GENETIC DIVERSITY ANALYSIS OF SOYBEAN (*Glycine max* L. Merr.)

MD ANAETH ULLAH RAFI

DEPARTMENT OF GENETICS AND PLANT BREEDING

SHER-E-BANGLA AGRICULTURAL UNIVERSITY

DHAKA-1207

June, 2022

GENETIC DIVERSITY ANALYSIS OF SOYBEAN (*Glycine max* L. Merr.)

By

MD ANAETH ULLAH RAFI

REG. NO.: 15-06374

A Thesis
Submitted to the Department of Genetics and Plant Breeding,
Faculty of Agriculture,
Sher-e-Bangla Agricultural University, Dhaka
in partial fulfillment of the requirements
for the degree
of

MASTER OF SCIENCE (MS)
IN
GENETICS AND PLANT BREEDING

SEMESTER: January-June, 2022

APPROVED BY:

Dr. Naheed Zeba	**Dr. Shahanaz Parveen**
Professor	Associate Professor
Department of Genetics and Plant Breeding	Department of Genetics and Plant Breeding
Supervisor	**Co-supervisor**

Dr. Shahanaz Parveen
Chairman
Department of Genetics and Plant Breeding

Dr. Naheed Zeba
Professor
Department of Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Dhaka-1207, Bangladesh
Mobile: +880 01913091772
E-mail: naheed0359@yahoo.com

CERTIFICATE

This is to certify that, the thesis entitled *'Genetic diversity analysis of soybean (Glycine max L. Merr.)'* is 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 in Genetics and Plant Breeding**, embodies the result of a piece of bona fide research work carried out by Md Anaeth Ullah Rafi, Registration number: 15-06374 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: June, 2022
Dhaka, Bangladesh

Dr. Naheed Zeba
Supervisor

DEDICATED

TO

MY BELOVED PARENTS

ACKNOWLEDGEMENTS

LIST OF CONTENTS

LIST OF CONTENTS (Contd.)

LIST OF CONTENTS (Contd.)

LIST OF TABLES

LIST OF PLATES

LIST OF FIGURES

LIST OF APPENDICES

SOME COMMONLY USED ABBREVIATIONS

Full word	Abbreviation
Agro Ecological Zone	AEZ
Analysis of variance	ANOVA
Food and Agricultural Organization	FAO
Bangladesh Agricultural Research Institute	BARI
Centimeter	Cm
Degree Centigrade	^0C
Co-efficient of the variation	CV
Days after sowing	DAS
Degrees of Freedom	df
At the rate	@
Et cetera	etc.
Mean sum of square	MSS
Heritability in broad sense	h^2b
Genetic Advance	GA
Genotypic correlation	r_g
Genotypic variance	σ^2_g
Genotypic Coefficient of Variation	GCV
Gram	g
Meter	m
Milliliter	mL
Metric ton	MT
Triple Super Phosphate	TSP
Muriate of Potash	MOP
Number	No.
Percent	(%)
Percentage of Coefficient of Variation	CV%
Phenotypic variances	σ^2_p
Phenotypic Coefficient of Variation	PCV
Phenotypic correlation	r_p
Randomized Complete Block Design	RCBD
Sher-e-Bangla Agricultural University	SAU
Square meter	m^2
Standard error	SE

GENETIC DIVERSITY ANALYSIS OF SOYBEAN (*Glycine max* L. Merr.)

ABSTRACT

This research was conducted using twenty soybean genotypes to assess the performance of yield and yield related characters during early 2022 from February to May. Variance analysis exhibited highly significance of differences for all the studied parameters. Phenotypic coefficient of variation was found higher for all the character than the genotypic coefficient of variation, indicating the influence of environment on the trait expression. The rage of the heritability was from 23.74 to 97.77. High heritability associated with high genetic advance of percent mean was observed for no. of branches per plant, no. of pods per plant, no. of seeds per pod, dry stover yield (g/plant) and dry seed yield (g/plant); that indicating the existence of additive gene action and simple selection based on this trait is possible for future breeding program. Calculation of correlation of coefficient revealed that, the dry seed yield per plant (g/plant) had positive and significant correlation with plant height (G= 0.76, P= 0.67), no. of branches per plant (G= 0.51, P= 0.42), pod length (G= 0.70, P= 0.66), no. of pods per plant (G= 0.67, P= 0.55), no. of seeds per pod (G= 0.84, P= 0.31), hundred seed weight (g) (G= 0.88, P= 0.48), and dry stover yield (g/plant) (G= 0.97, P= 0.68). The path analysis revealed the days to maturity (0.119), pod length (cm) (0.071), no. of pods per plant (0.477), no. of seeds per pod (0.289), hundred seed weight (g) (0.381), and dry stover yield (g/plant) (2.826) had positive direct effect on dry seed yield. Through the multivariate analysis it was found that the twenty genotypes of soybean were clustered into three different cluster. Cluster three contained the maximum number of genotypes (9) which are G5, G7, G9, G12, G15, G17, G18, G19 and G20. While the lowest number of genotypes (4) was noted in cluster I including G1, G11, G13, and G14. Considering the magnitude of the cluster mean and agronomic performance of the soybean genotypes, from the cluster I, G2 (BD-2325) for minimum days for flowering, G3 (BD-2326) for highest plant height, maximum number of pods per plant, and highest hundred seed weight (g), G4 (BD-2327) for minimum days for maturity, and G16 (BD-2341) for highest dry stover yield per plant. Besides, from the cluster II, G7 (BD-2331) was found to give maximum length of pod and highest dry seed yield of soybean. Therefore, considering the agronomic performance, these genotypes can be used as parent for desirable hybridization program of soybean in future.

CHAPTER I

INTRODUCTION

Soybean is globally grown as one of the major crops belonging to the family Fabaceae, which is one of the largest families of flowering plants and sub-family papilionaceae. It belongs to the genus *Glycine*, and several other species exist, including *Glycine soja* (wild), *Glycine tomentella*, and *Glycine gracilis*. However, the most commonly cultivated and consumed species of soybean is *Glycine max*, which chromosome number is 2n=2x=40 (Kawakami, 1930). It is an annual herbaceous plant that can grow up to two meters tall, and its leaves are trifoliate.

People grow soybean in a range of climates and soil types. It is highly adaptable. In Bangladesh, it is a very demandable crop and is cultivated all throughout the country. They are used for several purposes, including vegetable oil, animal feed, and as a food ingredient in many processed foods. Soybeans are also used to make soy milk, tofu, and many soy-based products that are very popular among vegans and vegetarians. In 2021, the total production of soybean was 14,500 metric tons in Bangladesh, and Jamalpur, Rajshahi, Rangpur, Dinajpur, and Pabna was found to produce the maximum soybean. This represents an increase of 16.92% from the previous year's production. In Bangladesh, during the 2019-2020 crop season the total area under soybean cultivation was 3,647 hectares (BBS, 2021).

It is widely cultivated in the whole world and Brazil covers the maximum area of soybean cultivation. In 2020, the total area under soybean cultivation was approximately 126 million hectares worldwide. Along with Brazil, the United States, Argentina, China, and India cultivate soybean mostly. In the same year, approximately 364 million tonnes of soybean were produced all over the world and the united state were the highest prouder with 120 million tonnes (FAO, 2021).

Soybeans have been cultivated for more than 5,000 years. It is believed that, soybean originated in East Asia, particularly in the location that now encompasses Japan, China, and Korea. in these countries Soybean cultivation, and consumption can be traced back to ancient times. It is assumed that around 5,000 to 9,000 years ago, it has been

domesticated from the wild soybean (*Glycine soja*) in China. From there, soybean cultivation had been spread throughout East Asia and other parts of the world. in the 18th century, Soybean was first introduced to the Western world. Dutch traders brought it to Europe. in the 19th century, it was introduced to North America. Now it is cultivated in North and South America, as well as in Asia, Europe, and Africa. The distribution of soybean is highly affected by the climate, weather, human activities, etc. (Chaudhary, 1997, Hymowitz, 2004; and Zhou *et al.*, 2008;).

Soybean is a nutrient-dense food that provides a wide range of essential vitamins, macronutrients, micronutrients, and minerals. It is an important source of protein, oil, and other nutrients for both humans and livestock. Soybeans have a high amount of protein, and they are considered a complete protein-packed source because they contain all the nine essential amino acids that the human body requires. They are also a good source of dietary fiber, calcium, iron, and other minerals. In one cup (172 grams) of cooked soybean can give 298 calories, 28.6 g of proteins, 17.1 g of carbohydrates, 10.3 g fiber, 3g of sugar. Besides, it also provides potassium 886 mg, phosphorus 704 mg, magnesium 280 mg, calcium 175 mg, iron 6.1 mg, zinc 4.9 mg, copper 1.7 mg, and manganese 1.6 mg. Moreover, Vitamin B is high in soybean, as thiamine (B1) 0.5 mg, riboflavin (B2) 0.3 mg, niacin (B3) 2.5 mg, pantothenic acid (B5) 1.2 mg, vitamin (B6) 0.3 mg, and folate (B9) 481 mg can also be found in one cup of cooked soybean (USDA, 2021). There has been some controversy surrounding the health effects of soybean consumption, particularly regarding its effects on the hormone levels.

However, most studies have shown that moderate soybean consumption is safe and may have health benefits, such as reducing the risk of heart disease and certain types of cancer. Soybean has been exhibited to improve lipid profiles, decrease blood pressure, reduce the risk of the cardiovascular disease, and improve the bone health by increasing bone density and reducing bone loss (Li *et al.*, 2014; Lui *et al.*, 2012; Taku *et al.*, 2012; and Zhang *et al.*, 2001). soybean is also a good source of phytochemicals, such as isoflavones, which have been found to have potential health benefits, including reducing the risk of heart disease and certain types of cancer (Ma *et al.*, 2008).

Soybean is one of the valuable crops in Bangladesh, with a growing demand for its various uses. For the production of soybean oil, soy milk, and tofu it is widely cultivated in Bangladesh. It also provides animal feed, it is an important ingredient in animal feed,

especially for poultry and fish. Soybean is used in the production of various industrial products such as biodiesel, soy-based plastics, and cosmetics; also used in the manufacturing of soap and candles. Soybean plays a very important role in soil health improvement and use for crop ration. Moreover, Soybean cultivation and processing provide employment opportunities for farmers and workers in Bangladesh. The growing demand for soybean products also creates income-generating opportunities for small and medium-scale businesses.

The soybean is a day-length sensitive crop. If the length of the day is less than 14 hours, then the yield is good. The favorable temperature ranges from 25 to 30°C for the soybean. Approximately 15°C soil temperature stimulates rapid germination and growth. The crop is well adapted to the location with an altitude ranging from 1200 to 1800 above sea level. It requires annual average rainfall ranging from 450 to 1500 mm. A broad range of well-drained soil types is good for soybean cultivation and loamy soil is considered as ideal. It can be grown between the pH of 5.5 to 6.5.

It is an important crop plant with a complex genetic background. The soybean genome has been fully sequenced, and a number of genetic researches have been carried out to understand its genetics and breeding. One of the key genetic features of soybean is its high level of genetic diversity. This diversity is thought to have arisen through a combination of natural selection and human selection for desirable traits over thousands of years of cultivation. A number of studies have focused on identifying the specific genetic loci responsible for important characteristics in soybean, including yield, disease resistance or tolerance, and seed composition (Schmutz, 2010).

The genetic diversity of soybean is the first and foremost step to understanding the variation among the genotypes for the improvement program. Analyzing genetic diversity among genotypes helps to identify the desirable traits for further crop improvement programs (Gaur *et al.,* 1978). To know the sources of genes for finding a particular trait within the available genotypes evaluation of genetic diversity is important (Tomooka, 1991). It helps to select the parents for hybridization programs (Anderson, 1957).

Keeping in view of the above facts the present investigation is being carried out to find out the high seed-yielding genotypes of soybean from the studied genotypes with the following objectives -

- To assess the amount of genetic variability among the twenty soybean genotypes;
- To evaluate the correlation and path coefficient for yield and yield-attributing characters of twenty soybean genotypes;
- To estimate the genetic diversity among the twenty soybean genotypes; and
- To fetch out promising genotypes for the further breeding program.

CHAPTER II

REVIEW OF LITERATURE

Evaluation of quantitative and qualitative parameters of soybean are receiving much importance in the world, as soybean is a one of the most common and important crops covering a wider range of area under its cultivation in the world. Knowledge on soybean's different yield attributing traits of the different varieties or germplasms under the varied agro-ecological situations are not well informed in Bangladesh or in the elsewhere in the world, research effort on the characterization, diversity analysis of soybean and comparative studies of the soybean seems to be negligible. Thinking about the magnitude of diversity for the seed yield and its component parameters, considerable interest to the breeders for planning, selecting, and execution of genetic improvement programs; a lot of such experiments or studies had been carried out over the years. Some of their findings are presented below-

2.1 Characterization and variability of soybean genotypes

Tandekar *et al.* (2022) carried out an investigation to study the genetic variability, heritability, and genetic advance among the twenty-five soybean genotypes. Analysis of variance expressed the significant genotypic differences for all the thirteen parameters. For most of the features, the difference between the phenotypic and genotypic coefficients of variation (PCV and GCV) were low, suggesting little environmental influence on their exhibition. For the number of pods per plant and the number of seeds per plant, high heritability, and genetic advance with a high GCV were noticed for soybean and indicating that, the improvement by phenotypic selection is possible. The traits with the higher heritability and genetic advance value may indicate their variability and the high selective value. Genetic variation is crucial to the productiveness of yield the improvement efforts since it is a major element in broadening the gene pools in any particular crop population.

A study for assessing genetic variability, heritability and genetic advance among yield and yield components of eighty-two soybean genotypes was conducted by Mofokeng (2021). Five plants per genotype were considered for the measurement of yield and yield related traits. Data were analyzed through the analysis of variance and genetic traits were estimated. The results revealed highly significant genotypic differences among the genotypes based on days to flowering, hundred seed weight, branch number per plant, pod weight per plant, seed number per plant, pod length, seed number per pod and yield. Heritability of the yield and yield components were ranged from 5.9% - 100%. The heighest heritable traits were hundred seed weight (100 %), seed number per pod (67.37%), and days to flowering (64.13 %). The genotypic variance (GV) ranged from 0.3% to 33% while phenotypic variation ranged from (PV) 1.5% to 44%. The phenotypic and genotypic coefficient of variations was high for the grain yield, moderate for the days to flowering and lowest for the hundred seed weight. The phenotypic coefficient of variations was higher than genotypic coefficient of variation (GCV) for all observed characters, indicating the impact of environmental factors. The genetic advance was high for most of the parameters, moderate for seed number per pod and hundred seed weight and low for the pod number per plant. The estimated genetic advance as percent of mean was high for all characters. There was vast variation recorded among the soybean genotypes.

Dutta *et al.* (2021) used forty soybean genotypes for two consecutive years kharif 2018 and 2019 to evaluate the genetic variability, heritability (h^2) and genetic advance (GA) for yield and other yield attributing parameters. The pooled analysis of variance exhibited significant variation among the soybean genotypes for all traits studied. The interaction of the year x treatment also presented a significant difference for most of the parameters. RVSM2011-35 was observed for the highest mean performance of seed yield/plant and a high value of the oil content over the two years, indicating that the genotype was found to be promising and could be use further. The estimates of phenotypic coefficient of variation (PCV) and the genotypic coefficient of variation (GCV) indicated that the values of PCV were slightly larger than GCV. The largest values of GCV and PCV were observed for the seed yield/plant, the number of seeds/pod and oil content. Higher values of heritability coupled with high genetic advance (GA) were noticed for seed yield per plant, the number of seeds per pod, oil content, days to 50% flowering, the number of branches, plant height, the number of

pods per plant, and 100 seed weight, advising that these characters could easily be modified through simple selection.

