

**SELECTION OF ELITE SOYBEAN (*Glycine max* L. Merrill)
GENOTYPES BASED ON MORPHO-AGRONOMIC TRAITS**

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June, 2020

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REGISTRATION No. 13-05407

A Thesis

submitted to the Department of Genetics and Plant Breeding

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: JANUARY - JUNE, 2020

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Dedicated

to

My Beloved Parents and Teachers



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CERTIFICATE

This is to certify that the thesis entitled “SELECTION OF ELITE SOYBEAN GENOTYPES BASED ON MORPHO-AGRONOMIC TRAITS” submitted to the Department of Genetics and Plant Breeding of 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, embodies the results of a piece of bona fide research work carried out by MD.KAMRUL HASAN, Registration No.13-05407 under my supervision and guidance. No part of this thesis has been submitted for any other degree or diploma.

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

Dated: June, 2020
Dhaka, Bangladesh

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ACKNOWLEDGEMENTS

All the praises and gratitude are to the Almighty Who has created everything of this universe and kindly enabled the author to complete his research work and to prepare this thesis for the Master of Science (MS) in Genetics and Plant Breeding.

*The author obediently expresses his profound respect, sincere appreciation, ever indebtedness to his reverend teacher and supervisor **Prof. Dr. Mohammad Saiful Islam**, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, for his continuous supervision, keen interest, scholastic guidance, encouragement and sympathy in the entire period of research work and preparation of this thesis.*

*The author feels proud to express his deepest sense of gratitude and immense indebtedness to his co-supervisor **Prof. Dr. Md. Sarowar Hossain**, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, for his innovative suggestion, continuous supervision, constructive criticisms and cordial assistance for the preparation of thesis.*

*The author expresses his sincere gratitude and thanks to his honorable chairman **Prof. Dr. Kazi Md. Kamrul Huda**, honorable teachers **Prof. Dr. Md. Shahidur Rashid Bhuiyan**, **Prof. Dr. Naheed Zeba**, **Prof. Dr. Firoz Mahmud**, **Prof. Dr. Jamilur Rahman**, **Prof. Dr. Md. Abdur Rahim**, **Prof. Dr. Md. Ashaduzzaman Siddiquee and others**, 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.*

*The author is also grateful to the Ministry of Science and Technology, People's Republic of Bangladesh for awarding a prestigious "NST" fellowship for conducting the research work. Finally the author is highly indebted to his beloved parents **Md. Abul Hosen and Mrs. Kamala Khatun** for their endless blessings and affection in all stages of my life.*

The author

June, 2020

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SOME COMMONLY USED ABBREVIATIONS

Full Word	Abbreviation	Full Word	Abbreviation
Advanced	<i>Adv.</i>	Etcetera	etc.
Agricultural	<i>Agril.</i>	Genetic Advance	GA
Agriculture	<i>Agric.</i>	Genetics	<i>Genet.</i>
Agriculturist	<i>Agricult.</i>	Genotype	G
Agronomy	<i>Agron.</i>	Genotypic coefficient of variation	GCV
Analysis of Variance	ANOVA	Genotypic variance	σ^2g
And others (at elli)	<i>et al.</i>	Gram	g
Applied	<i>Appl.</i>	Hectare	ha
As for example	e.g.	Heritability in broad sense	h^2b
Bangladesh Agricultural Development Corporation	BADC	National Least significant Difference	<i>Natl.</i> LSD
Bangladesh Agricultural Research Institute	BARI	Newsletter	<i>Newsl</i>
Biology	<i>Biol.</i>	Percentage	%
Biotechnology	<i>Biotechnol.</i>	Opinion	<i>Opin.</i>
Botany	<i>Bot.</i>	Particular pages	Pp.
Brasleira	<i>Bras.</i>	Percent	%
Breeding	<i>Breed.</i>	Phenotypic variance	σ^2g
Bulletin	<i>Bull.</i>	Phenotypic coefficient of variation	PCV
Centimeter	cm	Physiology	<i>Physiol.</i>
Chronica	<i>Chron.</i>	Proceeding	<i>Proc.</i>
Company	Co.	Progress	<i>Progr.</i>
Randomized Complete Block Design	RCBD	Research	<i>Res.</i>
Current	<i>Curr.</i>	Science	<i>Sci.</i>
Degree Celsius	$^{\circ}C$	Technical	<i>Tech.</i>
Degrees of freedom	df	Days after sowing	DAS
Ecology	<i>Ecol.</i>	Coefficient of variance	CV
Economy	<i>Econ.</i>	Kilogram	Kg
Environment	<i>Env.</i>	University	<i>Univ.</i>
Environmental	<i>Environ.</i>	Veterinary	<i>Vet.</i>
		Weight of hundred seed	WHS

**SELECTION OF ELITE SOYBEAN (*Glycine max* L. Merrill)
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ABSTRACT**

The present experiment was conducted by using eighteen advanced genotypes of Soybean (*Glycine max* L. Merrill) for selecting most promising genotypes at the experimental field of Sher-e-Bangla Agricultural University (SAU), Sher-e-Bangla Nagar, Dhaka-1207 during the period from mid-December, 2018 to mid-April, 2019 based on some morphological traits. The experiment consisted of one factor with three replications. The results indicated that the genotypes differed regarding all the characters studied. The phenotypic variance and coefficient of variation were higher than the genotypic variance and coefficient of variation in all the characters studied. Moderate to high heritability was observed for all characters except leaf length and number of primary branches per plant. High heritability coupled with high genetic advance in percent mean were observed for germination percentage, days to 50% flowering, plant height, number of pod per plant, number of seeds per plant and thousand seed weight. The characters germination percentage, days to 50% flowering, plant height, leaf length, number of pod per plant, number of seeds per pod and number of seeds per plant showed positive direct effect on yield. Therefore, importance had to be given for these characters in further breeding program to improve soybean yield. All the genotypes were grouped into four clusters having 5, 2, 6 and 5 genotypes, respectively. Cluster III comprised the maximum number (6) of genotypes followed by cluster I(5) and IV(5). The highest inter cluster distance (26.186) was observed between the cluster I and II. Likewise highest distant genotypes were G11(AGS-205) and G18 (BINA SOYBEAN 3) (1.362). Among the characters studied days to 50% flowering, number of primary branches per plant, number of seeds per pod, thousands seed weight were the important component characters having higher contribution to the genetic divergence of soybean. As a result, these traits could be emphasized during selection of parents for hybridization.

CHAPTER I

INTRODUCTION

Soybean (*Glycine max* L. Merrill) is an important legume crop that grows in the tropical, subtropical and temperate climates (Thuzar *et al.*, 2010). Soybean belongs to the botanical family Leguminosae under sub-family papilionaceae and is a self-pollinated crop. Soybean is known as "Golden bean" or "Miracle bean" or "Protein hope of future" is now being cultivated and consumed in Bangladesh. It is one of the most important protein and oilseed crops throughout the world. The crop is well adapted to many soil types and climatic conditions. It is a resident of eastern Asia, originally growing wild in China, Manchuria, Korea and Japan. Soybean (*Glycine max* L. Merrill) is one of the oldest crops grown in the world. The plant is classed more as an oil seed crop than a pulse. It is an annual plant that has been used in at least 3000 BC by ancient Chinese who considered soybean as an important and sacred crop (Vaughan and Geissler2008).

Soybean is an important legume with multifarious uses. It's cost effectiveness is ensured through its biological nitrogen fixation and in rotation with exhaustive crops such as maize and sorghum; it helps in replenishing and maintaining the soil fertility. According to FAO (2012), United States of America was the largest global producer of soybean with (82,054,000 tonnes) followed by Brazil (65,848,857 tonnes), Argentina (40100,197 tonnes)and then China (12,800,159 tonnes). Soybean is very suitable crop to fit into the cropping systems of Bangladesh. 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).

It provides a large amount of edible vegetable oil as well as soybean cake and meal which are high protein supplements in mixed feed rations for livestock. Azhari (1987) reported that soybean contains 20 to 22% of essential amino acids, and 40% of proteins. The experimental result by Malik *et al.*, (2006)

revealed that soybean contains 18-22% oil which comprises of 85% cholesterol free unsaturated fatty acids in comparison to conventional vegetable and animal fats. Soybean also has many food and industrial uses. Soybean food has been reported to provide protection against heart disease, cancer and other diseases (Carter and Wilson 1987). Because of its nutritional value there is a growing demand for soy foods such as soymilk, several types of tofu, soybean sprouts, soy nuts, cottage cheese like soybean curd rich in protein, and various vitamins and minerals (Rao *et al.*, 2002). Its seed contain 42-45% protein and 22% edible oil (Mondal *et al.*, 2001). Moreover, it contains minerals such as Fe, Cu, Mn, Ca, Mg, Zn, Co, P and K. Vitamins B1, B2, B6 and isoflavones are also available in soybean grains (Messina, 1997). Soybean oil is rich in polyunsaturated fatty acids, including the two essential fatty acids (linoleic and linolenic). In Bangladesh, human consumption of soybean is very little. Recently, soybean has become an important crop in Bangladesh for its increasing demand as an ingredient of poultry and fish meal. Therefore, a huge amount of soybean is imported every year.

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 of Bangladesh, 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).

Soybean is being cultivated in Bangladesh as a minor crop and little attention has been given on the improvement of its yield. In Bangladesh the average yield of soybean is very low in comparison with other soybean growing

countries of the world. Low production and acreage of soybean in Bangladesh result from lack of high yielding genotypes, poor technological intervention during production, competitions for a place in the existing cropping pattern and food habit. This shortcoming can be overcome by the development of high yielding varieties with wider adaptability and stability. Therefore the development of high yielding varieties of soybean is essential to compete economically with other crops as well as to gear up the production trend of this crop. The basic key to bring about the genetic improvement to a crop is to utilize the available or created genetic variability. If the variability in the population is largely due to genetic causes with least environmental effects it is easy to isolate superior soybean genotypes to improve yield. A critical review of genetic variability is therefore prerequisite for planning and evaluation of a breeding program. This is difficult to judge what proportion of the observed variability is heritable and what proportion is non-heritable.

The process of breeding in such population is primarily conditioned by the magnitude and nature of interaction of genotype and environment variations in plant characters. It is necessary to categorize the observed variability into its heritable and non-heritable components and to have an understanding of parameters such as genetic coefficient of variation, heritability and genetic advance. 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.

The screening of commonly grown soybean genotypes for low pH tolerance would provide a better understanding of the crops adaptation and the management requirements under low soil pH conditions. Raut *et al.* (2001) reported that acid tolerance in plants is often clearly identifiable through morphological and physiological symptoms. High acidic soil condition greatly influence on the physiological growth and yield contributing characters of

soybean (Uguru *et al.*, 2012; Kuswanto *et al.*, 2013). The cultivation of oil crop especially soybean is unknown to the farmers in this region due to the lack of local variety. The production performance of any crops depends on some physiological characteristics. To evaluate the morpho- physiological characteristics responsible for yield differences among the genotypes of soybean are useful in crop improvement.

Considering the above mentioned facts, the present investigations were undertaken with the following objectives:

1. To estimate the nature and magnitude of genetic diversity and selection of superior soybean genotypes
2. To know the nature of association of traits, direct and indirect relation between yield contributing characters of soybean genotypes

CHAPTER II

REVIEW OF LITERATURE

Soybean was first domesticated in the 11th century BC around northeast of China. Soybean belongs to the family Leguminosae under sub-family Papilionaceae that grows well in tropical, subtropical, and temperate climates. Soybean (*Glycine max* L. Merrill) is one of the world's pioneer sources of vegetable oil and plant protein, both of which are very well adapted to the nourishment of human beings. Extensive research works on soybean have been conducted in different parts of the world. Various studies on the variability, interrelationship, path co-efficient 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 II presented under the following heads:

2.1 Family and botany

Soybean (*Glycine max* L.Merrill) like peas, beans, lentils and peanuts, belongs to the large botanical family Leguminosae, in the subfamily Papilionidae, and is well adapted to many soil types and climatic conditions. The genus *Glycine*, consists of two subgenera, *Soja* and *Glycine*. Subgenus *soja* includes *Glycine max* and its annual wild relative *Glycine soja* which are native to eastern Asia, throughout China, Japan, Korea and part of Russia (Chen *et al.*,2015).

The crop grows well in the tropical, subtropical and temperate climates .Plant breeders have argued that within the soybean species, there are varieties which react differently to photoperiod, and classified them as long day, short day and day neutral plants (Borget, 1992). Singh *et al.* (2007) described soybean as being typically a short day plant, physiologically adapted to temperate climatic conditions. However, some have been adapted to the hot, humid, tropical climate. This affects the extent of vegetative growth, flower induction, production of viable pollen, length of flowering, pod filling and maturity characteristics (Norman *et al.*, 1995).Soybean plant has 40 chromosomes

($2n=2x=40$) and it is a self-fertile species with less than 1% out-crossing (Shurtleff and Aoyagi, 2007; IITA, 2009). The optimum temperature for soybean is 20°C – 30°C, with temperatures of 35°C and above considered inhibitory to production. The optimum rainfall amount is between 350 mm and 750 mm, well distributed throughout the growth cycle (Ngeze, 1993). Soybean is a short day plant and therefore, flowers in response to shortening days. Each variety has a critical day length that must be reached before it will start to flower. The best time to plant soybeans is between early and late June depending on the rains in Northern Ghana. Soybeans prefer fertile, well drained, loamy soils. Drought is a major limiting factor for soybean in the early wet season in respect to germination (Luo *et al.*, 2013).

"Soya" (or "Soy" in the United States), is a dicotyledonous plant that exhibits epigeal emergence. During germination, the cotyledons are pushed through the soil to the surface by an elongating hypocotyl. Because of the energy required to push the large cotyledons through heavy soils, soybean generally emerges best if they are planted no deeper than 5 cm. After emergence, the green cotyledons open and supply the developing leaves with stored energy, while capturing a small amount of light energy (Fehr *et al.*, 1971). The first leaves to develop are the unifoliolate leaves. Two of these single leaves appear directly opposite one another above the cotyledons. All subsequent leaves are trifoliolates, comprised of 3 leaflets (Mahama, 2011). Soybean development is characterized by two distinct growth phases. The first is the vegetative stages that cover development from emergence through flowering. The second is the reproductive stages from flowering through maturation. Plant stages are determined by classifying leaf, flower, pod, and or seed development (Fehr *et al.*, 1971; Gary and Dale, 1997).

The flowers are either purple or white, and are borne in auxiliary racemes on peduncles at the nodes. The papilionaceous flower consists of a tubular calyx of five sepals, a corolla of five petals (one banner, two wings and two keels), one pistil and nine stamens with a single separate posterior stamen. The stamens form a ring at the base of the stigma and elongate one day before

pollination, at which time the elevated anthers form a ring around the stigma and are self-pollinated (Acquaah, 2007). The plant produces a large number of flowers, but only about two-thirds to three quarters of them produce pods (Acquaah, 2007). The pods are also pubescent and range in colour from light-yellow to black. They are usually straight or slightly curved in shape, vary in length from two to seven centimeters, and consist of two halves of a single carpel which are joined by a dorsal and ventral suture.

The pod usually contains one to three seeds (occasionally four) (Asafo-Adjei *et al.*, 2005). The shape of the seed, usually oval, can vary amongst cultivars from almost spherical to elongated and flattened. The seeds are usually uncoloured and may be straw yellow, greenish-yellow green, brown, or black (Acquaah, 2007). Bicoloured seeds exist, such as yellow with a saddle of black or brown. The hilum is also coloured with various patterns such as yellow, buff, brown or black (Acquaah, 2007).

