Morphological Assessment of Drought Stress Tolerant Soybean Genotypes in Bangladesh

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Soybean (*Glycine max* (L.) Merr) is the most important commercial grain legume and oil seed crop which represents the most important plant source of vegetable oil and protein in the world. The water stress tolerance of the fifty soybean genotypes was evaluated in a glasshouse at the Bangladesh Institute of Nuclear Agriculture (BINA). The study was carried out to identify the drought tolerant soybean genotype(s) for improving yield under rainfed conditions in Bangladesh. Drought

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stress was induced by withholding water completely from 21 days after emergence. The water stress was continued until wilting symptom persisted on plant overnight. Water stress caused an overall reduction in some morphological and yield contributing characters such as plant hight, number of branches plant^{-1}, internode length, pod plant^{-1}, seeds pod^{-1}, hundred (100) seeds weight and finally the seed yield of soybean. The studied genotypes were categorized into four groups based on their yield reduction under drought stress conditions. Five genotypes YESOY-4, PK-416, Shohag, SBM-09 and Binasoybean-6 were categorized as tolerant (<35% yield reduction), fourteen genotypes were categorized as moderately tolerant (35%-60% yield reduction), twenty five genotypes were categorized as moderately susceptible (61%-80% yield reduction) and rest six genotypes were categorized as susceptible (>80% yield reduction). These five genotypes YESOY-4, PK-416, Shohag, SBM-09 and Binasoybean-6 study further for developing drought tolerant soybean verities which may be helpful for quality oil seed production.

1. INTRODUCTION

"Soybean (*Glycine max* [L.] Merr.) is one of the most economically important field crops worldwide, producing around 370 million tons annually" [1]. "Soybean is a highly nutritious legume for its protein and edible oil which is used for both human consumption and livestock feed" [2]. "Drought is a major ecological problem that severely limits the production of agriculture globally, particularly in the context of global warming" [3]. "Soybean is the world's primary source of protein and oil and is also acknowledged as a 'miracle crop' due to over 40% protein and 20% oil" [4,5,6,7,8]. "For the duration of its growth and development process, it requires a sufficient amount of water to achieve higher yields". [9]. "The plants of soybean are affected by drought at every stage of life" [10,11,12,13,14]. "Soybean is now an essential and dominant source of protein and oil with over 200 uses in feed, food and industrial applications. Recent studies indicate that the consumption of soybeans reduces cancer, blood serum cholesterol, osteoporosis and heart disease" [15]. "Also, soybeans are a good source of minerals, vitamins, folic acid, and isoflavones which are credited with the slow development of these diseases" [16]. Thus, the demand for many edible soybean products has increased dramatically.

"Drought affects several aspects of legume growth and development, including germination, shoot and root development, photosynthesis and the reproductive stage. As a result of climate change, drought is becoming one of the most unpredictable and uncontrollable factors affecting crop productivity and negatively affecting legume crops. Soybeans are susceptible to drought, particularly in the reproductive growth stage"

[17,18,19]. "Drought stress affected the yield and quality of soybeans. Drought frequently results in 40% losses in soybean production" [20,21]. "These losses become even greater when moisture stress occurs during both the vegetative and reproductive stages of the plant's life. Drought tolerance is the ability of plants to utilize a limited amount of water, leading to low tissue water potential, with higher efficiency regarding growth, biomass accumulation and reproduction" [22]. "Soybean is mainly grown in the late winter season in the greater Noakhali district of Bangladesh. In this area, rainfall (75%) is concentrated mainly during the summer monsoon season (June to September) and rain and irrigation water are scarce from October to May. Thus, the crop falls under acute water stress mostly at the flowering and pod-filling stages. Research on plant response to stress is becoming increasingly important, as most climate change scenarios suggest an increase in aridity in many areas of the globe" [23]. One of the main ways to maintain high soybean productivity in drought conditions is to develop more drought-tolerant varieties. Ku et al. [24] reported that "various indices/parameters have been adopted to quantify drought tolerance in soybean genotypes and other crops". The identification of drought-tolerant soybean genotypes by screening several key and stable traits with high heritability is an important step to improve drought tolerance in soybeans.Therefore, the present study was undertaken to screen for drought-tolerant soybean genotype(s) for improving the yield level of soybeans under rainfed cultivation in Bangladesh.

2. MATERIALS AND METHODS

The experiment was carried out at the Bangladesh Institute of Nuclear Agriculture

(BINA) glasshouse in Mymensingh. Fifty (50) soybean genotypes were used as experimental materials for this study. All these genotypes with their sources of collection are given in Table 1 [25]. Soil used in the plastic pot was sandy loam. 12 kg of air-dried soil, including cowdung at a 4:1 ratio, were added to the pot which was equivalent to 9 kg of oven-dry soil that retained roughly 28% moisture at field capacity (FC). The soil of the pot was fertilized uniformly with 0.15, 0.18, 0.36 and 0.1 g urea, TSP (triple super phosphate), MP (muriate of potash) and gypsum corresponding to 24-30-60-15 kg NPKS per hectare, respectively (Fertilizer Recommendation Gide -2018). Six healthy seeds per pot were sown. Most of the seedling emerged within 6-7 days after sowing. Seedlings were thinned out after two weeks of emergence keeping three healthy seedlings with uniform growth in each pot. Optimum soil moisture conditions were maintained for the seedling growth. During the evaluation of 50 genotypes, two treatments were applied: non-stress and water stress. Equal amount of water was applied to each pot before the stress treatment started. Drought stress was induced by withholding water completely from 21 days after emergence. The treatment was continued until wilting symptom persisted on plant throughout the night. After that they were re-watered to 50% field capacity. During the treatment period, wilting symptom was visually observed every day. In non-stress treatment, water was applied when it was needed. The experiment was designed as a completely randomized design under factorial arrangement with three replications (three plants per pot considered as one replication). The insecticide "Admire" @ 0.5 mL litre^{-1} of water was sprayed to protect Jasside. The pots were kept weed free throughout the growing season [26].

