## GENETIC VARIABILITY OF SOYBEAN GENOTYPES UNDER DROUGHT STRESS

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### Abstract

A field experiment was carried out to identify drought tolerant soybean genotypes from January to June 2015. Thirteen quantitative plant traits were studied to classify the genotype into different groups using multivariate analyses. A wide range of variation was observed and the genotypes were grouped into six clusters. The maximum number of genotypes (15) under control condition was concentrated in cluster 1 followed by cluster 2 (14), 3 (10), 4 (8), 6 (2) and 5 (1) whereas under drought condition the maximum number of genotypes (15) were gathered in cluster 4 followed by cluster 1 (12), 3 (11), 6 (6), 5 (4) and 2 (2). Principle component analysis (PCA) revealed that a single component described 100% variation in controlled condition and PC 1, 2 and 3 described 92% variation together in stress. The plant height, pods per plant, number of seeds per plant, yield per plant and 100-seed weight were the important discriminating variables in grouping the genotypes. The number of seeds per plant and 100-seed weight displayed the principal role in explaining the maximum variance in the genotypes. The clustering pattern of the genotypes revealed that G2 (G00006) followed by G37 (BD2336), G39 (BD2350), G47 (GMOT22) and G46 (BGH2033) produced higher seed yield. Considering all the plant characters studied G2, G39, G50 (Shohag), G37 and G47 were the best genotypes and they had great potential in varietal development.

Keywords: Genetic variability, seed yield, tolerance, water scarcity.

### Introduction

Soybean (*Glycine max* L.) is one of the oldest cultivated crops and the wide range of its climatic adaptability made the crop more popular world wide. In Bangladesh, soybean is a newly introduced crop and the cultivation is increasing gradually as the climatic and edaphic conditions of the country are favorable for soybean production. The recommended time for soybean cultivation is September 15 to October 15, December 15 to January 15 or May 15 to June 15.

The farmers of Bangladesh mostly sow the seeds in late-winter season in the southern part, especially in greater Noakhali, whereas during pre-winter in the northern part of Bangladesh. In both the seasons the soybean is grown mostly under rainfed conditions.

Even soybean is sown under optimum soil moisture conditions the crop suffers from water shortage at the later stages of growth with the depletion of stored soil moisture. When the crop is exposed to drought during vegetative stage, it will have less branching, shorter plant,

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minimum leaf area and consequently will produced low grain yield. Water participates in nearly all physiological and biochemical processes in plants, comprising approximately 90% of their mass (Farias *et al.*, 2007). Water is responsible for the thermal regulation of the plant, acting both to maintain the cooling and heat distribution and to promote mechanical support of the plant (Taiz and Zeiger, 2009). However, two-thirds of world food production is done under water stress conditions (Gerten and Rost, 2010) and thus, it is considered as the most damaging abiotic stress affecting modern agricultural production (Zhang *et al.*, 2006).

Soybean is also considered as a species sensitive to several abiotic stresses (Heerden and Krüger, 2000), when compared with other tropical legumes (Silveira et al., 2003), as well as others species (Younis et al., 2000). The total water requirement for the maximum productivity varies between 450 and 800 mm, depending on weather conditions, crop management practices and cycle timing (Embrapa, 2011 and Farias et al., 2007). Although the effects of various environmental factors interfere with the performance of crops, water restriction is the main limiting environmental factor that contributes to the failure for obtaining potential soybean vield (Casagrande et al., 2001). If soybean is exposed to drought at reproductive stage, flower drop may occur and that will lead to lower pods per plant and lighter seed weight. Moreover, having its day neutral plant character soybean may be grown in Bangladesh round the year. The vast area of char land of Bangladesh (1.0 mha) can also be used for cultivation of soybean. For expanding soybean in the under-exploited land, more

specifically in the northern Bangladesh as well as in the char lands, it is necessary to screen suitable genotypes for low soil moisture conditions prevailing during kharif I season. It is also important to analyze the physiomorphological changes of the crop due to low soil moisture conditions in order to understand the mechanisms of the crop tolerance to such situations under the climate change context of Bangladesh. Thus, this study was initiated to screen for drought tolerance among fifty high yield potential soybean genotypes.