2.2 Origin and distribution

Soybean is one of the oldest cultivated crops, but its early history is lost in antique. The first domestication of soybean has been traced to the eastern half of North China in the eleventh century B.C. or perhaps a bit earlier. Soybean has been one of the five main plant foods of China along with rice, wheat, barley and millet (Gibson and Benson, 2005). According to early authors (Hymowitz, 1984; Wilcox, 1987; Shurtleff *et al.*, 2014), soybean production was localized in China until after the Chinese- Japanese war of 1894-95, when the Japanese began to import soybean oil cake for use as fertilizer. Shipments of soybeans were made to Europe about 1908, and the soybean attracted world-wide attention. Europeans had been aware of soybeans as early as 1712 through the writing of a German botanist (Bertheau and Davison, 2011). It is believed that some soybean seed may have been sent from China by missionaries as early as 1740 and planted in France (Gibson and Benson, 2005). The first written reference to soy appears in a list of Chinese plants from 2853 B.C. Soybean is also referred to many times in ancient writings as one of the five grains essential to Chinese civilization. Western contact with soybeans and soy

foods was limited until Asians began to emigrate in large numbers to Europe and the U.S. in the 1800s. The crop grows in the tropical, subtropical and temperate climates regions (Evans, 1996).

Soy has been grown for three millennia in Asia and more recently, has been successfully cultivated around the world. Today, the world's top producers of soy are the United States, Brazil, Argentina, China and India (USDA, 2007). Soybean was first introduced to Africa in the early 19th century, through Southern Africa (Ngeze, 1993) and is now widespread across the continent (Wikipedia, 2009). However, Shurtleff and Aoyagi (2007) have stated that, it might have been introduced at an earlier date in East Africa, since that region had long traded with the Chinese. The same report indicates that soybean has been under cultivation in Tanzania in 1907 and Malawi in 1909. In Ghana, the Portuguese missionaries were the first to introduce the soybean in 1909. This early introduction did not flourish because of the temperate origin of the crop (Mercer-Quarshie and Nsowah, 1975). However, serious attempts to establish the production of the crop in Ghana started in the early 1970s. This was as a result of collaborative breeding efforts of Ghana's Ministry of Food and Agriculture (MoFA) and the International Institute of Tropical Agriculture (IITA) (Tweneboah, 2000).

A team from the International Soybean Programme (INTSOY) in Illinois, USA around 1977 prepared programme for soybean development in the country for the Grains and Legumes Development Board (GLDB) in Ghana and USDA. Their aim was to assist the Ghanaian government to design a five-year national soybean production, processing and utilization programme. GLDB and INTSOY projected that by 1978 about 4,800 ha of soybeans would be cultivated in Ghana and the nation would hence be self-sufficient in soy oil and meal and by 1982 over 50,000 acres of soybeans would be planted annually in Ghana respectively. (Mercer-Quarshie and Nsowah, 1975). Soybean production in Ghana and Africa is low compared to other countries and continent. (Addai, 2001). According to FAO (1982), production of soybean in Africa is about

0.05% of the world total. While the United States, the leading soybean production in the world harvest an average of over 2,000 kg/ha on its 27 million hectares of land in 1981, Africa countries harvest just over 900 kg/ha on 300,000 ha. The crop is cultivated mainly in the Northern, Upper West, Upper East, and Northern Volta regions in Ghana.

Among these geographical regions, the largest production occurs in Northern Ghana, which lays within the Guinea savannah and Sahel agro- ecological zones (Lawson *et al.*, 2008). The optimum temperature for soybean is 20 - 30°C, with temperatures of 35°C, and above considered inhibitory to production. The optimum soil temperature for germination and early seedling growth is 25 to 30°C. Soybean can grow and yield with as little as 180 mm of in-crop rain but could expect a 40 - 60 percent yield decline compared to optimal conditions.

2.3 Nomenclature of soybean

The American Piper demanded at length according to the 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 USA 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 must be *Glycine max* L. Merrill .

2.4 Importance of Soybean

Soybeans actually have hundreds of uses from industrial products like engine oil or crayons to food products and animal feeds. Soybeans are naturally rich in protein and oil and they have the highest natural source of dietary fiber, making them a very versatile crop in terms of how it is used. The soy cake is an excellent source of protein feed for the livestock industry in Ghana (MoFA and CSIR, 2005).

Aside from being a major source of quality protein and vitamin E, soy foods contain isoflavones, which seem to play a role in reducing the risk of heart attack, osteoporosis, breast cancer and prostate cancer (Misiko *et al.*, 2008). Packed with calcium, fiber and protein, soybeans are a healthy choice. The soybean, often referred to as the miracle crop, provides a sustainable source of protein and oil worldwide. Soy's properties allow its use in a variety of applications from animal feed and human consumption, to road fuel and other industrial uses (Abbey *et al.*, 2001; Caminiti *et al.*, 2007; Dugje *et al.*, 2009).

Because soy grows throughout the world, it represents a viable and renewable replacement for petrochemicals. Soy oil is also used in industrial paint, varnishes, caulking compounds, linoleum, printing inks, and other products. A 27 kg of soybeans yields about 5 kg of oil and about 22 kg of meal (Gibson and Benson, 2005). According to Masuda and Goldsmith (2009), soybeans are not only a valuable source of feed for livestock and fish but also a good source of protein for human diet. El- Agroudy *et al.* (2011) reported that soybeans contain 30 percent cholesterol free oil, 40 percent protein and also contain most essential vitamins required by human beings. As far as the soybean nutritional value is concerned, soybean serves as an excellent source of essential fatty acids, calcium, magnesium, lecithin, riboflavin, thiamine, fibre, foliate (folic acid), and iron. It aids in protecting the heart against oxidation (Page, 1998). Also, soybean powder is used for various preparations of food and drinks for babies and adult, such as mixing with pap for babies and even adults.

According to Ennin-Kwabiah and Osei-Bonsu, (1993) cited by Ennin *et al.*, (2005), soybean has high protein content, ranging from 36 to 56% of the dry weight which is approximately double the protein content of the indigenous legumes, cowpea (19% - 35%) and groundnut (25% - 30%). Therefore soybean has the potential of providing an inexpensive source of protein both for human consumption and animal feed preparation. Soybeans, like most legumes, meet most of its nitrogen needs by establishing a symbiotic relationship with the bacterium *Bradyrhizobium japonicum*.

Soybean like all other legumes also improves soil fertility by converting atmospheric nitrogen from the soil for its own use, which also benefits subsequent crops in rotation. It therefore reduces the amount of nitrogen fertilizer that farmers have to purchase to apply to their fields to improve productivity. This is an important benefit in Africa (Ghana; Southern Guinea Savanna), where soils are poor in nutrients and fertilizers are expensive and not available for farmers (MoFA and CSIR, 2005; IITA, 2009). They can fix as much as 120 kg N/ha during a growing season (Giller, 2001). About 85 percent of the world's soybeans are processed, or "crushed," annually into soybean meal and oil (Reenberg and Fenger, 2011).

Approximately 98 percent of the soybean meal that is crushed is further processed into animal feed with the balance used to make soy flour and proteins. Of the oil fraction, 95 percent is consumed as edible oil; the rest is used for industrial products such as fatty acids, soaps and biodiesel (Mpeperekhi *et al.*, 2000). Promotion of the nutritional and economic values of the crop is being done in Ghana by the Ministry of Food and Agriculture, and this has resulted in rapid expansion in production (Sarkodie-Addo *et al.*, 2006). In West Africa, soybean has become a major source of high quality and cheap protein for the poor and rural households. It is used in processing soy meat, cakes, 'dawadawa' (a local seasoning product for stews and soups), and food for babies, (Abbey *et al.*, 2001). It is also used to fortify various traditional foods such as soups, gari, sauces, stew, kenkey and banku to improve their nutritional levels (MoFA and CSIR, 2005).

Soybean is beneficial in the management of *Striga hemonthica*, an endemic parasitic weed of cereal crops in the savanna zone of Ghana, which causes severe losses in crop yield of up to 70 - 100% of millet, sorghum and maize. Soybean is non-host plant to *Striga*, but it produces chemical substances that stimulate the germination of *Striga* seeds. Germinated seeds subsequently die off within a few days because they cannot attach their root system to that of the soybean plant to draw food substances and water (MoFA and CSIR, 2005).

2.5 Planting date and replanting

According to Morgan (2005), early planting can reduce the proportion of branch nodes that became fertile, while late planting can reduce branch node number in soybean. Early planting was also found to increase seed yield, while late planting increased seed mass (Pedersen and Lauer, 2004). Prasad *et al.* (2008) concluded that, the combination of the factors affecting soybean seed yield production emphasizes the complexity of individual soybean plant compensation and seed yield recovery, however, according to Conley *et al.* (2008) plants can recover yield loss at or before stage R1 if there is a at least a final plant population of 247,500 plants /ha. Planting date effect on emergence is related to weather and soil conditions (Rosenzweig *et al.*,2001).

As soil and air temperatures increase during the planting season, the percent of emergence also should increase (Licht and Al-Kaisi, 2005). The soybean plant has a tremendous ability to compensate for missing plants. By developing more branches and podding more heavily, the effect of missing plants in the stand is often not detected in yields (Lichtenzweig *et al.*, 2006). Chauhan (2012) reported that, yield reduction that suffered with very poor stands may still be more profitable to the grower than a replanted field, which has additional costs associated with replanting and a reduced yield potential because of a delayed seeding date. Soybeans can compensate for missing plants when randomly placed gaps occur in the stand (Zaimoglu *et al.*, 2004). In field situation where poor stands are realized, management to control weeds is essential to prevent further yield losses due to the poor stand. The cost of maintaining the necessary weed control must be considered a cost of keeping a less than perfect stand. Growers who replant do so at a later planting date than is the optimum (Sacks *et al.*, 2010). A penalty to yield due to the delayed planting of 2 to 3 weeks is expected (Bastidas *et al.*, 2008). According to De Bruin and Pedersen (2009), plant density per meter of row achieved with replanting, along with possible gaps in a stand, will influence yield potential.

Fernández *et al.* (2009) observed that, there will likely be less difference in emergence between early- and late-planted soybeans with high quality seed than with low quality seed.

2.6 Harvest index

Harvest index which is useful for measuring the partitioning of photosynthesis 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 materials (Donald and Hamblin 1976). Increasing crop yield is connected with increased harvest index, probably.

2.7 Variability, heritability and genetic advance

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

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

Kumar *et al.* (2014) evaluated forty soybean genotypes for agro-morphological traits and genetic parameters of soybean. Analysis of variance and mean performance for yield and related components revealed the significant

differences among all the genotypes for all the characters. Correlation was also found significant with yield and its component traits. Nooghab *et al.* (2014); examined 14 soybean genotypes and a local check variety in a randomized complete block design with three replications to study of genetic diversity for yield and its components. Different traits such as plant height (cm), number of secondary stems, number of pods in secondary stems, number of pods in main stem, number of grain per plant, 1000-grain weight (g), pod length (cm), yield per plant (g) and yield (ton/ha) were investigated. Results of analysis of variance showed significant difference for the traits except number of secondary stems one. The highest CV was for yield per plant, number of pods in secondary stems, height of the first secondary stem and 1000-grain weight which are respectively 29.64, 28.89, 27.45 and 26.79. The lowest CV was for number of secondary stems and plant height that are respectively 14.37, 14.78 and 15.46. Emperor and Kao- hsiung-10 genotypes had the highest (5.113 ton/ha) and lowest (2.06 ton/ha) yield, respectively.

An experiment was conducted by Swapnil *et al.* (2014); with 12 soybean genotypes. The data of 13 yield component traits were recorded to study genetic variability, heritability, and genetic advance analysis. Analysis of variance among 12 genotypes revealed highly significant differences for all the characters except the number of grain per plant meant the presence of substantial amount of genetic variability. High genetic advance percent of mean in 13 yield component traits were observed for number of pod per plant, seed yield per hectare and seed yield per plant. Chandel *et al.* (2013); conducted an experiment to assume the genetic variability in 70 diverse soybean genotypes. The variability parameters like mean, range of variation, genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance were estimated for 15 different characters.

Analysis of variance expressed that mean squares due to genotype were found significant for all the traits under study except oil content, indicated that enormous phenotypic variability was present among the genetic materials

studied. The highest genotypic coefficient of variation was observed for number of pods per plant followed by number of primary branches per plant and number of clusters per plant. The magnitude of heritability was observed to be high for plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod, seed yield per plant, biological yield per plant and harvest index. Number of pods per plant and number of primary branches per plant showed high genetic advance. Ghodrati (2013), assessed 12 soybean genotypes for genotypic variation, phenotypic correlations and broad sense heritability for seed yield and some quality properties during three growing seasons. Significant differences were found for seed yield and quality characters which suggest sufficient genetic variation for efficient selection. High broad sense heritability (81%, 76%, 74%) and genetic advance (0.35, 0.20, 0.40) were found for the number of nodes per plant, days to flowering and plant height, respectively.

Patil *et al.* (2011) investigated a quantitative study to assess genetic diversity for 11 characters of soybean by Mahalanobis's D^2 statistics. The studies included 36 genotypes of soybean obtained from different eco-geographical regions of India, which showed that there was a substantial genetic diversity among the genotypes with D^2 values ranging from 33.64 to 379.08. Another study was made by Iqbal *et al.* (2010) in National Agriculture Research Centre, Islamabad to test the variability and association among 9 traits in 139 soybean genotypes. The traits viz., days to maturity, number of branches per plant, number of pods per plant, 100-seed weight (g), oil content, grain yield per plant (g), biological yield per plant (gm) and harvest index were studied. Results of analysis of variance showed significant differences among genotypes in terms of traits under study, which ensure the existence of genetic variation.

Arshad *et al.* (2006); evaluated 30 genotypes of soybean for days to 50% flowering, days to maturity, pod length, number of branches, number of unfilled, total pods, 100 seed weight and seed yield. Analysis of variance and mean performance for yield and its components revealed significant differences

among all the genotypes for all the characters examined. Another subsequent experiment was carried out by Bangar *et al.* (2003) which revealed that phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV). The GCV and PCV value were highest for branch number per plant and plant height among the characters. The GCV and PCV were of moderate high for the pod number per plant 100-seed weight (g) and seed yield per plant (g). Days to 50% flowering and days to maturity had very low GCV and PCV estimates. The differences between GCV and PCV magnitudes were very high for 100-seed weight (gm) and number of pods per plant.

An experiment was conducted with 90 genotypes of soybean by Chamundeswari and Aher (2003) and they found that days to maturity, plant height at maturity, number of clusters per plant, number of seeds per pod, 100-seed weight and grain yield per plant showed significant genetic variation. Genotypic coefficient of variation was highest for biological yield per plant. Plant height, number of pods per plant and biological yield per plant showed highest broad sense heritability. Similarly, Agarwal *et al.* (2001) studied genetic variability using 195 soybean germplasms. They found that GCV were moderate for days to flower initiation, days to flower termination and low for days to maturity. Heritability and genetic advance as percentage of mean were high for all the plant growth characters (except moderate GAM for days to maturity). Jain and Ramgiry (2000), found significant variation for yield per plant. High heritability values accompanied by genetic advance as a percentage of mean were recorded for seed yield, plant height and pods per plant. In parallel Mehetre *et al.* (2000) studied variability for 11 characters with 60 diverse genotypes of soybean. Their result revealed that pods per plant and seed yield per plant had high genotypic and phenotypic coefficient of variation.

They also said that plant height and pods per plant had high genotypic and phenotypic coefficient of variation and high heritability associated with high genetic advance as percentage of mean.

