

**EVALUATION OF YIELD AND YIELD CONTRIBUTING CHARACTERS
OF TWENTY GENOTYPES OF SOYBEAN (*Glycine max* L. Merrill)**

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DHAKA-1207, BANGLADESH**

JUNE, 2016

**EVALUATION OF YIELD AND YIELD CONTRIBUTING CHARACTERS
OF TWENTY GENOTYPES OF SOYBEAN (*Glycine max* L. Merrill)**

BY

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REGISTRATION NO. 10-03909

A thesis

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 (MS)
IN
GENETICS AND PLANT BREEDING
SEMESTER: Jan -June, 2016**

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CERTIFICATE

*This is to certify that the thesis entitled, "EVALUATION OF YIELD AND YIELD CONTRIBUTING CHARACTERS OF TWENTY GENOTYPES OF SOYBEAN *Glycine max L. Merrill*" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING**, embodies the result of a piece of bona fide research work carried out by **NAZMUL ALAM KHAN**; **Registration No. 10-03909**, under my supervision and guidance. No part of this thesis has been submitted for any other degree or diploma.*

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

*Dated: June, 2016
Dhaka, Bangladesh*

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*Dedicated to
My Beloved Parents*

ACKNOWLEDGEMENTS

First of all, the author expresses his gratitude to the “Omnipotent Creator” for his never-ending blessing, it is a great pleasure to express profound thankfulness to his respected parents, who entiled much hardship inspiring for prosecuting his studies, thereby receiving proper education.

*The author expresses his sincere gratitude, heartfelt respect and immense indebtedness to his reverend Supervisor, **Prof. Dr. Mohammad Saiful Islam**, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for his sincere guidance, scholastic supervision, constructive criticism and constant inspiration throughout the course and in preparation of the manuscript of the thesis.*

*The author wishes to extend his deepest gratitude and sincere appreciation to his Co-supervisor, **Prof. Dr. Md. Shahidur Rashid Bhuiyan** Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for his utmost cooperation and constructive suggestions to conduct the research work as well as preparation of the thesis.*

*He is grateful to **Prof. Dr. Kamal Uddin Ahmed**, Honourable Vice Chancellor, Sher-e-Bangla Agricultural University, Dhaka for providing me with all possible help during my studies.*

*He expresses his sincere respect to the Chairman, **Prof. Dr. Jamilur Rahman** and my honourable teachers **Prof. Dr. Md. Sarowar Hossain**, **Prof. Dr. Naheed Zeba**, **Prof. Dr. Firoz Mahmud**, **Associate Prof. Dr. Md. Ashaduzzaman Siddiquee** and **Associate Prof. Dr. Abdur Rahim**, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for their teaching, direct and indirect advice, encouragement and co-operation during the study period.*

*He would like to thank **Dr. Md. Abdul Malek**, Honourable principle Scientific Officer of Bangladesh Agricultural Research Institute (Plant Genetic Resources Centre, BARI) for his help to supply 20 breeding line of soybean.*

The author also would like to thank all the staff of Bagladesh Agricultural Research Institutte of BARI, Gazipur for their immense support.

The author also would like to thank Arif, Mati, Mitoo, Babu, Tania, Tonny and all of his family members and friends who have helped him with technical support to prepare this thesis paper.

He found no words to thank his parents Abdul Hakim Khan and Nazma Khanam for their unquantifiable love, sacrifice and never ending affection for bringing my dream to proper shape. They are my constant source of zeal, inspiration and enthusiasm in the critical moment of my studies.

June, 2016

The Author

SAU, Dhaka

Some commonly used abbreviations

Full word	Abbreviation	Full word	Abbreviation
Advanced	<i>Adv.</i>	Genotypic coefficient of variation	GCV
Agricultural	<i>Agril.</i>	Genotypic variance	δ^2g
Agriculture	<i>Agric.</i>	Gram	g
Agriculturist	<i>Agricult</i>	Hectare	Ha
Agronomy	<i>Agron.</i>	Heritability in broad sense	H^2_b
Analysis of variance	ANOVA	International	<i>Intl.</i>
And others	<i>et al.</i>	Journal	<i>J.</i>
Applied	<i>Appl.</i>	Mean sum of square	MS
As for example	e.g.	Meter	m
Bangladesh	BD	National	<i>Natl</i>
Bangladesh Agricultural Research Institute	BARI	International	<i>Intl.</i>
Bangladesh Institute of Nuclear Agriculture	BINA	Percent	%
Biology	<i>Biol.</i>	coefficient of variation	CV%
Biotechnology	<i>Biotechnol.</i>	Phenotypic variance	δ^2p
Centi-meter	cm	Phenotypic coefficient of variation	PCV
Company	Co.	Standard error	SE
Completely randomized design	CRD	Standard deviation	SD
Degree (Latitude and longitude)	°	Journal	<i>J.</i>
Degree Celsius	°C	Mean sum of square	MS
Degrees of freedom	df	Research	<i>Res.</i>
Environment	<i>Env.</i>	University	<i>Univ.</i>
Environmental	<i>Environ.</i>	Journal	<i>J.</i>
Environmental coefficient of variation	EVC		
Environmental variance	δ^2e		
Etcetera	etc.		
Genetic Advance	GA		
Genetic advance in percentage of mean	GAM		
Genotype	G		

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**EVALUATION OF YIELD AND YIELD CONTRIBUTING CHARACTERS OF
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By

NAZMUL ALAM KHAN

ABSTRACT

A field experiment was conducted during November 2016 to February 2017 to study the genetic variability, correlation, path coefficient analysis and genetic diversity for quantitative traits of twenty soybeans (*Glycine max* L. merill) genotypes in randomized complete block design with three replications at the research farm of Sher-E-Bangla Agricultural University, Dhaka. Experiment showed significant differences among the genotypes. Phenotypic variance was higher than that of genotypic variance for all the characters. Phenotypic coefficients of variation (PCV) was also close to genotypic coefficients of variation (GCV) for all the characters indicating that environment had influence on the expression of these characters. The high heritability coupled with high genetic advance in percent of mean observed in plant height, leaf breadth at top, leaf per plant, pods per plant, seeds per plant, hundred seed weight and seed yield per plant which would be select for future breeding program. High heritability coupled with low genetic advance in percent of mean was observed in germination percentage, leaf breadth at middle and leaf breadth at top. Germination percentage (0.404), plant height (1.464), leaf breadth at base (0.288), leaf breadth at middle (0.401), leaf breadth at top (0.426), pods per plant (0.908), seeds per plant (0.867), hundred seed weight (0.907) and days to maturity (0.535) showed highly significant and positive correlation with seed yield at genotypic levels revealed that selection based on these traits would ultimately improve the seed yield. Path coefficient analysis revealed that hundred seed weight (0.907) had the highest positive direct effect on seed yield. Hence, thrust has to be given for these characters in future breeding program to improve the yield in soybean. Multivariate analysis based on 13 agronomic characters indicated that the twenty genotypes were grouped into five distant clusters. The inter cluster distance was maximum between cluster I and cluster III (38.541). The highest intra-cluster distance was found in cluster V (4.76). It can be concluded genotypes G7 (ASOMEME), G8 (GMOT-13), G12 (BOSS) from cluster I, G10 (BARI SOYBEAN 5) and G18 (BINA SOYBEAN 3) from cluster III, G14 (BINA SOYBEAN 4), G15 (BINA SOYBEAN 1) and G16 (SOHAGH) from cluster V could be suitable for future hybridization program or in view of seed yield for releasing as soybean varieties.

INTRODUCTION

A legume crop called soybean (*Glycine max* L. Merrill) grown in tropical, sub-tropical and temperate region. The cultivated soybean belongs to the family leguminosae under sub-family papilionaceae and is a self-pollinated crop having chromosome number of $2n=40$. It is originated in China with *Glycine ussuriensis* as probable progenitor (Vavilov, 1951). Soybean (*Glycine max* L. Merrill.) is a “Miracle bean” having a great industrial value (Hossain *et al.*, 2003). It is a source of both plant protein and fat and is considered to be the most important oil and legume crop in the world, in terms of total production and international trade. Soybean seed contains about 40-45% protein and 18-20% oil and provides around 60% of the world supply of vegetable protein and 30% of the oil (Fehr, 1998). The protein of soybean is called complete protein because it supplies sufficient amount of various kinds of amino acids required for building and repairing the body tissues. Soya consumption may reduce the risk of colon cancer. It can be used for human food and for industrial purposes and also for livestock feed (Singh and Hymowitz, 1999). Soybean is second only to groundnut in terms of oil content (18 to 22% comprising 85% unsaturated fatty acids and is free from cholesterol) among food legumes, so it is highly desirable in the human diet (Antalina *et al.*, 1999). As a good source of protein, unsaturated fatty acids, minerals like Ca and P including vitamin A, B and D, soybean can meet up different nutritional needs (Rahman, 1982).

Soybean is not only used as oil but also it has multiple uses like; soya-chatni, soya-milk, soya-meat, soya-dhal, soya khichuri, soya-curd, soya flour, tofu, roasted soyabean snack and many other retail food products (Khaleque, 1985). It is also frequently used in mayonnaise, salad dressings, frozen foods, imitation dairy and meat products and commercially baked goods. Soybean oil won't interfere with the taste of the food because it has little flavor.

The present nutritional situation of Bangladesh is a matter of great concern. The prime nutritional problem of the country is that of protein-energy

malnutrition. Most of our people are suffering from malnutrition. Soybean can play an important role to meet up the protein deficiency problem. Soybean is regarded as an ideal food for the people of Bangladesh as it contains high quality of protein and reasonable quantity of oil as a source of energy (Khaleque, 1985). Due to high price of animal protein like meat, fish, egg, milk, etc. the poor people of our country cannot afford to take it. Soya protein products can replace animal-based foods (Henkel, 2000). Soybean was introduced in Bangladesh around 1942; but its cultivation did not expand satisfactorily. In recent years MCC, CDP, BARC, BARI, BAU, BCSIR and other some NGOs (GKF, RDRS etc.) are trying to expand its cultivation. This crop can be cultivated throughout the year with less or even without irrigation as a cash or food crop in many ecological conditions of Bangladesh. Many studies provide with evidence that supports the role of whole soya foods in a cancer-preventing diet (Amadou *et al.*, 2009). Consumption of soya may reduce the risk of colon cancer (Symolon *et al.*, 2004).

Soybean improves the soil by fixing the atmospheric nitrogen through *Rhizobium* bacteria that lives in root nodules. Steward (1966) stated that in a season the plants can fix 94 kg/ha nitrogen in the soil. According to Keyser and Li (1992) the *Bradyrhizobium japonicum* can fix atmospheric nitrogen about 300 kg/ha/year in symbiosis with soybean. The cultivation of soybean in Bangladesh doesn't expand satisfactorily. . Soybean is very suitable crop to fit into the cropping systems of Bangladesh. However according to the BBS report 2013-2014 areas being utilized under soybean cultivation was 150472 acres and total production was 112024 metric tons (BBS, 2016). A wide range of climatic and edaphic conditions are suitable for soybean cultivations. With well-adapted cultivars, soybean can be cultivated throughout the year in Bangladesh (Rahman, 1982; Haque *et al.*, 1976). In the northern part, it can also be grown in summer without affecting the production of transplant aman rice. Even, it can be grown in char and haor areas after receding flood water with no tillage and minimum inputs. But still the yield of soybean is very

discouraging compared to other soybean producing countries. This is mainly due to use of low yield potential varieties and poor cultivation technologies i.e. lack of application of inoculums, fertilizer etc. Seeds yield and protein content of soybean are both heritable traits (Imasande, 1992).

Breeding attempts have added greatly to improve yield potential, regional adaptation through tolerance or resistance to biotic and abiotic stress, plant variety and feed traits. Quantum of genetic variability and the degree to which heritable and non-heritable variations are associated with the characters should be given priorities for the degree of genetic improvement.

Yield is a very complex character and it is managed with a large number of genes and significantly affected from the environment and quality traits influence the yield both directly and indirectly. Thus assortment depending on these traits has greater possibility of success in comparison to selection for yield alone. Yield components and yield are usually linked mainly to linkage and pleiotropic effects of gene. The genotypic correlation indicates the extents to that the two characters are controlled by the exact same group of genes are experiencing the physiological basis of their expression. Information regarding direct and indirect effects which contribute in yield will be added advantages in improvement of the crop. Wright (1921) introduced path co efficient analysis technique through which it can be measured the direct and indirect role in various components which make the total correlation to yield. Depending on this study, the individual character is identified which help to facilitate in breeding program for better yield.

Paterson *et al.* (1991) suggested that evaluation of genetic diversity would promote the efficient use of genetic variations in the breeding program. The analysis of genetic divergence is destined to the identification of appropriate genitors in order to obtain hybrids with higher heterotic effect, which provide more segregation in recombination. For any crop improvement programme, analysis of genetic diversity is the first and foremost step. Information on genetic diversity among genotypes has several important applications for crop

improvement. This information can be useful to classify germplasm for identification of cultivars, assist in selection of parents for hybridization and reduce number of genotypes needed to ensure sampling of a broad range of genetic variability. Genetically diverse parent is a pre-requisite to improve the chances of selecting better segregants for various characters. When such parents utilized in cross breeding programme, they are likely to produce high heterotic effect and wide spectrum of variability (Barh *et al.*, 2014). Moreover, evaluation of genetic diversity is important to know the sources of genes for a particular trait within the available germplasm (Tomooka, 1991). Multivariate analysis act as a useful tool to quantify the degree of divergence between the biological populations at genotypic level and to assess the relative contribution of different components to the total divergence both inter and intra cluster level (Jangale *et al.*, 1994).

Mahalanobis (1936) developed D^2 statistics which provides a measure of degree of divergence between two genotypes which are under comparison. In an anthropometric survey Mahalanobis used this at first. It considers any character which creates variation and subsequent effect on other characters. This technique has been applied in various crops to choose genotypes for further breeding programs. Clustering of genotypes based on D^2 analysis will be useful in choosing suitable parental lines for heterosis breeding. These type of studies are also useful in parental selection for hybridization to recover superior transgressive segregants and it can further result into release of improved open pollinated varieties for commercial cultivation.

Therefore, the present investigation was undertaken on “Evaluation of Yield and Yield Contributing Characters of Twenty Genotypes of Soybean (*Glycine max* L. Merrill)” was under taken involving advanced breeding lines with the following objectives.

- ❖ To assess genetic diversity among the soybean genotypes.

- ❖ To assess variability present among the soybean genotypes.
- ❖ To know the association and contribution of yield contributing characters on yield.
- ❖ To identify the distant parents for future improvement through hybridization.
- ❖ To find out the superior genotypes for utilization as variety in future breeding program.

REVIEW OF LITERATURE

Soybean was domesticated in the 11th century BC around northeast of China. Soybean belongs to the family Leguminosae under sub-family Papilionaceae that grows in tropical, subtropical, and temperate climates. Soybean (*Glycine max* L. Merrill) is one of the world's leading sources of vegetable oil and plant protein, both of which are very well adapted to the nourishment of human beings. Extensive research works have been conducted on soybean in different parts of the world. Many studies on the variability, interrelationship, path coefficient analysis, heritability and genetic advance have been carried out in many countries of the world. Some such works relevant to the present investigation have been reviewed in this chapter. The review of literature concerning the studies presented under the following heads.

2.1 Acquaintance of soybean

The genus glycine has 10 species which are twining climbers or procumbent perennial herbs and subtropical or warm temperate regions. *Glycine max*, the most important species, is cultivated for grain, oil and fodder. Locally it's known as Garikalai and Talkalai (Kaul and Das, 1986).

2.2 Nomenclature of soybean

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) in 1914. 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 (Anonymous, 2015).

2.3.1 Plant height

Plant height is considered as an important plant character related to grain yield in soybean. Plant height has been found to vary from genotype to genotype. *Bangar et al.* (2003) reported that phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for plant height in soybean.

Sirohi et al. (2007) studied variability and correlation for twelve characters including plant height with 25 diverse genotypes of soybean and reported that plant height had high genotypic and phenotypic coefficient of variation and heritability associated with high genetic advance as percentage of mean indicating the possibility of improving this trait through direct selection. Similar result was also observed by *Khan et al.* (2000) in soybean through studying 86 diverse genotypes of soybean.

Data on sixteen yield related traits of 25 soybean genotypes were subjected to analysis of variance, heritability, correlation coefficient and path analysis in soybean by *Malik et al.* (2007) and reported highly significant differences among the genotypes for all the characters examined including plant height. High heritability was recorded for hundred grain weight, plant height, days to maturity, pods per plant and grain yield indicating the additive type of gene action governing the traits. Similar result was also reported by *Sultana et al.* (2005) through studying thirty genotypes of soybean.

According to *Archana et al.* (1999) were found high genotypic coefficient of variation for plant height and high heritability estimates accompanied with high genetic advance were found in 30 genotypes of soybean (*Glycine max*).

Mehetre et al. (1998_a), *Roy and Roquib* (1998) and *Shrivastava and Shukla* (1998) all have reported that plant height showed high genetic coefficient of variation. High heritability accompanied with high genetic advance.

Major et al. (1996) conducted an experiment with one hundred germplasm of soybean (*Glycine max*) in a random block design during 1992-1994. They observed high genetic advance for plant height. *Rajarathinam et al.* (1996)

studied genetic advance, heritability and genetic variability for 8 yield components in 35 genotypes of soybean (*Glycine max*). They reported high estimates of heritability and genetic advance for plant height.

Dobhal and Gautam (1995) observed a wide range of variability for plant height. They also observed high broad sense heritability coupled with high genetic advance for the same. Jagtap and Mchetre (1994) studied variability, heritability and genetic advance for 12 quantitative traits in 10 indigenous and exotic varieties of soybean (*Glycine max*). Highest genotypic coefficient of variation was observed for plant height.

2.3.2 Branching

Branch per plant is an important primary yield contributing characters. Bangars *et al.* (2003) found that the GCV and PCV estimates were the highest for branch number per plant. Similar result was also reported by Sultan *et al.* (2005) in soybean.

Malik *et al.* (2007) studied variability on branch number in 27 genotypes of soybean and reported that there had a wide range of variability in branch number ranging 0-4.6 per plant . Similar result was also reported by ZhongWen *et al.* (2009) in soybean.

Kamwal and Singh (2009) studied variability, heritability and character association for seed yield and its contributing traits in soybean and observed high genetic coefficient of variation along with high heritability for number of branches per plant.

High genetic coefficient of variation along with high heritability was observed for number of branches per plant (Bhandarker, 1999). Roy and Roquib (1998) also noticed that primary branches per plant had high heritability along with high values of genetic advance.

According to Sridhara *et al.* (1998) number of branches through of pods per plant seemed to be significant contributors to seed yield. Praneetha and Thamburaj (1997) studied vegetable soybean and indicated that branches per

plant can be considered for crop improvement in vegetable soybean. Rajarathinam *et al.* (1996) recorded heritability, genetic advance and genetic variability for 8 yield components in 35 genotypes of soybean (*Glycine max*). High estimates of heritability and genetic advance were recorded for number of primary branches per plant. Jagtap and Mehetre (1994) estimated variability, heritability and genetic advance for 12 quantitative characters in 10 indigenous and exotic varieties of *Glycine max*. Highest genotypic coefficient of variation was found in number of branches on main stem.

Roy and Roquib (1998) noticed that primary branches per plant had high heritability along with high values of genetic advance.