## **Materials and Methods**

A study was conducted at Bangabandhu Agricultural Sheikh Mujibur Rahman University, Gazipur, from January to June 2015. The soil of the experimental site was silty clay in surface and silty clay loam in sub surface region. The land preparation was done well by repeated ploughing and crossploughing followed by laddering. Urea, triple super phosphate, muriate of potash, gypsum and boric acid were applied at final land preparation as the source of N, P, K, S and B at the rate of 27.5, 37, 60, 20.5 kg and 1.7 kg ha<sup>-1</sup>, respectively (FRG, 2012). High yield potential fifty (50) soybean genotypes were used as planting material (Table 1). Seeds were sown by hand on 15 January, 2015 in lines maintaining 30 cm  $\times$  5 cm spacing. The experiment was laid out in a split-plot design with three replications. The water managements were allocated in the main plots and soybean genotypes in the sub-plots. The treatments were Factor A: Soybean genotypes; and Factor B: Water management such as (i) Irrigation as and when necessary (control) and (ii) Irrigation (50% of control) when wilting symptoms appeared in plants (drought). Appropriate cultural practices other

Genotype no.	Accession code	Remarks	Genotype no.	Accession code	Remarks
G1	G00001	Advanced line	G26	G00197	Advanced line
G2	G00006	Advanced line	G27	G00209	Advanced line
G3	G00008	Advanced line	G28	G00246	Advanced line
G4	G00009	Advanced line	G29	G00341	Advanced line
G5	G00010	Advanced line	G30	G00352	Advanced line
G6	G00011	Advanced line	G31	G00354	Advanced line
G7	G00012	Advanced line	G32	BD2326	Advanced line
G8	G00013	Advanced line	G33	BD2329	Advanced line
G9	G00017	Advanced line	G34	BD2331	Advanced line
G10	G00018	Advanced line	G35	BD2333	Advanced line
G11	G00025	Advanced line	G36	BD2334	Advanced line
G12	G00037	Advanced line	G37	BD2336	Advanced line
G13	G00043	Advanced line	G38	BD2340	Advanced line
G14	G00046	Advanced line	G39	BD2350	Advanced line
G15	G00051	Advanced line	G40	AGS191	Advanced line
G16	G0055	Advanced line	G41	AGS205	Advanced line
G17	G00075	Advanced line	G42	AGS313	Advanced line
G18	G00112	Advanced line	G43	AGS383	Advanced line
G19	G00135	Advanced line	G44	BARI Soybean 5	Variety
G20	G00152	Advanced line	G45	BARI Soybean 6	Variety
G21	G00154	Advanced line	G46	BGH2033	Advanced line
G22	BU Soybean 1	Variety	G47	GMOT22	Advanced line
G23	G00168	Advanced line	G48	PK262	Advanced line
G24	G00170	Advanced line	G49	PK472	Advanced line
G25	G00196	Advanced line	G50	Shohag	Variety

Table 1. List of soybean genotypes with their accession number used in the experiment

than water management were followed to raise a healthy crop. Regular irrigation was applied with a hosepipe attached to a water tape both in control and drought plots up to trifoliate stage (20 days after sowing) of soybean for seed germination and establishment of young seedling. After three leaf stage, irrigation was applied properly at regular intervals in control plots. However, irrigation was applied when wilting symptom appeared on more than 50% soybean plants in drought treated plots. Ten plants of each genotype in the row were selected for collecting the data on phenology, morphology and yield and yield attributes were recorded. Analysis of genetic variation among genotypes was performed with the program SPSS 16 following the procedure described by Rojas *et al.* (2000). Estimation of the degree of correlation was estimated among the different plant characters according to Pearson's co-efficient (Clifford and Stephenson, 1975). Thirteen qualitative

variables viz. days to 1st flowering, days to 80% flowering, days to maturity, plant height, plant dry weight, branches per plant, pods per plant, pod length, seeds per pod, pod wall dry weight, seeds per plant, 100-seed weight and yield per plant were considered in the cluster analysis and principal component analysis (PCA). Discriminant function analysis (DFA) and non-hierarchical K-mean cluster was performed to classify the genotypes into a number of groups (Nimnual et al., 2014). The DFA, PCA, chi-square test, structure matrix of variables, test of equality of group means were done through stepwise procedures. Descriptive analysis including range, mean and co-efficient of variation (CV) of the plant characters with frequency distribution was employed to estimate and describe the performance of the genotypes in terms of each character. Some of the parameters (% yield reduction) were calculated using Microsoft excel.