In 2021, Shilpashree *et al.* carried a study with soybean genotypes. Genetic variability of main observed traits in vegetable soybean genotypes and their divergence was calculated; as a result of the magnitude of genotypic variation, and phenotypic variation of traits varied among the soybean genotypes. All parameters showed the high heritability associated with high genetic advance % mean (GAM). Therefore, these traits are potential for the genetic improvement soybean.

Jandong *et al.* (2020) used 20 soybean genotypes in 2015 and 2016 to estimate the genetic variability, heritability genetic advance and genetic advance (% mean) for some agronomic and yield parameters for selection criteria in a future breeding program. Analysis of variance (ANOVA) presented significant variations among the soybean genotypes indicating that the planting materials were genetically divergent from each other. The phenotypic coefficient of variation (PCV) was a bit higher than the genotypic coefficient of variation (GCV) for all the studied parameters. Portraying the impact of the environmental factors in the variations. High value of PCV and GCV were observed for the traits such as plant height, number of pods, number of leaves, and seed yield, suggesting the presence of sufficient genetic variations for simple selection in these traits. High heritability along with high genetic advance observed for the plant height and number of pods suggests that selection could be productive for these characters.

The F2 progenies and parents were planted of soybean genotypes was evaluated by Hakima *et al.* (2020). Among the traits studied, number of pods per plant, seed weight per plant, and days to maturity had the highest coefficient of variability with the means of 48.2%, 52.6%, and 41.9%, respectively. Number of branches and days to flowering had given the smallest variability of 11.7% and 15.3% respectively. Among the agronomic parameters, number of pods per plant, plant height, and seed size and days to maturity had the highest coefficient of variability associated with the high heritability and genetic advance.

In 2018, Jain *et al.* investigated 24 genotypes soybean to study the genetic variability, genotypic, phenotypic and environmental coefficient of variation, broad sense heritability and genetic advance (% mean) for observations on 9 traits. ANOVA

indicated that, significant variations were found among the different genotypes for all the traits under the study. The maximum value for genotypic (GCV) and phonotypic coefficient of variation (PCV) were found by the test weight, harvest index, number of pods per plant, and plant height (cm). The PCV was noticed higher than the GCV which indicates the important impact of environment in the expression of the parameters. High heritability in broad sense and high genetic advance were recorded in the test weight, harvest index, number of pods per plant, and plant height. The combination of the high heritability and high genetic advance provide the clear image of the character in the simple selection process for crop improvement program.

An investigation to estimate the genetic variability in 124 diverse germplasm accessions of soybean was conducted by Neelima *et al.* (2018) for 13 different characters. The values of the phenotypic coefficient of variation (PCV) were higher than the genotypic coefficient of variation (GCV) for all the parameters, indicating the influence of environmental components. The magnitude of heritability was noticed high for all the characters under the experiment indicated that the larger portion for the total variations would be under the genetic control and selection based on phenotypic levels would be useful for the improvement of these characters. High estimates of heritability in broad sense coupled with the high genetic advance expressed as percentage of mean were recorded for plant height, number of pods per plant, number of branches per plant, and seed yield per row which may be attributed to the preponderance of the additive gene action and possess high selective value and thus, simple selection pressure could profitably be applied on this character for their improvement in future.

Getnet (2018) evaluated the genetic variability, heritability and genetic advance under of forty-nine soybean genotypes. The highest value for heritability was recorded for days to 50% flowering followed by days to maturity and days to the pod setting. Wide range of mean values was recorded in all the parameters evaluated. This indicates that the characters can be improved through the selection.

Chandrawat *et al.* (2017) conducted an experiment to evaluation of genetic variability present in the forty-one soybean genotypes and five checks (two local + three national checks) and observations were recorded on various yield and yield related characters viz., days to 50% flowering, plant height, days to maturity, number of branches per plant, 100 seed weight, number of pods per plant, harvest index, and grain yield per

plant at field level and in the laboratory the oil content, protein content and trypsin inhibitor content were analyzed. ANOVA showed the significant variability for all the studied parameters. High values of GCV and PCV were noted for characters viz., plant height (23.49, 25.84), number of pods per plant (35.45, 38.62), yield per plant (21.35, 24.86), and number of branches per plant (20.58, 24.22), which indicated the presence of high genetic variation. High heritability associated with high genetic advance observed for the traits viz., plant height, pods per plant, yield per plant, trypsin inhibitor content, branches per plant, and 100 seed weight which indicated presence of additive gene action and demands for population improvement by simple selection.

For the following parameters days to 50% flowering, days to 95% maturity, days to pod setting, plant height, number of branch per plant, number of seeds per pod, number of pods per plant, pod length, Biological yield, Leaf Area Index, hundred seed weight, grain yield, and harvest index; Desissa (2017) used sixteen soybean genotypes to estimate characters Genotypic and Phenotypic Variance, Genotypic coefficient of variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability in broad and genetic advance percent of mean. All the characters showed significant variation and the coefficient of variation were relatively lower. Heritability found high for all characters studied except number of branches per plant, harvest index, leaf area index, and days to flowering whereas expected genetic advance percent of mean ranged from low (1,98%) in harvest index to high in biological yield in ton/ha. High heritability and high genetic advance percent of mean for biological yield followed by the pod length and plant height indicates the presence of the additive genes in the trait and suggested that soybean improvement through selection of the trait.

2.2 Correlation of coefficient analysis of soybean

Amogne *et al.* (2020) used eighty-one soybean genotypes to assess their association of traits using quantitative, qualitative and quality traits in Dibate substation during 2018/2019 cropping season. Based on ANOVA, days to flowering, plant height, days to maturity, number of branches per plant, protein, hundred seed weight, and oil contents and yield exhibited highly significant differences. Positive and significant combination of plant height and number of pods per plant with the grain yield were recorded. Highly significant and positive phenotypic correlation with the grain yield was noted by the number of pods per plant (0.31).

An experiment with soybean was carried by Mishra (2019). The analysis exhibited that none of correlation was found significant in the parents. In the F1 population, days to 50 per cent flowering had a positive association with the days to maturity and 100-seed weight. Plant height, number of pod caring nodes per plant, number of seeds per plant, and number of pods per plant; number of pod caring nodes per plant number of seeds per plant, number of pods per plant; number of seeds per plant versus seed yield and number of the pods per plant had the positive associations. Similarly, in the F2 population days to maturity, plant height; number of the pod bearing nodes per plant, number seeds per plant; number of seeds per plant seed yield and number of pods per plant; seed yield versus 100-seed weight and number of pods per plant had positive association.

An investigation for the phenotypic correlation of the yield component traits using several environmental stratifications formulas was carried. The parameters such as total number of the pods per plant, number of branches/plant and number of pods with 2-3 grains showed significant and linear correlations with the grain yield in both methods of analysis. The mass of a thousand grains and plant height were highly associated with grain yield but mostly influenced by environmental effects (Ferrari *et al.*, 2018).

To evaluate the phenotypic and genotypic correlations between agronomic traits, having as main character grain yield, and to identify the indirect selection criteria for grain yield, Machado *et al.* (2017) conducted a research work. There was genetic variability for all parameters at 5% probability level through the F-test. Thirty significant phenotypic correlations were also noticed with values oscillating from 0.42 to 0.87, which indicated a high level of the association between some evaluated characters. Additionally, we verified that the phenotypic and genotypic correlations were essential of the same the direction, being the genotypic ones of superior magnitudes. Plants with the superior vegetative cycle had higher life cycles; this fact could be explained by significant phenotypic correlations between the number of days to blooming and number of days to maturity (0.76). Significantly positive phenotypic and genotypic correlations for total number of pods per plant and the grain yield per plant (0.84) were observed. Therefore, the phenotypic and genotypic correlations indicated high correlations between grain yield and number of branched nodes, the number of pods with two, and three seeds, and the total number of pods.

Balla *et al.* (2017) evaluated genotypic correlation to determine the effect of various traits as components of grain yield in 21 soybean (*Glycine max* L) genotypes. The 21 soybean genotypes were evaluated. Highly significant positive genotypic correlations were found for the grain yield with days to 50% flowering, plant height, days to maturity, number of pods/ plant, and fodder yield.

Khan *et al.* (2017) evaluated forty-six pea genotypes for thirteen morphological characters. (ANOVA) test revealed significant differences for all the traits among the genotypes. Days to first flowering, branches plant/ plant, plant height, pod length, hundred seed weight, seeds plant, and seed yield plant exhibited that they were controlled by additive gene action and simple selection for the future improvement of these parameters would be productive. The phenotypic variance was noticed higher than the corresponding genotypic variance for all the characters. Hundred seed weight had presented the highest heritability (95.97). Pod length, hundred seed weight, pods/ plant and seeds per plant exhibited significant positive genotypic and phenotypic correlation with the seed yield the genotypes.

A research work with soybean genotypes to know the contribution of each yield component to the productivity. The number of pods/ plant and seeds/ plant, 100 seed weight, and seed yield/ plant were determined. The number of pods/ plant showed high and positive correlation with productivity, while for the 100 seed weight; the correlation was high but negative (Silva *et al.*, 2015).

By Mahbub *et al.* (2015), twenty-eight soybean genotypes for eleven morphological characters was evaluated. Analysis of variance presented significant differences among the soybean genotypes for all the traits. Plant height, branches per plant, seed yield per plant, number of seeds per pod, number of pods per plant, and hundred seed weight showed that they were controlled by the additive gene action and selection of these traits would be productive for the improvement. The phenotypic variance was found higher than the corresponding genotypic variance. Genotypic coefficient of variation was observed the highest for seed yield per plant (31.45%) followed by the number of branches per plant (29.9%) and the plant height (27.42%). Days to maturity (99.93%) had the highest heritability in broad sense. Plant height and number of seeds per pod, , pod length, hundred seed weight, branches per plant and number of seeds per pod exhibited significant positive genotypic and phenotypic correlation with the seed yield.

During the kharif 2010-2011, Jain *et al.* (2015) experimented with 41 soybean genotypes to study the genetic variability, correlation of yield and its component factors. It was observed that, the PCV value was higher than the GCV value for all the parameters. The heritability values were high for all the nine observed characters. Correlation and path coefficient analysis for seed yield/ plant and its elements indicated that out of the nine characters, seed yield/ plant had showed the positive and significant association with the biological yield, pods per plant, and 100-seed weight. That indicating an intense selection for these traits will improve seed yield in soybean. Again, Onemli (2003) did experiment to understand the correlations and found that number of the pods were positively correlated with the plant height, pod length (cm), number of branches, number of pods per plant, and 1000 seed weight, but was found to have negatively correlated and a significant relationship with the number of the seeds per pod, seed length (cm), and pod length in soybean strains. The number of the pods and 1000 seeds had presented a negative effect on the soybean yield via number of pods. The genotypic correlation of coefficients was found higher than the phenotypic correlation coefficients.

Chaudhury and Sharma in 2003 reported that the pod yield per plant exhibited a positive phenotypic correlation with pod length, number of pods per plant; number grains per pod, and shelling percentage.

In 2001, Tiwari *et al.* exhibited that, the seed yield of soybean has shown a significant and positive relationship with the plant height1000 seed weight, number of pods per plant, and number of grains per pod and the harvest index.

2.3 Path coefficient analysis of soybean

Amogne *et al.* (2020) used eighty-one soybean genotypes for path analysis and found positive and high direct effect at the genotypic level was recorded by the number of pods per plant (0.38) and the number of nodules per plant (0.21). The positive direct effect on the grain yield was noted by the number of pods per plant (0.48) and the negative direct effect by the number of branches (-0.28). About 0.88 and 0.901 residuals was found from the genotypic and phenotypic direct and indirect effects, respectively.

An experiment was conducted with soybean and the path coefficient analysis study in parents, F1 and F2 populations revealed the existence of positive direct effect of 100-

seed weight, number seeds per plant and number of pods per plant on seed yield. Though, 100-seed weight had substantial positive direct effect, but indirect effect for all the characters was found to be negative. A reciprocal recurrent selection should be followed in order to exploit additive and non–additive genetic improvement of yield in soybean. However, while making the selection, the criteria should be based on major yield components like, number seeds per plant, number of pods per plant and 100-seed weight (Mishra, 2019).

In 2018, Ferrari *et al.* investigated soybean to extimate the direct and indirect effects of the characters on themselves and on the gran yield. The total number of pods should be prioritized for selecting the superior soybean genotypes due to its direct and indirect effects on the grain yield. It has presented constant in all the environmental conditions. The direct effects of the number of branches and the number of pods (with one grain) presented distinct effects on the yield in favorable and unfavorable environments.

During the kharif season, Machado *et al.* (2017) conducted research to perform the path analysis, having as main character grain yield, and to identify the indirect selection criteria. Through the path analysis, the character that contributed the most over the grain yield was the number of pods with three seeds as it showed the largest direct effect on grain yield per plant, as well as the strong indirect effect on the total number of pods. The path analysis determined the number of pods with three seeds as having the highest favorable effect on the grain yield, and thus, being useful for indirect selection toward prodeffctive soybean genotypes.

Balla *et al.* (2017) evaluated path coefficient analysis of twenty-one soybean genotypes to determine the effect of various traits as components of grain yield. Path analysis exhibited that the fodder yield, plant height, and days to maturity had the highest positive and direct effect on the grain yield. Number of pods/ plant via plant height gave the highest positive but indirect effect on the grain yield. These results indicated that, fodder yield, plant height, and days to maturity can be used as selection criteria for the future improvement of soybean grain yield.

Similarly, Khan *et al.* (2017) evaluated forty-six pea genotypes for thirteen yield related characters. In path analysis, internode length, plant height, hundred seed weight,

number of seeds pod, and seeds/ plant was noted to present positive direct effect on yield.

A research work with soybean genotypes to know the direct and indirect contribution of each yield component to the productivity Through path analysis, it was found that the number of seeds/ plant was the component of a more direct effect on the grain yield, and the effect of number of pods/ plant in the productivity is based on the indirect effect of the number of seed plant (Silva *et al.*, 2015).

Mahbub *et al.* (2015) investigated twenty-eight soybean genotypes for eleven morpho-physiological characters. In path analysis, hundred seed weight, seeds per pod, pod length, days to maturity, and plant height exhibited positive direct effect on the grain yield.

Jain *et al.* (2015) carried an investigation during the kharif 2010-2011 with 41 soybean genotypes to study the path coefficient analysis of yield and its component factors. That revealed that biological yield, number of pods /plant and 100 seed weight (g) were major parameters influencing the seed yield directly and indirectly. The outcomes indicated that the biological yield was responsible for the manipulation of seed yield in soybean.

In 2007, Inderjit *et al.* exhibited in their research that, pods per plant, 100 seed weight, seeds per pod, and days to maturity had direct and positive effect on the grain yield, while the plant's height, pods per the cluster and pod length had shown negative but direct effect on the grain yield of soybean.

Harpreet *et al.* (2007) carried and experiment and the path investigate revealed that direct effects were found highest value for the number of pods per plant, node at which the first fertile pod developed, number of the seeds per pod and pod length.

2.4 Diversity analysis of soybean

Shilpashree *et al.* (2021) conducted an investigation with soybean genotype for estimating their divergence. Genetic diversity is the prime requirement for the breeding, and magnitude of genetic diversity values were maximized among specific genotypes. The genotypes were grouped in eight clusters; cluster VIII and cluster I were considered

to have the most the diversity. Cluster VIII consisted of two soybean genotypes (GM-6 and GM-27), based on the mean outcomes of high yield attributing traits. Hence, these two (GM-6, GM-27) genotypes can be advanced for the commercial cultivation.

An investigate metabolic changes between the soybean variants carried out by Jung *et al.* (2021). Multivariate analyses showed the significant metabolic differences between soybean genotypes in seeds and leaves, with seeds showing accumulation of phytosterols, tocopherols, and carotenoids (BCE only), indicating the co-induction of the methylerythritol 4-phosphate and pathways of mevalonic acid. Principal component analysis exhibited metabolic discrimination between growth stages of soybean leaves and identified differences in leaf groups according to different soybean genotypes at 8, 12, and 16 weeks, with Wild showing the higher levels of environmental stress-related elements relative to BCE and Hybrid leaves. The metabolic profiling approach could be a useful tool to identify the metabolic links in various soybean cultivars.

