based foods lowers cholesterol, calms hot flashes, prevents breast and prostate cancer, aids weight loss, and wards off osteoporosis. Therefore the quality of soy protein is now recognized as being similar to that of meat protein. It is also a good source of minerals like Ca & P and vitamins namely A, B, C & D (Antalina, 1999). When Soybean is grown solely and/or in combination with other crops, it has great importance to improve the soil nutrient status and farming system (Agdew and Getnet, 2006).

This crop is called as “Golden Bean” or “Miracle Crop” of the 20th century, because of its versatile uses like; soya-dhal, soya-chatni, soya-curd, soya khichuri, soya-milk, soya-meat, soya flour, tofu, roasted soybean snack and multiple nutritional qualities. Due to its both qualities *viz.* high protein and oil content, soybean is considered as a wonder crop. Soybean is also recognized for its benefits to human health such as the cholesterol-lowering effect of protein.

Soybean (*Glycine max* L. Merr.) is reported to have originated in China (Nagata, 1960; Vavilov, 1951). The first half of the 20th century, China was the largest soybean producer and exporter country. Soybean cultivation developed rapidly in the USA after the 1950s and now the USA is the largest soybean producing country in the world followed by Brazil & Argentina. According to the World Agricultural Supply and Demand Estimates (WASDE) report 2017-2018, the global production of soybeans is forecast to be 337 million metric tons among them the United States is projected to produce 124.8 million metric tons of soybeans.

The cultivation of soybean in Bangladesh doesn't expand satisfactorily. According to the Bangladesh Bureau of Statistics (BBS) report, 2016-2017 areas being utilized under soybean cultivation was 155351 acres and total production was 96921 metric tons. The major soybean producing districts in Bangladesh is Noakhali. Laksmipur, Chittagong, Chandpur, Barisal and Bhola.

The soybean is a day length sensitive crop. Their yield is good enough where the length of the day is less than 14 hours. The temperature ranging from 25 to 30°C is considered favorable for most of the soybean varieties. It requires a minimum 15°C soil temperature for rapid germination and growth. The minimum temperature for effective growth of the soybean crop is 10°C. The crop is well adapted to areas with the altitude ranging from 1200 to 1800 above sea level and an annual average rainfall ranging from 450 to 1500 mm. Broad range of well-drained soil types is considered for soybean cultivation and loamy soil is ideal for soybean production. It can be grown between the p^H of 5.5 to 6.5.

Analysis of genetic diversity is the first and foremost step for any crop improvement programmed. Information on genetic diversity among genotypes has several important applications for crop improvement. Genetic diversity is important for the improvement of the crop has been stressed on both self and cross-pollinated crop (Gaur *et al.,* 1978; Murty and Anand, 1966; Griffing and Lindstrom, 1954). Genetic diversity as a main component that ascertains yield security in future (Batugal, 1999). Evaluation of genetic diversity is important to know the sources of genes for a particular trait within the available germplasm (Tomooka, 1991). Moreover, the quantification of genetic diversity through biometrical procedures has made it possible to choose genetically diverse parents for a successful hybridization program (Anderson, 1957; Rao, 1952).

Nogueira *et al.,* (2012) analyzing the correlations and path analysis over two sowing seasons in 90 soybean genotypes and concluded that the total number of pods per plant and number of nodes of the main stem could be used as an indirect selection basis for soybean grain yield. Scientists used path analysis in soybean, which partitions the genotypic correlations into direct and indirect effects of the traits (Iqbal *et al*., 2003; Board *et al*., 1999; Shukla *et al*., 1998; Taware *et al.,* 1997; Board *et al*., 1997; Akhter and Sneller, 1996; Shivashankar and Viswanatha, 1989) whereas, Ghafoor *et al*., (2003); Yadev *et al*., (2001) and Gafoor *et al*., (1990) have mentioned the worth of this technique in other legumes also. Path coefficients have been used in soybean for diverse type of studies, among them, yield components on different sowing types in soybean (Pandey and Torrie, 1973), identify indirect selection criteria in late sowings (Board *et al.,* 1997), weed interference with plant growth (Jordan, 1992), relationship between pod dehiscence with other agronomical characters (Tiwari and Bhatnagar, 1991), effect of the environment over yield (Board *et al.,* 1999), the effect of population density on yield (Ball *et al.,* 2001), yield components on soybean hybrids (Taware *et al.,* 1997), yield component between genotypes (Shukla *et al.,* 1998), varietal differences, yield components, oil and protein (Malik *et al.,* 2006a), genetic diversity to improve grain yield (Malik *et al.,* 2006b).

Yield is a complex entity and high yield is the major objectives in all breeding programs. It is a polygenic trait and influenced by many genetic factors as well as abiotic and biotic factors. Hence, direct and indirect selections are important to get a better yield. Therefore the direct selection for yield could be very difficult. A study of the correlation between different quantitative characters provides an idea of association that could be effectively exploited to formulate selection strategies for improving yield components. However, when more characters are involved in correlation study it becomes difficult to ascertain the traits which really contribute towards the yield. The path analysis under such a situation helps to determine the direct and indirect contribution of these traits towards the yield.

Keeping in view of the above facts the present investigations is being directed to screen out high seed yielding genotypes from the advance generation of soybean with the following objectives:

1) To assess the amount of genetic variability present among advance genotypes of soybean,
2) To estimate the genetic diversity among soybean genotypes and
3) To study the correlation and path coefficient analysis for seed yield and different yield contributing characters.

CHAPTER II

REVIEW OF LITERATURE

Soybean is one of the major important protein and oil 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 variability, divergence analysis using agro-morphogenic characters among different soybean genotypes. In this chapter, an attempt has been made to briefly review the work related to the present study.

2.1 Nomenclature of soybean

In 1914 the American Piper argued at length that, under American botanical rules, the soybean should be called *Soja max* (L.) Piper. (The L. stands for Linnaeus, who first identified the species). This name was used in the US until 1948. In 1917 the American Elmer Drew Merrill (1876-1956), later Dean of the University of California College of Agriculture, Berkeley campus, argued convincingly that according to International botanical rules, the correct botanical name of the soybean should be *Glycine max* (L.) Merrill. (Annonymous, 2015).

2.2 Variability, heritability and genetic advance

The success of crop breeding programs largely depends on the presence of the genetic variation and the inheritance of traits of interest. The importance of genetic variation assists the breeder to decide the proper strategy and selection criteria to be followed for improvement of the target traits. In addition, the correlation between seed yield and quality characters as well as oil content is of major interest. A critical review of genetic variability is, therefore, a prerequisite for planning and evaluation of a breeding program.

Barros *et al.* (2015) conducted a research on 11 progenies of soybean in an F3 generation in a randomized block design with six replications to estimate the expected gain from selection. It was concluded that there is genetic variability for the productivity among evaluated progenies and also to issuing capability of lateral branches in soybean, however, the selection seeking to intensify or reduce this characteristic does not imply achievement of productivity gains.

Nooghab *et al.* (2014) planted a local check and 14 soybean genotypes variety in a randomized complete block design with three replications to study of genetic diversity for yield and its components with three replications in 2013. Different traits such as plant height (cm), number of secondary stems, number of pods in secondary stems, number of pods in main stem, number of grain per plant, 100-grain weight (g), pod length (cm), yield per plant (g) and yield (kg/ha) were investigated. Results of analysis of variance showed a significant difference for the traits except for number of secondary stems. The highest CV was for yield per plant, number of the pod in secondary stems, the height of the first secondary stem and 100-grain weight which are respectively 29.64, 28.99, 27.45 and 26.79. The lowest CV was for a number of secondary stems and plant height that are respectively 14.37, 14.78 and 15.46. Kao-Hsiung-10 and Emperor genotypes had the lowest (2060 kg/ha) and highest (5113 kg/ha) yield respectively.

Kumar *et al.* (2014) forty soybean genotypes were evaluated for agro-morphological traits and genetic parameters. Mean performance and analysis of variance for yield and its components revealed significant differences among all the genotypes for all the characters. The correlation was also found significant with yield and its component traits.

Swapnil *et al.* (2014) conducted an experiment during Kharif 2011 in 12 soybean genotypes. The data were recorded for 13 yield component traits to heritability, study genetic variability and genetic advance analysis. Analysis of variance among 12 genotypes showed highly significant differences for all the characters except the number of grain per plant indicated the presence of a substantial amount of genetic variability. High genetic advance percent of mean in 13 yield component traits was observed for number of pod per plant, seed yield per plant and seed yield per hectare.

Ghodrati (2013) evaluated 12 soybean genotypes for phenotypic correlations, genotypic variation and broad sense heritability for seed yield and some quality properties during three growing seasons. Results showed significant differences for quality characters and seed yield which suggest sufficient genetic variation for efficient selection. High broad sense heritability (81%, 76%, 74%) and genetic advance (0.35, 0.20, 0.40) were obtained for the number of nodes plant^{-1}, days to flowering and plant height respectively.

Chandel *et al.* (2013) conducted an experiment to estimate the genetic variability in 70 diverse soybean genotypes. The variability parameters like mean, range of variation, the phenotypic and genotypic coefficient of variation, heritability in a broad sense and genetic advance were estimated for 15 different characters. Analysis of variance revealed that mean squares due to genotype were found significant for all the traits under study except oil content, indicated that enormous phenotypic variability was present among the genetic materials studied. The highest genotypic coefficient of variation was observed for a number of pods per plant followed by the number of primary branches per plant and the number of clusters per plant. The magnitude of heritability was observed to be high for plant height, number of primary branches per plant, number of pods per plant, number of clusters per plant, seed yield per plant, number of seeds per pod, biological yield per plant and harvest index. A number of primary branches per plant and number of pods per plant noted high genetic advance.

Hossain *et al.* (2013) investigated 56 genotypes of yard long bean through 20 agro-morphogenic characters. Analysis of variance revealed that significant differences present for each character among all 56 genotypes. A quantitative study was done by Patil *et al.* (2011) by Mahalanobis D^2 statistics to assess genetic diversity for 11 characters of soybean. The studies included 36 genotypes of soybean obtained from different eco-geographical regions of India, which showed that there was a substantial genetic diversity between the genotypes with D^2 values ranging from 33.64 to 379.08. Another study was carried out by Iqbal *et al.* (2010) in the National Agriculture Research Centre, Islamabad during autumn 2004 and 2005 to determine the variability and association among 9 traits in 139 soybean genotypes. The traits *viz.* plant height at maturity, days to maturity, number of branches per plant, oil content, number of pods per plant, 100-seed weight (g), grain yield per plant (g), biological yield per plant (g) and harvest index were studied. Results of analysis of variance showed significant differences among genotypes in terms of traits under study, which indicate the existence of genetic variation.

Arshad *et al.* (2006) evaluated 30 genotypes of soybean for days to flowering, days to maturity, number of branches, pod length, number of filled, unfilled pods and total pods, 100 seed weight and seed yield. Analysis of variance and mean performance for yield and its components revealed significant differences among all the genotypes for all the characters. Another experiment was carried out by Bangar *et al.* (2003) and revealed that phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV). The GCV and PCV estimates were highest for plant height and branch number per plant 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 PCV and GCV magnitudes were very high for a number of pod per plant and 1000-seed weight.

Chamundeswari and Aher (2003) conducted an experiment with 90 genotypes of soybean and they observed days to maturity, plant height at maturity, number of clusters 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 a number of pods per plant and plant height and biological yield per plant. Similarly, Agarwal *et al.* (2001) studied genetic variability 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 a percentage of the mean was 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 genetic advance as a percentage of the mean were noticed for plant height, pods per plant and seed yield. In parallel Mehetre *et al.* (2000) studied variability for 11 characters with 60 diverse genotypes of soybean. They reported that pods per plant and seed yield per plant had high phenotypic and genotypic coefficient of variation. They also reported that pods per plant and plant height had high genotypic and phenotypic coefficient of variation and high heritability associated with high genetic advance as a percentage of the mean.

Sing *et al.* (2000) reported that the genotypic coefficient of variation and phenotypic coefficient of variation was comparatively high for pods per plant, plant height and seed yield per plant. Pods per plant, plant height and seed yield per plant showed high heritability with high genetic advance as a percentage of the mean. Similarly, Bandarkar (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 the mean for plant height and days to maturity.

Archana *et al.* (1999) reported that plant height and 100-seed weight had a high genotypic coefficient of variation and high heritability accompanied with the high genetic advance percent of mean soybean. Another experiment conducted by Nehru *et al.* (1999) to estimate genetic advance and heritability for 16 yield and quality components in 49 genotypes of soybean and found days to maturity and 100 seed weight had high heritability but low genetic advance. Mehetre *et al.* (1998) reported that the genotypic coefficient 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. In a different experiment, Shrivastava and Shukla (1998) revealed a significant amount of variability for plant height, pods per plant and seed yield per plant in soybean. These characters had high heritability coupled with high expected genetic advance. In a different study, Mehetre *et al.* (1997) estimated high heritability accompanied by the high genotypic coefficient of variation for pod 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 a high genotypic coefficient of variation and heritability in vegetable soybean. Similarly, Major *et al.* (1996) observed high phenotypic and genotypic coefficient of variation for 100-seed weight and grin yield in soybean. They also observed plant height and grain yield per plant showed high genetic advance. In a different experiment, Rajarthinam *et al.* (1996) estimated genetic variability, heritability and genetic advance. They reported that high heritability and genetic advance were for plant height, 100 seed weight, pod per plant and seed yield per plant.

Dobhal and Gautam (1995) observed a wide range of variability for plant height, days to maturity, pod per plant, yield per plant in soybean germplasm and high broad sense heritability coupled with high genetic advance were observed for plant height, pods per plant and yield per plant. Similarly, Sing *et al.* (1995) observed pods per plant and yield per plant showed the maximum genotypic coefficient of variation in soybean. Pods per plant also showed the highest heritability.

Jagatap and Mehetre (1994) revealed that plant height and number of pods per plant showed the highest genotypic coefficient of variation in soybean. In another experiment conducted by Jangale *et al.* (1994) observed high heritability for 50% flowering, days to maturity, pods per plant and seeds per pod. On the other hand, Mahajan *et al.* (1994) reported that pods per plant and yield per plant showed the high genotypic coefficient of variation in soybean. High heritability was recorded for pods per plant. Similarly, Malhotra (1973) observed that seed yield had the highest coefficient of genetic variation and predicted genetic advance as a percentage of mean in soybean.

2.3 Correlation co-efficient

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

Kumar *et al.* (2014) conducted a research with 40 genotypes of soybean and reported that correlation was found significant with yield and its component traits. An analysis indicated that hundred seed weight had the highest effect on yield. In a different experiment, conducted by Ghodrati (2013) with 12 soybean genotypes and observed that there is a strong positive correlation (r = 0.61*) between seed yield and plant height. An increase in plant height leads to an increase in the number of nodes per plant, number of seeds per pod, number of pods per plant, number of seeds per plant and protein yield. It is, therefore, concluded that simultaneous selection for improving seed yield through increasing the number of pods per plant, number of nodes per plant and plant height would be an effective approach to increase seed yield as well as protein yield.

Iqbal *et al.* (2010) studied 139 genotypes of soybean and concluded that grain yield was positively and significantly correlated with all studied traits except plant height, which showed non-significant association during both years. Oil content showed significant and positive correlation with grain yield, 100-seed weight, and harvest index while significantly negative correlation was observed with days to maturity, plant height and number of branches per plant. Significantly positive correlations were observed for days to maturity and number of branches per plant; the number of pods per plant and biological yield per plant and harvest index; the number of branches per plant and number of pods per plant; 100-seed weight and oil content; harvest index and 100-seed weight and biological yield per plant. Results obtained from this study can make a better choice for soybean breeders for selecting genotypes among a large number of accessions.

Inderjit *et al.* (2007) conducted an association study which indicated that days to 50% flowering, pods per plant, cluster per plant and seeds per pod were significantly correlated with grain yield. In another research, Arshad *et al.* (2006) estimated that seed weight had a positive correlation with filled, unfilled and total pods. Grain yield had a positive and significant correlation with all the characters except days to flowering and seed yield per 5 plants. Moreover, it had a significant but negative correlation with days to maturity and also negatively correlated with un-filled pods. Days to maturity, number of branches, pod length, number of pods and 100 seed weight had positive direct effects on grain yield. High indirect effect was also exhibited via pod length by most of the traits hence these characters may be given more emphasis while selecting high yield soybean lines.

Avc and Ceyhan (2006) showed in a correlation study that the pod yield was significantly and positively correlated with pods per plant and 100 seed weight. In another study, Singh and Singh (2006) revealed that seed yield per plant had a significant and positive association with a number of pods per plant, plant height, harvest index and a number of grains per pod.

Chamundeswari and Aher (2003) studied with 90 genotypes of soybean and concluded that seed yield is positively correlated with the number of pods per cluster, number of pods per plant and biological yield per plant. A character association study was done by Sharma *et al.* (2003) in soybean and indicated that positive and significant association of seed yield per plant with biological yield per plant, pods per plant and pod length. The significant negative correlation of harvest index was observed with plant height. It can be predicted that selection for pods per plant, pod length and biological yield per plant would improve seed yield per plant. Recombination breeding may be suggested for the simultaneous improvement of biological yield per plant and harvest index.

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 phenotypic level. The number of days to 50% flowering was positively and significantly correlated with days to maturity but negatively with a number of seeds per pod and 100-grain weight at the genotypic level. Days to maturity were significantly correlated with plant height and days to 50% flowering at the phenotypic levels.

Onemli (2003) reported that the number of pods positively correlated with plant height, number of branches, pod length, number of pods per plant and 1000-seed weight, but was negatively correlated and significant correlations with the number of seeds per pod, seed length and pod length in soybean. A number of pods and 1000-seed had a negative effect on soybean yield via the number of pods. The genotypic correlation coefficients were higher than the phenotypic correlation coefficients. Pod yield per plant showed positive phenotypic correlation with pod length, number grains per pod, number of pods per plant and shelling percentage described by Chaudhury and Sharma (2003). In another experiment, Tiwari *et al.* (2001) revealed that seed yield exhibited a significant and positive correlation with plant height, number of pods per plant, 1000 seed weight, and number of grains per pod and harvest index.