## **Results and Discussion**

### Variation in plant characters

The soybean genotypes showed a wide range of variations in 13 quantitative characters both control and drought conditions (Table 2). The co-efficient of variation (CV) for days to first and 80% flowering was 12% in control but 117% in case of drought condition. It indicated that the variation for these two characters were more prominent in drought condition compare to control. Similarly, the CV for morphological attributes also illustrated a high level of diversity among the soybean genotypes. Yield and yield attributes such as

 
 Table 2. Descriptive statistics of the plant characters of tested soybean genotypes under both control and drought condition

Diant abaratara	Co	ntrol condition		Drought condition			
Plant characters	Range	Mean <sup>1</sup>	CV (%)	Range	Mean <sup>1</sup>	CV (%)	
Phenological							
Days to 1st flowering	40-64	53±6.17	12	38-61	51±6.06	117	
Days to 80% flowering	46-73	61±7.09	12	44-70	59±6.97	117	
Days to maturity	76-113	97±8.38	9	75-115	101±8.75	8.6	
Morphological							
Plant height (cm)	30-72.27	52.82±10.05	19	18.43-64.33	41.35±10.10	24.4	
Plant dry weight (g)	1.00-4.33	2.56±0.92	36	0.43-3.86	$1.82 \pm 0.82$	45.5	
Branches per plant (no.)	1.00-5.43	2.30±1.10	48	1-5	1.57±0.77	49	
Yield and yield attributes							
Pods per plant (no.)	10.80-57.33	27.32±10.79	39	6.53-55.51	22.55±10.65	47.2	
Pod length (cm)	3.08-5.32	3.96±0.45	11	3.02-5.02	3.82±0.47	12.2	
Seeds per pod (no.)	2.00-3.20	2.53±0.26	10	1.77-3.4	2.43±0.35	14.3	
Pod wall dry weight (g)	1.40-4.76	3.12±0.81	26	0.80-6.35	$2.50\pm0.98$	39.3	
Seeds per plant (no)	18.13-123.86	48.02±18.47	38	12.77-115.33	37.19±18.75	50.4	
100-seed weight (g)	5.66-25.13	12.10±3.32	27	6.37-21.46	11.68±2.94	25.2	
Yield per plant (g)	2.94-10.79	6.01±1.68	28	1.42-9.20	4.88±1.90	39	

<sup>1</sup>Mean±standard deviation

pods per plant (CV-39% for control and 47% for drought), pod wall dry weight (CV-26% for control and 39% for drought), number of seeds per plant (CV 38% for control and 50% for drought), seed yield per plant (CV 28% for control and 39 for drought) and 100-seed weight (CV-27% for control and 25% for drought) also showed a much variations among the genotypes. Anjum *et al.* (2013) reported that water deficit conditions disrupted the yield and yield related attributes in terms of grain number per pod, grain number per plant, 100-grain weight, biological yield per plant, seed yield per plant and harvest index in comparison to well watered conditions.

### **Correlation between plant characters**

The correlation coefficients were estimated for the 13 plant characters in both control and drought condition (Table 3). The strongest and significant positive correlation corresponded to days to first flowering and 80% flowering (1.00\*\*) in both treatments. This indicated that these two phenological characters were perfect positively correlated. Positive significant correlations were also shown between days to maturity with both days to first flowering and 80% flowering. Malek et al. (2014) observed that days to flowering and days to maturity were positively and highly correlated. Plant height and plant dry matter production also showed a strong positive correlation with days to first and 80% flowering as well as days to harvest in both treatments. On the other hand, branch per plant exhibited a weak and negative correlation with days to first and 80% flowering, weak and positive with plant height and plant dry matter production. Ngalamu et al. (2013) found that branch per plant significantly correlated with days to 50% flowering and pods per plant.

Yield and yield attributes under both control and drought condition i.e., pods per plant, pod length, seeds per pod, pod wall dry weight, total numbers of seeds per plant and yield per plant were highly correlated to each other. Pod wall dry weight had a strong positive correlation with plant weight  $(0.731^{**})$ , plant dry weight (0.819\*\*) and yield per plant (0.887\*\*). Mondal et al. (2011) observed that seed yield showed significant and positive correlations with the number of pods per plant. Under drought condition, pods per plant had strong positive correlation with plant height (0.678\*\*) and plant dry weight (0.652\*\*). Pod wall dry weight had a strong positive correlation with plant weight (0.672), plant dry weight  $(0.675^{**})$  and yield per plant  $(0.722^{**})$ . Total number of seeds under control condition had a positive correlation with pods per plant (0.887\*\*). Total number of seeds under drought condition had a positive correlation with pods per plant (0.897\*\*). Hundred-seed weight has a negative correlation with total number of seeds per plant (-0.638\*\*). Maleki1 et al. (2013) also reported that there was a significant reduction in seed per pod in water stress condition. Almost all plant characters studied had a strong positive correlation with yield in both conditions.