Forty-nine soybean genotypes were used by Getnet (2018) to evaluate the diversity among them. The result of this study indicated variations for all the traits evaluated. Divergence analysis arranged the 49 soybean genotypes into seven clusters. The principal component analysis revealed that five principal components PC1 to PC5 with Eigen values 4.27, 2.53, 1.91, 1.28 and 1.08 respectively, have accounted for 73.81% of the total variation.

Kumar *et al.* (2015) evaluated forty soybean genotypes for agro-morphological parameters and genetic parameters. ANOVA and mean performance for yield and its elements revealed highly significant differences among all the used genotypes for all the traits. Correlation was also found significant with the yield and its other component parameters. A path analysis presented that the hundred seed weight had the highest effect on yield. A Cluster diagram based on the agro-morphological traits had proposed two major clusters A and B. In the present experiment the data revealed that four principal components having greater than the one eigen values contributed 76.2 % of the total variation among the forty genotypes of soybean. The traits, which contributed more positively to the PC1 were total pods per plant (0.430), days to the maturity (0.418) and the filled pod per plant (0.411). Fertility percentage (0.577), yield per ha (0.350), and hundred seed weight (0.361) contributed more positively to PC2. The number of branches per plant (0.635) and the five pod length (0.644) contributed more

to the PC3 and PC4 respectively. MACS 1394, MAUS 612 and PS 1518 were found to be promising for mid altitudes of Meghalaya.

Singh *et al.* (2015) did molecular characterization and genetic diversity among the 82 soybean accessions by using 44 simple sequence repeat (SSR) markers. Of the 44 SSR markers used, 40 markers were found polymorphic among the 82 soybean accessions. These 40 polymorphic markers developed a total of 119 alleles, of which five were the unique alleles and four alleles were rare. The allele number for each SSR locus varied between 2-4 with an average of 2.98 alleles per marker. Polymorphic information content of SSRs ranged from 0.101 to 0.742 with an average of 0.478. Jaccard's similarity coefficient was also employed to study molecular diversity of 82 soybean accessions. The pairwise genetic similarity among the eighty-two soybean accessions varied from 0.28 to 0.91. The dendrogram illustrated based on the genetic similarities among the 82 soybean genotypes identified three major clusters. The majority of genotypes including four improved genotypes were grouped in a single subcluster IIIa of cluster III, indicating high genetic resemblance among the soybean germplasm collection in India. Again in 2014, Dong *et al.* conducted a n experiment with hundred vegetable soybeans using 53 simple sequence repeat (SSR) markers. A total of 296 alleles were found with an average of 5.61 alleles per SSR locus. The polymorphism information content (PIC) values of SSR markers ranged from 0.074 - 0.831, with the average of 0.573. Nei's genetic distance between genotypes ranged from 0 - 0.9434 with the average of 0.6286. These vegetable soybeans could be divided into 8 subgroups based on the STRUCTURE analysis, or 11 subgroups based on the unweighted pair group method with arithmetic average cluster. Further comparison showed that the UPGMA subgroups and STRUCTURE sub-groups were highly consistent. Genotypes in each classified groups exhibited great consistency with the origins of them. The molecular data and the cluster analysis also presented that germplasms from China were more diverse than those from other areas. These results gave us a deep insight into genetic structure of the vegetable soybeans in China and will help to improve the breeding strategies.

Lam *et al.* (2010) reported an analysis of the patterns of genome-wide genetic variation in the soybeans. they re-sequenced a total of 17 wild and 14 cultivated vegatables soybean genomes to an average of approximately ×5 depth and >90% coverage using

Illumina Genome Analyzer II platform. They compared the patterns of the genetic variation between the wild and cultivated soybeans and identified the higher allelic diversity in the wild soybeans. They suggested that marker-assisted breeding of soybean will be less challenging than the map-based cloning. they report linkage disequilibrium between the block location and the distribution, and they identified a set of 205, 614 tag SNPs that may be useful for the QTL mapping and association studies.

In 2014, Nooghab *et al.* studied fourteen genotypes of vegetable soybean. The genotypes had been clustered into five groups based on the morphologic traits including the seeds weight per plant (gm), the weight of 100 seeds (gm), pods length (cm), and yield (g/plant).

In 2013, Hossain *et al.* conducted an investigation using 56 genotypes of yard long bean for the 20 agro-morphogenic characters. Mahalanobis D^2 analysis had established the presence of the wide genetic diversity among the soybean genotypes through the development of nine clusters. Genotypes from different areas fell into the same cluster, indicating that the genetic diversity was not concurrent with the geographical diversity. They suggested that, genotypes of the cluster I and IX would be good to use for produce progeny which might show homeostasis over changing the environments and hybridization between the cultivars of cluster V could be used to increase the number of the pods per plant. The character, 100 seed weight (gm), contributed least (0.191%) and the contribution offered by the yield per plant was also minimum (0.512%) to total divergence.

Sihag *et al.* (2004) evaluated genetic diversity among the 160 soybean strains using the Mahalanobis D^2 statistic and had grouped the genotype into 8 clusters. The clustering exhibited that no definite relationship was existed between genetic the diversity and geographic diversity. The genotypes from same eco-geographic region were into the different clusters and genotypes from the different eco-geographic regions.

Vart *et al.* (2002) carried out an experiment to estimate the genetic diversity in 56 cultivars of soybean by using the D^2 statistic and classed them into 11 clusters. The clustering analysis was not influenced by the eco-geographical distribution of the genotypes.

In 2000, Das *et al.* analyzed the genetic divergence of 65 genotypes using the Mahalanobis D^2 statistic and 13 clusters were made by using the genotypes of soybean. Clustered soybean genotypes suggested that, no parallelism was available between the genetic divergence and the geographical distribution of the genotypes. The different cluster means revealed that the pods per plant and plant height had exhibited the maximum contribution towards the divergence.

Chowdhury *et al.* (1998) investigated 55 soybeans strains for calculating the genetic diversity among them by using the Mahalanobis D^2 technique. The genotypes were classified into different 7 clusters. The genetic divergence and the geographic distribution were not necessarily in relationship with the ten different characters, yield per plant, pods per plant, and effective nodes per the plant had contributed maximum on total divergence. The highest value for the inter-cluster distance observed between the clusters, that indicates highly divergent types existed in these classifications.

CHAPTER III

MATERIALS AND METHODS

The present experimental work with twenty soybean genotypes was carried out in the experimental location of the Sher-e-Bangla Agricultural University, Dhaka – 1207 during the period from February 2022 to May 2022. The study was entitled "Genetic Diversity Analysis of Soybean". The explicit information related to the materials and methods of this experimental work is discussed below:

3.1 Experimental location

The experimental field was at 90° 21" E longitude and 23° 42" N latitude at an altitude of 8.7 meters from sea level (www.distancesfrom.com).

3.2 Soil characteristics

The soil characteristics of the experimental site is a medium-high land; it has been grouped in the Modhupur Tract of the Agro-Ecological Zone (AEZ) 28 (www.banglapedia.com). The Madhupur Clay has developed an area with complex relief and soils. There are eleven distinguished types of soils in the region, with deep red-brown terraces, shallow red-brown terraces, and acid basin clays being the most common. Dark grey and thick clays make up the soil. They are highly acidic in nature, with a limited amount of moisture retention capacity, and level low fertility (Banglapedia). More details of the soil with chemical components are given in the appendix II.

3.3 Climate

During the experiment, there was a little amount of rain and the humidity percentage and temperature were moderate to high. Details of the meteorological information regarding the climate during that period was exhibited in appendix III.

3.4 Planting materials

The experimental materials used in this present study were collected from the BARI (Bangladesh Agriculture Research Institute). The name of the soybean genotypes along with the source are showed in Table 1.

Table 1. Name of selected twenty soybean genotypes used in the experiment with their source.

Sl. No.	Genotypes	Acc. No.	Source
1.	**G1**	BD-2324	BARI
2.	**G2**	BD-2325	BARI
3.	**G3**	BD-2326	BARI
4.	**G4**	BD-2327	BARI
5.	**G5**	BD-2329	BARI
6.	**G6**	BD-2330	BARI
7.	**G7**	BD-2331	BARI
8.	**G8**	BD-2332	BARI
9.	**G9**	BD-2333	BARI
10.	**G10**	BD-2334	BARI
11.	**G11**	BD-2335	BARI
12.	**G12**	BD-2336	BARI
13.	**G13**	BD-2337	BARI
14.	**G14**	BD-2338	BARI
15.	**G15**	BD-2339	BARI
16.	**G16**	BD-2341	BARI
17.	**G17**	BD-2342	BARI
18.	**G18**	BD-2345	BARI
19.	**G19**	BD-2350	BARI
20.	**G20**	BD-2353	BARI

3.5 Layout and design of the experiment

Randomize Complete Block Design (RCBD) was used to layout the experiment had 3 different replications. The total area under experiment was 200 m^2 and the spacing between rows were maintained 60 cm. Land preparation and showing of seeds are shown in plate 1A and plate 1B.

3.6 Manure and fertilizers application

Before sowing the soil was well pulverized with the help of farm division and dried in the sun for two days. Recommended amount of well-decomposed cow dung was mixed properly all throughout the plot with the soil (Handbook of Agricultural Technology. According to the fertilizer recommendation guide of the BADC (Bangladesh Agricultural Development Corporation), 2012 Fertilizer was applied on the field.

Table 2. Doses of manure and fertilizers

Sl. No.	Manure and fertilizer	Required amount
1	Cow dung	250 kg/h
2	Urea	50-60 kg/h
3	TSP	150-175 kg/h
4	MOP	100-120 kg/h
5	Gypsum	80-115 kg/h

3.7 Intercultural operations

After sowing the seedlings, to protect them from several damages, different intercultural practices were conducted for better growth. Required amount of water is given to the plant. Two times irrigation in every week is maintain to keep the soil moisture level good for the plant. To keep the area free from unwanted plants and allow the all nutrient and water for soybean plants only, regular weeding was conducted. After a week, filled is checked clearly and observed gap was filled with new soybean plant. Insecticides and pesticides were applied when necessary. They were treated to prevent unwanted diseases with Bavistin DF and Cupravit 50 WP. To control the Aphid and leaf miner Malathion 250 EC @ 0.5ml/l was used. Required amount of fungicide and pesticide were sprayed two times, first at the vegetative growth stage and next to the

early flowering time to protect them. Pesticide application and intercultural operation in the field are illustrated in plate 1C.

3.8 Harvesting

After the maturity stage, when the pod turns into golden yellow or straw colored to dark brown in color, harvesting of pods were conducted. Different varieties of soybean were harvested at different dates as they have varied maturity time periods.

3.9 Data recording

The data for the experiment were collected on three selected soybean plants of each genotype from each replication on the following traits. The data collection and recording are demonstrated in plate 1 (E-F).

3.9.1 Days to first flowering

When the first flower initiated on the soybean plant, that data was counted as days from the seed sowing date. Then average data from tree plant was used as days to first flowering.

3.9.2 Days to maturity

When the pods were matured, days from the seed sowing was counted to estimate to days to maturity.

3.9.3 Plant height (cm)

After harvesting the height of the plant was collected with the help of a centimeter scale.

3.9.4 No. of branches per plant

Branches of each plant is counted and average data was recorded per genotype.

3.9.5 Pod length (cm)

Pod was measured with the help of a centimeter scale and average data was collected.

3.9.6 No. of pods per plant

Number of pods per plant is counted and average data was collected for each genotype.

3.9.7 No. of seeds per pod

Seeds of each pod is counted and average data was recorded.

Plate 1. Different activities on the experimental field (A: preparation of land, B: sowing the seeds, C: Pesticides application, D: Intercultural operation, E: Inspection of field with supervisor during data collection, and F: Recording the data)

3.9.8 Hundred seeds weight (g)

Hundred seeds of a single plant is counted and then weight of that seeds were taken with the help of a weight machine. Then average of three plants per genotypes were collected.

3.9.9 Dry stover yield (g/plant)

Stover was collected and then weighted on the weight machine.

3.9.10 Dry seed yield (g/plant)

Seeds were dried under the sun. After that, they were weighted and average data was recorded.

3.10 Statistical analysis

Collected data of different parameter were statistically analyzed using STATICTIX-10 computer software program to get the significance among the soybean genotypes. To test the differences between the means of genotypes, Duncan's Multiple Range Test at 5% and 1% level of significance was conducted for all the parameters (Gomez and Gomez, 1984). Correlation of coefficient, path analysis and genetic diversity were determined with the help of R studio computer program.

3.10.1 Analysis of the Variance

The analysis of variance for several traits was carried out utilizing the collected data to compute the genetic variability among soybean strains as procedure given by the Cochran and Cox (1957). The level of the significance was tested at 5% and 1% by using the F test (probability). The model of ANOVA used is presented below:

Source of variation	df	MSS
Replication (r)	r-1	M1
Genotypes (g)	g-1	M2
Error (e)	(r-1) (g-1)	M3

Here,

r = Number of replications;

g = Number of genotypes;

df = degree of freedom;

To test significance of the differences between any of the two-adjusted genotypic mean, the standard error of the mean was evaluated by using the formula:

$$S.E = \sqrt{\frac{2Me}{r}} \left(1 + \frac{rqu}{q+1}\right)$$

Here,

S. E = Standard error of mean;

Me = Mean sum of the square for error (Intra block);

r = Number of the replications;

q = Number of populations in each sub-block; and

u = Weightage factor computed.

3.10.2 Study of Variability parameters

Estimation of the variability among the soybean stains for traits related to the dry seed yield per plant were narrated below:

3.10.2.1 Estimation of Genotypic and Phenotypic Variances

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

a. Genotypical variance, $\sigma_g^2 = \frac{MSG - MSE}{r}$

Here,

MSG = Mean sum of square for the genotypes;

MSE = Mean sum of square for the error; and

r = Replication numer.

b. Phenotypical variance, $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$

Here,

σ_e^2 = Environmental variance = Mean square of error (MSE).

3.10.2.2 Estimation of genotypic and phenotypic coefficient of variation

The following process was established by Burton (1952) to evaluate the genotypic coefficient of variation (GCV) and phenotypical coefficient of variation (PCV) for all the characters.

$$GCV = \frac{\sigma_g \times 100}{\bar{x}}$$

Here,

GCV = Genotypic coefficient of the variation;

σ_g = Genotypic standard deviation; and

$\bar{x}$ = Population means.

$$PCV = \frac{\sigma_p \times 100}{\bar{x}}$$

Here,

PCV = Phenotypic coefficient of the variation;

σ_p = Phenotypic standard deviation; and

$\bar{x}$ = Population means.

Phenotypical coefficients of variation (PCV) and genotypical coefficients of variation (GCV) were categorized into 3 categories by Sivasubramanian and Madhavamenon (1973).

    High = Which is greater than 20%

    Moderate = From 10 to 20%; and

    Low = From 0 to 10%.

3.10.2.3 Estimation of heritability in broad sense

To get the broad sense of heritability, a formula used which was given by Singh and Chaudhary (1985), which is presented below:

$$h_b^2(\%) = \frac{\delta_g^2}{\delta_p^2} \times 100$$

Here,

h_b^2=Heritability in the broad sense;

σ_g^2= Genotypic variance; and

σ_p^2= Phenotypic variance.

Categories for heritability were suggested by Robinson *et al.* (1966). They are:

Low = 0-30%;

Moderate = 30-60%; and

High = > 60%.

3.10.2.4 Estimation of genetic advance

To calculate the genetic advance for the different parameters under selection a process was suggested by Allard (1960), which is -

$$GA = \frac{\sigma_g^2}{\sigma_p^2} . K . \sigma_p$$

Here,

GA = Genetic advance;

σ_g^2 = Genotypic variance;

σ_p^2 = Phenotypic variance;

σ_p = Standard phenotypic deviation; and

K= Standard selection differential which is at 2.06 at 5% selection intensity.

