CHARACTER ASSOCIATION AND DIVERSITY ANALYSIS OF DIFFERENT GENOTYPES OF SOYBEAN (*Glycine max* L Merr.)

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

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ABSTRACT

An experiment was executed with 36 (Thirty six) soybean (*Glycine max* L. Merr.) genotypes at Bangabandhu Sheikh Mujibur Rahman Agricultural University by the period from December 2020 to April 2021, Salna, Gazipur. The aim of this study is to find the genetic variability, correlation and path coefficient analysis, for detecting the genetically diverse parents with elite agronomic performance and to find out the characters accountable for genetic divergence. The analysis of variance showed highly significant differences among the mean values for all traits. 36 (Thirty six) soybean genotypes for all the estimated traits shown high heritability, high to low genetic advance along with high to moderate GA%. This finding indicated that those traits were governed by additive gene so selection might be useful. As per the experiment number of branches/plant (0.08), number of nodes/plant (0.31), number of seeds/plant (0.07), 100 seed weight (g) (0.16) and seed yield/plant (0.45) were the important characters accountable for genetic divergence. Among the 6 (six) clusters, the highest inter cluster distance was observed between in cluster I and cluster VI (20.01) and the lowest between cluster V and cluster VI. For the highest seed yield/plant G1, along with the other genotypes belonging cluster III (G8, G13, G33) will be worthwhile selection for future crop improvement program.

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LIST OF ACRONYMS

FULL NAME	ABBREVIATION
Agro-Ecological Zone	AEZ
And others	*et. al.*
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Centimeter	cm
Degrees of freedom	d.f
Etcetera	etc.
Food and Agriculture Organization	FAO
Figure	Fig.
Genetic advance	GA
Genotypic variance	$\delta^2{}_g$
Heritability in broad sense	$h^2{}_b$
Journal	j.
Kilogram	Kg
Meter	m
Mean sum of square	MSS
Millimeter	mm
Murate of potash	MP
Percent	%
Phenotypic co-efficient of variation	PCV
Randomized complete block design	RCBD
Sher-e-Bangla Agricultural University	SAU
Standard error	SE
Triple super phosphate	TSP
Unites nations development program	UNDP

CHAPTER I

INTRODUCTION

Soybean (*Glycine max* L. Merill) is a leguminous crop has enormous appraise in agriculture as a suitable source of high quality protein and vegetable oil in one hand and nitrogen fixing ability on the other. It is a self-pollinated crop and belongs to the family fabaceae, sub-family faboideae and genus *Glycine*. The chromosome number of cultivated species of soybean is 2n = 40. China is reported to be the origin of cultivated soybean (*G. max* L. Merr.) with *Glycine ussuriensis* as probable progenitor (Vavilov, 1951; Nagata, 1960). There are wide variations in plant and seed characteristics of soybean.

Soybean is a grain legume crop and a popular source of vegetable protein and phytochemicals in many Asian countries (Rao et al., 2002). Soybean is known as "Golden bean" and miracle crop of 20th century. It is a multipurpose and attractive crop with countless possibilities of not only improving agriculture but also supporting industries. Day by day the demand of soybean is increasing for human food as well as feed for animal and fish. Despite the relatively low oil content of the seed (about 20% on moisture-free basis), soybeans are the largest single source of edible oil and account for roughly 50% of the total oilseed production of the world. (Awal, 2014). Soybean seed contains 38-42% good quality protein and 18-22% oil content. For human consumption soybean includes products such as soy milk, soy flour or tofu.

The crop is grown under warm conditions in the tropics, subtropics and temperate climates. This statistic shows the leading countries in soybean production worldwide from 2012/13 to 2020/21. From 2015/16 to 2018/2019, the United States was the leading global producer of soybeans with a production volume of 120.52 million metric tons in 2018/2019. As of May 2020, Brazil overtook the United States as the leading soybean producing country with a production volume of some 126 million metric tons in 2020/21 (FAO, 2021). Among all oilseeds produced in 2019-2020, in Bangladesh, soybeans accounted for 9 percent of total oilseed planted area. (BBS, 2019).

Seed yield of soybean is controlled by quantitative genes with low heritability that makes the response to selection for yield (Burton, 1987). A good knowledge of genetic resources might also help in identifying desirable cultivars for commercial cultivation. The progression of soybean genetic base may lead to the introduction of new favorable

alleles to polygenic traits (Mulato et al., 2010). The extent of genetic variability existing in population of germplasm determines the success of the crop improvement program. Heritability provides the proportion of total phenotypic variance that is attributed to genetic causes. The estimates of heritability only fail to specify the response to selection (Johnson et al., 1955).

Genetically diverse parent is a pre-requisite to improve the chances of selecting better segregants for various characters. When such parents utilized in cross breeding programme, they are likely to produce high heterotic effect and wide spectrum of variability (Barh et al., 2014). The knowledge of genetic diversity in the improvement of crop has been stressed on both self and cross pollinated crop.

Therefore, the present research was under taken with the following objectives:

- ➤ To find out the genetic variability and association among 9 (nine) traits in 36 (thirty six) soybean genotypes.
- ➤ To assess the characters influencing genetic divergence
- ➤ To screen out the genetically diverse parents with elite agronomic performance

CHAPTER II

REVIEW OF LITERATURE

The review of literatures contain report on the crop under study and other related crops studied by several investigators, which appears pertinent in understanding the problem which may help in the explanation and the interpretation of results of the present study. In this section, an attempt has been made to review the available information at home and aboard on direct and indirect genetic effects on the yield performance of different soybean genotypes.

2.1 Variability, Heritability and Genetic Advance:

(Vedna, 2018) conducted a field experiment to study of genetic variability, heritability and genetic advance and other quality characters in in 307 soybean germplasm lines. Higher phenotypic coefficients of variation were observed for for harvest index and biological yield/plant. High heritability coupled with high genetic advance were detected for harvest index followed by biological yield /plant, seed yield /plant, number of pods/plant and 100-seed weight specifying the predominance of additive gene action in controlling the trait.

The genotypes G00197 took maximum days (39.86) to 50% flowering (DAE) while G00221 took minimum days (36.06) to 50% flowering (Biswas et al., 2016). The investigation was carried out at the experimental field of the Bangabandhu Sheikh Mujibur Rahman Agricultural University by the period from january 2012 to April 2012, Salna, Gazipur.

Hapsari et al (2021) conducted an experiment to evaluate the performance of yield and yield components of soybean genotypes, as well as the relationship pattern among characters that affect the seed yield. The combined analysis of variance for yield and yield component showed a significant interaction effect between location and genotype for the number of branches, the number of empty pods, 100 seed weight, and seed yield. The performance of yield and yield components of soybean genotypes tested in Malang showed earlier maturity, taller plants, larger seed size, and higher seed yields when compared to research conducted in Probolinggo. In the selection for the best genotypes, ten genotypes were chosen for their large seed size criteria, while two genotypes were chosen for their relatively medium maturity (81 days) in the location of Malang. In

Probolinggo, of the ten genotypes, three genotypes with medium maturity, and three genotypes with medium seed size. The selected genotypes will proceed to the stage of the advanced yield trial. The association study revealed that soybean yield has a positive correlation with plant height, number of nodes, number of branches, number of filled pods, days to flowering, and days to maturity.

(Pankaj, 2013) carried out an experiment on plant characterization and seed quality of some dwarf soybean genotypes. The heritability estimates for the number of branches/plant was high, genetic advance was low and genetic advance in per cent of mean were found very high, shown that this trait was governed by additive gene where selection might be useful for crop improvement.

(Iqbal, 2010) A study was carried out in National Agriculture Research Centre, Islamabad during autumn 2004 and 2005 to determine the variability and association among 9 traits in 139 soybean genotypes. The traits viz., days to maturity, plant height at maturity, number of branches per plant, number of pods per plant, 100-seed weight (g), oil content, grain yield per plant (g), biological yield per plant (g) and harvest index were studied. Results of analysis of variance showed significant differences among genotypes in terms of traits under study, which indicate the existence of genetic variation. Correlation coefficient indicated that the grain yield was positively and significantly correlated with all studied traits except plant height, which showed non-significant association during both years. Oil content showed significant and positive correlation with grain yield, 100-seed weight, and harvest index while significantly negative correlation were observed with days to maturity, plant height and number of branches per plant. Significantly positive correlations were observed for: days to maturity and plant height and number of branches per plant; number of branches per plant and number of pods per plant; number of pods per plant and biological yield per plant and harvest index; 100-seed weight and oil content; harvest index and 100-seed weight and biological yield per plant. Results obtained from this study can make better choice for soybean breeders for selecting genotypes among large number of accessions.

2.2 Correlation Co-efficient:

Joshi, et al. (2017) field experiments were conducted with the title study on genetic variability, heritability and genetic advance in soybean (*G. max* L. Merrill). He found Days to 50% Flowering showed highly significant positive correlation with, Days to maturity, Plant height (cm), No. of nodes/plant, No. of pods/plant, No. of seeds/plant, at both genotypic and phenotypic level. These findings indicated that those traits are governed by the same gene and simultaneous improvement would be effective, while insignificant but positive genetic correlation was found with Number of branches/plant. Days to 50% Flowering showed significant negative correlation with 100 seed weight (g)

Karnwal, et al. (2009) found Days to maturity showed significant positive correlation with, Plant height (cm), Number of branches/ plant, No. of Nodes/plant, No. of Pods/plant, No. of Seeds/plant at both genotypic and phenotypic level indicated that if days to maturity increased these parameters will also be increased, governed by the same gene and simultaneous improvement would be effective. Insignificant and negative correlation was found with 100 seed weight (g).

Vedna, (2018) conducted a field experiment to study of genetic variability, heritability and genetic advance and other quality characters in in 307 soybean germplasm lines. Number of branches /plant, number of seeds /pod, biological yield/plant and harvest index exhibited significantly positive correlation with seed yield /plant both at phenotypic and genotypic levels. Two traits viz., harvest index and biological yield /plant could be considered as direct selection indices for yield improvement in soybean.

2.3 Path Co-efficient:

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

Harpreet et al. (2007) reported that direct effects were highest for number of pods per plant, node at which first fertile pod develops, number of seeds per pod and pod length which can serve as reliable for selection.

Islam, (2015) evaluated that yield per plot was positively correlated with pods per plant, seeds per pod, branches per plant, harvest index, days to maturity and plant height which revealed that selection based on these traits could significantly improved the grain yield of soybean. From the path coefficient analysis, it was observed that among the different

yield contributing characters pods per plant, seeds per pod, plant height, 100 seed weight contributed maximum direct positive effect to yield per plot. Negative direct effect was observed for days to flowering and days to maturity, but its correlation with yield was positive. It was due to its positive indirect effect

Aditya, et al. (2011) conducted that the Path analysis exposed that days to 50% flowering had positive direct effect (0.098) on yield. Days to 50% flowering exhibited positive indirect effect with days to maturity, plant height, number of branches / plant , number of pods/plant , number of nodes/plant and number of seeds/ plant , while showed a negative indirect effect through 100 seed weight.