Table 1. Experimental materials with their sources of collection

Genotypes	Sources of collection	Genotypes	Sources of collection
G-2120	BAU, Mymensingh	BS-3	BAU, Mymensingh
Gc-84040-27-1	BAU, Mymensingh	KADSING	BAU, Mymensingh
MTD-16	BAU, Mymensingh	AGS-302	BAU, Mymensingh
AGS-79	BAU, Mymensingh	GAURAB	BAU, Mymensingh
ASSET-93-19-1	BAU, Mymensingh	MTD-176	BAU, Mymensingh
PM-78-6-3-13	BAU, Mymensingh	JOYAWIYAJA	BAU, Mymensingh
G-2261	BAU, Mymensingh	AGS-314	BAU, Mymensingh
Pb-1/Shohag	BAU, Mymensingh	BS-13	BAU, Mymensingh
HIHS-WIHS	BAU, Mymensingh	LG-92P-1139	BAU, Mymensingh
MTD-451	BAU, Mymensingh	CH-1	BAU, Mymensingh
BRAGG	BAU, Mymensingh	ASSET-93-19-2	BAU, Mymensingh
GC-83005-9	BAU, Mymensingh	TAINANS	BAU, Mymensingh
SBG-1	BAU, Mymensingh	Lokon	BAU, Mymensingh
SY-35	BAU, Mymensingh	SBM-09	BAU, Mymensingh
NO-205	BAU, Mymensingh	SBM-15	BINA, Mymensingh
MTD-6	BAU, Mymensingh	SBM-18	BINA, Mymensingh
AGS-66	BAU, Mymensingh	SBM-22	BINA, Mymensingh
ACC-1222	BAU, Mymensingh	BINA-6	BINA, Mymensingh
BARI-6	BARI, Gazipur	SANTAR-05A	BAU, Mymensingh
BINA-2	BINA, Mymensingh	AGS-278	BAU, Mymensingh
BINA-3	BINA, Mymensingh	ASSET-93-19-5	BAU, Mymensingh
BINA-1	BINA, Mymensingh	G-10180	BAU, Mymensingh
BINA-4	BINA, Mymensingh	PK-416	BAU, Mymensingh
BARI-5	BARI, Gazipur	DAVIS	BAU, Mymensingh
MINA HAI	BAU, Mymensingh	YESOY- 4	BAU, Mymensingh

Abbreviations: BAU=Bangladesh Agricultural University, BARI=Bangladesh Agricultural Research Institute, BINA= Bangladesh Institute of Nuclear Agriculture, SBM=Soybean mutant

2.1 Data Collection

At harvest plants were cut at the base and the following data were recorded:

Plant height (cm): Plant height was considered as the height from ground level to the largest leaf of the plant.

Number of branches (no.): At the final harvest, number of branches of each plant was recorded.

Internode length (cm): The length between two nodes was measured from each plant for internode length.

Pod plant^{-1} (no.): The number of mature pods of each plant was recorded and mean was expressed on plant^{-1}basis.

Seeds pod^{-1} (no.): Pods from each plant were sun dried. The clean seeds were collected and counted.

Hundred (100) seeds weight (g): For each individual treatment, samples of well-dried 100-seeds were counted separately and weighed.

Seed yield plant^{-1} (g): Yield plant^{-1} of each pot was recorded individually and adjusted at 10% moisture content.

2.2 Tolerance Indices

Five drought tolerance and susceptible indices including relative performance (RP), mean productivity (MP), geometric mean productivity (GMP), tolerance (TOL) and drought susceptibility index (DSI) were calculated based on grain yield under water deficit and control conditions. Stress tolerance attributes were calculated by the following formulae:

Relative performance (RP) = value of a plant character under water stress condition / Value of that character under non – stress condition [27]

Mean productivity (MP) = $\dfrac{Yc + Ys}{2}$ [28]

Geometric mean productivity (GMP) = $(Yc \times Ys)^{\frac{1}{2}}$ [29]

Tolerance (TOL) = $(Yc - Ys)$ [28]

Drought susceptibility index (DSI) = $(1 - Ys/Yc)/(1 - \overline{Ys}/\overline{Yc})$,

Where,

Yc = the yield of a given genotype in control condition

Ys = the yield of a given genotype in stress condition

$\overline{Ys}$ = mean yield of all genotypes under control condition

$\overline{Yc}$ = mean yield of all genotypes under stress condition

Fig. 1. Screening of soybean genotypes under drought stress conditions at Glasshouse, BINA, Mymensingh. The tolerant genotypes remained fresh and vigorous but the susceptible genotypes were become wilted

2.3 Statistical Analysis

The recorded data were analyzed statistically using the STATISTIX-10 software package [30] and R-4.3.0 computer package program [31]. Ranking was done based on their yield reduction due to water stress over non-stress condition.