# Grouping of genotypes through multivariate analysis

The soybean genotypes were grouped into six groups by non-hierarchical K-mean cluster analysis considering thirteen quantitative plant characters. The maximum number of genotypes (15) under control condition was concentrated in cluster 1 followed by cluster 2 (14), 3 (10), 4 (8), 6 (2) and 5 (1) whereas the maximum number of genotypes (15) was

Table 3.	Correlat	ion coeffic	cient of th	irteen pla	int chara	cters of te	sted soyb	ean genot	ypes			
Traits	DFF	DEF	ΗΠ	Hd	PDW	BPP	РРР	ΡL	SPP	PWDW	TSN	HSW
Control c	ondition											
DEF	$1.00^{**}$											
HU	$0.76^{**}$	0.77**										
Hd	0.53**	0.54**	$0.46^{**}$									
PDW	0.64**	$0.64^{**}$	$0.70^{**}$	0.83**								
BPP	-0.27	-0.28	-0.39**	0.16	0.04							
ppp	0.34*	0.33*	0.13	$0.61^{**}$	$0.51^{**}$	0.53**						
PL	0.01	0.01	0.16	-0.15	0.05	-0.36**	-0.62**					
SPP	-0.34*	-0.34*	-0.21	-0.18	0.02	0.23	-0.19	0.32*				
PWDW	0.52**	0.52**	$0.51^{**}$	0.73**	0.82**	0.23	$0.64^{**}$	0.01	-0.09			
NST	0.21	0.21	0.09	0.58**	0.54**	0.66**	$0.88^{**}$	-0.49**	0.15	$0.62^{**}$		
MSH	0.20	0.20	0.37**	-0.17	0.016	-0.58**	-0.64**	0.72**	-0.07	-0.10	-0.64**	
ΥL	0.50**	0.50**	$0.51^{**}$	0.64**	$0.81^{**}$	0.19	0.58**	0.01	-0.01	$0.88^{**}$	0.60**	0.02
Drought	condition											
DEF	$1.00^{**}$											
ΗΠ	0.74**	0.74**										
Hd	0.56**	$0.56^{**}$	$0.61^{**}$									
PDW	0.64**	$0.64^{**}$	0.75**	$0.86^{**}$								
BPP	-0.09	-0.09	-0.25	0.29*	0.26							
ppp	0.49**	$0.49^{**}$	$0.41^{**}$	0.68**	0.65**	$0.54^{**}$						
PL	-0.01	-0.01	0.16	-0.01	0.08	-0.25	-0.49**					
SPP	-0.34*	-0.34*	-0.14	-0.21	-0.01	0.22	-0.28*	0.44**				
PWDW	0.57**	0.57**	$0.62^{**}$	0.67**	$0.67^{**}$	0.09	$0.62^{**}$	-0.01	-0.23			
ISN	0.38**	$0.38^{**}$	$0.36^{*}$	0.66**	$0.69^{**}$	0.72**	0.89**	-0.33*	0.06	$0.53^{**}$		
MSH	0.17	0.17	0.35*	0.02	0.14	-0.48**	-0.44**	0.68**	0.08	-0.02	-0.38**	
ΥL	0.56**	0.56**	0.69**	0.79**	0.88**	0.31*	0.75**	0.01	-0.07	0.72**	0.77**	0.11
** and * ( harvest, Pl per pod (n	Correlation i H = plant he o), PWDW	is significant ight (cm), PI = pod wall d	at the 1 and DW = plant c lry weight (g	5% level (2. hry weight (c ), TSN = tot	-tailed), resp m), BPP = t al number o	ectively. DH sranches per f seeds per p	FF = days to plant (no), F olant, HSW=	first flowerir PP = pods pe 100-seed we	ng, DEF = d er plant (cm sight (g) and	lays to 80% f ), PL = pod l l YL = yield	lowering, DJ ength (cm), S per plant (g)	H = days to PP = seeds

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concentrated in cluster 4 followed by cluster 1 (12), 3 (11), 6 (6), 5 (4) and 2 (2) under drought condition (Table 4).