Husna et al. (2011) conducted that the results of path coefficient analysis revealed the maximum direct contribution towards yield per plant with number of fruit per plant (0.680) followed by fruit weight (0.453) in 31 sweet gourd genotypes.

Bisen, et al (2015) observed correlation among yield determining components in 86 diverse maturity genotypes of soybean. Path coefficient analysis revealed that pods/plant had the direct effect on seed yield followed by 100 seed weight. Pods/plant affected seed yield negatively via indirect effects of plant height, pod height and seed/pod.

2.4 Genetic Diversity:

Kumar et al. (2010) conducted a survey of the nature and magnitude of genetic diversity of 40 soybean genotypes. D^2 analysis grouped the genotypes into two different cluster A and Cluster B The data revealed that four principal components having greater than one eigenvalues contributed 76.2 %.

Iqbal et al. (2015) studied genetic diversity among 139 soybean genotypes. A total of 17 bands have been identified for 139 Soybean genotypes which include 9 monomorphic bands and 8 polymorphic bands.

Sihag et al. (2004) studied genetic diversity among 160 soybean genotypes using Mahalanobis' D2 statistic and grouped the genotype into 8 clusters. The clustering pattern revealed that no definite relationship existed between genetic diversity and geographic diversity. The genotypes from the same eco-geographic region were classified in different clusters and genotypes from different eco-geographic regions were classified into one cluster.

Vart et al. (2002) estimated genetic diversity in 56 genotypes of soybean by using D2 statistic and grouped them into 11 clusters. The clustering pattern was not significantly influenced by the eco-geographical distribution of genotypes.

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

Nooghab et al. (2014) investigated 56 genotypes of soybean. The genotypes has been divided into five groups based on morphologic traits including seeds weight per plant (g), pods length (cm), weight of 100 seeds (g) and yield (kg/ha).

Liu et al. (2018) in comparative analysis with five legume species, genes related to defense responses were significantly overrepresented in *Glycine*-specific orthologous gene families. A total of 304 putative nucleotide-binding site (NBS)-leucine-rich-repeat (LRR) genes were identified in this genome assembly.

CHAPTER III

MATERIALS AND METHODS

This chapter clarifies the information concerning methodology that was used in carrying out the study of character association and diversity analysis of different genotypes of Soybean. A brief representation of experimental site, climate and soil, experimental materials, layout and design of the experiment, growing of crops, intercultural operations, harvesting, data recording procedure and statistical analysis were described below:

3.1 Description of the experimental site

3.1.1 Experimental period

By the period from December 2020 to April 2021, the experiment was executed at Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur.

3.1.2 Geographical location

The experimental area was located at 24°09'N latitude and 90°26'E longitude having an elevation of 8.2 m from sea level (Anon., 1995). The experimental field falls under the Agro-ecological zone of The Modhupur Tract, AEZ number 28. The experimental site was shown in the map of AEZ of Bangladesh in (Appendix I).

3.1.3 Climatic condition

The area belongs to sub-tropical climate, which is characterized by high temperature accompanied by moderately high rainfall during Kharif seasons (mid-March to mid-November) and scanty rainfall associated with moderately low temperature during the Rabi (mid-November to mid-March) season. Details of the meteorological data including temperature, rainfall, humidity and sunshine hour during the period of the experiment was presented in (Appendix II).

3.1.4 Characteristics of soil

The soil used in the experiment belongs to Salna soil series of Madhupur Tract (24°09'N latitude and 90°26'E longitude) with shallow Red Terrace type of soil under AEZ number 28 having pH around 6.0 (UNDP, 1988). The nutrient status of the farm soil under the experimental plot with in a depth 0-20 cm were collected and analyzed in the Soil Research and Development Institute, Dhaka. The physical and chemical properties of experimental soil are given in (Table 1).

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Table 1. Physical and chemical properties of experimental soil-

Soil properties	Analytical values
Sand%	17
Silt%	62
Clay%	22
Texture%	Silty clay
pH	6.1
Organic carbon%	0.61
Total nitrogen%	0.07
Phosphorus (gm g^{-1} soil)	18.9

3.2 Experimental materials

36 (Thirty six) soybean genotypes were used in this experiment, among them thirty two genotypes were collected from AVRDC, Taiwan; 3 from BARI and 1 from BSMRAU. Genotypes with accession number used in this experiment are shown in (Table 2).

Table 2. List of experimental materials

Sl. No.	Genotype	Accession number	Source
1	G1	AGS313	AVRDC, Taiwan
2	G2	G00151	AVRDC, Taiwan
3	G3	G00152	AVRDC, Taiwan
4	G4	G00149	AVRDC, Taiwan
5	G5	G00022	AVRDC, Taiwan
6	G6	G00150	AVRDC, Taiwan
7	G7	G00035	AVRDC, Taiwan
8	G8	G00001	AVRDC, Taiwan
9	G9	G00145	AVRDC, Taiwan
10	G10	G00067	AVRDC, Taiwan
11	G11	G00061	AVRDC, Taiwan
12	G12	G00090	AVRDC, Taiwan
13	G13	PK472	AVRDC, Taiwan
14	G14	GALAR JAN	AVRDC, Taiwan
15	G15	G00170	AVRDC, Taiwan
16	G16	G00354	AVRDC, Taiwan
17	G17	G00015	AVRDC, Taiwan
18	G18	G00113	AVRDC, Taiwan
19	G19	G00173	AVRDC, Taiwan
20	G20	G00042	AVRDC, Taiwan
21	G21	G00024	AVRDC, Taiwan
22	G22	G00108	AVRDC, Taiwan
23	G23	G00204	AVRDC, Taiwan
24	G24	G00068	AVRDC, Taiwan
25	G25	G00179	AVRDC, Taiwan
26	G26	G00089	AVRDC, Taiwan
27	G27	G00063	AVRDC, Taiwan
28	G28	G00121	AVRDC, Taiwan
29	G29	G00053	AVRDC, Taiwan
30	G30	G00060	AVRDC, Taiwan
31	G31	G00261	AVRDC, Taiwan
32	G32	G00197	AVRDC, Taiwan
33	G33	BD2353	BARI, Bangladesh
34	G34	BD2325	BARI, Bangladesh
35	G35	BD2338	BARI, Bangladesh
36	G36	BU Soybean 1	BSMRAU, Bangladesh

AVRDC=Asian Vegetable Research and Development Center, BARI=Bangladesh Agricultural Research Institute, BSMRAU=Bangabandhu Sheikh Mujibur Rahman Agricultural University.

3.3 Layout and design of the experiment

The study was set out in randomized complete block design (RCBD) with 3 (three) replications. The size of experimental area was 455 m^2 with length 35 m and width 13 m. The total area was divided into 3(three) equal blocks. Each block contains 36(thirty six) plots where 36(thirty six) soybean genotypes were allocated by random assignment. The seeds were shown in lines keeping row-to-row distance 30cm and 5cm between seeds within rows.

3.4 Growing of crops

3.4.1 Land preparation

The experimental plot was fast opened by moldboard plough. Afterwards it was prepared by deep, cross ploughing and harrowing followed by laddering. The plots were broken and weeds were removed from the field to obtain a desirable tilth.

3.4.2 Application of fertilizers and manure

In the course of final preparation of land the total cow dung, triple super phosphate, muriate of potash and borax have been used on the site. Urea was applied in 3 equal splits. First dose of Urea was placed at the time of final land preparation, Second and third dose at 20 and 40 days after sowing correspondingly. Dosage of manure and fertilizer that were applied is shown in (Appendix III).

3.4.3 Seed sowing

The seeds of 36 genotypes were sown on 8 December, 2020. At first, seeds were treated with provax-200 @ 2.0g Kg^{-1} seed for an hour before sowing. The seeds were covered by pulverized soil just after sowing and gently pressed with hand and light watering was done just to supply sufficient moisture need to quick germination. The seedlings were immersed 8 to 11 days after sowing.

3.4.4 Intercultural operation

The intercultural operations like thinning, weeding and plant protection measures were taken as and when necessary. The crop was protected from the attack of insect and pests by spraying of Dursban 20 EC @ 5.0 ml/L of water. The disease was controlled by applying Dithane M-45 @ 2.0 g/L of water at the base of the plants. Leaf mosaic virus affected leaves were clipped out.

3.4.5 Irrigation and after care

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

3.4.6 Harvesting

The plant was harvested at full maturity. Such maturity came with yellowing of leaves with completion of leaf shedding and the pod color mostly become dark brown. Different varieties were harvested at different dates as they reach maturity converting variable periods. Harvesting was started at 105 DAS (days after sowing) and continued up to 115 DAS.

3.5 Data recording

Different biometric traits related to yield and its contributing characters were documented namely; days to 50% flowering, days to maturity, plant height (cm), number of branches/plant, number of pods/plant, number of nodes/plant, number of seeds/plant, 100 seeds weight (g), seed yield/plant (g).

3.5.1. Days to 50% flowering

Determine as the days required from sowing to 50% anthesis of every entry.

3.5.2 Days to maturity

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

3.5.3 Plant height (cm)

The average height of plant at matured stage measured from the ground level to the tip in cm using meter scale.

3.5.4 Number of branches/plant

At 60 days after planting, the number of branches arising from the main stem above the ground was logged and the mean was calculated.

3.5.5 Number of pods/plant

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

3.5.6 Number of nodes/plant

The total number of nodes were counted from the main stem above the ground at matured stage and the mean was calculated.

3.5.7 Number of Seeds/plant

The total number of seeds per plant was collected and recorded and the mean value for each of the genotypes was calculated accordingly.

3.5.8 100 seed weight (g)

Weight of hundred seeds selected at random from each of the genotype was recorded and expressed in grams.

3.5.9 Seed yield/plant (g)

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

Plate 1. View of experimental site

3.6 Statistical analysis

Multivariate analysis was used to measure mean data of the characters. Univariate analysis of the individual character was done for all characters under study using mean values (Singh and Chaudhury, 1985) and was estimated using MSTAT-C computer program. Duncans multiple range test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range, and co-efficient of variation (CV%) were estimated using MSTAT-C. Multivariate analysis was done by computer using the GENESTAT 10.13 and Microsoft Excel 2018 software through four techniques namely; principal component analysis (PCA), principal co-ordinate analysis (PCO), cluster analysis and canonical vector analysis (CVA).