Johnson *et al.* (1955) suggested group for genetic advance. They are:

(<10%) = Low;

(10-20%) = Moderate; and

(>20%) = High.

3.10.2.5 Estimation of genetic advance in percentage of mean

To calculate the genetic advance in percentage of mean was done by following the formula, which was given by Comstock and Robinson (1952).

$$\text{GA in percent of mean} = \frac{\text{GA}}{\text{Grand mean}} \times 100$$

Johnson *et al.* (1955) suggested categories for genetic advance in percent of mean. They are:

Low = (<10%);

Moderate = (10-20%); and

High = (> 20%).

3.10.3 Correlation coefficient analysis

The correlation coefficient of the twenty genotypes of soybean was calculated to understand the relationship of characters with the yield and among the yield attributing studied traits. Both genotypic and phenotypic correlation coefficients were computed by using the variance and covariance products, using the formula which was suggested by Al-Jibouri *et al.* (1958).

- $r_{gxy} = \dfrac{Cov_{gxy}}{\sqrt{\sigma^2_{gx}} \cdot \sqrt{\sigma^2_{gy}}}$

Here,

$r_g(xy)$= The genotypic correlation the coefficients of x;

Cov_{gxy}= The genotypic covariance of x;

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

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

- $r_{pxy} = \dfrac{Cov_{pxy}}{\sqrt{\sigma^2_{px}} \cdot \sqrt{\sigma^2_{py}}}$

Here,

$r_p(xy)$= The phenotypic correlation the coefficients y;

Cov_{pxy} = The phenotypic the covariance of y;

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

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

The obtained value of the 'r' was compared with the tabulated 'r' value with n-2 degrees of freedom at the 5% and 1% level of significance, where, n is representing the number of the pairs of observations. Thus, the data gained from the various experimental objectives were subjected to the pertinent statistical analysis to draw the relevant inference towards genetic divergence of soybean populations.

3.10.4 Path coefficient analysis

Dewey and Lu (1959) had given a formula to estimate the path analysis. Similar procedure was suggested by the Singh and Chaudhary (1985). Path coefficient analysis was obtained by utilizing simple correlation values. In path analysis, the correlation coefficient is segregate into the direct and indirect independent variables on the dependent variable.

$$r_{yx1} = P_{yx1} + P_{yx2}r_{x1x2} + P_{yx3}r_{x1x3} + \ldots\ldots\ldots\ldots + P_{yx11}.r_{x1x11}$$

$$r_{yx2} = P_{yx1}r_{x1x2} + P_{yx2} + P_{yx3}r_{x2x3} + \ldots\ldots\ldots\ldots + P_{yx11}.r_{x2x11}$$

$$r_{yx3} = P_{yx1}r_{x1x3} + P_{yx2}r_{x2x3} + P_{yx3} + \ldots\ldots\ldots\ldots + P_{yx11}.r_{x3x11}$$

To estimated values of the direct and indirect effect of the correlated characters, say x1, x2 and x3 yield y, a set of simultaneous equations is needed to be formulated as presented below:

Here,

   r= simple correlation coefficient; and

   P= path coefficient (unknown).

P's in the above equations may be conveniently decoded, arranging them in matrix form. Total correlation, say between x1 and y is thus partitioned as illustrate bellow:

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

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

$P_{yx3}r_{x1x3}$ = the indirect effect of the x1 via x3 on y.

After estimating the direct and indirect effect of the characters, the residual effect (R) was computed by using the formula presented below (Singh and Chaudhary, 1985):

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

Here,

$P_{RY}^2 = (R^2)$;

Hence, residual effect, $R = (P_{RY}^2)^{1/2}$;

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

r_{iy}=Correlation of the character with yield;

3.10.5 Analysis of diversity

Among the strains of soybean genetic diversity was assessed by the procedure of the Mahalanobis's (1936) distance (D^2) general statistic and its auxiliary analyses. Clustering was conducted by using the non-hierarchical classification. The quantification of genetic diversity through the biometrical procedures had made it possible to choose the genetically diverse parents for the future hybridization program (Rao, 1952). There are several analyses, which are as follows:

3.10.5.1 Principal Component Analysis (PCA)

Principal Component analysis is one of multivariate techniques which is used to access the inter-relationships among several parameters and it could be obtain from the sum of squares and the products matrix for the parameters. Thus, PCA find out the linear combinations that maximize the variations contained within them, thereby exhibiting most of the important variability in a smaller number of the dimensions. Therefore, Principles components were evaluated from correlation matrix and genotypes scores obtained for first products and flourishing components with the latent roots greater than unity (Jeger *et al.*, 1983). Different morphological parameters, attribution towards the divergence is discussed from the latent vectors of first two principal components.

3.10.5.2 Principal Coordinate Analysis (PCO)

Principal Coordinates Analysis is a process to explore the similarities or dissimilarities of data. It starts with a similarity of matrix or dissimilarity of matrix (= distance matrix) and assigns for the each item a location in a low-dimensional space. By using PCO we can visualize individual differences.

3.10.5.3 Canonical Vector Analysis (CVA)

Canonical vector analysis is use to observe the linear combination of the original variabilities that maximize ratio of between the groups to within group variations. It's also giving the functions of the main variables that will help to discriminate between the groups. Consequently, in this analysis a series of ortho-gonal transformations sequentially happens, maximizing the ratio of among the groups to the within group variations. The canonical vector is based upon roots and vectors of the WB, where W is pooled within the groups covariance matrix and B is among groups covariance matrix.

3.10.5.4 Cluster Analysis (CA)

The used genotypes are divided into some number of exclusive groups by cluster analysis. Clustering was obtaned by using non-hierarchical classification.

3.10.5.5 Calculation of D^2 values

The Mahalanobis's distance (D^2) values were computed from the transformed uncorrelated means of studied parameters according to Rao (1952). The D^2 values were evaluated for all the possible combinations between all studied genotypes. In simpler form D^2 statistic is defined by the following formula-

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

Here,

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

X = Number of characters

3.10.5.6 Calculation of average intra-cluster distances

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

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

Here,

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

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

3.10.5.7 Calculation of average inter-cluster distances

Average inter-cluster distances were computed by the following process, which was reported by Singh and Chaudhury (1985).

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

Here,

$\sum D_{ij}{}^{2}$ = the sum of the distances between all possible combinations of the strains in cluster i and j;

n_i = Number of the populations in cluster I; and

n_j = Number of the populations in cluster j.

3.10.5.8 Cluster diagram

Using the values of the intra and inter-cluster distances, a scatter or cluster diagram was drawn, that was also suggested by Singh and Chaudhury (1985). It gives a brief idea of pattern of diversity among the strains included in a cluster.

CHAPTER IV

RESULTS AND DISCUSSION

The study was carried out at the research field of Sher-e-Bangla Agricultural University, during 2021-2022. Plant breeding depends on genetic variation. Information related to the degree of diversity and nature is the prerequisite for making a breeding program effective. Genotypic variation is related to phenology, morphology, and yield, so knowledge related to them will help to screen desirable genotypes for the hybridization programs. this chapter includes the result and their interactions on the basis of -

Estimation of genetic variability, heritability and genetic advance,

Analysis of correlation of coefficient,

Path analysis, and

Diversity analysis.

4.1 Estimation of genetic variability, heritability and genetic advance

Analysis of variance presented that; significant differences were found for all the characters which indicated the presence of variation among the genotypes for all the characters (Table 3). In Table 4 maximum value, minimum value, mean, and standard error of ten parameters of soybean genotypes namely, days to first flowering, days to maturity, plant height (cm), no. of branches per plant, Pod length (cm), no. of Pods per plant, no. of Seeds per pod, hundred seed weight(g), dry stover yield (g/plant), and dry seed yield (g/plant) have been shown. Genotypic variance (GV), Environmental variance (EV), Phenotypic variance (PV), Genotypic coefficient variation (GCV), Environmental coefficient variation (ECV), Phenotypic coefficient variation (PCV), heritability, genetic advance (GA), and genetic advance as % mean of the observed parameters of soybean genotype have been exhibited in Table 5.

4.1.1 Days to first flowering

The shortest duration for first flowering was noticed in G2 (29.56), followed by G10 (31.92) and G7 (34.15). While, the longest period for first flowering in soybean was observed in G1 (46.55), followed by G11 (43.18) and G13 (42.62) in Table 4.

Table 3. Analysis of variance for ten characters of twenty soybean genotypes

Source of variations	df	Mean Sum of Square									
		DFF	DM	PH	NBPP	PL	NPPP	NSPP	HSW	DSY	DrSY
Replication	2	6.66	11.16	0.81	0.10	0.01	24.32	0.11	4.04	0.82	32.79
Genotype	19	12.70**	4.94*	73.73**	1.71**	0.35**	556.90**	2.01**	6.57**	38.69**	137.88**
Error	38	1.32	2.55	1.30	0.05	0.004	4.20	0.02	0.73	3.13	14.05
CV (%)		3.24	2.54	1.72	3.05	1.78	2.53	4.81	5.29	4.40	2.96

Here,

*= Significant at 5 % level of probability, **= Significant at 1 % level of probability, df = Degree of freedom

DFF= Days to first flowering,
DM= Days to maturity,
PH= Plant height (cm),
NBPP= No. of branches per plant,

PL= Pod length (cm),
NPPP= No. of pods per plant,
NSPP= No. of seeds per pod,

HSW= Hundred seed weight(g),
DSY= Dry stover yield (g/plant), and
DrSY= Dry seed yield (g/plant).

Table 4. Mean performance of ten characters of twenty genotypes of soybean

Genotypes	DFF	DM	PH	NBP	PL	NPPP	NSPP	HSW	DSY	DrSY
G1	46.55a	73.48ab	59.13hi	5.17ij	2.49hi	62.94lm	3.12a-e	11.68e	13.30e	17.50f
G2	29.56f	63.25c-f	72.42ab	6.80d-g	3.66b-d	96.12c	2.70b-h	16.30bc	19.90a-d	32.70a-c
G3	35.49d	63.5cd	73.89a	7.77a-d	3.62b-e	128.64a	3.13a-e	21.92a	20.93ab	33.87ab
G4	34.9cd	60.4f	72.57ab	8.23ab	3.68b-d	78.56fg	3.60a	17.39b	20.47a-c	31.16a-c
G5	37.25c	62.45c-f	67.22de	6.30e-i	3.16e-g	75.77gh	2.57c-h	13.82c-e	20.37a-c	35.80a
G6	36.17cd	60.47ef	65.89ef	6.57e-g	3.38c-f	96.01c	3.10a-f	16.09bc	20.53a-c	32.70a-c
G7	34.15de	62.94c-f	66.22ef	6.37e-h	4.28a	72.34hi	2.23g-i	14.00c-e	19.37a-d	36.60a
G8	36.33cd	63.35c-e	67.65de	7.20b-f	3.32d-f	99.8bc	2.97a-g	16.29bc	19.20b-d	31.26a-c
G9	35.93cd	64.32cd	71.33bc	7.33a-e	3.10fg	67.42jk	2.40d-i	15.44b-d	17.87cd	30.77a-d
G10	31.92ef	63.85cd	71.21bc	7.90a-d	3.87ab	101.18b	3.47ab	16.13bc	18.27b-d	32.65a-c
G11	43.18b	71.62b	57.36i	4.70j	2.72gh	65.27kl	1.73ij	12.05e	11.40ef	15.20f
G12	35.55cd	63.51cd	61.57g	6.47e-g	3.74b-d	84.3de	3.10a-f	15.40b-d	17.83cd	31.90a-c
G13	42.62b	75.8a	58.64i	5.23h-j	3.07fg	56.56n	1.20j	12.50e	10.00f	19.30ef
G14	41.03b	73.39ab	51.4j	8.07a-c	2.18i	59.4mn	1.75ij	11.45e	10.50ef	16.50f
G15	36.44cd	64.18cd	69.42cd	8.40a	3.41b-f	70.1ij	2.77b-h	14.38bb-e	18.40b-d	29.50a-d
G16	34.84cd	63.64cd	66.85e	7.03c-f	3.70b-d	80.57ef	3.23a-c	16.05bc	22.17a	32.09a-c
G17	35.01cd	64.86c	58.66i	6.43e-g	3.36c-f	72.35hi	2.30f-i	13.14c-e	19.90a-d	27.10cd
G18	34.66cde	61.81d-f	57.4i	6.53e-g	3.33d-f	87.47d	3.20a-d	15.86bc	20.06a-d	31.03a-c
G19	34.58cde	61.89d-f	64.26f	5.83g-j	3.51b-f	69.34ijk	2.36e-i	14.46b-e	18.53b-d	24.60de
G20	36.3cd	64.05cd	61.53gh	6.13f-i	3.83a-c	72.27hi	2.06hi	12.13e	17.35d	19.50ef
Mean	36.63	65.138	64.731	6.723	3.3705	79.8205	2.6495	14.824	17.82	28.09
Min	29.56	60.4	51.4	4.7	2.18	56.56	1.2	11.45	10.00	15.20
Max	46.55	75.8	73.89	8.4	4.28	128.64	3.6	21.92	22.17	36.60
SE	0.66	0.92	0.66	0.12	0.04	1.18	0.07	0.49	1.44	3.06

Here,

DFF= Days to first flowering,
DM= Days to maturity,
PH= Plant height (cm),
NBPP= No. of branches per plant,

PL= Pod length (cm),
NPPP= No. of pods per plant,
NSPP= No. of seeds per pod,

HSW= Hundred seed weight(g),
DSY= Dry stover yield (g/plant), and
DrSY= Dry seed yield (g/plant).

Table 5. Estimation of genetic parameters of ten characters of twenty soybean genotypes

	EV	GV	PV	ECV	GCV	PCV	h^2_b	GA	GA %
DFF	1.32	3.79	5.11	3.24	5.49	6.37	74.21	3.46	9.74
DM	2.55	0.79	3.35	2.54	1.42	2.91	23.74	0.90	1.42
PH	1.30	24.14	25.44	1.72	7.43	7.63	94.89	9.86	14.91
NBPP	0.05	0.56	0.60	3.05	10.59	11.02	92.33	1.47	20.97
PL	0.004	0.12	0.124	1.78	9.27	9.44	96.42	0.69	18.76
NPPP	4.20	184.23	188.43	2.53	16.74	16.93	97.77	27.65	34.10
NSPP	0.02	0.66	0.68	4.82	30.34	30.72	97.54	1.66	61.73
HSW	0.73	1.95	2.68	5.29	8.63	10.12	72.69	2.45	15.15
DSY	3.13	11.86	14.98	9.92	19.33	21.72	79.13	6.31	35.41
DrSY	14.05	41.28	55.33	13.35	22.87	26.48	74.61	11.43	40.70

Here,

PV= Phenotypic variance;
GV= Genotypic variance;
EV= Environmental variance

PCV= Phenotypic coefficient variation;
GCV= Genotypic coefficient variation;
ECV= Environmental coefficient variation;

h^2_b= Heritability;
GA= Genetic advance; and
GA (%)= Genetic advance as % of mean.

DFF= Days to first flowering,
DM= Days to maturity,
PH= Plant height (cm),
NBPP= No. of branches per plant,

PL= Pod length (cm),
NPPP= No. of pods per plant,
NSPP= No. of seeds per pod,

HSW= Hundred seed weight(g),
DSY= Dry stover yield (g/plant), and
DrSY= Dry seed yield (g/plant).

The phenotypic variance (5.11) was higher than the genotypic variance (3.79) and the difference between them was smaller, suggesting the influence of environment was minimum for the appearance of this parameter. Both the genotypic coefficient variation (5.49) and Phenotypic coefficient variation (6.37), were low. The estimated heritability in broad sense was high (74.21) with low genetic advance (3.46) and high genetic advance (9.74) in % of mean, suggesting presence of additive gene action for expressing this trait and simple selection based on this parameter will be effective (Table 5).

