

Morphological assessment of drought stress tolerant soybean genotypes in Bangladesh

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 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 height, 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 varieties which may be helpful for quality oil seed production.

Keywords: phenotypic assessment, soybean, water stress

1. Introduction

"Soybean (*Glycine max* [L.] Merr.) is one of the most economically important field crops worldwide, producing around 370 million tons annually" (USDA, 2023). "Soybean is a highly nutritious legume for its protein and edible oil which is used for both human consumption and livestock feed" (Kodadinne Narayana, 2024). "Drought is a major ecological problem that severely limits the production of agriculture globally, particularly in the context of global warming" (Wen *et al.*, 2021).

33 “Soybean is the world's primary source of protein and oil and is also acknowledged as a ‘miracle
34 crop’ due to over 40% protein and 20% oil” (Tripathi and Tiwari, 2004; Tiwari & Tripathi, 2005;
35 Mishra *et al.*, 2020; Upadhyay *et al.*, 2020a; Upadhyay *et al.*, 2020b). “For the duration of its growth
36 and development process, it requires a sufficient amount of water to achieve higher yields”. (Buezo
37 *et al.*, 2018). “The plants of soybean are affected by drought at every stage of life” (Dhanda *et al.*,
38 2004; Kachare, 2017; Kachare *et al.*, 2019; Mishra *et al.*, 2021; Sharma *et al.*, 2021). “Soybean is
39 now an essential and dominant source of protein and oil with over 200 uses in feed, food and
40 industrial applications. Recent studies indicate that the consumption of soybeans reduces cancer,
41 blood serum cholesterol, osteoporosis and heart disease” (Birt *et al.*, 2004). “Also, soybeans are a
42 good source of minerals, vitamins, folic acid, and isoflavones which are credited with the slow
43 development of these diseases” (Wilson, 2004). Thus, the demand for many edible soybean
44 products has increased dramatically.

45 “Drought affects several aspects of legume growth and development, including germination, shoot
46 and root development, photosynthesis and the reproductive stage. As a result of climate change,
47 drought is becoming one of the most unpredictable and uncontrollable factors affecting crop
48 productivity and negatively affecting legume crops. Soybeans are susceptible to drought, particularly
49 in the reproductive growth stage” (Oya *et al.*, 2004, Joshi *et al.*, 2016, Farooq *et al.*, 2017). “Drought
50 stress affected the yield and quality of soybeans. Drought frequently results in 40% losses in
51 soybean production” (Specht *et al.*, 1999; Pathan *et al.*, 2007). “These losses become even greater
52 when moisture stress occurs during both the vegetative and reproductive stages of the plant's life.
53 Drought tolerance is the ability of plants to utilize a limited amount of water, leading to low tissue
54 water potential, with higher efficiency regarding growth, biomass accumulation and reproduction”
55 (Ingram & Bartels, 1996). “Soybean is mainly grown in the late winter season in the greater
56 Noakhali district of Bangladesh. In this area, rainfall (75%) is concentrated mainly during the
57 summer monsoon season (June to September) and rain and irrigation water are scarce from
58 October to May. Thus, the crop falls under acute water stress mostly at the flowering and pod-filling
59 stages. Research on plant response to stress is becoming increasingly important, as most climate
60 change scenarios suggest an increase in aridity in many areas of the globe” (Petit *et al.*, 1999). One
61 of the main ways to maintain high soybean productivity in drought conditions is to develop more
62 drought-tolerant varieties. Ku *et al.* (2013) reported that “various indices/parameters have been
63 adopted to quantify drought tolerance in soybean genotypes and other crops”. The identification of
64 drought-tolerant soybean genotypes by screening several key and stable traits with high heritability
65 is an important step to improve drought tolerance in soybeans. Therefore, the present study was
66 undertaken to screen for drought-tolerant soybean genotype(s) for improving the yield level of
67 soybeans under rainfed cultivation in Bangladesh.

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2. Material and Methods

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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

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

97 2.1. Data collection

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

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

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

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

104 **Pod plant⁻¹ (no.):** The number of mature pods of each plant was recorded and mean was
105 expressed on plant⁻¹ basis.

106 **Seeds pod⁻¹ (no.):** Pods from each plant were sun dried. The clean seeds were collected and
107 counted.

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

110 **Seed yield plant⁻¹ (g):** Yield plant⁻¹ of each pot was recorded individually and adjusted at 10%
111 moisture content.