3.6.1 Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula

Genotypic variance (σ^2g) =$\frac{GMS-EMS}{r}$

GMS = Genotypic mean sum of squares

EMS = Error mean sum of square

r = number of replications

Phenotypic variance (σ^2p) = σ^2g + EMS

Where,

σ^2 g = Genotypic variance

EMS = Error mean sum of square

3.6.2 Estimation of genotypic and phenotypic correlation co-efficient

It used to calculate the genotypes and phenotypes for all possible combinations. The genotypic co-variance component between the two features was derived the same as the corresponding variance component with the phenotypic covariance component. The components of covariance were used to calculate genotypic and phenotypic data. The relationship between the character pairs is the following:

Genotypic Correlation ($r_{gxy)} = \frac{\sigma^2 gxy}{\sqrt{\sigma^2 gx \sigma^2 gy}}$

Where,

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

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

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

Phenotypic correlation (r_{gxy}) $= \dfrac{\sigma pxy}{\sqrt{\sigma^2 px \sigma^2 py}}$

Where,

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

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

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

3.6.3 Estimation of genotypic and phenotypic co-efficient of variation

Genotypic and phenotypic co-efficient of variation were calculated by the formula.

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

Where,

$\sigma^2 g$ = Genotypic variance

$\bar{x}$ = Population mean similarly,

The phenotypic co-efficient of variation was calculated from the following formula. Phenotypic co-efficient variation (PCV) $= \sqrt{\dfrac{\sigma^2 ph}{\bar{x}}}$

Where,

$\sigma^2 ph$ = Phenotypic variance

x = Population mean

3.6.4 Estimation of heritability

Broad sense heritability was estimated by the following formula. $h^2_b\% = \dfrac{\sigma^2 g}{\sigma^2 ph}$

Where,

h^2_b= Heritability in broad sense

$\sigma^2 g$ = Genotypic Variance

$\sigma^2 ph$ = Phenotypic Variance

3.6.5 Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated using the formula.

Genetic advance (GA) = K. h^2 b. σ_{ph}

$$GA = K. \frac{\sigma^2 g}{\sigma^2 \sigma ph} . \sigma ph$$

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

σ_{ph} = Phenotypic standard deviation

h^2b = Heritability in broad sense

σ^2 = Genotypic variance

$\sigma^2 ph$ = Phenotypic variance

3.6.6 Estimation of genetic advance mean's percentage

Genetic advance as percentage of mean was calculated from the following formula

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

3.6.8 Estimation of path co-efficient analysis

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

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

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

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

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

Where, $r's$ denotes simple correlation co-efficient and $P's$ denote path co-efficient (Unknown). $P's$ in the above equation may be conveniently solved by arranging them in matrix from. Total correlation, say between x1 and y is thus partitioned follows:

P_{yx1}= The direct effect of x1 via x2 on y.

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

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

3.6.7 Multivariate analysis

Mahalanobis's (1936) generalized distance (D^2) statistical program is more reliable as necessary knowledge while selection of parents from about a mass of features which is available before the crossing. General distance (D^2) and auxiliary analyzes assessed the genetic diversity of genotypes. The Biometric methods have enabled genetically diversified parents to be chosen as a parenting program by quantifying genetic diversity. The main component analysis, cluster analysis and Canonical Vector analysis (CVA) are efficient analysis of the components. Multivariate parameters namely Principal Component analysis, Cluster analysis and Canonical Vector analysis (CVA) which quantify the differences among several quantitative traits are efficient method of evaluating genetic diversity. These are as follows:

3.6.7.1 Principal component analysis (PCA)

To study inter-relationships between several characters and to apply the sum of squares and matrix of products for the characters, one of the most important multivariable techniques is PCA. PCA therefore identifies linear combinations of a set of variables which maximize variation within them and shows a smaller number of dimensions to show the most original variability. The main components were therefore calculated from the correlation matrix and genotype ratings were obtained for the first components. Which has the maximum variance accounting property and subsequent latent roots components larger than unity. The contribution of different morphological characteristics to divergence from latent vectors of the first two main components is discussed.

3.6.7.2 Cluster analysis (CA)

A non-hierarchical classification was selected for dividing the genotypes of a data set into some number of mutually exclusive groups clustering. The algorithm is used in genstat to search for the optimal values of the selected criterion. Beginning with some initial grade 49 the algorithm divides the genotype into the number of groups required repeatedly. As long as that transfer improves the value of the criterion, genotypes are transferred from one group to another. If the criterion is not improved with a further transfer, the algorithm moves to a second stage, which examines the effect of swooping two different class genotype types etc.

3.6.7.3 Canonical vector analysis (CVA)

Complementary to D^2 statistic, Canonical variate analysis is a category of multivariate analysis where canonical vectors and roots representing different axes of differentiation and the amount of variation accounted for by each of such axes respectively and derived. Canonical variate analysis computed linear combination of original variability that maximized the ratio between ground and within group variations, thereby giving functions of the original variables that could be used to discriminate between the groups. Thus in this analysis, a series of orthogonal transformation was done sequentially for maximizing the ratio of the groups to within group variations.

3.6.7.4 Selection of varieties for future hybridization program

Divergence is typically used for the identification of different genotypes for purposes of hybridization. The most divergent genotypes of these different clusters are expressed by clusters that are separated by the largest statistical distance (D2). For the efficient hybridization program Singh and Chaudhur varieties or lines have been selected (1985). In selecting genotypes for the hybridization program, the following points should be considered accordingly:

i. Choice of cluster from which genotypes are selected for use as parents

ii. Selection of particular genotypes from the selected clusters

iii. Relative contribution of the characters to the total divergence

iv. Other important characters of the genotypes performance

CHAPTER-IV

RESULTS AND DISCUSSION

The present experimentation was accompanied for character association and genetic diversity analysis of different genotypes of soybean. Mean performance, genetic variability, correlation coefficient, path analysis and genetic diversity analysis on different yield attributes and yields of soybean genotypes were estimated. The experimental results obtained have been displayed with the help of Table and possible interpretation was provided under the following headings and sub-headings:

4. 1Genetic components of variation

Analysis of variance and mean performance of different yield and yield attributes of 36 (thirty six) soybean genotypes were presented in (Table 3). The analysis of variance showed highly significant differences (P>0.05) among the mean values for all traits i.e. days to 50% flowering, days to maturity, plant height (cm), number of branches/plant, number of nodes/plant, number of pods/plant, number of seeds/plant, 100 seed weight (g) and seed yield/plant (Table 4). Therefore, there is a noteworthy opportunity for selecting majority of the traits in the genotypes.

Table 3: The analysis of variance of nine characters of 36 soybean genotypes

SV	df	Days to 50% flowering	Days to Maturity	No of Branches /plant	Plant height (cm)	No of pods /plant	No. of Nods/plant	Seeds / plant	100 seed weight (g)	Seed yield/plant(g)
Replication	2	2.01	1.59	0.14	0.14	0.47	0.20	1.42	0.24	0.11
Genotype	35	200.05**	277.30**	6.85**	563.50**	365.11**	12.55**	1797.33**	34.38**	10.79**
Error	70	1.62	4.43	0.19	1.34	0.43	0.11	0.55	0.13	0.11
CV (%)		2.29	1.94	13.26	3.06	2.37	3.61	1.40	2.83	5.34

SV=Sources of variation, df =Degrees of freedom, CV(%)=Percentage of coefficient of variation, **Significant at 1% level.

4.2 Genetic variability, heritability and genetic advance

The extent of genetic variability existing in population of germplasm determines the success of the crop improvement program. Heritability provides the proportion of total phenotypic variance that is attributed to genetic causes. The estimates of heritability only fail to specify the response to selection (Johnson et al., 1955). Consequently, the heritability estimates appears to be more significant when accompanied by estimates of genetic advance. The genetic advance in per cent of mean (GAM) was also estimated. The evaluations of mean, range, genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic advance in per cent mean for all the nine characters of thirty six soybean genotypes were studied and the results are presented in (Table 4).

Table 4. Mean performance of nine characters of 36 soybean genotypes

Genotypes	Days to 50% flowering	Days to Maturity	No of branches /plant	Plant height (cm)	No of pods /plant	No. of nodes/plant	Seeds / plant	100 seed weight (g)	Seed yield/plant
G1	66.67c	121.00bc	4.70c-f	58.77c	28.90gh	10.93c	73.12f	16.26c	12.25a
G2	49.67l-n	102.00no	3.17j-l	31.80j-l	23.90m	8.53jk	43.31q	13.09g	5.57i-k
G3	54.00gh	106.00lm	2.17n-q	52.97e	26.20kl	9.63d-f	45.29p	18.07b	8.14c
G4	48.33n-p	110.00i-k	3.40i-k	30.77k-m	27.07jk	9.00g-j	52.31m	15.11de	7.86cd
G5	50.67k-m	114.33e-h	5.17b-d	45.80g	53.43b	12.23b	132.26a	6.22p	7.23ef
G6	54.67fg	104.00m-o	2.13n-q	33.13j	28.30g-i	9.33f-h	53.82l	15.55d	8.19c
G7	52.67g-k	107.00k-m	3.17j-l	45.70g	17.70qr	6.77n	35.38u	13.69f	4.91l-n
G8	57.67e	113.00f-i	4.73c-e	61.27b	34.90e	12.10b	59.69h	11.96hi	7.10e-g
G9	51.00j-l	100.67o	1.57q-s	30.53lm	16.13s	9.43e-g	43.41q	10.24lm	4.46no
G10	51.33i-l	104.67mn	1.00s	29.97l-n	24.33m	6.93n	39.34s	14.58e	4.50no
G11	57.33e	95.00p	2.80k-n	23.57q	14.57t	7.70m	37.81t	10.76kl	3.42p
G12	57.33e	105.67lm	4.00f-i	43.93gh	21.33o	8.23kl	32.53vw	17.80b	5.78i
G13	74.00a	124.67a	4.53d-g	55.43d	27.93h-j	12.03b	55.48jk	11.45ij	7.460de
G14	70.67b	111.00h-j	5.83b	45.60g	43.27c	12.90a	110.18b	6.22p	6.49h
G15	46.33pq	114.00e-h	1.90p-r	25.60op	17.47qr	6.63no	32.02wx	16.21c	5.24j-l
G16	65.67c	116.33d-f	3.10j-l	49.50f	35.83e	10.70c	41.76r	13.34fg	5.33i-l
G17	53.33g-i	108.67j-l	3.93g-i	37.97i	55.47a	9.10g-i	102.35c	6.34p	6.67gh
G18	51.00j-l	104.00m-o	3.03j-m	23.93pq	26.63k	9.93de	38.80st	17.66b	7.42d-f
G19	61.67d	124.00ab	2.13n-q	24.43pq	18.43pq	8.83h-j	43.29q	10.03m	4.30o
G20	46.67o-q	93.00pq	2.63l-o	19.00r	17.20r	9.90de	42.85qr	14.84e	6.59gh
G21	70.00b	116.33d-f	3.70h-j	50.53f	52.73b	11.80b	94.86d	11.53ij	11.34b

Table 4.(cont''d)