4.1.2 Days to maturity

In table 4, It was observed that minimum days to maturity was taken by G4 (60.40), followed by G6 (60.47) and G18 (61.81). On the other hand, maximum period of days was consumed by G13 (75.8), followed by G14 (73.39) and G11 (71.62).

The phenotypic variance, genotypic variance, environmental coefficient variation, genotypic coefficient variation, and Phenotypic coefficient variation were observed 3.35, 0.79, 2.54, 1.42, and 2.91 respectively. The phenotypic variance was slightly higher than the genotypic variance. Similarly, Phenotypic coefficient variation was a bit higher than the genotypic coefficient variation, that indicating the effect of environment for expressing the trait. Low heritability (23.74) combined with low genetic advance (% mean) (1.42) was observed, suggesting the presence of non-additive gene action and simple selection based on this trait is not possible (Table 5). Similar results were reported by Dutta *et al.* in 2021.

4.1.3 Plant height (cm)

The longest plant was observed in G3 (73.89), followed by G4 (72.57) and G2 (72.42); while shortest soybean plant was noticed in G14 (51.4), followed by G11 (57.36) and G18 (57.4) in Table 4.

The genotypic variance (24.14) was slightly lower than the phenotypic variance (25.44). Moreover, the Phenotypic coefficient variation (7.63) was recorded slightly higher than the genotypic coefficient variation (7.43). These indicating the environmental effect on the expression of this character. High heritability (94.89) associated with low genetic advance (9.86) and low genetic advance % of mean (14.91) was recorded in table 5. In 2021, Shilpashree *et al.* also exhibited same types of outcomes.

4.1.4 No. of branches per plant

Highest no. of branches was recorded in G15 (8.4), followed by G4 (8.23) and G14 (8.07)**,** whereas, the lowest no. of branches was noticed in G11 (4.7), followed by G1 (5.17) and G13 (5.23) in Table 4.

 The genotypic variance (0.56), phenotypic variance (0.60), Phenotypic coefficient variation (11.02), and genotypic coefficient variation (10.59) was observed in Table 5. The genotypic coefficient of variance was noted slightly lower than the phenotypic coefficient of variance, which means the environment has an effect on the exhibition of the trait. A high genetic advance in percent of the mean (20.97) associated with high heritability (92.33) was observed, indicating the additive gene action and allowing simple selection.

4.1.5 Pod length (cm)

G7 (4.28), followed by G10 (3.87) and G20 (3.83) exhibited the longest length of pod; on the other hand, G14 (2.18), followed by G1 (2.49) and G11 (2.72) was found to produce the smallest length of the pod in Table 4 (Plate 2).

In table 5, the genotypic variance, phenotypic variance, Phenotypic coefficient variation, and genotypic coefficient variation were found 0.12, 0.124, 9.44, and 9.27 respectively. The phenotypic variance was slightly higher than the genotypic variance. High heritability (96.42) coupled with the moderate genetic advance in % of the mean (18.76) for pod length was observed in Table 5.

4.1.6 No. of pods per plant

Maximum number of pods were noted in G3 (128.64), followed by G10 (101.18) and G8 (99.8); whereas G13 (56.56), followed by G14 (59.4) and G1 (62.94) was found to produce minimum no. of pods (Table 4).

The genotypic variance (184.23), phenotypic variance (188.43), Phenotypic coefficient variation (16.93), and the genotypic coefficient variation (16.74) were observed for soyabean genotypes. The phenotypic variance was slightly larger than the genotypic variance, indicating influence of the environment on this parameter. High genetic

Plate 2. Pods of twenty soybean genotypes

advance in percent of mean (34.10) was found coupled with high heritability (97.77), suggesting action of additive gene. So, simple selection is possible based on this parameter (Table 5). Shilpashree *et al.* found similar outcome in 2021.

4.1.7 No. of Seeds per pod

Lowest number of seed were noticed in G13 (1.2), followed by G11 (1.73) and G14 (1.75). On the other hand, highest number of seed was found in G4 (3.60), followed by G10 (3.47) and G16 (3.23) in Table 5.

The genotypic variance (0.66) was noticed little smaller than the phenotypic variance (0.68). The Phenotypic coefficient variation (30.72) was slightly higher than the genotypic coefficient variation (30.34), indicating the effect of nature. Both heritability (97.54) and genetic advance in percent mean (61.73) were found high, indicating additive gene action and express the possibility of simple selection (Table 5). In 2020, similar result reported by Hakima *et al.*

4.1.8 Hundred seed weight (g)

Highest weight of hundred seed per plant was found in G3 (21.92), followed by G4 (17.39) and G8 (16.29). On the contrary, lowest weight of hundred seed was observed in G14 (11.45), followed by G1 (11.68) and G11 (12.05) in Table 4.

genotypic variance, phenotypic variance, genotypic coefficient variation, and Phenotypic coefficient variation was recorded 1.95, 2.68, 8.63, and 10.12 respectively. Here, the genotypic variance is slightly smaller than the phenotypic variance, which means the environment have influence on the exhibition of the character. High heritability (72.69) associated with moderate genetic advance in % of mean (15.15) in Table 5. Similar result was found in several previous investigation (Mofokeng, 2021; Hakima *et al.*, 2020; and Jain *et al.*, 2018).

4.1.9 Dry stover yield (g/p)

Maximum dry stover yield was noted in G16 (22.17), followed by G3 (20.93), G4 (20.47), and G6 (20.53); while the minimum yield of dry stover was found in G13 (10.00), followed by G14 (10.50) and G11 (11.4) in Table 4.
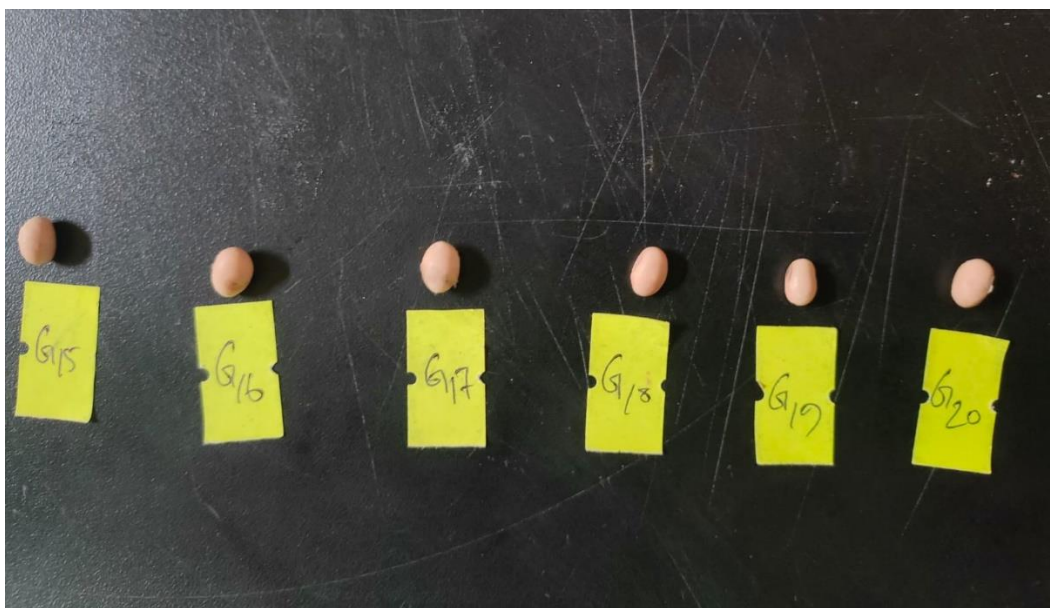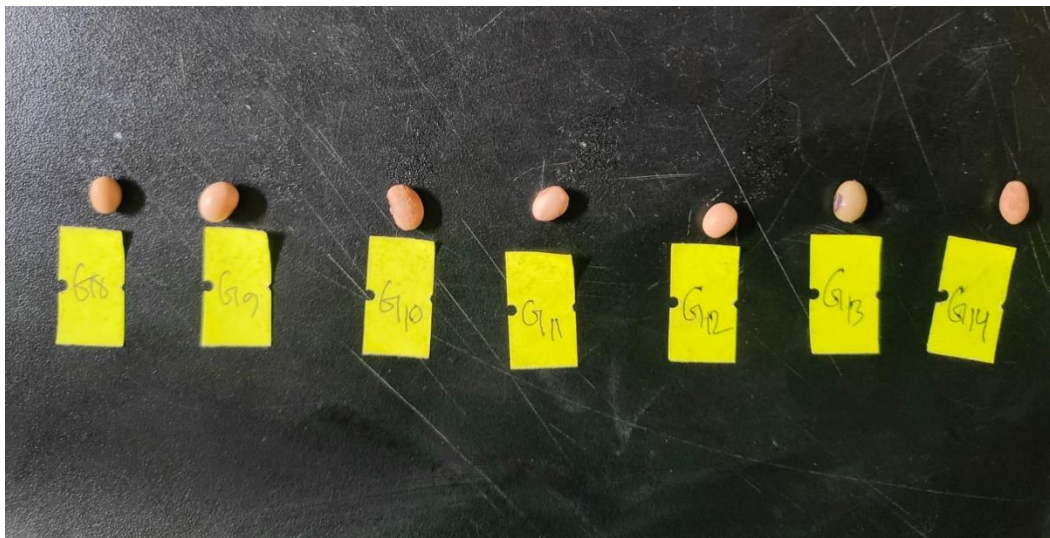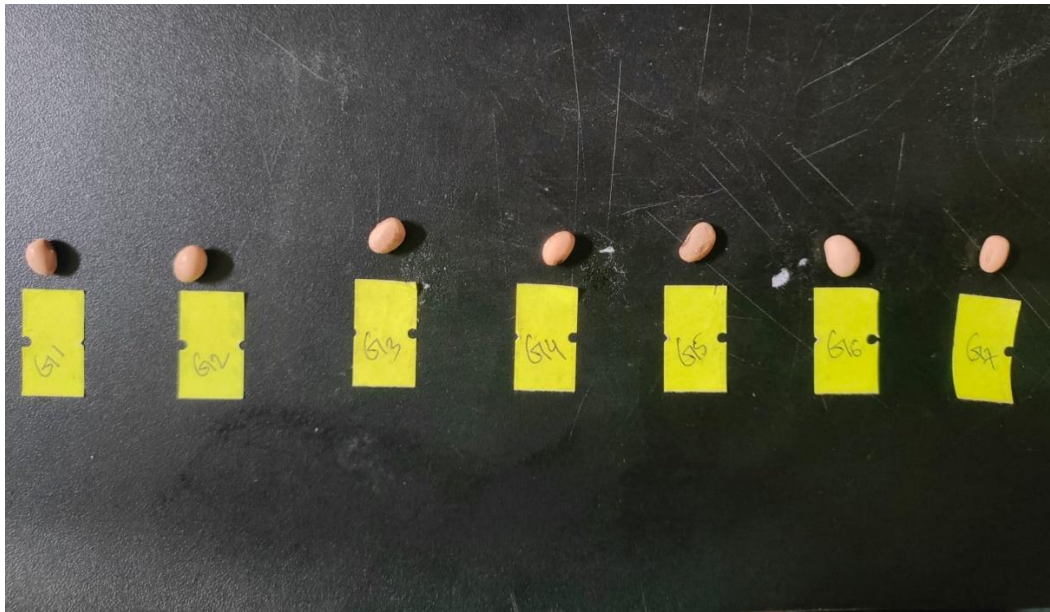
Plate 3. Seed of twenty soybean genotypes

Genotypic variance (11.86) was recorder smaller than the phenotypic variance (14.98). the Phenotypic coefficient variation and the genotypic coefficient variation was found 21.72 and 19.33 respectively. They indicating the influence of the environment for relating this character. High heritability (79.13), low genetic advance (6.31) and high genetic advance in percent of mean (35.41) were observed in Table 5.

4.1.10 Dry seed yield (g/plant)

Highest dry seed yield of soybean was recorded in G7 (36.60), followed by G5 (35.8) and G3 (33.87). On the other hand, lowest yield of dry seed was noted in G11 (15.20), followed by G14 (16.50) and G1 (17.50) (Table 4).

The phenotypic variance, genotypic variance, Phenotypic coefficient variation, and genotypic coefficient variation were observed 55.33, 41.28, 26.48, and 22.87, respectively. The phenotypic variance was moderately higher than the genotypic variance, indicating environment impact on the trait expression. High heritability (74.61) along with high genetic advance in percent of mean (40.70) was noted suggesting the presence of additive gene action. So that, simple selection can be possible based on this character (Table 5). Similar result was found by Getnet in 2018 and Jandong *et al.* in 2020.

4.2 Analysis of correlation of coefficient

Evaluation of correlation coefficient provides the detail information how yield of crops depends on different yield attributing traits. Yield of the crops is a very complex product and being influenced by the several inter-dependable quantitative and qualitative characters. Thus, selection for the plant yield may not be productive, unless the other yield related parameters are directly or indirectly taken into the consideration. When the selection is practiced for the improvement of characters highly associated with plant yield, a bunch of other correlated traits are impacted simultaneously. Hence, information regarding to the association of characters with the yield and other yield contributing parameters, provided knowledge to a plant breeder for making advancement through the selection provide a clear information about the contribution in respect of the association by genetic and non-genetic products. The correlation of the co-efficient (genotypic and phenotypic) and the parameter correlated with the plant yield were exhibited in Table 6.

Table 6. Genotypic (G) and phenotypic (P) correlation coefficients among different pairs of yield and yield attributing characters in twenty soybean genotypes

Characters		DM	PH	NBP	PL	NPPP	NSPP	HSW	DSY	DrSY
DFF	G	-0.029	-0.309	0.127	-0.242	-0.136	-0.114	-0.199	-0.88**	-0.84**
	P	-0.017	-0.273*	0.095	-0.199	-0.155	-0.092	-0.096	-0.63**	-0.64**
DM	G		0.122	0.076	-0.095	0.213	0.357	-0.139	-0.98**	-0.86**
	P		0.017	0.050	-0.075	0.090	0.129	-0.049	-0.84**	-0.72**
PH	G			0.628**	-0.212	0.528*	0.372	0.569**	0.70**	0.76**
	P			0.566**	-0.199	0.517**	0.360**	0.442**	0.61**	0.67**
NBP	G				-0.075	0.399	0.445*	0.304	0.55*	0.51*
	P				-0.086	0.393**	0.417**	0.269*	0.23	0.42**
PL	G					-0.051	-0.319	-0.067	0.78**	0.70**
	P					-0.057	-0.309*	-0.028	0.59**	0.66**
NPPP	G						0.196	0.877**	0.64**	0.67**
	P						0.190	0.718**	0.58**	0.55**
NSPP	G							0.247	0.73**	0.84**
	P							0.219	0.65**	0.31*
HSW	G								0.77**	0.88**
	P								0.57**	0.48**
DSY	G									0.97**
	P									0.68**

Here,

DFF= Days to first flowering,
DM= Days to maturity,
PH= Plant height (cm),
NBPP= No. of branches per plant,

PL= Pod length (cm),
NPPP= No. of pods per plant,
NSPP= No. of seeds per pod,

HSW= Hundred seed weight(g),
DSY= Dry stover yield (g/plant), and
DrSY= Dry seed yield (g/plant).

4.2.1 Days to first flowering

Days to first flowering exhibited significant and negative correlation with plant height (P= -0.273*), dry stover yield (g/plant) (G= -0.88**, P= -0.63**), and dry seed yield (g/plant) (G= -0.84**, P= -0.64**); while it expressed non-significant and negative correlation with days to maturity (G= -0.029, P= -0.017), plant height (cm) (G= -0.309), pod length (cm) (G= -0.242, P= -0.199), no. of pods per plant (G= -0.136, P= -0.155), no. of seeds per pod (G= -0.114, P= -0.092), and hundred seed weight (g) (G= -0.199, P= -0.096). On the other hand, days to first flowering showed non-significant but positive relation with no. of branches per plant (G= 0.127, P= 0.095). Desissa (2017) found the same outcomes.