3. RESULTS AND DISCUSSION

3.1 ANOVA for Morphological Traits of Soybean Genotypes

The results of the analysis of variance (ANOVA) of the quantitative traits of the tested genotypes are presented in Table 2. Statistical analyses performed on various agro-morphological traits revealed the presence of significant variation for all the traits of the tested genotypes. The differences among genotypes for all the traits under study viz., plant height (cm), branch plant[-1], internode length (cm), pod plant[-1], seed plant[-1], 100 seed wt. (gm) and seed yield plant[-1] (gm) were highly significant (***$P \leq$ 0.001). The analysis of variance results showed that there was a considerable amount of variation among the tested genotypes.

3.2 Descriptive Statistics Analysis

Range of values obtained from 50 soybean genotypes for 7 traits, mean of the traits with standard error, genotypic (GV) and phenotypic (PV) variance, genotypic (GCV) and phenotypic coefficient of variation (PCV), genetic advance (GA), genetic advance as per cent (GAM) of mean and broad sense heritability (h^2b) has been furnished in Table 3.

3.2.1 Mean and range values

The range and mean values for the 7 traits are presented in Table 3. The results indicated significant differences among the soybean genotypes for growth, yield and yield related traits. Plant height (cm) ranged from 21cm to 100cm with an average height of 62.31cm. The range observed for branch plant[-1] was the lowest (0) to highest (7) with an overall mean of 3.24, Internode length (cm) having a range between minimum 2 cm to maximum 12 cm with a mean 5.17 cm. The number of pods per plant ranged from 8 to 61 with an average of 33.67. The number of seeds per plant was likely to be 10 to 121 with an average value of 68.40. Regarding seed related traits, the lightest 100 seed weight was 5.75g and the heaviest was 10.70g with an

average weight of 8.56g (Table 3). The range and mean values of the studied traits suggested the existence of sufficient variability among the studied soybean genotypes and thus offered ample scope for their potential improvement.

3.2.2 Genotypic and phenotypic coefficients of variation

High GCV was observed for seed yield plant[-1] (56.29g), branch plant[-1] (46.57), seed plant[-1] (44.36), pod plant[-1] (42.90) and plant height (28.99 cm). On the contrary, moderate values were observed for internode length (18.87 cm) and 100 seed wt. (13.84g).

High PCV was observed for seed yield plant[-1] (56.40g), branch plant[-1] (47.47), seed plant[-1] (44.44), pod plant[-1] (43.24) and plant height (29.14 cm). On the contrary, moderate values were observed for internode length (23.30 cm) and 100 seed wt. (13.95g).

The per cent genotypic and phenotypic coefficient of variation (GCV and PCV) for plant height (28.99 cm and 29.14 cm), branch plant[-1] (46.57 and 47.47), pod plant[-1] (42.90 and 43.24), seed plant[-1] (44.36 and 44.44), 100 seed wt. (13.84g and 13.95g) and seed yield plant[-1] (56.29g and 56.40g) were very close to each other (Table 3) indicating that the characters were less influenced by the environment. Therefore, selection based on phenotype alone can be effective for the improvement of these traits.

Additionally, all of these explored values (Table 3) were close to each other providing evidence that these parameters were under the control of additive gene effects and that effective selection could be possible for the improvement of these characters. Reliable selection could be made for these traits based on phenotypic expression.

3.2.3 Heritability and genetic advance

Estimating heritability is of tremendous significance to the breeder, as its magnitude indicates the accuracy with which a genotype can be recognized by its phenotypic expression. High heritability (>60%) accompanied with high to moderate genotypic and phenotypic coefficient of variation and genetic advance which indicates that most likely the heritability is due to additive gene effects for these traits, selection may be effective in early generations. The high heritability of those traits indicated that the

influence of the environment on these characters is negligible or low. Therefore, selection can be effective based on the phenotypic expression of these traits in the individual plant by implementing simple selection methods.

High heritability does not always indicate a high genetic gain; heritability should be used together with the genetic advance in predicting the ultimate effect of selecting superior varieties [32]. The estimates of high heritability (>60%) coupled with high genetic advance (>20%) were recorded for plant height (cm) (h^2b= 99%, GA= 59.43%), branch plant[-1] (h^2b= 96.25%, GA=94.13%), pod plant[-1] (h^2b= 98.46%, GA=87.70%), seed plant[-1] (h^2b= 99.63%, GA=91.22%), 100 seed wt. (gm) (h^2b= 98.47%, GA=28.30%) and seed yield plant[-1] (gm) (h^2b= 99.58%, GA= 115.71%) in (Table 3), which exhibited good scope for improving these traits through phenotypic selection due to the additive gene action.

Heritability for all the characters was high, indicating the low influence of the environment on the studied characters. The maximum heritability was recorded for seed plant[-1] (99.63%) and the minimum for internode length (cm) (65.53%). According to Johnson et al. [33], estimating heritability in conjunction with genetic advancement is more beneficial in forecasting the gain under selection.

3.2.4 Principal Component Analysis

The computed eigenvalues of seven variables of 50 soybean genotypes were subjected to principal component analysis; their eigenvalues, variability% and cumulative explained variance are present in the following Table 4. Eigenvalues of the first 7 principal components had been shown in the scree plot (Fig. 2) which revealed that the first principal component explained the majority of variation expressed by the population. Among the seven PCs, two PCs with an eigenvalue greater than 1 explained 77.07% of the entire morphological variation. The PC1, PC2, and PC3 explained 58.58%, 77.07% and 88.62% of the whole morphological variation, respectively (Table 4).