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

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119 2.2. Tolerance indices

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

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125 Relative performance (RP) = $\frac{\text{Value of a plant character under water stress condition}}{\text{Value of that character under non - stress condition}}$
126 (Asana and Williams, 1965)

127 Mean productivity (MP) = $\frac{Y_c + Y_s}{2}$ (Hossain *et al.*, 1990)

128 Geometric mean productivity (GMP) = $(Y_c \times Y_s)^{1/2}$ (Fernandez, 1992)

129 Tolerance (TOL) = $(Y_c - Y_s)$ (Hossain *et al.*, 1990)

130 Drought susceptibility index (DSI) = $(1 - Y_s/Y_c)/(1 - \bar{Y}_s/\bar{Y}_c)$,

131 Where,

132 Y_c = the yield of a given genotype in control condition

133 Y_s = the yield of a given genotype in stress condition

134 \bar{Y}_s = mean yield of all genotypes under control condition

135 \bar{Y}_c = mean yield of all genotypes under stress condition

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137 **2.3 Statistical analysis**

138 The recorded data were analyzed statistically using the STATISTIX-10 software package (Statistix
139 10. 2013) and R-4.3.0 computer package program (R Studio 2020). Ranking was done based on
140 their yield reduction due to water stress over non-stress condition.

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142 **3. Results & Discussion:**

143 **3.1. ANOVA for morphological traits of soybean genotypes**

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

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152 **Table 2. Analysis of variance (ANOVA) of seven yield contributing traits with significance**
153 **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 x 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

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

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156 **3.2. Descriptive Statistics Analysis**

157 Range of values obtained from 50 soybean genotypes for 7 traits, mean of the traits with
158 standard error, genotypic (GV) and phenotypic (PV) variance, genotypic (GCV) and

159 phenotypic coefficient of variation (PCV), genetic advance (GA), genetic advance as per cent
160 (GAM) of mean and broad sense heritability (h^2b) has been furnished in Table 3.

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162 **Mean and range values**

163 The range and mean values for the 7 traits are presented in Table 3. The results indicated
164 significant differences among the soybean genotypes for growth, yield and yield related traits. Plant
165 height (cm) ranged from 21cm to 100cm with an average height of 62.31cm. The range observed
166 for branch plant⁻¹ was the lowest (0) to highest (7) with an overall mean of 3.24, Internode length
167 (cm) having a range between minimum 2 cm to maximum 12 cm with a mean 5.17 cm. The number
168 of pods per plant ranged from 8 to 61 with an average of 33.67. The number of seeds per plant was
169 likely to be 10 to 121 with an average value of 68.40. Regarding seed related traits, the lightest 100
170 seed weight was 5.75g and the heaviest was 10.70g with an average weight of 8.56g (Table 3). The
171 range and mean values of the studied traits suggested the existence of sufficient variability among
172 the studied soybean genotypes and thus offered ample scope for their potential improvement.

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174 **Genotypic and phenotypic coefficients of variation**

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

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

181 The per cent genotypic and phenotypic coefficient of variation (GCV and PCV) for plant height
182 (28.99 cm and 29.14 cm), branch plant⁻¹ (46.57 and 47.47), pod plant⁻¹ (42.90 and 43.24), seed
183 plant⁻¹ (44.36 and 44.44), 100 seed wt. (13.84g and 13.95g) and seed yield plant⁻¹ (56.29g and
184 56.40g) were very close to each other (Table 3) indicating that the characters were less influenced
185 by the environment. Therefore, selection based on phenotype alone can be effective for the
186 improvement of these traits.

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

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194 **Heritability and genetic advance**

195 Estimating heritability is of tremendous significance to the breeder, as its magnitude indicates the
 196 accuracy with which a genotype can be recognized by its phenotypic expression. High heritability
 197 (>60%) accompanied with high to moderate genotypic and phenotypic coefficient of variation and
 198 genetic advance which indicates that most likely the heritability is due to additive gene effects for
 199 these traits, selection may be effective in early generations. The high heritability of those traits
 200 indicated that the influence of the environment on these characters is negligible or low. Therefore,
 201 selection can be effective based on the phenotypic expression of these traits in the individual plant
 202 by implementing simple selection methods.

203 High heritability does not always indicate a high genetic gain; heritability should be used together
 204 with the genetic advance in predicting the ultimate effect of selecting superior varieties (Muchie and
 205 Fentie, 2016). The estimates of high heritability (>60%) coupled with high genetic advance (>20%)
 206 were recorded for plant height (cm) ($h^2b= 99\%$, $GA= 59.43\%$), branch plant⁻¹ ($h^2b= 96.25\%$,
 207 $GA=94.13\%$), pod plant⁻¹ ($h^2b= 98.46\%$, $GA=87.70\%$), seed plant⁻¹ ($h^2b= 99.63\%$, $GA=91.22\%$),
 208 100 seed wt. (gm) ($h^2b= 98.47\%$, $GA=28.30\%$) and seed yield plant⁻¹ (gm) ($h^2b= 99.58\%$, $GA=$
 209 115.71%) in (Table 3), which exhibited good scope for improving these traits through phenotypic
 210 selection due to the additive gene action.