4.2.2 Days to maturity

Days to maturity expressed positive but non-significant correlation with plant height (cm) (G= 0.122, P= 0.017), no. of branches per plant (G= 0.076, P= 0.050), no. of pods per plant (G= 0.213, P= 0.090), and no. of seeds per pod (G= 0.357, P= 0.129). It showed negative and significant relation with dry stover yield (g/plant) (G= -0.98**, P= -0.84**) and dry seed yield (g/plant) (G= -0.86**, P=-0.72**). On the contrary, it exhibited negative and non-significant relation with pod length (cm) (G= -0.095, P= -0.075), and hundred seed weight(g) (G= -0.139, P= -0.049).

4.2.3 Plant height (cm)

Plant height (cm) was found to produce positive and highly significant correlation with no. of branches per plant (G= 0.628**, P= 0.566**), no. of pods per plant (G= 0.528*, P= 0.517**), no. of seeds per pod (P= 0.360**), hundred seed weight (g) (G= 0.569**, P= 0.442**), dry stover yield (g/plant) (G= 0.70**, P= 0.61**) and dry seed yield (g/plant) (G= 0.76**, P= 0.67**). Moreover, it expressed positive but non-significant correlation with no. of seeds per pod (G= 0.372). Whereas, it was found to express negative and non-significant correlation with pod length (cm) (G= -0.212, P= -0.199). Desissa in 2017 exhibited same outcomes in his experiment.

4.2.4 No. of branches per plant

No. of branches per plant exhibited significant and positive combination with the no. of pods per plant (P= 0.393**), no. of seeds per pod (G= 0.445*, P= 0.417**), hundred seed weight(g) (P= 0.269*), dry stover yield (g/plant) (G= 0.55*), and dry seed yield

(g/plant) (G= 0.51*, P= 0.42**). While, it showed positive but non-significant correlation with no. of pods per plant (G= 0.399), hundred seed weight(g) (G= 0.304), and dry stover yield (g/plant) (P= 0.23). On the other hand, pod length (cm) (G= -0.075, P= -0.086) was found to have negative and non-significant correlation with no. of branches per plant.

4.2.5 Pod length (cm)

Pod length (cm) showed positive and significant correlation with dry stover yield (g/plant) (G= 0.78**, P= 0.59**), and dry seed yield (g/plant) (G= 0.70**, P= 0.66**). Pod length (cm) was found to exhibit negative but significant correlation with no. of seeds per pod (P= -0.309*). Whereas, it produced non-significant and negative combination with no. of pods per plant (G= -0.051, P= -0.057), no. of seeds per pod (G= -0.319), and hundred seed weight(g) (G= -0.067, P= -0.028).

4.2.6 No. of pods per plant

No. of pods per plant showed positive and highly significant relation with hundred seed weight(g) (G= 0.877**, P= 0.718**), dry stover yield (g/plant) (G= 0.64**, P= 0.58**) and dry seed yield (g/plant) (G= 0.67**, P= 0.55**). Besides, it presented non-significant but positive correlation with no. of seeds per pod (G= 0.196, P= 0.190). In 2017, similar result was noticed by Balla.

4.2.7 No. of Seeds per pod

No. of seeds per pod was found to express positive and significant correlation with dry stover yield (g/plant) (G= 0.73**, P= 0.65**) and dry seed yield (g/plant) (G= 0.84**, P= 0.31*). while it also exhibited positive and non-significant correlation with hundred seed weight(g) (G= 0.247, P= 0.219).

4.2.8 Hundred seed weight (g)

hundred seed weight (g) presented significant and positive correlation with dry stover yield (g/plant) (G= 0.77**, P= 0.57**) and dry seed yield (g/plant) (G=0.88**, P= 0.48**).

4.2.9 Dry stover yield (g/plant)

dry stover yield (g/plant) had positive and significant correlation with dry seed yield (g/plant) (G= 0.97**, P= 0.68**).

4.3 Path co-efficient analysis

Evaluation of path co-efficient express the association or combination of the independent variables with the dependent variable is due to their direct or indirect impact on it through the other characters. This analysis was conducted considering dry seed yield per plant as the dependent trait and its attributes parameters were considered as the independent variables namely, days to first flowering, days to maturity, plant height (cm), no. of branches per plant, pod length (cm), no. of pods per plant, no. of seeds per pod, hundred seed weight (g) and dry stover yield (g/plant). Each element has two ways of actions, one is the direct influence on dry seed yield and the another one is the indirect effect through component parameters which are not expressed from the correlation observation. The estimates of the direct and indirect effects of yield related traits on dry seed yield (g/plant) are presented in Table 7.

4.1.1 Days to first flowering

Path analysis expressed that, days to first flowering had negative and direct effect (**-0.225**) on dry seed yield of soybean. Moreover, it expressed positive and indirect effect on days to maturity (0.007), plant height (cm) (0.069), pod length (cm) (0.054), no. of pods per plant (0.030), no. of seeds per pod (0.026), hundred seed weight (g) (0.045), and dry stover yield (g/plant) (0.010). Whereas, it had negative indirect effect on no. of branches per plant (-0.029). In 2017, Machado *et al.* exhibited similar result.

4.1.2 Days to maturity

Through the path analysis days to maturity presented positive and direct effect (**0.119**) dry seed yield of soybean. It also expressed positive and indirect effect on plant height (cm) (0.014), no. of branches per plant (0.009), no. of pods per plant (0.025) and no. of seeds per pod (0.042). On the other hand, it had negative indirect influence on days to first flowering (-0.004), pod length (cm) (-0.011), hundred seed weight (g) (-0.017), and dry stover yield (g/plant) (-0.022). Silva *et al.* showed similar outcome in 2015.

Table 7. Path analysis showing direct and indirect effects of different traits on dry seed yield of twenty soybean genotypes

Characters	DFF	DM	PH	NBP	PL	NPPP	NSPP	HSW	DSY	Genotypic correlation with yield
DFF	**-0.225**	-0.004	0.023	-0.029	-0.017	-0.065	-0.033	-0.076	-2.500	-0.84**
DM	0.007	**0.119**	-0.009	-0.018	-0.008	0.102	0.103	-0.053	-2.781	-0.86**
PH	0.069	0.014	**-0.076**	-0.146	-0.015	0.252	0.108	0.217	1.987	0.76**
NBP	-0.029	0.009	-0.047	**-0.233**	-0.005	0.191	0.129	0.116	1.545	0.51*
PL	0.054	-0.011	0.016	0.017	**0.071**	-0.025	-0.092	-0.025	2.201	0.70**
NPPP	0.030	0.025	-0.039	-0.093	-0.004	**0.477**	0.057	0.334	1.798	0.67**
NSPP	0.026	0.042	-0.028	-0.104	-0.023	0.094	**0.289**	0.094	2.054	0.84**
HSW	0.045	-0.017	-0.043	-0.071	-0.005	0.418	0.071	**0.381**	2.173	0.88**
DSY	0.010	-0.022	-0.022	-0.084	-0.021	0.081	-0.027	0.149	**2.826**	0.97**

Residual effect: 0.0251

Here,

DFF= Days to first flowering;
DM= Days to maturity;
PH= Plant height (cm);
NBPP= No. of branches per plant;

PodL= Pod length (cm);
NPodPP= No. of pods per plant;
NSPP= No. of seeds per pod;

HSW= Hundred seed weight (g);
DSY= Dry stover yield (g/plant); and
DSeedY= Dry seed yield (g/plant).

4.1.3 Plant height (cm)

plant height (cm) was noticed to exhibit negative but direct effect (**-0.076**) on dry seed yield. Moreover, it had positive and indirect impact on days to first flowering (0.023) and pod length (cm) (0.016). Whereas, plant height presented indirectly negative effect on days to maturity (-0.009), no. of branches per plant (-0.047), no. of pods per plant (-0.039), no. of seeds per pod (-0.028), hundred seed weight (g) (-0.043) and dry stover yield (g/plant) (-0.022). Balla *et al.* in 2017 reported similar outcomes.

4.1.4 No. of branches per plant

No. of branches per plant was recorded to give negatively direct influence (**-0.233**) on dry seed yield of soybean. Besides, it exhibited positive and indirect effect on only pod length (cm) (0.017). Except that, no. of branches presented negative and indirect effect on days to first flowering (-0.029), days to maturity (-0.018), plant height (cm) (-0.146), no. of pods per plant (-0.093), no. of seeds per pod (-0.104), hundred seed weight (g) (-0.071), and dry stover yield (g/plant) (-0.084).

4.1.5 Pod length (cm)

pod length (cm) showed positive and direct impact (**0.071**) on soybean's dry seed yield. Moreover, it had negative and indirect effect on

days to first flowering (-0.017), days to maturity (-0.008), plant height (cm) (-0.015), no. of branches per plant (-0.005), no. of pods per plant (-0.004), no. of seeds per pod (-0.023), hundred seed weight(g) (-0.005), and dry stover yield (g/plant) (-0.021).

4.1.6 No. of pods per plant

No. of pods per plant exhibited positive and direct effect (**0.477**) on yield per plant. It also presented negatively indirect effect on days to first flowering (-0.065) and pod length (cm) (-0.025). Whereas, it exhibited positive indirect effect on days to maturity (0.102), plant height (cm) (0.252), no. of branches per plant (0.191), no. of seeds per pod (0.094), hundred seed weight (g) (0.418), and dry stover yield (g/plant) (0.081).

4.1.7 No. of Seeds per pod

No. of seeds per pod was found to show direct and positive effect (**0.289**) on dry seed yield (g/plant). It also presented positive indirect effect on days to maturity (0.103), plant height (cm) (0.108), no. of branches per plant (0.129), no. of pods per plant

(0.057), hundred seed weight (g) (0.071), and dry stover yield (g/plant) (-0.027). On the other hand, it had negative and indirect effect on days to first flowering (-0.033) and pod length (cm) (-0.092). Chaudhury and Sharma in 2003 reported similar result

4.1.8 Hundred seed weight (g)

Hundred seed weight (g) expresses positive and direct effect (**0.381**) on dry seed yield (g/plant). Besides, it had positive but indirect effect on plant height (cm) (0.217), no. of branches per plant (0.116), no. of pods per plant (0.334), no. of seeds per pod (0.094), and dry stover yield (g/plant) (0.149). On the contrary, it showed negative indirect effect on days to first flowering (-0.076), days to maturity (-0.053), and pod length (cm) (-0.025).

4.1.9 Dry stover yield (g/plant)

Dry stover yield (g/plant) was noticed to exhibit positive and direct effect (**2.826**) on dry seed yield (g/plant). It also showed positive indirect effect on plant height (cm) (1.987), no. of branches per plant (1.545), pod length (cm) (2.201), no. of pods per plant (1.798), no. of seeds per pod (2.054), and hundred seed weight (g) (2.173). Whereas, it had negative indirect effect on days to first flowering (-2.500) and days to maturity (-2.781),. In 2015, Jain *et al.* exhibited similar results.

4.4 Diversity analysis

By using the computer software program R genetic diversity was. It involves several analyses namely, principal component analysis (PCA), Vector, eigen value determination, clustering, and analysis of inter-cluster distance. Therefore, numerous multivariate techniques were needed to represent results more clearly and it was also reported by many researchers (Bashar, 2002; Juned *et al.*, 1988, and Ario, 1987). In the evaluation of genetic diversity in soybean multivariate techniques were used.

4.4.1 Principal component analysis (PCA)

With the help of Principal component analysis, we can easily estimate the important polygenic traits which have importance in breeding program for variety development. The genotype scores and correlation matrix collected from the first components and the succeeding components with roots greater than the unity, the principal components were calculated. Eigen values of the ten principal components axes and the percentage

Table 8. Eigen values, Percent variation, and Cumulative % of Percent variation showing for ten characters of twenty soybean genotypes

Parameters	Eigen values	Percent variation	Cumulative % of Percent variation
DFF	6.63	66.30	66.31
DM	1.06	10.62	76.92
PH	0.69	6.88	83.0
NBP	0.55	5.52	89.32
PodL	0.37	3.78	93.10
NPodP	0.26	2.57	95.66
Nseed	0.18	1.79	97.45
HSW	0.12	1.21	98.66
DSY	0.09	0.78	99.43
DSeedY	0.06	0.63	100.00

of grand total variation accounting for them, they were gained from the principal component analysis are presented in Table 8. The presented values exhibited that, the cumulative eigen values of the five principal components accounted for 93.10% of total variation among the ten studied parameters of soybean genotypes. Out of the five principal component PC1, PC2, PC3, PC4 and PC5 accounted for 66.30%, 10.62%, 6.88%, 5.52% and 3.78% of the total variations, respectively.

4.4.2 Non- hierarchical Clustering

With the help of a covariance matrix with application of non-hierarchical clustering, the twenty soybean genotypes were classified into three different clusters. Among the obtained, clusters 9 genotypes were found in cluster III; which is the largest cluster. On the other hand, cluster I have 4 genotypes and it was the smallest cluster. Rest of the seven genotypes were noticed in cluster II in table 9. These results confined that; the clustering pattern of the genotypes were according to the principal component analysis. Kumar et al., (1998) exhibited five clustering, Joshi and Kohli (2003) assessed the pattern and magnitude of the genetic divergence using non-hierarchical Euclidean cluster analysis in the 73 tomato (*Lycopersicon esculentum*) genotypes of diverse origin for several quantitative and qualitative parameters. According to the principal component analysis, these results would corroborate the genotype clustering patterns. The non-hierarchical clustering corroborated PCA findings, thereby confirming the PCA outcomes. Soybean genotypes were grouped into clusters, suggesting a broad ranges of genetic variations.

Table 9. Distribution of twenty soybean genotypes into distinguished cluster

Cluster	Number of populations	Genotypes
I	4	G1, G11, G13, and G14
II	7	G2, G3, G4, G6, G8, G10 and G16
III	9	G5, G7, G9, G12, G15, G17, G18, G19 and G20

- **Cluster I**

Cluster I had four genotypes as G1, G11, G13, and G14 (Table 9). In table 10, it was observed that clustering mean values, it was observed that cluster I produced the highest mean values for days to first flowering (43.35) and days to maturity (73.57). While, for plant height (cm) (56.63), no. of branches per plant (5.79), pod length (cm) (2.62), no. of pods per plant (61.04), no. of seeds per pod (1.95), hundred seed weight (g) (11.92), dry stover yield (g/plant) (11.31), and dry seed yield (g/plant) (17.10).

- **Cluster II**

Cluster II had exhibited seven genotypes, which are G2, G3, G4, G6, G8, G10 and G16 (Table 9). it was also observed to give the highest cluster mean result for most of the characters. In Table 10, plant height (cm) (70.07), no. of branches per plant (7.36), pod length (cm) (3.60), no. of pods per plant (97.27), no. of seeds per pod (3.17), hundred seed weight (g) (17.17), dry stover yield (g/plant) (20.23) and dry seed yield (g/plant) (32.49) had shown the maximum mean of cluster values, except the days to first flowering (34.18) and days to maturity (62.64) showed the minimum cluster mean.

- **Cluster III**

In cluster III, maximum number of genotypes of soybean were found. They are 9 in number which are had exhibited seven genotypes, which are G5, G7, G9, G12, G15, G17, G18, G19 and G20 (Table 9). All the parameters showed moderate cluster mean values, which were days to first flowering (35.54), days to maturity (63.33), Table 10, plant height (cm) (64.18), no. of branches per plant (6.64), pod length (cm) (3.52), no. of pods per plant (74.60), no. of seeds per pod (2.55), hundred seed weight (g) (14.30), dry stover yield (g/plant) (18.97) and dry seed yield (g/plant) (29.61) exhibited in table 10.

4.4.3 Development of scatter diagram

By using the components of I as X axis and component II as the Y axis, a two-dimensional scatter diagram was constructed (Figure 1). The twenty genotypes were apparently distributed into the three cluster on the scatter diagram, with three different color red, green, and blue for cluster I, cluster II and cluster III, respectively, in purpose of proper understanding.