Rajanthinam *et al.* (1996) recorded heritability genetic advance and genetic variability for 8 yield components in 35 genotypes of soybean (*Glycine max*). High estimates of heritability and genetic advance were recorded for number of primary branches per plant.

2.3.3 Days to flowering

Genetic variability was studied by Sirohi *et al.* (2007) using 25 soybean genotypes and found that GCV was moderate for days to flowering whereas high for days to maturity.

Heritability and genetic advance as per centage of mean were high for days to flowering. Similar result was also observed by Agrawal *et al.* (2001) in soybean.

Khan *et al.* (2000) studied heritability among yield determining components in 86 diverse maturity genotypes of soybean and found that heritability value for days to maturity was 90.98%.

Bhandarkar (1999) found high genotypic and phenotypic coefficient of variation for days to flowering. According to them heritability and genetic advance was also high for days to flowering Jangale *et al.* (1994) studied 34 genotypes of soybean (*Glycine max*) and showed considerable variation for the

10 characters. High heritability was observed for days to initiation of flowering and days to 50% flowering.

2.3.4 Days to maturity

Days to maturity are one of the important criteria of any crop yields. It is influenced by genotypes and various environmental factors. Variation, heritability and genetic advance for days to maturity are usually studied for developing early maturing varieties. Several workers found significant genetic variation among different genotypes of soybean.

Chettri *et al.* (2003) evaluated 18 elite soybean genotypes and found that days to maturity was significantly correlated with plant height and path coefficient estimates showed that days to maturity positively affected grain yield. Bhandarkar (1999) observed high genetic coefficient of variation, heritability and genetic advance as percent of mean for days to maturity, which indicated the presence of further scope for improvement in these traits.

Nehru *et al.* (1999) derived heritability from data on I6 yield and quality components of 49 soybean genotypes grown during Kharif 1988. They observed that the days to maturity had high heritability, but low genetic advance. Mehetre *et al.* (1998_a) conducted an experiment with 41 soybean genotypes in field traits during 1994-96. They observed significant variation for days to maturity. Dobhal and Goutam (1995) conducted an experiment during 1991 and 1992 with 65 lines of soybean (*Glycine max*). A wide range of variability was observed for days to maturity. Jangale *et al.* (1994) studied 34 genotypes of soybean (*Glycine max*) and observed considerable variation for the 10 characters. They recorded high heritability for days to maturity. Ghatge and Kadu (1993) recorded information on heritability and genetic advance from data on 16 yield components in 58 promising genotypes of soybean. Highest variability was observed for days to maturity. Heritability was high for days to 50 percent flowering followed by days to maturity.

Bhandarkar (1999) observed high genetic coefficient of variation heritability and genetic advance as percent of mean for days to maturity which indicates further scope for improvement in this traits.

Sultana *et al.* (2005) reported that genotypic coefficient of variation was high for days to maturity in soybean.

2.3.5 Number of pods per plant

Pods per plant is the primary yield components of soybean variation of this character was invariably studied in connection with yield. In general, the higher is the pod number the higher is the seed yield and height was observed by several researchers.

Mehetre *et al.* (1998_a) showed significant variation for pods per plant. High heritability values accompanied by high genotypic coefficient of variation for pods per plant. Roy and Roquib (1998) observed pods per plant had high heritability along with high values of genetic advance. Shrivastava and Skula (1998) estimated genetic parameters of variation. A significant amount of variability was observed for pods per plant. Pods per plant was the major yield contributing characters in soybean.

Mehta *et al.* (2000) observed number of pods per plant high genotypic coefficient of variation and phenotypic coefficient of variation. High heritability accompanied with high genetic advance as percentage of mean for number of pods per plant indicated that this may be controlled by additive gene action. Bhandarkar (1999) observed a high coefficient of variation and moderate heritability for mature pods per plant which indicated further scope for improvement in this trait.

Scoffel *et al.* (1996) studied the behavior of soybean yield components and found that soybean yield components vary according to cultivar and sowing date. The number of pods per plant was the yield component that had the most effect on the yield Chandankar *et al.* (2000) recorded considerable variability among 25 genotypes of soybean for number of pods per plant.

Mehta *et al.* (2000) observed that the high heritability accompanied with high genetic advance as percentage of mean for number of pods per plant. According to them this trait might be controlled by additive gene action. Bhandarkar (1999) also observed a high coefficient of variation and moderate heritability for mature pods per plant, which indicated further scope for improvement in this trait.

Mehetre *et al.* (1998_a) showed significant variation for pods per plant. They reported high heritability values accompanied by high genotypic coefficient of variation for pods per plant. Roy and Roquib (1998) observed pods per plant had high heritability along with high values of genetic advance. Shrivastava and Shukla (1998) estimated genetic parameters of variation in soybean. A significant amount of variability was observed for pods per plant, which was the major yield contributing character in soybean. Mehetre *et al.* (1997_a) investigated 41 soybean genotypes and showed significant variation for pods per plant. High heritability accompanied by high GCV was also observed for pods per plant. Praneetha and Thamburaj (1997) observed high genotypic coefficient of variation and heritability for pod yield per plant. Rajarathinam *et al.* (1996) estimates genetic advance, heritability and genetic variability for 8 yield components in 35 genotypes of soybean (*Glycine max* L.). High estimates of heritability and genetic advance were recorded for pod number per plant. Dobhal and Goutam (1995) observed a wide range for variability for pods per plant. High broad sense heritability coupled with high genetic advance was also observed for pods per plant. According to Singh *et al.* (1995) the maximum genotypic coefficient of variation and highest heritability were recorded for pods per plant.

Sirohi *et al.* (2007) studied variability for seed yield and yield components among 25 soybean genotypes and found that pods per plant and seed yield had high genotypic and phenotypic variation of variation and had high heritability associated with high genetic advance.

Thirty soybean genotypes were evaluated for estimating genotypic coefficient of variation, phenotypic coefficient of variation for yield attributes and yield in soybean by Bandyopadhyay (2003). High heritability along with high genetic advance was recorded for pods per plant. Similar result was also reported by Malik *et al.* (2007) in soybean.

Sultana *et al.* (2005) studied with a view to find out genetic variability, correlation and path coefficient analysis for yield and its quantitative characters in 30 soybean genotypes and found significant variation in pods per plant. The higher genetic variability was found in pods per plant followed by hundred seed weight. High heritability together with high genetic advance in percentage of mean were observed for pods per plant, Hundred seed weight and branch per plant. Similar result was also reported by Karnwal and Singh (2009) in soybean.

2.3.6 Seeds per pod

Seeds per pod are an important primary yield component. Normally, higher number of seeds per pod is desirable. Chandankar *et al.* (2000) studied the genetic divergence among 25 genotypes of soybean and found considerable variability among the genotypes for number of seeds per pod. Also Jangle *et al.* (1994) on studying 34 genotypes of soybean (*Glycine max*) reported that considerable variation exists for the 10 characters including seeds per pod. They estimated high heritability for number of seeds per pod. Malhotra (1973) found significant variation in 37 soybean varieties for some characters. He observed highest coefficient of genotypic variation and predicted genetic advance as a percentage of mean with number of seeds per pod.

2.3.7 Hundred seed weight

It is an important grain character, which is directly related to seed yield of soybean. Hundred seed weight that reflects the seed size is also an important

component trait. It differs widely from genotype to genotype and influenced by some factors of production. A good numbers of research works have been conducted on this character.

Cho-Jinwoong *et al.* (2004) studied the effects of crop density on the growth and yield of soybean cultivars and observed that the plant density significantly affected seed weight.

Archana *et al.* (1999) studied genetic variability, heritability and genetic advance in 30 genotypes of soybean (*Glycine max*). They observed high genotypic coefficient of variation for hundred seed weight. The same showed high heritability estimates accompanied with high genetic advance, which indicated the possibility of being controlled by additive gene action and selection may be effective. Bhandarkar (1999) observed high heritability and genetic advance as percent of mean for hundred seed weight, which indicated the possibilities of improvement of this traits contributing to yield. Nehru *et al.* (1999) reported that hundred seed weight had high heritability, but low genetic advance.

Mehetre *et al.* (1998_a) studied hundred seed weight, which showed high genetic coefficient of variation, high heritability values accompanied by high genetic advance. In other study Mehetre *et al.* (1997) reported high heritability accompanied by high GCV for hundred seed weight. Major *et al.* (1996) also observed high genotypic and phenotypic coefficients of variation for hundred seed weight.

2.3.8 Harvest index

Harvest index measures the partitioning of photosynthates to economic yield and is considered as one of the most important physiological yield component (Donald and Hamblin, 1976). Harvest index is the ratio of the grain yield to the biological yield (Donald, 1962) and the biological yield is the total yield of plant material (Donald and Hamblin 1976). Increased harvest index results increased crop yield, probably because of improved portioning of dry matter to reproductive parts (Paniappan, 1985).

Chandankar *et al.* (2000) studied the genetic divergence among 25 genotypes of soybean and recorded considerable variability among the genotypes for harvest index. Shrivastava and Shukla (1998) evaluated nine yield related traits of soybean at Jabalpur during Kharif 1994 and 1995 and the data were used for estimating genetic parameters of variation. Biological yield had high heritability coupled with high-expected genetic advance.

2.3.9 Yield per plant

Yield is the most important characters almost in every breeding programme. It is a complex trait influenced largely by a number of characters and factors of production. A good number of reports revealed the existence of variability in yield among different genotypes of soybean.

According to Boros (2003) seed number per plant had the highest direct effect on seed yield per plant and lower direct effects on pods per plant and hundred seed weight.

According to Chettri *et al.* (2003) grain yield was significantly correlated with days to maturity and number of grain per pod at the genotypic level and hundred seed weight did not show any correlation with grain yield. They concluded that the number of grain per pod, days to maturity, number of pods per plant and plant height positively affected grain yield.

Nawracca and Uczkiewiwcz (2003) analyzed the variability of yield component traits and found highest variability for seed yield per plant ($V = 57.08\%$).

Osinaka and Laudanski (2002) showed close relationship among the productivity traits such as seed weight, seed number and pod number of plant.

Agarwal *et al.* (2001) conducted an experiment in India during the Kharif season of 1998. Rabi season of 1999 and Kharif season of 1999 to evaluate 196 soybean genotypes. Cluster per plant and pods per plant were the most important selection criteria for increasing seed yield. Raut *et al.* (2001) found that seed yield showed positive significant association with number of pods per

plant, 100 seed weight and harvest index both at genotypic and phenotypic levels.

Shrivastava *et al.* (2001) observed highest positive direct effects on seed yield for the number of branches per plant, followed by days to maturity, plant height, 100 seed weight, biological yield and harvest index. Plant height on the other hand had a negative effect on yield. Sudaric *et al.* (2001) conducted a research to assess the genetic advance, seed yield and quality of 29 promising lines compared to four standard cultivars. Phenotypic variability, wide sense heritability, genetic gain and relative genetic gain from selection were calculated for seed yield. Results of biometrical analyses indicated that advances in yield and quality had been achieved.

Mehta *et al.* (2000) studied variability for eleven characters with 60 diverse genotypes of soybean. Seed yield per plant had high genotypic and phenotypic coefficient of variation and indicated the possibility of improving this trait through direct selection. Bhandarkar (1999) observed a high genetic coefficient of variation for yield per plant. Moderate heritability was observed for seed yield per plant. Siahsar and Rezia (1999) evaluated 285 soybean lines and found that the maximum variation in seed yield could be attributed to the pods/plant, seeds/pod and 100 seed weight. It was concluded that in order to improve soybean cultivars, selection, should focus on plant with higher number of pods per plant and higher seed weights.

Mehetre *et al.* (1998_a) showed significant variation for yield per plant. High heritability values accompanied by high genetic coefficients of variation and high genetic advance were observed for yield per plant. Shrivastava and Shukia (1998) revealed a significant amount of variability for seed yield per plant and had high heritability coupled with high-expected genetic advance Mehetre *et al.* (1997_a) estimated high heritability accompanied by high genotypic coefficient of variation for yield per plant. Pranetha and Thamburaj (1997) studied variability in vegetable soybean and observed that the yield per plant had high genotypic coefficients of variation and heritability.

Major *et al.* (1996) revealed that genotypic and phenotypic coefficient of variation and genetic advance were high for grain yield. Rajarathinam *et al.* (1996) estimated genetic advance, heritability and genetic variability in 35 genotypes of soybean (*Glycine max*). They recorded high heritability and genetic advance for seed yield of soybean. Dobhal and Gautam (1995) estimated a wide range of variability for yield per plant; high broad sense heritability coupled with high genetic advance for yield per plant. Singh *et al.* (1995) observed maximum genotypic coefficient of variation occurred for grain yield per plant.

2.4 Variability, heritability and genetic advance

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

2.5 Correlation co-efficient

Correlation studies showed that the pod yield was significant positive correlated with pods per plant and hundred seed weight (Ave and Ceyhan, 2006). Seed yield per plant had significant and positive association with number of pods per plant, plant height, harvest index, and number of grains per pod (Singh and Singh, 2006). Chamnundeswari and Aher (2003) conducted an experiment with ninety genotypes of soybean. They reported that seed yield showed positive correlation with number of pods per cluster, number of clusters per plant, number of pods per plant and biological yield per plant. Character association studies conducted by Sharma *et al.* (2003) and indicated that positive and significant association of seed yield per plant with biological yield per plant, pods per plant and pod length. Significant negative correlation of harvest index was observed with plant height. It can be predicted that selection for pods per plant pod length and biological yield per plant would

improve seed yield per plant Recombination breeding may be suggested for simultaneous improvement of biological yield per plant and harvest index.

Dogney *et al.* (1998) reported that the number of seeds per pod and hundred seed weight had a high positive direct effect on yield in soybean. Number of seeds per pod, days to maturity had medium to low direct effect on seed yield. Peluzio *et al.* (2012) revealed the negative correlation between days to maturity and pods per plant in soybean. Again, Saurabh *et al.* (1998) conducted an experiment and observed significant and positive correlations between plant height and pods per plant in soybean. Significant positive correlations of seed yield with plant height, pod length, number of pods per plant and straw yield per plant were reported by Devendra *et al.* (1998).

Jadhav *et al.* (1995) observed that number of branches, pods and seeds per plant pod length and pod weight per plant were positive and high significantly correlated with seed yield in soybean. Yield is higher correlated with yield and yield contributing characters. Again, Wu *et al.* (1995) revealed that seed yield had positively correlation with pods per plant, plant height in summer soybean. Seed yield was influenced by hundred seed weight, pods per plant and nodes per main stem among these high yielding genotypes. In another study, Mahajan *et al.* (1993); informed that grain yield per plant had positively correlated with pods per plant (0.75), branches per plant (0.52) in soybean. Days to maturity (0.47) and plant height were the most important yield contributing characters.

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

Onemli (2003) reported that the number of pods positively correlated with plant height, number of branches, pod length, seed length, number of pods per plant and 1000-seed weight, but was negatively correlated and significant

correlations with number of seeds per pod, seed length and pod length in soybean. Number of pods and thousand seed had negative effect on seed yield via the number of pods. The genotypic correlation coefficients found higher than the phenotypic correlation coefficients. Pod yield per plant showed positive phenotypic correlation with pod length, number of grains per pod, number of pods per plant and shelling percentage (Chaudhary and Sharma, 2003).

Chand (1999), reported that the genotypic correlation coefficients higher than the phenotypic and environmental correlation coefficients in soybean. Seed yield was positively correlated with days to flowering and maturity, plant height and branches per plant and pods per plant in terms of genotype and phenotypic correlation coefficients. No correlation between hundred seed weight and seed yield per plant was established. Plant height was negatively correlated with hundred 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.

2.6 Path co-efficient

Khan *et al.* (2000) observed correlation among yield determining components in 86 diverse maturity genotypes of soybean. Path coefficient analysis revealed that pods per plant had the direct effect on seed yield followed by 100-seed weight. Pods per plant affected seed yield negatively via indirect effects of plant height, pod length and seed per pod. In another study, Rajanna *et al.* (2000) estimated significant and positive correlation of number of pods per plant, number of clusters per plant and 100-seed weight with seed yield in soybean. Days to maturity, plant height and number of branches per plant exhibited significant positive correlation with number of clusters per plant and number of pods per plant. Path analysis indicated effect on seed yield per plant.

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

plant was the strongest forces influencing yield. Saad (1995) observed that the path analysis showed direct contribution of yield components to seed yield for cultivars was in the descending order number of pods per plant, 100-seed weight, number of seeds per pod and plant height, while highest indirect effects were exerted by number of seeds per pod via number of pods per plant in soybean. Major *et al.* (1996) reported that the grain yield showed significant and positive correlation with branches per plant, pods per plant and 100-seed weight in soybean. Path analysis revealed that pods per plant and 100-seed weight had high direct and positive effects on grain yield.

Shrivastava *et al.* (2001) observed highest positive direct effects on seed yield or the number of branches per plant, followed by days to 50% flowering and days to maturity, plant height, hundred seed weight, biological yield and harvest index. Plant height, on the other hand, had a negative effect on yield in a path coefficient analysis of yield contributing traits in soybean. The highest direct effect was exhibited by pods per plant, indirect effects, especially through the seeds per pod in pea (Ave and Ceyhan, 2006). Pods per plant, hundred seed weight, seeds per pod and days to maturity had positive direct effect on grain yield, while plant height, pods per cluster and pod length had negative direct effect on grain yield (Singh and Singh, 2006). The results of path analysis revealed that direct effects were highest for number of pods per plant, node at which first fertile pod develops, number of branches, number of seeds per pod and pod length which can serve as reliable variable for selection (Harpreet *et al.*, 2007).

2.7 Genetic diversity

Genetic diversity for quantitative traits assessment has been of prime importance in many contexts particularly in differentiating well defined populations. The germplasm in a self-pollinated crop can be considered as heterogeneous sets of groups, since each group being homozygous within it. Selecting the parents for breeding program in such crops is critical because, the success of such program depends upon the segregants of hybrid derivatives

between the parents, particularly when the aim is to improve the quantitative characters like yield. To help the breeder in the process to identify the parents that nick better, several methods of divergence analysis based on quantitative traits have been proposed to suit various objectives. Among them, Mahalanobis' generalized distance occupies a unique place and an efficient method to gauge the extent of diversity among genotypes, which quantify the difference among several quantitative traits. A summary of literature available on this aspect in soybean is presented below.

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

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

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

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

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

Chowdhury *et al.* (1998) conducted an experiment to assess genetic diversity among 55 soybean using Mahalanohis' D^2 -statistic. The genotypes fell in seven clusters of different sizes. Genetic divergence and geographic distribution were not necessarily related of the ten different characters, pods per plant, yield per plant and effective nodes per plant contributed maximum on the total divergence. The highest inter-cluster distance was observed between I and V followed by I and VI indicates that highly divergent types existed in these clusters. Sanjay *et al.* (1998) reported genetic divergence of 30 advanced breeding lines of soybean and were grouped into 7 clusters, of which cluster I and II contained the most important genotypes. Cluster I was characterized by high yield per plant (23.72 g), 100-120 pods per plant, a reproductive phase high harvest index and high seed weight, cluster II contained genotypes almost similar to those in cluster I. Dobhal (1995) observed significant variability among 65 soybean genotypes for 12 yield components, allowing genotypes to be grouped into 17 clusters. D^2 analysis revealed that yield per plant, number of pods per plant, pod length and seed per pod made a high contribution towards total genetic distance.

