

## MORPHO-PHYSIOLOGICAL CHARACTERIZATION OF SOYBEAN GENOTYPES UNDER SUBTROPICAL ENVIRONMENT

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Soybean is a promising oilseed crop in rice-based cropping systems in South and Southeast Asia. In spite of immense scope of its expansion, the crop is not being popular to the farmers because of poor yield of the existing cultivars. Therefore, this study evaluated eighty-soybean genotypes of diverse growth habits with a view to searching genotype(s) of desirable morpho-physiological characters and high yield potential. Sixteen quantitative plant traits were evaluated to classify the genotypes into different groups using various multivariate methods. A wide range of variation was found in almost all qualitative plant traits. The study reveals that plants tend to become taller as the phenological cycle is longer. Seed yield was the product of the number of pods per plant, pod weight and seeds per pod. The first three components of principal component analysis explained 75% of the total variations of the soybean genotypes. Using Dendrogram from cluster analysis, the genotypes were grouped into six clusters. The maximum number of genotypes was concentrated in cluster 5 followed by clusters 4. The phenology, plant height, the number of pods and seed yield were the important discriminating variables in grouping the genotypes. The number of pods per plant displayed the principal role in explaining the maximum variance in the genotypes. The clustering pattern of the genotypes revealed that the genotypes under cluster 2 and cluster 6 were long statures, late maturing and produced higher seed yield. The genotype G00003 under cluster 2 is the best entry giving the highest seed yield. From cluster 6, the genotype G00209 could be the better choice for much better seed yield. The cluster 3

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genotypes were comparatively early maturing and gave reasonable yield. It is concluded that the genotypes under clusters 2 and 6 and 3 can be important resources for developing a high yielding variety and sustainability of growing soybean in the subtropical conditions.

*Key words:* genotypes, morpho-physiology, multivariate analysis, soybean

## INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is a species of legume native to East Asia recognized as an oilseed rather than a pulse. It is a versatile and fascinating crop of the 21st century because of its innumerable possibilities of not only improving agriculture but also supporting industries and medicinal sectors worldwide (FIGUEIREDO, 2014). Soybean provides cholesterol-free oil, high-quality protein, and carbohydrate (RAHMAN *et al.*, 2011). Recently soybean is widely used as fish meal (PHUMEE *et al.*, 2011; KADER *et al.*, 2012) and poultry feed (SERRANO *et al.*, 2013). South and Southeast Asia are dominated by rice-based cropping systems where the areas under oilseeds have been declining since 1970. Rapid increase in population and a gradual reduction of cultivable land are becoming a challenge to the sustainability of cultivating soybean in the region. The present dietary pattern is highly imbalanced where there is excessive consumption of cereals, but a deficit of pulse and oilseeds. In general, yield potential of soybean is high and the crop can be an excellent source of the balanced diet to the resource-poor people. For instance, Bangladesh has to import 850 tons of soybean oil at a cost of taka 68 million to fulfill the nutritional requirements (BBS, 2011). Despite suitable climatic and edaphic conditions in Bangladesh yield of soybean is around 1.64 tons against 3.0 tons per ha in the world (MALEK *et al.*, 2013; MOA, 2010). Low yield of soybean in Asia region is due to lack of high yielding varieties. Soybean can be cultivated throughout the year in Bangladesh. The crop is grown all over the country but there is an enormous possibility of expanding soybean cultivation in the southern coastal region, and some other accreted and fallow lands of the country. Considering these, the attempts are being continued on searching the short-duration and high yield potential soybean genotypes which can fit well in rice-based cropping system of tropical and subtropical regions of Asia. Therefore, the study aims at assessing the genetic variability in morpho-physiological characters of soybean genotypes and to identify the genotypes with high yield potentials.

## MATERIALS AND METHODS

Eighty genotypes of soybean formed the treatment variables in the study. A list of genotypes with their identifiers and sources is given in Table 1. Out of 80 entries, 67 genotypes obtained from the AVRDC-World Vegetable Center, Taiwan, 4 obtained from Japan, and 9 obtained from Bangladesh Agricultural Research Institute. The genotypes were evaluated at the Field Research site of Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur located at 24°5' N latitude and 90°16' E longitude during the period from November 2013 to May 2014.