3.2.5 Biplot analysis based on principal component analysis

"A biplot is a principal component that represents variables superimposed on a plot as vectors where the relative length of vectors represents the relative proportion of variability in each variable represented on the biplot. If the angle between vectors of two traits is < 90° both are positively correlated whereas if the angle is > 90° there is a negative correlation. Both vectors show no correlation if the angle is 90°" [34]. "It is mostly used to determine the components where the effect is more to create the genotypic variation. The traits having highest values have the greatest influence on the total variation. Biplot analysis determines varietal stability in the multi-environmental trial" [35]. In the Dim1 and Dim2 biplot graphs, it was evident that pod/plant and seed plant[-1] had a strong positive correlation. Moreover, seed plant[-1] and seed yield plant[-1] (gm) had a strong positive correlation among them; 100 seed wt. (gm) and seed yield plant[-1] (gm) had a strong positive correlation with each other. Plant height (cm) and seed yield plant[-1] (gm) had a strong negative correlation with each other while both of them revealed a negative correlation with branch plant[-1] and pod plant[-1] (Fig. 3).
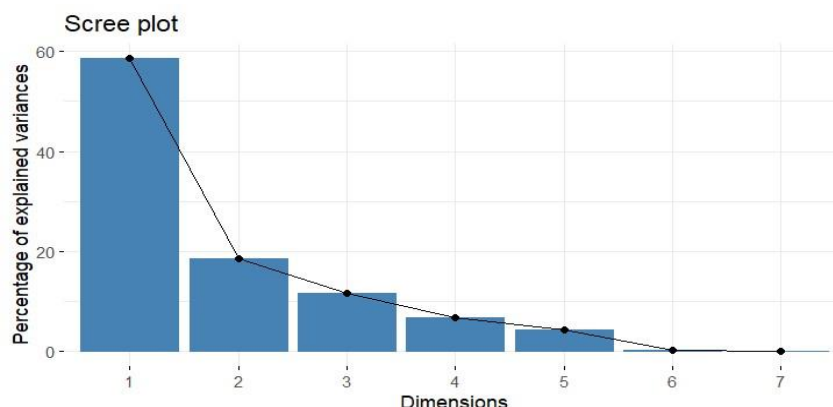

Fig. 2. Scree plot explaining how much variation each principal component capturedfrom the data along with the breakdown point of principal components

Table 2. Analysis of variance (ANOVA) of seven yield contributing traits with significance levels in Soybean Genotypes

Source of Variation	Df	Plant height (cm)	Branch Plant^{-1}	Internode length (cm)	Pod Plant^{-1}	Seed Plant^{-1}	100 seed Wt (gm)	Seed yield Plant^{-1} (gm)
Genotype	49	1280***	5.97***	6.81***	307***	1289***	4.373***	16.68***
Treatment	1	55570***	328.65***	441.65***	47401***	201554***	134.884***	2068.03***
Genotype × Treatment	49	113***	2.46***	5.03***	37***	183***	0.729***	1.61***
Residuals	200	2	0.09	0.46	1	1	0.021	0.03

P Value ≤ 0.05 (*), P Value ≤0.01 (**) and P Value ≤ 0.001 (***)

Table 3. Descriptive statistics for seven agronomic characters of soybean

Characters	Range	Mean±SE	PV($ɜ^2$p)	GV($ɜ^2$g)	PCV (%)	GCV (%)	GA	GAM (%)	h^{2}b
Plant Height (cm)	21-100	62.31±1.18	201.3961	199.3785	29.1405	28.9941	28.9414	59.4279	99
Branch Plant^{-1}	0-7	3.24±0.09	1.0842	1.0435	47.4734	46.5738	2.0645	94.1261	96.25
Internode Length (cm)	2-12	5.17±0.11	0.8517	0.5581	23.3049	18.8652	1.2458	31.4596	65.53
Pod Plant^{-1}	8-61	33.67±0.85	83.2311	81.9507	43.2375	42.9036	18.5045	87.6991	98.46
Seed Plant^{-1}	10-121	68.40±1.75	356.4419	355.1271	44.4437	44.3616	38.7487	91.2163	99.63
100 Seed Wt. (gm)	5.75-10.70	8.56±0.07	1.2113	1.1928	13.9518	13.8448	2.2326	28.3018	98.47
Seed Yield Plant^{-1} (gm)	0.80-12.73	6.12±0.18	3.8788	3.8625	56.4048	56.2861	4.0401	115.7069	99.58

Abbreviations: PV($ɜ^2$p) = Phenotypic Variance, GV ($ɜ^2$g) = Genotypic Variance, PCV= Phenotypic Coefficient of Variation, GCV= Genotypic Coefficient of Variation, GA= Genetic Advance, GAM (%) = Genetic Advance as Percentage of Mean, h2b= Broad Sense Heritability

Table 4. Eigenvalues of the correlation matrix of seven yield contributing traits in Soybean Genotypes

Principle component	EigenValues	Proportion of Variance	Percent of Variation (%)	Cumulative Proportion (%)
PC1	4.1008	0.5858	58.58%	58.58%
PC2	1.2943	0.1849	18.49%	77.07%
PC3	0.8086	0.1155	11.55%	88.62%
PC4	0.4658	0.06654	6.65%	95.28%
PC5	0.3049	0.04355	4.36%	99.63%
PC6	0.0205	0.00294	0.29%	99.93%
PC7	0.0051	0.00073	0.07%	100%