The clustering group revealed that cluster 6 in control and cluster 2 in drought were the best as compared to others (Table 5) for the highest dry matter accumulation, production more branches per plant, higher number of seeds per pod as well as per plant and improved seed yield per plant. Other groups were characterized by days to flowering, plant height, growth duration and seed size. Cluster 4 was characterized by the shortest plant height, shortest growth duration and the lowest seed yield in control condition. Similarly, all the dwarf, short-durated and lower yield genotypes were placed in cluster 6 in case of drought condition. Cluster 3, 4 and 5 showed moderate features in all the plant characters under studied

## Principal component analysis

Based on the correlation matrix, thirteen plant characters were analyzed using Principal Component Analysis (PCA). A linear transformation of thirteen plant characters was performed by PCA that generated a new

set of thirteen independent variables. These were described by latent root (Eigen value) and latent vectors. Under control condition, the use of PCA revealed that the first PC had Eigen values more than 1 and explained 100% variations where, first three PCs had Eigen values more than 1 and explained 49.74%, 28.98% and 13.45% of total variation individually 92% variations together under drought condition (Table 6). Under control condition the variables with high positive contribution to PC 1 were days to first flowering, days to 80% flowering, branches per plant, pods per plant, seeds per pod, pod wall dry weight, total number of seeds per plant and yield per plant (Table 6). The rest of the variables had high negative contribution to PC 1. Under drought condition, the variables with high positive contribution to PC 1 were days to maturity, days to harvest, pods per plant, pod wall dry weight, total number of seeds per plant and yield per plant. Flowering time is an important trait related to drought adaptation, where a short life cycle can lead to drought escape (Araus et al., 2002). Sofi et al. (2014) evaluated genetic variability among 300 genotypes of common bean under PCA.

Table 4. Clusters of 50 soybean genotypes classified by K-mean clustering

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G16, G18, G25,
38, G39, G41,
G13, G19, G22,
and G40
and G26

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		Clu	sters in con	ntrol cond	ition			Clus	ters in dro	ught condi	tion	
Plant characters		2	3	4	5	9	1	2	3	4	5	9
No. of genotypes	15	14	10	8	1	2	12	2	11	15	4	6
Phenological												
Days to first flowering	52	58	55	43	57	56	55	56	55	48	58	42
Days to 80% flowering	59	67	63	50	99	64	63	64	63	56	67	48
Days to maturity	95	106	67	84	111	66	110	104	103	98	107	84
Morphological												
Plant height (cm)	50.36	57.56	59.88	37.50	40.41	70.30	50.51	61.59	43.96	36.46	38.56	25.56
Plant dry weight (g)	2.09	3.21	3.12	1.32	2.2780	3.85	2.63	3.40	2.02	1.28	1.87	0.63
Branches per plant (no)	2.31	1.34	3.08	2.45	1	5	1.23	4.63	1.64	1.42	1.01	1.87
Yield and yield attributes												
Pods per plant (no)	27.18	22.84	39.95	15.37	10.80	52.50	22.50	54.06	33.33	17.98	13.82	9.64
Pod length (cm)	3.72	4.24	3.73	4.17	5.32	3.40	4.13	3.33	3.33	3.84	4.49	3.82
Seeds per pod (no)	2.37	2.53	2.47	2.83	2.37	2.92	2.46	2.82	2.12	2.47	2.52	2.66
Pod wall dry weight (g)	2.94	3.36	3.81	2.03	2.83	3.96	3.11	3.41	3.04	2.17	2.12	1.04
Seeds per plant (no)	44.23	41.84	64.13	33.75	18.13	111.18	38.29	112.27	45.70	30.98	24.43	18.40
100-seed weight (g)	11.07	14.44	9.88	12.61	25.13	6.10	14.22	7.16	9.30	11.08	15.58	11.39
Yield per plant (g)	5.25	6.63	7.43	4.26	5.52	7.45	6.30	8.63	5.70	3.96	4.22	2.07