Seeds of the genotypes were sown in rows and 10 cm apart from each other in the field on 23 November 2013. Appropriate cultural practices were followed to raise a healthy crop. In each line, 50 plants were grown and each plant was considered as single replicate. Data related to morpho-physiological, phenological and yield and yield attributes were recorded. Six plants of each genotype in the row were selected for collecting the data. Descriptive analysis including range, mean, CV and skewness of plant characters. The performance of the genotypes was

described in terms of each character. Quantitative variables considered in the descriptive analysis were plant height, the number of leaves, the number of branches, leaf area, plant components dry weight: i.e. stem, leaf, petiole and reproductive parts and SPAD value as morpho-physiological attributes; days to flowering, days to maturity as phenological attributes and the number of pods per plant, pod weight, number of seeds per pod, seed weight and grain yield as yield and yield attributes.

*Table 1. Soybean genotypes used for morpho-physiological characterization*

Sl. No.	Genotype identifier	Source
1	G00001	AVRDC, Taiwan
2	G00003	AVRDC, Taiwan
3	G00009	AVRDC, Taiwan
4	G00011	AVRDC, Taiwan
5	G00015	AVRDC, Taiwan
6	G00020	AVRDC, Taiwan
7	G00022	AVRDC, Taiwan
8	G00035	AVRDC, Taiwan
9	G00042	AVRDC, Taiwan
10	G00044	AVRDC, Taiwan
11	G00050	AVRDC, Taiwan
12	G00051	AVRDC, Taiwan
13	G00057	AVRDC, Taiwan
14	G00060	AVRDC, Taiwan
15	G00063	AVRDC, Taiwan
16	G00067	AVRDC, Taiwan
17	G00068	AVRDC, Taiwan
18	G00069	AVRDC, Taiwan
19	G00070	AVRDC, Taiwan
20	G00073	AVRDC, Taiwan
21	G00078	AVRDC, Taiwan
22	G00080	AVRDC, Taiwan
23	G00081	AVRDC, Taiwan
24	G00082	AVRDC, Taiwan
25	G00083	AVRDC, Taiwan
26	G00090	AVRDC, Taiwan
27	G00112	AVRDC, Taiwan
28	G00113	AVRDC, Taiwan
29	G00119	AVRDC, Taiwan
30	G00120	AVRDC, Taiwan
31	G00121	AVRDC, Taiwan
32	G00122	AVRDC, Taiwan
33	G00123	AVRDC, Taiwan
34	G00124	AVRDC, Taiwan
35	G00125	AVRDC, Taiwan
36	G00126	AVRDC, Taiwan

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37	G00127	AVRDC, Taiwan
38	G00129	AVRDC, Taiwan
39	G00130	AVRDC, Taiwan
40	G00136	AVRDC, Taiwan
41	G00139	AVRDC, Taiwan
42	G00147	AVRDC, Taiwan
43	G00150	AVRDC, Taiwan
44	G00151	AVRDC, Taiwan
45	G00152	AVRDC, Taiwan
46	G00154	AVRDC, Taiwan
47	G00156	AVRDC, Taiwan
48	G00157	AVRDC, Taiwan
49	G00161	AVRDC, Taiwan
50	G00163	AVRDC, Taiwan
51	G00164	AVRDC, Taiwan
52	G00165	AVRDC, Taiwan
53	G00166	AVRDC, Taiwan
54	G00167	AVRDC, Taiwan
55	G00168	AVRDC, Taiwan
56	G00196	AVRDC, Taiwan
57	G00197	AVRDC, Taiwan
58	G00209	AVRDC, Taiwan
59	G00252	AVRDC, Taiwan
60	G00256	AVRDC, Taiwan
61	G00283	AVRDC, Taiwan
62	G00288	AVRDC, Taiwan
63	G00293	AVRDC, Taiwan
64	G00322	AVRDC, Taiwan
65	G00346	AVRDC, Taiwan
66	G00352	AVRDC, Taiwan
67	G00354	AVRDC, Taiwan
68	BD2324	BARI, Bangladesh
69	BD2325	BARI, Bangladesh
70	BD2327	BARI, Bangladesh
71	BD2332	BARI, Bangladesh
72	BD2335	BARI, Bangladesh
73	BD2353	BARI, Bangladesh
74	BD2355	BARI, Bangladesh
75	AGS313	BARI, Bangladesh
76	GMD2093	BARI, Bangladesh
77	JP-VR TACHMAH	Japan
78	ENREI	Japan
79	STRESSS LAND	Japan
80	LDUSVR	Japan