Singh *et al.* (2000); investigated that genotypic coefficient of variation and phenotypic coefficient of variation was comparatively high, for seed yield per plant, pods per plant and plant height. Seed yield per plant, pods per plant and plant height showed high heritability with high genetic advance as a percentage of mean. Similarly Bhandarkar (1999) noticed high co-efficient of variation and moderate heritability for pods per plant and seed yield per plant in soybean. High heritability and genetic advance as percent of mean for plant height and days to maturity was observed by him. Archana *et al.* (1999); reported that plant height and 100-seed weight had high genotypic coefficient of variation and high heritability accompanied with high genetic advance percent of mean soybean. Another research conducted by Nehru *et al.* (1999) to estimate genetic advance and heritability for 16 yield and quality components in 49 genotypes of soybean. They found days to maturity and 100 seed weight had high heritability but low genetic advance. Subsequently, Mehetre *et al.* (1998), reported that genotypic coefficient of variation was high for plant height, 100-seed weight and yield per plant in soybean. High heritability along with high genetic advance were also observed for plant height, 100 seed weight and yield per plant. In a separate experiment, Shrivastava and Shukla (1998), revealed a significant amount of variability for plant height, seed yield per plant and pods per plant in soybean. All these characters had high heritability coupled with high expected genetic advance. In a different study Mehetre *et al.* (1997) recorded high heritability accompanied by high genotypic coefficient of variation for pod pods per plant, 1000-seed weight and yield per plant in soybean.

Praneetha and Thamuraj (1997), examined that pods per plant and yield per plant had high genotypic coefficient of variation and heritability in vegetable soybean. Similarly, Major *et al.* (1996) observed high genotypic and phenotypic coefficient of variation for 100-seed weight and grain yield in soybean. They also observed plant height and grain yield per plant showed high genetic advance. In a different experiment Rajarthnam *et al.* (1996) estimated

genetic advance, heritability and genetic variability. High heritability and genetic advance for plant height, pod per plant, 100 seed weight and seed yield per plant were recorded by them.

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

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

2.8 Correlation co-efficient

The interrelationship of different characters with yield determines the efficiency of selection in breeding programs. It nearly indicates the intensity of association. Where phenotypic correlation reflects the observed relationship, genotypic correlation underline the true relationship among characters. Selection procedures could be different depending on the relative contribution of each traits. The following paragraphs give review of literature on correlation between different characters in 18 soybean genotypes. Kumar *et al.* (2014); studied 40 genotypes of soybean and revealed that correlation was found significant with yield and its component traits. An analysis indicated that

hundred seed weight had highest effect on yield. In a separate experiment, conducted by Ghodrati (2013) with 12 soybean genotypes and observed that there is a strong positive correlation ($r = 0.61^*$) between seed yield and plant height. An Increase of number of nodes per plant, number of pods per plant, number of seeds per pod, number of seeds per plant and protein yield is proportional to increase in plant height. It is, therefore, understood that simultaneous selection for improving seed yield through increasing the number of nodes per plant, number of pods per plant and plant height would be an effective move to increase seed yield as well as protein content.

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

Inderjit *et al.* (2007); made an association studies which indicated that pods per plant, cluster per plant, seeds per pod and days to 50% flowering were significantly correlated with grain yield. In a different research, Arshad *et al.* (2006) estimated that seed weight had positive correlation with unfilled, filled and total pods. Grain yield had positive and significant correlation with all the characters except days to flowering and seed yield per plant.

Moreover, it had significant but negative correlation with days to maturity and un-filled pods. Positive direct effects on grain yield was found with days to maturity, branches, pod length, pods and 100 seed weight. High indirect effect was also exhibited via pod length by most of the traits hence these characters should be given more emphasis while selecting high yielding soybean lines. Avc and Ceyhan (2006), performed a correlation studies that the pod yield was significantly and positively correlated with pods per plant and 100 seed weight. In another study, Singh and Singh (2006) found that 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.

Chamundeswari and Aher (2003), studied with 90 genotypes of soybean. They showed that seed yield is positively correlated with number of pods per cluster, number of pods per plant and biological yield per plant. A character association study was done by Sharma *et al.* (2003) in soybean and indicated that positive and significant association of seed yield per plant with biological yield per plant, pods per plant and pod length. 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.

A report by Chettri *et al.* (2003); revealed that grain yield was significantly correlated with days to maturity and number of grain per pod in soybean at the phenotypic level. Days to maturity were significantly correlated with plant height and number of pods per plant at the phenotypic levels. Where, number of days to 50% flowering was positively and significantly correlated with days to maturity but number of seeds per pod and 100 grain weight was negatively correlated at the genotypic level. Path coefficient result showed that number of grain per pod, days to maturity and number of pods per plant positively affected grain yield. Onemli (2003), reported that the number of pods were positively correlated with plant height, number of branches, pod length, seed

length, number of pods per plant and 1000-seed weight, but was negatively correlated and significant correlations with number of seeds per pod, seed length and pod length in soybean. Number of pods and 1000-seed had negative effect on soybean yield via the number of pods. The genotypic correlation coefficients were higher than the phenotypic correlation coefficients. Pod yield per plant showed positive phenotypic correlation with pod length, number grains per pod, number of pods per plant and shelling percentage described by Chaudhury and Sharma (2003).

A path coefficient analysis of yield-contributing traits in soybean was experimented by Shrivastava *et al.* (2001). They observed high positive direct effects on seed yield for the number of branches per plant, followed by days to 50% flowering, days to maturity, plant height, 100-seed weight, biological yield and harvest index. On the other hand, plant height had a negative effect on yield. In a different experiment, Khan *et al.* (2000) observed correlation among yield determining components in 86 diverse maturity genotypes of soybean. Path coefficient analysis revealed that pods per plant had the direct effect on seed yield followed by 100 seed weight. Pods per plant affected seed yield negatively via indirect effects of plant height, pod height and seed per pod.

Singh *et al.* (2000); reported that leaf area had positive direct effect on biological yield but negative effect on seed yield in soybean. In another study, Rajanna *et al.* (2000) found significant and positive correlation of number pods per plant, number of clusters per plant and 1000-seed weight with seed yield in 40 soybean genotypes. Days to maturity, plant height and number of branches per plant exhibited significant and positive correlation with number of clusters per plant and number of pods per plant. Path analysis indicated effect on seed yield per plant. Genotypic correlation coefficients higher than the phenotypic and environmental correlation coefficients in soybean was reported by Chand (1999). Seed yield was positively correlated with days to flowering and maturity plant height, number of branches and pods per plant in terms of

genotypic and phenotypic correlation coefficients. No correlation was found between 100-seed weight. The characters which showed significant positive correlation with yield were also positively correlated among themselves, except days to maturity with seeds per plant.

Dogney *et al.* (1998); revealed that number of seeds per pod and 100 seed weight had a high positive direct effect on yield in soybean. Number of seeds per pod, days to maturity had medium to low direct effect on seed yield. In another study, Saurabh *et al.* (1998) determined significant and positive correlations between plant height and pods per plant in soybean.

Sridhara *et al.* (1998) conducted an another experiment reported that number of pods per plant and number of seeds per plant directly contributed the most to yield attribute in soybean. Pod length, seed number, plant height and number of branches through number of pods per plant seemed to be significant contributors of seed yield. In a study, Peluzio *et al.* (1998) revealed that the negative correlation between days to maturity and pods per plant in soybean. In a different study, Ramgiry and Raha (1997) observed that genotypic correlation coefficients were higher than phenotypic correlation coefficients in soybean. Seed yield per plant showed positive correlations with seeds per plant and nods perplant.

Praneetha and Thamuraj (1997), revealed that pods per plant and single pod weight in soybean were the most important yield determinants because of their high direct and indirect effects. Another study was conducted by Mehetre *et al.* (1997) with 4 soybean genotypes. Yield per plant was highly significant and positively correlated with 100 seed weight but non-significant and positively correlated with leaf area. Path coefficient analysis indicated that the number of branches per plant exerted the highest positive direct effect followed by contribution of 100 seed weight, number of pods per plant. The highest indirect positive effect was found for number of pods per plant.

Major *et al.* (1996); reported that the grain yield showed significant and positive correlation with branches per plant, pods per plant and 100 seed weight in soybean. Path analysis revealed that 100 seed weight had high direct and positive effects on grain yield. In a different study, Rahman *et al.* (1996) revealed a significant and positive correlation between pods per plant and 100 seed weight with seed yield in soybean. Plant height and days to maturity showed the significant and positive correlation with pods per plant. The number of pods per plant and seeds per pod had higher direct effect on yield.

Rajarthnam *et al.* (1996); found that seed yield was significantly correlated with plant height, number of primary branches per plant and pod number in soybean. In another study, Shinde *et al.* (1996) reported that the genotypic correlations were higher than the phenotypic ones in soybean. Seed yield per plant showed highly significant and positive correlations with plant height, pods per plant and seeds per pod. Seeds per pod was significantly correlated with yield and its direct effect was very strong.

Dobhal and Gautam (1995), showed that yield per plant was positively and significantly 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. Another study was conducted by Saad (1995) and he observed that the path analysis showed direct contribution of yield components to seed yield for cultivars was in the descending order of pods per plant, 100 seed weight, number of seeds per pod and plant height, while highest indirect effects were exerted by number of seeds per pod via number of pods per plant in soybean. Wu *et al.* (1995); revealed that seed yield was positively correlated with pods per plant, plant height in summer soybean. Seed yield was influenced by 100 seed weight, pods per plant and nodes per main stem among these high yielding genotypes. In a different study, Jadhav *et al.* (1995) observed that number of branches per plant, pods per plant, seeds per plant, pod length and pod weight per plant were positively and highly significantly correlated with seed yield in soybean. Yield

is highly correlated with yield and yield contributing characters. Mishra *et al.* (1994); reported that the number of seeds and pods per plant had a substantial contribution towards the seed yield in soybean. Path coefficient analysis showed the positive direct effect of 100 seed weight, number of seeds per plant and number of pods per plant on seed yield. Another experiment was carried out by Singh *et al.* (1994) and they revealed that grain yield per plant showed high positive association with number of pods per plant and days to maturity in soybean. Plant height showed high positive correlation with days to maturity.

Mahajan *et al.* (1994); informed that grain yield per plant was positively correlated with eight characters in 51 soybean genotypes grown in India during the kharif of 1990. Seed yield was correlated with ($r=0.75$) with branches per plant (0.52), days to 50% flowering (0.48), maturity (0.47) and plant height. In a different study, Das *et al.* (1984) reported that highly significant positive correlation between seed yield and pods per plant and a significant positive correlation between seed yield and seeds per pod in soybean. Pods per plant and 100 seed weight showed very high direct effects on seed yield.

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

2.9 Path coefficient

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

Inderjit *et al.* (2007); reported that pods per plant, 100 seed weight, seeds per pod and days to maturity had positive direct effect on grain yield, while plant

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

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

Path coefficient analysis done by Mohan *et al.* (2005) revealed that number of pods per plant and shelling percentage had the maximum direct effect on green pod yield. Thus, due importance should be given to these characters for improvement of yield. In an experiment in India, Chettri *et al.* (2003) reported that grain yield was significantly correlated with days to maturity and number of grain per pod in soybean at the genotypic level. Days to maturity and number of grains per pod were also correlated. Days to maturity were significantly correlated with plant height and days to 50% flowering at phenotypic levels. The number of days to 50% flowering was positively and significantly correlated with days to maturity but negative with number of seeds per pod and 100 grain weight at the genotypic level. Path coefficient estimates showed that the number of grain per pod, days to maturity, number of pods per plant and plant height positively affected grain yield.

A path coefficient analysis of yield contributing traits in soybean was conducted by Shrivastava *et al.*(2001).They observed highest positive direct

effects on seed yield for the number of branches per plant, followed by days to 50% flowering and days to maturity, plant height, 100 seed weight, biological yield and harvest index. Plant height, on the other hand, had a negative effect on yield. In a different study, Khan *et al.* (2000) observed correlation among yield components in 86 diverse maturity genotypes of soybean. Path coefficient analysis revealed that pods per plant had the direct effect on seed yield followed by 100 seed weight. Pods per plant affected seed yield negatively via indirect effects of plant height, pod height and seed per pod.

Rajanna *et al.* (2000); estimated significant and positive correlation of number of pods per plant, number of cluster per plant and 100 seed weight with seed yield in soybean. Days to maturity, plant height and number of branches per plant exhibited correlation with number of cluster per plant and number pods per plant. Path analysis indicated effect on seed yield per plant. And number of pods per plant. Path analysis indicated effect on seed yield per plant. Another experiment was conducted by Mehetre *et al.* (1997) with 4 soybean genotypes and they observed yield per plants was highly significant and positively correlated with 100 seed weight but non-significant and positively correlated with leaf area. Path coefficient analysis indicated that the number of branches per plant exerted highest positive direct effect followed by contribution of 100 seed weight, number of pods per plant. The highest indirect positive effect was found for number of pods per plant. Pranneetha and Thamuraj (1997), revealed that pods per plant and single pod weight in soybean were the most important yield determinants because of their high direct and indirect effects. In a different study, Major *et al.* (1996) reported that grain yield showed significant and reported that the grain yield showed significant and positive correlation with branches per plant, pods per plant and 100 seed weight in soybean. Path analysis revealed that pods per plant and 100 seed weight had high direct and positive effects on grain yield.

Dobhal and Gautam (1995), showed that yield per plant was positively and significantly associated with pods per plant and days to maturity at both

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

Mishra *et al.* (1994); reported that the number of seeds per plant and pods per plant had a substantial contribution towards the seed yield in soybean. Path coefficient analysis showed the positive direct effect of 100 seed weight, number of seeds per plant and number of pods per plant on seed yield. In a different study, Singh *et al.* (1994) revealed that grain yield per plant showed high positive association with number of pods per plant and days to maturity in soybean. Plant height showed high positive correlation with days to maturity. Plant height, days to maturity, number of pods per plant had a low positive direct effect on grain yield.

2.10 Genetic divergence among soybean germplasms

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

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

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

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

To assess genetic diversity Patil *et al.* (2011) worked out by mahalanobis D^2 with 36 genotypes for 11 characters. Thirty six genotypes were grouped into six clusters. The clustering pattern revealed that genetic diversity was not necessarily associated with geographical diversity in this crop. The hybridization program has been suggested on the basis of inter cluster divergence and cluster means for the character studied. To study genetic

diversity and association between yield and its components 120 genotypes were evaluated for 10 characters. The study indicated presence of considerable genetic divergence among the genotypes. The genotypes were grouped into six clusters. To get the desirable segregants the hybridization among the genotypes of cluster III and IV, cluster V and VI and cluster I and VI as the inter cluster distance was greater between these clusters ,Inderjit *et al.*(2007).

Singh *et al.* (2007); evaluated 120 genotypes for 10 characters to study genetic diversity and association between yield and its components. The study indicated presence of considerable genetic divergence among the genotypes. The genotypes were grouped into six clusters. To get the desirable segregants the hybridization among the genotypes of cluster III and VI, cluster V and VI and cluster I and VI as the inter cluster distance was greater between these clusters. Another study was carried out by Arshad *et al.* (2006) and they evaluated genetic diversity in 33 soybean genotypes. Cluster diagram based on Euclidean dissimilarity revealed three clusters at 50% linkage distance, cluster I consisted 14 genotypes, cluster II 8 and cluster III 11 genotypes. The accessions in the cluster III were of short duration and high yielding having high seed weight.

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

In another experiment, Vart *et al.* (2002) estimated genetic diversity in 56 genotypes of soybean by using D^2 statistic and grouped them into 11 clusters. The clustering pattern was not significantly influenced by the eco-geographical distribution of genotypes. In a different study, Das *et al.* (2000) stated that, genetic divergence of 65 genotypes using Mahalanobis D^2 statistics and

grouped the genotypes into 13 clusters. Grouping pattern of the genotypes suggested no parallelism between genetic divergence and geographical distribution of the genotypes. Variance of cluster means revealed that pods per plant and plant height had the maximum contribution towards divergence.