Genotypes	Days to 50% flowering	Days to maturity	No of branches /plant	Plant height (cm)	No of pods /plant	No. of nodes/plant	Seeds / plant	100 seed weight (g)	Seed yield/plant
G22	65.33c	111.00h-j	4.37e-h	42.60h	42.47c	8.87h-j	88.51e	7.73o	6.54h
G23	54.33gh	93.33pq	1.00s	23.67q	19.37p	4.97q	31.06xy	14.65e	4.35o
G24	51.00j-l	104.00m-o	2.27n-q	25.07o-q	15.70s	6.93n	29.97y	15.48d	4.31o
G25	62.00d	108.33j-l	3.17j-l	26.47o	25.53l	8.80ij	50.37n	10.16m	5.09k-m
G26	58.00e	122.67ab	4.13e-h	44.50 g	27.73ij	10.03d	42.08r	16.35c	6.90f-h
G27	53.67gh	94.33p	1.27rs	32.47jk	22.40n	7.90lm	35.20u	12.00hi	4.22o
G28	53.00g-j	96.33p	2.33m-p	33.07j	15.43st	6.63no	33.30v	14.76e	4.70m-o
G29	52.33h-k	108.67j-l	2.10n-q	24.50pq	13.20u	5.83p	25.18z	19.44a	4.653m-o
G30	51.33i-l	118.00cd	4.10e-i	28.53n	19.47p	10.13d	38.45st	13.23fg	5.11j-m
G31	44.67q	114.67d-g	5.30bc	31.30j-m	37.60d	8.97g-j	57.09i	11.96hi	6.53h
G32	48.67m-o	90.33q	1.97o-r	50.73f	25.43l	8.00lm	41.74r	13.24fg	5.08k-m
G33	56.67ef	124.33ab	5.77b	81.93a	32.43f	12.90a	54.28kl	10.46lm	5.63ij
G34	72.00ab	112.67g-i	3.13j-l	29.80mn	29.07g	9.07g-i	46.92o	11.34jk	5.17j-m
G35	49.33l-n	116.67de	1.70p-s	26.50o	24.37m	6.17op	55.59j	8.88n	4.95l-n
G36	39.67r	95.67p	7.60a	38.77i	33.10f	7.07n	64.76g	12.22h	7.93cd
Mean	55.63	108.51	3.31	37.78	27.64	9.03	52.90	12.86	6.15
Min	39.67	90.33	1.00	19.00	13.20	4.97	25.18	6.22	3.42
Max	74.00	124.67	7.60	81.93	55.47	12.90	132.26	19.44	12.25
SE (±)	1.04	1.72	0.36	0.94	0.53	0.27	0.60	0.30	0.27
LSD (0.05)	2.07	3.43	0.71	1.88	1.07	0.53	1.20	0.59	0.53

SE=Standard Error, LSD=Least Significant Difference

4.2.1 Days to 50% Flowering

The result of analysis of variance indicated significantly (P>0.05) higher amount of variability present among the genotypes for the character days to 50% flowering (Table 3). The finding clearly showed that there exists high variability for days to 50% flowering among the genotypes studied. The lowest days to 50% flowering was observed in G36 (39.67 days) while the highest was in G13 (74.00 days). The average days to 50% flowering was recorded around 55.63 days with a range from 39.67 to 74.00 days (Table 4). The genotypes G00197 took maximum days (39.86) to 50% flowering (DAE) while G00221 took minimum days (36.06) to 50% flowering. (Biswas *et al.*, 2016). The phenotypic variation (67.76) appeared to be slightly higher than the genotypic variation (66.14), signifying that the environment has less influence on the expression of the genes controlling this trait. The difference between the genotypic co-efficient of variation (14.62) and phenotypic coefficient of variation (14.80) were close to each other (Table 5) indicating minor environmental influence on this character. The heritability (97.61%) estimates for this trait was high, genetic advance (16.55) was at moderate level and genetic advance over percentage of mean (29.75) were found moderately high, revealed the possibility of predominance of additive gene effect and selection might be effective.

Table 5. Estimation of genetic parameters nine characters of 36 soybean genotypes

Character	Phenotypic variance	Genotypic variance	PCV (%)	GCV (%)	Heritability (%)	GA	GA (%)
Days to 50% flowering	67.76	66.14	14.80	14.62	97.61	16.55	29.75
Days to maturity	95.39	90.96	9.00	8.79	95.35	19.18	17.68
No of branches/plant	2.41	2.22	46.97	45.06	92.03	2.94	89.05
Plant height (cm)	188.72	187.39	36.36	36.23	99.29	28.10	74.37
No of pods /plant	121.99	121.56	39.96	39.89	99.65	22.67	82.03
No. of nodes/plant	4.26	4.15	22.85	22.57	97.51	4.14	45.91
Seeds /plant	599.48	598.93	46.28	46.26	99.91	50.39	95.26
100 seed weight (g)	11.55	11.42	26.43	26.28	98.85	6.92	53.83
Seed yield/plant	3.67	3.56	31.14	30.68	97.06	3.83	62.26

PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, GA= Genetic advance, GA (%)= Genetic advance as percentage of mean

4.2.2 Days to maturity

Days to maturity varied significantly among the studied soybean genotypes (Table 3). The average days to maturity was recorded around 108.51days with a range from 90.33 to 124.67 days. The highest days to maturity (124.67 days) was found in G13, while the lowest days to maturity (90.33 days) was found in G32 (Table 4). The phenotypic variance (95.39) appeared to be higher than the genotypic variance (90.96) recommended there is effect of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 8.79 and 9.00 respectively which were close to each other (Table 5). There was a very little difference between phenotypic and genotypic co-efficient of variation, indicating minimal environmental influence on this character. The heritability (95.35%) estimates for this trait was high, genetic advance (19.18) moderately high and genetic advance in percent of mean (17.68) was found moderately high (Table 5), shown that this trait was governed by additive gene as a result selection for this trait may be useful. High heritability of genetic advance was reported for days to maturity in soybean (Hapsari, et al, 2021).

4.2.3 Number of branches/plant

The number of branches/plant varied among the soybean genotypes (Table 3). Significantly higher number (7.6) of branches was recorded in G36, while the lowest was in G10 with the mean of 3.31. The phenotypic variance (2.4) appeared to be slightly higher than the genotypic variation (2.22), signifying that the environment has less influence on the expression of the genes controlling this trait. The phenotypic co-efficient of variation and the genotypic co-efficient of variation were 46.97 and 45.06 respectively (Table 5) which revealed presence of considerable variability among the genotypes. The heritability (92.93%) estimates for this trait was high, genetic advance (2.94) was low and genetic advance in per cent of mean (89.50) were found very high, shown that this trait was governed by additive gene where selection might be useful for crop improvement. The result corroborated with that of (Pankaj, 2013).

4.2.4 Plant Height

The maximum plant height 81.93cm was observed in G33 while the lowest plant height in G20 (19.00cm) with the mean of 37.78cm. The genotypic and phenotypic variance was observed 187.39 and 188.72 respectively (Table 5) for plant height displays low environmental influence. the phenotypic co-efficient of variation (36.36) was marginally higher than the genotypic co-efficient of variation (36.23),specifies that the apparent variation is governed by the genotypes with less influence of the environment. The heritability (99.29%) estimates for this trait was very high, genetic advance (28.10) was moderately high and genetic advance in per cent of mean (74.37) was found also high (Table 5), shown that this trait was governed by additive gene would be beneficial for selection which was parallel to the earlier findings by Jam and Ramgiry (2000). The phenotypic variation in plant height is displayed in (Plate 2)
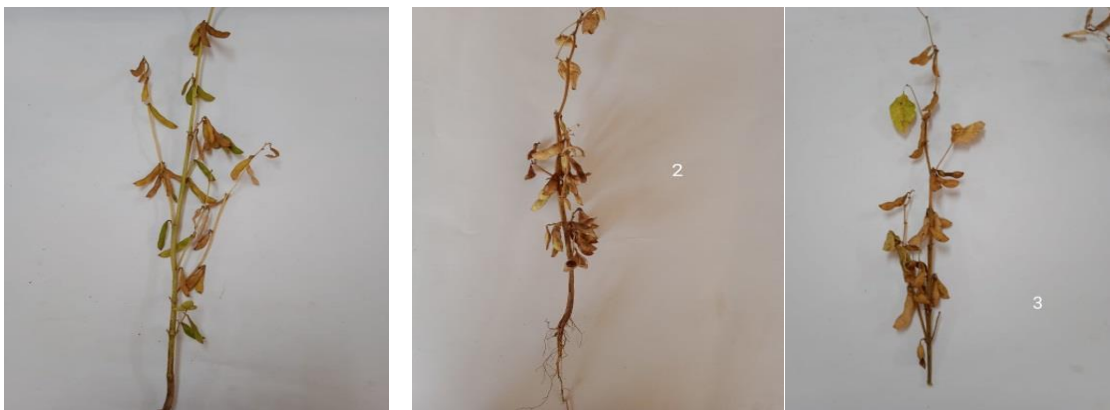
G1   G2   G3

G4   G5   G6

G7

G8

G9

G10

G11

G12

pk472

G13

G14

G15   **G16**   **G17**

G21   **G22**   **G25**

G30   **G31**   **G36**

Plate 2. Showing morphological variation in plant hight among different soybean genotypes (G1-G36)

4.1.5 Number of nodes/plant

The number of nodes/plant varied among the soybean genotypes (Table 3). Significantly higher number (12.90) of nodes was recorded in G14, while the lowest was in G23 (4.97) with the mean of 9.30. The phenotypic variance (4.26) appeared to be slightly higher than the genotypic variation (4.15), signifying that the environment has less influence on the expression of the genes controlling this trait. The phenotypic co-efficient of variation and the genotypic co-efficient of variation were 22.85 and 22.57 respectively (Table 5) which revealed the apparent variation is governed by the genotypes with less influence of the environment. The heritability (97.51) estimates for this trait was high, genetic advance (4.14) was low and genetic advance in per cent of mean (45.91) was found high, shown that this trait was governed by additive gene where selection might be useful for crop improvement.

4.1.6 Number of pods/plant

Significant mean sum of square for pods per plant indicated that considerable variation for this trait exists in soybean (Table 3). The number of pods/plant was ranged from 13.20 to 55.47 with mean of 27.64. The least number of pods/plant was observed in genotype G29 while maximum number of pods per plant was found in the genotype G17 (Table 4). The phenotypic variance (121.99) appeared to be slightly higher than the genotypic variation (121.56), signifying that the environment has very less influence on the expression of the genes controlling this trait. The phenotypic co-efficient of variation and the genotypic co-efficient of variation were 39.96 and 39.89 respectively (Table 5), which revealed the apparent variation is governed by the genotypes with less influence of the environment. The heritability (99.65%) estimates for this trait was high, genetic advance (22.67) was moderately and genetic advance in per cent of mean (82.03) was found high, shown that this trait was governed by additive gene where selection might be useful for crop improvement. High heritability coupled with high genetic advance were detected for seed yield/plant, followed by number of pods/plant and 100-seed weight representing the predominance of additive gene action in controlling the trait (Vedna, 2018).