MATERIALS AND METHODS

An experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh during the period from November 2016 to February 2017 to evaluate twenty of soybean genotypes. The experiment was conducted to deal with major objectives of thesis work. A brief description about the locations of the experimental site, characteristics of soil, climate, materials, layout and design of the experiment, land preparation, manuring and fertilizing, intercultural operations, harvesting, data recording procedure, statistical analysis etc. which are presented as follows:

3.1 Experimental site

The research work relating to evaluation of yield and yield contributing characters of twenty soybean genotypes was conducted at the Sher-E-Bangla Agricultural University Farm, Dhaka-1207 during November 2016 to February 2017.

3.2 Geographical location

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

3.3 Climate

The experimental area has subtropical climate, characterized by high temperature, high relative humidity and scanty rainfall associated with moderately low temperature during the Rabi season (October-March). Weather

information regarding temperature, relative humidity, rainfall and sunshine hours prevailed at the experimental site during the study period presented in Appendix II.

3.4 Characteristics of soil

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

3.5 Planting materials

The material comprised of 20 genotypes of soybean. The genetically pure and physically healthy seeds of these genotypes were obtained from the Germplasm Bank of Bangladesh Agricultural Research Institute (BARI), Gazipur and Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh. List of the genotypes are given in Table 1.

Table 1: The code and accession name of 20 soybean genotypes used in the study

Genotypic Code	Genotypic Name	Genotypic Code	Genotypic Name	Genotypic Code	Genotypic Name
G1	TAS-4	G8	GMOT-13	G15	BINA SOYBEAN 1
G2	DJS 9207	G9	AGS-205	G16	SOHAGH
G3	AGS- 95	G10	BARI SOYBEAN 5	G17	BARI SOYBEAN 6
G4	K-16	G11	FV-4PL-NICE-7	G18	BINA SOYBEAN 3
G5	GMOT-95	G12	BOSS	G19	BINA SOYBEAN 2
G6	ASSET-93	G13	AGS-79	G20	LOCAL
G7	ASOMEME	G14	BINA SOYBEAN 4		

Source: OSRC= Oil Seed Research Center, BARI= Bangladesh Agricultural Research Institute

BINA= Bangladesh Institute of Nuclear Agriculture

3.6 Design and layout of the experiment

The study was laid out in randomized complete block design (RCBD) with three (3) replications. The plot size was 120 m² and distance of 30 cm from block to block, 30 cm from each row within each line. Each plot has a single row of 1m length. Plant to plant distance was 10 cm. The genotypes were randomly distributed to each row within each block.

3.7 Land preparation

The selected field for growing soybean was first opened at 20 October, 2016 with power tiller and was exposed to the sun for a week. Then the land was prepared to obtain good tilth by several ploughing, cross ploughing and laddering . Subsequent operations were done with harrow, spade and hammer. Weeds and stubbles were removed; larger clods were broken into small particles, and finally attained into a desirable tilth to ensure proper growing conditions.

The plot was partitioned into the unit plots according to the experimental design as mentioned earlier. Proper irrigation and drainage channels were prepared around the plots. Each unit plot was prepared and raised upto 5 cm height from the drains. The bed soil was made friable and the surface of the bed was leveled.

3.8 Manure and fertilizer application

The plots were fertilized with cow dung, urea, TSP and MP at the amount of 1 ton, 45 kg, 62.5 kg, 50 kg per ha, respectively. The entire cow dung, TSP, MP and half of the urea were applied at the time of final land preparation. The remaining half of urea was applied as top dressing in two installments, first after 21 days and second after 42 days of sowing.

3.9 Seed sowing

Seeds of the twenty soybean genotypes were sown on 01 November 2016. The seedlings were emerged five to twelve days after sowing.

3.10 Intercultural operation

Four weeding and thinning were done on same date, which were 23, 35,50 and 60 days after sowing. Other intercultural operations were done as per need.

3.11 Pesticide application

During the cropping period, since there was no significant pest infestation in the field, hence no control measure was undertaken. In order to prevent disease infestation, “Ripcord” was used for 2 times at an interval of 12 days from 22 November to 16 December 2016. There were different types of weeds which were controlled effectively by hand weeding.



Plate 1: Photograph showing land preparation and seed sowing



Plate 2: Photograph showing twenty different genotypes of soybean plants in experimental plot



Plate 3: Photograph showing intercultural operation practice in the experimental plot



Plate 4: Photograph showing inspection of experimental site by supervisor

3.12 Harvesting

Pods were picked on the basis of horticultural maturity, size, color and age being determined for the purpose of consumption throughout the harvesting period. Harvesting was done in late January.

3.13 Data recording

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

3.13.1 Germination percentage

The numbers of germinated seeds were recorded from each plot and percentage was calculated.

3.13.2 Days to 50% flowering

The days determined as the days required from sowing to 50% anthesis.

3.13.3 Plant height (cm)

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

3.13.4 Primary branches per plant

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

3.13.5 Length of leaves (cm)

The lengths of leaves from ten randomly selected plants were measured.

3.13.6 Diameter of leaves (cm)

The breadth of leaves at base, at middle and top were measured from ten randomly selected plants.

3.13.7 Leaves per plant

The numbers of leaf ten randomly selected plants were counted.

3.13.8 Pods per plant

The mean numbers of pods were recorded from ten randomly selected plants.

3.13.9 Seeds per pod

The average numbers of seeds from ten randomly selected pods were counted.

3.13.10 Seeds per plant

The mean numbers of seeds from ten randomly selected plants were counted.

3.13.11 Hundred seed weight (g)

Weight of hundred seeds were measured from selected plants at random from each plant was expressed in grams.

3.13.12 Days to plant maturity

The number of days taken from sowing to 80 per cent of the green pods to dry was taken as days to maturity.

3.13.13 Seed yield per plant

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

3.14 Statistical analysis

Mean data of the characters were subjected to multivariate analysis. Univariate analysis of the individual character was done for all characters under study using the mean values (Singh and Chaudhury, 1985) and was estimated using MSTAT-C computer 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. Multivariate analysis was done by computer using

GENSTAT 5.13 and Microsoft Excel 2007 software through four techniques viz., principal coordinate analysis (PCO), cluster analysis (CVA).

3.14.1 Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.*, (1955). Genotypic variances (σ^2_g) were obtained by subtracting Error MS from Genotypic MS and dividing by the number of replications as shown below:

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

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of square

r = number of replications

The phenotypic variance (σ^2_p) were derived by adding genotypic variance (σ^2_g) with error variance (σ^2_e) as given by following formula-

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

Where,

σ^2_g = Genotypic variance

σ^2_e = Error variance

3.14.2 Estimation of genotypic and phenotypic co-efficient of variation

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

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

Where,

σ_g = Genotypic standard deviation

\bar{x} = Population mean

Similarly, the phenotypic co-efficient of variation was calculated from the following formula-

$$\text{Phenotypic co-efficient variation (PCV)} = \frac{\sigma_p}{\bar{X}} \times 100$$

Where,

σ_p = Phenotypic standard deviation

\bar{x} = Population mean

3.14.3 Estimation of heritability

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

$$\text{Heritability (H}_b \text{ \%)} = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

H_b = Heritability in broad sense

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

3.14.4 Estimation of genetic advance

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

$$\text{Genetic advance (GA)} = K \times \frac{\sigma_g^2}{\sigma_p^2} \times \sigma_p$$

Where,

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

σ_p = Phenotypic standard deviation

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

3.14.5 Estimation of genetic advance mean's percentage

Genetic advance as percentage of mean was calculated from the following formula as proposed by Comstock and Robinson (1955).

$$\text{Genetic advance (\% mean)} = \frac{\text{Genetic advance}}{\text{Population mean}} \times 100$$

3.14.6 Estimation of genotypic and phenotypic correlation co-efficient

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

The genotypic co-variance component between two traits and have the phenotypic co-variance component were derived in the same way as for the corresponding variance components. The co-variance components were used to

compute genotypic and phenotypic correlation between the pair of characters, are presented as follows:

$$\text{Genotypic correlation } (r_{gxy}) = \frac{\sigma^2_{gxy}}{\sqrt{(\sigma^2_{gx} \times \sigma^2_{gy})}}$$

Where,

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

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

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

$$\text{Phenotypic correlation } (r_{pxy}) = \frac{\sigma^2_{pxy}}{\sqrt{(\sigma^2_{px} \times \sigma^2_{py})}}$$

Where,

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

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

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

3.14.7 Path co-efficient analysis

Path co-efficient analysis was done 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 co-efficient is partitioned into direct and indirect independent variables on the dependent variable.

In order to estimate direct & indirect effect of the correlated characters, say x1, x2 and x3 on yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

$$r_{yx1} = p_{yx1} + p_{yx2} r_{x1x2} + P_{yx3} r_{x1x3}$$

$$r_{yx2} = p_{yx1} r_{x1x2} + p_{yx2} + P_{yx3} r_{x2x3}$$

$$r_{yx3} = p_{yx1} r_{x1x3} + p_{yx2} r_{x2x3} + p_{yx3}$$

Where, r's denotes simple correlation co-efficient and P's denote path co-efficient (Unknown). P's in the above equations may be conveniently solved by arranging them in matrix form. Total correlation, say between x_1 and y is thus partitioned as follows:

p_{yx1} = The direct effect of x_1 on y.

$p_{yx2} r_{x1x2}$ = The indirect effect of x_1 via x_2 on y

$p_{yx3} r_{x1x3}$ = The indirect effect of x_1 via x_3 on y

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

$$P_{RY}^2 = 1 - \sum p_{iy} \cdot r_{iy}$$

Where,

$$P_{RY}^2 = (R^2); \text{ and hence residual effect, } R = (P_{RY}^2)^{1/2}$$

p_{iy} = Direct effect of the character on yield

r_{iy} = Correlation of the character with yield

3.15 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance (D^2) statistic and its auxiliary analyses. The parent's selection in hybridization programme based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) suggested that the quantification of genetic diversity through biometrical procedures had made it

possible to choose genetically diverse parents for a hybridization programme. Multivariate analysis viz. principal component analysis, principal coordinate analysis, cluster analysis and canonical vector analysis (CVA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

3.15.1 Principal component analysis (PCA)

Principal component analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity. Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.15.2 Principal co-ordinate analysis (PCO)

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

3.15.3 Cluster analysis (CA)

Cluster analysis divides the genotypes of a data set into some number of mutually exclusive groups. Clustering was done using non-hierarchical classification. In Genstat, the algorithm is used to search for optimal values of chosen criterion proceeds as follows. Starting from some initial classification of the genotypes into required number of groups, the algorithm repeatedly

transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

3.15.4 Canonical vector analysis (CVA)

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

3.15.5 Calculation of D² values

The Mahalanobis's distance (D²) values were calculated from transformed uncorrelated means of characters according to Rao (1952), and Singh and Chaudhury (1985). The D² values were estimated for all possible combinations between genotypes. In simpler form

D² statistic is defined by the formula

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

Where,

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

x = Number of characters

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

3.15.6 Computation of average intra-cluster distances

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

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

Where,

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

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

3.15.7 Computation of average inter-cluster distances

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

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

Where,

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

n_i = Number of populations in cluster i

n_j = Number of populations in cluster j

3.15.8 Cluster diagram

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

RESULTS AND DISCUSSION

The results found from the experiment are discussed and presented in this section. The data collected from twenty soybean genotypes on yield and yield contributing characters were calculated and analyzed statistically are presented in the following headings:

4.1 Genetic parameters

4.2 Genetic variability, heritability and genetic advance

4.3 Correlation co-efficient

4.4 Path co-efficient analysis

4.5 Multivariate analysis

4.1 Genetic parameters

The analysis of variance of this experimental data shows significantly differences exist in all the characters under study *viz.*, germination percentage, days to 50% flowering, plant height (cm), primary branches per plant, primary branches per plant, breadth of leaves (cm), leaf per plant, number of pods per plant, number of seeds per pod, seeds per plant, weight of hundred seeds (g), days to maturity, seed yield per plant so it is clear that, selection for all the traits among genotypes have a great impact and good scope of improvement. The analysis of variances, means of all 13 characters are presented in Table 2. ANOVA is given in appendix IV.

Table 2. Range, mean, CV (%) and standard deviation of 20 soybean genotypes

Parameters	Range		Mean	CV (%)	SD	SE
	Min	Max				
Germination percentage %	83.33	95.33	91.22	2.38	2.17	0.82
Days of 50% flowering	39.00	48.00	41.92	4.69	1.97	0.74
Plant height (cm)	21.33	63.33	43.47	13.61	5.92	2.24
Length of leaves (cm)	5.27	8.37	6.89	10.41	0.72	0.27
Leaf breadth base (cm)	2.33	4.10	3.16	9.89	0.31	0.12
Leaf breadth middle (cm)	2.93	5.80	4.57	9.97	0.46	0.17
Leaf breadth top (cm)	1.60	3.67	2.42	9.90	0.24	0.09
Primary branches per plant	2.33	4.67	3.52	18.85	0.66	0.25
Leaf per plant	9.67	20.00	15.37	9.90	1.52	0.58
Pods per plant	10.67	28.67	18.92	15.78	2.98	1.13
Seed per pod	2.00	3.00	2.60	18.96	0.49	0.19
Seeds per Plant	40.00	81.00	58.10	6.94	4.03	1.52
100 seed weight (gm)	8.67	16.33	12.13	9.40	1.14	0.43
Days to maturity	84.33	91.33	87.83	1.30	1.14	0.43
Seed yield per plant (gm)	4.35	12.01	7.21	11.30	0.82	0.31

4.2 Genetic variability, heritability and genetic advance

The achievement of crop improvement program relies on the amount of genetic variability present in germplasm or in the population. The extent of genetic variability can determine the pace and quantum of genetic improvement through hybridization followed by selection or through selection. Phenotypic variance indicates the degree of variation in phenotypic values whereas genotypic variance indicates variation created in genotypic values. Heritability indicates target in determining the relative amount of portion of variation which are heritable.

The presence of little gap between GCV and PCV for all the characters under study, suggested that traits which are being studied have low environmental effect. The estimates of heritability alone fail to estimate the response to selection (Johnson *et al.*, 1955). Therefore, the heritability estimates seems to be more significant when accompanied by estimates of genetic advance. The genetic advances as percent mean was also estimated.

The estimates of range, mean, phenotypic and genotypic coefficients of variation, genetic advance and genetic advance as per cent mean for all the characters, heritability were studied and the results are presented in Table 3 and depicted in Fig. 1. The average performance of soybean genotypes for different growth characters and yield components are presented in table 2.

4.2.1 Germination percentage

The mean of germination percentage of 20 genotypes was 91.2. Significant differences were found among the genotypes with respect to germination percentage (Table 2). The values ranged from 83.33% to 95.33%, in the genotype “BOSS” and “LOCAL” respectively (Appendix VII). From the analysis it is found that phenotypic variance (12.28) was higher than genotypic variances (7.58). It indicates that influence of environment on the expression of trait controlling genes was higher and considerable. The genotypic co-efficient of variation was found 3.02 and phenotypic co-efficient of variation was found

3.84. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation found very low which indicates less environmental effect on this character. The estimation of heritability (61.73%) for this trait was moderately high, genetic advance was found 4.46 and genetic advance over percentage of mean was found 4.89 which is low indicates non-additive genes controlled the trait (Table 3).

4.2.2 Days to 50% flowering

The mean number of days to 50% flowering was 41.92. Significant differences were found among the genotypes with respect to days to 50% flowering (Table 2). The values ranged from 39.00 to 48.00, in the genotype “BINA SOYBEAN 1” and “ASOMEME” respectively (Appendix VII). The genotypic variance was found 3.05 and phenotypic variance was found 6.92. From the analysis it is found that phenotypic variances (6.92) were higher than genotypic variances (3.05). It indicates that influence of environment on the expression of trait controlling genes was higher and considerable. The genotypic co-efficient of variation was found 4.16 and phenotypic co-efficient of variation was found 6.28. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation found very low which indicates less environmental effect on this character. The estimation of heritability (44.05) for this trait was moderately high, genetic advance was found 2.39 and

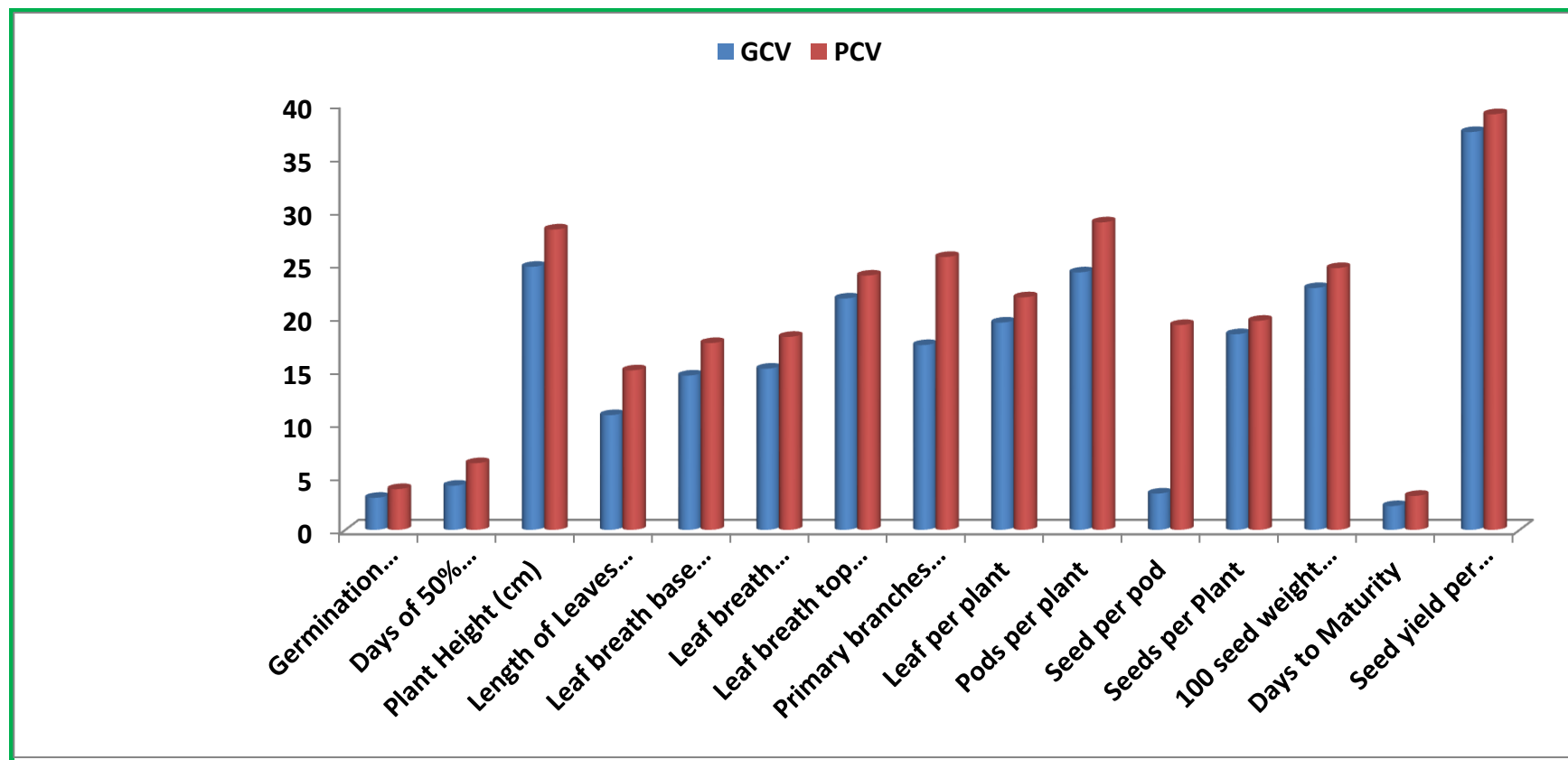


Figure 1. Bar graph showing genotypic and phenotypic variability of different characters for twenty in soybean genotypes