Shrivastava *et al.* (2001); studied the divergence among 50 soybean genotypes for nine yield component characters and the genotypes were grouped into five clusters, based on D^2 values. In another experiment, Chaudhary *et al.* (1985) assessed genetic diversity among 55 soybean using Mahalanobis' D^2 technique. The genotypes fell in 7 clusters of different sizes. Genetic divergence and geographic distribution were not necessarily related of the ten different characters, pods per plant, yield per plant and effective nodes per plant contributed maximum on the total divergence. The highest inter-cluster distance observed between the clusters indicates highly divergent types existed in these clusters. Rahman (1996), estimated genetic divergence among 16 genotypes of soybean using Mahalanobis' D^2 statistics. The genotypes were grouped into 7 clusters. The inter-cluster average D^2 values showed maximum distance between cluster I and III. The genetically diverse genotypes from these groups could be used as a parent in hybridization programme for getting desirable segregants. Germplasms in use of these characters of respective cluster would offer a better scope of improvement of the crop through rational selection. A different experiment was conducted by Sanjay *et al.* (1998) and they reported genetic divergence of 30 advanced breeding lines of soybean and were grouped into 7 clusters. Of which two clusters contained the most important genotypes. One cluster characterized by high yield per plant, pods per plant, a reproductive phase high harvesting index and high seed weight, another cluster contained genotypes almost similar to those in previous cluster.

Chaudhary *et al.* (1985); studied 30 genotypes of soybean for genetic divergence using Mahalanobis' D^2 statistics and reported that genotypes were clustered in 6 six diverse groups. From the study, they concluded that geographical isolation may not be the only factor causing genetic diversity but

also 100 seed weight and yield per plant were the main contributors of total divergence. In another experiment, Mehetre *et al.* (1997) observed 41 genotypes of soybean which were grouped into 12 different clusters. Genetic diversity was independent of geographic area. From the cluster mean values donor for different characters are recommended.

Praneetha and Thamuraj (1996), observed that 15 and 22 genotypes of soybean were grouped into 6 and 3 clusters respectively on the basis of D^2 analysis of 14 clusters. In another study, Dobhal (1995) found significant variability among 65 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 contribute highest to total genetic distance.

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

A different experiment was carried out by Mehetre *et al.* (1994) and they determined genetic divergence among 51 genotypes of soybean and genotypes were grouped into 10 clusters. From the clustering pattern they concluded that diversity and geographic distribution were independent of each other. Using the Mahalanobis' D^2 , Ghatge and Kadu (1993) estimated genetic diversity statistics in soybean too. Their examined genotypes were grouped into 7 clusters. The clustering pattern expressed that genetic diversity did not have a strong association with geographical origin.

CHAPTER III

MATERIALS AND METHODS

The present research work was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka-1207, during the rabi season (December, 2018 to April,2019). The experiment location, materials used and methods followed in different operations during the experiment as well as in data collection are described here under the following sub-heads:

3.1 Experimental site

The site is situated between 23°74' N latitude and 90° 35' F longitude with an elevation 8.2 m from sea level (Appendix I). The experimental field belongs to the Agro-ecological zone of “The Modhupur Tract”, AEZ-28. 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.

3.2 Climate

The research area is situated in the subtropical zone, characterized by heavy rainfall during Kharif season (April to September), and scanty in Rabi season (October to March). Rabi season is characterized by plenty of sunshine. Information regarding average monthly maximum and minimum temperature, rainfall and relative humidity, soil temperature as recorded by the Dhaka meteorology centre, Agargoan. Dhaka, during the period of study has been presented in Appendix II.

3.3 Soil

The soil of the research area was non-calcareous dark grey and belongs to the Madhupur Tract (UNDP, 1988) under AEZ 28. The selected plot *was* medium high land and soil series was Tejgoan with a pH of 5.6. The analytical data of the soil sample collected from the experimental area was analyzed in the SRDI, Soil Testing laboratoiy, Khamarbari, Dhaka (Appendix III).

3.4 Planting materials

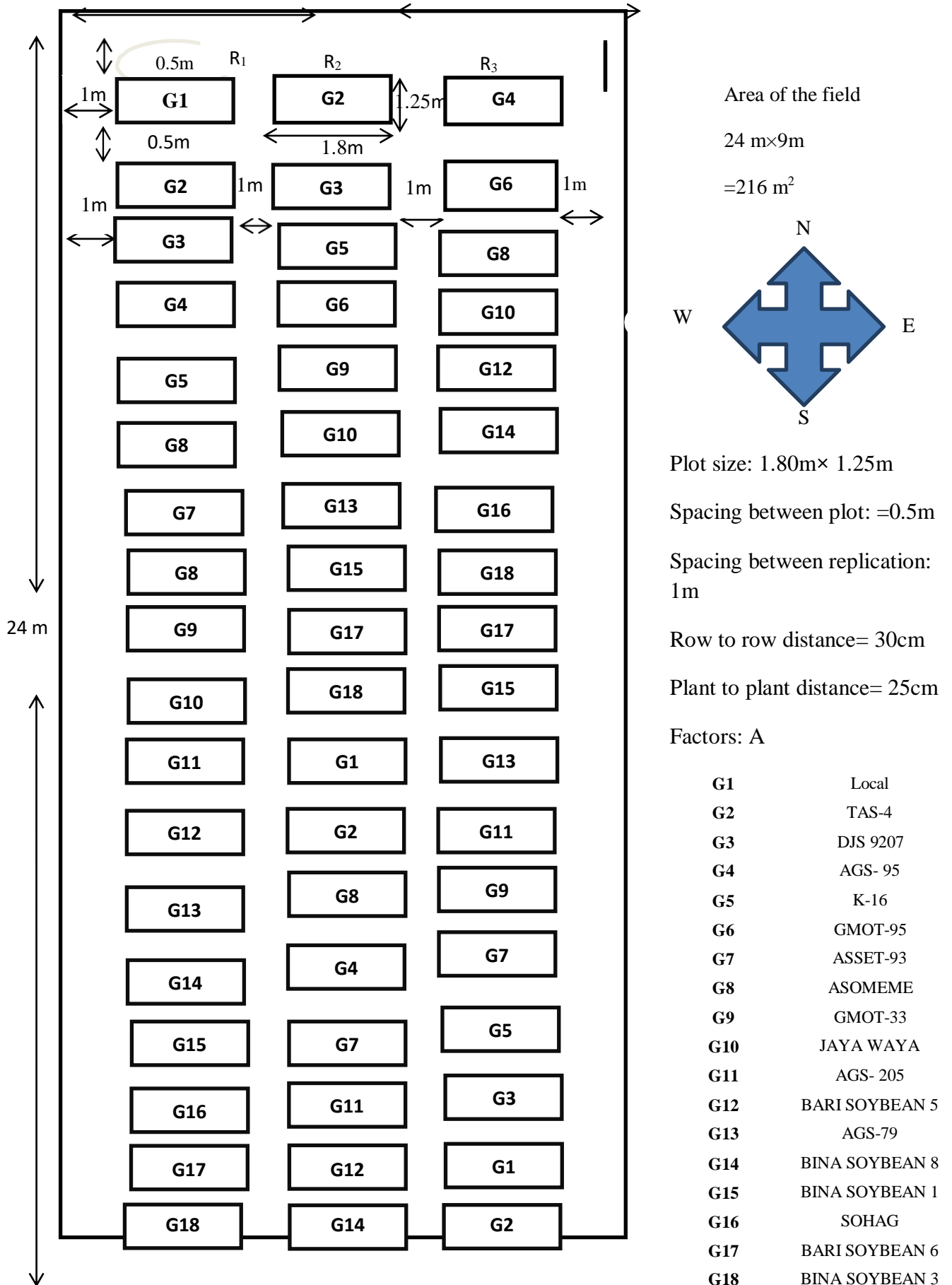
The experiment was designed for selection of elite soybean genotypes based on morpho-agronomic traits. There were 18 genotypes of soybean. The genetically pure and physically healthy seeds of these genotypes were obtained from the Department of Genetics and Plant Breeding, SAU, Germplasm Bank of Bangladesh Agricultural Research Institute (BARI), Gazipur and Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh. List of the genotypes are given in Table1.

Table 1: The code and accession name of 18 soybean genotypes used in the experiment

Code of Genotypes	Accession Name
G1	Local
G2	TAS-4
G3	DJS 9207
G4	AGS- 95
G5	K-16
G6	GMOT-95
G7	ASSET-93
G8	ASOMEME
G9	GMOT-33
G10	JAYA WAYA
G11	AGS- 205
G12	BARI SOYBEAN 5
G13	AGS-79
G14	BINA SOYBEAN 8
G15	BINA SOYBEAN 1
G16	SOHAG
G17	BARI SOYBEAN 6
G18	BINA SOYBEAN 3

Source: OSRC= Oil Seed Research Center, BARI= Bangladesh Agricultural Research Institute BINA= Bangladesh Institute of Nuclear Agriculture

Figure 1: Layout of the experiment



3.5 Design and layout

The experiment was laid out following Randomized Complete Block Design (RCBD) with three replications. The total area of the experimental plot was 216 m² (24 m x 9 m) which was divided into three equal blocks and each block was divided into 18 plots for distribution 18 treatments randomly. The size of each plot was 1.8 m x 1.25 m with a plant spacing 30 cm × 25 cm.

3.6 Land preparation

The land which was selected to conduct the experiment was opened on 8december, 2018 with the help of a power tiller and then it was kept open to sun for 7 days prior to further ploughing. Afterwards it was prepared by ploughing and cross ploughing followed by laddering. Deep ploughing was done to have a good tilth, which was necessary for getting better yield of this crop. The weeds and stubbles were removed after each laddering. Simultaneously the clods were broken and the soil was magic until good tilth.



Picture 1: Seed bed preparation

3.6.1 Application of manures and fertilizers

The following doses of manures and fertilizers recommended by Rashid, (1999) were applied to the experimental plots to grow the crop.

Table 2: Doses of manure and fertilizers in soybean field

Manures/Fertilizers	Dose/ha	Dose/plot *
Well decomposed cow dung	1 tons	225.00g
Urea	45 kg	10.12g
Triple Super Phosphate (TSP)	62.2 kg	14.06 g
Murate of potus (MOP)	50 kg	11.25 g

*Unit plot size was 1.8 m x 1.25 m= 2.25 m²

3.6.2 Sowing of seed

Seeds of the eighteen soybean genotypes were sown on 12 December 2018. The seedlings were emerged five to twelve days after sowing. Each unit plot (1.8 m × 1.25 m) was accumulated with 30 numbers of plants.



Picture 2: Sowing of seed

3.7 Intercultural operations

3.7.1 Weeding

Plots were kept free from weeds by regular weeding. The weeds were eradicated very carefully with roots were done as per necessity.

3.7.2 Irrigation and drainage

Irrigation and drainage were done as necessity.

3.7.3. Pest management

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 January to 16 February 2019. There were different types of weeds which were controlled effectively by hand weeding.

3.7.4 Diseases management

The crop was healthy and disease free and no fungicide were used.

3.7.5 Harvesting

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

3.8 Data collection

Data on the following parameters were recorded from the sample plants during the course of experiment. Ten plants were sampled randomly from each unit plot for collection of per plant data. The whole plot was harvested to record per plot data. Data were collected on different growth and yield component and yield. The plants in the outer rows and at the extreme end of the middle rows were excluded from the random selection to avoid the border effect. The following parameters were recorded.

3.8.1 Germination percentage

The numbers of germinated seeds were recorded from each plot and percentage was calculated. The days determined as the days required from sowing to 50% anthesis.

3.8.2 Days to 50% flowering

The days to 50% flowering were observed and noted on. The days determined as the days required from sowing to 50% flowering.

3.8.3 Plant height (cm)

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

3.8.4 Primary branches per plant

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

3.8.5 Leaf length (cm)

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

3.8.6 Number of pods per plant

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

3.8.7 Number of seeds per pod

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

3.8.8 Number of seeds per plant

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

3.8.9 Thousands seed weight (g)

Weight of thousands seed were measured from selected plants at random from plant and expressed in grams.

3.8.10 Seed yield

Average seed yield from ten randomly selected plants was recorded in ton/ha.

3.9 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 STATISTIX 10 computer programme. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV %) were also estimated using STATISTIX 10. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2000 software through four techniques viz., Principal Component Analysis (PCA), Principal Coordinate

Analysis (PCO), Cluster Analysis (CA) and Canonical Variate Analysis (CVA).

3.9.1 Estimation of genetic parameters

$$\text{Genotypic variance } (\delta^2g) = \frac{MSG - MSE}{r}$$

Where,

MSG = Mean Square due to Genotypes.

MSE = Mean Square Error

r = Number of replication

$$\text{Phenotypic variance } (\sigma^2p) = \sigma^2g + \sigma^2e$$

Where,

σ^2g = Genotypic variance

σ^2e = Environmental variance = MSE

3.9.2 Estimation of genotypic coefficient of variation and phenotypic coefficient of variation

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

Where,

σ^2g = Genotypic variance

\bar{x} = Population mean

$$\text{Phenotypic Co-efficient of Variation (PCV\%)} = \frac{\sqrt{\sigma^2p}}{\bar{x}} \times 100$$

Where,

σ^2p = Phenotypic variance

\bar{x} = Population mean

3.9.3 Estimation of heritability

Heritability in broad sense was estimated using the given formula suggested by Johnson *et al.* (1955).

$$\text{Heritability, } h^2_b = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

3.9.4 Estimation of genetic advance

Expected genetic advance under selection was estimated using the formula suggested by Johnson *et al.*, 1955.

$$\text{Genetic advanced (GA)} = \frac{\sigma^2_g}{\sigma^2_p} \times K \times \sigma_p$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

σ_p = Phenotypic standard deviation

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

3.9.5 Estimation of genetic advance in percent of mean

Estimate by the following formula suggested by Comstock and Robinson (1952)

$$\text{Genetic advance in percent of mean GA(\%)} = \frac{\text{GA}}{\bar{X}} \times 100$$

Where,

GA = Expected Genetic Advance

\bar{X} = Population mean

3.9.6 Estimation of correlation

The genotypic and phenotypic correlation estimated by the formula suggested by Miller *et al.* (1958).

$$\text{Genotypic correlation } r_{gxy} = \frac{Cov_{gxy}}{\sqrt{(\sigma^2_{g_x} \times \sigma^2_{g_y})}}$$

Where,

Cov_{gxy} = Genotypic covariance between the trait x and trait y

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

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

Similarly,

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

Where,

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

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

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

3.9.7 Path co-efficient analysis

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1959) 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 and indirect effect of the correlated characters, say x1, x2 and x3 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 x1 and y is thus partitioned as follows:

P_{yx1} = The direct effect of x1 on y.

$P_{yx2}r_{x1x2}$ = The indirect effect of x1 via x2 on y.

$P_{yx3}r_{x1x3}$ = The indirect effect of x1 via x3 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):

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

Where,

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

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

r_{iy} = Correlation of the character with yield

3.9.8 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:

3.9.9 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

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.

3.9.10 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).

3.9.11 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 soon.

3.9.12 Canonical variate 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 variate are based upon the roots and vectors of WB , where W is the pooled within groups covariance matrix and B is the among groups co variance matrix.