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Analysis of genetic variation of the genotypes was performed with the program SPSS 16 following the procedure described by ROJAS *et al.*, 2000; ISLAM *et al.*, 2007). Estimation of the degree of correlation was estimated among the different plant characters according to Pearson's coefficient (CLIFFORD and STEPHENSON, 1975). Sixteen qualitative variables enlisted before considered in the cluster analysis, Principal Component Analysis (PCA) and Discriminant Function Analysis (DFA). Non-hierarchical K-mean cluster and DFA was performed to classify the genotypes into a number of groups. The cluster analysis indicates the grouping of a large number of genotypes into several clusters having similar characteristics on the basis of variables considered in the analysis. DFA was employed for conformity of the results on grouping the genotypes. DFA indicated whether a particular set of variables is useful in separating in previously delineated groups. The discriminatory functions play the vital role in identifying the set of variables contributed more in clustering a large number of genotypes into homogeneous groups. Through stepwise procedures of DFA, PCA, chi-square test, structure matrix of variables, the test of equality of group means was done.

## RESULT AND DISCUSSION

### *Variability in plant characters*

The range of variation in sixteen quantitative characters of the eighty-soybean genotypes is presented in Table 2. A wide range of variation was observed in all the plant characters of the genotypes. Except for SPAD value and phenological characters, the other plant traits showed a high variability based on the coefficient of variation as suggested by BOTEZ *et al.* (1995). However, variations were much wider in pods plant<sup>-1</sup> followed by seed yield, reproductive plant parts, and pod weight. This indicates that yield and yield contributing characters displayed much wider range of variability rather than morpho-physiological characters. The frequency distribution of all the plant characters showed a normal distribution with slightly skewed towards left or right. Among the characters, the number of branches and days to maturity showed a distribution with negative skewness and others are positively skewed. The high positive skewness in the number of leaves, reproductive part dry weight, days to flowering and yield and yield contributing characters excluding grain weight indicates most of the genotypes are concentrated on the left in frequency distribution tables in these characters.

### *Correlation between plant characters and seed yield*

The correlation coefficient among the plant characters showed that out of 120 coefficient, 76 were highly significant at p 0.01, 17 were significant at p 0.05 and others were insignificant (Table 3). According to REDDY (1990) the coefficient higher than 0.50 were considered as strongly correlated ( $r \geq 0.50$ ) and less than 0.50 as weakly to moderately correlated. Among the plant characters related to morpho-physiology of plant highest, strong and significant positive correlation corresponded to petiole dry weight (DW) and stem DW (0.95\*\*). Except for leaf DW, all other morpho-physiological characters had moderate to strong correlations with seed yield. The seed yield relationship was negative with SPAD values and reproductive parts DW. However, a strong positive relationship existed between plant height and the number of leaves with seed yield. FAISAL *et al.* (2011) also observed that plant height had positive and highly significant correlation with seed yield,

Phenological characters showed exhibited significant positive correlation with plant height. It indicates that plants tend to become taller as the phenological cycle become longer.

Reproductive parts DW exhibited moderately to strong negative significant correlation with phenological periods indicating that plants having longer phenological period produced lesser amounts of reproductive parts. Days to flowering rather than days to maturity showed more strong relations with yield contributing characters and seed yield. MACHIKOWA *et al.* (2005) reported that days to flowering and maturity were highly and positively correlated with yield components in soybean.

Table 2. Descriptive statistics of the plant characters of 80 soybean genotypes

Plant character	Range	Mean	Std. Deviation	CV (%)	Skewness
Morpho-physiological					
Plant height (cm)	12.8-74.0	37.4	16.03	43	0.33
Number of leaf	6.5-51.0	20.6	8.62	42	1.01
Branch plant <sup>-1</sup>	1.0-8.8	4.6	1.57	34	-0.06
Leaf area (dm <sup>2</sup> )	0.60-13.90	4.92	2.60	53	0.83
Stem dry weight (g)	0.21-3.76	1.53	0.75	49	0.71
Leaf dry weight (g)	0.32-5.85	2.60	1.06	41	0.52
Petiole dry weight (g)	0.06-1.75	0.62	0.39	63	0.83
Reproductive part dry weight (g)	0-1.12	0.31	0.28	90	1.03
SPAD value	33.3-52.9	42.14	4.72	11	0.38
Phenological					
Days to flowering	45-77	54	6.92	13	1.45
Days to maturity	90-133	120	10.93	9	-0.67
Yield and yield attributes					
Pods plant <sup>-1</sup>	1.33-112.50	23.46	23.98	102	1.85
Pod weight (g plant <sup>-1</sup> )	0.37-26.27	6.86	5.99	87	1.20
Seeds plant <sup>-1</sup>	1.00-2.90	1.65	0.46	28	1.03
100-seed weight (g)	4.84-26.24	12.44	4.21	34	0.32
Seed yield (g plant <sup>-1</sup> )	0.19-15.64	4.12	3.67	91	1.18