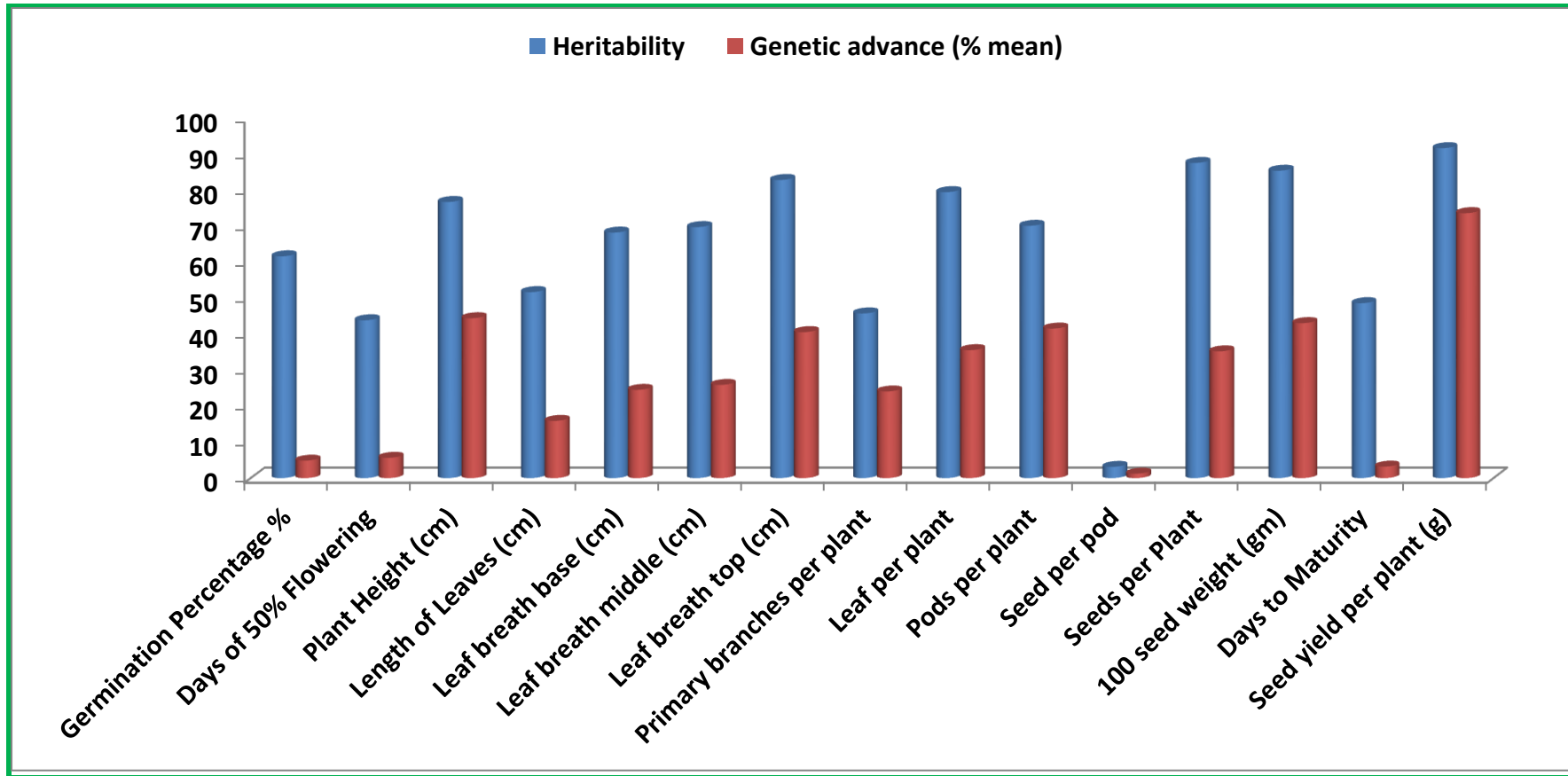


Figure 2. Bar graph showing heritability and genetic advance over mean of soybean genotypes

Table 3. Estimation of genetic parameters of different characters of twenty soybean genotypes

Parameters	σ^2_p	σ^2_g	σ^2_e	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
Germination Percentage %	12.28	7.58	4.70	3.84	3.02	2.38	61.73	4.46	4.89
Days of 50% Flowering	6.92	3.05	3.87	6.28	4.16	4.69	44.05	2.39	5.69
Plant Height (cm)	150.46	115.48	34.99	28.22	24.72	13.61	76.75	19.39	44.62
Length of Leaves (cm)	1.07	0.55	0.51	15.01	10.80	10.41	51.84	1.10	16.03
Leaf breadth base (cm)	0.31	0.21	0.10	17.57	14.52	9.89	68.29	0.78	24.72
Leaf breadth middle (cm)	0.69	0.48	0.21	18.15	15.17	9.97	69.82	1.19	26.11
Leaf breadth top (cm)	0.33	0.28	0.06	23.90	21.75	9.90	82.83	0.99	40.78
Primary branches per plant	0.81	0.37	0.44	25.64	17.38	18.85	45.95	0.85	24.27
Leaf per plant	11.29	8.97	2.32	21.86	19.49	9.90	79.47	5.50	35.79
Pods per plant	29.87	20.96	8.91	28.89	24.20	15.78	70.17	7.90	41.76
Seed per pod	0.25	0.01	0.24	19.26	3.42	18.96	3.15	0.03	1.25
Seeds per Plant	130.54	114.28	16.26	19.66	18.40	6.94	87.54	20.60	35.46
100 seed weight (gm)	8.91	7.61	1.30	24.60	22.73	9.40	85.39	5.25	43.27
Days to Maturity	7.91	3.86	4.05	3.20	2.24	2.29	48.78	2.83	3.22
Seed yield per plant (g)	7.93	7.26	0.66	39.03	37.36	11.30	91.62	5.31	73.66

σ^2_p = Phenotypic variance, σ^2_g = Genotypic variance and σ^2_e = Environmental variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation.

over percentage of mean was found 5.69 which is low indicating non- additive genes controlled the trait (Table 3).

4.2.3 Plant height (cm)

The mean number of plant height was 43.47. Significant differences were found among the genotypes with respect to plant height (Table 2). The values ranged from 21.33 cm to 63.33 cm, in the genotype “TAS-4”and “SOHAGH” respectively (Appendix VII). The genotypic variance was found 115.48 and phenotypic variance was found 150.46. From the analysis it is found that phenotypic variance (150.46) was higher than genotypic variances (115.48). It indicates that influence of environment on the expression of trait controlling genes was little bit higher but not considerable because their gap is very little. The genotypic co-efficient of variation was found 24.72 and phenotypic co-efficient of variation was found 28.22. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation was found very low which indicates less environmental effect on this character. The estimation of heritability (76.75%)for this trait was moderately high, genetic advance was found 19.39 and genetic advance over percentage of mean was found 44.62 which is medium indicating both additive and non- additive genes controlled the trait (Table 3).

4.2.4 Primary branches per plant

Maximum number of branches were recorded in K-16 (4.67) and the minimum number of main branches were recorded in AGS-79 (2.33) (Table 2) (Appendix VII). The mean of Primary branches per plant is 3.52. The phenotypic variance (0.81) appeared to be higher than the genotypic variance (0.37) suggested considerable influence of environment on the expression of the genes controlling this trait (Figure 1). The genotypic co-efficient of variation and phenotypic co-efficient of variation were 17.38 and 25.64 respectively (Table 3) which indicated presence of considerable variability among the genotypes. The heritability (45.95%) estimates for this trait was moderate, genetic advance

(0.85) was low and genetic advance in per cent of mean (24.27) were found low (Table 3), revealed that this trait was governed by non-additive gene. Bangar *et al.* (2003) reported that phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV).

4.2.5 Length of leaves (cm)

The mean number of length of leaves was 6.89. Significant differences were found among the genotypes with respect to length of leaves (Table 2). The values ranged from 5.27 cm to 8.37 cm, in the genotype “DJS 9207” and “SOHAGH” respectively (Appendix VII). The genotypic variance was found 0.55 and phenotypic variance was found 1.07. From the analysis it is found that phenotypic variance (1.07) was higher than genotypic variance (0.55). It indicates that influence of environment on the expression of trait controlling genes was higher and considerable. The genotypic co-efficient of variation was found 10.80 and phenotypic co-efficient of variation was found 15.01. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation was found very low which indicates less environmental effect on this character. The estimation of heritability (51.84%) for this trait was moderate, genetic advance was found 1.10 and genetic advance over percentage of mean was found 16.03 which is low indicating non-additive gene controlled the trait (Table 3).

4.2.6 Breadth of leaves (cm)

The mean diameter of leaves was 3.16 cm at the base, 4.57 cm at the middle and 2.42 cm at the top. Significant differences were found among the genotypes with respect to diameter of leaves (Table 2) (Appendix VII). The values ranged from 2.33 cm to 4.10 cm, in the genotype “ASOMEME” and “SOHAGH” at the base; 2.93 cm to 5.80 cm, in the genotype “ASOMEME” and “BINA SOYBEAN 1” at the middle and 1.60 cm to 3.67 cm, in the genotype “DJS 9207” and “BINA SOYBEAN 4” at the top respectively (Appendix VII). The genotypic variance was found 0.21 at the base 0.48 at the middle and 0.48 at the top and phenotypic variance was found 0.31 at the base,

0.69 at the middle and 0.33 at the top. From the analysis it is found that phenotypic variance was higher than genotypic variances. It indicates that influence of environment on the expression of trait controlling genes was higher and considerable. The genotypic co-efficient of variation was found 14.52 at the base, 15.17 at the middle and 21.75 at the top and phenotypic co-efficient of variation was found 17.57 at the base 18.15 at the middle and 23.90 at the top. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation was found very low which indicates less environmental effect on this character. The estimation of heritability (68.29%) for this trait was moderately high, genetic advance was found 0.78 and genetic advance over percentage of mean was found 24.72 which is low indicating non-additive genes controlled the leaf breadth at the base. The estimation of heritability (69.82%) for this trait was moderately high, genetic advance was found 1.19 and genetic advance over percentage of mean was found 26.11 which is low indicating non-additive genes controlled the leaf breadth at the middle. The estimation of heritability (82.83%) for this trait was moderately high, genetic advance was found 0.99 and genetic advance over percentage of mean was found 40.78 which is moderate indicating both additive and non-additive genes controlled the leaf breadth at the top (Table 3).

4.2.7 Leaves per plant

The mean no of leaf per plant is 15.37. The no of leaf shows significant phenotypic and difference among the different type of genotypes. The range of no of leaf per plant is 9.67 to 20.00, in the genotype “AGS-79” and “BINA SOYBEAN 3” respectively (Table 2) (Appendix VII). The phenotypic variation was found 11.29 and the genotypic variation was found 8.97. Here we found that phenotypic variance (11.29) was higher than the genotypic variance (8.97). It indicates that influence of environment on the expression of trait controlling genes was higher and considerable. The genotypic co-efficient of variation was found 19.49 and phenotypic co-efficient of variation was found 21.86. The difference between phenotypic co-efficient of variation and genotypic co-

efficient of variation was found low which indicates less environmental effect on this character. The estimation of heritability (79.47%) for this trait was moderately high, genetic advance was found 5.50 and genetic advance over percentage of mean was found 35.79 which were medium indicating non-additive gene controlled the trait (Table 3).

4.2.8 Number of pods per plant

The number of pods per plant was ranged from 10.67 to 28.67 with mean of 18.92. The minimum number of pods per plant was observed in accession “GMOT-13”, maximum number of pods per plant was found in the genotype “BINA SOYBEAN 3” (Table 2) (Appendix VII). The phenotypic variance (29.87) appeared to be higher than the genotypic variance (20.96) suggested influence of environment on the expression of the genes controlling this trait. The genotypic coefficient of variation and phenotypic co-efficient of variation were 24.20 and 28.89 respectively (Table 2) which indicated presence of inherent variability among the population with the possibility of high potential for selection. The heritability (70.17%) estimates for this trait was moderately high, genetic advance (7.90) was moderately high and genetic advance in per cent of mean (41.76) was found moderate (Table 3), revealed that this trait was governed by both additive gene and non-additive gene and selection for this trait might be rewarding.

4.2.9 Number of seeds per pod

The phenotypic variation in seeds of twenty soybean genotypes is illustrated in Plate 3. The values ranged from 2.00 to 3.00 with a mean of 2.60. The genotype “BINA SOYBEAN 2” had highest number of seeds per pod while it was lowest in the “GMOT-13” (Table 2) (Appendix VII). The phenotypic variance (0.25) appeared to be lower than the genotypic variance (0.01). The genotypic co-efficient and phenotypic co-efficient of variation were 3.42 and 19.26 respectively (Table 2) indicating minimal influence of environment on the expression of the genes controlling this trait.

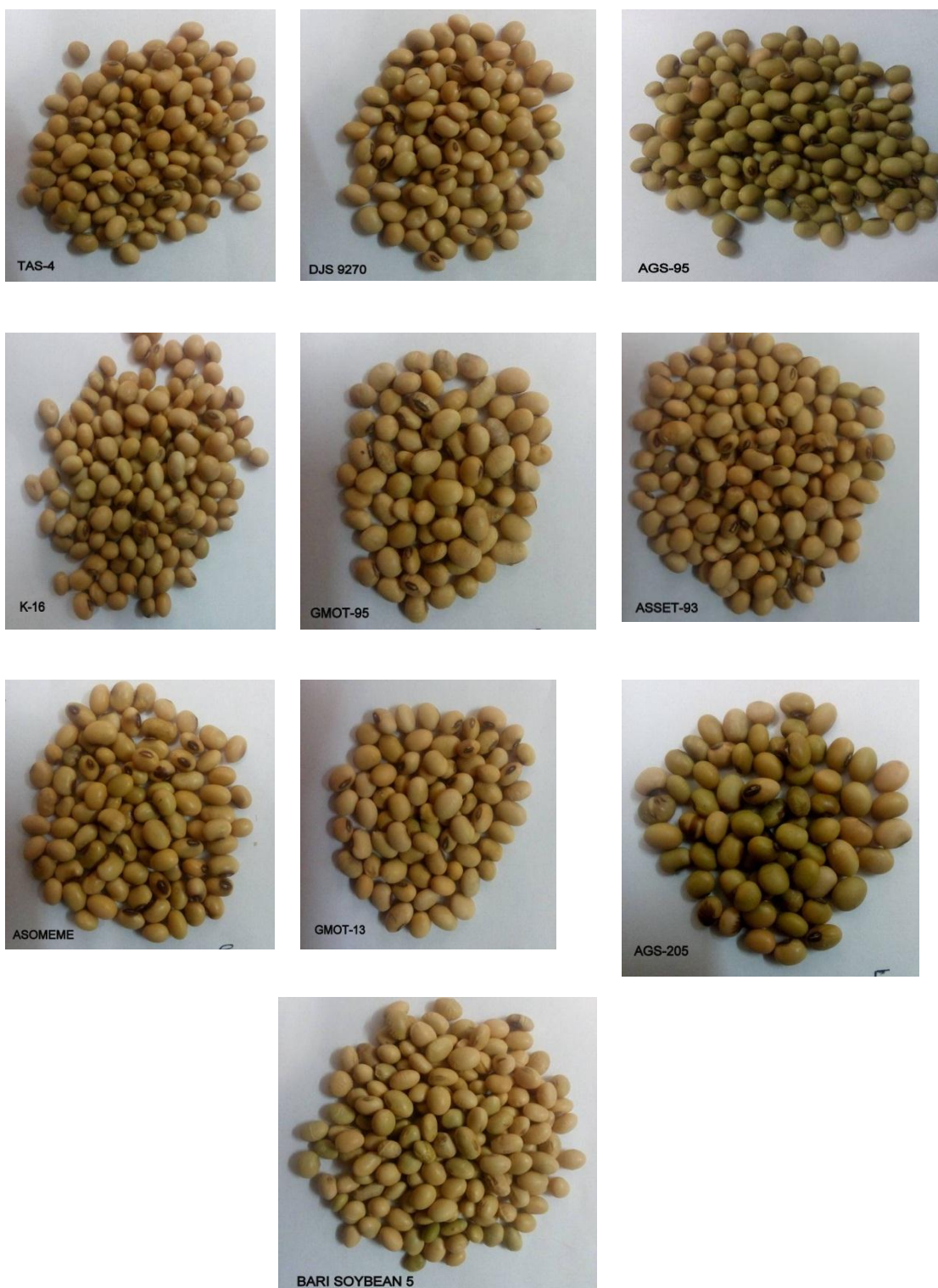


Plate 5. Photograph showing phenotypic variation in seeds of experimental soybean genotypes G1-G10

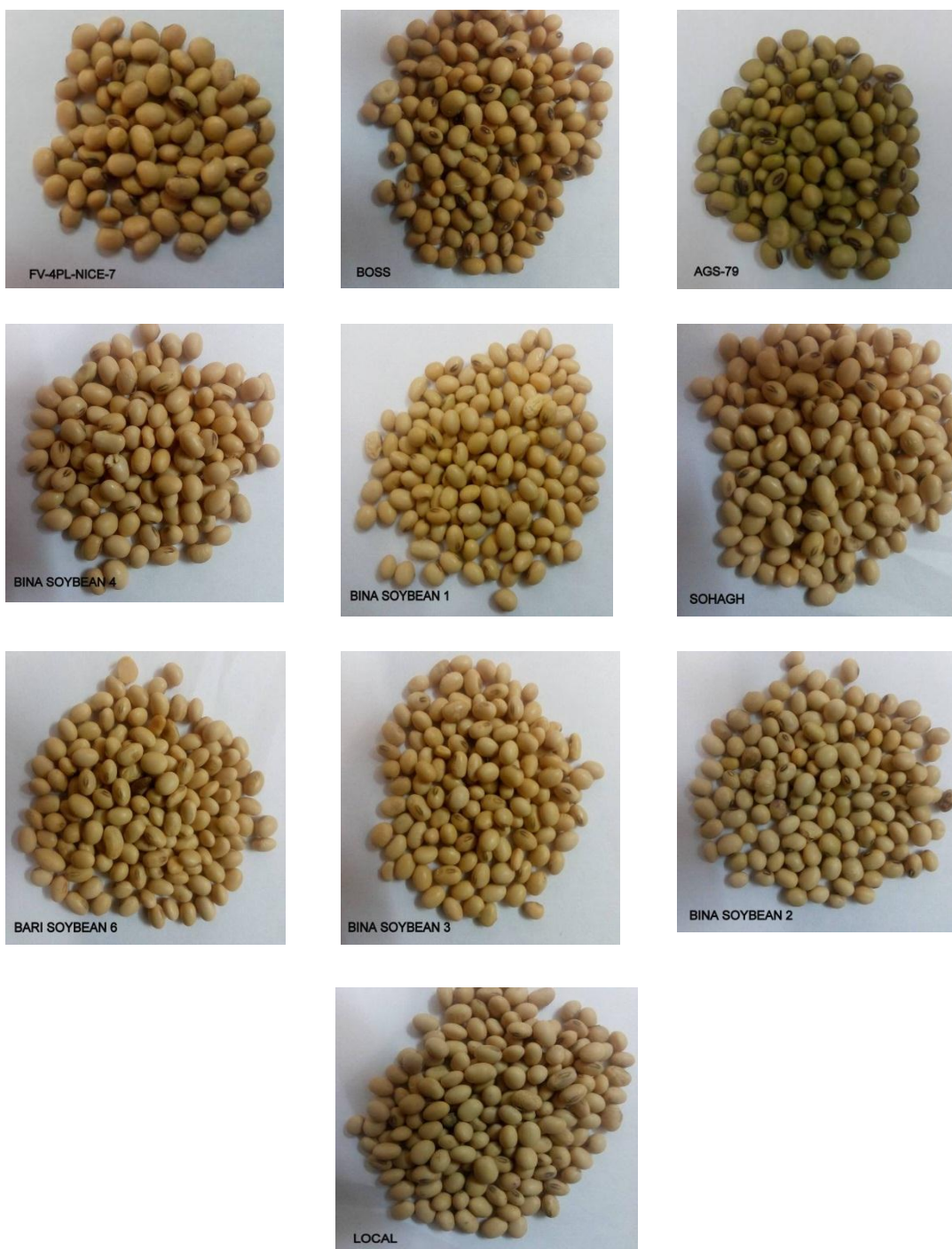


Plate 6. Photograph showing phenotypic variation in seeds of experimental soybean genotypes G11-G20

The heritability (3.15%) estimates for this trait was low, low genetic advance (0.03) and genetic advance in percent of mean (1.25) was found very low (Table 3). revealed that this trait was governed by non-additive gene.