211 Heritability for all the characters was high, indicating the low influence of the environment on the
 212 studied characters. The maximum heritability was recorded for seed plant⁻¹ (99.63%) and the
 213 minimum for internode length (cm) (65.53%). According to Johnson et al. (1955), estimating
 214 heritability in conjunction with genetic advancement is more beneficial in forecasting the gain under
 215 selection.

216

217 **Table 3. Descriptive statistics for seven agronomic characters of soybean**

Charact ers	Range	Mean±S E	PV(σ^2p)	GV(σ^2g)	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±0.0 9	1.0842	1.0435	47.4734	46.5738	2.0645	94.1261	96. 25
Internod e Length	2-12	5.17±0.1 1	0.8517	0.5581	23.3049	18.8652	1.2458	31.4596	65. 53

(cm)									
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

218 Abbreviations: PV(σ^2_p) = Phenotypic Variance, GV (σ^2_g) = Genotypic Variance, PCV= Phenotypic Coefficient of Variation, GCV= Genotypic Coefficient of
 219 Variation, GA= Genetic Advance, GAM (%) = Genetic Advance as Percentage of Mean, h²_b= Broad Sense Heritability

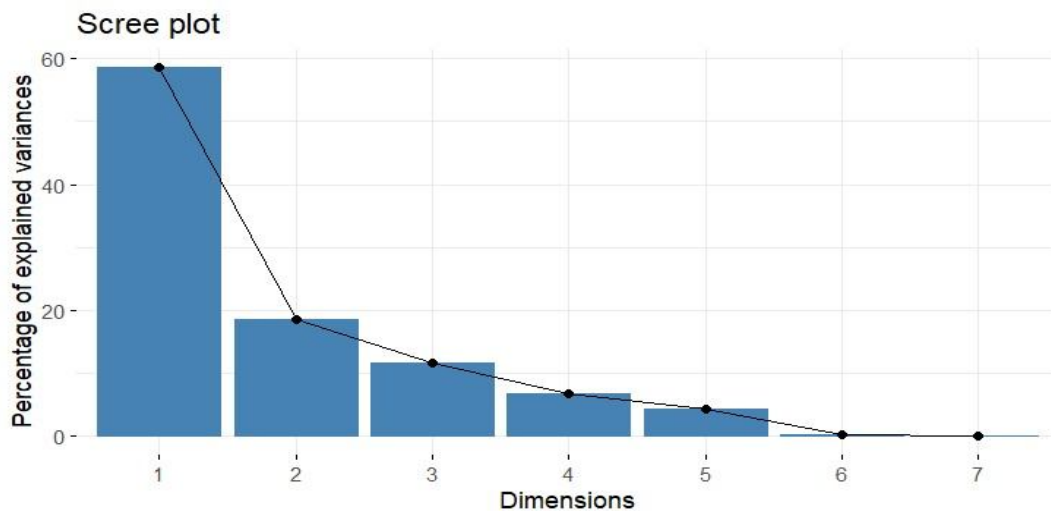
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221 3.2. Principal Component Analysis

222 The computed eigenvalues of seven variables of 50 soybean genotypes were subjected to
 223 principal component analysis; their eigenvalues, variability% and cumulative explained
 224 variance are present in the following Table 4. Eigenvalues of the first 7 principal
 225 components had been shown in the scree plot (Figure 2) which revealed that the first
 226 principal component explained the majority of variation expressed by the population.
 227 Among the seven PCs, two PCs with an eigenvalue greater than 1 explained 77.07% of the
 228 entire morphological variation. The PC1, PC2, and PC3 explained 58.58%, 77.07% and
 229 88.62% of the whole morphological variation, respectively (Table 4).