Table 5. Eigenvectors with principal components of seven yield contributing traits in Soybean Genotypes

| Eigen Vectors	Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7
	Plant height (cm)	-0.2744	0.5744	0.3969	-0.1484	-0.6440	-0.0200	0.0020
	Branch/plant	-0.3484	0.4121	0.3602	-0.0796	0.7566	-0.0107	-0.0111
	Internode length (cm)	-0.1068	0.5727	-0.8033	0.1189	0.0338	-0.0002	-0.0059
	Pod/plant	-0.4534	-0.2501	-0.1633	-0.2980	-0.0375	-0.7841	-0.0151
	Seed/plant	-0.4601	-0.2311	-0.1439	-0.2873	-0.0499	0.4933	-0.6212
	100 Seed Wt. (gm)	-0.3851	-0.1117	0.1009	0.8858	-0.0752	-0.0924	-0.1737
	Seed Yield/plant (gm)	-0.4758	-0.2095	-0.0993	-0.0380	-0.0454	0.3645	0.7639
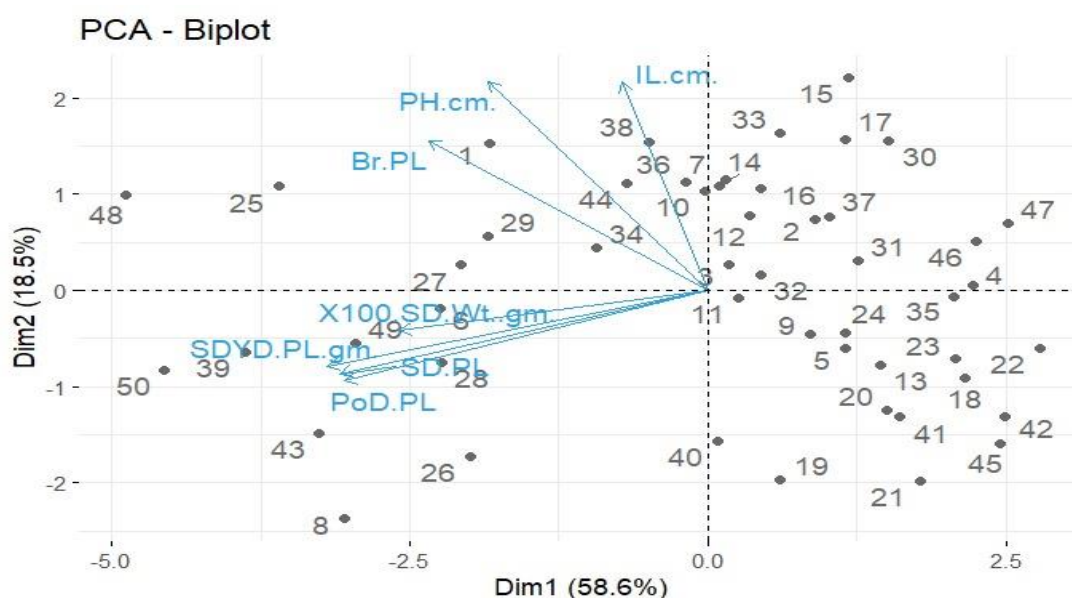
Fig. 3. Principal Components Analysis (PCA) ordination graph; Dim1 vs Dim2 biplot.
[Position of soybean genotypes from the selected genotypes along the first two axes obtained from PCA where PH (cm) = Plant Height (cm), Br/PL = Branch/Plant, IL (cm) = Internode Length (cm), PoD/PL = Pod/Plant, SD/PL = Seed/Plant, 100 SD Wt (gm) = 100 Seed Wt. (gm) and SDYD/PL (gm) = Seed Yield/Plant (gm)]

Again, biplot analysis showed the trait profiles of the genotypes, especially, those genotypes positioned far away from the origin and the results indicated a correlation between traits with genotypes. In the Dim1 and Dim2 biplot, it is indicated that genotype PK-416 has better seed yield plant[-1] (gm). ASSET-93-19-1 can be selected based on 100 seed wt. (gm). KADSING can be selected based on pod plant[-1] and seed plant[-1]. Biplot results indicated a correlation between traits with genotypes. It represented suitable genotypes for selection through the seven specific traits in consideration.

3.3 Cluster Analysis

The study of morphological traits can be successfully used for the estimation of genetic diversity and cultivar development because they provide a straightforward way of quantifying genetic variation. The analysis of variance based on plant means revealed significant differences among the genotypes for all the characters studied indicating a considerable amount of genetic variability for all the characters and therefore, diversity analysis was carried out. The distribution pattern in the D2 analysis indicated that 50 genotypes fell into six clusters (Table 6 and Fig. 4).

Clusters IV (12%) and V (12%) had 24% of the genotypes containing six genotypes each. Clusters III and VI contained five genotypes each (Table 6). On the contrary, cluster I contained nineteen genotypes (38%) and cluster II contained nine genotypes (18%). The fifty soybean genotypes were grouped by the

Pearson method using quantitative and qualitative traits as shown in Fig. 4.