Sing *et al.* (2000) reported that leaf area had positive direct effect on biological yield but it showed negative effect on seed yield in soybean. In another study, Rajanna *et al.* (2000) estimated a significant and positive correlation of number 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 an 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, number of branches and pods per plant in terms of genotypic and phenotypic correlation coefficients. No correlation between 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.

Dogney *et al.* (1998) investigated that number of seeds per pod and 100 seed weight had a high positive direct effect on yield in soybean. Number of seeds per pod, days to maturity had medium to the low direct effect on seed yield. In a different study, Saurabh *et al.* (1998) estimated significant and positive correlations between plant height and pods per plant in soybean. Another experiment was conducted by Sridhara *et al.* (1998) and they reported that number of pods per plant and number of seeds per plant directly contributed the most to yield in soybean. Plant height, pod length, seed number and number of branches through number of pods per plant seemed to be significant contributors to seed yield. Significant positive correlations of seed yield with plant height, pod length, number of pods per plant and straw yield per plant were reported by Devendra *et al.* (1998). In a different study, Peluzio *et al.* (1998) revealed that the negative correlation between days to maturity and pods per plant in soybean. In a different study, 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 Thamuraj (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. Another study was conducted by Mehetre *et al.* (1997) 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.

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 100 seed weight had high direct and positive effects on grain yield. In a different study, Rahman *et al.* (1996) revealed a significant and positive correlation between pods per plant and 100 seed weight with seed yield in soybean. Plant height and days to maturity sowed 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.

Rajarthinam *et al.* (1996) found that seed yield was significantly correlated with plant height, pod number and number of primary branches per plant in soybean. In another study, 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 significantly and positively associated with pods per plant and days to maturity both at genotypic and phenotypic levels in soybean. Path analysis revealed that pod per plant was the strongest forces influencing yield. Another study was conducted by Saad (1995) and he observed that the path analysis showed direct contribution of yield components to seed yield for cultivars was in the descending order of pods per plant, number of seeds per pod, 100 seed weight 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 the main stem among these high yielding genotypes. In a different study, Jadhav *et al.* (1995) observed that number of branches per plant, pods per plant, seeds per plant, pod length and pod weight per plant were positively and highly significantly correlated with seed yield in soybean. Yield is highly 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. Another experiment was carried out by Singh *et al.* (1994) and they 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.

Mahajan *et al.* (1994) informed that grain yield per plant was positively correlated with eight characters in 51 soybean genotypes grown in India during the Kharif of 1990. Seed yield was correlated with (r=o.75) with branches per plant (0.52), days to 50% flowering (0.48), maturity (0.47) and plant height. In a different study, Das *et al.* (1984) reported that 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.

Juneje and Sharma (1971) observed that seed yield was positively correlated with number of branches and pods per plant, days to flowering and days to pod formation.

2.4 Path coefficient

Presuming yield is a contribution of several characters which are correlated among themselves and to the yield, path coefficient analysis was developed (Dewey and Lu, 1959; Wright, 1921). Unlike the correlation coefficient which measures the extent of the relationship, path coefficient measures the magnitude of the direct and indirect contribution of component characters to a complex character and it has been defined as a standardized regression coefficient which splits the correlation coefficient into direct and indirect effects.

Inderjit *et al.* (2007) reported that pods per plant, seeds per pod, 100 seed weight and days to maturity had direct positive effect on grain yield, while plant_height, pods per cluster and pod length had negative direct effect on grain yield. In another experiment, the results of path analysis revealed that direct effects were highest for number of pods per plant, node at which first fertile pod develops, number of seeds per pod and pod length which can serve as reliable for selection (Harpreet *et al.,* 2007).

Avc and Ceyhan (2006) found the highest direct effect was exhibited by pods per plant, indirect effects, especially through the seeds per pod in pea. A different study was conducted by Arshad *et al.* (2006) and they reported that days to maturity, branches, pod length and 100 seed weight had positive direct effects on grain yield. High indirect effect was also exhibited via pod length by most of the traits hence these characters may be given more emphasis while selecting high yield soybean lines. In a different study, Singh and Singh (2006) showed that pods per plant, 100 seed weight, seeds per pod and days to maturity had positive direct effect on grain yield.

Shrivastava *et al.* (2001) 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. On the other hand, plant height had a negative effect on yield. In a different study, Khan *et al.* (2000) observed correlation among yield components in 86 diverse maturity genotypes of soybean. Path coefficient analysis revealed that pods per plant had the direct effect on seed yield followed by 100 seed weight. Pods per plant affected seed yield negatively via indirect effects of pod height, plant height and seed per pod.

Path coefficient analysis done by Mohan *et al.* (2005) revealed that number of pods per plant and shelling percentage had the maximum direct effect on green pod yield. Thus, due importance should be given to these characters for the improvement of yield. In an experiment in India, 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 phenotypic levels. The number of days to 50% flowering was positively and significantly correlated with days to maturity but negative with number of seeds per pod and 100-grain weight at the genotypic level. Path coefficient estimates showed that the number of grin per pod, days to maturity, number of pods per plant and plant height positively affected grain yield.

Rajanna *et al.* (2000) estimated significant and positive correlation of number of pods per plant, number of cluster per plant and 100 seed weight with seed yield in soybean. Days to maturity, plant height and number of branches per plant exhibited correlation with number pods per plant and number of cluster per plant. Path analysis indicated an effect on seed yield per plant and number of pods per plant. Another experiment was conducted by Mehetre *et al.* (1997) with 4 soybean genotypes and they observed yield per plants 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 highest positive direct effect followed by a contribution of 100 seed weight, number of pods per plant. The highest indirect positive effect was found for number of pods per plant.

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

Dobhal and Gautam (1995) showed that yield per plant was positively and significantly associated with pods per plant and days to maturity at both genotypic and phenotypic levels in soybean. Path analysis revealed that pod per plant was the strongest forces influencing yield. Another experiment was conducted by Saad (1995) and he observed that path analysis showed direct contribution of yield components to seed yield for cultivars was in the descending order number of pods per plant, 100 seed weight, number of seeds per pod and plant height, while highest indirect effects were exerted by number of seeds per pod via number of pods per plant in soybean.

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

2.5 Genetic divergence using agro-morphogenic traits among soybean germplasm

Genetic diversity analysis is used to identify specific parents for realizing heterosis and recombination in breeding program. Several workers have followed the technique of Mhalanobis's 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 (1966). Of them, Mahalanobis D^2 statistics was extensively used by the researchers. The Mahalanobis technique has been followed by several workers on a wide range of crop species.

Kumar *et al.* (2014) conducted a research with 40 genotypes of soybean to understand the extent of genetic diversity. A Cluster diagram based on agro-morphological traits proposed two major clusters A and B. The data revealed that four principal components having greater than one eigenvalue contributed 76.2 % of the total variation among forty genotypes of soybean. The traits, which contributed more positively to PC1 were total pods per plant (0.430), days to maturity (0.418) and filled pod per plant (0.411). Fertility percentage (0.577), hundred seed weight (0.361) and yield per ha (0.350) contributed more positively to PC2. Number of branches per plant (0.635) and five pod length (0.644) contributed more to PC3 and PC4 respectively.

Nooghab *et al.* (2014) studied with 14 genotypes of soybean genotypes. The genotypes have been divided into five groups based on morphologic traits including seeds weight per plant (g), pods length (cm), the weight of 100 seeds (g) and yield (kg/ha). In another study, Hossain *et al.* (2013) investigated 56 genotypes of yard long bean through 20 agro-morphogenic characters. Mahalanobis D^2 analysis established the presence of wide genetic diversity among the genotypes through the formation of nine clusters. Genotypes of different sources fell into the same cluster, indicating that genetic diversity was not concurrent with geographical diversity. They suggested genotypes of cluster I and IX would produce progeny which may show homeostasis over changing environments and hybridization between the genotypes of cluster V could be used to increase the number of pods per plant. The character, 100 seed weight, contributed least (0.19%) and the contribution offered by yield per plant was also minimum (0.51%) to total divergence.

Patil *et al.* (2011) worked out by Mahalanobis D^2 with 36 genotypes for 11 characters to assess genetic diversity. Thirty-six genotypes were grouped into six clusters. The clustering pattern revealed that genetic diversity was not necessarily associated with geographical diversity in this crop. The hybridization program has been suggested on the basis of inter-cluster divergence and cluster means for the character study. To study genetic diversity and association between yield and its components 120 genotypes were evaluated for 10 characters. The study indicated the presence of considerable genetic divergence among the genotypes. The genotypes were grouped into six clusters. To get the desirable segregants the hybridization among the genotypes of cluster III and IV, cluster V and VI and cluster I and VI as the inter-cluster distance was greater between these clusters (Inderjit *et al.*, 2007).

Singh *et al.* (2010) evaluated 120 genotypes for 10 characters to study genetic diversity and association between yield and its components. The study indicated presence of considerable genetic divergence among the genotypes. The genotypes were grouped into six clusters. To get the desirable segregants the hybridization among the genotypes of cluster III and VI, cluster V and VI and cluster I and VI as the inter-cluster distance was greater between these clusters. Another study was conducted by Arshad *et al.* (2006) and they evaluated genetic diversity in 33 soybean genotypes. Cluster diagram based on Euclidean dissimilarity revealed three clusters at 50% linkage distance, cluster I consisted 14 genotypes, cluster II 8 and cluster III 11 genotypes. The accessions in the cluster III were of short duration and high yielding having high seed weight.

Sihag *et al.* (2004) studied genetic diversity among 160 soybean genotypes using Mahalanobis 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. In another experiment, Vart *et al.* (2002) estimated genetic diversity in 56 genotypes of soybean by using D^2 statistic and grouped them into 11 clusters. The clustering pattern was not significantly influenced by the eco-geographical distribution of genotypes. In a different study, Das *et al.* (2000) stated that, genetic divergence of 65 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. The variance of cluster means revealed that pods per plant and plant height had the maximum contribution towards divergence.

Shrivastava *et al.* (2001) studied the divergence among 50 soybean genotypes for nine yield component characters and the genotypes were grouped into five clusters, based on D^2 values. In another study, Chowdhury *et al.* (1998) assessed genetic diversity among 55 soybeans using Mahalanobis D^2 technique. The genotypes fell in 7 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 observed between the clusters indicates highly divergent types existed in these clusters.

Praneetha and Thamuraj (1997) observed that 15 and 22 genotypes of soybean were grouped into 6 and 3 clusters respectively on the basis of D^2 analysis of 14 clusters. In another study, Dobhal (1995) observed significant variability among 65 genotypes for 12 yield components, allowing genotypes to be grouped into 17 clusters. D^2 analysis revealed that number of pods per plant, pod length, yield per plant and seed per pod made a high contribution towards the total genetic distance.

Rahman (1996) estimated genetic divergence among 16 genotypes of soybean using Mahalanobis D^2 statistics. The genotypes were grouped into 7 clusters. The inter-cluster average D^2 values showed the maximum distance between cluster I and III. The genetically diverse genotypes from these groups could be used as a parent in the hybridization programme for getting desirable segregants. Germplasm much in use of these characters of the respective cluster would offer a good scope of improvement of the crop through rational selection. A different experiment was conducted by Sanjay *et al.* (1998) and they reported a genetic divergence of 30 advanced breeding lines of soybean and were grouped into 7 clusters. Of which two clusters contained the most important genotypes. One cluster characterized by high yield per plant, pods per plant, a reproductive phase high harvesting index and high seed weight, another cluster contained genotypes almost similar to those in the previous cluster.

Chowdhury *et al.* (1996) observed 30 genotypes of soybean for genetic divergence using Mahalanobis D^2 statistics and reported that genotypes were clustered in 6 diverse groups. They demonstrated that geographical isolation may not be the only factor causing genetic diversity but also 100 seed weight and yield per plant were the main contributors of total divergence. In another experiment, Mehetre *et al.* (1997) observed 41 genotypes of soybean were grouped into 12 different clusters. Genetic diversity was independent of geographic region. From the cluster mean values donor for different characters is suggested.

Kumar and Nadarajan (1994) studied 11 yield components in 64 genotypes of soybean for genetic divergence and reported that genotypes were clustered in 11 diverse groups. A different experiment was carried out by Mehetre *et al.* (1994) and they estimated genetic divergence among 51 genotypes of soybean and genotypes were grouped into 10 clusters. The clustering pattern showed that diversity and geographic distribution were independent of each other. Using the Mahalanobis D^2, Ghatge and Kadu (1993) estimated genetic diversity 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

This chapter interprets information concerning the methodology that was used in the execution of the experiment. It comprises a brief description of locations of experimental site, planting materials, climate and soil, layout and design of the experiment, plot preparation, fertilizing, intercultural operations, harvesting, data recording procedure, statistical analysis etc. which are presented as follows:

3.1 Experimental site

The experiment was conducted in the experimental area of Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh during the period from December 2017 to May 2018. Location of the site is 23°74' N latitude and 90°35' E longitude with an elevation of 8 meters from sea level in Agro-ecological zone of "Madhupur Tract" (AEZ-28) (Anonymous, 1988). The experimental site is shown on the map of AEZ of Bangladesh in (Appendix I).

3.2 Climate and soil

The experimental site was situated in the subtropical climatic zone and moderately low temperature prevails from December to May (Rabi season) which is suitable for soybean growing in Bangladesh. Weather information and physicochemical properties of the soil are presented in (Appendix II and Appendix III respectively). The soil of the experimental site belongs to the Agroecological region of “Madhupur Tract” (AEZ No. 28). The soil was clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH value ranging from 5.47 to 5.63 and organic carbon content is 0.82% (Appendix III). The records of air temperature, humidity and rainfall during the period of the experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix II).

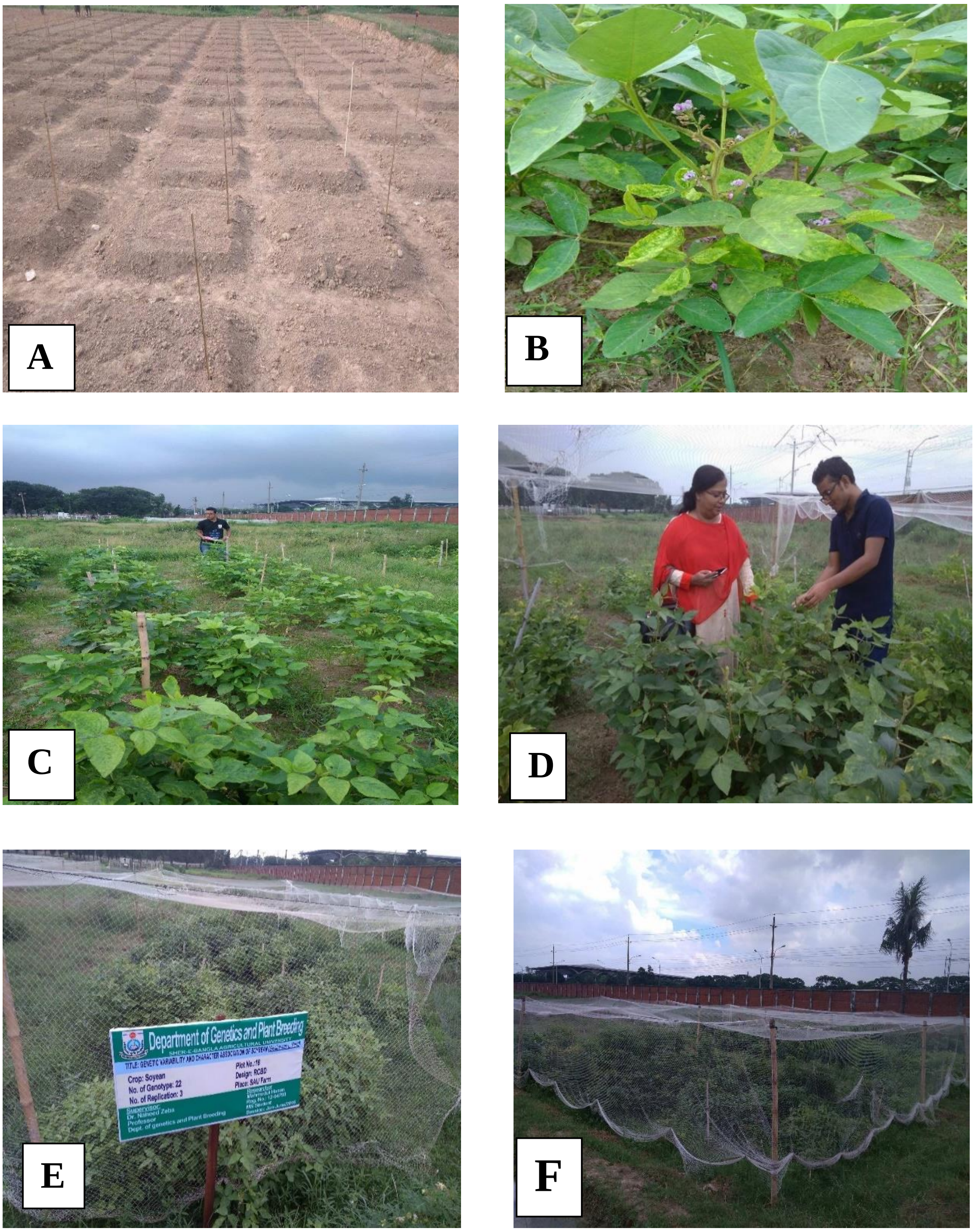


Plate 1. Different steps of experimental method. A. Plots preparation for seed sowing B. Plants in the main pots. C. Several plots in the main field, D. Supervisor visited. E. Banner with tagging, F. Experimental plots cover by net.

3.3 Experimental materials

The experimental material consisted of 22 genotypes of advance generation of soybean collected from Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh for the research work. List of the genotypes is given in Table 1.

3.4 Design and layout of the experiment

The experiment was laid out and evaluated during Rabi season 2017-2018 in Randomize Complete Block Design (RCBD) that included 22 genotypes. The experiment was conducted in 3 replications. The twenty-two genotype were planted each on a 3 m X 1.5 m plot size having 4 rows including 2 borders. The spacing between rows, plants, plots and replication was 60 cm, 10 cm, 50 cm and 50 cm respectively.