Among the yield attributing characters, pod weight showed the highest and strong positive correlation (0.98\*\*) with seed yield. The number of pods plant<sup>-1</sup> and seeds pod<sup>-1</sup> also presented strong and significant positive correlation with seed yield. MUKHEKAR *et al.* (2004) found that pods plant<sup>-1</sup> had the highest contribution to the seed yield and can be considered as most reliable yield indicator in soybean. However, seed weight showed a significant negative correlation with seed yield (-0.27\*) indicating that plants produced smaller seed exhibiting lower seed weight produced higher seed yield. This was because the genotypes having higher 100-seed weight produced a lower number of pods plant<sup>-1</sup>. MONDAL *et al.* (2011) also observed a significant negative association of seed yield with seed size (100-seed weight). Higher seed yield was attributed to the higher number of pods plant<sup>-1</sup> and seeds pod<sup>-1</sup>. The strong positive correlations for almost all plant characters indicate that plant performance can be attributed mostly to genetic differences rather than environmental influences.

Table 3. Correlation coefficient of 16 plant characters of 80 soybean genotypes

	pht	nl	br	la	sdw	ldw	pdw	repro	df	dm	spad	ppp	pw	spp	sw	yi
pht	1															
nl	0.46**	1														
br	0.36**	0.82**	1													
la	0.71**	0.27*	0.27*	1												
sdw	0.67**	0.18	0.19	0.90**	1											
ldw	0.41**	0.02	0.15	0.82**	0.82**	1										
pdw	0.58**	0.07	0.10	0.88**	0.95**	0.85**	1									
repro	-0.37**	-0.65**	-0.54**	-0.21	-0.16	-0.01	-0.05	1								
df	0.45**	0.35**	0.27*	0.44**	0.41**	0.20	0.36**	-0.37**	1							
dm	0.41**	0.42**	0.37**	0.36**	0.23*	0.21	0.20	-0.57**	0.29**	1						
spad	-0.72**	-0.34**	-0.27*	-0.59**	-0.59**	-0.27*	-0.53**	0.24*	-0.44**	-0.24*	1					
ppp	0.60**	0.66**	0.42**	0.38**	0.35**	-0.03	0.25*	-0.40**	0.51**	0.29**	-0.65**	1				
pw	0.56**	0.47**	0.29**	0.44**	0.38**	0.04	0.29**	-0.30**	0.53**	0.22	-0.65**	0.85**	1			
spp	0.50**	0.43**	0.16	0.23*	0.23*	-0.15	0.16	-0.27*	0.36**	0.16	-0.64**	0.82**	0.75**	1		
sw	-0.31**	-0.31**	-0.23*	-0.07	-0.07	0.15	-0.07	0.21	-0.23*	-0.17	0.32**	-0.51**	-0.24*	-0.47**	1	
yi	0.59**	0.51**	0.29**	0.46**	0.40**	0.04	0.31**	-0.30**	0.50**	0.22*	-0.68**	0.89**	0.98**	0.80**	-0.27*	1

\*\* Correlation is significant at the 0.01 level (2-tailed). \* Correlation is significant at the 0.05 level (2-tailed).

df-Days to flowering, dm-Plant height, nl-Number of leaf, spad-SPAD value, sdw-Stem dry weight, ldw-Leaf dry weight, pdw-Petiole dry weight, repro-Reproductive parts dry weight, la-Leaf area, br-Branch plant<sup>-1</sup>, ppp-Pods plant<sup>-1</sup>, pw-Pod weight, spp-Seeds plant<sup>-1</sup>, sw-100 seed weight, yi-Seed yield (g plant<sup>-1</sup>).

### Grouping of genotypes

K-means non-hierarchical cluster analysis was done using 16 quantitative plant characters for grouping the soybean genotypes into six clusters where the genotypes under each cluster were highly comparable. A dendrogram was prepared on the basis of cluster analysis (Figure 1). The tree was cut at the rescaled distance of 4.5 to produce classes that were maximally related to other specific variables of interest. The maximum number of genotypes (25) was concentrated in cluster 5 followed by cluster 4 (21), 1 (18), 3(9), 2 (5) and 6 (2). A total number of genotypes for each cluster and mean of each cluster for the 16 plant characters are presented in Table 4.