4.2.10 Seeds per plant

The mean number of seeds per plant was 58.10. Significant differences were found among the genotypes with respect to number of seeds per plant (Table 2). The values ranged from 40.00 to 81.00, in the genotype “GMOT-13” and “BARI SOYBEAN 5” respectively (Appendix VII). The genotypic variance was found 114.28 and phenotypic variance was found 130.54. From the analysis it is found that phenotypic variance (130.54) was higher than genotypic variances (114.28). It indicates that influence of environment on the expression of trait controlling genes was higher and considerable. The genotypic co-efficient of variation was found 18.40 and phenotypic co-efficient of variation was found 19.66. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation was found very low which indicates less environmental effect on this character. The estimation of heritability (87.54%) for this trait was moderately high, genetic advance was 20.60 found and genetic advance over percentage of mean was found 35.46 which is medium indicating both additive and non-additive genes controlled the trait (Table 3).

4.2.11 Hundred seed weight (g)

The mean hundred seed weight noticed was 12.13gm with a range of 8.67gm-16.33gm. The line “AGS-79” showed the minimum hundred seed weight and the maximum hundred seed weight was recorded in the accession “BINA SOYBEAN 2” (Table 2) (Appendix VII). The phenotypic variance appeared 8.91 to be higher than the genotypic variance 7.61 suggested no considerable influence of environment on the expression of the genes controlling this trait. There was a very little difference between phenotypic 24.60 and genotypic co-efficient of variation 22.73, indicating minor environmental influence on this character. Heritability (85.39%) estimates for this trait was moderately high, genetic advance (5.25) was low and genetic advance in

per cent of mean (43.27) was found moderately high, revealed that this trait was governed by additive gene (Table 3).

4.2.12 Days to maturity

The mean of days to maturity was 87.83 days. Significant differences were found among the genotypes with respect to days to maturity (Table 2) (Appendix VII). The values ranged from 84.33 to 91.33 days, in the genotype “AGS-79” and “BINA SOYBEAN 1” respectively (Appendix VII). The genotypic variance was found 3.86 and phenotypic variance was found 7.91. From the analysis it is found that phenotypic variances (7.91) were higher than genotypic variances (3.86). It indicates that influence of environment on the expression of trait controlling genes was higher and considerable. The genotypic co-efficient of variation was found 2.24 and phenotypic co-efficient of variation was found 3.20. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation was found very low which indicates less environmental effect on this character. The estimation of heritability (48.78%) for this trait was moderately high, genetic advance was 2.83 found low and genetic advance over percentage of mean was found 3.22 which is low indicating non-additive genes controlled the trait (Table 3).

4.2.13 Seed yield per plant (g)

The mean seed yield was 7.21gm. Significant differences were found among the genotypes with respect to seed yield (Table 2). The values ranged from 4.35gm to 12.01gm, in the genotype “GMOT-13” and “BINA SOYBEAN 2” respectively (Appendix VII). The genotypic variance was found 7.26 and phenotypic variance was found 7.93. From the analysis it is found that phenotypic variances (7.93) were higher than genotypic variances (7.26). It indicates that influence of environment on the expression of trait controlling genes was higher and considerable. The genotypic co-efficient of variation was found 37.36 and phenotypic co-efficient of variation was found 39.03. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation was found very low which indicates less environmental

effect on this character. The estimation of heritability (91.62%) for this trait was high, genetic advance was 5.31 found low and genetic advance over percentage of mean was found 73.66 which is high indicating additive genes controlled the trait (Table 3).

4.3 Correlation co-efficient

Yield is the resultant of combined effect of several quantitative traits and environment. Understanding the interaction of characters among themselves and with environment has been of great use in the plant breeding. The analysis of the relationship among those traits and their association with seed yield is very much essential to establish selection criteria. 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 4. For clear understanding correlation coefficients are separated into genotypic and phenotypic level in Table 4. Where the genotypic correlation coefficients were higher than their phenotypic correlation coefficients, it indicates that the genetic reason of association. While phenotypic correlation coefficient were higher than genotypic correlation coefficient indicating suppressing effect of the environment which modified the expression of the characters at phenotypic level. The depicted genotypic and phenotypic correlation coefficient among yield and yield contributing characters of soybean are shown in Figure 3 and Figure 4 respectively.

4.3.1 Germination percentage

Germination percentage had positive and significant correlation with plant height (0.277), leaf breadth at middle (0.544), pods per plant (0.455), seeds per plant (0.462), hundred seed weight (0.303) and seed yield per plant (0.404) at genotypic level. With primary branches per plant (-0.334) had negative and significant relationship at genotypic level (Table 4). Leaf breadth at middle

(0.402), seeds per pod (0.264), seeds per plant (0.380) and seed yield per plant (0.335) had positive and significant relationship at phenotypic level (Table 5).

4.3.2 Days to 50% flowering

Days of 50% flowering had positive and significant correlation with primary branch per plant (0.582) and seeds per pod (1.632) at genotypic level. With plant height (-0.540), leaf breadth at base (-0.585), leaf breadth at middle (-0.690), leaf breadth at top (-0.502) and hundred seed weight (-0.297) had negative and significant relationship at genotypic level (Table 4). With leaf breadth at base (-0.432), leaf breadth at middle (-0.401) and leaf breadth at top (-0.305) had negative and significant relationship at phenotypic level. With primary branch per plant (0.370) had positive and significant relationship at phenotypic level (Table 5).

4.3.3 Plant height (cm)

Plant height had positive and significant correlation with plant height (0.894), leaf breadth at base (0.681), leaf breadth at middle (0.577), leaf breadth at top (0.786), hundred seed weight (0.617) and seed yield per plant (0.464) at genotypic level. With primary branch per plant (-0.632) and seed per pod (-0.825) had negative and significant relationship at genotypic level (Table 4). With primary branches per plant (-0.376) had negative and significant relationship at phenotypic level. With leaf length (0.455), leaf breadth at base (0.458), leaf breadth at middle (0.458), leaf breadth at top (0.600), hundred seed weight (0.493) and seed yield per plant (0.397) had positive and significant relationship at phenotypic level (Table 5).

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

	GP	DF	PH	LL	LBB	LBM	LBT	PBP	LPP	PPP	SP	SPP	HSW	DM	SYP
GP	1														
DF	-0.200	1													
PH	0.277*	-0.540**	1												
LL	-0.037	-0.221	0.894**	1											
LBB	0.042	-0.585**	0.681**	0.523**	1										
LBM	0.544**	-0.690**	0.577**	0.526**	0.691**	1									
LBT	0.016	-0.502**	0.786**	0.695**	0.939**	0.567**	1								
PBP	-0.334**	0.582**	-0.632**	-0.457**	-0.464**	-0.529**	-0.634**	1							
LPP	0.141	0.012	-0.065	-0.201	-0.274*	0.014	-0.317*	0.358**	1						
PPP	0.455**	0.112	0.188	-0.033	-0.178	0.277*	0.031	-0.299*	0.307*	1					
SP	0.043	1.632**	-0.825**	-0.131	-1.306**	-0.339**	-0.748**	0.961**	1.091**	0.681**	1				
SPP	0.462**	0.119	0.174	-0.010	-0.158	0.168	0.075	-0.389**	0.215	1.011**	1.140**	1			
HSW	0.303*	-0.297*	0.617**	0.176	0.621**	0.518**	0.660**	-0.357**	0.020	0.631**	-0.643**	0.581**	1		
DM	0.056	0.189	-0.035	-0.141	0.547**	0.159	0.578**	-0.121	-0.350**	0.292*	0.025	0.373**	0.597**	1	
SYP	0.404**	-0.143	0.464**	0.091	0.288*	0.401**	0.426**	-0.422**	0.146	0.908**	0.102	0.867**	0.907**	0.535**	1

** = Significant at 1%.

* = Significant at 5%.

GP = Germination percentage %, DF = Days of 50% flowering, PH = Plant height (cm), LL = Length of leaves (cm), LBB = Leaf breadth base (cm), LBM = Leaf breadth middle (cm), LBT = Leaf breadth top (cm), PBP = Primary branches per plant, LPP = Leaf per plant, PPP = Pods per plant, SP = Seeds per pod, SPP = Seeds per plant, HSW = 100 seed weight (gm), DM = Days to maturity and SYP = Seed yield per plant (g).

Table 5. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of soybean

	GP	DF	PH	LL	LBB	LBM	LBT	PBP	LPP	PPP	SP	SPP	HSW	DM	SYP
GP	1														
DF	-0.073	1													
PH	0.202	-0.198	1												
LL	0.128	-0.233	0.455**	1											
LBB	0.023	-0.432**	0.545**	0.353**	1										
LBM	0.402**	-0.401**	0.458**	0.218	0.504**	1									
LBT	-0.027	-0.305*	0.600**	0.471**	0.781**	0.431**	1								
PBP	-0.145	0.370**	-0.376**	-0.313*	-0.344**	-0.263*	-0.409**	1							
LPP	0.137	0.042	-0.046	-0.185	-0.226	0.066	-0.294*	0.244	1						
PPP	0.183	0.060	0.189	-0.087	-0.059	0.130	0.016	-0.113	0.177	1					
SP	0.264*	0.215	-0.130	0.225	-0.133	-0.078	-0.117	0.010	0.118	0.079	1				
SPP	0.380**	0.065	0.160	-0.092	-0.088	0.145	0.038	-0.246	0.183	0.816**	0.189	1			
HSW	0.229	-0.172	0.493**	0.131	0.433**	0.421**	0.540**	-0.227	-0.026	0.488**	-0.052	0.501**	1		
DM	0.039	0.004	0.020	-0.094	0.259*	0.173	0.283*	-0.021	-0.166	0.167	-0.044	0.261*	0.396**	1	
SYP	0.335**	-0.084	0.397**	0.030	0.225	0.340**	0.350**	-0.276*	0.102	0.733**	0.065	0.840**	0.885**	0.383**	1

** = Significant at 1%.

* = Significant at 5%.

GP = Germination percentage %, DF = Days of 50% flowering, PH = Plant height (cm), LL = Length of leaves (cm), LBB = Leaf breadth base (cm), LBM = Leaf breadth middle (cm), LBT = Leaf breadth top (cm), PBP = Primary branches per plant, LPP = Leaf per plant, PPP = Pods per plant, SP = Seeds per pod, SPP = Seeds per plant, HSW = 100 seed weight (gm), DM = Days to maturity and SYP = Seed yield per plant (g).

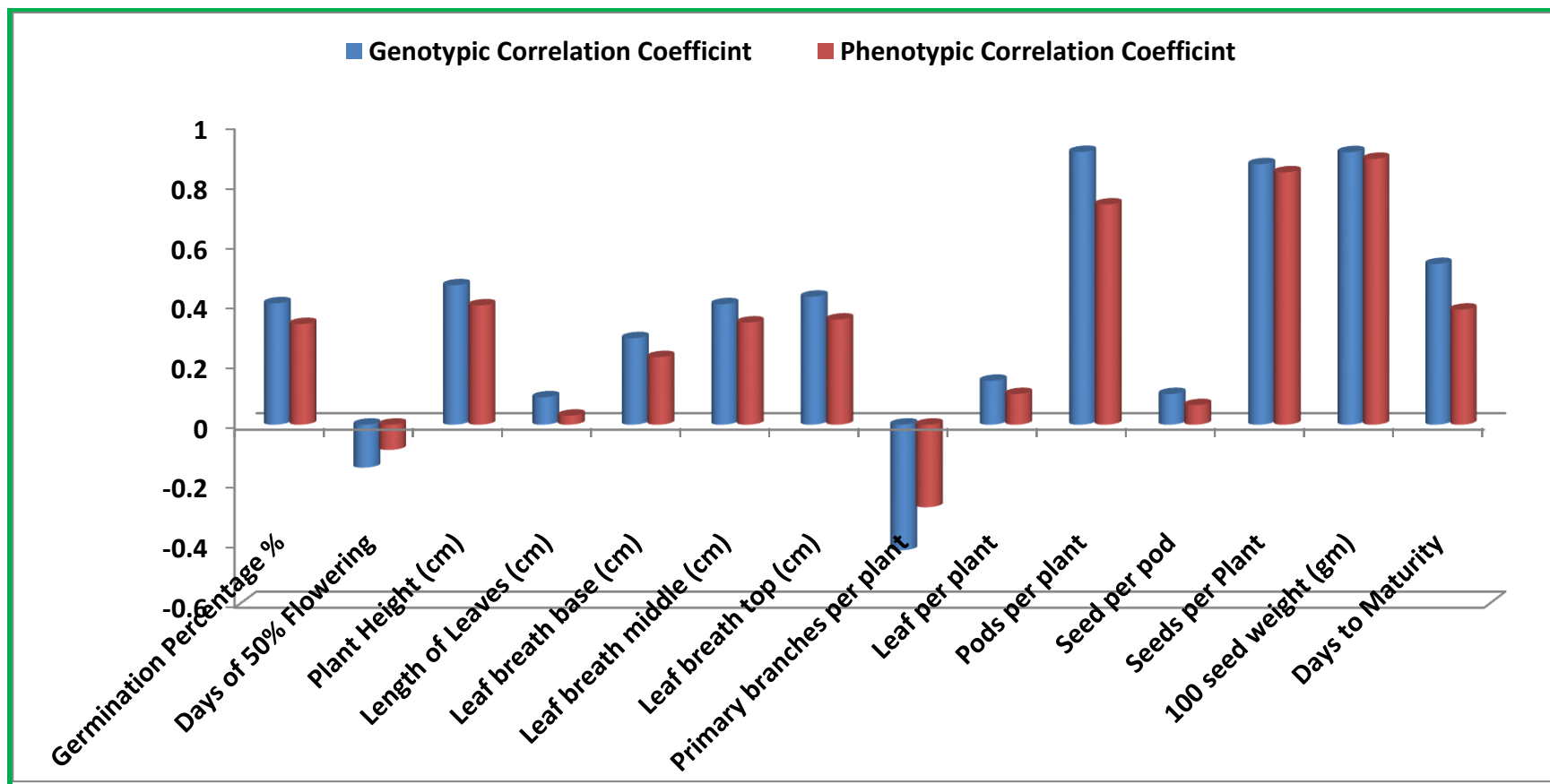


Figure 3. Bar graph showing genotypic and phenotypic correlation coefficient of fourteen characters with yield in soybean

4.3.4 Primary branches per plant

Primary branches per plant had positive and significant correlation with days of 50% flowering (0.582), leaf per plant (0.358) and seed per pod (0.961) at genotypic level. With germination percentage (-0.334), plant height (-0.632), leaf length (-0.457), leaf breadth base (-0.464), leaf breadth middle (-0.529), leaf breadth top (-0.634), pods per plant (-0.299), seed per plant (-0.389), hundred seed weight (-0.357) and seed yield per plant (-0.422) had negative and significant relationship at genotypic level (Table 4). With days of 50% flowering (0.370) had positive and significant relationship at phenotypic level. With plant height (-0.376), leaf length (-0.313), leaf breadth at base (-0.344), leaf breadth at middle (-0.263), leaf breadth at top (-0.409) and seed yield per plant (-0.276) had negative and significant relationship at phenotypic level (Table 5).

4.3.5 Length of leaves (cm)

Leaf length had positive and significant correlation with plant height (0.894), leaf breadth at base (0.523), leaf breadth at middle (0.526) and leaf breadth at top (0.695) at genotypic level. With primary branch per plant (-0.457) had negative and significant relationship at genotypic level (Table 4). With plant height (0.455), leaf breadth at base (0.353) and leaf breadth at top (0.471) had positive and significant relationship at phenotypic level. With primary branch per plant (-0.313) had negative and significant relationship at phenotypic level (Table 5).

4.3.6 Breadth of leaves (cm)

Breadth of leaves at base had positive and significant correlation with plant height (0.681), leaf length (0.523), leaf breadth at middle (0.691), leaf breadth at top (0.939), hundred seed weight (0.621), days of maturity (0.547) and seed yield per plant (0.288) at genotypic level. With days of 50% flowering (-0.585), primary branch per plant (-0.464), leaf per plant (-0.274) and seed per pod (-1.306) had negative and significant relationship at genotypic level (Table 4).

With plant height (0.545), leaf length (0.353), leaf breadth at middle (0.504), leaf breadth at top (0.781), hundred seed weight (0.433) and days of maturity (0.259) had positive and significant relationship at phenotypic level. With days of 50% flowering (-0.432) and primary leaf (-0.344) per plant had negative and significant relationship at phenotypic level (Table 5).

Breadth of leaves at middle had positive and significant correlation with germination percentage (0.544), plant height (0.577), leaf length (0.526), leaf breadth at base (0.691), leaf breadth at top (0.567), pod per plant hundred seed weight (0.518) and seed yield per plant (0.401) at genotypic level. With days of 50% flowering (-0.690), primary branch per plant (-0.529) and seed per pod (-0.339) had negative and significant relationship at genotypic level (Table 4). With germination percentage (0.402), plant height (0.458), leaf breadth at base (0.504), leaf breadth at top (0.431), hundred seed weight (0.421) and seed yield per plant (0.340) had positive and significant relationship at phenotypic level. With days of 50% flowering (-0.401) and primary branch per plant (-0.263) had negative and significant relationship at phenotypic level (Table 5).