3.5 Manure and fertilizers application

The soil was well pulverized and dried in the sun and only well-decomposed cow dung was mixed with the soil according to the recommendation guide Handbook of Agricultural Technology, BARI, 2011. According to the fertilizer recommendation guide of BADC, 2012 Fertilizer dose 20:20:40:10 NPKS Kg/ha was applied uniformly over the soil. Well decomposed cow dung was calculated for each plot considering the dose of 1-hectare soil at the depth of 20 cm.

3.6 Intercultural operations

Necessary watering and intercultural operations were given as and when required. Weeding was performed in all plots as and when required to keep plants free from weeds. Diseases and pest is a limiting factor to soybean production. Experimental soybean plants were treated with Bavistin DF and Cupravit 50 WP to prevent unwanted diseases problem @1g/l and 2g/l respectively. Aphid and leaf miner is an important pest of soybean during the growing stage. They were controlled by Malathion 250 EC @ 0.5ml/l. Those

Table 1. Name and origin of 22 soybean genotypes used in the study

Sl. No.	**Genotypes No.**	**Name/Acc No. (BD)**	**Source**
1	G1	GM0011	Supervisor
2	G2	GM0009	Supervisor
3	G3	GM0001	SAU
4	G4	GM0015	Co-supervisor
5	G5	GM0020	Co-supervisor
6	G6	GM0016	Co-supervisor
7	G7	GM0019	Co-supervisor
8	G8	GM0017	Co-supervisor
9	G9	GM0018	SAU
10	G10	GM0022	Co-supervisor
11	G11	GM0012	Co-supervisor
12	G12	GM0013	SAU
13	G13	GM0014	Co-supervisor
14	G14	GM0003	Supervisor
15	G15	GM0008	Co-supervisor
16	G16	GM0010	Co-supervisor
17	G17	GM0021	Co-supervisor
18	G18	GM0007	Co-supervisor
19	G19	GM0006	Co-supervisor
20	G20	GM0005	Co-supervisor
21	G21	GM0004	Supervisor
22	G22	GM0002	Supervisor

SAU=Sher-e-Bangla Agricultural University fungicide and pesticide were sprayed two times, first at vegetative growth stage and next to the early flowering stage to manage pest and diseases.

3.7 Harvesting

Harvesting of fruits was done after the maturity stage. Mature pods were harvested when the pods turned golden yellow to dark brown in color. Different varieties were harvested at different dates as they reach maturity in variable periods of time.

3.8 Data recording

Different biometric traits related to yield and its contributing characters were recorded *viz.* Days to first flowering, days to 50% flowering, days to physiological maturity, days to harvest maturity, plant height (cm), number of branch per plant, pod length, pod wide, pod height, number of pod per plant, number of seed per pod, seed yield per plant, weight of 100 seeds (g), seed yield per plot (kg), seed yield per hectare (ton). Data were recorded in respect of the following parameters:

3.8.1 Days to first flowering

Days to first flowering was recorded from the date of sowing to date of first flowering in each plot.

3.8.2 Days to 50% flowering

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

3.8.3 Days to physiological maturity

Number of days taken from the date of sowing till physiological maturity of the pods.

3.8.4 Days to harvest maturity

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

3.8.5 Plant height (cm)

The height of the plant at a mature stage measured in centimeters from the ground level to the tip of the main stem.

3.8.6 Number of branch per plant

The number of branches per plant from the main stem above ground was recorded and the mean was calculated**.**

3.8.7 Pod length

The length of the pod at the mature stage measured in millimeters.

3.8.8 Pod wide

The wide of the pod at the mature stage measured in millimeters.

3.8.9 Pod height

The height of the pod at the mature stage measured in millimeters

3.8.10 Number of pods per plant

The total number of pods per plant was counted and recorded. The average number of pods per plant for each of the genotype was calculated.

3.8.11 Number of seeds per pod

Number of seeds present per pod was counted from each plant and the average was calculated for each of the genotypes.

3.8.12 Seed yield per plant (g)

The weight of the total seeds of an individual plant in grams was taken after harvest.

3.8.13 Weight of 100 seeds (g)

The weight of a hundred seeds from each of the genotype which is randomly was recorded and expressed in grams.

3.8.14 Seed yield per plot (kg)

Weighing the seeds produced in a plot.

3.8.15 Seed yield per hectare

Weighing the seeds produced in a plot and then converted into kg per hectare.

3.9 Statistical analysis

For each character the data were recorded and averaged to obtain mean data. Mean data of characters were subjected to multivariate analysis. Univariate analysis of the individual character was done for all characters under study using mean values (Singh *et al.* 1985) and was estimated using MSTAT-C computer program. 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, the multivariate analysis was done by computer using the GENESTAT and Microsoft Excel 2016 software through four techniques *viz*. Principal Component Analysis (PCA), Principle Co-ordinate Analysis (PCO), Cluster Analysis and Canonical Vector Analysis (CVA).

3.9.1 Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were calculated by the following formulae given by Johnson *et al*. (1955).

a. Genotypic variance, $\delta^2 g = \frac{MSG-MSE}{r}$

Where, MSG= Mean sum of square for genotype

MSE= Mean sum of square for error, and

r = Number of replication

b. Phenotypic variance, $\delta^2 p = \delta^2 g + \delta^2 e$

Where, $\delta^2 g =$ Genotypic variance,

$\delta^2 e$ = Environmental variance=Mean square of error

3.9.2 Estimation of genotypic and phenotypic co-efficient of variation

The genotypic and phenotypic co-efficient of variation in percent were computed by the following formula (Burton, 1952).

Genotypic co-efficient of variation (GCV%) = $\frac{\delta_g \times 100}{\bar{X}}$

Phenotypic co-efficient of variation (PCV%) = $\frac{\delta_p \times 100}{\bar{X}}$

Where, δ_g = Genotypic standard deviation

δ_p = Phenotypic standard deviation

$\bar{X}$ = Population mean.

The PCV and GCV values are ranked as low, medium and high (Shivasubramanian and Menon, 1973) and are mentioned below:

0-10% - Low

10-20% - Moderate

>20% - High

3.9.3 Estimation of heritability

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

h^2_b (%) = $\frac{\delta^2 g}{\delta^2 p} \times 100$

Where,

h^2_b= Heritability in broad sense

$\delta^2 g$ = Genotypic variance

$\delta^2 p$ =Phenotypic variance

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

0-30% - Low

30-60% - Moderate

60% and above - High

3.9.4 Estimation of genetic advance

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

$$GA = \frac{\delta^2 g}{\delta^2 p} K.\, \delta_p$$

Where, GA= Genetic advance

δ^2_g = Genotypic variance

δ^2_p = Phenotypic variance

δ_p = Phenotypic standard deviation

K = Selection differential which is equal to 2.06 at 5% selection intensity

3.9.5 Estimation of genetic advance in the percentage of mean

Genetic advance in the percentage of the mean was calculated by the following formula given by Johnson *et al.* (1955).

Genetic Advance in the percentage of mean $= \frac{Genetic\ Advance}{Grand\ mean} \times 100$

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

0-10% - Low

10-20% - Moderate

20% and above - High

3.9.6 Estimation of simple correlation co-efficient

Simple correlation co-efficient was estimated by the following formula (Clarke, 1980; Singh and Chaudhary, 1985).

$$r = \frac{\sum xy - \frac{\sum x . \sum y}{N}}{\sqrt{[\{\sum x2 - \frac{(\sum x)2}{N}\}\{\sum y2 - \frac{(\sum y)2}{N}\}]}}$$

Where,

$\sum$ = Summation

x and y are two variable correlated

N = Number of observations

3.9.7 Estimation of genotypic and phenotypic correlation co-efficient

The genotypic and phenotypic correlation co-efficient was estimated by the formula (Johnson *et al.*1955; Hanson *et al.* 1956).

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

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

$\sigma^2{}_{gx}$ = Genotypic variance of the trait x

$\sigma^2{}_{gy}$ = Genotypic variance of the trait y

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

Where, σ_{pxy} = Phenotypic co-variance between the traits x and y

$\sigma^2{}_{px}$ = Phenotypic variance of the trait x

$\sigma^2{}_{py}$ = Phenotypic variance of the trait y

3.9.8 Estimation of path co-efficient analysis

Path co-efficient analysis was carried out according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985) using simple correlation values. In path analysis, correlation coefficient is partitioned into direct and indirect independent variables on the dependent variable.

In order to estimate direct and indirect effect of the correlated characters, say, xl, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) are required to be formulated as shown below:

$r_{yx1} = P_{yxl} + P_{yx2} r_{xlx2} + P_{yx3}\, r_{x1x3}$

$r_{yx2} = P_{yxl} r_{x1x2} + P_{yx2} + P_{YX3}\, r_{x2x3}$

$r_{yx3} = P_{yxl} r_{x1x3} + P_{yx2} r_{x2x3} + P_{yx3}$

Where, r´s denotes simple correlation co-efficient and P´s denote path co-efficient (Unknown). P´s in the above equation may be conveniently solved by arranging them in matrix from.

Total correlation, say between x_1 and y is thus partitioned follows:

Pyx1= The direct effect of x1 via x_2 on y.

$P_{yx2}r_{x1x2}$= The indirect effect of x1 via x_2 on y.

$P_{yx3}r_{x1x3}$= The indirect effect of x1 via x_3 on y.

3.10. Multivariate analysis

Genetic diversity was estimated following Mahalanobis's (1936) generalized distance (D^2). Selection of parents in hybridization programme based on Mahalanobis D2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) reported that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a successful hybridization program. Statistical analysis such as Mahalanobis D^2 and Canonical Variate Analysis (CVA), which quantify the differences among several quantitative traits are an efficient method of evaluating genetic diversity. Mean data of each quantitative character were subjected to both univariate and multivariate analysis. Mean, range, co-efficient of variation (CV) and the correlation was estimated using MSTAT computer program. Multivariate analysis *viz.* Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CLU) and Canonical Variate Analysis (CVA) were done by using GENSTAT program.

3.10.1 Principle component analysis

Principle component analysis (PCA), one of the multivariate techniques, is used to examine the inter-relationship among several characters and can be done from sum of squares and product matrix for the characters. Therefore, principle component was computed from the correlation matrix and genotypes scores obtained from the first components (which has the property of accounting for the maximum variance) and succeeding components with latent roots greater than unity. The contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.10.2 Principle co-ordinate analysis

The principal coordinate analysis is equivalent to PCA but it is used to calculate inter-unit distances. Through the use of all dimensions of P it gives the minimum distance between each pair of the N points using similarity matrix (Digby *et al*. 1989).

3.10.3 Cluster analysis (CA)

To divide the genotypes of a data set into some number of mutually exclusive groups clustering was done using non-hierarchical classification. In GENSTAT, the algorithm was used to search for optimal values of chosen criteria. Starting from some initial classification of the genotypes into the 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 examine the effect of swooping two genotypes of different classes and so on.

3.10.4 Canonical variate analysis (CVA)

Canonical Variate Analysis, complementary to D2 statistic, is a sort of multivariate analysis where canonical vectors and roots representing different axes of differentiation and the amount of variation accounted for by each of such axes respectively and derived. Canonical Variate Analysis computed linear combination of original variability that maximized the ratio between ground and within group variations, thereby giving functions of the original variables that could be used to discriminate between the groups. Thus in this analysis, a series of orthogonal transformation was done sequentially for maximizing the ratio of the groups to within-group variations.

3.10.5 Calculation of D^2 values

The Mahalanobis distance (D^2) values are 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 statastic is defined by the formula

$$\mathrm{D}^2 = \sum_i^x \boldsymbol{d_i^2} = \sum_i^x \left(\boldsymbol{Y_i^j} - \boldsymbol{Y_j^k}\right) \qquad \textbf{(j≠k)}$$

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.

3.10.6 Computation of average intra-cluster distances

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

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

Where,

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

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

3.10.7 Computation of average inter-cluster distances

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

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

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

$n_i =$ Number of populations in cluster i.

$n_j =$ Number of populations in cluster j.

3.10.8 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 Chaudhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

CHAPTER IV

RESULTS AND DISCUSSION

The major function of parent selection is diversity. The degree of diversity of the parents is the pre-requisite of an effective breeding programme. The experiment was conducted to determine the variability among 22 genotypes of soybean as well as to study the genetic diversity, correlation and path co-efficient for seed yield and different yield contributing characters. The data were recorded on different parameters such as days to 50% flowering, days to physiological maturity, days to harvest maturity, plant height (cm), number of branch per plant, pod length (mm), pod wide (mm), pod height (mm), number of pod per plant, number of seed per pod, seed yield per plant, weight of 100 seeds (g), seed yield per plot (kg), seed yield per hectare (ton). The data were statistically analyzed and results obtained from statistical analysis have been presented under the following headings.

4.1 Genetic parameters

The analysis of variance indicated a significantly higher amount of variability present among the genotypes for all the characters studied except pod wide, seed per pod, seed yield per plot and seed yield per hectare. (Appendix V). The results clearly indicated that there exists high variability for yield and yield components among the genotypes studied. Therefore there is a lot of scope for selection for the majority of the traits in the genotypes. The mean sum of squares of all the 15 characters is presented in Appendix V.

4.2 Genetic variability, heritability and genetic advance

The mean performance of soybean genotypes for various yield components is presented in Appendix IV. The success of a crop improvement program depends on the extent of genetic variability existing in the germplasm or population. Genetic variability is prerequisite for any crop improvement programme as it provides wider scope for selection. The heritability is one of the genetic parameters, which most contribute to the breeder work. It provides the proportion of total phenotypic variance that is attributed to genetic causes. High heritability joined with high genetic advance can be used as a guide in soybean breeding. The narrow gap between PCV and GCV for all the characters presence under these study, suggested that these traits studied has low environmental influence. Heritability estimates were considered in conjunction with genetic advance. Otherwise, the estimates of heritability alone fail to indicate the response to selection (Johnson *et al.*, 1955). Therefore, the heritability estimates appears to be more meaningful when accompanied by estimates of genetic advance. The genetic advance as percent of the mean (GAM) was also estimated. The extent of variation among the genotypes in respect of fifteen characters was studied and estimates of mean, range, genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic advance as percent mean for all the characters were studied and the results are interpreted in Table 2 and illustrated in Figure 1 and 2.

4.2.1 Days to first flowering

The variance due to days to first flowering showed that the genotypes differed significantly and ranged from 46.33 days after sowing (DAS) in (G2) to 74.33 DAS in (G13) with mean value 65.32 days after sowing (DAS) (Appendix IV). The phenotypic variance (59.03) appeared to be higher than the genotypic variance (58.29) suggested there is an influence of environment on the expression of the genes controlling this trait. The difference between the phenotypic coefficient of variation (11.76) and genotypic coefficient of variation (11.69) was low, which indicated the presence of low variability among the genotypes. The heritability (98.74) estimates for this trait was high, genetic advance (15.63) was moderate on the other hand, genetic advance in percent of the mean (23.29) were found high,

Table 2. Estimation of genetic parameters in fifteen characters of twenty two genotypes in soybean

Traits	GenMS	Min	Max	Mean	CV(%)	σ^2_g	σ^2_e	σ^2_P	GCV	ECV	PCV	h^2_b	GA	GA (% mean)
FF	175.60**	46.33	74.33	65.32	1.32	58.29	0.75	59.03	11.69	1.32	11.76	98.74	15.63	23.92
D50%F	196.31**	56.33	86.00	75.15	0.93	65.27	0.49	65.76	10.75	0.93	10.79	99.25	16.58	22.06
DPM	480.04**	82.00	135.33	117.11	0.90	159.64	1.11	160.76	10.79	0.90	10.83	99.31	25.94	22.15
DHM	465.91**	91.33	144.67	129.05	0.99	154.76	1.62	156.38	9.64	0.99	9.69	98.96	25.49	19.76
PH	1525.96**	29.55	105.22	76.21	6.80	499.70	26.88	526.57	29.33	6.80	30.11	94.90	44.86	58.86
BPP	3.59**	2.55	6.22	4.51	14.87	1.05	0.45	1.50	22.68	14.87	27.12	69.93	1.76	39.06
PoL	18.45**	33.01	42.58	36.48	6.39	4.34	5.43	9.77	5.71	6.39	8.57	44.43	2.86	7.84
PoW	1.48	6.02	9.88	7.83	3.61	0.47	0.08	0.55	8.72	3.61	9.44	85.40	1.30	16.61
PoH	2.28*	4.48	8.77	5.27	4.78	0.74	0.06	0.80	16.30	4.79	16.99	92.07	1.70	32.22
PPP	4566.60**	27.00	138.89	76.61	19.64	1446.71	226.45	1673.17	49.65	19.64	53.39	86.47	72.86	95.10
SPP	0.11	2.33	3.11	2.75	10.19	0.01	0.08	0.09	3.92	10.19	10.92	12.87	0.08	2.89
SYPP	106.32**	11.27	32.88	20.63	16.15	31.74	11.10	42.84	27.31	16.15	31.73	74.09	9.99	48.42
100SW	44.02**	6.63	20.00	12.08	6.31	14.48	0.58	15.06	31.50	6.32	32.13	96.14	7.69	63.63
YPP	0.24	0.58	1.58	1.02	15.29	0.07	0.02	0.09	26.01	15.31	30.19	74.26	0.47	46.18
YPH	0.93	1.17	3.13	2.03	14.92	0.28	0.09	0.37	26.09	14.95	30.07	75.29	0.95	46.64

** Significant at 1%   * Significant at 5%

Legend:

FF= First flowering, D50F = Days to 50% flowering, DPM= Days of physiological maturity, DHM= Days of harvest maturity, PH = Plant height (cm), BPP= Branches per plant, PoL= Pod length, PoW= Pod wide, PoH= Pod height, PPP= Pod per plant, SPP= Seed per pod, SYPP= Seed yield per plant, 100SW= 100 Seed weight, YPP= Yield per plot, YPH= Yield per hectare, MS = mean sum of square, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance, σ^2e = Environmental variance, PCV = Phenotypic Coefficient of variation, GCV= Genotypic coefficient of variation and ECV= Environmental coefficient of variation, h^2_b = Heritability in broad sense, GA= Genetic advance.