3.9.13 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

Mahalanobis' D² statistics

First the variation among the materials were tested by Wilkin's criteria 'Λ'.

$$\Lambda = \frac{|W|}{|S|} = \frac{\text{Determination of error matrix}}{\text{Determination of error + variety matrix}}$$

$$\text{Now, 'v'}_{(stat)} = -m \log_e \Lambda = - \{n-(p+q+1)/2\} \log_e \Lambda$$

Where,

$$m = n-(p+q+1)/2$$

p = number of variables or characters

q = number of varieties – 1 (or df for population)

n = df for error + varieties

$$e = 2.7183$$

Data were then analysed for D² statistics according to Rao (1952). Error variance and covariance matrix obtained from analysis of variance and covariance were inverted by pivotal condensation method. Using the pivotal elements the original means of the characters (X₁, X₂.....X₈) were transformed into a set of uncorrelated variables (Y₁, Y₂..... Y₈).

Now, the genetic divergence between two varieties/lines (suppose V_i and V_j) was calculated as –

8

$$D^2_{ij} = \sum_{k=1} (V_{ik} - V_{jk})^2$$

$k = 1$

Where,

D^2_{ij} = Genetic divergence between 'i' th and 'j' th genotypes

V_{ik} = Transformed mean of the 'i' th genotype for 'k' th character

V_{jk} = Transformed mean of the 'j' th genotype for 'k' th character

The D^2 values between all the studied genotypes were arranged in order of relative distances from each other and were used for clusters formation, as suggested by Rao,1952.

$$\text{Average intra-cluster } D^2 = \frac{\sum D^2_i}{n}$$

Where,

$\sum D^2_i$ = Sum of distances between all possible combinations (n) of the genotypes included in a cluster.

N = All possible combinations.

3.9.14 Cluster diagram

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

CHAPTER IV

RESULTS AND DISCUSSION

The results of the analyses of variance in respect of all the parameters studied in the present investigation are presented and discussed in this chapter. The results on the different parameters are presented in Tables and Appendices for ease of discussion under the following sub-headings and possible interpretations are also given whenever necessary. A summary of the analyses of variance of the data in respect of all the parameters studied are shown in the Appendices (IV to VI)

The results found from the experiment are discussed and presented in this section. The data collected from 18 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 Multi variate analysis

4.1 Genetic parameters

The analysis of variance of this experimental data showed significantly differences exist in all the characters under study *viz.*, germination percentage, days to 50% flowering, plant height (cm), primary branches per plant, leaf length (cm), number of pods per plant, number of seeds per pod, seeds per plant, weight of thousands seed (g), seed yield ,so it was clear that, selection for all the traits among genotypes had a great impact and good scope of improvement. Genetic parameters of all 10 characters are presented in table 3 and ANOVA is given in appendix V.

Table 3. Estimation of genetic parameters in ten characters of eighteen genotypes in soybean

Traits	Range	Mean	MS	CV%	σ^2_g	σ^2_p	σ^2_e	GCV	PCV	ECV	h^2_b	GA	GA(% mean)
GP	81-96	91.63	71.05**	0.54	23.603	23.85	0.2473	5.302	5.33	0.028	98.963	9.956	10.866
FP	38.33-49	42.57	29.60**	2.69	9.429	10.742	1.3126	7.213	7.698	0.486	87.781	5.927	13.921
PH	46.38-62.77	56.16	43.17**	4.64	12.125	18.928	6.8036	6.200	7.747	1.547	64.056	5.741	10.223
NPBP	6.00-9.00	7.72	2.40**	10.23	0.593	1.217	0.62418	9.969	14.285	4.316	48.702	1.107	14.331
LL	5.70-8.67	7.41	2.38*	14.37	0.416	1.549	1.13321	8.702	16.801	8.10	26.826	0.688	9.285
NPPP	29-41.33	33.20	35.02**	3.09	11.324	12.378	1.0545	10.135	10.596	0.461	91.481	6.630	19.968
NSPP	2.00-4.00	3.00	1.13**	17.46	0.288	0.562	0.27451	17.876	24.991	7.115	51.163	0.790	26.339
NSP	66-165.33	100.09	2013.64**	18.08	562.073	889.493	327.42	23.686	29.797	6.111	63.190	38.823	38.787
TSW	7.67-20.67	11.70	38.97**	8.58	12.656	13.665	1.0087	30.396	31.584	1.188	92.618	7.053	60.261
Y	1.24-2.62	1.73	0.27**	1.75	0.090	0.091	0.00092	17.364	17.452	0.088	98.992	0.616	35.589

GP= Germination percentage, FP=Days to fifty percent flowering, PH= Plant height (cm), NPBP= Number of primary branches per plant, LL=Leaf length (cm), NPPP= Number of pods per plant, NSPP= Number of seeds per pod, NSP=Number of seeds per plant, TSW=Thousands seed weight (g), Y= Yield (ton/ha)., MS = mean sum of square, σ^2 =Phenotypic variance, σ^2_g = Genotypic variance, σ^2_e =Environmental variance, PCV = Phenotypic Coefficient of Variation, GCV= Genotypic Coefficient of Variation, ECV= Environmental Coefficient of Variation, h^2_b =Heritability, GA=Genetic advance, GA% mean=Genetic advance in percentage of mean, CV%=Percentage of coefficient of variation

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 were 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 . The average performance of soybean genotypes for different growth characters and yield components are presented in Appendix IV.

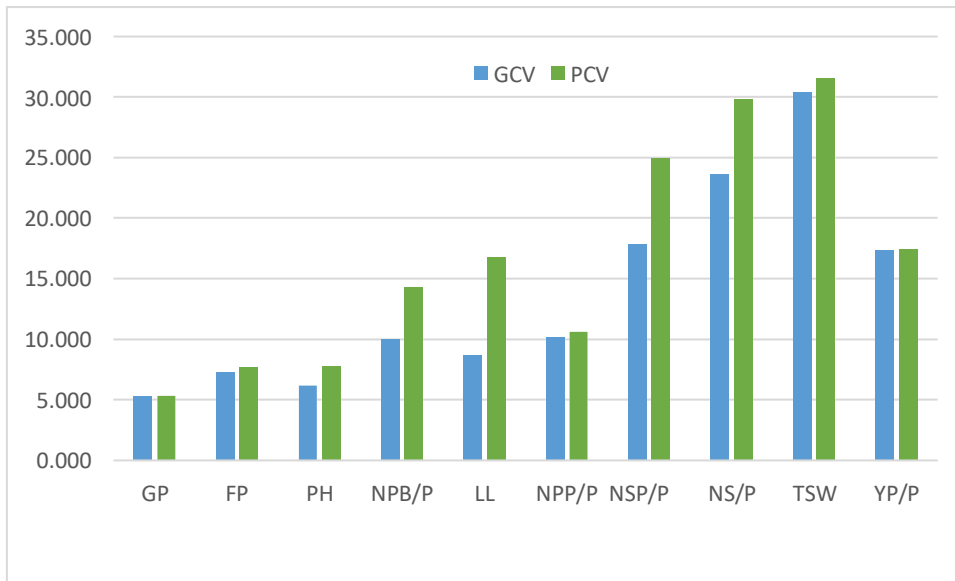


Figure 2: Genotypic and phenotypic variability in soybean.

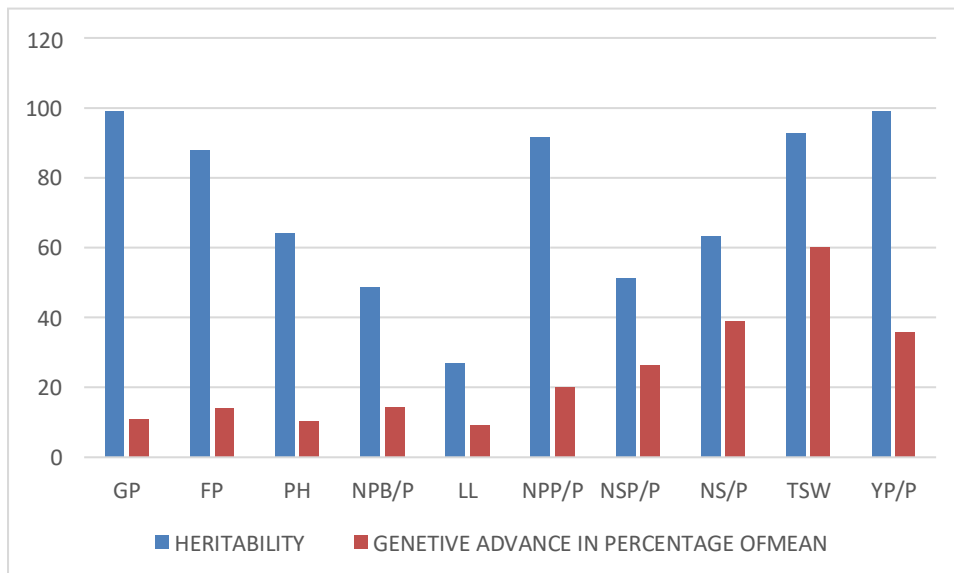


Figure 3: Heritability and genetic advance over mean in soybean

4.2.1 Germination percentage

The mean of germination percentage of 18 genotypes was 91.63. Significant differences were found among the genotypes with respect to germination percentage (Appendix IV). The values ranged from 81% to 96%, in the genotype “LOCAL” and “AGS-205” respectively (Appendix IV). From the analysis it was found that phenotypic variance (23.85) was higher than genotypic variances (23.603). It indicated that influence of environment on the expression of trait controlling genes was higher but not considerable. The phenotypic co-efficient of variation was found 5.33 and genotypic co-efficient of variation was found 5.302. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation found very low which indicated less environmental effect on this character. The estimation of heritability (98.963%) for this trait was moderately high, genetic advance was found 9.956 and genetic advance over percentage of mean was found 10.866 which was low indicated non- additive genes controlled the trait (Table 3).

4.2.2 Days to 50% flowering

The variance due to days to 50% flowering showed that the genotypes differed significantly and ranged from 49 days after sowing (DAS) in AGS-205 to 38.33 DAS in “LOCAL” with mean value 42.57 days after sowing (DAS) (Appendix IV). The Genotypic, phenotypic and environmental variances observed were 9.429, 10.742 and 1.3126, respectively (Table 3). The phenotypic variance appeared to be closed to the genotypic variance suggested least influence of environment in expression of the genes controlling this trait. It was observed that there was little difference between the genotypic co-efficient of variation (7.213) and phenotypic coefficient of variation (7.698) (Table 3) indicating minor environmental influence on this character. Therefore, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. Bangar *et al.* (2003) reported that phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) which agreed with the result of this experiment. The heritability (87.781%) estimates for this trait was moderately high, genetic

advance (5.927) was at moderate level and genetic advance over percentage of mean (13.921) were found low (table 3), indicating both additive and non-additive genes controlled the traits. Genetic advances in per cent of mean were low with the findings of Nehru *et al.* (1999). On the other hand high heritability with high genetic advance in percent of mean was observed by Agarwal *et al.* (2001), Jain and Ramgiry (2000) and Mehetre *et al.* (2000).

4.2.3 Plant height (cm)

The mean for plant height was recorded 56.16 cm. It ranged from 46.38 cm to 62.77 cm (Table 3). The analysis of variance revealed highly significant differences among the genotypes with respect to plant height (Appendix VI). The maximum plant height (62.77 cm) was recorded by the genotype ‘AGS-205’ and the lowest plant height (46.38 cm) was recorded by ‘LOCAL’ (Appendix IV). The genotypic and phenotypic variance was observed 12.125 and 18.928 respectively for plant height with low environmental influence. The phenotypic co-efficient of variation (7.747) was higher than the genotypic co-efficient of variation (6.20), which indicated presence of considerable variability among the genotypes for this trait. The heritability (64.056%) estimates for this trait was moderately high, genetic advance (5.741) was low and genetic advance in per cent of mean (10.223) was found very low, revealed that this trait was governed by both additive and non-additive genes controlled the traits. Therefore, selection for this trait will not be effective. Plant height exhibited high heritability and high genetic advance as percent mean in soybean which is partially similar to the earlier findings by Kumar *et al.* (2014) and Ghodrati (2013).

4.2.4 Number of primary branches per plant

Considerable differences among the genotypes studied in case of number of primary branches per plant. Mean sum of square was found 2.40 and ranged from 6.00 to 9.00 with a mean value of 7.72. Maximum number of primary branches were recorded in AGS- 205 and GMOT-33 and LOCAL genotype showed the minimum number of main branches (Appendix IV). The Phenotypic variance (1.217) appeared to be higher than the genotypic variance

(0.593) suggested considerable influence of environment on the expression of the genes controlling this trait (Figure 2). The genotypic co-efficient of variation and phenotypic co-efficient of variation were 9.969 and 14.285, respectively which indicated presence of considerable variability among the genotypes. The heritability (48.702%) estimates for this trait was medium, genetic advance (1.107) was low and genetic advance in per cent of mean (14.331) were found low also, revealed that this trait was governed by both additive and non-additive genes. Bangar *et al.* (2003) reported that phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV).

4.2.5 Leaf length (cm)

Leaf length showed significance variation due to different variety of soybean and it was significance at 5% level (Table no. 3 and Appendix IV). Where “GMOT-33” performed the highest leaf length (8.67cm) at observation, the lowest value was found in “BARI SOYBEAN 6” which was 5.70cm. In case of leaf length mean sum of square significant (2.38) in soybean indicated considerable difference among the genotypes studied (Table 3). It ranged from 5.70 to 8.67 with a mean value of 7.41. The phenotypic variance (1.549) appeared to be higher than the genotypic variance (0.416) suggested considerable influence of environment on the expression of the genes controlling this trait (Figure 2). The heritability (26.826%) estimates for this trait was low, genetic advance (0.688) was low and genetic advance in per cent of mean (9.285) were also found low, revealed that this trait was governed by non-additive gene. Therefore, selection would be effective for this trait.

4.2.6 Number of pods per plant

Significant mean sum of square for pods per plant (35.02) indicated that considerable variation for this trait exists in soybean (Table 3). The number of pods per plant was ranged from 29 to 41.33 with mean of 33.20. The minimum number of pods per plant was observed in genotype “BINA SOYBEAN 3” while maximum number of pods per plant was found in the genotype “AGS-205” (Appendix IV). The phenotypic variance (12.378) appeared to be higher

than the genotypic variance (11.324) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic coefficient of variation and phenotypic co-efficient of variation were 10.135 and 10.596, respectively which indicated presence of considerable variability among the genotypes. The heritability (91.481%) estimates for this trait was very high, genetic advance (6.630) was low and genetic advance in per cent of mean (19.968) was found also low, revealed that this trait was governed by both additive and non-additive genes. Selection for this trait would be effective on the basis of this trait. Pods per plant showed high heritability with high genetic advance in soybean which is halfly similar to the earlier findings by Chandel *et al.* (2013) and Dobhal and Gautam (1995).

4.2.7 Number of seeds per pod

The values ranged from 2.00 to 4.00 with a mean of 3.00. The genotype “ags-205” had highest number of seeds per pod while it was lowest in the “K-16” (Table 3 and Appendix IV). The phenotypic variance (0.562) appeared to be higher than the genotypic variance (0.288). The genotypic co-efficient and phenotypic co-efficient of variation were 17.876 and 24.991 respectively (Table 3) indicating minimal influence of environment on the expression of the genes controlling this trait. The heritability (51.163%) estimates for this trait was medium, low genetic advance (0.790) and genetic advance in percent of mean (26.339) was found medium low (Table 3). revealed that this trait was governed by non-additive gene. Therefore, selection on the basis of this trait would take long time. Whereas, Nooghab *et al.* (2014) observed total genetic distance was highest for seeds per pod.