Table 10. Cluster mean for ten characters of twenty soybean genotypes

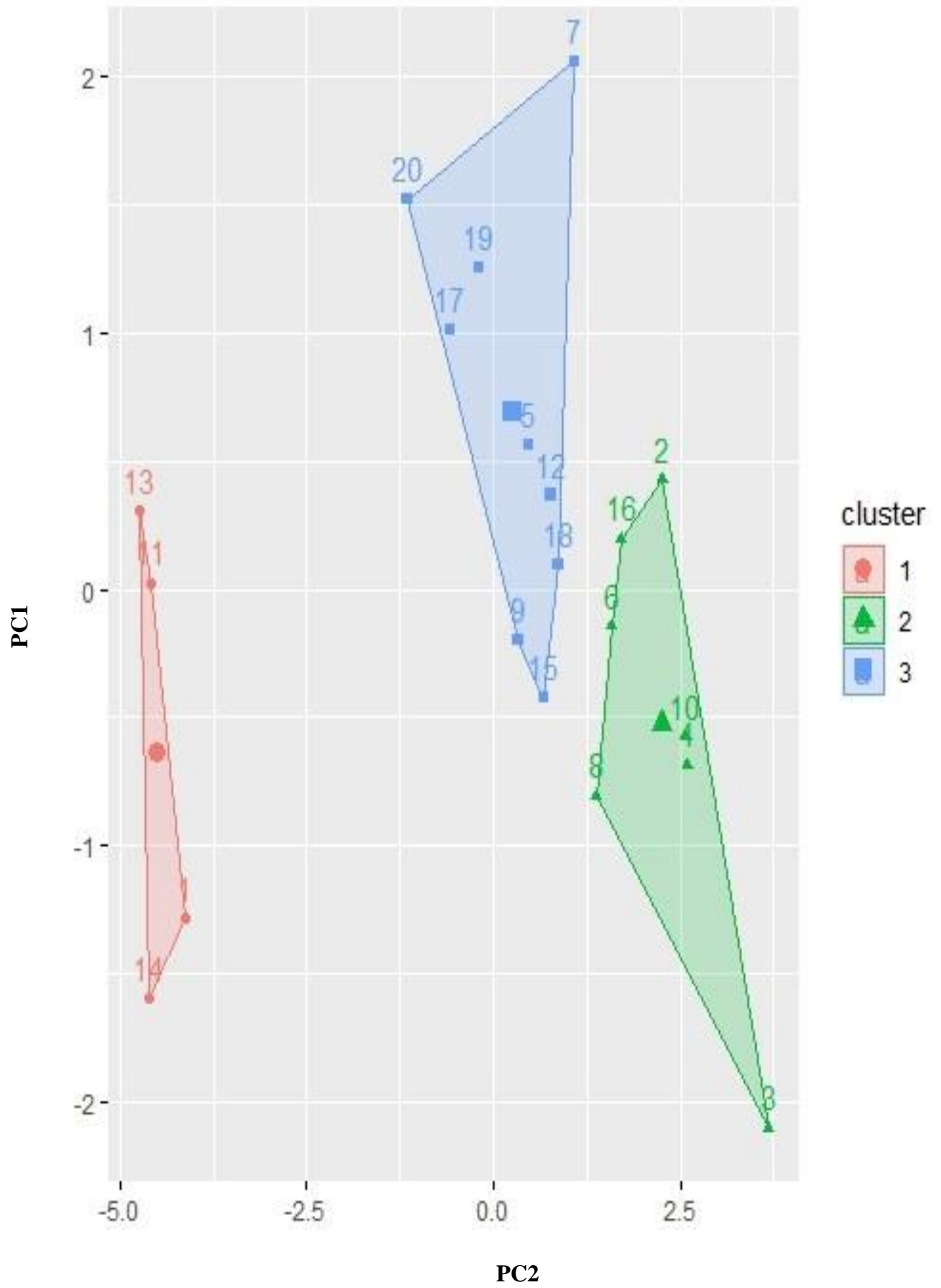| Characters	I	II	II
Days to first flowering	43.35	34.18	35.54
Days to maturity	73.57	62.64	63.33
Plant height (cm)	56.63	70.07	64.18
No. of branches per plant	5.79	7.36	6.64
Pod length (cm)	2.62	3.60	3.52
No. of pods per plant	61.04	97.27	74.60
No. of seeds per pod	1.95	3.17	2.55
Hundred seeds weight (g)	11.92	17.17	14.30
Dry stover yield (g/plant)	11.31	20.23	18.97
Dry seed yield (g/plant)	17.10	32.49	29.61

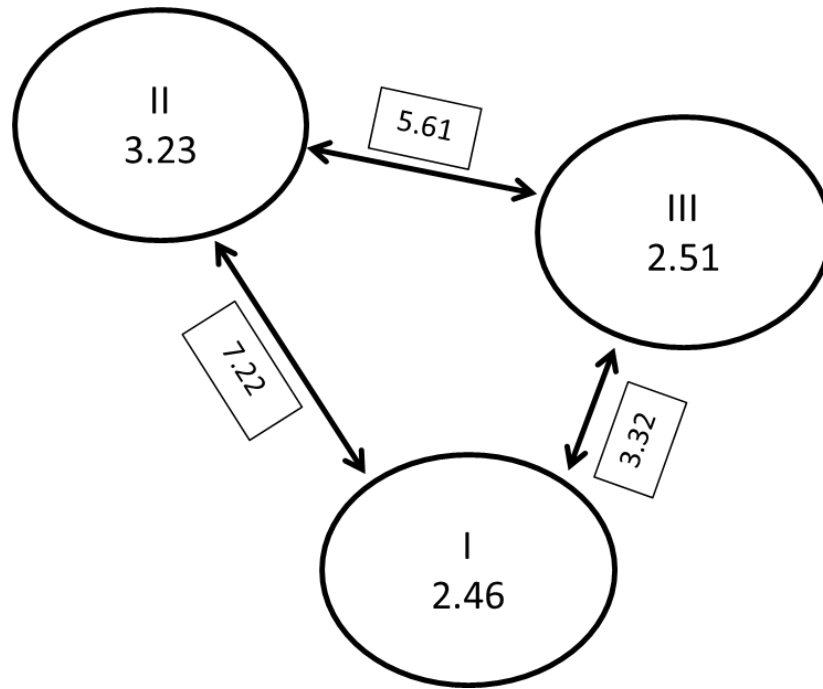Figure 1. Scatter diagram of twenty soybean genotypes

Figure 2. Intra (Bold) and inter cluster distances (D^2) of twenty genotypes of
        soybean

4.4.4 Canonical variate analysis

The inter-genotypic distances and the intra-cluster genotypic distances are presented in table 11, as suggested by Singh *et al.* (1977). Cluster I which (2.46) is composed of four genotypes showed the lowest intra cluster distances and cluster II was found to exhibited the highest value for intra-cluster distance (3.23), and it composed of seven soybean genotypes. The coordinates were obtained from the Principal Component analysis (PCA), that were used as input at Principal Coordinate Analysis (PCO) to access the distances among the points presented by by Digby *et al.* (1989). PCA was mostly used for the graphical representation of the points while the PCO was used to evaluate the minimum distance straight line between the each pair of points. To get the inter-cluster Mahalanobis's D^2 values canonical variate analysis was runed. Table 11, illustrating the intra-cluster and inter-cluster distance. The maximum inter-cluster distances was found between the cluster I and cluster II, which is (7.22), indicating wider genetic diversity among the genotypes. The lowest inter-cluster distance was found between the cluster I and Cluster III, which was (3.23).

Table 11. Intra (Bold) and inter cluster distance of twenty soybean genotypes

Clusters	I	II	III
I	**2.46**	7.22	3.23
II		**3.23**	5.61
III			**2.51**

4.4.5 Relative contribution of individual character to the genetic divergence in soybean

It was measured through the vectors (vector I and II) for different studied traits. Vectors (Vector I and II) for different parameters in this experiment are exhibited in Table 12. In vector the crucial characters were responsible for the genetic divergence in the major axis of differentiation were, plant height (cm), no. of branches per plant, pod length (cm), no. of pods per plant, no. of seeds per pod, hundred seed weight(g), dry stover yield (g/plant), and dry seed yield (g/plant) and in vector II the second axis of differentiation for dry stover yield (g/plant), and dry seed yield (g/plant). The dry stover yield (g/plant) (0.9163 and 0.1926), and dry seed yield (g/plant) (0.9020 and 0.1169) was noticed positive for both vector I and vector II. Srinivas *et al.* (2013) and Hasan *et al.* (2015) showed similar result.

Table 12. Latent vectors for ten characters of twenty soybean genotypes

Components	Vector-1	Vector-2
I	-0.8497	-0.3160
II	-0.89101	-0.2748
III	0.8199	-0.1066
IV	0.5870	-0.4454
V	0.7548	-0.6591
VI	0.7778	-0.3474
VII	0.7416	-0.3403
VIII	0.8485	-0.3622
IX	0.9163	0.1926
X	0.9020	0.1169

4.4.6 Selection of soybean genotypes as parent for the further hybridization program

Identification and determination of genetically diverse parents is a prerequisite and crucial step for a hybridization program in plant breeding. Three factors namely, the selection of specific variety from the clusters, determination of a particular cluster among them, and the relative attribution of the parameters to the total genetic divergence) were considered for selecting the parents for a plant breeding program, as reported by Chaudhary *et al.* in 1977. Thorough the use of knowledge of genetic diversity of the crops is most important for the parental selection that would maximizes genetic improvement (Rahman *et al.*, 2011). So, in the present study soybean genotypes were to be selected on the basis of specific parameters. Considering the magnitude of the cluster mean and agronomic performance of the soybean genotypes, from the cluster I, G2 (BD-2325) for minimum days for flowering, G3 (BD-2326) for highest plant height, maximum number of pods per plant, and highest hundred seed weight (g), G4 (BD-2327) for minimum days for maturity, and G16 (BD-2341) for highest dry strove yield per plant. Besides, from the cluster II, G7 (BD-2331) was found to give maximum length of pod and highest dry seed yield of soybean. Therefore, considering the agronomic performance, these genotypes can be used as parent for desirable hybridization program of soybean in future.

CHAPTER III

SUMMARY AND CONCLUSION

This research was conducted using twenty soybean genotypes to assess the performance of yield and yield related characters. Randomized complete block design (RCBD) with three specific replications was used in the experimental location at the Sher-e-Bangla Agricultural University, Dhaka-1207, during early 2022 from February to May. Data on different morphological characters namely, days to first flowering, days to maturity, plant height (cm), no. of branches per plant, pod length (cm), no. of pods per plant, no. of seeds per pod, hundred seed weight (g), dry stover yield (g/plant), and dry seed yield (g/plant) was recorded.

Variance analysis exhibited highly significance of differences for all the studied parameters. Shortest period for days to first flowering was recorded for G2 (29.56), while the maximum period was observed for G1(46.55); days to maturity was found minimum for G4 (60.40), whereas minimum days observed for G13 (75.8); Highest result for plant height (cm) was noticed in G3 (73.89), while shortest plant was found in G14(51.4); no. of branches per plant was noted highest in G15 (8.4), on the contrary, lowest number was recorded in G11 (4.7); the highest pod length (cm) was noticed in G7 (4.28) and the lowest length of pod was seen in G1 (2.49); no. of pods per plant was found maximum in G3 (128.64), while the lowest number was in G13 (56.56); no. of seeds per pod was noticed highest in G4 (3.60), whereas the minimum value found in G13(1.2); hundred seed weight (g) was maximum in G3 (21.92) and minimum in G14 (11.45); maximum dry stover yield (g/plant) was collected in G16 (22.17 g), while the minimum was in G13 (10.00 g); and dry seed yield (g/plant) showed the maximum value in G7 (36.6 g) and minimum value was found in G11 (15.2 g). Phenotypic coefficient of variation was found higher for all the character than the genotypic coefficient of variation. Similarly, the phenotypic variance was higher than the genotypic variance for all the parameters, indicating the influence of environment on the trait expression. High heritability associated with high genetic advance of percent mean was observed for no. of branches per plant, no. of pods per plant, no. of seeds per plant, dry stover yield (g/plant) and dry seed yield (g/plant); that indicating the

existence of additive gene action and simple selection based on this trait is possible for future breeding program.

Calculation of correlation of coefficient revealed that, the dry seed yield per plant (g/plant) had positive and significant correlation with plant height (G= 0.76, P= 0.67), no. of branches per plant (G= 0.51, P= 0.42), pod length (G= 0.70, P= 0.66), no. of pods per plant (G= 0.67, P= 0.55), no. of seeds per pod (G= 0.84, P= 0.31), hundred seed weight (g) (G= 0.88, P= 0.48), and dry stover yield (g/plant) (G= 0.97, P= 0.68).

The path analysis revealed the days to maturity (0.119), pod length (cm) (0.071), no. of pods per plant (0.477), no. of seeds per pod (0.289), hundred seed weight (g) (0.381), and dry stover yield (g/plant) (2.826) had positive and direct effect on dry seed yield.

Through the multiverse analysis it was found that the twenty genotypes of soybean were clustered into three different cluster. There the cluster three contained the maximum number of genotypes (9) which are G5, G7, G9, G12, G15, G17, G18, G19 and G20. While the lowest number of genotypes (4) was noted in cluster I including G1, G11, G13, and G14. Considering the magnitude of the cluster mean and agronomic performance of the soybean genotypes, from the cluster I, G2 (BD-2325) for minimum days for flowering, G3 (BD-2326) for highest plant height, maximum number of pods per plant, and highest hundred seed weight (g), G4 (BD-2327) for minimum days for maturity, and G16 (BD-2341) for highest dry strove yield per plant. Besides, from the cluster II, G7 (BD-2331) was found to give maximum length of pod and highest dry seed yield of soybean. Therefore, considering the agronomic performance, these genotypes can be used as parent for desirable hybridization program of soybean in future.

REFERENCES

Al–Jibouri, H., Miller, P.A. and Robinson, H.F. (1958). Genotypic and environmental variances and co-variances in an upland cotton cross of the interspecific origin. *Agron. J.* **50**(10): 633–636.

Amogne, A., Atnaf, M., and Bantayehu, M. (2020). Correlation and path coefficient analysis in soybean (*Glycine Max* L.) Merrill) genotypes in Dibate, Northwestern Ethiopia. *Int. J. Eng. Sci.* **4**(6): 1–5.

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

Ario, O.J. (1987). Measurement and classification of genetic diversity in okra (Abelmoschus esculentus). *Annals of App. Bio.* **116**: 335–340.

Balla, M.Y.B. and Ibrahim, S.E. (2017). Genotypic correlation and path coefficient analysis of soybean [*Glycine max* (L.) Merr.] for yield and its components. *Agri. Res. Tech.; Open Access J.* **7**(3).

BBS. (2021). Bangladesh Bureau of Statistics. Agricultural Statistical Yearbook of Bangladesh 2020.

Bashar, M.K. (2002). The genetic and Morpho-physiological basis of heterosis in the rice. Ph.D. thesis, BSMRAU, Gazipur.

Burton, G.W. (1952). Quantitative inheritance in the grass pea. Proc. 6th Grassl. Cong. **1**: 277–283.

Chandrawat, K.S., Baig, K.S., Hashmi, S., Sarang, D. H., Kumar, A. and Dumai, P.K. (2017). Study on genetic variability, heritability and genetic advance in soybean. *Int. J. Pure App. Biosci.* **5**(1): 57–63.

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

Chaudhary, D. P. (1977). Soybean: cultivation and uses. New India Publishing.

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

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

61

Cochran, W.G. and Cox, G. (1957). Experimental design. John Willing and Sons (2nd ed.). New York. **pp**.615.

Comstock, K. and Robinson, P.R. (1952). Estimation of genetic advance. *Indian J. Hill.* **6**(2): 171–174.