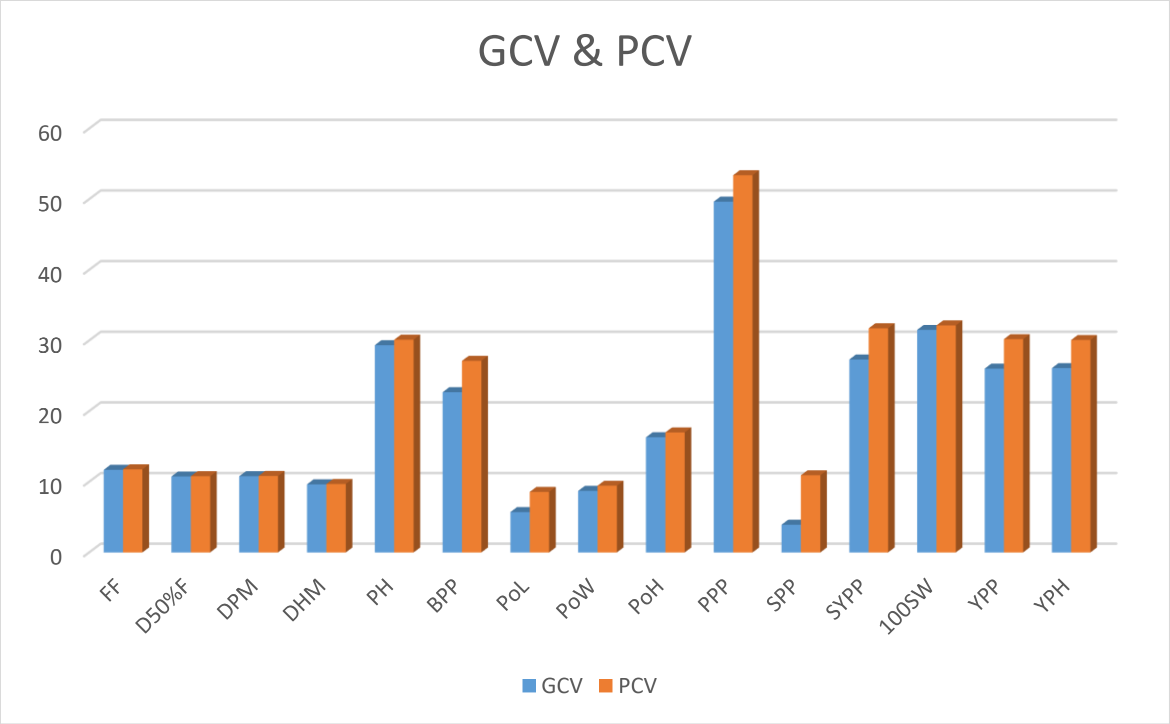


Figure 1. Genotypic and phenotypic variability in soybean

FF= First flowering, D50F = Days to 50% flowering, DPM= Days of physiological maturity, DHM= Days of harvest maturity, PH = Plant height (cm), BPP= Branches per plant, PoL= Pod length, PoW= Pod wide, PoH= Pod height, PPP= Pod per plant, SPP= Seed per pod, SYPP= Seed yield per plant, 100SW= 100 Seed weight, YPP= Yield per plot, YPH= Yield per hectare

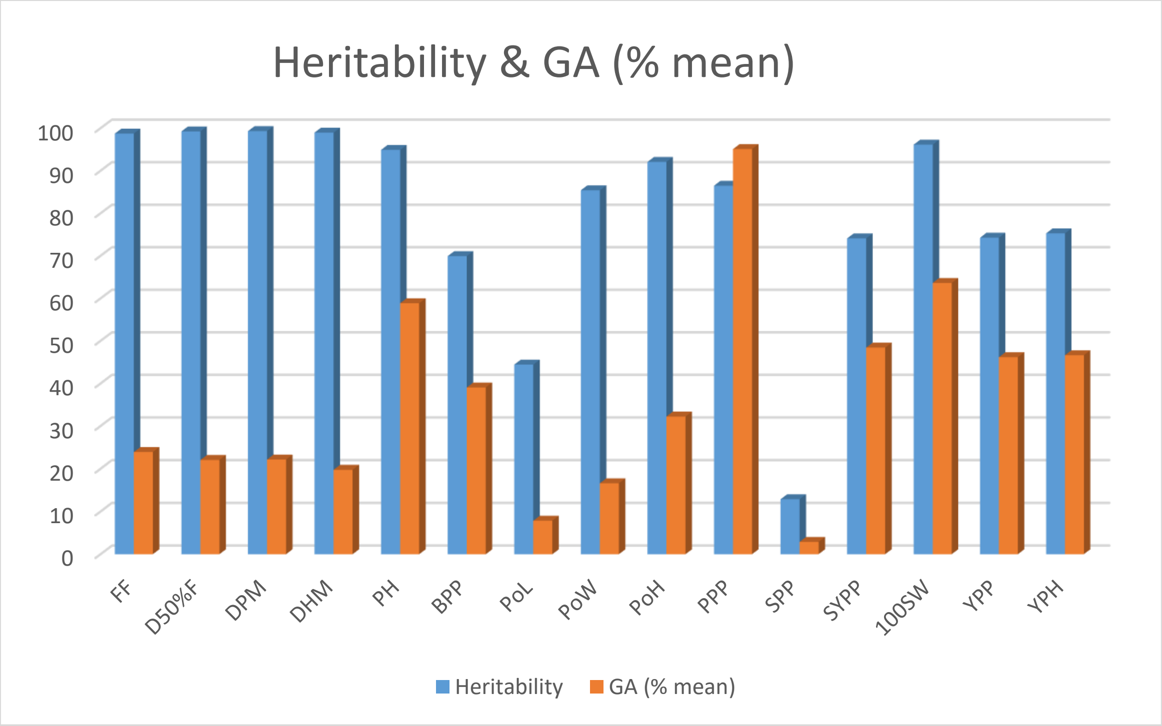


Figure 2. Heritability and genetic advance over mean in soybean.

FF= First flowering, D50F = Days to 50% flowering, DPM= Days of physiological maturity, DHM= Days of harvest maturity, PH = Plant height (cm), BPP= Branches per plant, PoL= Pod length, PoW= Pod wide, PoH= Pod height, PPP= Pod per plant, SPP= Seed per pod, SYPP= Seed yield per plant, 100SW= 100 Seed weight, YPP= Yield per plot, YPH= Yield per hectare

revealed that this character was governed by additive gene and selection for this character would be effective.

4.2.2 Days to 50% flowering

The variance due to days to 50% flowering showed that the genotypes differed significantly and ranged from 56.33 days after sowing (DAS) in G3 to 86 DAS in G12 with mean value 75.15 days after sowing (DAS) (Appendix IV). The Genotypic, phenotypic and environmental variances observed were 65.27, 65.76 and 0.49, respectively (Table 2). The phenotypic variance appeared to be closed to the genotypic variance suggested no influence of environment on the expression of the genes controlling this trait.

The difference between the genotypic co-efficient of variation (10.75) and phenotypic coefficient of variation (10.79) was close to each other (Table 2 and Figure 1) indicating a minor environmental influence on this character. The heritability (99.25) estimates for this trait was high, genetic advance (16.58) was at moderate level and genetic advance over a percentage of the mean (22.06) was found high, revealed the possibility of the predominance of additive gene effect and selection might be effective for producing varieties. Bangar *et al.* (2003) reported that phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV).

4.2.3 Days to physiological maturity

With respect to days to physiological maturity, mean values ranged from 82 days after sowing in G2 to 135.33 days after sowing in G16. The overall mean for days to physiological maturity was 117.11 days (Appendix IV). The genotypic co-efficient of variation and phenotypic co-efficient of variation were 10.79 and 10.83, respectively which were close to each other (Table 2). There was a very little difference between phenotypic and genotypic co-efficient of variation, indicating a minimal environmental influence on this character. The heritability (99.31%) estimates for this trait was high, genetic advance (25.94) high and genetic advance in percent of the mean (22.15) was found high, revealed that this trait was governed by additive gene and selection might be effective for producing varieties.

4.2.4 Days to harvest maturity

The value ranged from 91.33 to 144.67 with a mean of 129.05. The genotype G2 had the lowest and G16 was the highest in the genotype (Appendix IV). The phenotypic variance (156.38) appeared to be higher than the genotypic variance (154.76) suggested there is an 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 9.64 and 9.69, respectively which were close to each other (Table 2). There was a very little difference between phenotypic and genotypic co-efficient of variation, indicating a minimal environmental influence on this character. The heritability (98.96%) estimates for this trait was high, genetic advance (25.49) high and genetic advance in percent of the mean (19.76) was found moderate, revealed that this trait was governed by the additive gene. So selection for this trait may be rewarding. Jangale *et al.* (1994) observed that high heritability was observed for days to maturity. Bhandarkar (1999) reported that high heritability and genetic advance for days to maturity in soybean.

4.2.5 Plant height (cm)

The mean for plant height was recorded 76.21 cm. It ranged from 29.55 cm to 105.22 cm (Table 2). The maximum plant height (105.22 cm) was recorded by the genotype ‘G13’ and the lowest plant height (29.55 cm) was recorded by ‘G2’ (Appendix IV). The analysis of variance revealed highly significant differences among the genotypes with respect to plant height. The genotypic and phenotypic variance was observed 499.70 and 527.57, respectively for plant height with high environmental influence. The phenotypic co-efficient of variation (30.11) was higher than the genotypic co-efficient of variation (29.33), which indicated the presence of considerable variability among the genotypes for this trait. The heritability (94.90%) estimates for this trait was high, genetic advance (44.86) was a high and genetic advance in percent of the mean (58.86) was found high, revealed that this trait was governed by the additive gene. Therefore, selection for this trait will be effective. Plant height exhibited high heritability and high genetic advance as percent mean in soybean which is similar to the earlier findings by Kumar *et al.* (2014) and Ghodrati (2013).

4.2.6 Branches per Plant

Branches per plant were ranged from 2.55 in G20 and 6.22 in G13 with mean value of 4.51 (Table 2). The genotypic variance and phenotypic variance for this trait were 1.05 and 1.50 respectively (Table 2). The phenotypic variance appeared to be closed to the genotypic variance suggested no influence of environment on the expression of the genes controlling this trait. The phenotypic co-efficient of variation (27.12) was higher than the genotypic co-efficient of variation (22.68), indicates that the apparent variation is not only due to genotypes but also due to the influence of the environment. The heritability estimates for this trait was high (69.93) with low genetic advance (1.76) and high genetic advance in percent of the mean (39.06) indicated that this trait was controlled by additive gene and selection for this character would be effective.

4.2.7 Pod length

The mean for pod length was recorded 36.48 mm. It ranged from 33.01 mm to 42.58mm cm (Table 2). The maximum pod length (42.58 mm) was recorded by the genotype ‘G1’ and the lowest pod length (33.01 mm) was recorded by ‘G12’ (Appendix IV). The genotypic and phenotypic variance was observed 4.34 and 9.77 respectively for pod length with high environmental influence. The phenotypic co-efficient of variation (8.57) was higher than the genotypic co-efficient of variation (5.71), which indicated the presence of considerable variability among the genotypes for this trait. The heritability (44.43%) estimates for this trait was moderate, genetic advance (2.86) was a low and genetic advance in percent of the mean (7.84) was found low, revealed that this trait was governed by additive or non-additive gene. Therefore, selection for this trait will not be effective.

4.2.8 Pod wide

The value ranged of pod wide from 6.02 mm to 9.88 mm with a mean of 7.83 mm. The genotype G2 had the lowest and G1 was the highest in the genotype (Appendix IV). The genotypic and phenotypic variance was observed 0.47 and 0.55 respectively (Table 2) for pod length suggested no influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient and phenotypic co-efficient of variation were 8.72 and 9.44, respectively indicating the minimal influence of environment on the expression of the of variation genes controlling this trait. The heritability (85.40) estimates for this trait was high, genetic advance (1.30) was a low and genetic advance in percent of the mean (16.61) were found moderate, revealed that this character was governed by additive or non-additive gene and selection for this character would not be effective.

4.2.9 Pod height

The mean for pod height was recorded 5.27 mm. It ranged from 4.48 mm to 8.77 mm (Appendix IV). The maximum pod length (8.77 mm) was recorded by the genotype ‘G2’ and the lowest pod length (4.48 mm) was recorded by ‘G5’ (Appendix IV). The phenotypic variance, genotypic variance observed were 0.80 and 0.74 respectively (Table-2). The phenotypic variance appeared to be closed to the genotypic variance suggested no influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient and phenotypic co-efficient of variation were 16.30 and 16.99, respectively indicating the minimal influence of environment on the expression of the of variation genes controlling this trait. The heritability (92.07) estimates for this trait was high, genetic advance (1.70) was low on the other hand, genetic advance in percent of the mean (32.22) was found high, revealed that this character was governed by additive gene and selection for this character would be effective.

4.2.10 Pod per plant

The number of pods per plant was ranged from 27 to 138.89 with a mean of 76.61. The minimum number of pods per plant was observed in G1 while a maximum number of pods per plant was found in the genotype G13 (Appendix IV). The phenotypic variance (1673.17) appeared to be higher than the genotypic variance (1446.71) suggested a high influence of environment on the expression of the genes controlling this trait. The phenotypic co-efficient of variation (53.39) was higher than the genotypic co-efficient of variation (49.65), indicates that the apparent variation is not only due to genotypes but also due to the influence of the environment. The heritability (86.47) estimates for this trait was high, genetic advance (72.86) was a high and genetic advance in percent of the mean (95.10) were found very high, revealed that this character was governed by additive gene and selection for this character would be effective.

4.2.11 Seed per pod

The mean for seed per pod was recorded 2.75 and ranged from 2.33 to 3.11 (Appendix IV). The maximum seed per pod (3.11) was recorded by the genotype 'G6' and the lowest pod length (2.33) was recorded by 'G22' (Appendix IV). The phenotypic variance (0.09) appeared to be higher than the genotypic variance (0.01) suggested the considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient and phenotypic co-efficient of variation were 3.92 and 10.92, respectively indicating the presence of considerable variability among the genotypes. The heritability (12.87%) estimates for this trait is low, genetic advance (0.08) was very low and genetic advance in percent of the mean (2.89) was found low (Table 2), revealed that this trait was governed by the non-additive gene. Selection on the basis of this traits would not be effective.

4.2.12 Seed yield per plant

Seed yield per plant was ranged from 11.27 in G11 and 32.88 in G13 with mean value of 20.63 (Appendix IV). The phenotypic variance was 42.88 which is higher than the genotypic variance 31.74 and slightly high difference between the GCV (27.31) and PCV (31.73) indicates that the apparent variation is not only due to genotypes but also due to the influence of the environment. Heritability was found 74.09 where genetic advance and genetic advance in the percentage of the mean was recorded as 9.99 and 48.42 respectively. High heritability accompanied by low genetic advance along with high genetic advance in percentage of mean revealed that the expression of this trait is controlled by additive gene and thus selection for this trait might be rewarding.

4.2.13 Weight of hundred seeds (g)

The mean for Weight of hundred seeds was recorded 12.08 g and ranged from 6.63 g to 20 g. The maximum Weight of hundred seeds (20 g) was recorded by the genotype 'G1' and the lowest Weight of hundred seeds (6.63 g) was recorded by 'G17' (Appendix IV). The phenotypic variance (15.06) appeared to be higher than the genotypic variance (14.48) 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 26.01 and 30.19, respectively indicating considerable environmental influence on this character. The heritability (96.14%) estimates for this trait was high, genetic advance (7.69) was low but genetic advance in percent of mean (63.63) were found high, revealed that this character was governed by additive gene and selection for this character would be effective.

4.2.14 Yield per plot (kg)

Seed yield per plot was ranged from 0.58 kg in G11 and 1.58 kg in G13 with mean value of 1.02 kg (Appendix IV). The Phenotypic variance was 0.09 which is closed to the genotypic variance 0.07 and slightly high difference between the GCV (26.01) and PCV (30.19) indicates that the apparent variation is not only due to genotypes but also due to the influence of the environment. Heritability was found 74.26 where genetic advance and genetic advance in the percentage of mean was recorded as 0.47 and 46.18 respectively. High heritability accompanied by low genetic advance along with high genetic advance in percentage of mean revealed that the expression of this trait is controlled by additive gene and thus selection for this trait might be rewarding.

4.2.15 Yield per hectare

The mean for yield per hectare was recorded 2.03 ton and ranged from 1.17 ton to 3.13 ton. The maximum Yield per hectare (3.13 ton) was recorded by the genotype ‘G13’ and the lowest Yield per hectare (1.17 ton) was recorded by ‘G11’ (Appendix IV). The phenotypic variance (0.37) appeared to be higher than the genotypic variance (0.28) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient and phenotypic co-efficient of variation were 26.09 and 30.07, respectively indicating presence of considerable variability among the genotypes. The heritability (75.29%) estimates for this trait is high, genetic advance (0.95) was very low but genetic advance in percent of mean (46.64) was found high (Table 2), revealed that this trait was governed by additive gene. Selection on the basis of this traits would be effective.

4.3 Correlation co-efficient

Yield is the resultant of combined effect of several quantitative characters and environment. Hence Knowledge about the interaction of characters among themselves and environment has been of great use in the plant breeding. Correlation studies along with path analysis provide a better understanding of the association of different characters with fruit yield. So selection may not be effective unless the other contributing components influence the yield directly or indirectly.

A positive correlation between desirable characters is favorable to the plant breeder because it helps in simultaneous improvement of both the characters. From this it would be possible to bring about genetic up-gradation in one character by selection of the other of a pair. On the other hand, a negative correlation will hinder the simultaneous expression of both the characters with high values. In such situations some economic compromise has to be made. Hence, an attempt has been made to study the character association in the soybean at both levels.