Breadth of leaves at Top had positive and significant correlation with plant height (0.786), leaf length (0.695), leaf breadth at base (0.939), leaf breadth at middle (0.567), hundred seed weight (0.660), days of maturity (0.578) and seed yield per plant (0.426) at genotypic level. With days of days of 50% flowering (-0.502), primary branch of plant (-0.634), leaf per plant (-0.317) and seed per pod (-0.748) had negative and significant relationship at genotypic level (Table 4). With plant height (0.600), leaf length (0.471), leaf breadth at base (0.781), leaf breadth at middle (0.431), hundred seed weight (0.540), days of maturity (0.283) and seed yield per plant (0.350) had positive and significant relationship at phenotypic level. With days of 50% flowering (-0.305), primary branch per plant (-0.409) and leaf per plant (-0.294) had negative and significant relationship at phenotypic level (Table 5).

4.3.7 Leaves per plant

Leaf per plant had positive and significant correlation with primary branch per plant (0.358), pods per plant (0.307) and seed per pod (1.091) at genotypic level. With leaf breadth at base (-0.274), leaf breadth at top (-0.317) and days of maturity (-0.350) had negative and significant relationship at genotypic level (Table 4). With leaf breadth at top (-0.294) had negative and significant relationship at phenotypic level (Table 5).

4.3.8 Number of pods per plant

Number of pod per plant had positive and significant correlation with germination percentage (0.455), leaf breadth at middle (0.277), leaf per plant (0.307), seed per pod (0.681), seed per plant (1.011), hundred seed weight (0.631), days of maturity (0.292) and seed yield per plant (0.908) at genotypic level. With primary branch per plant (-0.299) had negative and significant relationship at genotypic level (Table 4). With seed per plant (0.816), hundred seed weight (0.488) and seed yield per plant (0.733) had positive and significant relationship at phenotypic level (Table 5).

4.3.9 Number of seeds per pod

Number of seed per pod had positive and significant correlation with days of 50% flowering (1.632), primary branch per plant (0.961), leaf per plant (1.091), pod per plant (0.681) and seed per plant (1.140) at genotypic level. With plant height (-0.825), leaf breadth at base (-1.306), leaf breadth at middle (-0.339), leaf breadth at top (-0.748) and hundred seed weight (-0.643) had negative and significant relationship at genotypic level (Table 4). With germination percentage (0.264) had positive and significant relationship at phenotypic level (Table 5).

4.3.10 Seeds per plant

Seeds per plant had positive and significant correlation with germination percentage (0.462), pod per plant (1.011), seed per pod (1.140), hundred seed

weight (0.581), days of maturity (0.373) and seed yield per plant (0.867) at genotypic level. With primary branch per plant (-0.389) had negative and significant relationship at genotypic level (Table 4). With germination percentage (0.380), pods per plant (0.816), hundred seed weight (0.501), days of maturity (0.261) and seed yield per plant (0.840) had positive and significant relationship at phenotypic level (Table 5).

4.3.11 Hundred seed weight (g)

Weight of hundred seed weight had positive and significant correlation with germination percentage (0.303), plant height (0.617), leaf breadth at base (0.621), leaf breadth at middle (0.518), leaf breadth at top (0.660), pods per plant (0.631), seed per plant (0.581), days of maturity (0.597) and seed yield per plant (0.907) at genotypic level. With days of 50% flowering (-0.297), primary branch per plant (-0.357) and seed per pod (-0.643) had negative and significant relationship at genotypic level (Table 4). With plant height (0.493), leaf breadth at base (0.433), leaf breadth at middle (0.421), leaf breadth at top (0.540), pod per plant (0.488), seed per plant (0.501), days of maturity (0.396) and seed yield per plant (0.885) had positive and significant relationship at phenotypic level (Table 5).

4.3.12 Days to maturity

Seeds per plant had positive and significant correlation with leaf breadth at base (0.547), leaf breadth at top (0.578), pods per plant (0.292), seed per plant (0.373), hundred seed weight (0.597) and seed yield per plant (0.535) at genotypic level. With leaf per plant (-0.350) had negative and significant relationship at genotypic level (Table 4). With leaf breadth at base (0.259), leaf breadth at top (0.283), seed per plant (0.261), hundred seed weight (0.396) and seed yield per plant (0.383) had positive and significant relationship at phenotypic level (Table 5).

4.2.13 Seed yield per plant

Seeds per plant had positive and significant correlation with germination percentage (0.404), plant height (0.464), leaf breadth at base (0.288), leaf breadth at middle (0.401), leaf breadth at top (0.426), pods per plant (0.908), seed per plant (0.867), hundred seed weight (0.907) and days of maturity (0.535) at genotypic level. With primary branch per plant (-0.422) had negative and significant relationship at genotypic level (Table 4). With germination percentage (0.335), plant height (0.397), leaf breadth at middle (0.340), leaf breadth at top (0.350), pods per plant (0.733), seeds per plant (0.840), hundred seed weight (0.885) and days of maturity (0.383) had positive and significant relationship at phenotypic level. With primary branch per plant (-0.276) had negative and significant relationship at phenotypic level (Table 5).

4.4 Path coefficient analysis

Association of character determined by correlation co-efficient may not provide an exact picture of the relative importance of direct and indirect influence of each of yield components on seed yield per plant. 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. Though correlation analysis denotes the association pattern of components traits with yield, they basically represent the overall effect of a particular trait on yield rather than providing cause and effect relationship. The technique of path coefficient analysis developed by Wright (1921) and demonstrated by Dewey and Lu (1959) facilitates the portioning of correlation coefficients into direct and indirect contribution of various characters on yield. It is standardized partial regression coefficient analysis. As such, it measures the direct effect of one variable upon other. Such information would be of great value in enabling the breeder to exclusively identify the important component traits of yield and use the genetic resources for improvement in a planned way.

In path coefficient analysis the direct effect of a trait on seed yield per plant and its indirect effect through other characters were calculated and the results are presented in Table 6.

4.4.1 Direct effect

Nine out of thirteen characters had positive direct effect on yield per plant. The characters which had positive direct effects are days to 50% flowering (0.061), leaf breadth at base (0.005), leaf breadth at middle (0.032), leaf breadth at top (0.014), leaf per plant (0.026), pod per plant (0.038), seeds per pod (0.007), seeds per plant (0.418), hundred seed weight (0.701). However characters viz., germination percentage (-0.048), plant height (-0.044), leaf length (-0.056), primary branches per plant (-0.101) and days of maturity (-0.087) had negative direct effect on seed yield per plant (Table 6).

4.4.2 Indirect effect

4.4.2.1 Germination percentage

Germination percentage showed a positive indirect effect on seed yield through leaf length (0.002), leaf breadth at middle (0.017), primary branch per plant (0.034), leaf per plant (0.004), pods per plant (0.017), seeds per plant (0.193) and hundred seed weight (0.212). Germination percentage has indirect negative effect on seed yield through days to 50% flowering (-0.012), plant height (-0.012), days to maturity (-0.005) (Table 6).

4.4.2.2 Days to 50% flowering

Days to 50% flowering showed a positive indirect effect on seed yield through germination percentage (0.010), plant height (0.024), leaf length (0.012), pods per plant (0.004), seeds per pod (0.011), seeds per plant (0.050). Days to 50% flowering has indirect negative effect on seed yield through leaf breadth at base (-0.003), leaf breadth at middle (-0.022), leaf breadth at top (-0.007), primary branch of plant (-0.059), hundred seed weight (-0.208), days to maturity (-0.017) (Table 6).

4.4.2.3 Plant height (cm)

Plant height showed a positive indirect effect on seed yield through leaf breadth at base (0.003), leaf breadth at middle (0.019), leaf breadth at top (0.011), primary branch per plant (0.064), pods per plant (0.007), seeds per plant (0.073), hundred seed weight (0.433) and days to maturity (0.003). Plant height has indirect negative effect on seed yield through germination percentage (-0.013), days to 50% flowering (-0.033), leaf length (-0.050), leaf per plant (-0.002) and seeds per pod (-0.005) (Table 6).

4.4.2.4 Primary branches per plant

Primary branch per plant showed a positive indirect effect on seed yield through germination percentage (0.016), days to 50% flowering (0.036), plant height (0.028), leaf length (0.026), leaf per plant (0.009), seeds per pod (0.006) and days to maturity (0.011). Primary branch per plant has indirect negative effect on seed yield through leaf breadth at base (-0.002), leaf breadth at middle (-0.017), leaf breadth at top (-0.009), pods per plant (-0.011), seeds per plant (-0.163) and hundred seed weight (-0.250) (Table 6).

Table 6. Partitioning of genotypic correlations into direct (bold) and indirect effects of fourteen important characters of soybean by path analysis

	Effect via														Genotypic correlation with yield
	GP	DF	PH	LL	LBB	LBM	LBT	PBP	LPP	PPP	SP	SPP	HSW	DM	
GP	-0.048	-0.012	-0.012	0.002	0.000	0.017	0.000	0.034	0.004	0.017	0.000	0.193	0.212	-0.005	0.404**
DF	0.010	0.061	0.024	0.012	-0.003	-0.022	-0.007	-0.059	0.000	0.004	0.011	0.050	-0.208	-0.017	-0.143
PH	-0.013	-0.033	-0.044	-0.050	0.003	0.019	0.011	0.064	-0.002	0.007	-0.005	0.073	0.433	0.003	0.464**
LL	0.002	-0.014	-0.039	-0.056	0.002	0.017	0.010	0.046	-0.005	-0.001	-0.001	-0.004	0.123	0.012	0.091
LBB	-0.002	-0.036	-0.030	-0.030	0.005	0.022	0.013	0.047	-0.007	-0.007	-0.009	-0.066	0.435	-0.048	0.288*
LBM	-0.026	-0.042	-0.025	-0.030	0.003	0.032	0.008	0.053	0.000	0.011	-0.002	0.070	0.363	-0.014	0.401**
LBT	-0.001	-0.031	-0.035	-0.039	0.004	0.018	0.014	0.064	-0.008	0.001	-0.005	0.031	0.462	-0.050	0.426**
PBP	0.016	0.036	0.028	0.026	-0.002	-0.017	-0.009	-0.101	0.009	-0.011	0.006	-0.163	-0.250	0.011	-0.422**
LPP	-0.007	0.001	0.003	0.011	-0.001	0.000	-0.004	-0.036	0.026	0.012	0.007	0.090	0.014	0.031	0.146
PPP	-0.022	0.007	-0.008	0.002	-0.001	0.009	0.000	0.030	0.008	0.038	0.005	0.422	0.442	-0.025	0.908**
SP	-0.002	0.100	0.036	0.007	-0.006	-0.011	-0.010	-0.097	0.028	0.026	0.007	0.476	-0.450	-0.002	0.102
SPP	-0.022	0.007	-0.008	0.001	-0.001	0.005	0.001	0.039	0.006	0.039	0.008	0.418	0.407	-0.033	0.867**
HSW	-0.014	-0.018	-0.027	-0.010	0.003	0.017	0.009	0.036	0.001	0.024	-0.004	0.243	0.701	-0.052	0.907**
DM	-0.003	0.012	0.002	0.008	0.003	0.005	0.008	0.012	-0.009	0.011	0.000	0.156	0.418	-0.087	0.535**

Residual effect: 0.00073

** = Significant at 1%.

* = Significant at 5%.

GP = Germination percentage %, DF = Days of 50% flowering, PH = Plant height (cm), LL = Length of leaves (cm), LBB = Leaf breadth base (cm), LBM = Leaf breadth middle (cm), LBT = Leaf breadth top (cm), PBP = Primary branches per plant, LPP = Leaf per plant, PPP = Pods per plant, SP = Seeds per pod, SPP = Seeds per plant, HSW = 100 seed weight (gm), DM = Days to maturity and SYP = Seed yield per plant (g).

4.4.2.5 Length of leaves (cm)

Leaf length showed a positive indirect effect on seed yield through germination percentage (0.002), leaf breadth at base (0.002), leaf breadth at middle (0.017), leaf breadth at top (0.010), primary branch per plant (0.046), hundred seed weight (0.123) and days to maturity (0.012). Leaf length has indirect negative effect on seed yield through days to 50% flowering (-0.014), plant height (-0.039), leaf per plant (-0.005), pods per plant (-0.001), seed per pod (-0.001) and seed per plant (-0.004) (Table 6).

4.4.2.6 Breadth of leaves (cm)

Leaf breadth at base showed a positive indirect effect on seed yield through leaf breadth at middle (0.022), leaf breadth at top (0.013), primary branch per plant (0.047) and hundred seed weight (0.435). Leaf breadth at base has indirect negative effect on seed yield through germination percentage (-0.002), days to 50% flowering (-0.036), plant height (-0.030), leaf length (-0.030), leaf per plant (-0.007), pods per plant (-0.007), seed per pod (-0.009), seed per plant (-0.066) and days to maturity (-0.048) (Table 6).

Leaf breadth at middle showed a positive indirect effect on seed yield through leaf breadth at base (0.003), leaf breadth at top (0.008), primary branch per plant (0.053), pods per plant (0.011), seed per plant (0.070) and hundred seed weight (0.363). Leaf breadth at middle has indirect negative effect on seed yield through germination percentage (-0.026), days to 50% flowering (-0.042), plant height (-0.025), leaf length (-0.030), seed per pod (-0.002) and days to maturity (-0.014) (Table 6).

Leaf breadth at top showed a positive indirect effect on seed yield through leaf breadth at base (0.004), leaf breadth at middle (0.018), primary branch per plant (0.064), pods per plant (0.001), seed per plant (0.031) and hundred seed weight (0.462). Leaf breadth at top has indirect negative effect on seed yield through germination percentage (-0.001), days to 50% flowering (-0.031), plant

height (-0.035), leaf length (-0.039), leaf per plant (-0.008), seed per pod (-0.005) and days to maturity (-0.050) (Table 6).

4.4.2.7 Leaves per plant

Leaf per plant showed a positive indirect effect on seed yield through days to 50% flowering (0.001), plant height (0.003), leaf length (0.011), pods per plant (0.012), seed per pod (0.007), seed per plant (0.090), hundred seed weight (0.014) and days to maturity (0.031). Leaf per plant has indirect negative effect on seed yield through germination percentage (-0.007), leaf breadth at base (-0.001), leaf breadth at top (-0.004) and primary branch per plant (-0.036) (Table 6).

4.4.2.8 Number of pods per plant

Number of pods per plant showed a positive indirect effect on seed yield through days to 50% flowering (0.007), leaf length (0.002), leaf breadth at middle (0.009), primary branch per plant (0.030), leaf per plant (0.008), seed per pod (0.005), seed per plant (0.422) and hundred seed weight (0.442). Number of pods per plant has indirect negative effect on seed yield through germination percentage (-0.022), plant height (-0.008), leaf breadth at base (-0.001), days to maturity (-0.025) (Table 6).

4.4.2.9 Number of seeds per pod

Number of seeds per pod showed a positive indirect effect on seed yield through days to 50% flowering (0.100), plant height (0.036), leaf length (0.007), leaf per plant (0.028), pods per plant (0.026) and seeds per plant (0.476). Number of seeds per pod has indirect negative effect on seed yield through germination percentage (-0.002), leaf breadth at base (-0.006), leaf breadth at middle (-0.011), leaf breadth at top (-0.010), primary branch per plant (-0.097), hundred seed weight (-0.450) and days to maturity (-0.002) (Table 6).

4.4.2.10 Seeds per plant

Seeds per plant showed a positive indirect effect on seed yield through days to 50% flowering (0.007), leaf length (0.001), leaf breadth at middle (0.005), leaf breadth at top (0.001), primary branch per plant (0.039), leaf per plant (0.006), pods per plant (0.039), seeds per pod (0.008) and hundred seed weight (0.407). Seeds per plant has indirect negative effect on seed yield through germination percentage (-0.022), plant height (-0.008), leaf breadth at base (-0.001) and days to maturity (-0.033) (Table 6).

4.4.2.11 Hundred seed weight (g)

Weight of hundred seeds showed a positive indirect effect on seed yield through leaf breadth at base (0.003), leaf breadth at middle (0.017), leaf breadth at top (0.009), primary branch per plant (0.0360), leaf per plant (0.001), pods per plant (0.024) and seeds per plant (0.243). Weight of hundred seeds has indirect negative effect on seed yield through germination percentage (-0.014), days to 50% flowering (-0.018), plant height (-0.027), leaf length (-0.010), seeds per pod (-0.004) and days to maturity (-0.052) (Table 6).

4.4.2.12 Days to maturity

Days to maturity showed a positive indirect effect on seed yield through days to 50% flowering (0.012), plant height (0.002), leaf length (0.008), leaf breadth at base (0.003), leaf breadth at middle (0.005), leaf breadth at top (0.008), primary branch per plant (0.012), pods per plant (0.011), seeds per plant (0.156) and hundred seed weight (0.418). Days to maturity has indirect negative effect on seed yield through germination percentage (-0.003) and leaf per plant (-0.009) (Table 6).

4.5 Multivariate analysis

4.5.1 Principal component analysis (PCA)

Analysis of yielded eigen values of each principal component axes of coordination of genotypes in which the first axes accounted 35.591% of the total variation among the genotypes, while four of these with Eigen values above unity accounted for 76.419% presented in Table 7. Graphical representation of scree plot of the fifteen characters by using eigen values of component axes are shown in Figure 4. Dendrogram showing five different clusters of twenty soybean genotypes in figure 5. Component plot distances of different variables of soybean genotypes were shown in Figure 6.

In order to assess the diversity and grouping genotypes based on the characteristics and parameter was performed principal component analysis. PCA shows that the first four traits correspond to the whole percentage of the variance in the dataset. The first four main PCAs are extracted from the complicated components, the total cumulative variance of these four factors amounted to 76.419% and these components had eigen values >1 . The PCA grouped the estimated soybean variables into four main components which PCA_1 accounted for about 35.591% of the variation; PCA_2 for 21.564%; PCA_3 for 10.891% and PCA_4 for 8.373% . The first PCA was related to leaf length, plant height, leaf breadth at base, leaf breadth at middle and leaf breadth at top whereas the second PCA was related to seed yield per plant, seeds per plant, pods per plant, hundred seed weight, leaf per plant.