4.2.8 Number of seeds per plant

Significant mean sum of square for number of seeds per plant (2013.64) in soybean indicated existence of considerable variation for this trait (Table 3). The germplasm genotypes differed significantly for this character. The values ranged from 66 to 165.33 with a mean of 100.09. The genotype AGS-205 had highest number of seeds per plant while it was lowest in the genotype K-16 (Appendix IV). The phenotypic variance (889.493) appeared to be higher than

the genotypic variance (562.073) suggested considerable influence of environment on the expression of the of variation genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 23.686 and 29.797, respectively where there were little difference to each other (Table 3). The heritability (63.190%) estimates for this trait was high, genetic advance (38.823) and genetic advance in percent of mean (38.787) was found considerable high (Table 3), revealed that this trait was governed by additive gene. Therefore selection for this trait would be effective. Similar findings was reported by Chandel *et al.*(2013).

4.2.9 Thousands Seed weight (g)

The mean sum of square for thousands seed weight was found 38.97 in soybean which significantly indicated considerable differences among the genotypes studied (Table 3). The mean thousand seed weight noticed was 11.70 with a range of 7.67-20.67 g. The genotype TAS-4 showed the minimum thousands seed weight and the maximum thousand seed weight was recorded in the genotype “AGS-205”. The genotypic variance appeared (12.656) to be lower than the phenotypic variance (13.665) suggested considerable influence of environment on the expression of the genes controlling this trait. There was a very little difference between phenotypic (31.584) and genotypic co-efficient of variation (30.396), indicating minor environmental influence on this character. Heritability (92.618%) estimates for this trait was very high, genetic advance (7.053) was low and genetic advance in per cent of mean (60.261) was found high, revealed that this trait was governed by additive gene. Selection performed on the basis of this trait would be effective which is coupled with the earlier findings of Kumar *et al.* (2014); Nooghab *et al.* (2014) and Arshad *et al.* (2006).

4.2.10 Yield (ton/ha)

Significant mean sum of square for yield (0.27) in soybean indicated existence of considerable variation for this trait (Table 3). The germplasm genotypes differed significantly for this character. The values ranged from 1.24 to 2.62 with mean value 1.73 ton/ha. AGS-205 performed maximum yield where LOCAL genotype performed lower yield. The phenotypic variance (0.091) appeared to be same as the genotypic variance (0.090) suggested very little influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient and phenotypic co-efficient of variation were 17.364 and 17.452, respectively indicating presence of considerable variability among the genotypes. The heritability (98.992%) estimates for this trait is high, genetic advance (0.616) was very low but genetic advance in percent of mean (35.589) was found moderate (Table 2), revealed that this trait was governed by additive gene. Selection on the basis of this traits would be effective.

4.3 Correlation co-efficient

As yield is the resultant of combined effect of several component characters and environment, understanding the interaction of characters among themselves and with environment has been of great use in the plant breeding. Correlation studies along with path analysis provide a better understanding of the association of different characters with fruit yield. So selection may not be effective unless the other contributing components influence the yield directly or indirectly. When selection pressure is applied for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated characters. Hence knowledge regarding association of character with yield and among themselves provides guideline to the plant breeders for making improvement through selection with a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factors (Dewey and Lu, 1959). Pearson correlation analysis among yield and its contributing characters are shown in Table 4.

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

Trait		GP	FP	PH	NPBP	LL	NPPP	NSPP	NSP	TSW
FP	G	0.432**								
	P	0.411**								
PH	G	0.514**	0.521**							
	P	0.422**	0.380**							
NPBP	G	0.196 ^{NS}	0.878**	0.525**						
	P	0.147 ^{NS}	0.619**	0.356**						
LL	G	0.118 ^{NS}	0.634**	0.750**	0.510**					
	P	0.057 ^{NS}	0.306*	0.095 ^{NS}	0.181 ^{NS}					
NPPP	G	0.271*	0.919**	0.533**	0.795**	0.568**				
	P	0.255 ^{NS}	0.840**	0.417**	0.561**	0.298*				
NSPP	G	-0.047 ^{NS}	0.019 ^{NS}	0.014 ^{NS}	0.198 ^{NS}	-0.242 ^{NS}	0.240 ^{NS}			
	P	-0.035 ^{NS}	0.023 ^{NS}	-0.060 ^{NS}	0.158 ^{NS}	0.065 ^{NS}	0.177 ^{NS}			
NSP	G	0.112 ^{NS}	0.455**	0.312*	0.505**	0.098 ^{NS}	0.662**	0.883**		
	P	0.088 ^{NS}	0.354**	0.139 ^{NS}	0.357**	0.178 ^{NS}	0.545**	0.918**		
TSW	G	0.380**	0.902**	0.654**	0.745**	0.709**	0.960**	0.256 ^{NS}	0.668**	
	P	0.362**	0.805**	0.530**	0.493**	0.377**	0.900**	0.149 ^{NS}	0.496**	
Y	G	0.472**	0.899**	0.747**	0.818**	0.563**	0.914**	0.214 ^{NS}	0.621**	0.946**
	P	0.467**	0.828**	0.610**	0.574**	0.297*	0.874**	0.163 ^{NS}	0.502**	0.914**

GP=Germination percentage, FP=Days to 50% flowering, PH= Plant height (cm), NPBP= Number of primary branches per plant, LL=Leaf length (cm), NPPP= Number of pods per plant, NSPP= Number of seeds per pod, NSP=Number of seeds per plant, TSW=Thousands seed weight (g), Y= Yield (ton/ha)

The genotypic correlation coefficients in most cases were higher than their phenotypic correlation coefficients indicating the genetic reason of association. While phenotypic correlation coefficient were higher than genotypic correlation coefficient indicating suppressing effect of the environment which modified the expression of the characters at phenotypic level. The depicted of genotypic and phenotypic correlation coefficient among yield and yield contributing characters of soybean are shown in table4.

4.3.1 Germination percentage

Germination percentage had positive and highly significant correlation with days to 50% flowering (0.432 and 0.411), plant height (0.514 and 0.422), thousand seed weight (0.380 and 0.362) and seed yield (0.472 and 0.467) at both genotypic and phenotypic level. It had also positive and significant correlation with number of pod per plant (0.271) at genotypic level. On the other hand germination percentage had negative but non significant relationship with number of seed per pod (-0.047 and -0.035) at both genotypic and phenotypic level (Table4).

4.3.2 Days to 50% flowering

The correlation of days to 50% flowering with plant height (0.521 and 0.380), number of primary branch per plant (0.878 and 0.619), leaf length (0.634 and 0.306), number of pods per plant (0.919 and 0.840), number of seed per pod (0.455 and 0.0.354), thousand seed weight (0.902 and 0.805) and yield (0.899 and 0.828) was positive and highly significant at both the genotypic and phenotypic levels (Table 4).

4.3.3 Plant height (cm)

A highly significant and positive association of number of primary branches per plant (0.525 and 0.356), number of pods per plant (0.533 and 0.417) thousand seed weight (0.654 and 0.530) and yield (0.747 and 0.610) was present with plant hight at both the genotypic and phenotypic levels (Table 4).

4.3.4 Number of primary branches per plant

The number of primary branch showed a positive and highly significant association with days to 50% flowering (0.878 and 0.619), plant height (0.525 and 0.356), number of pod per plant (0.795 and 0.561), thousands seed weight (0.745 and 0.493) and yield (0.818 and 0.574) at both genotypic and phenotypic levels (Table 4).

4.3.5 Leaf length cm)

The leaf length showed a highly positive and significant association with days to 50% flowering (0.634 and 0.306), number of pod per plant (0.568 and 0.298) , thousand seed weight (0.709 and 0.377) and yield (0.563 and 0.297) at both the genotypic and phenotypic levels (Table4).

4.3.6 Number of pods per plant

Number of pods per plant had positive and significant correlation with days to 50% flowering (0.919 and 0.840), plant height (0.533 and 0.417), number of primary branches per plant (0.795 and 0.561), leaf length (0.568 and 0.298), number of seeds per plant (0.662 and 0.545), thousands seed weight (0.960 and 0.900) and seed yield (0.914 and 0.874) at both genotypic and phenotypic level (table 4).

4.3.7 Number of seeds per pod

A highly significant and positive association of number of seed per plant at both the genotypic and phenotypic levels was observed with number of seeds per plant (0.883 and 0.918). But all other characters showed non-significant results.

4.3.8 Number of seeds per plant

A highly significant and positive association of number of seed per plant at both the genotypic and phenotypic levels was observed with days to50% flowering (0.455 and 0.354), number of primary branches per plant (0.505 and 0.357), number of pod per plant (0.662 and 0.545), number of seeds per plant (0.883and0.918),thousands seed weight (0.668 and 0.496) and yield (0.621 and 0.502)(table 4).

4.3.9 Thousands seed weight (g)

A highly significant and positive association of thousands seed weight (gm) at both the genotypic and phenotypic levels was observed with germination percentage (0.380 and 0.362), days to 50% flowering (0.902 and 0.805), plant height (0.654 and 0.530), leaf length (0.709 and 0.377), number of pod per plant (0.960 and 0.900), number of seeds per plant (0.668 and 0.496) and yield per plant (0.946 and 0.914). There were no negative correlation among the 10 characters (table 4).

4.3.10 Yield (ton/ha)

A highly significant and positive association of soybean yield at both the genotypic and phenotypic levels was observed with germination percentage (0.472 and 0.467), days to 50% flowering (0.899 and 0.828), plant height (0.747 and 0.610), number of primary branch per plant (0.818 and 0.574), leaf length (0.563 and 0.297), number of pod per plant (0.914 and 0.874), number of seeds per plant (0.621 and 0.502) and yield (0.946 and 0.914). There were no negative correlation among the characters (table 4).

4.4 Path coefficient analysis

Though correlation analysis indicates the association pattern of component traits with yield, they simply represent the overall influence of a particular trait on yield rather than providing cause and effect relationship. The path coefficient analysis technique was developed by Wright (1921) and demonstrated by Dewey and Lu (1959) facilitates the partitioning of correlation coefficients into direct and indirect contribution of various characters on yield. It is standardized partial regression coefficient analysis. As such, it measures the direct influence of one variable upon other. Such information would be of great value in enabling the breeder to specifically identify the important component traits of yield and utilize the genetic stock for improvement in a planned way. In path coefficient analysis, the direct effect of a trait on yield of plant and its indirect effect through other characters were computed and the results are presented in Table 5.

4.1 Direct effect

Seven out of nine characters had positive direct effect on yield per plant. The characters which had positive direct effects are germination percentage (0.508), days to 50% flowering (1.886), plant height (0.417), leaf length (1.442), number of pod per plant (3.173), number of seeds per plant (1.204) and number of seeds per plant (0.031). However characters viz., number of primary branches per plant (-1.080), thousands seed weight (-4.813) had negative direct effect on seed yield per plant (Table5).

4.2 Indirect effect

4.2.1 Germination percentage

Germination percentage showed a positive indirect effect on seed yield through days to 50% flowering (0.814), plant height (0.215), leaf length (0.170), number of pods per plant (0.859), number of seeds per plant (0.003) . Number of primary branches per plant (-0.212), number of seeds per pod (-0.057) and thousands seed weight (-1.828) had indirect negative effect on seed yield (Table5).

4.4.2 Days to 50% flowering

Path analysis revealed that days to 50% flowering had positive direct effect (0.1.886) on yield. Days to 50% flowering showed positive indirect effect with germination percentage (0.219), plant height (0.217), leaf length (0.914), number of pods per plant (2.915), number of seed per pod (0.022) and number of seeds per plant (0.014) (Table 5). It had a negative indirect effect through number of primary branches (-0.948), and thousands seed weight (-4.341).

4.4.3 Plant height (cm)

Path analysis revealed that plant height had positive direct effect (0.417) on yield. Germination percentage (0.261), days to 50% flowering (0.983), leaf length (1.082), number of pods per plant (1.692), number of seeds per pod (0.016) and number of seeds per plant (0.010) had indirect influence on yield. It had negative indirect effect on number of primary branches (-0.567) and thousands seed weight (-3.146)

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

Direct Effect	GP	FP	PH	NPBP	LL	NPPP	NSPP	NSP	TSW	Y
GP	0.508	0.814	0.215	-0.212	0.170	0.859	-0.057	0.003	-1.828	0.472**
FP	0.219	1.886	0.217	-0.948	0.914	2.915	0.022	0.014	-4.341	0.899**
PH	0.261	0.983	0.417	-0.567	1.082	1.692	0.016	0.010	-3.146	0.747**
NPBP	0.100	1.655	0.219	-1.080	0.735	2.523	0.238	0.016	-3.588	0.818**
LL	0.060	1.196	0.313	-0.551	1.442	1.803	-0.291	0.003	-3.412	0.563**
NPPP	0.137	1.733	0.223	-0.859	0.819	3.173	0.289	0.020	-4.622	0.914**
NSPP	-0.024	0.035	0.006	-0.214	-0.349	0.762	1.204	0.027	-1.234	0.214NS
NSP	0.057	0.859	0.130	-0.546	0.141	2.099	1.064	0.031	-3.214	0.621**
TSW	0.193	1.701	0.273	-0.805	1.022	3.047	0.309	0.021	-4.813	0.946**

Residual effect: 0.2

GP=Germination percentage, FP=Days to fifty percent flowering, PH= Plant height (cm), NPBP=Number of primary branches per plant, LL=Leaf length (cm), NPPP= Number of pods per plant, NSPP= Number of seeds per pod, NSP=Number of seeds per plant, TSW=Thousands seed weight (g), Y=Yield (ton/ha).

4.4.4 Number of primary branches per plant

Number of branches per plant had negative direct effect (-1.080) on yield. This character influenced the yield per plant indirectly through germination percentage (0.100), day to days to 50% flowering (1.655), plant height (0.219), leaf length (0.735), number of pod per plant (2.523), number of seed per pod (0.238) and number of seeds per plant (0.016). Thousand seed weight (-3.588) had negative indirect effect on the other hand (table 5).

4.4.5 Leaf length (cm)

Path analysis revealed that leaf length had positive direct effect (1.442) on yield. Leaf length showed indirectly positive influence for germination percentage (0.060), days to 50% flowering (1.196), plant height (0.313), number pod per plant (1.803) and number of seeds per plant (0.003). It had negative indirect effect for number of primary branch (-0.551), number of seed per pod (-0.291) and thousand seed weight (-3.412) showed on table 5.

4.4.6 Number of pods per plant

Number of pod per plant had the direct positive effect on yield (3.173) whereas it had positive indirect effect through germination percentage (0.137), days to 50% flowering (1.733), plant height (0.223), leaf length (0.819), number pod per pod (0.289) and number of seeds per plant (0.020) (Table 5). However, it had indirect negative effects through number of primary branches per plant (-0.859), and thousand seed weight (-4.622) (table 5).

4.4.7 Number of seeds per pod

Path analysis evidenced that Number of seeds per pod had positive direct effect (1.204) on yield whereas, it showed indirect positive effects on seed yield by days to 50% flowering (0.035), plant height (0.006), number of pods per plant (0.762) and number of seeds per plant (0.027). It showed indirect negative effect on seed yield through germination percentage (-0.024), number of primary branch per plant (-0.214), leaf length (-0.349) and thousand seed weight (-1.234) which were non-significant (Table 5).

4.4.8 Number seeds per plant

Path analysis revealed that Number of seeds per plant had positive direct effect (0.031) on yield whereas, it showed indirect positive effects on seed yield by germination percentage (0.057), days to 50% flowering (0.859), plant height (0.130), leaf length (0.141), number of pods per plant (2.099) and number of seeds per pod (1.064) (Table 5). It showed indirect negative effect on seed yield through number of primary branch per plant (-0.546) and thousands seed weight (-3.214) showed in (Table 5).