Pearson correlation analysis among yield and its contributing characters are shown in Table 3. For clear understanding correlation coefficients are separated into genotypic and phenotypic level in Table 4**.** When phenotypic correlation coefficient were higher than genotypic correlation coefficient indicating suppressing effect of the environment which modified the expression of the characters at phenotypic level. Where the genotypic correlation coefficients were higher than their phenotypic correlation coefficients, it indicates that the genetic reason of association. The depicted of genotypic and phenotypic correlation coefficient among yield and yield contributing characters of soybean are shown in Figure 3**.**

4.3.1 Days to first flowering

Days to first flowering showed significant positive association with days to 50% flowering (G=0.979, P=0.977), day to physiological maturity (G=0.731, P=0.729),

Table 3. Pearson correlation coefficients among different pairs of yield and yield contributing characters in 22 genotypes of soybean.

	FF	D50F	DPM	DHM	PH	BPP	PoL	PoW	PoH	PPP	SPP	SYPP	100SW	YPP	YPH
FF		0.977**	0.729**	0.721**	0.744**	0.581**	-0.395	-0.120	-0.690**	0.635**	-0.291	0.492*	-0.641**	0.504*	0.497*
D50%F			0.712**	0.701**	0.729**	0.565**	-0.402	-0.175	-0.645**	0.658**	-0.225	0.520*	-0.654**	0.537**	0.532*
DPM				0.984**	0.766**	0.650**	-0.367	0.157	-0.596*	0.688**	-0.356	0.601**	-0.681**	0.607**	0.600**
DHM					0.725**	0.626**	-0.300	0.203	-0.644**	0.678**	-0.357	0.598**	-0.634**	0.602**	0.596**
PH						0.613**	-0.473*	-0.218	-0.561**	0.822**	-0.146	0.729**	-0.769**	0.736**	0.730**
BPP							-0.417	-0.183	-0.232	0.810**	-0.206	0.611**	-0.762**	0.610**	0.610**
PoL								0.599**	0.011	-0.609**	0.302	-0.524*	0.553**	-0.515*	-0.510**
PoW									-0.253	-0.349	-0.146	-0.245	0.365	-0.238	-0.246
PoH										-0.315	0.248	-0.222	0.437*	-0.236	-0.237
PPP											-0.198	0.908**	-0.753**	0.907**	0.905**
SPP												-0.169	0.096	-0.163	-0.160
SYPP													-0.481*	0.998**	0.998**
100SW														-0.487*	-0.485*
YPP															0.999**

FF= Days to first flowering, D50F = Days to 50% flowering, DPM= Days of physiological maturity, DHM= Days of harvest maturity, PH = Plant height (cm), BPP= Branches per plant, PoL= Pod length, PoW= Pod wide, PoH= Pod height, PPP= Pod per plant, SPP= Seed per pod, SYPP= Seed yield per plant, 100SW= 100 Seed weight, YPP= Yield per plot, YPH= Yield per hectare

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

Traits		D50F	DPM	DHM	PH	BPP	PoL	PoW	PoH	PPP	SPP	SYPP	100SW	YPP	YPH
DFF	G	0.979**	0.731**	0.725**	0.752**	0.615**	-0.475*	-0.123	-0.702**	0.651**	-0.510*	0.524*	-0.648**	0.538**	0.529*
	P	0.977**	0.729**	0.721**	0.744**	0.581**	-0.395	-0.12	-0.690**	0.635**	-0.291	0.492*	-0.641**	0.504*	0.497*
D50%F	G		0.714**	0.702**	0.737**	0.606**	-0.487*	-0.183	-0.654**	0.677**	-0.395	0.551**	-0.661**	0.568**	0.562**
	P		0.712**	0.701**	0.729**	0.565**	-0.402	-0.175	-0.645**	0.658**	-0.225	0.520*	-0.654**	0.537**	0.532*
DPM	G			0.987**	0.772**	0.690**	-0.434*	0.158	-0.607**	0.708**	-0.641**	0.636**	-0.687**	0.642**	0.633**
	P			0.984**	0.766**	0.650**	-0.367	0.157	-0.596*	0.688**	-0.356	0.601**	-0.681**	0.607**	0.600**
DHM	G				0.733**	0.670**	-0.356	0.206	-0.653**	0.699**	-0.653**	0.632**	-0.638**	0.636**	0.628**
	P				0.725**	0.626**	-0.3	0.203	-0.644**	0.678**	-0.357	0.598**	-0.634**	0.602**	0.596**
PH	G					0.645**	-0.563**	-0.22	-0.579**	0.842**	-0.303	0.766**	-0.787**	0.774**	0.764**
	P					0.613**	-0.473*	-0.218	-0.561**	0.822**	-0.146	0.729**	-0.769**	0.736**	0.730**
BPP	G						-0.538**	-0.193	-0.241	0.860**	-0.435*	0.646**	-0.836**	0.638**	0.641**
	P						-0.417	-0.183	-0.232	0.810**	-0.206	0.611**	-0.762**	0.610**	0.610**
PoL	G							0.687**	0.009	-0.716**	0.708**	-0.653**	0.659**	-0.642**	-0.628**
	P							0.599**	0.011	-0.609**	0.302	-0.524*	0.553**	-0.515*	-0.510**
PoW	G								-0.27	-0.362	-0.337	-0.263	0.378	-0.26	-0.264
	P								-0.253	-0.349	-0.146	-0.245	0.365	-0.238	-0.246
PoH	G									-0.323	0.454*	-0.239	0.447*	-0.251	-0.252
	P									-0.315	0.248	-0.222	0.437*	-0.236	-0.237
PPP	G										-0.351	0.929**	-0.783**	0.925**	0.921**
	P										-0.198	0.908**	-0.753**	0.907**	0.905**
SPP	G											-0.416	0.165	-0.408	-0.385
	P											-0.169	0.096	-0.163	-0.16
SYPP	G												-0.521*	1.000**	1.000**
	P												-0.481*	0.998**	0.998**
100SW	G													-0.528*	-0.523*
	P													-0.487*	-0.485*
YPP	G														1.000**
	P														0.999**

FF= Days to first flowering, D50F = Days to 50% flowering, DPM= Days of physiological maturity, DHM= Days of harvest maturity, PH = Plant height (cm), BPP= Branches per plant, PoL= Pod length, PoW= Pod wide, PoH= Pod height, PPP= Pod per plant, SPP= Seed per pod, SYPP= Seed yield per plant, 100SW= 100 Seed weight, YPP= Yield per plot, YPH= Yield per hectare

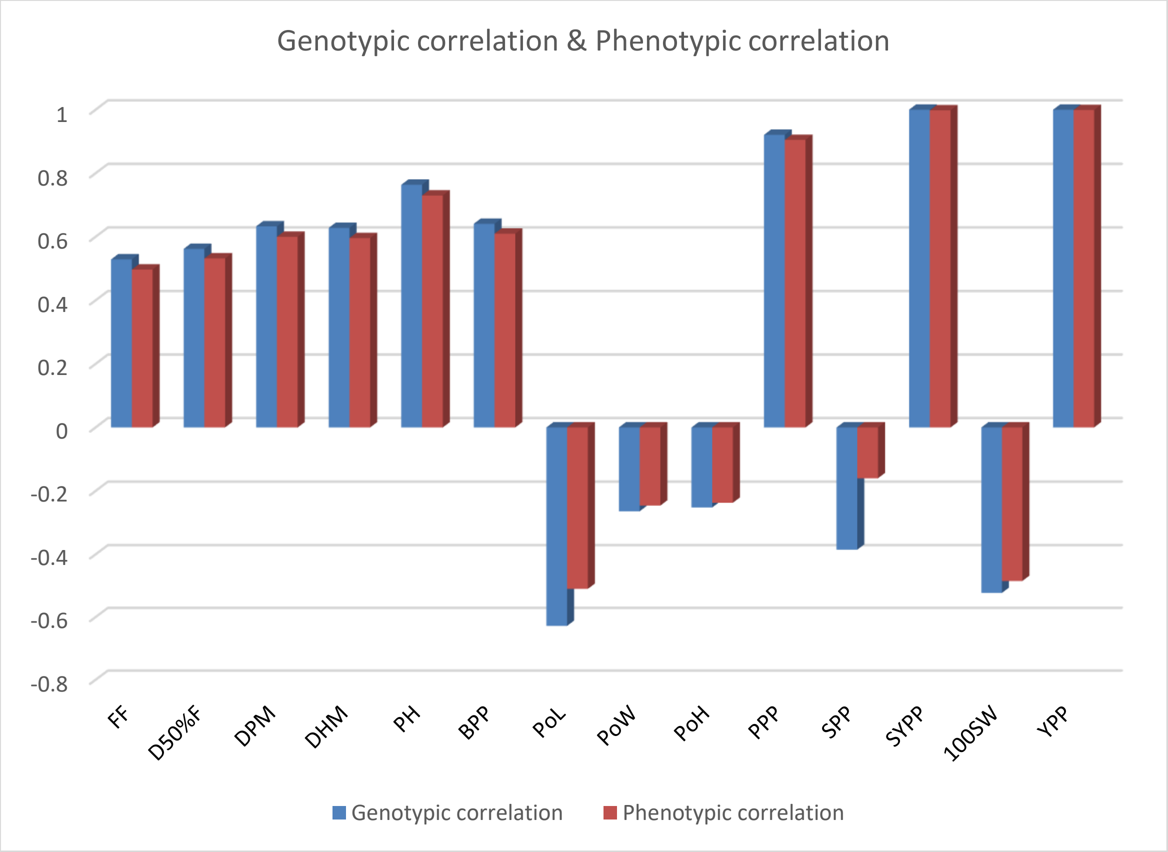


Figure 3. Genotypic and phenotypic correlation of different characters with yield

FF= First flowering, D50F = Days to 50% flowering, DPM= Days of physiological maturity, DHM= Days of harvest maturity, PH = Plant height (cm), BPP= Branches per plant, PoL= Pod length, PoW= Pod wide, PoH= Pod height, PPP= Pod per plant, SPP= Seed per pod, SYPP= Seed yield per plant, 100SW= 100 Seed weight, YPP= Yield per plot, YPH= Yield per hectare.

days to harvest maturity (G=0.725, P=0.721), number of branches per plant (G=0.615, P=0.581), pod per plant (G=0.651, P=0.635), seed yield per plant (G=0.524, P=0.492), yield per plot (G=0.538, P=0.504) and yield per hectare (G=0.529, P=0.497) at both the genotypic and phenotypic levels. Significant negative association was found in case of pod height (G=-0.702, P=-0.690), weight of hundred seeds (G=-0.648, P=-0.641) at both the genotypic and phenotypic levels.

4.3.2 Days to 50% flowering

Days to 50% flowering showed highly positive significant interaction with days to physiological maturity (G=0.714, P=0.712), days to harvest maturity (G=0.702, P=0.701), plant height (G=0.737, P=0.723), number of branches per plant (G=0.606, P=0.565), number of pod per plant (G=0.677, P=0.658), seed yield per plant (G=0.551, P=0.520), yield per plot (G=0.568, P=0.537) and yield per hectare (G=0.562, P=0.532) at both the genotypic and phenotypic levels. Other characters such as, pod height (G=-0.654, P=-0.645) and weight of hundred seeds (G=-0.661, P=-0.654) showed significant negative correlation with days to 50% flowering at both the genotypic and phenotypic level. Inderjit *et al.* (2007) reported that days to 50% flowering were significantly correlated with grain yield which was contradictory to present findings.

4.3.3. Days to physiological maturity

Days to physiological maturity had significant positive association with day to harvest maturity (G=0.987, P=0.984), plant height (G=0.772, P=0.766), number of branches per plant (G=0.690, P=0.650), number of pod per plant (G=0.708, P=0.688), seed yield per plant (G=0.636, P=0.601), yield per plot (G=0.642, P=0.607) and yield per hectare (G=0.633, P=0.600) at both the genotypic and phenotypic levels (Table 4). Significant negative association was found in case of pod height (G=-0.607, P=-0.596) and weight of hundred seeds (G=-0.687, P=-0.681) at both the genotypic and phenotypic levels.

4.3.4. Days to harvest maturity

Days to harvest maturity had significant positive association with plant height (G=0.733, P=0.7625), number of branches per plant (G=0.670, P=0.626), number of pod per plant (G=0.699, P=0.678), seed yield per plant (G=0.632, P=0.598), yield per plot (G=0.636, P=0.602) and yield per hectare (G=0.628, P=0.596) at both the genotypic and phenotypic levels (Table 4). Significant negative association was found in case of pod height (G=-0.653, P=-0.644) and weight of hundred seeds (G=-0.638, P=-0.634) at both the genotypic and phenotypic levels. Chand (1999) observed that maturity of soybean was positively correlated with seed yield.

4.3.5 Plant height

A highly significant and positive association of plant height at both the genotypic and phenotypic levels was observed with number of branches per plant (G=0.670, P=0.626), number of pod per plant (G=0.699, P=0.678), seed yield per plant (G=0.632, P=0.598), yield per plot (G=0.636, P=0.602) and yield per hectare (G=0.628, P=0.596). Pod length (G=-0.563, P=-0.473), pod height (G=-0.579, P=-0.561), weight of hundred seeds (G=-0.787, P=-0.769) showed significant negative correlation with plant height at both the genotypic and phenotypic level.

4.3.6 Branches per plot

Number of branches per plot had significant positive association with number of pod per plant (G=0.860, P=0.810), seed yield per plant (G=0.646, P=0.611), yield per plot (G=0.638, P=0.610) and yield per hectare (G=0.641, P=0.610) at both the genotypic and phenotypic levels (Table 4). Significant negative association was found in case of the weight of hundred seeds (G=-0.836, P=-0.762) at both the genotypic and phenotypic levels.

4.3.7 Pod length

Pod length had significantly positive association with pod wide (G=0.687, P=0.599) and weight of hundred seeds (G=0.659, P=0.553) at both genotypic and phenotypic levels (Table 4). Significant negative association was found in case of number of pod per plant (G=-0.716, P=-0.609) and seed yield per plant (G=-0.653, P=-0.524) at both the genotypic and phenotypic levels.

4.3.8 Pod wide

Pod wide had non-significantly negative association with pod height, number of pod per plants, seed per pod, seed yield per plant, the weight of hundred seeds, yield per plot and yield per hectare at both genotypic and phenotypic levels (Table 4).

4.3.9 Pod height

Pod height had significantly positive association with the weight of hundred seed (G=0.447, P=0.437) at both genotypic and phenotypic levels (Table 4).

4.3.10 Number of pod per plant

Number of pod per plant had significantly positive correlation with seed yield per plant (G=0.929, P=0.908), yield per plot (G=0.925, P=0.907) and yield per hectare (G=0.921, P=0.905) at both genotypic and phenotypic levels (Table 4). Significant negative association was found in case of seed yield per plant (G=-0.783, P=-0.753) at both the genotypic and phenotypic levels.

4.3.11 Number of seed per pod

A non-significant and negative association of number of seed per plant at both the genotypic and phenotypic levels was observed with seed yield per plant, yield per plot and yield per hectare.

4.3.12 Seed yield per plant

A highly significant and positive association of seed yield per plant at both the genotypic and phenotypic levels was observed with yield per plot (G=0.1.000, P=0.998) and yield per hectare (G=1.000, P=0.998). Significant negative association was found in case of weight of hundred seeds (G=-0.521, P=-0.481) at both the genotypic and phenotypic levels.

4.3.13 Weight of hundred seeds

Significant negative association was found in case of yield per plot (G=-0.528, P=-0.487) and yield per hectare (G=-0.523, P=-0.485) at both the genotypic and phenotypic levels.

4.3.14 Yield per plot

Yield per plot had significant positive association with yield per hectare (G=1.000, P=0.999) at both the genotypic and phenotypic levels.

4.4 Path coefficient analysis

Path coefficient analysis is a means of measuring the direct and indirect effects of one variable through the other variables on the end product. In order to find out a clear picture of the inter-relationship between seed yield per plant and other yield attributes, direct and indirect effects were worked out using path analysis at phenotypic level which also measured the relative importance of each component. Seed yield per plant was considered as a resultant (dependent) variable and days to first flowering, days to 50% flowering, days to physiological maturity, days to harvest maturity, plant height, branches per plant, pod length, pod wide, pod height, pod per plant, seeds per pod, weight of seed yield per plant, hundred seeds weight, weight of yield per plot, weight of yield per hectare were causal (independent) variables.

Wright (1921) developed the path coefficient analysis technique and later demonstrated by Deway and Lu (1959) facilitates the portioning of correlation coefficients into direct and indirect contribution of various characters on yield. It is standardized partial regression coefficient analysis. As such, it measures the direct influence of one variable upon other. Estimation of direct and indirect effect of path co-efficient analysis is presented in Table 5.

4.4.1 Days to first flowering

The path analysis showed that days to first flowering had negative direct effect (-0.236) on yield per plant (Table 5). Where it showed positive indirect effect with day to 50% flowering (0.181), days to physiological maturity (0.070), plant height (0.010), branches per plant (0.020), pod length (0.004), pod wide (0.014), pod height (0.050), pod per plant (0.009), seeds per pod (0.010), weight of yield per plot (0.466). It had a negative indirect effect on day to harvest maturity (-0.025), weight of seed yield per plot (-0.020).

4.4.2 Days to 50% flowering

Days to 50% flowering had positive direct effect (0.186) on yield per plant (Table 5). It showed positive indirect effect with days to physiological maturity (0.068), plant height (0.009), branches per plant (0.019), pod length (0.004), pod wide (0.016), pod height (0.047), pod per plant (0.009), seeds per pod (0.009), weight of yield per plot (0.497) and negative indirect effect on days to first flowering (-0.229), day to harvest maturity (-0.025), weight of seed yield per plot (-0.023), hundred seeds weight (-0.025).