Table 7. Factor analysis for different traits of twenty soybean genotypes

Characters	Component			
	PCA	PCA2	PCA3	PCA4
Length of leaves (cm)	0.884	-0.162	0.017	0.305
Plant height (cm)	0.853	0.199	-0.006	-0.123
Leaf breadth top (cm)	0.783	0.169	0.493	-0.183
Leaf breadth base (cm)	0.697	0.059	0.432	-0.411
Leaf breadth middle (cm)	0.641	0.295	-0.179	-0.382
Primary branches per plant	-0.621	-0.224	-0.009	0.189
Seed yield per plant (g)	0.243	0.943	0.086	-0.048
Seeds per plant	0.033	0.922	-0.126	0.236
Pods per plant	-0.004	0.904	-0.161	0.132
100 seed weight (gm)	0.38	0.757	0.272	-0.244
Days to maturity	-0.024	0.499	0.723	-0.071
Leaf per plant	-0.192	0.228	-0.633	0.042
Germination percentage %	0.233	0.461	-0.469	-0.06
Seed per pod	-0.015	0.157	-0.23	0.816
Days of 50% flowering	-0.475	0.034	0.204	0.709
Eigen value	5.339	3.235	1.634	1.256
Cumulative%	35.591	57.155	68.046	76.419

Table 8. Eigen values and yield percent contribution of different characters of soybean genotype

Principal component axes	Eigen values	Percent variation	Cumulative % of percent variation
I	5.339	35.591	35.591
II	3.235	21.564	57.155
III	1.634	10.891	68.046
IV	1.256	8.373	76.419
V	.997	6.647	83.066
VI	.903	6.018	89.084
VII	.577	3.847	92.931
VIII	.347	2.314	95.245
IX	.271	1.805	97.050
X	.202	1.344	98.394
XI	.094	.630	99.024
XII	.072	.478	99.502
XIII	.060	.400	99.901
XIV	.014	.095	99.996
XV	.001	.004	100.000

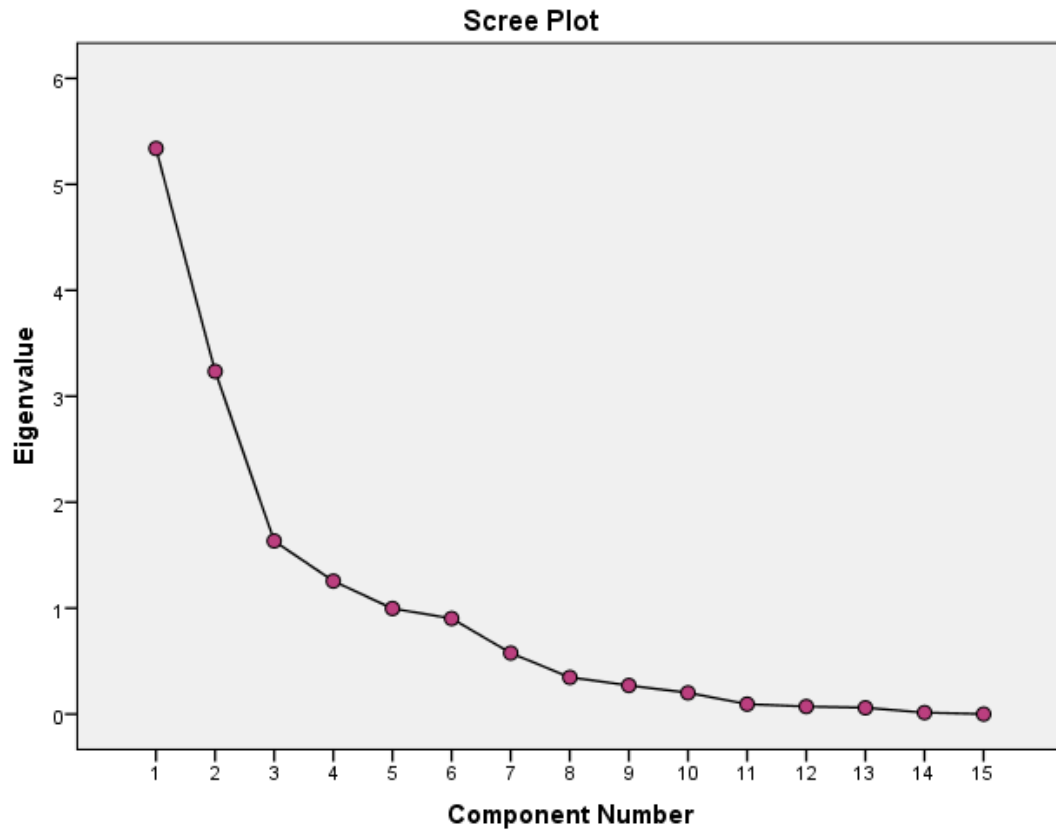


Figure 4: Graphical representation of scree plot of the fifteen characters by using eigen values of component axes

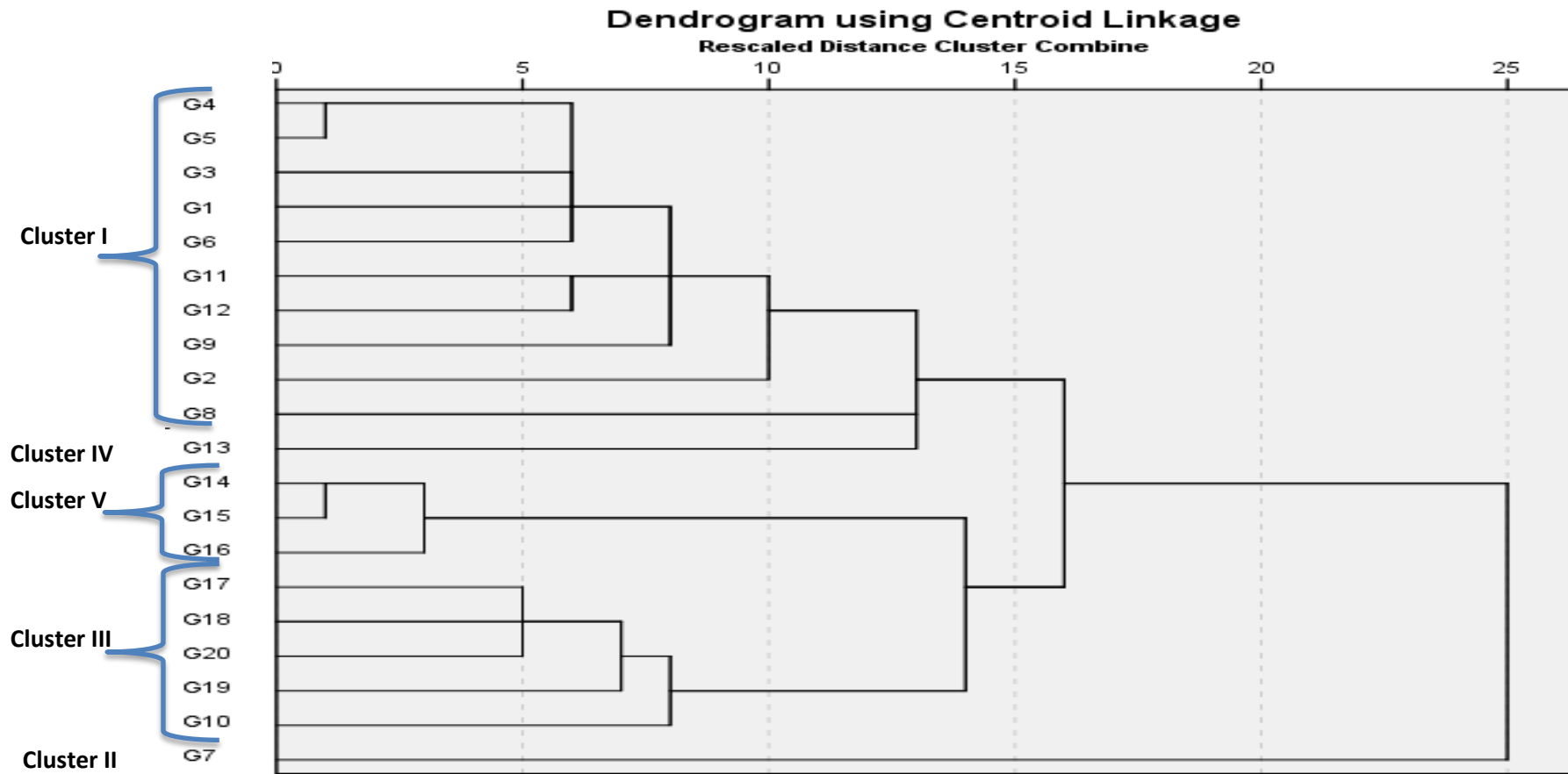


Figure 5: Dendrogram showing five different clusters of twenty soybean genotypes

and germination percentage. The third PCA consist variables that are related solely to days to maturity and the fourth PCA was related to seeds per pod, days to 50% flowering and primary branches per plant (Table 6).

4.5.2 Nonhierarchical clustering

With the application of covariance matrix for nonhierarchical clustering, 20 soybean genotypes were grouped into five different clusters. It is stated that highest 50% genotypes were included in cluster I and it was followed by 25% in cluster III, 15% in cluster V, 5% in cluster II and IV. The composition of clusters with different genotypes is presented in Table 8.

From Table 9 cluster I had the maximum 10 genotypes (G1, G2, G3, G4, G5, G6, G8, G9, G11, G12) followed by cluster III (G10, G17, G18, G19, G20) had 5 genotype, cluster V (G14, G15, G16) had three genotype, cluster II (G7) and cluster IV (G13) had only one genotypes (Table 8).

The result confirmed the clustering pattern off the genotype according to the principal component analysis. Composition of various clusters regarding their genotypes in each cluster is presented in Table 9. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. For that reason it can be said that the results obtained through PCA were established by nonhierarchical clustering.

Table 9. Distribution of different genotypes of soybean in different clusters

Cluster no.	Name of Genotypes	No. of populations	Percentage	Genotypes
I	G1, G2, G3, G4, G5, G6, G8, G9, G11, G12	10	50%	TAS-4,DJS 9207,AGS-95,K-16, GMOT-95, ASSET-93, GMOT-13, AGS-205, FV-4PL- NICE-7, BOSS
II	G7	1	5%	ASOMEME
III	G10, G17, G18, G19, G20	5	25%	BARI SOYBEAN 5, BARI SOYBEAN 6, BINA SOYBEAN 3, BINA SOYBEAN 2, LOCAL
IV	G13	1	5%	AGS-79
V	G14, G15, G16	3	15%	BINA SOYBEAN 4, BINA SOYBEAN 1, SOHAGH
Total		20		

4.5.3 Canonical variate analysis

Canonical variate analysis was performed to compute the inter-cluster Mahalanobis's values. Statistical distances represent the index of genetic diversity among the clusters. The inter cluster D^2 values are given in Table 10 and the nearest and farthest cluster from each cluster based on D^2 value is given in Table 11. The inter cluster D^2 values were maximum (38.541) between the cluster I and III cluster, followed by III and IV (36.024) and I and V (30.102). The higher inter-cluster distances between these clusters indicate to obtain wide spectrum variability of population. However, the highest inter cluster distance was observed between clusters I and III indicated the genotypes in these clusters were diverse than other clusters. Cluster I was the most diverse as many other clusters showed maximum inter cluster distance with it. The lowest inter-cluster distance was observed between cluster I and II (16.140), followed by IV and V (17.722). The minimum distance observed between clusters indicated close relationship among the genotypes.

The intra cluster D^2 values in Table 7 showed that highest intra-cluster distance was found in cluster V (4.76), followed by I (3.765). The lowest intra-cluster distance was observed in cluster II (0.00) and IV (0.00). The inter cluster distances were larger than the intra cluster distances which indicated wider genetic diversity among the genotypes of different groups.

Table 10: Intra (Bold) and inter cluster distances (D^2) for soybean genotypes

Cluster	I	II	III	IV	V
I	3.765	16.140	38.541	21.690	30.102
II		0.00	25.036	27.117	25.868
III			2.67	36.024	23.370
IV				0.00	17.722
V					4.76

Table 11. The nearest and farthest clusters from each cluster based on D^2 values in soybean genotype

Sl No.	Cluster	Nearest cluster with D^2 values	Farthest cluster with D^2 values
1	I	II (16.140)	III (38.541)
2	II	I (16.140)	IV (27.117)
3	III	II (25.036)	I (38.541)
4	IV	V (17.722)	III (36.024)
5	V	IV (17.722)	I (30.102)

4.5.4 Principal co-ordinate analysis (PCO)

The results obtained from principal co-ordinate analysis showed that highest inter genotypic distance was observed between G7 (ASOMEME) and G15 (AGS-79), followed by G7 (ASOMEME) and G14 (BINA SOYBEAN 8), G7 (ASOMEME) and G16 (SOHAGH) where inter genotypic distance values were 6.72, 6.26 and 6.01 respectively (Table 12). The lowest inter-genotypic distances was observed in G4 (K-16) and G5 (GMOT-95) followed by G14 (BINA SOYBEAN 8) and G15 (BINA SOYBEAN 1), G14 (BINA SOYBEAN 8) and G16 (SOHAGH) where inter genotypic distances were 0.28, 0.34 and 0.40 respectively (Table 12).

Table 12: Ten highest and ten lowest inter genotypic distance among the 20 soybean genotypes through Squared Euclidean Distance

Highest distance				Lowest distance			
SI No.	Genotype		Distance	SI No.	Genotype		Distance
01	G7	G15	6.721609	01	G4	G5	0.285335
02	G7	G14	6.267528	02	G14	G15	0.346613
03	G7	G16	6.01681	03	G14	G16	0.400332
04	G7	G18	5.755531	04	G17	G18	0.730159
05	G8	G18	5.04423	05	G18	G20	0.748411
06	G12	G18	4.461675	06	G11	G12	0.781039
07	G10	G12	4.415889	07	G15	G16	0.786672
08	G2	G16	4.400473	08	G3	G4	0.790287
09	G5	G15	4.400305	09	G1	G5	0.825379
10	G5	G14	4.299205	10	G17	G20	0.826472

4.5.5 Cluster mean analysis

The cluster means of 15 different characters (Table 13) were indicated and compared and indicated considerable differences among clusters for all the characters studied. Maximum germination percentage was found in cluster IV (94.33) whereas minimum was found in cluster II (87.00). Maximum days of 50% flowering were found in cluster II (48.00) whereas minimum was found in cluster V (40.00). Maximum plant height was found in cluster V (58.89) whereas minimum was found in cluster II (24.33). Maximum length of leaves was found in cluster V (7.83) whereas minimum was found in cluster II (5.93). Maximum leaf breadth at base was found in cluster V (4.04) whereas minimum was found in cluster II (2.33). Maximum leaf breadth at middle was found in cluster V (5.42) whereas minimum was found in cluster II (2.93). Maximum leaf breadth at top was found in cluster V (3.51) whereas minimum was found in cluster II (1.73). Maximum primary branches per plant were found in cluster II (4.67) whereas minimum was found in cluster IV (2.33). Maximum leaves per plant were found in cluster III (17.13) whereas minimum was found in cluster IV (9.67). Maximum pods per plant were found in cluster III (24.87) whereas minimum was found in cluster I (15.87). Maximum seeds per pod were found in cluster II (3.00) whereas minimum was found in cluster IV (2.33). Maximum seeds per plant were found in cluster III (72.20) whereas minimum was found in cluster I (50.60). Maximum hundred seed weight was found in cluster V (15.44) whereas minimum was found in cluster IV (8.67). Maximum days of maturity were found in cluster V (90.33) whereas minimum was found in cluster IV (84.33). Maximum seed yield per plant was found in cluster III (11.01) whereas minimum was found in cluster IV (4.93) (Table 13).

Table 13. Cluster mean of yield and yield related characters of soybean genotypes

Characters	I	II	III	IV	V
Germination Percentage %	90.30	87.00*	93.00	94.33**	91.67
Days of 50% Flowering	41.90	48.00**	42.07	41.00	40.00*
Plant Height (cm)	38.93	24.33*	46.67	45.67	58.89**
Length of Leaves (cm)	6.76	5.93*	6.69	7.27	7.83**
Leaf breadth base (cm)	3.08	2.33*	3.07	2.53	4.04**
Leaf breadth middle (cm)	4.43	2.93*	4.74	4.10	5.42**
Leaf breadth top (cm)	2.21	1.73*	2.41	2.03	3.51**
Primary branches per plant	3.83	4.67**	3.27	2.33*	2.89
Leafs per plant	16.40	11.67	17.13**	9.67*	12.11
Pods per plant	15.87*	20.67	24.87**	16.33	19.44
Seeds per pod	2.60	3.00**	2.67	2.33*	2.44
Seeds per Plant	50.60*	61.33	72.20**	56.67	59.00
100 seed weight (gm)	10.20	9.33	15.27	8.67*	15.44**
Days to Maturity	86.83	90.00	88.60	84.33*	90.33**
Seed yield per plant (g)	5.13	5.73	11.01**	4.93*	9.10

* Minimum value ** Maximum value

4.5.6 Cluster diagram

With the help of D^2 values within and between clusters, an arbitrary cluster diagram (Figure 7) was constructed, which showed the relationship between different genotypes. However, the diagram was not following exact scale. It was apparent from the (Fig 6) that the genotypes from the cluster V were far diverse (30.102) from the genotypes of the cluster I and where the genotypes belonging to I- II were the least diverse (16.140). Genotypes of cluster III and II (25.036) and IV -II (27.117) were moderately diverse from each other.

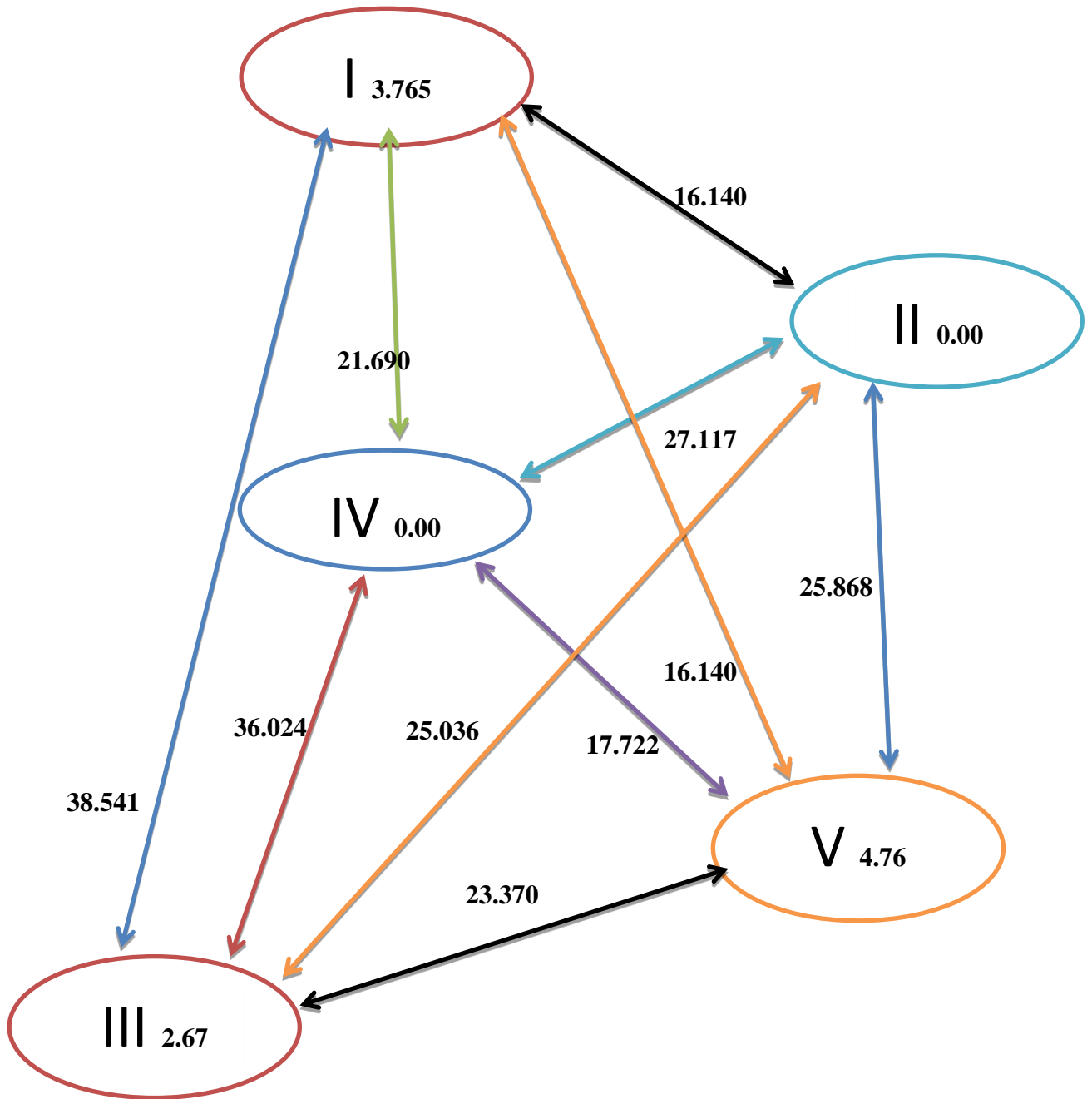


Figure 7: Intra and inter cluster distances of twenty soybean genotypes

4.5.7 Selection of genotypes as parent for hybridization programme

Identification and utilization of diverse germplasm is the central issue in plant breeding. Three factors (choice of particular cluster, selection of specific variety from a 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). Through knowledge of genetic diversity of the crop is necessary for parental selection that maximizes genetic improvement (Rahman et al. 2011). More accurate and complete description of genotypes and patterns of genetic diversity could help determinate future breeding strategies and facilitate introgression of diverse germplasm into the current commercial soybean genetic base (Baranek et al. 2002). Principal component analysis is useful as it gives information about the groups where certain traits are more important allowing the breeders to conduct specific breeding program (Salimi et al. 2012). Genetically distant parents are usually able to produce highest heterosis. Considering magnitude of genetic distance, contribution of different characters towards the total divergence, magnitude of cluster means for different characters and field performance the genotype G7 (ASOMEME) from the cluster II and G15 (BINA SOYBEAN 1) from cluster V, G7 (ASOMEME) from the cluster II and G14 (BINA SOYBEAN 4) from cluster V, G7 (ASOMEME) from the cluster II and G16 (SOHAGH) from cluster V, G7 (ASOMEME) from the cluster II and G18 (BINA SOYBEAN 3) from the cluster II, G8 (GMOT-13) from the cluster I and G18 (BINA SOYBEAN 3) from the cluster II would be suitable parent for highest yield for future hybridization programme.