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238 Figure 2. Scree plot explaining how much variation each principal component
 239 captured from the data along with the breakdown point of principal components

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

241 **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%

242

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

244 **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	-0.4758	-0.2095	-0.0993	-0.0380	-0.0454	0.3645	0.7639	

	Yield/plant (gm)							
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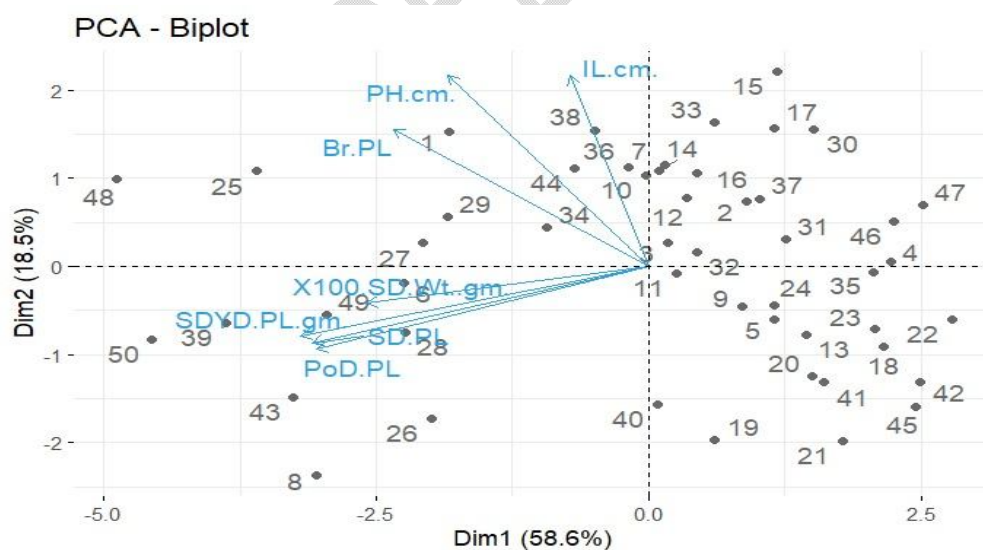
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246 **Biplot analysis based on principal component analysis**

247 “A biplot is a principal component that represents variables superimposed on a plot as vectors
 248 where the relative length of vectors represents the relative proportion of variability in each variable
 249 represented on the biplot. If the angle between vectors of two traits is $< 90^\circ$ both are positively
 250 correlated whereas if the angle is $> 90^\circ$ there is a negative correlation. Both vectors show no
 251 correlation if the angle is 90° ” (Sabaghnia *et al.* 2011). “It is mostly used to determine the
 252 components where the effect is more to create the genotypic variation. The traits having highest
 253 values have the greatest influence on the total variation. Biplot analysis determines varietal stability
 254 in the multi-environmental trial” (Farshadfar, 2013). In the Dim1 and Dim2 biplot graphs, it was
 255 evident that pod/plant and seed plant⁻¹ had a strong positive correlation. Moreover, seed plant⁻¹ and
 256 seed yield plant⁻¹ (gm) had a strong positive correlation among them; 100 seed wt. (gm) and seed
 257 yield plant⁻¹ (gm) had a strong positive correlation with each other. Plant height (cm) and seed yield
 258 plant⁻¹ (gm) had a strong negative correlation with each other while both of them revealed a
 259 negative correlation with branch plant⁻¹ and pod plant⁻¹ (Figure 3).

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 272 **Figure 3. Principal Components Analysis (PCA) ordination graph; Dim1 vs Dim2**
 273 **biplot.** [Position of soybean genotypes from the selected genotypes along the first two axes obtained from PCA where PH (cm) = Plant

274 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
 275 Wt. (gm) and SDYD/PL (gm) = Seed Yield/Plant (gm)]

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

285 3.3. Cluster Analysis

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

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 293 **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,

318 Clusters IV (12%) and V (12%) had 24% of the genotypes containing six genotypes each.
 319 Clusters III and VI contained five genotypes each (Table 6). On the contrary, cluster I
 320 contained nineteen genotypes (38%) and cluster II contained nine genotypes (18%). The
 321 fifty soybean genotypes were grouped by the Pearson method using quantitative and
 322 qualitative traits as shown in Figure 4.

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324 3.4. Heatmap

325 The relative correlation among the yield-related traits is indicated by the gradient of color;
 326 the lemon color denotes the highest genotypic correlation, and the red color means the
 327 lowest genotypic correlation. Heatmap generated exploiting the genotypic correlation
 328 matrix (Figure 5) showed that pod plant⁻¹ is highly correlated with seed plant⁻¹ followed by
 329 100 seed wt. (gm). Seed plant⁻¹ is highly positively correlated with 100 seed wt. (gm). 100
 330 seed wt. (gm) is positively correlated with the pod plant⁻¹, seed plant⁻¹ and seed yield plant⁻¹
 331 ¹ (gm). Pod plant⁻¹, seed plant⁻¹, 100 seed wt. (gm) and seed yield plant⁻¹ (gm) are highly
 332 negatively correlated with internode length (cm).