4.4.3 Days to physiological maturity

Day to physiological maturity had positive direct effect (0.093) on yield. This character influenced the yield per plant indirectly through days to 50% flowering (0.134), plant height (0.009), branches per plant (0.021), pod length (0.004), pod

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

Characters	Direct effect						Indirect effect								Genotypic correlation with yield
		FF	D50F	DPM	DHM	PH	BPP	PoL	PoW	PoH	PPP	SPP	SYPP	100SW	YPP	
FF	-0.236		0.181	0.070	-0.025	0.010	0.020	0.004	0.014	0.050	0.009	0.010	-0.020	-0.024	0.466*	0.529*
D50%F	0.186	-0.229		0.068	-0.025	0.009	0.019	0.004	0.016	0.047	0.009	0.009	-0.023	-0.025	0.497*	0.562**
DPM	0.093	-0.168	0.134		-0.037	0.009	0.021	0.004	-0.002	0.044	0.009	0.010	-0.027	-0.027	0.570**	0.633**
DHM	-0.038	-0.166	0.132	0.091		0.009	0.020	0.004	-0.006	0.047	0.008	0.009	-0.027	-0.024	0.570**	0.628**
PH	0.009	-0.169	0.133	0.071	-0.026		0.019	0.003	0.019	0.039	0.009	0.007	-0.036	-0.030	0.716**	0.764**
BPP	0.032	-0.119	0.097	0.057	-0.017	0.009		0.005	0.017	0.022	0.009	0.009	-0.026	-0.025	0.571**	0.641**
PoL	-0.009	0.054	-0.072	-0.044	-0.008	-0.020	-0.025		-0.048	-0.019	-0.020	-0.020	0.004	0.003	-0.405	-0.628**
PoW	-0.063	0.025	-0.033	0.009	-0.013	-0.005	-0.008	0.001		0.010	-0.005	-0.003	0.009	0.013	-0.202	-0.264
PoH	-0.068	0.159	-0.117	-0.054	0.024	-0.005	-0.009	-0.004	0.009		-0.005	-0.006	0.008	0.017	-0.202	-0.252
PPP	0.006	-0.143	0.114	0.059	-0.026	0.006	0.020	-0.002	0.022	0.022		0.005	-0.053	-0.031	0.922**	0.921**
SPP	-0.038	0.021	-0.052	-0.045	-0.015	-0.025	-0.027	-0.024	-0.022	-0.034	-0.025		-0.023	-0.021	-0.056	-0.385
SYPP	-0.063	-0.104	0.083	0.047	-0.023	0.003	0.014	-0.003	0.013	0.012	0.004	0.001		-0.019	1.034	1.000**
100SW	0.041	0.145	-0.123	-0.066	0.020	-0.011	-0.024	-0.004	-0.028	-0.035	-0.010	-0.009	0.017		-0.436*	-0.523*
YPP	1.044	-0.107	0.084	0.047	-0.024	0.002	0.013	-0.003	0.011	0.012	0.003	0.000	-0.063	-0.020		1.000**

Residual Effect=0.4392225

** Significant at 1%
 * Significant at 5%

FF= First flowering, D50F = Days to 50% flowering, DPM= Days of Physiological Maturity, DHM= Days of Harvest Maturity, PH = Plant height (cm), BPP= Branches per Plant, PoL= Pod length, PoW= Pod wide, PoH= Pod Height, PPP= Pod per Plant, SPP= Seed per pod, SYPP= Seed Yield per Plant, 100SW=100 Seed Weight, YPP= Yield per plot, YPH= Yield per Hectare height (0.044), pod per plant (0.009), seeds per pod (0.010), weight of yield per plot (0.570). It had a negative indirect effect through days to first flowering (-0.168), days to harvest maturity (-0.037), pod wide (-0.002), weight of seed yield per plant (-0.027), hundred seeds weight (-0.027).

4.4.4 Days to harvest maturity

Day to harvest maturity had negative direct effect (-0.038) on yield. Day to harvest maturity showed indirectly positive influence for days to 50% flowering (0.132), days to physiological maturity (0.091), plant height (0.009), branches per plant (0.020), pod length (0.004), pod height (0.047), pod per plant (0.008), seeds per pod (0.009), and weight of yield per plot (0.570). It had a negative indirect effect through day to first flowering (-0.166), pod wide (-0.006), weight of seed yield per plant (-0.027), hundred seeds weight (-0.024).

4.4.5 Plant height

Plant height had positive direct effect (0.009) on yield. Days to 50% flowering (0.133), days to physiological maturity (0.071), branches per plant (0.019), pod length (0.003), pod wide (0.019), pod height (0.039) pod per plant (0.009), seeds per pod (0.007), weight of yield per plot (0.716) positively influenced the yield per plant indirectly (Table 5). It had a negative indirect effect through day to first flowering (-0.169), day to harvest maturity (-0.026), weight of seed yield per plant (-0.036), hundred seeds weight (-0.030).

4.4.6 Branches per plant

Number of branches per plant had positive direct effect (0.032) on yield. This character influenced the yield per plant indirectly through days to 50% flowering (0.097), days to physiological maturity (0.057), plant height (0.009), pod length (0.005), pod wide (0.017), pod height (0.022), pod per plant (0.009), seeds per pod (0.009), weight of yield per plot (0.571). It had a negative indirect effect through day to first flowering (-0.119), day to harvest maturity (-0.017), weight of seed yield per plant (-0.026), hundred seeds weight (-0.025).

4.4.7 Pod length

Pod length had negative direct effect (-0.009) on yield. Day to first flowering (0.054), weight of seed yield per plant (0.004), hundred seeds weight (0.003) positively influenced the yield per plant indirectly (Table 5). It had a negative indirect effect through days to 50% flowering (-0.072), days to physiological maturity (-0.044), days to harvest maturity (-0.008), plant height (-0.020), branches per plant (-0.025), pod wide (-0.048), pod height (-0.019), pod per plant (-0.020), seeds per pod (-0.020), weight of yield per plot (-0.405).

4.4.8 Pod wide

Pod wide had negative direct effect (-0.063) on yield. Day to first flowering (0.025), day to physiological maturity (0.009), pod length (0.001), pod height (0.010), weight of seed yield per plant (0.009), hundred seeds weight (0.013) positively influenced the yield per plant indirectly (Table 5). It had a negative indirect effect through days to 50% flowering (-0.033), days to harvest maturity (-0.013), plant height (-0.005), branches per plant (-0.008), pod per plant (-0.005), seeds per pod (-0.003), weight of yield per plot (-0.202).

4.4.9 Pod height

Path analysis revealed that pod length had negative direct effect (-0.068) on yield, whereas it had positive indirect effect through day to first flowering (0.159), day to harvest maturity (0.024), pod wide (0.009), weight of seed yield per plant (0.008), hundred seeds weight (0.017). However, it had indirect negative effects through days to 50% flowering (-0.117), days to physiological maturity (-0.054), plant height (-0.005), branches per plant (-0.009), pod length (-0.004), pod per plant (-0.005), seeds per pod (-0.006), weight of yield per plot (-0.202).

4.4.10 Pod per plant

Number of pod per plant had the direct positive (0.006) effect on yield. This character influenced the yield per plant indirectly through days to 50% flowering

(0.114), days to physiological maturity (0.059), plant height (0.006), branches per plant (0.020), pod wide (0.022), pod height (0.022), seeds per pod (0.005), weight of yield per plot (0.922). It had a negative indirect effect through day to first flowering (-0.143), day to harvest maturity (-0.026), pod length (-0.002), weight of seed yield per plant (-0.053), hundred seeds weight (-0.031).

4.4.11 Seed per pod

Path analysis evidenced that seed per pod had negative direct effect (-0.038) on yield whereas, it showed indirect positive effects on seed yield by day to first flowering (0.021). It showed indirect negative effect on seed yield through days to 50% flowering (-0.052), days to physiological maturity (-0.045), days to harvest maturity (-0.015), plant height (-0.025), branches per plant (-0.027), pod length (-0.024), pod wide (-0.022), pod height (-0.034), pod per plant (-0.025), weight of seed yield per plant (-0.023), hundred seeds weight (-0.021), weight of yield per plot (-0.056).

4.4.12 Seed yield per plot

Seed yield per plot had negative direct effect (-0.063) on yield and it had positive and indirect influence on seed yield through days to 50% flowering (0.083), days to physiological maturity (0.047), plant height (0.003), branches per plant (0.014), pod wide (0.013), pod height (0.012), pod per plant (0.004), seeds per pod (0.001), weight of yield per plot (1.034). However it showed negative indirect effect with yield through day to first flowering (-0.104), day to harvest maturity (-0.023), pod length (-0.003), weight of hundred seed (-0.019).

4.4.13 Weight of 100 seed (g)

Weight of 100 seed had positive direct effect (0.041) on yield. Day to first flowering (0.145), day to harvest maturity (0.020), weight of seed yield per plant (0.017) positively influenced the yield per plant indirectly (Table 5). However, it had indirect negative effects through days to 50% flowering (-0.123), days to physiological maturity (-0.066), plant height (-0.011), branches per plant (-

0.024), pod length (-0.004), pod wide (-0.028), pod height (-0.035), pod per plant (-0.010), seeds per pod (-0.009), weight of yield per plot (-0.436).

4.4.14 Yield per plot (kg)

Yield per plot had positive direct effect (1.044) on yield. It had positive indirect effect through days to 50% flowering (0.084), days to physiological maturity (0.047), plant height (0.002), branches per plant (0.013), pod wide (0.011), pod height (0.012), pod per plant (0.003), seeds per pod (0.000). However, it had indirect negative effects through day to first flowering (-0.107), day to harvest maturity (-0.024), pod length (-0.003), weight of seed yield per plant (-0.063), hundred seeds weight (-0.020).

4.5 Multivariate analysis

4.5.1 Principal component analysis (PCA)

Principal component analysis was calculated with twenty two genotypes of soybean which gives Eigen values of principal component axes of coordination of genotypes with the first axes 57.52% of the total variation among the genotypes. First seven Eigen values for seven principal coordination axes of genotypes accounted for 97.12% variation showed in Table 6. Based on principal component scores I and II obtained from the Principal component analysis (Appendix VI), a two-dimensional scatter diagram (Z1-Z2) using component score I as X axis and component score II as Y axis was Constructed, which has been presented in Figure 4. The scatter diagram revealed that there were three apparent clusters and the genotypes were distantly located from each other, which indicated that considerable diversity existed among the genotypes.

4.5.2 Canonical variate analysis

Inter-cluster distances was compute by Canonical Variate Analysis (CVA). The intra and inter-cluster distance (D^2) values were shown in Table 7. When inter-

Table 6. Eigen values and yield percent contribution of 15 characters in 22 genotypes of soybean

Component	Eigen values	Percent variation	Cumulative % of Percent variation
I	8.63	57.52	57.52
II	2.21	14.70	72.22
III	1.27	8.49	80.71
IV	1.02	6.81	87.52
V	0.71	4.70	92.22
VI	0.42	2.77	94.99
VII	0.32	2.13	97.12
VIII	0.18	1.17	98.29
IX	0.15	0.97	99.26
X	0.07	0.46	99.72
XI	0.03	0.19	99.91
XII	0.01	0.07	99.98
XIII	0.00	0.01	99.99
XIV	0.00	0.01	100.00
XV	0.00	0.00	100.00

Table 7. Intra (Bold) and inter cluster distances (D^2) for 22 genotypes of soybean

Cluster	III	II	I
I	19.764	26.478	**0.755**
II	10.45	**0.385**	
III	**0.615**		

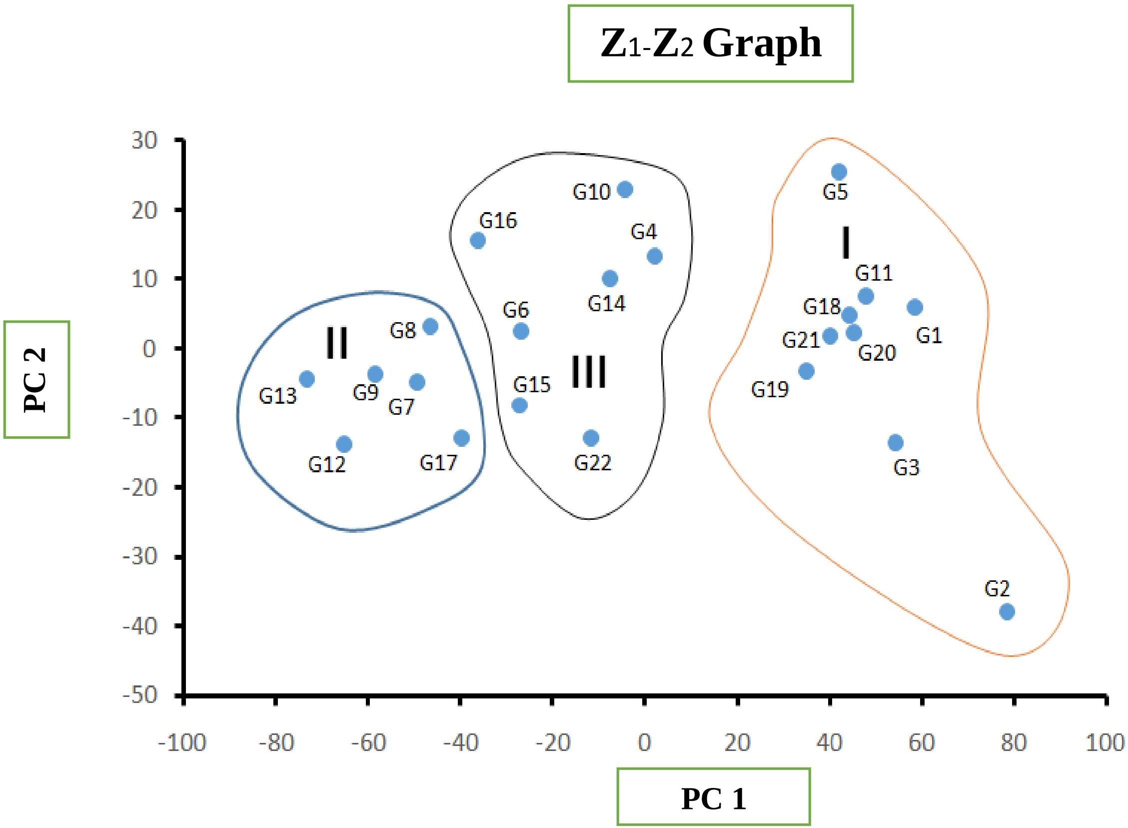


Figure 4. Scatter diagram of 22 soybean genotypes based on their principle component scores superimposed with clustering

cluster distances were higher than the intra- cluster distances, it's indicating broader genetic diversity among the genotypes of different groups. The highest inter-cluster distance was observed between lusters I and II (26.478), followed by between clusters I and III (19.764). In contrast, the lowest inter-cluster distance was observed between cluster II and III (10.45). However, the maximum inter-cluster distance was observed between the clusters I and II (26.478) indicating genotypes from these two clusters if involved in hybridization may produce a wide spectrum of segregating population. On the other hand, the maximum intra-cluster distance was found in cluster I (0.755), which contained of 9 genotypes, while the minimum distance was found in cluster II (0.385) that comprises 6 genotypes. Inter and intra cluster distances were showed in Table 7. Cluster I consists of nearest cluster with D^2 values cluster III (19.764) and farthest cluster with D^2 values II (26.478) (Table 8). Cluster II consists of nearest cluster with D^2 values cluster III (10.45) and farthest cluster with D^2 values I (26.478). Cluster III consists of nearest cluster with D^2 values cluster II (10.45) and farthest cluster with D^2 values I (19.764). According to scatter diagram all the genotypes were apparently distributed into three clusters (Figure 5). It is occupied that higher amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. In the present study the maximum distance existence both cluster II and I at the same level. So the crosses between the genotypes belonging cluster II with cluster I might produce high heterosis. Also the crosses between genotypes from cluster II with I might produce high level of segregating population. So the genotypes belonging to cluster II and cluster I might be selected for future hybridization program.

4.5.3 Principal coordinate analysis (PCO)

Inter genotypic distances as (D^2) as attained by principal coordinate analysis (PCO) for all possible combinations between the couple of genotypes. Inter genotypic distances, as obtained from principal coordinate analysis showed that the highest distance was observed between the G13 and G2 (Table 9).The lowest

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

Sl. No.	**Cluster**	**Nearest Cluster with D^2 values**	**Farthest Cluster with D^2 values**
1	**I**	III (19.764)	II (26.478)
2	**II**	III (10.45)	I (26.478)
3	**III**	II (10.45)	I (19.764)

Table 9. Ten highest and ten lowest inter genotypic distance among 22 genotypes of soybean

10 highest inter genotypic distances				**10 lowest inter genotypic distances**			
Sl	Genotypes	Genotypes	Values	Sl	Genotypes	Genotypes	Values
1	G13	G2	2.480	1	G8	G7	0.139
2	G12	G2	2.411	2	G9	G7	0.160
3	G9	G2	2.264	3	G9	G8	0.201
4	G13	G1	2.244	4	G10	G4	0.206
5	G12	G1	2.217	5	G21	G19	0.227
6	G8	G2	2.199	6	G20	G18	0.241
7	G7	G2	2.195	7	G21	G18	0.265
8	G17	G2	2.187	8	G17	G6	0.296
9	G13	G11	2.143	9	G14	G4	0.312
10	G16	G2	2.122	10	G15	G7	0.333

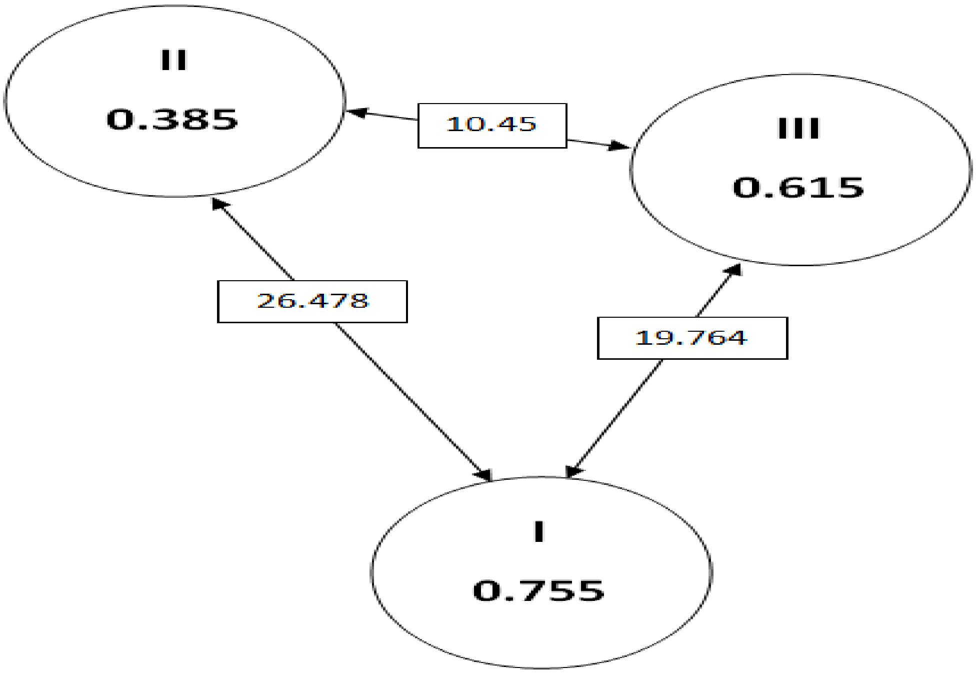


Figure 5. Intra and inter cluster distances (D^2) of 22 genotypes of soybean.

distance was observed between the G8 and G7. The difference between the highest and the lowest inter genotypic distance indicated the prevalence of variability among the 22 genotypes of soybean studied.