4.4.9 Thousands seed weight (g)

Path analysis revealed that thousands seed weight negative direct effect (-4.813) on yield whereas, it showed indirect positive effects on seed yield by germination percentage (0.193), days to 50% flowering (1.701), plant height (0.273), leaf length (1.022), number of pods per plant (3.047) and number of seeds per plant (0.021) (Table 5). It showed indirect negative effect on seed yield through number of primary branch per plant (-0.805) which is coupled with the earlier findings by Inderjit *et al.* (2007).

4.5 Genetic diversity

4.5.1 Principal component analysis (PCA)

Principal component analysis was carried out with eighteen genotypes of soybean which gives Eigen values of principal component axes of coordination of genotypes with the first axes totally accounted for the variation among the genotypes. First six eigen values for six principal coordination axes of genotypes accounted for 98.54% variation showed in Table 6. Based on principal component scores I and II obtained from the Principal component analysis (Appendix VI), a two-dimensional scatter diagram (Z1-Z2) using component score I as X axis and component score II as Y axis was constructed, which has been presented in Figure 4. The scatter diagram revealed that there were four apparent clusters. The genotypes were distantly located from each other, which indicated that considerable diversity existed among the genotypes.

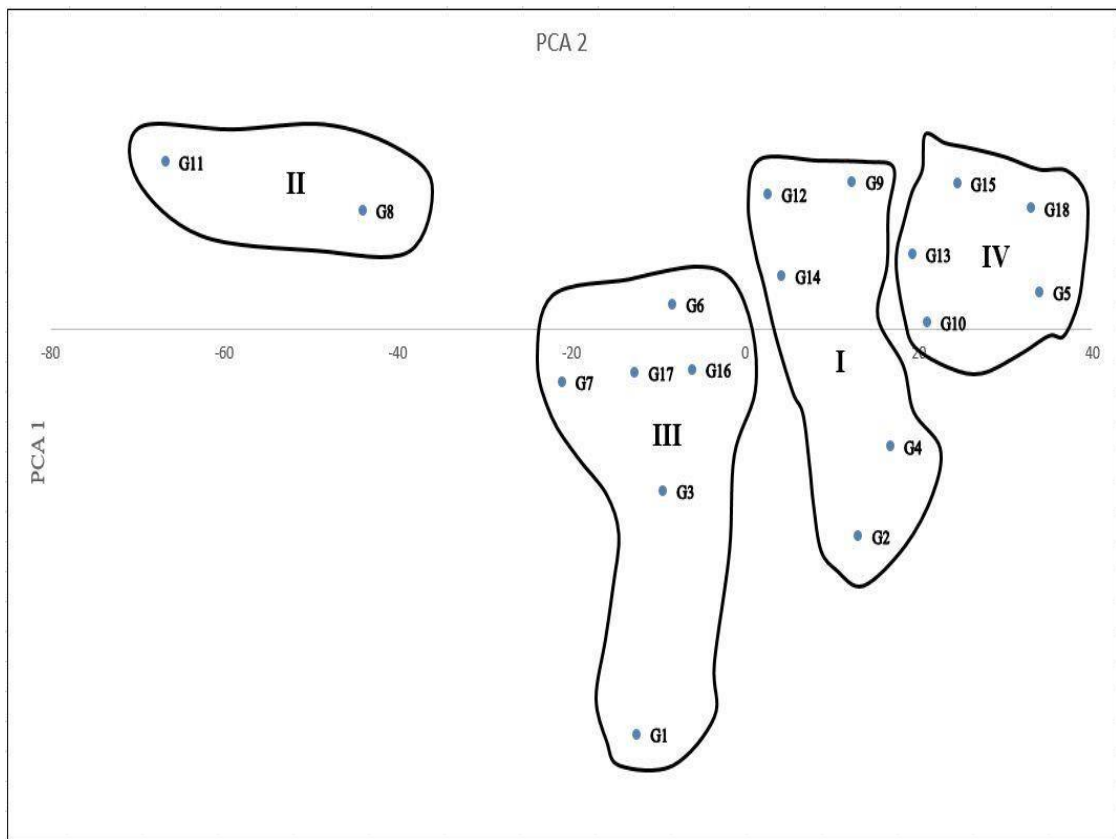


Figure 4. Scatter distribution of 18 genotypes of soybean based on their principal component scores super imposed with clustering.

4.5.2 Canonical variate analysis

Canonical Variate Analysis (CVA) was done to compute the inter-cluster distances. The intra and inter-cluster distance (D^2) values were shown in Table 7. In this experiment, the inter-cluster distances were higher than the intra-cluster distances thus indicating broader genetic diversity among the genotypes of different groups. The highest inter-cluster distance was observed between clusters II and I (26.186), followed by between clusters II and IV (23.881), II and III (19.008). In contrast, the lowest inter-cluster distance was observed between cluster I and IV (5.093). 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 cluster II and I as well as IV and II indicated the genotypes in these clusters were diverse than those clusters. The minimum distance was observed between clusters I and IV (5.093) and clusters III and I (7.921) indicate close relationship among the genotypes included. So the crossing the genotypes derived from cluster I and II will bring desired result. On the other hand, the maximum intra-cluster distance was found in cluster I (0.451), which contained of 5 genotypes, while the minimum distance was found in cluster II (0.283) that comprises 2 genotypes. Inter and intra cluster distances were showed in Table 7. Cluster I consists of nearest cluster with D^2 values cluster IV (8.53) and farthest cluster with D^2 values II (16.41) (Table 8). Cluster II consists of nearest cluster with D^2 values cluster III (7.90) and farthest cluster with D^2 values IV (21.90). Cluster III consists of nearest cluster with D^2 values cluster II (7.90) and farthest cluster with D^2 values IV (15.15). Cluster IV consists of nearest cluster with D^2 values cluster I (8.53) and farthest cluster with D^2 values II (21.90). A two-dimensional scatter diagram was constructed using component I as X-axis and component II as Y-axis, showing in the relative position. According to scatter diagram all the genotypes were apparently distributed into four clusters (Table 9).

Table 6. Eigen values and yield percent contribution of 10 characters of 18 genotypes of soybean

Parameters	Eigen values	Percent variation	Cumulative % of variation
Germination percentage	5.4849	54.85	54.85
Days to fifty percent flowering	1.7625	17.63	72.48
Plant height (cm)	0.997	9.97	82.45
Number of primary branches per plant	0.735	7.35	89.8
Leaf length (cm)	0.496	4.96	94.76
Number of pods per plant	0.3782	3.78	98.54
Number of seeds per pod	0.0638	0.64	99.18
Number of seeds per plant	0.0502	0.5	99.68
Thousands seed weight (g)	0.031	0.31	99.99
Yield (ton/ha).	0.0014	0.01	100

Table 7. Intra (bold) and inter cluster distances (D^2) for 18 genotypes of soybean

	I	II	III	IV
I				
	0.451			
II				
	26.186	0.283		
III				
	7.921	19.008	0.431	
IV				
	5.093	23.881	8.565	0.338

It is assumed that maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. Furthermore, for a practical plant breeder, the objective is to achieve high level production in addition to high heterosis. In the present study the maximum distance existence between cluster II and I. So the crosses between the genotypes belonging cluster II with cluster I might produce high heterosis. Also the crosses between genotypes from cluster II with IV might produce high level of segregating population. So the genotypes belonging to cluster II and cluster IV might be selected for future hybridization programme.

4.5.3 Principal coordinate analysis (PCO)

Inter genotypic distances as (D^2) as obtained by principal coordinate analysis (PCO) for all possible combinations between the pairs of genotypes. Inter genotypic distances, as obtained from principal coordinate analysis showed that the highest distance was observed between the G11 and G18 (1.362) (Table 8). The lowest distance was observed between the G14 and G16 (0.2225). The difference between the highest and the lowest inter genotypic distance indicated the prevalence of variability among the 18 genotypes of soybean studied.

Table 8. Ten highest and ten lowest inter genotypic distance among 18 genotypes of soybean

Highest Distance			Lowest Distance		
Genotypes		Distance	Genotypes		Distance
G11	G18	1.362	G14	G16	0.2225
G5	G11	1.3334	G4	G14	0.2272
G2	G11	1.2794	G4	G10	0.2274
G1	G11	1.2698	G16	G17	0.2303
G11	G13	1.2171	G9	G12	0.2379
G10	G11	1.1645	G3	G16	0.2511
G8	G18	1.1285	G4	G15	0.259
G11	G15	1.115	G5	G10	0.2765
G4	G11	1.094	G10	G15	0.2815
G5	G8	1.0853	G8	G11	0.2826

4.5.4 Nonhierarchical clustering

Eighteen *Glycine max* L. Merrill. genotypes were grouped into four different clusters through non-hierarchical clustering (Table 9). These results confirmed the clustering pattern of the genotypes obtained through principal component analysis. Cluster III had highest number of six genotypes (33.33%) followed by cluster IV and cluster I both (27.78%) constituted by five genotypes each. On the other hand, cluster II constituted by two genotypes (11.11%). Cluster III had maximum six genotypes namely G1 (LOCAL), G3 (DJS9207), G6(GMOT-95), G7(ASSET-93), G16(SOHAG), G17(BARI SOYBEAN 6). Cluster I represents 5 genotypes namely G2 (TAS-4), G4 (AGS-95), G9 (GMOT-33), G12 (BARI SOYBEAN 5) and G14(BINA SOYBEAN 8). Cluster IV represents five genotypes namely G5 (K-16), G10 (JAYA WAYA), G13 (AGS-79), G15 (BINA SOYBEAN 1), G18 (BINA SOYBEAN 3). Last of all cluster II had minimum 2 genotypes G8 (ASOMEME) and G11 (AGS-205). The results confirmed the clustering pattern of the genotypes according to the principal component analysis. 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 non hierarchical clustering. Clustering pattern of 18 genotypes of soybean is presented in figure 4 and figure 5.

4.5.5 Cluster mean analysis

The cluster means of 10 different characters (Table 10) were compared and indicated considerable differences between clusters for all the characters studied. Maximum germination percentage were found in cluster II (94.7) whereas minimum was found in cluster III (90.17). Maximum days to 50% flowering were observed in cluster II (48.15), whereas minimum days to 50%

Table 9. Distribution of genotypes in different clusters

Cluster no.	Genotypes	No. of genotypes
I	G2, G4, G9, G12, G14	5
II	G8, G11	2
III	G1, G3, G6, G7, G16, G17	6
IV	G5, G10, G13, G15, G18	5

Table 10. Cluster mean values of 10 different characters of 18 genotypes of soybean

Parameters	I	II	III	IV
Germination percentage	91	94.7	90.17	92.8
Days to fifty percent flowering	43	48.15	40.7	42.12
Plant height (cm)	54.38	62	54.42	57.66
Number of primary branches per plant	7.8	9	7.5	7.4
Leaf length (cm)	7.94	8.05	6.93	7.18
Number of pods per plant	33.12	40.15	32.17	31.72
Number of seeds per pod	2.74	3.85	3.52	2.32
Number of seeds per plant	90.22	154.15	112.27	73.72
Thousands seed weight (g)	11.8	19.35	10.28	10.26
Yield (ton/ha)	1.72	2.35	1.57	1.66

flowering in cluster III (40.7). Then maximum plant heights were observed in II (62) whereas minimum plant height were observed in cluster I (54.38). Maximum number of primary branches was observed in cluster II (9) and minimum (7.4) in cluster IV. Cluster II showed highest number of leaf length (8.05) and cluster III showed lowest (6.93). Maximum (40.15) and minimum (31.72) number of pod per plant were observed in cluster II and IV, respectively. The maximum number of seeds per pod was present in cluster II (3.85) and minimum number in cluster IV (2.32). Number of seeds per plant was highest in cluster II with a mean value of (154.15) and it was least in genotypes belongs to the cluster IV (73.72). The maximum thousand seed weight was found in cluster II (19.35) whereas minimum in cluster IV (10.26). The highest yield per plant was present in cluster II (2.35) and lowest in cluster III (1.57).

4.5.6 Cluster diagram

With the help of D^2 values within and between clusters, an arbitrary cluster diagram (Figure 5) was constructed, which showed the relationship between different genotypes. However, the diagram was not following exact scale. It was apparent from the Figure 5 that the genotypes included in the cluster I was far diverse (26.186) from the genotypes of the cluster II and where the genotypes belonging to I and IV was the least diverse (5.093). Genotypes of cluster II-III (19.008) and II-IV (23.881) were moderately diverse from each other.

4.5.7 Contribution of characters towards divergence of the genotypes

Contribution of characters towards the divergence obtained from canonical variate analysis is presented in Table 11. In this method vectors was calculated to represent the varieties in the graphical form (Rao, 1952). This is helpful in cluster analysis as it facilitated the study of group constellation and also serves as a pictorial representation of the configuration of various groups. The latent vectors (Z1 and Z2) obtained from principal component analysis (PCA). The absolute magnitude of the coefficients in the first two canonical vectors also

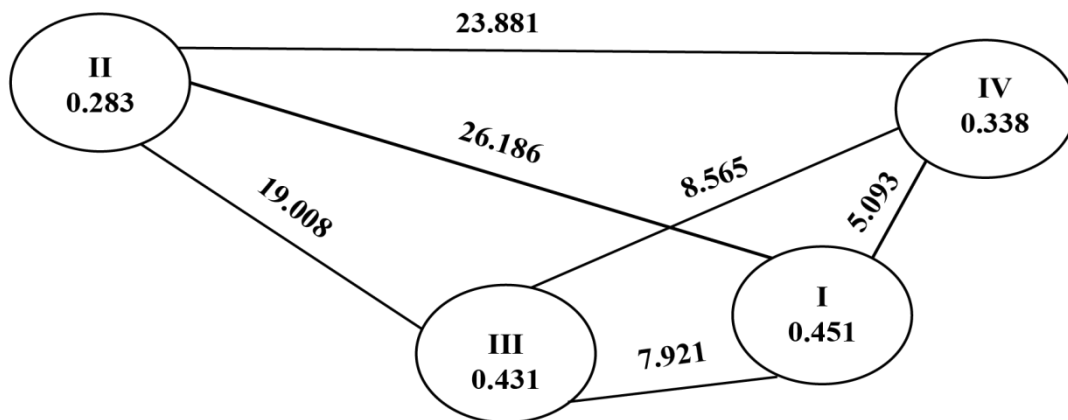


Figure 5. Intra and inter cluster distances (D^2) of 18 genotypes in soybean.

Table 11. Relative contributions of the ten characters of 18 genotypes of soybean to the total divergence

Parameters	Vector 1	Vector 2
Germination percentage	-0.234	0.168
Days to fifty percent flowering	1.647	-1.407
Plant height (cm)	0.946	-0.443
Number of primary branches per plant	1.017	0.341
Leaf length (cm)	-3.151	1.012
Number of pods per plant	-5.091	3.368
Number of seeds per pod	-49.408	31.9
Number of seeds per plant	1.757	-0.91
Thousand seed weight (g)	1.153	0.114
Yield (ton/ha)	-31.794	7.957

reflected to a great extent, the importance of primary and secondary differentiation. The character which gave absolute magnitude for vector I was considered to be responsible for primary differentiation. Likewise, the characters, which gave higher absolute magnitude for vector II was considered to be responsible for secondary differentiation. If the same character gave equal magnitude for both vectors then the characters was considered responsible for primary as well as secondary differentiation. The important characters responsible for genetic divergence in the axis of differentiation in vector I (Z1) were days to 50% flowering (1.647), plant height (0.946), number of primary branch per plant (1.017), number of seed per plant (1.757) and thousand seed weight (1.153). These characters were important because all these characters had positive signs in first axis. Germination percentage (0.168), number of primary branches per plant (0.341), leaf length (1.012), number of pods per plant (3.368), number of seeds per pod (31.9), thousand seed weight (0.114) and yield (7.957) had positive sign in vector II (Z2), second axis of differentiation. On the other hand, germination percentage (-0.234), leaf length (-3.151), number of pod per plant (-5.091), number of seeds per pod (-49.408) and yield per plant (-31.794) possessed the negative sign in the first axis of differentiation and days to 50% flowering (-1.407), plant height (-0.443) and number of seed per plant (-0.91) possessed negative signs in the second axis of differentiation that means these had minor role in the genetic divergence. Number of primary branch per plant and thousand seed weight had positive sign in both the axis, which indicated that they were the important component characters having higher contribution to genetic divergence among the genotypes studied.