Diant share stars	PC under control condition	PC und	ler drought co	ondition
Plant characters	1 <sup>st</sup>	1 st	2 <sup>nd</sup>	3 <sup>rd</sup>
Phenological				
Days to first flowering	1	0.126	0.657	0.716
Days to 80% flowering	1	0.126	0.657	0.716
Days to maturity	-1	0.987	0.092	-0.072
Morphological				
Plant height (cm)	-1	-0.872	0.014	0.171
Plant dry weight (g)	-1	-0.596	0.464	-0.608
Branches per plant (no)	1	-0.85	-0.498	0.083
Yield and yield attributes				
Pods per plant (no)	1	0.679	-0.656	0.299
Pod length (cm)	-1	-0.046	0.991	-0.09
Seeds per pod (no)	1	0.52	0.438	-0.567
Pod wall dry weight (g)	1	0.826	-0.053	-0.077
Seeds per plant (no)	1	0.844	-0.516	0.088
100-seed weight (g)	-1	0.195	0.912	-0.025
Yield per plant (g)	1	0.99	0.084	-0.101

Table 6. Latent vectors associated with the 1<sup>st</sup> principal components (PC)

### Discriminant function analysis (DFA)

Stepwise DFA was done to determine the set of discriminatory functions contributed in separating 50 genotypes into six distinct clusters. It provides a graphical view illustrating the existence of groups (Singh et al., 1991). Function 1 alone explained 59.70 and 65.90% whereas function 2 explained 25.10 and 23% of total variance under control and drought condition, respectively (Table 7). Hence, the function 1 and function 2 accounted for a cumulative of 84.70 and 88.90% of total variance in control and drought condition, respectively. Under control condition, all discriminatory functions except function 5 were statistically significant at a probability level of 0.000 according to chi-square test. Function 5 was statistically significant at a probability level of 0.034. Similarly, all discriminatory functions except function 4 and

5 were statistically significant at a probability level of 0.000 according to chi-square test in drought condition. Function 4 and 5 were statistically significant at a probability level of 0.085 and 0.166, respectively (Table 8). The genotypes were classified into six groups according to the first two discriminatory functions. Under control condition, the first function clearly separated group 6 from group 4, 5 and other groups were intermediate. Genotypes situated at the right side of the diagram produced the highest number of seeds per plant and that of the left side produced the lowest number of seeds per plant based on X ordinate (Fig. 1). Therefore, function 1 separated group (cluster) 4 and 5 very clearly from group 6 based on the number of seeds per plant. Cluster 1, 2 and 3 were intermediate in number of seeds per plant. On the other hand, the genotypes scattered on the upper part of the diagram required more days to maturity

Functions	Eigen value		Varian	ce (%)	Cumula	tive (%)	Canonica	l correlation
Functions	Control	Drought	Control	Drought	Control	Drought	Control	Drought
1	10.300ª	18.451ª	59.70	65.9	59.7	65.9	0.955	0.974
2	4.325ª	6.427ª	25.10	23.0	84.7	88.9	0.901	0.930
3	1.973ª	2.843ª	11.40	10.2	96.1	99.0	0.815	0.860
4	0.497ª	0.191ª	2.90	0.7	99.0	99.7	0.576	0.401
5	0.170ª	0.087ª	1.00	0.3	100.0	100.0	0.381	0.283

 Table 7. Discriminant function analysis using Eigen values

First 5 canonical discriminant functions were used in the analysis.

Table 8. Discriminant functions that analyze by Wilks' Lambda

Test of	Wilks' l	Lambda	Chi-s	quare	Degrees o	f freedom	Significance	e level
Function(s)	Control	Drought	Control	Drought	Control	Drought	Control	Drought
1 through 5	0.003	0.001	247.143	282.854	30	30	0	0
2 through 5	0.036	0.027	142.875	155.234	20	20	0	0
3 through 5	0.192	0.201	70.959	69.017	12	12	0	0
4 through 5	0.571	0.772	24.11	11.127	6	6	0	0.085
5	0.855	0.92	6.759	3.597	2	2	0.034	0.166



Fig. 1. Graphical illustration of the discriminant function analysis of six groups of 50 soybean genotypes under control and drought condition. The encircled accessions indicate the groups obtained through cluster analysis.

and harvest and that of the lower part required lesser days to maturity and harvest based on Y ordinate. Therefore, function 2 separated group 5 and group 2 very clearly from group 4 and group 6 based on day required to maturity and harvest. Group 4 was early maturing and group 5 was late maturing. Similar trend was also exhibited under drought condition (Fig. 2).