4.5.4 Non-hierarchical clustering

From covariance matrix the computations gave non-hierarchical clustering among 22 genotypes of *Glycine* and grouped them into three clusters. The clustering pattern obtained coincided with the apparent grouping patterns performed by principal component analysis (PCA). So, the results obtained through PCA were confirmed by non-hierarchical clustering.

Composition of different clusters with their corresponding genotypes in each cluster is presented in Table 10. Cluster I had the maximum number of nine genotype comprising G1 (GM0011), G2 (GM0009), G3 (GM0001) , G5 (GM0020), G11 (GM0012), G18 (GM0007), G19 (GM0006), G20 (GM0005) and G21 (GM0004) where cluster II had the minimum six genotype G7 (GM0019), G8 (GM0017), G9 (GM0018), G12 (GM0013), G13 (GM001114) and G17 (GM0021).

4.5.5 Cluster mean analysis

The cluster means of 15 different characters (Table 11) were compared and indicated considerable differences between clusters for all the characters studied. The maximum days to first flower were noticed in cluster II (71.78), whereas the minimum days to first flower were noticed in cluster I (60.26). The maximum days to 50% flowering were observed in cluster II (82.33), whereas the minimum days to 50% flowering in cluster I (69.67). The maximum days to physiological maturity were noticed in cluster II (126.61), whereas the minimum days to physiological maturity were noticed in cluster I (106.15). The maximum days to harvest maturity were noticed in cluster II (138.94), whereas the minimum days to harvest maturity were noticed in cluster I (119.04). The maximum plant heights were noticed in cluster II (95.51), whereas the minimum plant height were noticed in cluster I (53.07). The maximum number of branches per plant

Table 10. Distribution of genotypes in different clusters

Cluster	Number of population	Genotypes
I	9	G1, G2, G3, G5, G11, G18, G19, G20 and G21
II	6	G7, G8, G9, G12, G13 and G17
III	7	G4,G6, G10, G14, G15, G16 and G22

Table 11. Cluster mean values of 15 different characters of 22 genotypes of soybean

Parameters	**I**	**II**	**III**
FF	60.26	71.78	66.29
D50%F	69.67	82.33	76.05
DPM	106.15	126.61	123.05
DHM	119.04	138.94	133.43
PH	53.07	95.51	89.44
BPP	3.57	5.57	4.80
PoL	38.16	34.21	36.27
PoW	8.06	7.38	7.90
PoH	5.56	4.93	5.20
PPP	36.55	125.83	85.93
SPP	2.82	2.72	2.68
SYPP	15.54	27.22	21.52
100SW	15.82	9.16	9.78
YPP	0.78	1.32	1.07
YPH	1.56	2.64	2.13

FF= First flowering, D50F = Days to 50% flowering, DPM= Days of physiological maturity, DHM= Days of harvest maturity, PH = Plant height (cm), BPP= Branches per plant, PoL= Pod length, PoW= Pod wide, PoH= Pod height, PPP= Pod per plant, SPP= Seed per pod, SYPP= Seed yield per plant, 100SW= 100 Seed weight, YPP= Yield per plot, YPH= Yield per hectare

was noticed in cluster II (5.57) and the minimum (3.57) in cluster II. Cluster I showed the highest pod length (38.16) and cluster II showed the lowest (34.21). The highest pod wide were noticed in cluster I (8.06), whereas the minimum pod wide noticed in cluster II (7.38). The maximum pod height were noticed in cluster I (5.56), whereas the minimum pod height were noticed in cluster II (4.93). The maximum (125.83) and the minimum (36.55) number of pod per plant were observed in cluster II and I, respectively. The maximum number of seed per plant was observed in cluster I (2.82), whereas the minimum number of seed per plant was observed in cluster III (2.68). The maximum (27.22) and the minimum (15.54) seed yield per plot were noticed in cluster II and I, respectively. Weight of 100 seed was the highest in cluster I (15.82) and the minimum in cluster II (9.16). The maximum yield per plot were observed in cluster II (1.32) and the minimum in cluster I (0.78). The maximum yield per hectare was observed in cluster II (2.64), whereas the minimum yield was observed in cluster I (1.56).

4.5.6 Contribution of characters towards divergence of the genotypes

The characters contribution towards the divergence obtained from principle component analysis is presented in Table 12. The character, which gave highest absolute magnitude for vector 1, was considered to be responsible for primary differentiation. Same as, the characters, which gave highest absolute magnitude for vector 2 was considered to be responsible for secondary differentiation. If same character given equal magnitude for both the vectors than the characters considered responsible for primary as well as secondary differentiation. In vector 1 (Z_1), the important characters responsible for genetic divergence in the axis of differentiation were pod length (0.2018), pod wide (0.0752), pod height (0.1821), number of seed per pod (0.1014), weight of 100 seed (0.2707). In vector 2 (Z_2), the second axis of differentiation days to first flowering (0.2176), days to 50% flowering (0.1730), day to physiological maturity (0.2511), day to harvest maturity (0.2825), plant height (0.0202), pod length (0.3195), pod wide (0.5069) and weight of 100 seeds (0.0212) were important because all these

Table 12. Relative contributions of the 15 characters of 22 genotypes of soybean to the total divergence

Parameters	Vector-1	Vector-2
FF	-0.2784	0.2176
D50%F	-0.2795	0.1730
DPM	-0.2912	0.2511
DHM	-0.2852	0.2825
PH	-0.3061	0.0202
BPP	-0.2660	-0.0577
PoL	0.2018	0.3195
PoW	0.0752	0.5069
PoH	0.1821	-0.4526
PPP	-0.3193	-0.1802
SPP	0.1014	-0.1881
SYPP	-0.2873	-0.2239
100SW	0.2707	0.0212
YPP	-0.2886	-0.2142
YPH	-0.2879	-0.2190

FF= First flowering, D50F = Days to 50% flowering, DPM= Days of physiological maturity, DHM= Days of harvest maturity, PH = Plant height (cm), BPP= Branches per plant, PoL= Pod length, PoW= Pod wide, PoH= Pod height, PPP= Pod per plant, SPP= Seed per pod, SYPP= Seed yield per plant, 100SW= 100 Seed weight, YPP= Yield per plot, YPH= Yield per hectare

characters had positive signs. On the other hand, days to first flowering (-0.2784), days to 50% flowering (-0.2795), days to physiological maturity (-0.2912), days to harvest maturity (-0.2852), plant height (-0.3061), number of branches per plant (-0.2660), number of pod per plant (-0.3193), seed yield per plant (-0.2873), yield per plot (-0.2886) and yield per hectare (-0.2879) possessed the negative sign in the first axis of differentiation and number of branches per plant (-0.0577), pod height (-0.4526), number of pod per plant (-0.1802), number of seed per pod (-0.1881), seed yield per plant (-0.2239), yield per plot (-0.2142) and yield per hectare (-0.2190) possessed negative signs in the second axis of differentiation that means these had minor role in the genetic divergence.

4.5.7 Selection of genotypes as parent for hybridization program

Identification and selection of genetically diverse parents is an urgent step for hybridization program. Three factors (selection of specific variety from a cluster, choice of particular cluster and relative contribution of the character to the total divergence) should be considered for selecting parents for a breeding program (Chaudhary *et al.*, 1977). Thorough knowledge of genetic diversity of the crop is necessary for parental selection that maximizes genetic improvement (Rahman *et al.*, 2011). So, in the present study genotypes were to be selected on the basis of specific objectives. From the crosses between genetically distance parents a high heterosis could be produced. Considering the magnitude of cluster mean and agronomic performance the genotype G2 (GM0009) for the minimum days to 50% flowering and day to harvest maturity from cluster I, G13 (GM0014) for the maximum plant height, branches per plant, pod per plant and yield from cluster II, G1 for maximum weight of 100 seed and pod length from cluster I. Therefore considering group distance and other agronomic performance G2 and G13 soybean genotypes may be suggested for future hybridization program.

SUMMARY AND CONCLUSION

The experiment was conducted during the period from December 2017 to May 2018 in rabi season in the experimental field of Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka. The aim of the study was to identify the characters contributing to genetic diversity, identify divergent parent for hybridization program, asses the magnitude of genetic divergence in genotypes, determine the variability in respect of yield, identify yield contributing characters, the degrees of association among the characters and their direct and indirect effects of 22 genotypes of soybean [*Glycine max* (L). Merr.]. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Data on various yield attributing characters such as, day to first flowering, days to 50% flowering, day to physiological maturity, day to harvest maturity, plant height (cm), number of branches per plant, pod length (mm), pod wide (mm), pod height (mm), number of pod per plant, number of seeds per plant, 100 seed weight (g), seed yield per plot and yield ton/ha were recorded. 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 except pod wide, seed per pod, seed yield per plot and seed yield per hectare. The genotype G2 was the lowest days to first flowering (46.33 DAS) while G13 was the highest days to first flowering (74.33 DAS). The genotype G3 was the earliest to 50% days flowering (56.33 DAS) while G12 was late to days of 50% flowering (86). The genotype G2 was the lowest days to physiological maturity (82 DAS) while G16 was height days to physiological maturity (135.33 DAS). The genotype G2 was the lowest days to physiological maturity (91.33 DAS) while G16 was height days to physiological maturity

(144.67 DAS). The maximum plant height (105.22 cm) was recorded by the genotype G13 and the lowest plant height (29.55 cm) was recorded by G2. The maximum number of branches recorded in G13 (6.22) and G20 (2.55) genotype showed the minimum number of branches. The minimum pod length was recorded by the genotype G12 (33.01 mm) and G1 (42.58 mm) showed the maximum pod length. The maximum pod wide was recorded by the genotype G1 (9.88 mm) and G2 (6.02 mm) showed the minimum pod wide. The minimum pod height was recorded by the genotype G5 (4.48 mm) and G2 (8.77 mm) showed the maximum pod height. The genotype G1 was the minimum number of pod per plant (27) while genotype G13 was the maximum number of pod per plant (138.89). The minimum number of seed per pod was recorded by the genotype G22 (2.33) and G6 (3.11) showed the maximum number of seed per pod. The genotype G11 (11.27 g) showed the minimum seed yield per plant and the maximum seed yield per plant was recorded in the G13 (32.88 g). The genotype G17 (6.63 g) showed the minimum hundred seed weight and the maximum hundred seed weight was recorded in the G1 (20 g). In case of yield, genotype G11 (1.17 ton) produced the minimum and G13 (3.13 ton) produced highest yield ton per hectare.

Genetic diversity of twenty-two soybean genotypes based on fifteen characters was measured through multivariate analysis. The 22 genotypes fell into three distant clusters. The cluster I comprised the maximum number of genotypes (9). The cluster II and III comprised 6 and 7 genotypes, respectively. The highest inter-cluster distance (26.478) was observed between the cluster I and II and the highest distant genotypes were G2 and G13. The lowest inter-cluster distance (10.45) was observed between the cluster II and III. The inter-cluster distances were larger than the intra-cluster distances. The intra-cluster distance in the entire three clusters was more or less low indicating that the genotypes within the same cluster were closely related. Day to first flowering, days to 50% flowering, day to physiological maturity, day to harvest maturity, plant height and number of branches per plant were the important component characters having higher contribution to the genetic divergence. Number of pod per plant, pod length, number of seed per pod, seed yield per plant, the weight of hundred seeds, seed yield per plot and seed yield per hectare was the yield contributing character. The result of the present study revealed that a wide variability exists among the collected soybean genotypes.

Furthermore, from the findings of the present study, the following conclusions could be drawn:

- Wide range of genetic diversity existed among 22 soybean genotypes which were grouped into three clusters and most diverse genotypes were G2 (GM0009) and G13 (GM0014). That variability could be used for future breeding program of soybean in Bangladesh.

- High heritability coupled with high genetic advance in percent of mean was observed in plant height, number of branches per plant, Pod per plant, seed yield per plant, weight of 100 seed, yield per plot and yield per hectare. Hence, yield improvement in soybean would be achieved through selection of these characters.

- Highly significant positive association of seed yield per plant was observed with days to first flowering, days to 50% flowering, days to physiological, days to harvest maturity, plant height, number of branches per plant, number of pod per plant, seed yield per plant and yield per plot. This results suggested that seed yield per plant can be increased by improving these characters.

- Days to 50% flowering, days of physiological maturity, plant height, number of branches per plant, pod per plant, weight of 100 seed and yield per plot showed positive direct effect on yield. So yield improvement was associated with these characters. So yield improvement was associated with these characters.

- The genotypes of clusters I was more diverse from the genotypes of cluster II.
- 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:

- Genotypes G2 (GM0009) and G13 (GM0014) could be included in future hybridization program in the response of increase soybean yield.

- The maximum variability was found for days to first flowering, days to 50% flowering, days of physiological maturity, days of harvest maturity, plant height and number of branches per plant. So selection based on these characters could be effective for the improvement of soybean yield.

- The genotypes of cluster I and II could be used as parents for the further breeding program to develop soybean variety.

REFERENCES

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

Akhter, M. and Sneller, C.H. (1996). Yield and yield components of early maturing soybean genotypes in the mid-south. *Crop Sci*. **36**: 877-882.

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

Antalina, (1999). Recent research and industrial achievement for soybean in Japan. *Proceeding of RIELT-JIRCAS Workshop on Soy Research*; Sep. 28, 2000.

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

Anonymous. (2015). North Carolina Soybean Producers Associations, Inc. http://ncsoy.org/media-resources/uses-of-soybeans

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

Arshad, M., Ali, N. and Ghafoor, A. (2006). Character correlation and path coefficient in soybean *Glycine max* (L.) Merr. *Pakistan J. Bot.* **38**(1): 121-130.

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

Ball, R., McNew, R., Vories, E., Keisling, T., and Purcell, L. (2001). Path analyses of population density effects on short-season soybean yield. *Agron. J.* **93**:187 - 195.

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

Barros, J.P.A., Sediyama, T., Silva, F.C.D.S., Bezerra, A.R.G., Rosa, D. P. and Oliveira, D.S. (2015). Estimates of genetic parameters and efficiency in selection for branching capacity in soybean genotypes. *J. Agron.* **15**: 39-44.

Batugal, P.A. (1999). The role of International cooperation in the development of biotechnology in coconut. **In**: Current advances in coconut biotechnology. C. Oropeza, J.L. Verdeil, G.R. Ashburner, R. Cardena and J.M. Samantha, (eds.). Kluwer Academic Publisher, London. pp. 19-30.

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

Board, J.E., Kang, M.S. and Harville, B.G. (1997). Path analyses identify indirect selection criteria for yield of late-planted soybean. *Crop Sci.* **37**: 879-884.

Board, J.E., Kang, M.S. and Harville, B.G. (1999). Path analyses of the yield formation process for late-planted soybean. *Agron. J.* **91**: 128-135.

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

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

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

Chandel, K.K., Patel, N.B. and Patel, J. B. (2013). Genetic variability analysis in soybean (*Glycine max* L. Merr.). *AGRES Intl. e-J.* **2**(3): 318-325.

Chaudhary, B.D., Kakar, S.N. and Singh, R.K. (1977). Estimation of genetic parameters in barley (*Hordeum vulgare* L.). *Theol. Appl. Genet.* **49**(4): 153-156.

Chowdhury, M.A.Z., Alam, M.S., Rahim, M.A., and Mirza, S.H. (1996). Genetic divergence for yield and its morphological components in soybean. *J. Asiatic Soc. Bangladesh Sci.* **22**:125-130.

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

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

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

Clarke, G.M. (1980). Statistics and experimental design. 2nd Edition. Edward Arnold. London. Pp 196

Cooper, R.L. (1975). Modifying morphological and physiological characteristics of soybean to maximize yields. **In**: World Soybean Research L.D. Hil, (ed.). Proc. World Soybean Research Conference. The Interstate Printers and Publishers, Danvile, IL. pp. 230-236.

Das, A. and De. D. (2000). Nutritive value of Guatemala grass (*Tripsacum laxum*) as affected by method of conservation. *J. Hill Res*. **13**(2): 119-121

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

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

Digby, P.N., Gaiway and Lane, P. (1989). Genstat 5, A second course. Oxford Science Publication, Oxford. pp: 103-108.

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

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

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

Ghafoor, A., Gulbaz, F.N., Afzal, M., Ashraf, M. and Arshad, M. (2003). Inter-relationship between SDS-PAGE markers and agronomic traits in chickpea (*Cicer arietinum* L.). *Pakistan J. Bot.* **35**(4): 613-624.

Ghafoor, A., Zubair, M. and Malik, B.A. (1990). Path analysis in mash (*Vigna mungo* L.). *Pakistan J. Bot.* **22**(2): 160-167.

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

Ghodrati, G. (2013). Study of genetic variation and broad sense heritability for some qualitative and quantitative traits in soybean (*Glycine max* L.) genotypes. *Curr. Opin. Agric.* **2**(1): 31-35.

Gopalan, C., Ramashastry, B.V. and Balasubramanian, S.C., (1994). Nutritive Value of Indian Foods, Indian Council of Medical Research. pp.24-26

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

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

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

Hossain, M.K., Alam, N., Silva, J.A.T., Biswas, B.K. and Mohsin, G.M. (2013). Genetic relationship and diversity based on agro-Morphogenic characters in yard long bean (*Vigna sesquipedalis* L. Fruw) germplasm. *Intl. J. Plant. Breed.* **7**(2): 129-135.