4.1.7 Number of seeds/plant

The highest number of seeds/plant (132.26) was observed in G5 while the lowest number in G29 (25.18) with the mean of 52.90 (Table 4). The genotypic and phenotypic variance was observed 598.93 and 599.48 respectively (Table 5) suggested low influence of environment on the expression of the of variation genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 46.26 and 46.28, respectively which were close to each other (Table 2). The heritability (99.91%) estimates for this trait was very high, genetic advance (50.39) and genetic advance in percent of mean (95.26) were estimated high and very high correspondingly (Table 2), explained that this trait was governed by additive gene. Therefore selection for this trait would be effective. A similar finding was reported by (Chandel et al., 2013). Phenotypic variation of seeds of genotypes studied shown in plate 5.

4.1.8 100 seed weight (g)

100 seed weight (g) significantly varied among the soybean genotypes (Table 3). Meaningfully higher was 100 seed weight (g) recorded in G29 (19.44), while the lowest was in G5 (6.22g) with the mean of 12.86g. The finding was identical with the finding of (Sultana, D., 2015). The phenotypic variance (11.55) appeared to be slightly higher than the genotypic variation (11.42), signifying that the environment has very fewer influence on the expression of the genes controlling this trait. The phenotypic co-efficient of variation and the genotypic co-efficient of variation were 26.43 and 26.28 respectively (Table 5) which revealed the apparent variation is governed by the genotypes with less influence of the environment. The heritability (98.85%) estimates for this trait was high, genetic advance (6.92) was low and genetic advance in per cent of mean (53.83) was found high, shown that this trait was governed by additive gene where selection might be suitable for crop improvement which was in accordance with Awal (2014).

4.1.9 Seed yield/plant (g)

Seed yield/plant varied significantly among the studied soybean genotypes (Table 3). Significantly higher seed yield/plant was noted (12.25g) in G1, while the lowest was in G11 (3.42g) with the mean of 6.15g.The phenotypic variance (3.67) appeared to be slightly higher than the genotypic variation (3.56), signifying that the environment has very low influence on the expression of the genes controlling this trait. The phenotypic

co-efficient of variation and the genotypic co-efficient of variation were 31.14 and 30.68 respectively (Table 3) which revealed presence of considerable variability among the genotypes. The heritability (97.06%) estimates for this trait was high, genetic advance (3.83) was low and genetic advance in per cent of mean (89.50) was noted very high, shown that this trait was governed by additive gene where selection might be useful for crop improvement. which was in accordance with (Iqbal, et al., 2010) findings.

| G1 | G2 | G3 |

| G4 | G5 | G7 |

| G9 | G10 | G11 |

G12

G14

G15

G16

G17

G19

G20

G21

G22

G23

G24

G25

G27   G28   G29

G31   G33   G34

G35   G36
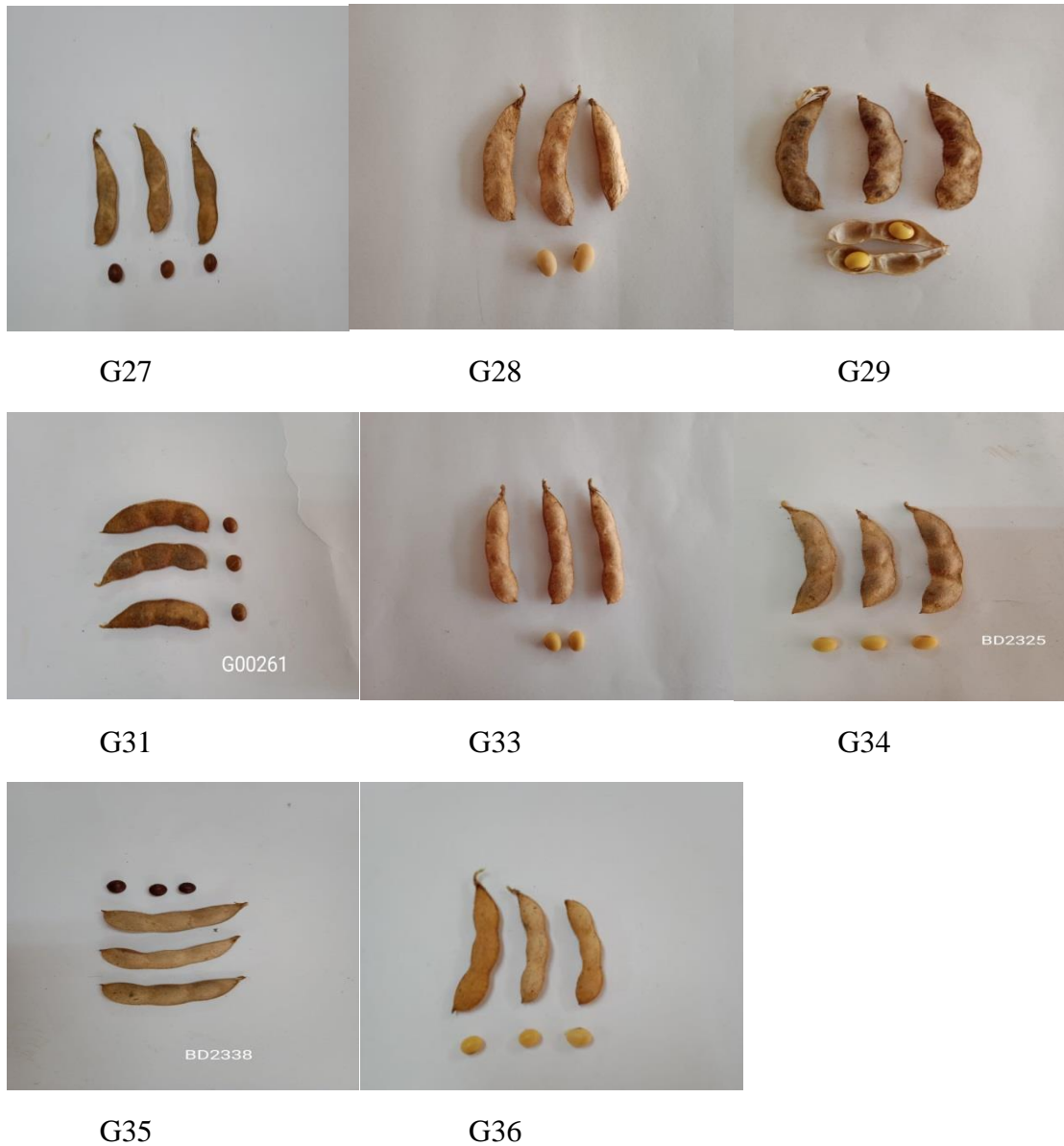
Plate 3. Showing morphological variation in seeds among different soybean genotypes (G1-G36)

4.2. Correlation co-efficient

Yield is a complex product being influenced by several inter-dependable quantitative characters. Thus, selection for yield may not be effective unless the other yield components influence it directly or indirectly are taken in to concern. When selection pressure is exercised for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated characters. Hence knowledge regarding association of character with yield and among themselves provides guideline to the plant breeder for making improvement through selection provide a clear

understanding about the contribution in respect of establishing the association by genetic and non-genetic factors. Coefficients of phenotypic and genotypic correlation among different yield components of nine characters of 36 soybean genotypes were discussed character wise days to 50% flowering, days to maturity, plant height (cm), number of branches/plant, number of nodes/plant, No. of pods/plant, No. of seeds/plant, 100 seed weight (g) and seed yield/plant in (Table 6).

Days to 50% flowering

Days to 50% flowering showed highly significant positive correlation with, Days to maturity (0.487 and 0.472), plant height (0.377 and 0.371), no. of nodes/plant (0.504 and 0.494), no. of pods/plant (0.299 and 0.296), no. of seeds/plant (0.286 and 0.283), seed yield/plant (0.255 and 0.251) both at genotypic and phenotypic levels (Table 4). These findings indicated that those trait are governed by the same gene and simultaneous improvement would be effective, while insignificant but positive genetic correlation was found with number of branches/plant (0.148 and 0.135). Days to 50% flowering showed significant negative correlation with 100 seed weight (g) (Table 4). Inderjit, et al (2007) reported that days to 50% flowering were significantly correlated with grain yield.

Table 6. Coefficients of phenotypic and genotypic correlation among different yield components of nine characters of 36 soybean genotypes

Character		Days to 50%flower ing	Days to maturity	No of branches /plant	Plant height (cm)	No of pods /plant	No. of nods/plant	Seeds / plant	100 seed weight (g)
Days to maturity	r_g	0.487**							
	r_p	0.472**							
No of branches /plant	r_g	0.148	0.392**						
	r_p	0.135	0.360**						
Plant height (cm)	r_g	0.377**	0.430**	0.539**					
	r_p	0.371**	0.416**	0.515**					
No of pods /plant	r_g	0.299**	0.342**	0.580**	0.465**				
	r_p	0.296**	0.333**	0.562**	0.462**				
No. of nods/plant	r_g	0.504**	0.540**	0.586**	0.644**	0.593**			
	r_p	0.494**	0.514**	0.553**	0.636**	0.585**			
Seeds/plant	r_g	0.286**	0.299**	0.581**	0.366**	0.893**	0.585**		
	r_p	0.283**	0.291**	0.558**	0.365**	0.892**	0.577**		
100 seed weight (g)	r_g	-0.260**	-0.187	-0.349**	-0.149	-0.586**	-0.353**	-0.701**	
	r_p	-0.258**	-0.181	-0.327**	-0.146	-0.582**	-0.348**	-0.697**	
Seed yield/plant	r_g	0.255**	0.330**	0.485**	0.458**	0.549**	0.538**	0.526**	0.092
	r_p	0.251**	0.317**	0.453**	0.448**	0.541**	0.521**	0.520**	0.094

**. Correlation is significant at the 0.01 level

Days to maturity

Days to maturity showed significant positive correlation with plant height (0.430 and 0.416), number of branches/plant (0.392 and 0.360), no. of nodes/plant (0.540 and 0.514), no. of pods/plant (0.342 and 0.333), no. of seeds/plant (0.299 and 0.291) both at genotypic and phenotypic level indicated that if days to maturity increased these parameters will also be increased (Table 6). These findings indicated that those traits are governed by the same gene and simultaneous improvement would be effective. On the other hand insignificant and negative correlation was found with 100 seed weight (g). Karnwal, et al. (2009) observed that maturity of soybean was positively correlated with seed yield.

Plant height (cm)

Plant height (cm) exhibited highly significant positive correlation with number of nodes/plant (0.644 and 0.636), no. of pods/plant (0.465 and 0.462), no. of seeds/plant (0.366 and 0.365), seed yield/plant (0.458 and 0.448) both at genotypic and phenotypic level (Table 6) directed that if plant height increased these parameters will also be increased, governed by the same gene and simultaneous improvement would be effective. Insignificant and negative correlation was found with 100 seed weight (-0.149 and -0.146). Saurabh, et al. (1998) observed that significant and positive correlations between plant height and pods per plant.