3.4 Heatmap

The relative correlation among the yield-related traits is indicated by the gradient of color; the lemon color denotes the highest genotypic correlation, and the red color means the lowest genotypic correlation. Heatmap generated exploiting the genotypic correlation matrix (Fig. 5) showed that pod plant[-1] is highly correlated with seed plant[-1] followed by 100 seed wt. (gm). Seed plant[-1] is highly positively correlated with 100 seed wt. (gm). 100 seed wt. (gm) is positively correlated with the pod plant[-1], seed plant[-1] and seed yield plant[-1] (gm). Pod plant[-1], seed plant[-1], 100 seed wt. (gm) and seed yield plant[-1] (gm) are highly negatively correlated with internode length (cm).

3.5 Genotypic Path Coefficient

"High correlation coefficients may not always give the true picture or could mislead the decision because the correlation between two variables may be due to a third factor. Therefore, it is necessary to analyze the cause and effect relationship between dependent and independent variables to reveal the nature of the relationship between the variables. Path coefficient analysis furnished a method of partitioning the correlation coefficient into direct and indirect effects and provided information on the actual contribution of a trait to the yield" [36,37].

Table 6. Frequency distribution in different clusters of soybean genotypes

| Cluster Number	Number of Genotypes	Per cent (%)	Name of Genotypes
I	19	38	G-2120, Gc-84040-27-1, MTD-16, G-2261, MTD-451, GC-83005-9, SY-35, NO-205, MTD-6, AGS-66, MTD-176, JOYAWIYAJA, AGS-314, BS-13, LG-92P-1139, ASSET-93-19-2, TAINANS, Lokon and SANTAR-05A
II	9	18	AGS-79, SBG-1, Binasoybean-1, Binasoybean-4, CH-1, SBM-18, SBM-22, ASSET-93-19-5 and G-10180
III	5	10	ASSET-93-19-1, BRAGG, BARI soybean-6, SBM-15 and AGS-278
IV	6	12	PM-78-6-3-13, MINA HAI, KADSING, AGS-302, GAURAB and DAVIS
V	6	12	Pb-1/Shohag, BS-3, SBM-09, Binasoybean-6, PK-416 and YESOY-4
VI	5	10	HIHS-WIHS, ACC-1222, Binasoybean-2, Binasoybean-3 and BARI soybean-5
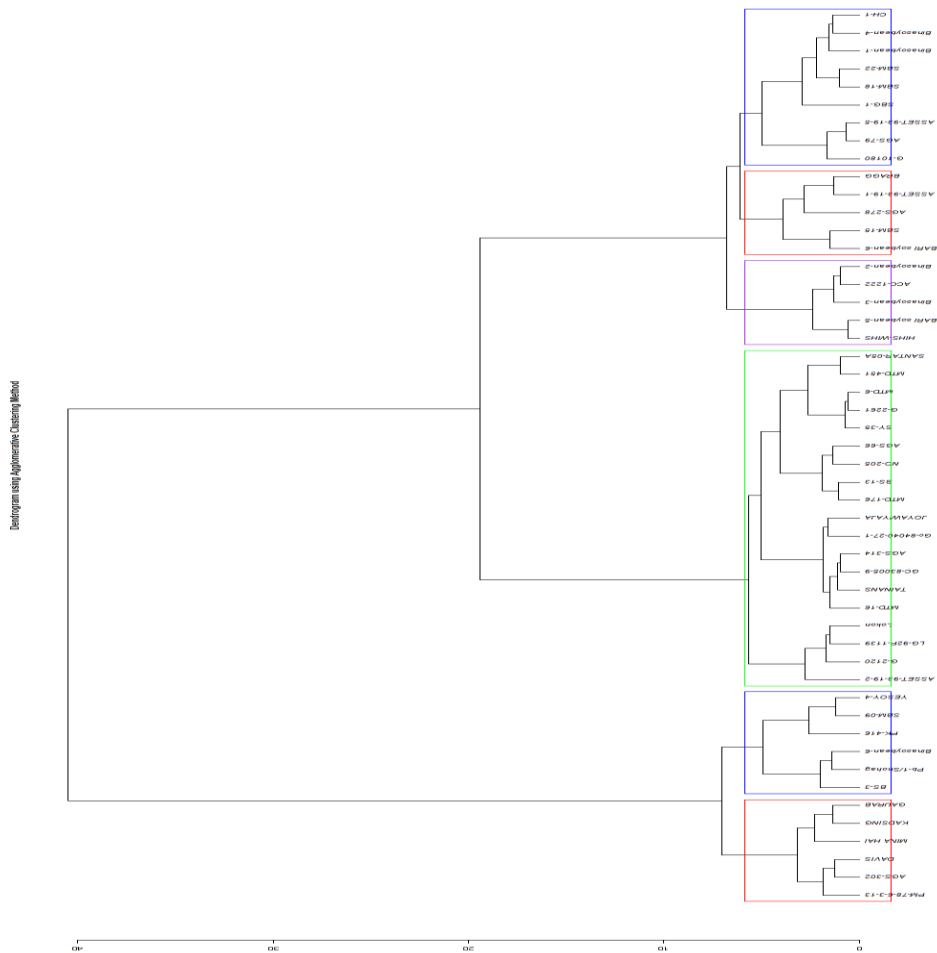
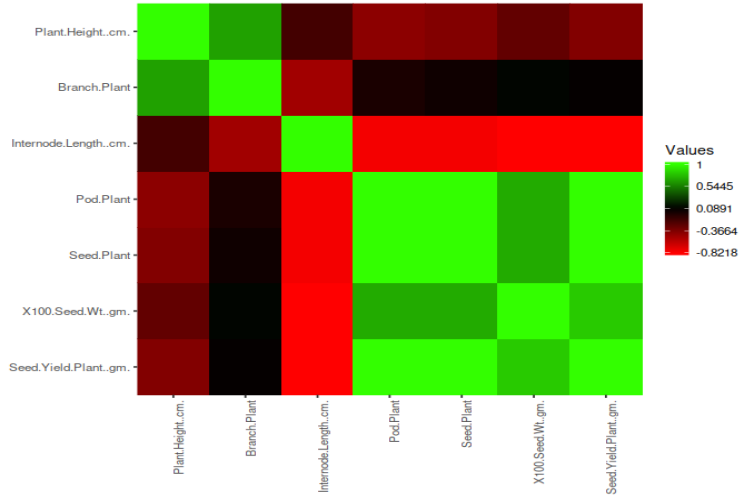**Fig. 4. Dendrogram showing the distribution of soybean genotypes into clusters using Ward's method**