4.5.8 Selection of genotypes as parent for hybridization program

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 G11 (AGS-205) from the cluster II and G18 (BINA SOYBEAN 3) from cluster IV, G8 (ASOMEME) from the cluster II and G2 (TAS- 4) from cluster I, G11 (AGS-205) from the cluster II and G8 (ASOMEME) from cluster II would be suitable parent for highest yield for future hybridization programme.

CHAPTER V

SUMMARY AND CONCLUSIONS

The research work was conducted with a view to find out the best promising soybean genotypes, to know the yield potentiality of different soybean genotypes, to know the nature of association of traits, direct and indirect relation between yield contributing characters of soybean genotypes, to cluster the genotypes according to their performance and to find out contribution of clusters to variability to identify divergent parent for hybridization program, the degrees of association among the characters under study and their indirect and direct effects of 18 genotypes of soybean (*Glycine max* L. Merrill) at the experimental field of Sher-E-Bangla Agricultural University farm, Dhaka, during robi season (December, 2018 to April, 2019) in RCBD with 3 replications

The most important findings of the present study have been summarized on the basis of the characters under study. Seeds were sown in experimental field in Randomized Complete Block Design (RCBD) with three replications. Data on various yield attributing characters such as, germination percentage, days to 50% flowering, plant height (cm), number of primary branches per plant, leaf length (cm), number of pods per plant, number of seeds per pod, number of seeds per plant, thousands seed weight (gm) and yield (ton/ha) were recorded. The salient findings of the present study have been summarized on the basis of the characters studied. The analysis of variance showed significant differences among the genotypes for all the characters. Where several genotypes performed above 95% germination percentage, some showed nearly 80% also “LOCAL” was the earliest to days of 50% flowering (38 DAS) while “AGS-205” was late to days of 50% flowering (49 DAS). The maximum plant height (62.77 cm) was recorded by the genotype ‘AGS-205’ and the lowest plant height (46.38 cm) was recorded by ‘LOCAL’. Maximum (9) number of primary branches recorded in “ASOMEME” and “AGS-205” on contrary “LOCAL” genotype showed the minimum number of primary branches (6).

The highest (8.67 cm) leaf length was recorded by the genotype 'GMOT-33' and 'BARI SOYBEAN 6' showed lowest leaf length. Where "AGS-205" bore maximum number of pod per plant, the genotype "BINA SOYBEAN 3" showed the minimum in case. Highest number of seeds per pod was recorded in the accession "AGS-205" and lowest in "K-16". Highest number of seeds per plant was observed in the accession "AGS-205" and lowest in "K-16". The weight of thousand seeds was highest (20.67 gm) in "AGS-205" genotypes and lowest (7.67 gm) in "TAS-4". Finally maximum 2.62 ton/ha yield was recorded for "AGS-205" lowest in "LOCAL" genotypes (1.24 ton/ha). Soybean yield showed significant and positive correlation at both genotypic and phenotypic level with all observed characters except number of seeds per pod which showed non-significant correlation. The phenotypic variance and co-efficient of variance were higher than genotypic variance and co-efficient of variance studied.

Path coefficient analysis revealed that Seven out of nine characters had positive direct effect on yield per plant. The characters which had positive direct effects are germination percentage (0.508), days to 50% flowering (1.886), plant height (0.417), leaf length (1.442), number of pods per plant (3.173), number of seeds per plant (1.204) and number of seeds per plant (0.031). However characters viz., number of primary branch per plant (-1.080), thousand seed weight (-4.813) had negative direct effect on seed yield per plant. High heritability (98.992) was recorded for yield per plant followed by germination percentage (98.963) and lowest heritability was in leaf length (26.826). Genetic diversity of eighteen soybean genotypes based on ten characters was measured through multivariate analysis. The 18 genotypes divided into four distant clusters. The cluster III comprised the maximum number of genotypes (6). The cluster I, II, and IV comprised 5, 2 and 5 genotypes, respectively. The highest inter-cluster distance (26.186) was found between the cluster I and II and the highest distant genotypes were G11 (AGS-205) and G18 (BINA SOYBEAN3). The lowest inter cluster distance (5.093) was observed between the cluster I and IV.

The inter-cluster distances were larger than the intra-cluster distances. The intra-cluster distance in the entire four clusters was more or less indicating that the genotypes within the same cluster were closely related. The result of the present study revealed that a wide variability exists among the collected soybean genotypes. Furthermore, there were also genotypes of different yield contributing characters with yield of soybean. From the findings of the present study, the following conclusions could be drawn:

- ❖ Wide range of genetic diversity existed among 18 soybean genotypes which were grouped into four clusters and most diverse genotypes were G11(AGS-205) and G18 (BINA SOYBEAN 3). That variability could be used for future breeding program of soybean in Bangladesh.
- ❖ High heritability coupled with high genetic advance in percent of mean was observed in germination percentage, days to 50% flowering, number of pods per plant, number of seeds per plant, thousands seed weight. Hence, yield improvement in soybean would be achieved through selection of these characters.
- ❖ Germination percentage, days to 50% flowering, plant height, leaf length, number of pods per plant, number of seeds per pod, number of seeds per plant showed positive direct effect on yield. So, yield improvement was associated with these characters.
- ❖ The genotypes of clusters II was more diverse from the genotypes of cluster I. 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 G11 (AGS-205), G8 (ASOMEME), G18 (BINA SOYBEAN 3), G6 (GMOT-43) could be included in future study in view of seed yield for releasing as soybean varieties.
- The genotypes of cluster I and II could be used as parents for further breeding program to develop soybean variety in order to get higher yield.

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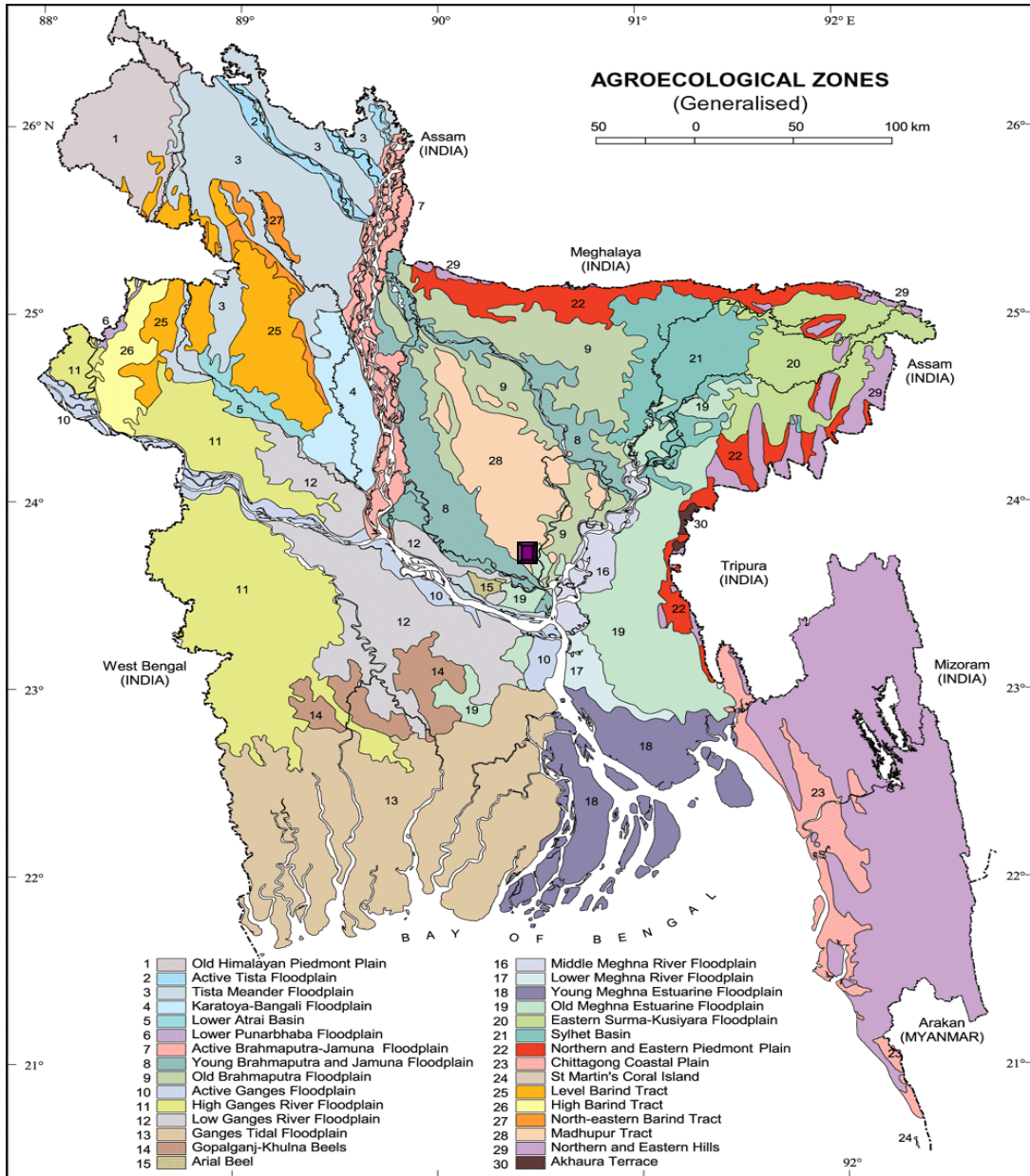
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APPENDICES

Appendix I: Map showing the experimental site under the study



Appendix II: Monthly record of temperature, relative humidity and rainfall, of the experimental site during the period from October, 2018 to June, 2019.

Months	Temperature (°C)		Relative humidity	Rainfall
	Maximum	Minimum	(%)	mm
October, 2018	31.6	23.8	65	172.3
November, 2018	29.6	19.2	53	34.4
December, 2018	26.4	14.1	50	12.8
January, 2019	25.4	12.7	46	7.7
February, 2019	28.16	15.5	37	28.9
March, 2019	32.5	20.4	38	65.8
April, 2019	33.7	23.6	42	156.3
May, 2019	32.9	24.5	59	339.4
June, 2019	32.1	26.1	72	340.4

Source: Bangladesh Meteorological Department (Climate & weather division) Agargaon, Dhaka-1207.

**Appendix III: Characteristics of Sher-e-Bangla Agricultural University
(SAU) Farm soil analyzed by Soil Resources Development
Institute (SRDI), Khamarbari, Farmgate, Dhaka**

Morphological feature	Characteristics
Location	SAU Farm, Dhaka
AEZ	Madhupur Tract (28)
General soil type	Shallow red brown terrace soil
Land type	High land
Soil series	Tejgaon
Topography	Fairly leveled
Flood level	Above flood level
Drainage	Well drained

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

Variety	GP	FP	PH	NPBP	LL	NPPP	NSPP	NSP	TSW	Y
G1	81.00	38.33	46.38	6.00	6.18	31.00	3.67	114.00	8.00	1.24
G2	85.00	39.00	52.72	8.00	7.45	29.33	3.00	88.00	7.67	1.45
G3	87.00	40.33	57.03	8.00	8.00	30.00	3.67	110.33	8.67	1.53
G4	85.33	41.33	53.50	7.00	7.75	31.33	2.67	83.67	11.00	1.62
G5	88.00	42.67	57.94	8.00	6.52	33.00	2.00	66.00	10.00	1.70
G6	90.00	42.33	59.14	8.00	6.62	36.00	3.00	108.00	14.00	1.91
G7	91.00	41.33	57.60	8.00	8.28	33.00	3.67	121.33	12.67	1.71
G8	93.67	47.33	61.20	9.00	7.64	39.00	3.67	143.00	18.00	2.10
G9	92.67	46.67	54.94	9.00	8.67	37.00	2.33	86.67	16.00	1.94
G10	88.00	43.33	56.96	8.00	8.05	34.00	2.33	79.00	10.00	1.63
G11	95.67	49.00	62.77	9.00	8.50	41.33	4.00	165.33	20.67	2.62
G12	96.00	47.67	53.20	8.00	8.35	36.00	2.67	96.67	14.00	1.88
G13	96.00	43.00	56.03	8.00	6.22	30.33	2.67	81.00	9.00	1.67
G14	96.00	40.33	57.57	7.00	7.35	32.00	3.00	96.00	10.33	1.73
G15	96.00	42.33	57.53	7.00	7.14	32.33	2.33	75.33	12.33	1.80
G16	96.00	40.33	52.94	7.00	6.83	32.00	3.33	106.67	9.00	1.52
G17	96.00	41.67	53.52	8.00	5.70	31.00	3.67	113.33	9.33	1.63
G18	96.00	39.33	59.89	6.00	8.08	29.00	2.33	67.33	10.00	1.47
MIN	81.00	38.33	46.38	6.00	5.70	29.00	2.00	66.00	7.67	1.24
MAX	96.00	49.00	62.77	9.00	8.67	41.33	4.00	165.33	20.67	2.62
MEAN	91.63	42.57	56.16	7.72	7.41	33.20	3.00	100.09	11.70	1.73

GP= Germination percentage, FP=Days to Fifty percent flowering, PH= Plant Height (cm), NPBP= Number of primary branches per plant, LL=Leaf length (cm), NPPP= Number of pods per plant, NSPP= Number of seeds per pod, NSP=Number of seeds per plant, TSW=Thousands seed weight (g), Y= Yield (ton/ha).

Appendix V : Analysis of variance of 10 yield and yield contributing characters of soybean

Source	DF	Mean sum of square									
		GP	FP	PH	NPBP	LL	NPPP	NSPP	NSP	TSW	Y
Replication	2	4.130	15.685	6.034	7.389	2.858	2.741	0.667	1026.130	3.185	0.003
Genotype	17	71.055**	29.600**	43.177**	2.402**	2.380*	35.025**	1.137**	2013.640**	38.976**	0.272**
Error	34	0.247	1.313	6.804	0.624	1.133	1.055	0.275	327.420	1.009	0.00092

*, 5% level of significant

** , 1% level of significant

GP= Germination percentage, FP=Days to fifty percent flowering, PH= Plant height (cm), NPBP= Number of primary branches per plant, LL=Leaf length (cm), NPPP= Number of pods per plant, NSPP= Number of seeds per pod, NSP=Number of seeds per plant, TSW=Thousands seed weight (g), Y= Yield (ton/ha).

Appendix VI : Z1-Z2 score of 18 genotypes of soybean

Genotype	PCA 1	PCA 2
G1	-12.44	-16.54
G2	13.09	-8.46
G3	-9.42	-6.61
G4	16.77	-4.8
G5	33.95	1.5
G6	-8.32	1.01
G7	-21.07	-2.16
G8	-44.03	4.84
G9	12.37	6.01
G10	20.98	0.27
G11	-66.74	6.81
G12	2.67	5.5
G13	19.27	3.05
G14	4.25	2.16
G15	24.46	5.94
G16	-6.06	-1.65
G17	-12.66	-1.79
G18	32.94	4.92

Pictorial Board



Picture 3: Seed bed preparation



Picture 4: Seeds ready for sowing



Picture 5: Sowing seed



Picture 6: Irrigation in experiment field



Picture 7: Rising Plant



Picture 8: Field visit by respected supervisor



Picture 9: Data Collection