Number of branches/plant

Number of branches/plant showed highly significant positive correlation with, plant height (0.539 and 0.515), no. of nodes/plant (0.586 and 0.553), no. of pods/plant (0.580 and 0.562), no. of seeds/plant (0.581 and 0.558) both at genotypic and phenotypic level (Table 6) indicated that if number of branches/plant increased these parameters will also be increased (Table 6). On the other hand insignificant and negative correlation was found with 100 seed weight (-0.349 and -0.327). Aditya, et al. (2011) reported that number of branches/plant was positively correlated with seed yield.

Number of nodes/plant

Number of nodes/plant exhibited highly significant positive correlation with number of seeds/plant (0.585 and 0.577), seed yield/plant (0.538 and 0.521) both at genotypic and phenotypic level (Table 6) directed that if number of nodes/plant increased these

parameters will also be increased and simultaneous improvement would be effective. Insignificant and negative correlation was found with 100 seed weight (-0.353 and -0.348).

Number of pods/plant

Number of pods/plant showed highly significant positive correlation with, number of nodes/plant (0.593 and 0.585), number of seeds/plant (0.893 and 0.892), seed yield/plant (0.549 and 0.541) both at genotypic and phenotypic level (Table 6). This finding indicated that those traits are governed by the same gene and simultaneous improvement would be effective, while significant negative correlation with 100 seed weight (-0.586 and -0.582) (Table 6).

Number of seeds/plant

Number of seeds/plant noted highly significant positive correlation with seed yield/plant (0.526 and 0.520) both at genotypic and phenotypic level (Table 6). This finding indicated that those traits are governed by the same gene and simultaneous improvement would be effective, while significant negative correlation with 100 seed weight (-0.701 and -0.697) (Table 6). Jain, et al (2014) reported that seeds per plant significantly correlated with seed yield.

100 seed weight (g)

100 seed weight (g) exhibited insignificant but positive correlation, at both genotypic and phenotypic level with seed yield/plant (0.092 and 0.094) (Table 6). Ave and Ceyhan, (2006) found that hundred seed weight significantly correlated with pod yield.

4.3 Path co- efficient analysis

Portioning of genotypic correlation of thirty six genotypes, yield and its contributing traits in Soybean are presented in Table 7 and discussed character wise as follows.

Association of character determined by correlation co-efficient may not provide an precise picture of the relative importance of direct and indirect influence of each of yield components. In order to find out a clear picture of the inter relationship between yield per plant and other yield attributes, direct and indirect effects were worked out using path analysis at phenotypic level which also measured the relative importance of each component. Estimation of direct and indirect effect of path co-efficient analysis for soybean showed in (Table 7).

4.1 Days to 50% flowering

Path analysis exposed that days to 50% flowering had positive direct effect (0.098) on yield. Days to 50% flowering exhibited positive indirect effect with days to maturity (0.048), plant height (0.037), number of branches/plant (0.015), number of pods/plant (0.029), number of nodes/plant (0.050) and number of seeds/plant (0.28), while showed a negative indirect effect through 100 seed weight (-0.026) (Table 7). Aditya, et al. (2011) reported that days to 50% flowering showed sufficient positive direct effect with seed yield.

Days to maturity

Days to maturity showed positive direct effect (0.024) on yield. Days to maturity exhibited positive indirect effect with days to 50% flowering (0.011), plant height (0.010), number of branches/plant (0.009), number of pods/plant (0.008), number of nodes/plant (0.013) and number of seeds/plant (0.007), while showed a negative indirect effect through 100 seed weight (-0.004) (Table 7).

Number of branches/ plant

Number of branches/plant exposed positive direct effect (0.024) on yield. Number of branches/plant exhibited positive indirect effect with days to 50% flowering (0.017), Days to maturity (0.044), plant height (0.061), number of pods/plant (0.066), number of nodes/plant (0.066) and number of seeds/plant (0.066), while showed a negative indirect effect through 100 seed weight (-0.040) (Table 7).

Plant height (cm)

Plant height (cm) showed positive direct effect (0.024) on yield. exhibited positive indirect effect with days to 50% flowering (0.013), Days to maturity (0.014), numbers of branches/plant (0.018) , number of pods/plant (0.016), number of nodes/plant (0.022) and number of seeds/plant (0.012), while showed a negative indirect effect through 100 seed weight (-0.052) (Table 7).

Number of pods/plant

Path analysis exposed that number of pods/plant had positive direct effect (0.089) on yield. number of pods/plant exhibited positive indirect effect with days to 50% flowering

(0.026), days to maturity (0.030), plant height (0.041), number of branches/plant (0.051), number of nodes/plant (0.053) and number of seeds/plant (0.073), while showed a negative indirect effect through 100 seed weight (-0.052) on yield (Table 7).

Number of nodes/plant

Number of nodes/plant showed positive direct effect (0.137) on yield. It exhibited positive indirect effect with days to 50% flowering (0.069), days to maturity (0.074), numbers of branches/plant (0.088), plant height (0.088) number of pods/plant (0.081), and number of seeds/plant (0.080), while showed a negative indirect effect through 100 seed weight (-0.048) (Table 7).

Table 7. Partitioning of genotypic into direct and indirect effects of morphological characters of 36 Soybean genotypes by path coefficient analysis

Character	Direct effect	Days to 50%flowering	Days to maturity	No. of branches /plant	Plant height (cm)	No. of pods /plant	No. of nodes/plant	Seeds / plant	100 seed weight (g)	Genotypic Correlation with yield
Days to first flowering	**0.098**		0.011	0.017	0.013	0.026	0.069	0.248	-0.228	**0.255****
Days to maturity	**0.024**	0.048		0.044	0.014	0.030	0.074	0.259	-0.164	**0.330****
No of branches /plant	**0.113**	0.015	0.009		0.018	0.051	0.080	0.503	-0.305	**0.485****
Plant height (cm)	**0.033**	0.037	0.010	0.061		0.041	0.088	0.317	-0.131	**0.458****
No of pods /plant	**0.089**	0.029	0.008	0.066	0.016		0.081	0.773	-0.513	**0.549****
No. of nodes/plant	**0.137**	0.050	0.013	0.066	0.022	0.053		0.507	-0.309	**0.538****
Seeds / plant	**0.866**	0.028	0.007	0.066	0.012	0.079	0.080		-0.613	**0.526****
100 seed weight (g)	**0.874**	-0.026	-0.004	-0.040	-0.005	-0.052	-0.048	-0.607		**0.092**

Residual effect= 0.23 **correlation is significant at the 0.01 level

Number of seeds/plant

Number of seeds/plant showed positive direct effect (0.866) on yield (Table 7). It exhibited positive indirect effect with days to 50% flowering (0.248), days to maturity (0.259), numbers of branches/plant (0.503), plant height (0.317), number of pods/plant (0.773), number of nodes/plant (0.507), while showed a negative indirect effect through 100 seed weight (-0.607) on yield (Table 7).

100 seed weight (g)

Path analysis exposed that 100 seed weight (g) had highest positive direct effect (0.874) on yield. 100 seed weight (g) exhibited negative indirect effect with days to 50% flowering (-0.305), days to maturity (-0.164), plant height (-0.131), number of branches /plant (-0.305), number of pods/plant (-0.513), number of nodes/plant (-0.309) and number of seeds/plant (-0.613) (Table 7).

4.4 Genetic diversity analysis of soybean genotypes

More than one multivariate technique was required to represent the results more clearly and it was obvious from the results of many researchers (Bashar, 2002; Uddin, 2001). In the analysis of genetic diversity multivariate techniques were used.

4.4.1 Principal component analysis (PCA)

Principal components were computed from the correlation matrix from genotype scores obtained from first components and succeeding components with latent roots greater than the unity. The PCA yielded eigen values of each principal component axes with the first axes totally accounting for the variation. PCA was carried out with 36 (thirty six) soybean genotypes. The first principal component axes accounted for 50.52% of the total variation while principal components two and three accounted for 15.18%, 11.8% respectively (Table 8). Principal component analysis exposed that genotypes, viz. JS-95-60, JS-20-103, JS20-69, JS-20-114, JS-20-49 and JS-335, were diverged from each other Bisen, (2015). Depending on the values of principal component scores 2 and 1 obtained from the principal component analysis, a two-dimensional scatter diagram was formed (Z1 - Z2) using component score 1 as X-axis and component score 2 as Y-axis was constructed, which has been presented in (Figure 1). The position of the genotypes in the scatter diagram was apparently distributed into six groups, which indicated that there existed considerable diversity among the genotypes.

Table 8. Eigen value, variance (%) and cumulative (%) total variance of the principal components

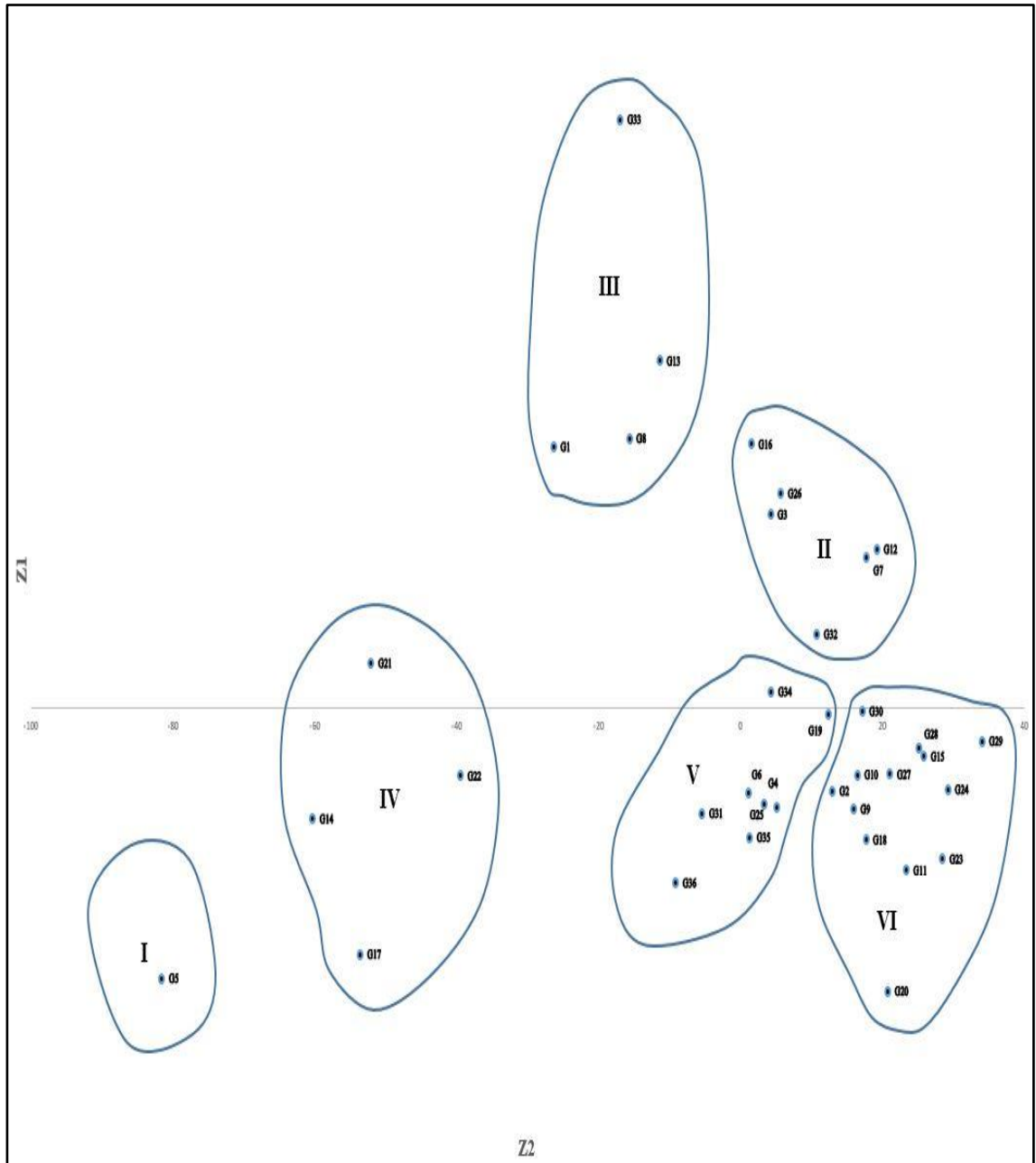| Principle component axes	Eigen value	Variance (%)	Cumulative (%) total variance
I	4.55	50.52	50.52
II	1.37	15.18	65.7
III	1.06	11.8	77.5
IV	0.66	7.33	84.83
V	0.53	5.93	90.76
VI	0.34	3.79	94.55
VII	0.29	3.23	97.78
VIII	0.14	1.55	99.33
IX	0.06	0.68	100