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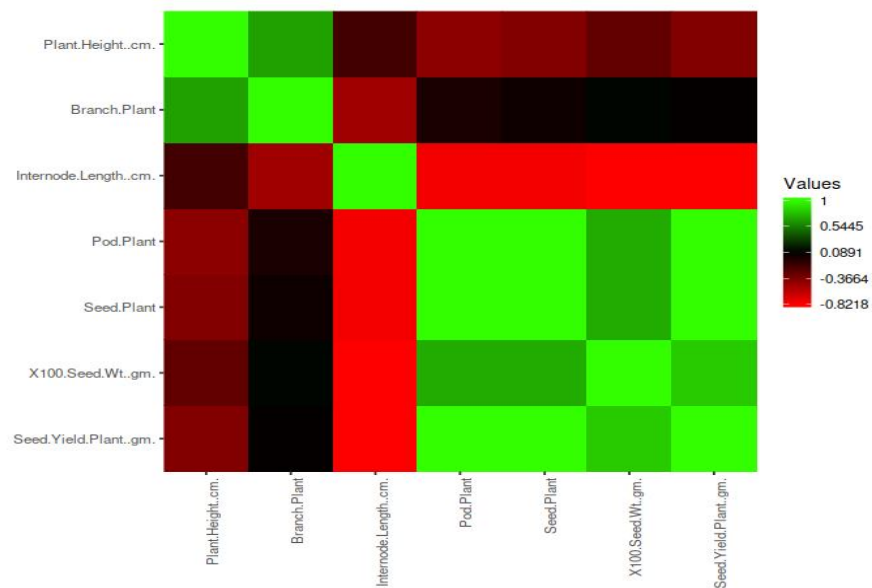
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347 Figure 5. Heatmap generated exploiting the genotypic correlation matrix revealing the relevance
 348 among the traits in drought condition

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” (Dewey and Lu, 1959; Begum *et al.*, 2016).

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 (Al-Amin *et al.*, 2019). The traits having a high positive correlation along with high direct effects are expected to be useful as selection criteria in crop improvement programs (Pavan *et al.*, 2011).

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.

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	0.0509	0.1328	-0.0154	0.0392	0.1303	0.3379

(cm)						
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

381 **Residue = 0.7501**

382 In the case of the present study, the residual effect was 0.7501 indicating that the six traits explain
383 24.99% of variability in hundred seed weight. The reason seems to be a very high correlation
384 between some traits with seed weight (gm).

385

386 **3.6. Stress tolerance indices:** The various stress tolerance indices employed in this
387 experiment are presented in Table 8. The TOL values in Binasoybean-6 (3.84), Shohag
388 (3.85), YESOY-4 (3.88), SBM-09 (3.91), and PK-416 (3.81) were the lowest (3.91). Shohag,
389 Binasoybean-6, PK-416, YESOY-4, and SBM-09 had the highest mean productivity (MP)
390 and geometric mean productivity (GMP). Similar to this, YESOY-4, PK-416, Shohag, SBM-
391 09, and Binasoybean-6 produced the highest relative productivity (RP). From 0.51 to 1.45
392 was the genotypic variance of the drought sensitivity index (DSI) (Table 3). The YESOY-4
393 (0.51), PK-416 (0.56), Shohag (0.56), SBM-09 (0.57), and Binasoybean-6 had the lowest
394 DSI values (0.58). Binasoybean-1 has the greatest DSI (1.45). According to Teran and
395 Singh (2002), drought-resistant lines have a relatively low DSI compared to drought-
396 susceptible lines. The selection of tolerant genotypes of various crops, such as french bean
397 (Choudhury *et al.*, 2010), wheat (Bazzaz, 2013 and Shafazadeh *et al.*, 2004), and soybean,
398 has been widely used and found to be effective when grouping genotypes based on
399 susceptibility index under stress conditions. Teran and Singh (2002) reported that drought
400 resistant lines had relatively low DSI values while the drought susceptible lines had high
401 DSI values (Mannan *et al.*, 2012). The most successful strategy for breeding soybeans for
402 drought resistance, according to Ramirez-Vallejo and Kelly (1998) and Schneider *et al.*
403 (1997), would be based first on selection for high geometric yield and then selection among
404 the high-yielding individuals for low to moderate levels of the drought susceptibility index.

405

406 **Table 8. Seed yield plant⁻¹ in both non-stress and water stress condition and different**
 407 **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

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

411

412 **4. Conclusion:**

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

419

420 **DISCLAIMER (ARTIFICIAL INTELLIGENCE)**

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

424

425 **COMPETING INTERESTS**

426 Authors have declared that no competing interests exist.

427

428 **Authors' contributions**

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

431

432 **Ethical Issues**

433 There is no ethical issue.

434

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