Fig. 5. Heatmap generated exploiting the genotypic correlation matrix revealing the relevance among the traits in drought condition

The phenotypic path analysis was performed by exploiting six yield contributing attributes and path coefficient values of all the characters with seed weight (gm) are presented in Table 7. Path coefficient analysis denotes the components of the correlation coefficient within different traits into the direct and indirect effects and indicates the relationship in a more meaningful way [38]. The traits having a high positive correlation along with high direct effects are expected to be useful as selection criteria in crop improvement programs [39].

In this study, the path analysis had been conducted considering only the effects of five profound seed related traits on hundred seed weight. The highest positive direct contribution on seed weight was contributed greatly by seed plant^{-1} (0.3948), branch plant^{-1} (0.1969), pod plant^{-1} (0.1301) and plant height (cm) (0.0509). On the contrary, the negative direct effect on seed weight was exerted by internode length (cm) (-0.0522). The highest positive indirect effects were recorded in seed plant^{-1} (0.1282) following branch plant^{-1} (0.0617), plant height (cm) (0.0392) and internode length (cm) (0.0142) via pod plant^{-1}. The same trend was detected for pod plant^{-1} (0.3889), branch plant^{-1} (0.1956), plant height (cm) (0.1303) and internode length (cm) (0.0464) via seed plant^{-1}.

The highest negative indirect effect was detected in pod plant^{-1} (-0.0057), seed plant^{-1} (-0.0061), branch plant^{-1} (-0.0126) and plant height (cm) (-0.0154) via internode length (cm).

The pattern of interaction of the other potential yield components can be precisely explained by the residual effects. It ascertains the most effective way for the causal factors to explain the dependent factor's variability.

In the case of the present study, the residual effect was 0.7501 indicating that the six traits explain 24.99% of variability in hundred seed weight. The reason seems to be a very high correlation between some traits with seed weight (gm).

3.6 Stress Tolerance Indices

The various stress tolerance indices employed in this experiment are presented in Table 8. The TOL values in Binasoybean-6 (3.84), Shohag (3.85), YESOY-4 (3.88), SBM-09 (3.91), and PK-416 (3.81) were the lowest (3.91). Shohag, Binasoybean-6, PK-416, YESOY-4, and SBM-09 had the highest mean productivity (MP) and geometric mean productivity (GMP). Similar to this, YESOY-4, PK-416, Shohag, SBM-09, and Binasoybean-6 produced the highest relative productivity (RP). From 0.51 to 1.45 was the genotypic variance of the drought sensitivity index (DSI) (Table 3). The YESOY-4 (0.51), PK-416 (0.56), Shohag (0.56), SBM-09 (0.57), and Binasoybean-6 had the lowest DSI values (0.58). Binasoybean-1 has the greatest DSI (1.45). According to Teran and Singh (2002), drought-resistant lines have a relatively low DSI compared to drought-susceptible lines.The selection of tolerant genotypes of various crops, such as french bean [40], wheat [41,42], and soybean, has been widely used and found to be effective when grouping genotypes based on susceptibility index under stress conditions. Teran and Singh [43] reported that drought resistant lines had relatively low DSI values while the drought susceptible lines had high DSI values [44]. The most successful strategy for breeding soybeans for drought resistance, according to Ramirez-Vallejo and Kelly [45] and Schneider et al. [46], would be based first on selection for high geometric yield and then selection among the high-yielding individuals for low to moderate levels of the drought susceptibility index.

Table 7. Partitioning of phenotypic correlations into direct (Bold) and indirect (Unbold) effects of seven important characters of fifty soybean genotypes by path analysis

Characters	Plant height (cm)	Branch/plant	Internode length (cm)	Pod/plant	Seed/plant	100 Seed Wt (gm)
Plant height (cm)	0.0509	0.1328	-0.0154	0.0392	0.1303	0.3379
Branch/plant	0.0344	0.1969	-0.0126	0.0617	0.1956	0.4759
Inter node length (cm)	0.0150	0.0477	-0.0522	0.0142	0.0464	0.0711
Pod/plant	0.0154	0.0933	-0.0057	0.1301	0.3889	0.6220
Seed/plant	0.0168	0.0975	-0.0061	0.1282	0.3948	0.6312

Residue = 0.7501

Table 8. Seed yield plant⁻¹ in both non-stress and water stress condition and different drought tolerance indices