Figure 1. Scatter diagram of 36 soybean genotypes of based on their principal component scores

Table 9. Distribution of 36 soybean genotypes into six different clusters

Cluster number	Number of genotypes	Name of genotypes
I	1	G5
II	6	G3, G7, G12, G16, G26, G32
III	4	G1, G8, G13, G33
IV	4	G14, G17, G21, G22
V	8	G4, G6, G19, G25, G31, G34, G35, G36
VI	13	G2, G9, G10, G11, G15, G18, G20, G23, G24, G27, G28, G29, G30

4.5.4 Non-hierarchical clustering

Thirty six *G. max* L. Merr. genotypes were grouped into six different clusters through non-hierarchical clustering (Table 9). These results confirmed the clustering pattern of the genotypes obtained through principal component analysis. Cluster VI (G2, G9, G10, G11, G15, G18, G20, G23, G24, G27, G28, G29, G30) contained the highest number (13) of soybean genotypes followed by Cluster V (G4, G6, G19, G25, G31, G35, G36), Cluster II (G3, G7, G12, G16, G26, G32). Cluster III (G1, G8, G13, G33) and Cluster IV (G14, G17, G21, G22) both contain 4 genotypes. On the contrary, cluster I (G5) contains only 1 genotype.

4.4.4 Canonical variate analysis (CVA)

To compute the inter-cluster distances canonical variate analysis was done. The intra and inter-cluster distance D^2 values were shown in Table 10. As per this experiment, the inter-cluster distances were higher than the intra-cluster distances hence indicating broader genetic diversity among the genotypes of different groups. Cluster I and cluster VI showed highest inter-cluster distance demonstrating that genotypes from these two clusters if involved in hybridization may yield a wide spectrum of segregating population followed by between cluster I and V (16.604), cluster I and III (16.158), cluster IV and VI (13.983), between cluster II and IV (12.167), between cluster IV and V (10.491), between cluster III and IV (9.844), between cluster III and V (7.247), between cluster I and IV (6.484), between cluster II and III (5.39, between cluster II and VI (4.323), between cluster II and V (3.552), between cluster V and VI (3.504). On the other hand,

the minimum intra-cluster distance was found in cluster I (0), which contained single genotype, while the maximum intra-cluster distance was found in cluster V (0.806) that consists of 8 genotypes.

Table 10. Average inter-cluster distance (D^2) and intra-cluster distance (bold) for 36 genotypes of soybean

	I	II	III	IV	V	VI
I	**0**					
II	18.601	**0.647**				
III	16.158	5.39	**0.610**			
IV	6.484	12.167	9.844	**0.672**		
V	16.604	3.552	7.247	10.491	**0.806**	
VI	20.01	4.323	9.54	13.983	3.504	**0.737**

4.5.3 Principal coordinate analysis (PCO)

The difference between the highest and the lowest inter genotypic distance indicated the occurrence of variability among the 36 genotypes of soybean studied. The highest inter genotypic distance was noted between the G5 and G29 (2.64), as got from principal coordinate analysis, followed by G5 and G23 (2.48), G14 and G29 (2.48), G14 and G23 (2.36), G17 and G29 (2.34), G21 and G29 (2.34), G5 and G24 (2.33), G5 and G15 (2.27), G21 and G23 (2.20). On the other hand, the lowest inter genotypic distance was observed in G25 and G34 (0.26) and trails the ascending order as follows G15 and G24 (0.28), G24 and G28 (0.31), g10 and G27 (0.32), G24 and G29 (0.37), G8 and G13 (0.37), G4 and G6 (0.38), G2 and G30 (0.39), G15 and G28 (0.40), G2 and G25 (0.41). (Table 11).

Table 11. Ten of each lower and higher inter genotypic distances (D^2) between pairs of soybean genotypes

Highest 10 inter genotypic distances				Lowest 10 inter genotypic distances			
Sl	Genotypes	Genotypes	Values	Sl	Genotypes	Genotypes	Values
1	G5	G29	2.64	1	G25	G34	0.26
2	G5	G23	2.48	2	G15	G24	0.28
3	G14	G29	2.48	3	G24	G28	0.31
4	G14	G23	2.36	4	G10	G27	0.32
5	G17	G29	2.34	5	G24	G29	0.37
6	G21	G29	2.34	6	G8	G13	0.37
7	G5	G24	2.33	7	G4	G6	0.38
8	G5	G15	2.27	8	G2	G30	0.39
9	G21	G23	2.20	9	G15	G28	0.40
10	G5	G28	2.20	10	G2	G25	0.41

4.5.5 Cluster mean analysis

Cluster mean for nine yield and yield contributing characters of 36 soybean genotypes are shown in (Table 12). Cluster mean analysis was associated and directed extensive differences between clusters for all the characters studied. In cluster IV (64.83), days to 50% flowering was maximum followed by cluster III (63.75), cluster II (56.06), cluster V (54.04) and cluster I (50.67) took the lowest time to 50% flowering. The cluster III took maximum time to reach the maturity (120.75 days) while cluster II took the minimum days (108 days). The genotype included in cluster I had the highest number of branches/plant (5.17). On the other hand, the genotypes in cluster VI had the lowest number of branches/plant (2.24). The maximum plant height was noted in cluster III (64.35) while the cluster VI possessed the minimum plant height (27.05). Maximum number of pods/plant was observed in cluster I (53.43) whereas minimum was in cluster VI (18.91). In case of number of nodes/plant the highest value was noted in cluster I (12.23) and lowest was in cluster VI (7.8). In analyzing the number of seeds/plant cluster I also showed the highest mark which was 132.26 although the lowest was in cluster VI. After investigation of 100 seed weight (g) cluster II showed the highest value (15.41) however cluster IV was the lowest (7.95). Highest seed yield/plant was noted in cluster III (8.11) although lowest was in cluster VI (4.96).

Table 12. Cluster mean for nine yield and yield contributing characters of 36 soybean genotypes

Characters	I	II	III	IV	V	VI
Days to 50% flowering	50.67	56.06	63.75	64.83	54.04	51.46
Days to maturity	114.33	108.00	120.75	111.75	110.75	102.15
Number of branches /plant	5.17	3.09	4.93	4.46	3.57	2.24
Plant height (cm)	45.80	47.89	64.35	44.17	30.15	27.05
Number of pods /plant	53.43	25.70	31.04	48.49	27.93	18.91
Number of nods/plant	12.23	8.89	11.99	10.67	8.41	7.80
Seeds/plant	132.26	39.8	60.64	98.97	53.02	36.21
100 seed weight (g)	6.22	15.41	12.53	7.95	11.91	14.38
Seed yield/plant (g)	7.23	6.02	8.11	7.76	6.25	4.96

4.4.5 Contribution of characters towards divergence of the genotypes

Principal component analysis which provides the knowledge over contribution of characters towards the divergence is presented in (Table 13). Vector 1 (Z1) which was obtained from PCA, the important characters accountable for genetic divergence in the axis of differentiation were number of branches/plant (0.08), number of nodes/plant (0.31) and seed yield/plant (0.45). On the other hand, vector 2 (Z2) which was the second axis of differentiation were number of pods/plant (0.05), number of nodes/plant (0.04), number of seeds/plant (0.07) and 100 seed weight (g) (0.16). Moreover these parameters are important in genetic diversity because all these characters had positive signs. In opposition, characters that possessed the negative sign in both the first axis of differentiation and second axis of differentiation were days to 50% flowering (-0.08; -0.04), days to maturity (-0.05; -0.02) and plant height (cm) (-0.06; -0.17) mean those had minor role in the genetic diversity.

Table 13. Latent vectors of nine characters of 36 soybean genotypes

Characters	Vector 1	Vector 2
Days to 50% flowering	-0.08	-0.04
Days to maturity	-0.05	-0.02
Number of branches /plant	0.08	-0.12
Plant height (cm)	-0.06	-0.17
Number of pods /plant	-0.04	0.05
Number of nodes/plant	0.31	0.04
Number of seeds / plant	-0.22	0.07
100 seed weight (g)	-0.20	0.16
Seed yield/plant	0.45	-0.45

4.4.6 Selection of genotype as parents for future hybridization program

Selection of genetically diverse parents is the crucial assignment for any plant breeding Activities. As per considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster means and agronomic performance the genotype G1 (AGS313) for the highest seed yield/plant (Table 3), along with the other genotypes belonging cluster III (G8, G13, G33) would be meaningful. For the minimum days to maturity the genotypes included in cluster VI (G2, G9, G10, G11, G15, G18, G20, G23, G24, G27, G28, G29, G30) and for the maximum 100 seed weight from cluster II (G3, G7, G12, G16, G26, G32), for the highest number of branches/plant, number of pods/plant, number of seed/plant G5 belonging cluster I might be worthwhile selection for future crop improvement program.