SUMMARY AND CONCLUSION

The experiment was conducted with a view to identify the characters contributing to genetic diversity, identify divergent parents for hybridization program, identify the characters which contribute to genetic diversity, measure the magnitude of genetic divergence in genotypes and find out the variability regarding yield and some yield contributing characters, the degrees of association among the characters under study and their indirect and direct effects of 20 genotypes of soybean (*Glycine max L. Merrill*) at the experimental plot of Sher-E-Bangla Agricultural University farm, Dhaka, during November 2016 to February 2017. The most important findings of the present study have been summarized on the basis of the characters under study.

The ANOVA (analysis of variance) showed significant differences among the genotypes for all the characters under study. The accession “LOCAL” showed highest germination percentage (95.33%) while the lowest (83.33%) was recorded in “BOSS”. The minimum days to 50% flowering was 39.00 days in the genotype “BINA SOYBEAN 1” and maximum was to 48.00 in the genotype “ASOMEME”. The lowest plant height was 21.33 cm in “TAS-4” and highest was 63.33 cm in the genotype “SOHAGH”. The minimum number of primary branches per plant was 2.33 in “AGS-79” and maximum was 4.67 in “K-16”. The minimum length of leaves was 5.27cm in “DJS 9207” and maximum was 8.37cm in “SOHAGH”. The genotype “ASOMEME” showed minimum breadth of leaves at the base was 2.33cm whereas “SOHAGH” showed maximum breadth of leaves at the base 4.10cm. The genotype “ASOMEME” showed minimum breadth of leaves at the middle was 2.93cm whereas “BINA SOYBEAN 1” showed maximum breadth of leaves at the middle was 5.80cm. The genotype “DJS 9207” showed minimum breadth of leaves at the top was 1.60cm whereas “BINA SOYBEAN 4” showed maximum breadth of leaves at the top was 3.67cm. The genotype “AGS-79” showed minimum leaf per plant was 9.67 whereas “BINA SOYBEAN 3” showed

maximum leaf per plant 20.00. Minimum number of pod per plant was 10.67 in the genotype “GMOT-13” whereas “BINA SOYBEAN 3” showed maximum number of pod per plant 28.67. The genotype “GMOT-13” showed minimum number of seed per pod 2.00 whereas maximum number of seed per pod 3.00 showed in “BINA SOYBEAN 2”. The genotype “GMOT-13” showed minimum number of seed per plant 40.00 whereas “BARI SOYBEAN 5” showed maximum number of seed per plant 81.00. Minimum weight of hundred seed was 8.67gm showed in the genotype “AGS-79” whereas “BINA SOYBEAN 2” showed maximum number of seed per plant was 16.33gm. The genotype “AGS-79” showed minimum days to maturity was 84.33 whereas maximum days to maturity 91.33 was shown in “BINA SOYBEAN 1”. The genotype “GMOT-13” showed minimum seed yield per plant was 4.35gm whereas “BINA SOYBEAN 2” showed maximum seed yield per plant was 12.01gm.

The phenotypic variance was higher than genotypic variance in all the characters under study. Phenotypic coefficients of variation were also near to genotypic coefficients of variation for all of the characters under study. High heritability (> 60%) was observed for most of the characters under study. The highest heritability was found for seed yield per plant (91.62%). The high heritability coupled with high genetic advance in percent of mean was observed in plant height, leaf breadth at top, leaf per plant, pods per plant, seeds per plant, hundred seed weight and seed yield per plant which would be selected for future breeding program. High heritability coupled with low genetic advance in percent of mean was observed in germination percentage, leaf breadth at middle and leaf breadth at top. Low heritability and low genetic advance in percent of mean was observed in days to 50% flowering, leaf length, primary branch per plant, seeds per pod and days to maturity.

Correlation revealed that highly significant positive association of seed yield per plant with germination percentage, plant height, leaf breadth at middle, leaf breadth at top, pods per plant, seed per pod, hundred seed weight and days to

maturity at both genotypic and phenotypic level. Genotypic correlation coefficients were larger in values as compared to their respective phenotypic correlation coefficient. This indicates greater contribution of genetic factor in the development of the association.

Hundred seed weight showed the highest positive direct effect with seed yield. On the other hand highest negative direct effect on seed yield was shown by primary branch per plant. Days to 50% flowering, leaf breadth at base, leaf breadth at middle, leaf breadth at top, leaf per plant, pods per plant, seeds per pod and seeds per plant also showed positive direct effect with seed yield. The highest indirect effect of leaf breadth at top observed with hundred seed weight. Hundred seed weight showed high direct effect on seed yield indicated that direct selection for this trait might be successful and there is a great extent of possibility of improving seed yield through selection based on those characters.

Genetic diversity of twenty soybean genotypes based on thirteen characters was measured through multivariate analysis. The 20 genotypes clustered into five distant clusters. The cluster I comprised the maximum number 10 of genotypes, followed by cluster III comprised of 5 genotypes. The cluster V, IV and II comprised 3, 1 and 1 genotypes, respectively. The highest inter-cluster distance (38.541) was observed between the cluster I and III and the highest distant genotypes were G7 (ASOMEME) and G15 (BINA SOYBEAN 1). The lowest inter-cluster distance (16.140) was observed between the cluster I and II and the lowest distance genotypes were G4 (K-16) and G5 (GMOT-95). The inter-cluster distances were larger than the intra-cluster distances. The intra cluster distances in the entire five clusters were more or less low indicating that the genotypes within the same cluster were closely related. Though genotypically distant parents are able to produce higher heterosis but in different experiments it was also revealed that higher heterosis for yield and its components could be obtained from the crosses between the intermediate divergent parents than extreme ones.

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

1. The genotype of clusters I was more diverse from the genotypes of cluster III.
2. Wide genetic diversity was found in 20 genotypes of soybean, which were grouped into five clusters and most diverse genotypes were G7 (ASOMEME) and G15 (BINA SOYBEAN 1). That variability could be used for future breeding program of soybean in Bangladesh.
3. Germination percentage, plant height, leaf breadth at middle, leaf breadth at top, pods per plant, seeds per pod and seeds per plant showed highly significant and positive correlation with seed yield at both genotypic and phenotypic levels. This results suggested that seed yield per plant can be increased by improving these characters.
4. High heritability coupled with high genetic advance in percent of mean was observed in plant height, leaf breadth at top, leaf per plant, pods per plant, seeds per pod, hundred seed weight and seed yield per plant. Hence, yield improvement in soybean would be achieved through selection of these characters.
5. Days to 50% flowering, leaf breadth at base, leaf breadth at middle, leaf breadth at top, leaf per plant, seeds per pod, seeds per plant and hundred seed weight showed positive direct effect on yield. So yield improvement was associated with these characters.
6. Further collection of soybean germplasms would be continued for getting more variability and desired traits in soybean.

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

- Genotypes G7 (ASOMEME), G8 (GMOT-13), G12 (BOSS) from cluster I, G10 (BARI SOYBEAN 5) and G18 (BINA SOYBEAN 3) from cluster III, G14 (BINA SOYBEAN 4), G15 (BINA SOYBEAN 1) and G16 (SOHAGH) from cluster V would be suitable for future hybridization program.
- The genotypes of cluster I and III could be used as parents for future breeding program to develop soybean variety.

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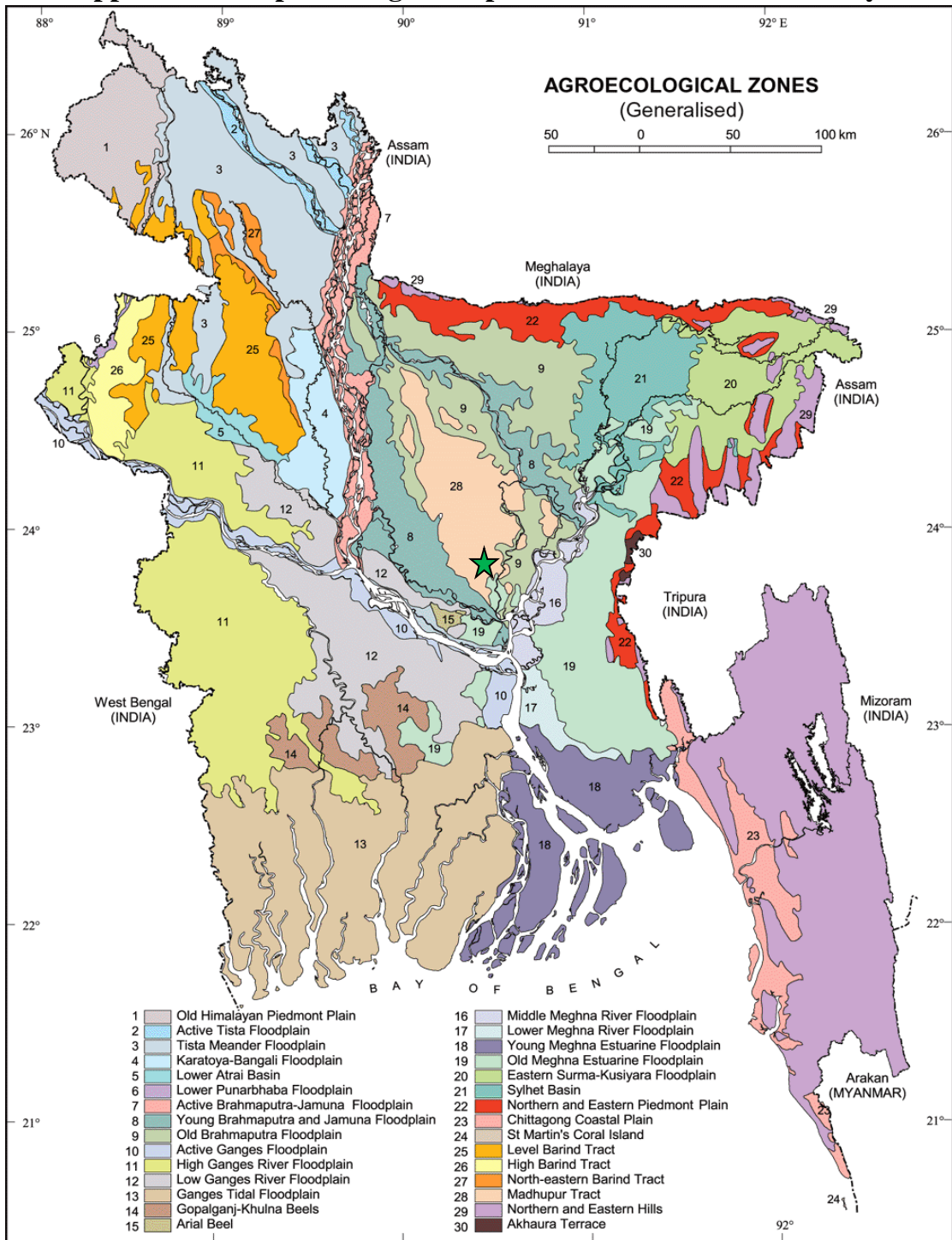
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APPENDICES

Appendix I: Map showing the experimental site under the study



Green Star = Experimental Area

Appendix II: Monthly average record of air temperature, rainfall, relative humidity, sunshine hours of the experimental site during study period from November 2016 to March 2017

Month	Air temperature (°c)		Relative humidity (%)	Rainfall(mm) total	Sunshine (hr)
	Maximum	Minimum			
November, 2016	30	15	75	2	8.5
December, 2016	29	13	79	0	8.3
January, 2017	28.1	11.1	72	1	7.5
February, 2017	33.9	12.2	55	1	8.7

**Source: Bangladesh Meteorological Department (Climate & Weather Division)
Agargaon Dhaka-1212**

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

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(%)	0.84
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)	6.3
10	CEC	11.23

Source: Soil Resource and Development Institute (SRDI), Dhaka 1207

Appendix IV: Analysis of variance of different characters of twenty soybean genotypes

Characters/Variety	Mean sum of square		
	Replication (r-1) = 2	Genotype (g-1) = 19	Error (r-1)(g-1) = 38
Germination percentage %	4.02	27.45**	4.70
Days of 50% flowering	4.12	13.01**	3.87
Plant height (cm)	87.22	381.42**	34.99
Length of leaves (cm)	0.48	2.18**	0.51
Leaf breadth base (cm)	0.09	0.73**	0.10
Leaf breadth middle (cm)	0.06	1.65**	0.21
Leaf breadth top (cm)	0.03	0.89**	0.06
Primary branches per plant	0.32	1.56**	0.44
Leaf per plant	1.32	29.22**	2.32
Pods per plant	2.07	71.79**	8.91
Seeds per pod	0.05	0.27	0.24
Seeds per plant	19.40	359.09**	16.26
100 seed weight (gm)	4.62	24.12**	1.30
Days to maturity	1.67	15.63**	4.05
Seed yield per plant (g)	3.38	22.45**	0.66

** Significant at 1% level of probability

Appendix V : Analysis of variance for regression

Model	Sum of squares	df	Mean square	F	Sig.
Regression	142.132	14	10.152	322.896	0.000
Residual	0.157	5	0.031		
Total	142.289	19			

Appendix VI: Partial correlation and linear regression coefficients of yield contributing attributes on yield of soybean

Attributes	Partial correlation	Linear regression coefficients (beta)	t-test for significance (for beta)
Germination percentage %	-0.657	-0.047	-1.946
Days of 50% flowering	0.066	0.004	.148
Plant Height (cm)	-0.131	-0.013	-.295
Length of leaves (cm)	0.432	0.037	1.070
Leaf breadth at base (cm)	0.223	0.024	.512
Leaf breadth at middle (cm)	0.368	0.028	.885
Leaf breadth at top (cm)	-0.546	-0.074	-1.457
Primary branches per plant	-0.032	-0.002	-.072
Leaf per plant	0.611	0.036	1.727
Pods per plant	-0.588	-0.129	-1.625
Seeds per pod	-0.603	-0.060	-1.691
Seeds per plant	0.946**	0.671	6.544**
100 seed weight (gm)	0.992**	0.630	17.479**
Days to maturity	-0.086	-0.007	-.193

*** = Significant at 0.1%.

** = Significant at 1%.

Appendix VII: Mean performance of different characters of twenty soybean genotypes

Gen	GP	DF	PH	LL	LBB	LBM	LBT	PBP	LPP	PPP	SP	SPP	HSW	DM	SYP
G1	91.33	42.33	21.33	6.37	2.83	4.23	2.17	3.67	17.00	15.67	3.00	57.33	9.33	89.67	5.38
G2	94.00	40.33	29.00	5.27	3.00	5.60	1.60	4.33	17.67	20.33	2.33	52.00	11.33	86.33	5.90
G3	93.67	42.00	45.33	7.53	3.23	5.00	2.23	4.67	17.67	13.33	2.67	48.33	9.67	89.00	4.68
G4	89.00	41.67	43.33	6.83	2.70	3.97	2.03	4.67	18.00	16.67	2.67	50.33	11.67	85.67	5.87
G5	91.00	43.00	37.00	6.00	2.80	3.87	2.10	4.33	17.00	17.67	2.67	56.33	9.67	85.00	5.42
G6	92.33	45.00	44.33	7.77	3.03	4.33	2.24	3.33	18.67	21.00	3.00	61.67	9.67	86.67	6.00
G7	87.00	48.00	24.33	5.93	2.33	2.93	1.73	4.67	11.67	20.67	3.00	61.33	9.33	90.00	5.73
G8	90.00	42.67	40.00	5.80	3.63	3.70	2.33	3.67	11.67	10.67	2.00	40.00	11.67	89.33	4.68
G9	92.67	40.67	49.00	7.77	3.13	5.30	2.30	2.67	14.67	16.00	3.00	53.67	8.67	84.67	4.66
G10	92.33	40.00	32.00	5.67	2.90	4.13	2.23	3.00	16.00	27.00	2.67	81.00	14.33	91.33	11.66
G11	85.67	41.00	45.00	6.63	3.27	3.93	2.73	3.33	19.33	12.33	2.33	42.33	10.33	86.00	4.36
G12	83.33	40.33	35.00	7.67	3.20	4.37	2.33	3.67	12.33	15.00	2.33	44.00	10.00	86.00	4.35
G13	94.33	41.00	45.67	7.27	2.53	4.10	2.03	2.33	9.67	16.33	2.33	56.67	8.67	84.33	4.93
G14	93.00	40.67	55.33	8.07	3.97	5.53	3.67	3.00	11.33	21.67	2.33	59.33	15.33	90.67	9.05
G15	91.33	39.00	58.00	7.07	4.10	5.80	3.40	2.33	13.00	18.67	2.33	60.00	14.67	91.33	8.81
G16	90.67	40.33	63.33	8.37	4.07	4.93	3.47	3.33	12.00	18.00	2.67	57.67	16.33	89.00	9.43
G17	91.00	44.33	52.67	6.77	2.87	5.00	2.43	3.33	16.67	27.67	2.33	74.00	15.67	89.33	11.58
G18	92.67	40.67	57.33	7.20	3.33	4.83	2.47	3.00	20.00	28.67	2.67	78.33	15.33	86.33	12.01
G19	93.67	43.33	42.67	6.83	3.50	5.27	2.77	3.33	14.67	19.00	3.00	63.67	16.33	89.33	10.39
G20	95.33	42.00	48.67	6.97	2.77	4.47	2.17	3.67	18.33	22.00	2.67	64.00	14.67	86.67	9.41

GP = germination percentage %, DF = days of 50% flowering, PH = plant height (cm), LL = length of leaves (cm), LBB = leaf breadth base (cm), LBM = leaf breadth middle (cm), LBT = leaf breadth top (cm), PBP = primary branches per plant, LPP = leaf per plant, PPP = pods per plant, SP = seed per pod, SPP = Seeds per Plant, HSW = 100 seed weight (gm), DM = days to maturity and SYP = seed yield per plant (g)