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

Desissa, D.H. (2017). Genetic variability, heritability and genetic advances of soybean (*Glycine max* (L.) Merrill) varieties grown at bako tibe in Western Ethiopia. *AJPSKY*. **7**(5):20–26.

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

Digby, P., Galway, N. and Lane, P. (1989). GENSTAT 5: A Second Course. Oxford Science. Oxford Science Publications, Oxford. **pp**.103–108.

Dong, D., Fu, X., Yuan, F., Chen, P., Zhu, S., Li, B., Yang, Q. Yu, X., and Zhu, D. (2014). Genetic diversity and population structure of vegetable soybean (*Glycine max* (L.) Merr.) in China as revealed by SSR markers. *Genet. Resour. Crop Evol.* **61**:173–183

Dutta, P., Goswami, P.K., and Borah, M. (2021). Assessment of genetic variability, heritability and genetic advance in soybean genotypes. *EJPB.* **12**(4): 1461-1465.

Ferrari, M., Carvalho, I.R., Pelegrin, A.J., Nardino, M., Szareski, V.J., Olivoto, Rosa, T.C., Follmann, D.N., Pegoraro, C., Maia, L.C. and Souza, V.Q. (2018). Path analysis and phenotypic correlation among yield components of soybean using environmental stratification methods. *AJCS.* **12**(02):193–202.

FAO. (2021). Food and Agriculture Organization of the United Nations. FAOSTAT - Crops. Retrieved from http://www.fao.org/faostat/en/#data/QC.

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

Getnet, B.E. (2018). Genetic variability, heritability and expected genetic advance as indices for selection in soybean [*Glycine max* (L.) Merrill] varieties. *Am. J. Life Sci.* **6**(4): 52–56.

Gomez, K.A. and Gomez, A.A. (1984). Statistical procedures for the agricultural research (2 ed.). John wiley and sons, NewYork, p.680.

Hakima, L., Suyamtob, and Paturohmana, E. (2020). Genetic variability, heritability and expected genetic advances of quantitative characters in f2 progenies of soybean crosses. *Indones. J. Agric. Sci.* **15**: 11–16.

Hasan, R.A.K.M., Hossain, M.K., and Alam, N. (2015). Assessment of genetic divergence in the chili (Capsium annum L.) genotypes. *Plant Genet. Trait.* **6**(3): 1– 5.

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

Hymowitz, T. (2004). The introduction of soybean to the Americas and factors relating to its spread. **In**: Soybeans: Improvement, Production, and Uses; **pp**. 1–7.

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

Jain, R.K., Joshi, A., Chaudhary, H.R., Dashora, A., and Khatik, C.L. (2018). Study on genetic variability, heritability and genetic advance in soybean [*Glycine max* (L.) Merrill]. *Legume Research*. **18**: 1–5.

Jain, S., Srivastava, S.C., Singh, S.K., Indapurkar, Y.M., and Singh, B.K. (2015). Studies on genetic variability, character association and path analysis for yield and its contributing traits in soybean [*Glycine max* (L.) Merrill]. *Legume Res.* **38**(2): 182–184.

Jandong, E.A., Uguru, M.I., and Okechukwu, E.C. (2020). Estimates of genetic variability, heritability and genetic advance for agronomic and yield traits in soybean (*Glycine max* L.). *African. J. Biotechnol.* **19**(4): 201–206.

Jeger, M.I., Garethojones, D. and Griffith, E. (1983). Components of partial resistance of the wheat seedlings of septoria nod rum. *Euphytica*. **32**: 575–584.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of the genetic and environmental variability in soybean. *Agron. J.* **47**:314–318.

Joshi, A. and Kohli, U.K. (2003). Genetic divergence for quantitative and qualitative characters in the tomato (*Lycopersicon esculentum*). *Indian J. Agric. Sci.* **73**(2):110–113.

Juned, S.A., Jackson, M.T. and Catty, J.P. (1988). Diversity in wild potato species Chacoense Bitt. *Euphytica*. **37**(2): 149–156.

Jung, J.W., Park, S.Y., Oh, S.D., Jang, Y., Suh, S.J., Park, S.K., Ha, S.H., Park, S.U., and Kim, J.K. (2021). Metabolomic variability of different soybean genotypes:

β-Carotene enhanced (*Glycine max*), wild (*Glycine soja*), and hybrid (*Glycine max × Glycine soja*) soybeans. *Foods*. **10**: 2421.

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

Khan, M.R.A., Mahmud, F., Reza, M. A. Mahbub, M.M., Shirazy, B.J., and Rahman, M.M. (2017). Genetic diversity, correlation and path analysis for yield and yield components of pea (*Pisum sativum* L.). *WJAS*. **13**(1): 11–16.

Kumar, A., Pandey, A. Aochen, C., Pattanayak, A. (2015). Evaluation of genetic diversity and interrelationships of agromorphological characters in soybean (*Glycine max*) genotypes. *Proc. Natl. Acad. Sci., India, Sect. B Biol. Sci.* **85**(2): 397–405.

Kumar, Raj and Kang, G.S. (1998). Genetic diversity among the Andigena potatoes. *J. of the Indian Potato Ass.* **25**(1–2): 21–24.

Lam, H., Xu, X., Liu, X., Chen, W., Yang, G., Wong, F., Li, M., He, W., Qin, N., Wang, B., Li, J., Jian, M., Wang, J., Shao, G., Wang, J., Sun, S.S., & Zhang, G. (2010). Resequencing of 31 wild and cultivated soybean genomes identifies patterns of genetic diversity and selection. *Nature Genetics.* **42**(12).

Li, S.S., Kendall, C.W., and de Souza, R.J. (2014). Dietary pulses, satiety and food intake: a systematic review and meta-analysis of acute feeding trials. Obesity (Silver Spring). **22**(8): 1773–1780.

Lui, X.X., Li, S.H., and Chen, JZ, (2012). Effect of soy isoflavones on blood pressure: a systematic review and meta-analysis of randomized controlled trials. *Nutr. Metab. Cardiovasc Dis.* **22**(6): 463–470.

Ma, D.F., Qin, L.Q., Wang, P.Y., and Katoh, R. (2008). Soy isoflavone intake increases bone mineral density in the spine of menopausal women: meta-analysis of randomized controlled trials. *Clin. Nutr.* **27**(1): 57–64.

Machado, B.Q.V., Nogueira, A.P.O., Hamawaki, O.T., Rezende, G.F., Jorge, G.L., Silveira, I.C., Medeiros, L.A., Hamawaki, R.L., and Hamawaki, C.D.L. (2017). Phenotypic and genotypic correlations between soybean agronomic traits and path analysis. **16**:234–238

Mahalanobis, P.C. (1936). On the generalized distance in the statistics. *Proc. Natl. Inst. Sci. India.* **2**:49–55.

Mahbub, M.M., Rahman, M.M., Hossain, M.S., Mahmud, F., and Kabir, M.M.M. (2015). Genetic variability, correlation and path analysis for yield and yield components in soybean. **15**(2): 231–236.

Messina, M.J. and Loprinzi, C.L. (2001). Soy for breast cancer survivors: a critical review of the literature. *J. Nutr.* **131**(11): 3095–3108.

Mishra, A.K. (2019). Association analysis in diverse populations of soybean. *Soybean Res.* **17**(1&2): 30–39.

Mofokeng, M.A. (2021). Genetic variability, heritability and genetic advance of soybean (*Glycine max*) genotypes based on yield and yield-related traits. *AJCS.* **15**(12): 1427–1434.

Neelima, G., Mehtre, S.P., and Narkhede, G.W. (2018). Genetic variability, heritability and genetic advance in soybean. *Int. J. Pure App. Biosci.* **6**(2): 1011–1017.

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

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

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

Rao, C.R. (1952). Advanced Statistical Methods in Biometrical Research. John Wiley and Sons, New York. **pp**. 45–110.

Robinson, H.F., Comstock, R.E. and Harvey, P. (1966). Quantitative genetics in relation to the breeding on the centennial of mendelism. *Indian J. Genetics.* **26**(A): 171–87.

Schmutz, J. (2010). Genome sequence of the paleopolyploid soybean. *Nature*, **463**(7278), 178–183.

Shilpashree, N., Devi, S.N., Manjunathagowda, D.C., Muddappa, A., Abdelmohsen, S.A.M., Tamam, N., Elansary, H.O., El-Abedin, T.K.Z., Abdelbacki, A.M.M., and Janhavi, V. (2021). Morphological characterization, variability and diversity among vegetable soybean (*Glycine max* L.) genotypes. *Plants*; **10**: 671.

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

Silva, A.F., Sediyama, T., Silva, F.C.S., Bezerra, A.R.G., Ferreira, L.V. (2015). Correlation and path analysis of soybean yield components. *IJPAES.* **5**(1): 177–179.

Singh, G., Gireesh, C., Shivakumar, M., Arya, M., Agarwal, D.K., and Husain, S.M. (2015). Molecular characterization and genetic diversity analysis of soybean (*Glycine max* (L.) Merr.) germplasm accessions in India. *Physiol. Mol. Biol. Plants.* **21**(1): 101–107.

Singh, H.N., Srivastava, J.P. and Prasad, R. (1977). Genetic variability and correlation studies in the bitter gourd. *Indian J. Agri. Sci.* **47**(12): 604–607.

Singh, R.K. and Choudhary, B.D. (1985). Biometrical Methods in the Quantitative Genetic Analysis. Kalyani. **pp**. 87–95.

Sivasubramanian, J. and Madhavamenon, P. (1973). Genotypic and phenotypic variability in the rice. *Madras Agric. J.* **12**: 15–16.

Srinivas, B., Thomas, B. and Gogineni, S. (2013). Genetic Divergence for Yield and its Component Traits in the Chili (Capsicum frutescens L) Accecessions of Kerala. Intl. *J. Sci. Res.* **6**(14): 442–446.

Taku, K., Melby, M.K., and Takebayashi, J. (2012). Effect of soy isoflavone extract supplements on menopausal symptoms in menopausal women: a systematic review and meta-analysis. *Menopause.* **19**(7): 776–790.

Tandekar, K., Rohit, and Thakur, K. (2022). Assessment of genetic variability, heritability and genetic advance in soybean (*Glysin max* L.) Genotypes. *Int. J. Plant. Soil. Sci.* **34**(23): 557–561.

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

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

USDA Food Data Central. (2021). Soybeans, mature cooked, boiled, without salt. https://fdc.nal.usda.gov/fdc-app.html#/food-details/170588/nutrients.

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

Zhang, X., Shu, X.O., Li, H. (2001). A prospective cohort study of soy food consumption and risk of breast cancer in women. *Arch Intern Med.* **165**(21): 2483–2488.

Zhou, X., Ge, S., Zhang, L., & Yang, Z. (2008). Ecological adaptation and origin of soybean. *J. Integ. Plant Bio.* **50**(7): 789–795.

APPENDICES

Appendix I. Map showing the experimental destination under the investigation
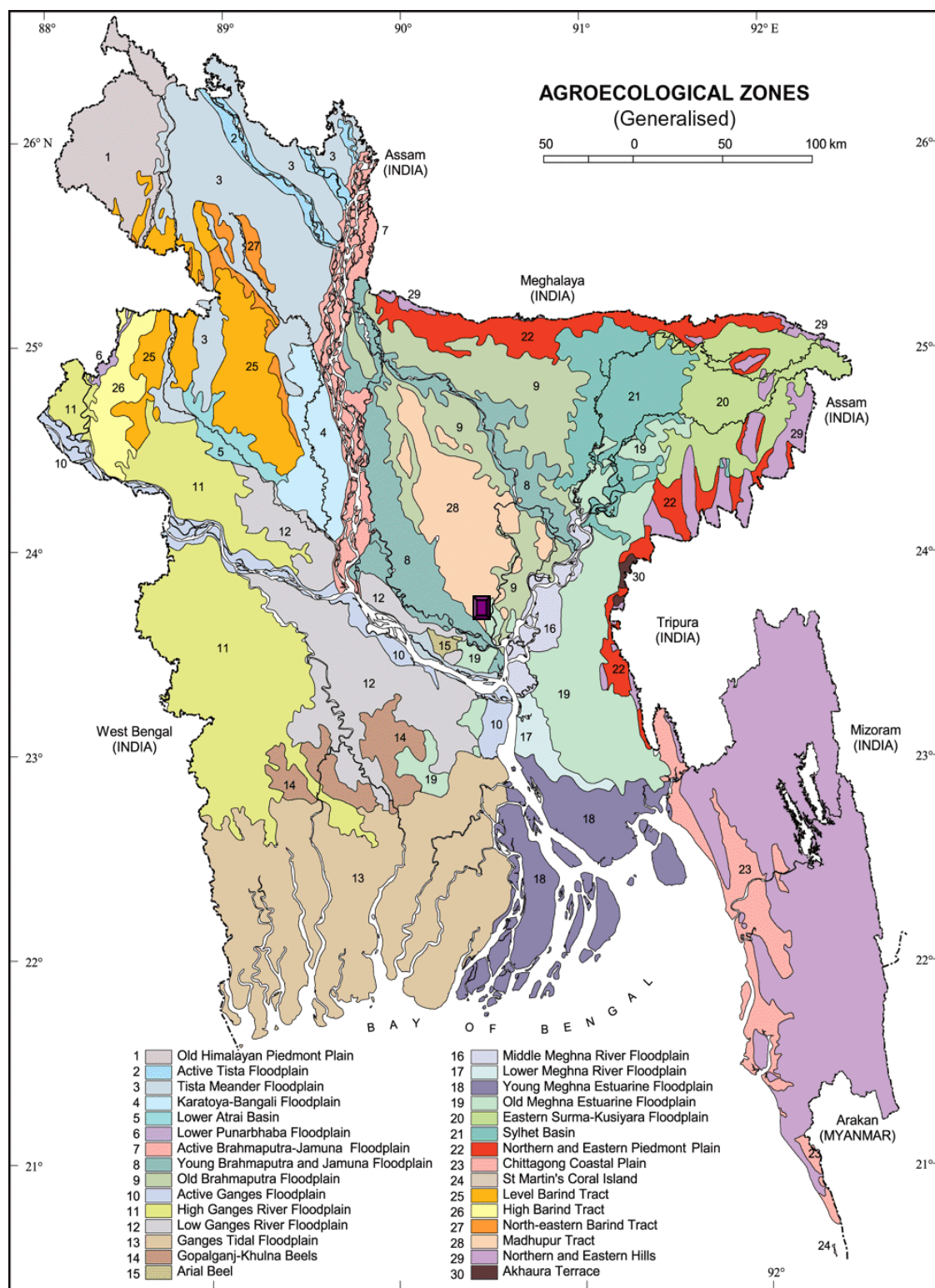
The experimental area under study

Appendix II. Morphological, physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site

A. **Physical composition of the soil (experimental area)**

Separates of soil	%
Sand	38.92
Silt	27.45
Clay	39.66
Texture class	Clay loam

B. **Chemical composition of the soil (experimental area)**

Sl. No.	Soil characteristics of the location	Analytical data
1	Organic carbon (%)	0.81
2	Total N (kg/plant)	1792.00
3	Available N (kg/ ha)	54.00
4	Available P (kg/plant)	67.00
5	Exchangeable K (kg/plant)	89.50
6	Total S (ppm)	225.00
7	Available S (ppm)	17.00
8	Total P (ppm)	840.00
9	pH (1: 2.5 soil to water)	5.57
10	CEC	12.23

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

Appendix III. Monthly average temperature, relative humidity and total rainfall of the experimental site during the period from February, 2021 to May, 2022

Month	Avg. Temperature (ºC)	Relative Humidity (%)	Total Rainfall (mm)
February, 2022	23.6	58	1
March, 2022	26.5	56	28
April, 2022	29.4	59	56
May, 2022	28.7	63	78

Source: Bangladesh Meteorological Department (Climate Division, Dhaka Station), Agargaon, Dhaka – 1207