Genotypes	Seed yield plant⁻¹ (g)		Tolerance indices				
	NS	WS	MP	GMP	RP	DSI	TOL
G-2120	10.8	4.93	7.87	7.30	0.46	0.90	5.87
Gc-84040-27-1	7.8	2.553	5.18	4.46	0.33	1.12	5.25
MTD-16	8.5	3.15	5.83	5.17	0.37	1.05	5.35
AGS-79	7.47	1.223	4.35	3.02	0.16	1.39	6.25
ASSET-93-19-1	7.3	2.4	4.85	4.19	0.33	1.12	4.90
PM-78-6-3-13	10.3	5.867	8.08	7.77	0.57	0.72	4.43
G-2261	7.25	2.72	4.99	4.44	0.38	1.04	4.53
Pb-1/Shohag	11.4	7.547	9.47	9.28	0.66	0.56	3.85
HIHS-WIHS	7.6	2.943	5.27	4.73	0.39	1.02	4.66
MTD-451	7.743	3.18	5.46	4.96	0.41	0.98	4.56
BRAGG	7.74	3.077	5.41	4.88	0.40	1.00	4.66
GC-83005-9	7.74	2.947	5.34	4.78	0.38	1.03	4.79
SBG-1	7.473	2.753	5.11	4.54	0.37	1.05	4.72
SY-35	7.567	2.777	5.17	4.58	0.37	1.05	4.79
NO-205	6.333	1.627	3.98	3.21	0.26	1.24	4.71
MTD-6	7.3	2.31	4.81	4.11	0.32	1.14	4.99
AGS-66	6.84	2.04	4.44	3.74	0.30	1.17	4.80
ACC-1222	6.817	2.16	4.49	3.84	0.32	1.14	4.66
BARI-6	9	3.613	6.31	5.70	0.40	1.00	5.39
BINA-2	7.357	2.707	5.03	4.46	0.37	1.05	4.65
BINA-3	7.21	2.7	4.96	4.41	0.37	1.04	4.51
BINA-1	6.91	0.88	3.90	2.47	0.13	1.45	6.03
BINA-4	8.077	1.933	5.01	3.95	0.24	1.27	6.14
BARI-5	8.33	2.73	5.53	4.77	0.33	1.12	5.60
MINA HAI	10.1	6.077	8.09	7.83	0.60	0.66	4.02
BS-3	10	5.973	7.99	7.73	0.60	0.67	4.03
KADSING	9.517	4.837	7.18	6.78	0.51	0.82	4.68
AGS-302	10.3	5.49	7.90	7.52	0.53	0.78	4.81
GAURAB	10.2	4.587	7.39	6.84	0.45	0.92	5.61
MTD-176	8.507	1.68	5.09	3.78	0.20	1.34	6.83
JOYAWIYAJA	8.72	2.25	5.49	4.43	0.26	1.24	6.47
AGS-314	9.533	2.83	6.18	5.19	0.30	1.17	6.70
BS-13	9.05	2.423	5.74	4.68	0.27	1.22	6.63
LG-92P-1139	8.933	4.157	6.55	6.09	0.47	0.89	4.78
CH-1	9.043	1.573	5.31	3.77	0.17	1.38	7.47
ASSET-93-19-2	8.3	2.7	5.50	4.73	0.33	1.12	5.60
TAINANS	9.8	2.237	6.02	4.68	0.23	1.28	7.56
Lokon	7.653	3.36	5.51	5.07	0.44	0.93	4.29
SBM-09	11.387	7.473	9.43	9.22	0.66	0.57	3.91
SBM-15	9.65	3.867	6.76	6.11	0.40	1.00	5.78
SBM-18	7.993	2.27	5.13	4.26	0.28	1.19	5.72
SBM-22	6.84	1.6	4.22	3.31	0.23	1.28	5.24
BINA-6	11.04	7.2	9.12	8.92	0.65	0.58	3.84
SANTAR-05A	8.9	3.6	6.25	5.66	0.40	0.99	5.30
AGS-278	9.15	2.03	5.59	4.31	0.22	1.30	7.12
ASSET-93-19-5	8.357	1.273	4.82	3.26	0.15	1.41	7.08
G-10180	8.277	1.2	4.74	3.15	0.14	1.42	7.08
PK-416	11.7	7.793	9.75	9.55	0.67	0.56	3.91
DAVIS	10.653	6.537	8.60	8.34	0.61	0.64	4.12
YESOY-4	12.677	8.8	10.74	10.56	0.69	0.51	3.88

Abbreviations: NS=Non-stress, WS=Water stress, MP=Mean productivity, GMP=Geometric mean productivity, RP=Relative productivity, DSI=Drought sensitivity index, TOL=Tolerance, BAU=Bangladesh Agricultural University, BARI=Bangladesh Agricultural Research Institute, BINA= Bangladesh Institute of Nuclear Agriculture, SBM=Soybean mutant

4. CONCLUSION

The five soybean genotypes YESOY-4, PK-416, Shohag, SBM-09 and Binasoybean-6 were found as drought stress tolerant based on of yield reduction percentage, the degree of different tolerance indices, descriptive statistics analysis, principal component analysis, cluster analysis, heatmap and genotypic path coefficient. Multi-locations adaptive trial in different drought prone area may be conducted to confirm the field performance of those genotypes. However, this work will be helpful for the development of drought tolerant soybean varieties in Bangladesh.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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