#### **Representative genotypes**

The relative position of genotypes indicated the cumulative response of variables representing of function 1 and function 2 under control condition (Fig. 2). Group centroid of each cluster represented the optimum values of function 1 and function 2 that was resulted from the cumulative effects of all genotypes oriented under that cluster based on their response to the optimum response of that group.

The deviation of the genotypes in response of discriminating variables was very close to the group centroid and might be considered as the most representative (might not be the best) of that group. Accordingly the genotype G10



Fig. 2. Graphical illustration of genotypes under each cluster by DFA based on plant characters under control condition.

(G00018) in group 1, G8 (G00013) in group 2, G32 (BD2326) in group 3, G21 (G00154) in group 4, G36 (BD2334) in group 5 and G46 (BGM-2033) in group 6 might be considered as more representative genotypes of their respective groups under control condition.

On the other hand, G2 (G00006) in group 1, G37 (BD2336) in group 2, G41 (AGS-205) in group 3, G40 (AGS-191) in group 4, G42 (AGS-313) in group 5 and G17 (G00075) in group 6 might be considered as more representative genotype of their respective groups under drought condition (Fig. 3).



Fig. 3. Graphical illustration of genotypes under each cluster by DFA based on plant characters under drought condition.

## Selection of genotypes for drought tolerance on the basis of yield

Considering yield as the main target, five genotypes (G2, G8, G43, G12 and G49) from cluster 2 and three genotypes (G39, G50 and G45) from cluster 3 were top yielder in control and drought condition, respectively (Table 9). Among the genotypes, G2 (G00006) produced the highest yield in both control (10.79 g) and drought (9.2 g) treatments. Similarly, G39 (BD2350) was the second top yielder in control and G37 (BD2336) in drought. The lowest yield was found in G38 (BD2340) and G25 (G00196) in control and drought, respectively. Other genotypes had yield per plant less than 8.00 g per plant. Drought stress

caused changes in photosynthetic pigments and components (Anjum *et al.*, 2003), damaged photosynthetic apparatus (Fu and Huang, 2001) and diminished activities of Calvin cycle enzymes, which are important causes of reduced crop yield (Monakhova and Chernyad, 2002). These genotypes showed considerable variation in percent reduction of yield subjected to drought stress. Similar yield reduction of soybean was also observed by Samarah *et al.* (2006).

## Conclusion

There existed a wide range of variation in morphological and phenotypic characters as well as yield performance of 50 soybean

	Con	trol condition			Drought	t condition	
Cluster	Genotype no.	Accession code.	Yield per plant (g)	Cluster no	Genotype no.	Accession code.	Yield per plant (g)
6	G37	BD2336	7.91	2	G37	BD2336	8.78
6	G46	BGM2033	6.98	2	G46	BGM2033	7.49
3	G19	G00135	8.52	1	G1	G00001	6.14
3	G32	BD2326	7.03	1	G2	G00006	9.2
3	G33	BD2329	5.98	1	G8	G00013	5.77
3	G35	BD2333	6.33	1	G12	G00037	6.92
3	G38	BD2340	5.86	1	G14	G00046	5.50
3	G39	BD2350	10.66	1	G16	G00055	5.69
3	G44	BARI Soybean 5	5.96	1	G18	G00112	5.36
3	G45	BARI Soybean 6	7.26	1	G25	G00196	4.86
3	G47	GMOT22	8.28	1	G27	G00209	5.25
3	G50	Shohag	8.42	1	G43	AGS383	6.53
2	G2	G00006	10.79	1	G47	GMOT22	7.59
2	G8	G00013	8.31	1	G49	PK472	6.77
2	G43	AGS383	7.73	3	G39	BD2350	8.52
2	G12	G00037	7.27	3	G50	Shohag	6.82
2	G49	PK472	7.25	3	G45	BARI Soybean 6	6.58

Table 9. Yield performance of soybean genotypes according to their respective clusters

genotypes. Out of 13 variables, the number of seeds per plant played the most dominant role in explaining the maximum variance in both control and drought conditions. The genotype G2 (G0006) and G39 (BD2350) showed high stability in yield performance under control and drought stress. These genotypes can be used as breeding materials for genetic improvement of the crop.

### Acknowledgement

The research work was funded by Research Management Committee (RMC), 2014-2015 of Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur-1706, Bangladesh.

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