CHAPTER V

SUMMARY AND CONCLUSION

By the period from December 2020 to April 2021, the experiment was executed at Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur with the title "CHARACTER ASSOCIATION AND DIVERSITY ANALYSIS OF DIFFERENT GENOTYPES OF SOYBEAN (*Glycine max* L. Merr.)". 36 (thirty six) soybean genotypes were used in this experiment, among them 32 (thirty two) genotypes were collected from AVRDC, Taiwan; 3 (three) from BARI and 1(one) from BSMRAU in randomized complete block design (RCBD) with three replications. Different biometric traits related to yield and its contributing characters were considered for observation namely; days to 50% flowering, days to maturity, plant height (cm), number of branches/plant, number of pods/plant, number of nodes/plant, number of seeds/plant, 100 seeds weight (g), seed yield/plant (g). The analysis of variance showed highly significant differences among the mean values for all traits. Significant mean sum of squares due to yield and yield attributing characters exposed existence of considerable variability in material studied for improvement of various traits.

The lowest days to 50% flowering was observed in G36 (39.67 days) while the highest was in G13 (74.00 days). The highest days to maturity (124.67 days) was found in G13, while the lowest days to maturity (90.33 days) was found in G32. Significantly higher number (7.6) of branches was recorded in G36, while the lowest was in G10. The maximum plant height 81.93cm was observed in G33 while the lowest plant height in G20 (19.00cm). Significantly higher number (12.90) of nodes was recorded in G14, though the lowest was in G23 (4.97) with the mean of 9.30. The number of pods/plant was ranged from 13.20 to 55.47 with mean of 27.64. The least number of pods/plant was observed in genotype G29 while maximum number of pods per plant was found in the genotype G17. The highest number of seeds/plant (132.26) was observed in G5 while the lowest number in G29 (25.18) with the mean of 52.90. Meaningfully higher was 100 seed weight (g) recorded in G29 (19.44), while the lowest was in G5 (6.22g) with the mean of 12.86g. Significantly higher seed yield/plant was noted (12.25g) in G1, while the lowest was in G11 (3.42g) with the mean of 6.15g.

The highest genotypic and phenotypic coefficient of variation was recorded, for number of branches (45.06 % and 46.97%). which revealed presence of considerable variability

among the genotypes. 36 soybean genotypes for all the estimated traits shown high heritability, high to low genetic advance along with high to moderate GA% this finding indicated that those traits were govern by additive gene so selection might be useful.

Correlation analysis exposed that seed yield/plant showed the high positive and significant correlation at both genotypic and phenotypic level with days to 50% flowering (0.255; 0.251), days to maturity (0.330; 0.317), plant height (0.458; 0.448), number of branches/plant (0.0.485; 0.453), number of nodes/plant (0.538; 0.521), no. of pods/plant (0.549; 0.541), no. of seeds/plant (0.526; 0.520) except 100 seed weight (g). Seed yield/plant positive but insignificant correlation with 100 seed weight (0.092; 0.094).

Path analysis exposed that days to 50% flowering had positive direct effect (0.098) on yield. Days to 50% flowering exhibited positive indirect effect with days to maturity (0.048), plant height (0.037), number of branches/plant (0.015), number of pods/plant (0.029), number of nodes/plant (0.050) and number of seeds/ plant (0.28), while showed a negative indirect effect through 100 seed weight (-0.026). On the other hand 100 seed weight (g) had highest positive direct effect (0.874) on yield. 100 seed weight (g) exhibited negative indirect effect with days to 50% flowering (-0.305), days to maturity (-0.164), plant height (-0.0131), number of branches/plant (-0.305), number of pods/plant (-0.513), number of nodes/plant (-0.309) and number of seeds/plant (-0.613).

36 (thirty six) (*G. max* L. Merr.) genotypes were grouped into six different clusters through non-hierarchical clustering. As per this experiment, the inter-cluster distances were higher than the intra-cluster distances hence indicating broader genetic diversity among the genotypes of different groups. Cluster I and cluster VI showed highest inter-cluster distance while cluster I reveled minimum intra cluster distance.

From the outcomes of the experiment, the following conclusions could be drawn:

  i.   Considerable genetic variability existed among the soybean genotypes, for all the estimated traits shown high heritability, high to low genetic advance along with high to moderate GA%.

  ii.   Number of branches/plant (0.08), number of nodes/plant (0.31), number of seeds/plant (0.07), 100 seed weight (g) (0.16) and seed yield/plant (0.45) were the important characters accountable for genetic divergence.

iii.   For the highest seed yield/plant G1, along with the other genotypes belonging cluster III (G8, G13, G33) will be worthwhile selection for future crop improvement program.

Recommendations

I.   The experiment may be conducted in kharif season.
II.   There is need of in-depth study on qualitative and processing parameters along with resistance to different biotic and abiotic stresses.
III.   More number of genotypes may be collected from different sources of Bangladesh and included in further studies.
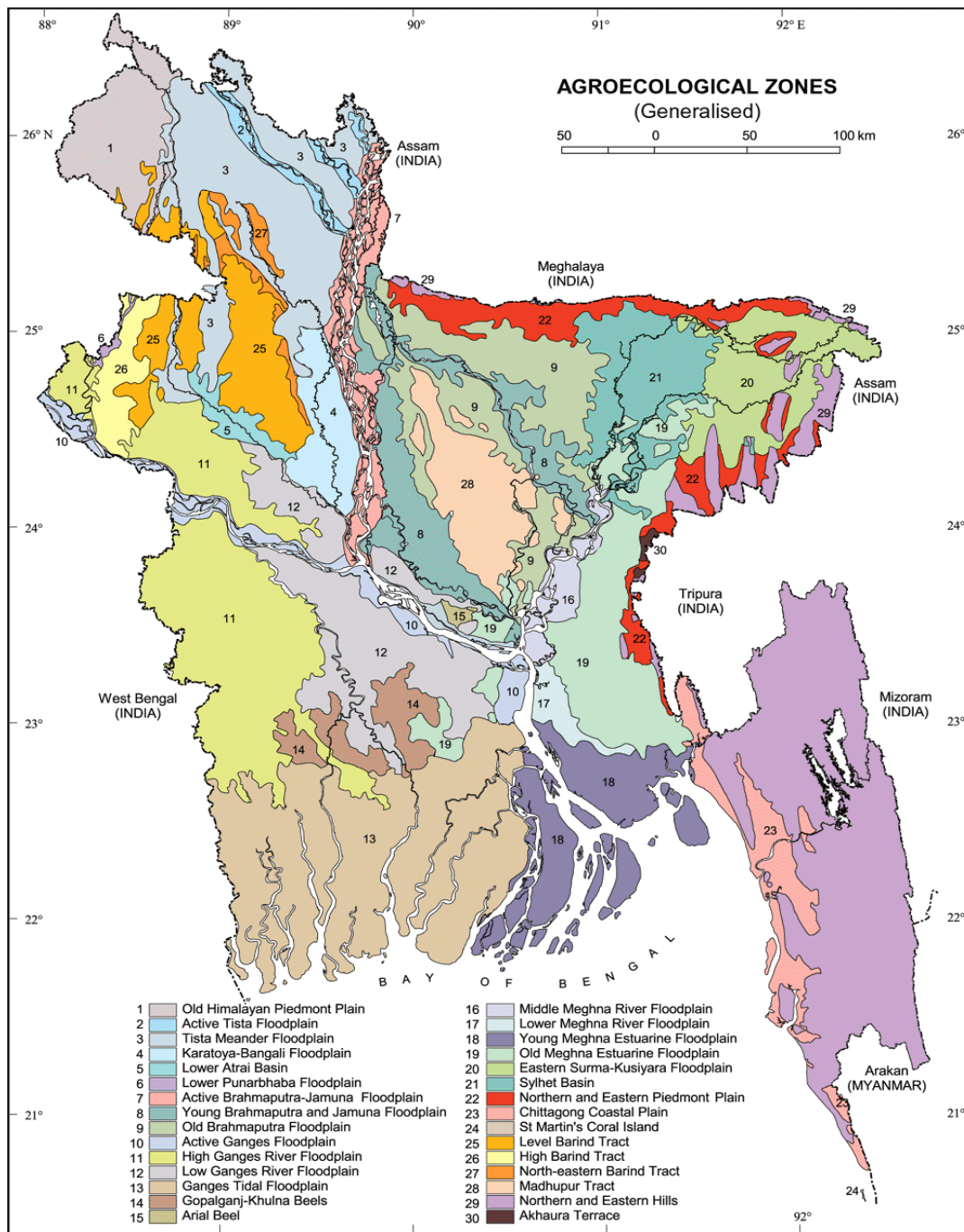
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APPENDIX I. Map Showing The Experimental Site Under The Study

AGROECOLOGICAL ZONES
(Generalised)

1	Old Himalayan Piedmont Plain	16	Middle Meghna River Floodplain
2	Active Tista Floodplain	17	Lower Meghna River Floodplain
3	Tista Meander Floodplain	18	Young Meghna Estuarine Floodplain
4	Karatoya-Bangali Floodplain	19	Old Meghna Estuarine Floodplain
5	Lower Atrai Basin	20	Eastern Surma-Kusiyara Floodplain
6	Lower Punarbhaba Floodplain	21	Sylhet Basin
7	Active Brahmaputra-Jamuna Floodplain	22	Northern and Eastern Piedmont Plain
8	Young Brahmaputra and Jamuna Floodplain	23	Chittagong Coastal Plain
9	Old Brahmaputra Floodplain	24	St Martin's Coral Island
10	Active Ganges Floodplain	25	Level Barind Tract
11	High Ganges River Floodplain	26	High Barind Tract
12	Low Ganges River Floodplain	27	North-eastern Barind Tract
13	Ganges Tidal Floodplain	28	Madhupur Tract
14	Gopalganj-Khulna Beels	29	Northern and Eastern Hills
15	Arial Beel	30	Akhaura Terrace

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Appendix II. Monthly record of air temperature, rainfall, relative humidity, rainfall and sunshine of the experimental site during the period from December, 2020 to April, 2021.

Month	*Air temperature (°c)		*Relative humidity (%)	*Rainfall (mm)	*Sunshine (hr)
	Maximum	Minimum			
December, 2020	23.2	14.2	90	00	6.3
January, 2021	25.4	10.4	82	00	6.6
February, 2021	30.3	11.1	87	23.5	6.8
March, 2021	34.7	21.5	85	30.7	7.1
April, 2021	36.2	22.6	88	46.2	7.1

Source: http://bsmrau.edu.bd/age/weather-data/

Appendix III. Physical and chemical properties of experimental soil

Soil properties	Analytical values
Sand%	17
Silt%	62
Clay%	22
Texture%	Silty clay
pH	6.1
Organic Carbon%	0.61

Source: Soil Resources Development Institute (SRDI), Khamarbari, Dhaka

Appendix IV. Dosage of manures and fertilizers

Nutrients	Manures/Fertilizers used as	Dose (Kg ha^{-1})
Organic matter	Cow dung	10,000
N	Urea	60
P	TSP	175
K	MoP	120
S	Gypsum	115
B	Boron	10