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

Iqbal, S., Mahmood, T., Tahira, Ali, M., Anwar, M. and Sarwar. M. (2003). Path-coefficient analysis in different genotypes of soybean [*Glycine max* (L.) Merr.]. *Pakistan J. Biol. Sci.* **6**(12): 1085-1087.

Iqbal, Z., Arshad, M., Ashraf, M., Naeem, R., Malik, M.F. and Waheed, A. (2010). Genetic divergence and correlation studies of soybean [*Glycine max* (L.) merr.] genotypes. *Pakistan J. Bot.* **42**(2): 971-976.

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

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

Jain, P.K. and Ramgiry, S.R. (2000). Genetic diversity of metric traits in Indian germplasm of soybean (*Glycine max* L. Merr.). *Adv. Plant Sci.* **13**: 127-31.

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

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

Jordan, N. (1992). Differential interference between soybean (*Glycine max*) varieties and common cocklebur (*Xanthium strumarium*): A path analysis. *Weed Sci.* **40**(4):614 - 620.

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

Karpechenko, G.D. (1925). On the chromosome of phaseolinae. *Bull. Appl. Bot. Plant Breed*. **14**: 143-148.

Kawakami, J. (1930). Chromosome numbers in leguminosae. *Bot. mag. Tokyo.* **44**: 319-329.

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

Kumar, A., Pandey, A., Aochen, C. and Pattanayak, A. (2014). Evaluation of genetic diversity and interrelationships of agro-Morphological characters in soybean (*Glycine max* L. Merr.) genotypes. *Natl. Acad. Sci. India* **85**(2): 397-405.

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

Lambert, J. M. and Williams, W. T. (1966). Multivariate methods in plant ecology, IV. Comparison of informational analysis and association analysis. *J. Ecol.* **54**: 635-664.

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

Mahalanobis, P.C. (1936). On the generalized distance in statistics. *Natl. Inst. Sci. India.* **12**: 49-55.

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

Malik, M., Qureshi, A., Ashraf, M., and Ghafoor, A. (2006a). Genetic variability of the main yield related characters in soybean. *Int. J. Agric. Biol.* **8**(6):815 - 819.

Malik, M., Qureshi, A., and Ghafoor, A. (2006b).Utilization of diverse germplasm for soybean yield improvement. *Asian J. Plant Sci.* **5**(4):663 - 667.

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

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

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

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

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

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

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

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

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

Nogueira A.P.O., Sediyama, T., Sousa, L.B., and Hamawaki O.T., (2012). Análise de trilha e correlações entre caracteres em soja cultivada em duas épocas de semeadura. *Biosci. J.* **28:** 877-888.

Nooghab, N.A.S., Jelodar, N.B. and Bagheri, N. (2014). Genetic diversity evaluation of different varieties of soybean (*Glycine max* L.) based on morphological traits. *J. Bio. Env. Sci.* **5**(5): 221-228.

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

Patil, S.S., Naik, M.R., Patil, A.B. and Ghodke, U.R. (2011). Genetic diversity in soybean. *Legume Res.* **34**(1): 68-70.

Pandey, J. and Torrie, J. (1973). Path coefficient analysis of seed yield components in soybeans (*Glycine max* (L.) Merr.).*Crop Sci.* **13**:505 **-** 507.

Peluzio, J.M., Sediyama, C.S., Sediyama, T. and Reis, M.S. (1998). Phenotypic correlations between genotype and environment some characters soybean in Pedro Afonso. *Tocantins.* **45**: 303-308,

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

Qiu J.L. and Change R.Z., (2010).The Origin and History of Soybean. MA, USA, Cambridge Press.

Rao, C.R. (1952). Advanced statistical methods in biometrical research. John Willy and sons. New York. 390.

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

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

Rahman, M.M., Rasul, M.G., Bashar M.K., Syed M.A. and Islam, M.R. (2011). Parent selection for transplanted Aman rice breeding by morphological, physiological and molecular diversity analysis. *Libyan Agric. Res. Centre J. Int.* **2**: 26-28.

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

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

Robinson, H. F., R. E. Comstock and P. M. Harvey (1949). Estimates of heritability and the degree of dominance in Corn. *Agron. J.* 41: 353 - 359.

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

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

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

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

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

Shivasubramanian, S. and Menon, M. (1973). Heterosis and inbreeding depression in rice. *Madras Agril. J.* **60**: 1139.

Shivashankar, G. and Viswanatha, S.R. (1989). Soybean introduction and improvement in Karnataka state of India. 4th Conferencia Mundial de Investigación en soja, Buenos Aires.

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

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

Shukla, S.; Singh, K.; and Pushpendra. (1998). Correlation and path coefficient analysis of yield and its components in soybean (*Glycine max* L. Merrill). Soybean Gen. *Newsl.* **25**:67 - 70.

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

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

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

Singh, J. and Yadav, H.S. (2000). Factors determining seed yield in early generation of soybean. *Crop Res. Hisar*. **20**: 233-243.

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

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

Singh .G. (2010) .The Soybean: Botany, Production and Uses pp 1. Printed and bound in the UK by CPI Antony Rowe.

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

Swapnil, S.S., Singh, V.J., Gampala, S. and Rangare, N.R. (2014). Assessment of genetic variability of the main yield related characters in soybean. *Intl. J. Food Agric. Vet. Sci.* **4**(2): 69-74.

Tiwari, S. P. and Bhatnagar, P. S. (1991). Pod shattering as related to other agronomic attributes in soybean. *Trop. Agric.* (Trinidad) **68**(1):102 - 103.

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

Taware, S., Halvankar, G., Raut, V., and Patil, V. (1997). Variability, correlation and path analysis in soybean hybrids. Soybean Gen. *Newsl.* **24**:96 – 98

Tomooka, N. (1991). Genetic diversity and landrace differentiation of mungbean, *Vigna radiata* (L.) wilczek and evaluation of its wild relatives (The subgenus ceratotrophics) as breeding materials. *Tech. Bull. Tropical Res. Centre Japan*. **28**: 1.

Vavilov, N.I. (1951). Phytogeographic basis of plant breeding. The origin, variation, immunity and breeding of cultivated plants. *Chronica Bot.* **13**: 1-366.

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

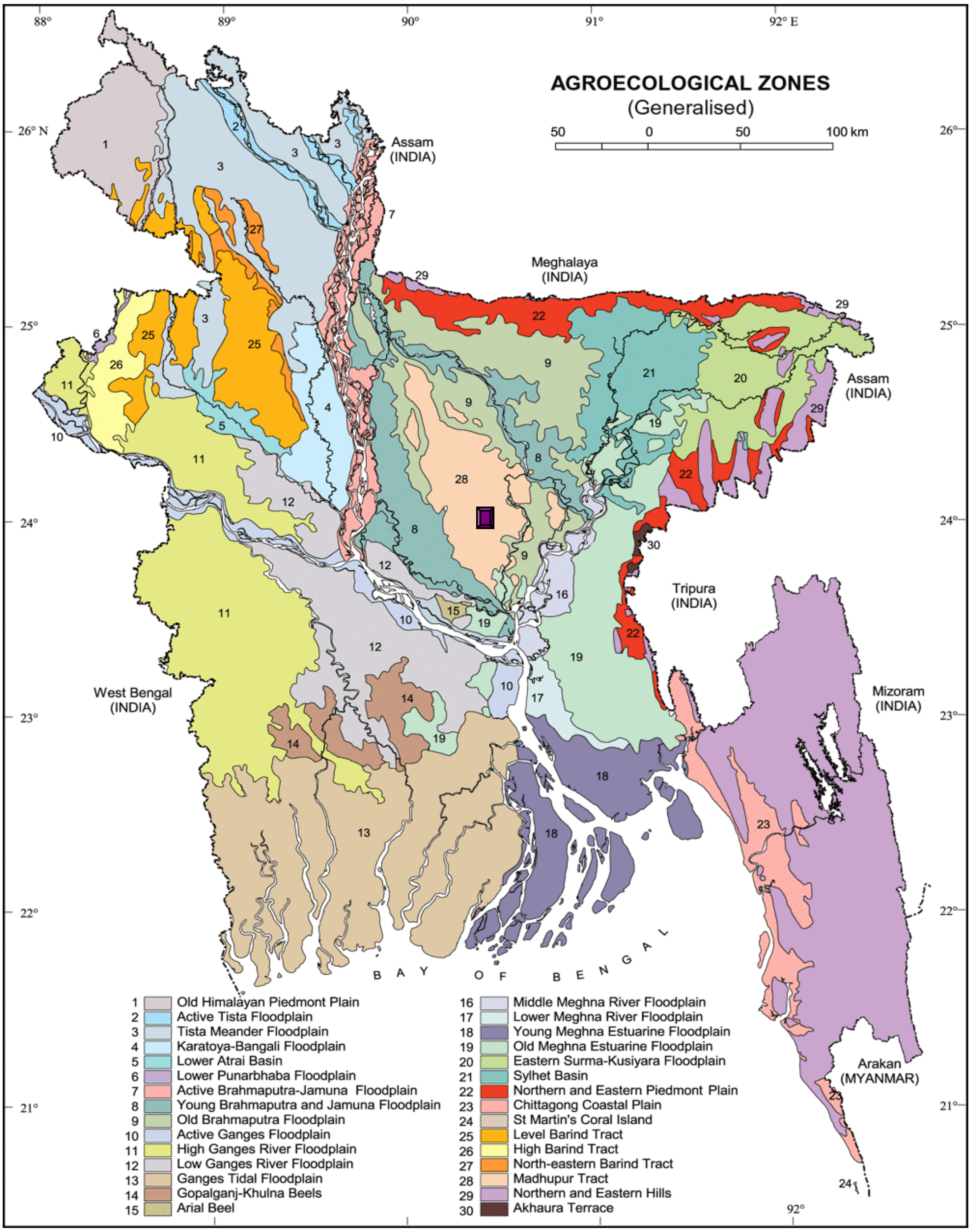
Wright, S. (1921). Correlation and causation. *J. Agric. Res.* **20**: 202-209.

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

Yadev, G.C., Singh, P.K., Singh, B.B. and Verma, R. (2001). Genetic variability and Path coefficients in urdbean. *Indian J. Pulses Res.* **14**(2): 143-144.

APPENDICES

Appendix 1. Map showing the experimental site under study



🟪 Experimental area under study

Appendix II. Monthly average temperature, relative humidity and total rainfall of the experimental site during the period from December, 2017 to May 2018.

Month	Air temperature (°C)			Relative Humidity (%)	Rainfall (mm) (total)
	Maximum	**Minimum**	**Average**		
December, 2017	31	23	27	55	63.9
January, 2018	28	20	24	43	0
February, 2018	32	22	27	40	3.2
March, 2018	37	25	31	44	34.1
April, 2018	36	28	32	54	327.1
May, 2018	35	28	31.5	65	689.8

Source: Bangladesh Metrological Department (Climate and Weather division), Agargaon, Dhaka-1207.

Appendix III. Morphological, physical and chemical characteristics of initial soil (0-12cm depth) of the experimental pot

A. Physical composition of the soil

Soil separates	% Composition
Sand	36.90
Silt	26.40
Clay	36.66
Texture class	Clay loam

B. Chemical composition of the soil

SL No.	Soil characteristics	Analytical Data
01.	Organic carbon(%)	0.82
02	Total N(kg/ha)	1790.00
03	Total S(ppm)	225.00
04	Total P(ppm)	840.00
05	Available N (kg/ha)	54.00
06	Available P(kg/ha)	69.00
07	Exchangeable K (kg/ha)	89.00
08	Available S(ppm)	16.00
09	PH(1:2.5 soil to water)	5.55
10	CEC	11.23

Source: Central library, Sher-e-Bangla Agricultural University, Dhaka-1207

Appendix IV. Mean performance of various growth parameter and yield components of 15 characters of 22 genotypes of soybean.

Treatment	FF	D50F	DPM	DHM	PH	BPP	PoL	PoW	PoH	PPP	SPP	SYPP	100SW	YPP	YPH
G1	52.67	61.67	114.67	128.00	47.33	3.66	42.58	9.88	6.02	27.00	2.89	15.60	20.00	0.78	1.53
G2	46.33	57.33	82.00	91.33	29.55	3.33	35.08	6.02	8.77	31.11	3.00	15.67	17.82	0.77	1.56
G3	48.67	56.33	101.33	118.33	46.00	2.94	38.19	8.04	5.43	39.55	2.89	15.73	14.20	0.76	1.53
G4	64.33	73.00	120.67	129.33	90.11	4.50	34.72	7.68	5.10	66.33	2.56	16.80	9.76	0.82	1.67
G5	69.67	76.67	115.67	125.33	75.43	3.66	38.72	7.84	4.48	27.44	2.78	12.85	13.33	0.65	1.30
G6	70.67	81.00	116.00	129.33	98.50	5.77	40.49	7.49	4.96	96.11	3.11	19.80	6.90	1.00	2.01
G7	71.33	79.67	129.33	143.00	87.89	5.66	33.65	7.26	4.84	121.33	2.44	26.53	10.19	1.30	2.57
G8	71.67	83.67	130.67	144.33	92.55	5.22	34.51	7.59	4.57	114.11	2.56	26.41	10.07	1.28	2.60
G9	71.00	79.67	130.00	143.67	96.50	5.89	35.14	7.34	5.10	127.67	2.78	26.25	10.04	1.27	2.53
G10	72.33	80.67	126.67	136.33	92.22	4.11	33.55	7.86	5.21	67.55	2.56	16.01	9.27	0.81	1.55
G11	68.33	79.67	121.33	134.33	34.00	5.11	37.45	8.43	5.44	38.44	2.67	11.27	11.24	0.58	1.17
G12	74.00	86.00	121.67	134.33	98.66	5.00	33.01	7.04	4.54	137.33	2.78	29.32	8.03	1.42	2.83
G13	74.33	84.33	131.00	142.67	105.22	6.22	34.74	7.84	5.38	138.89	2.78	32.88	10.02	1.58	3.13
G14	61.67	73.33	124.67	135.67	87.22	4.66	37.30	7.80	4.79	77.11	2.78	19.77	8.52	0.98	1.97
G15	62.00	70.67	124.33	133.00	83.11	6.11	34.82	8.22	5.43	103.67	2.56	24.97	9.05	1.25	2.50
G16	68.33	80.33	135.33	144.67	99.22	3.78	35.71	7.95	5.10	97.55	2.89	29.41	11.27	1.46	2.90
G17	68.33	80.67	117.00	125.67	92.22	5.44	34.22	7.24	5.14	115.67	3.00	21.96	6.63	1.10	2.17
G18	61.33	70.67	105.33	118.33	65.39	3.00	36.93	8.17	5.27	36.22	2.89	16.62	16.55	0.84	1.63
G19	65.33	74.00	104.33	117.67	61.05	4.11	38.70	7.93	4.68	49.11	2.67	18.64	16.00	0.93	1.87
G20	64.67	77.33	104.33	118.67	57.99	2.55	39.56	7.95	4.89	38.11	2.67	16.22	17.57	0.84	1.70
G21	65.33	73.33	106.33	119.33	60.88	3.78	36.21	8.28	5.10	42.00	2.89	17.24	15.66	0.87	1.74
G22	64.67	73.33	113.67	125.67	75.67	4.67	37.31	8.33	5.78	93.21	2.33	23.91	13.70	1.17	2.30
Min	**46.33**	**56.33**	**82.00**	**91.33**	**29.55**	**2.55**	**33.01**	**6.02**	**4.48**	**27.00**	**2.33**	**11.27**	**6.63**	**0.58**	**1.17**
Max	**74.33**	**86.00**	**135.33**	**144.67**	**105.22**	**6.22**	**42.58**	**9.88**	**8.77**	**138.89**	**3.11**	**32.88**	**20.00**	**1.58**	**3.13**
Mean	**65.32**	**75.15**	**117.11**	**129.05**	**76.21**	**4.51**	**36.48**	**7.83**	**5.27**	**76.61**	**2.75**	**20.63**	**12.08**	**1.02**	**2.03**

Appendix V. Analysis of variance and LSD of 15 yield and yield contributing characters of soybean

Sources of variation	df	FF	D50%F	DPM	DHM	PH	BPL	PoL	PoW	PoH	PPP	SPP	SYPP	100SW	YPP	YPH
Genotypes	21	175.603**	196.309**	480.044**	465.914**	1525.963**	3.587**	18.449**	1.48	2.278*	4566.598**	0.113	106.320**	44.023**	0.236	0.934
Replication	2	1.682	2.652	4.288	0.318	79.976	1.418	1.999	0.037	0.164	723.818	0.053	43.926	0.512	0.091	0.335
Error	42	0.745	0.493	1.113	1.62	26.878	0.45	5.428	0.08	0.064	226.455	0.079	11.098	0.582	0.024	0.092

FF= Days to first flowering, D50F = Days to 50% flowering, DPM= Days of Physiological Maturity, DHM= Days of Harvest Maturity, PH = Plant height (cm), BPP= Branches per Plant, PoL= Pod length, PoW= Pod wide, PoH= Pod Height, ,PPP= Pod per Plant, SPP= Seed per pod, SYPP= Seed Yield per Plant, 100SW=100 Seed Weight, YPP= Yield per plot, YPH= Yield per Hectare

* Significant at 5% level of probability

** Significant at 1% level of probability

Appendix VI. Z_1-Z_2 score of 22 genotypes of soybean

Genotype number	**PC1**	**PC2**
G1	58.57	6.03
G2	78.44	-37.96
G3	54.33	-13.54
G4	2.16	13.28
G5	42.06	25.49
G6	-27.07	2.44
G7	-49.45	-4.85
G8	-46.64	3.28
G9	-58.58	-3.65
G10	-4.39	22.93
G11	47.85	7.66
G12	-65.44	-13.88
G13	-73.36	-4.46
G14	-7.65	10.16
G15	-27.35	-8.19
G16	-36.41	15.57
G17	-39.95	-12.94
G18	44.41	4.7
G19	34.94	-3.31
G20	45.18	2.29
G21	40.24	1.91
G22	-11.87	-12.94