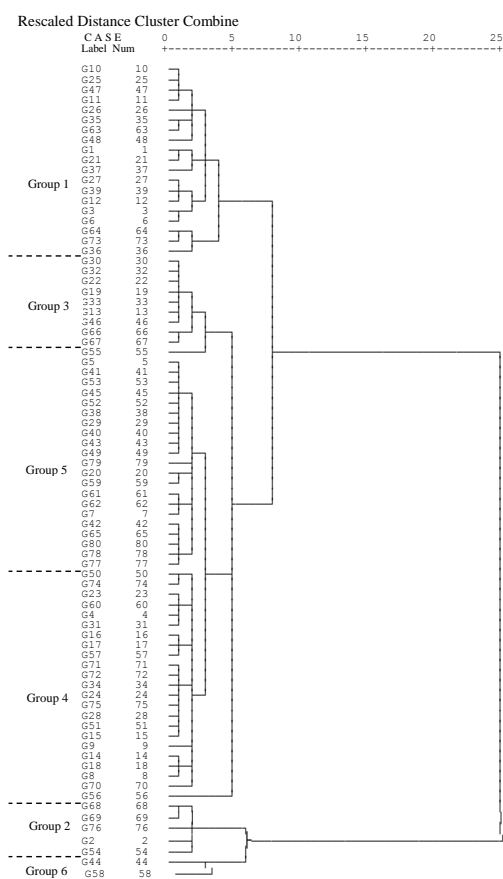


Figure 1. Dendrogram from cluster analysis using 16 quantitative plant characters on 80 soybean genotypes

The genotypes of this cluster 1 were characterized by comparatively tall stature and all other morpho-physiological characters were intermediate. The performance in respect of almost all morphological and yield attributes of the genotypes under cluster 2 was comparable and followed by the genotypes grouped under cluster 6. The remarkable differences were the longest growth duration of the genotypes under cluster 2. Cluster 3 genotypes produced the lowest number of leaves and branches, but the highest DW of reproductive plant parts and comparatively shorter



growth duration, and all other characters were intermediate and gave substantial seed yield. The genotypes in the cluster 4 performed very poorly in almost all the morphological characters but showed the highest SPAD values. The genotypes were also characterized with the shortest growth duration and poorer yield attributes and seed yield. Cluster 5 genotypes were almost similar to the genotypes grouped under cluster 4 in respect of all the characters but slightly better in morphological characters and worse in yield contributing characters resulting to the lowest seed yield. Cluster 6 genotypes were outstanding having the best performance in respect of almost all the morphological and yield contributing characters, and seed yield. However, the genotypes look less time to flower but having comparatively longer duration to mature indicating the longest reproductive phase. The genotypes were also having smaller seed size.

*Table 4. Comparison profile of the six groups of soybean genotypes classified by k-means clustering*

Plant characters	Clusters					
	1	2	3	4	5	6
No. of genotypes	18	5	9	21	25	2
Morpho-physiological						
Plant height (cm)	55.5	54.4	32.4	23.3	32.4	63.3
Number of leaf	23.8	35.5	12.5	16.7	19.6	45.9
Branch plant <sup>-1</sup>	5.2	6.1	2.8	3.9	4.7	7.9
Leaf area (dm <sup>2</sup> )	6.61	7.49	4.50	2.97	4.80	7.00
Stem dry weight (g)	1.90	2.14	1.44	1.09	1.49	2.24
Leaf dry weight (g)	2.74	2.68	2.43	2.16	2.94	2.49
Petiole dry weight (g)	0.78	0.83	0.65	0.40	0.62	0.90
Reproductive part DW (g)	0.17	0	0.58	0.52	0.23	0.10
SPAD value	38.4	35.9	40.6	45.8	44.1	35.6
Phenological						
Days to flowering	57	73	52	51	52	45
Days to maturity	125	130	112	107	127	128
Yield and yield attributes						
Pods plant <sup>-1</sup>	35.72	81.30	23.55	9.75	8.32	101.41
Pod weight (g)	11.66	17.29	9.27	2.94	2.77	19.09
Seeds pod <sup>-1</sup>	1.92	2.39	1.85	1.41	1.34	2.80
100-seed weight (g)	11.81	6.79	13.29	13.27	13.56	5.52
Seed yield (g plant <sup>-1</sup> )	6.95	11.01	5.93	1.60	1.48	12.88

### ***Principal Component Analysis***

Principal Component Analysis (PCA) explained clearly and concisely the genetic diversity of soybean genotypes. PCA is useful because it gives information about the groups of genotypes, where it may show certain traits that are important for the breeding programs. Based on the correlation matrix, 16 plant characters were analyzed using PCA. The use of PCA revealed that the first three principal components (PCs) had Eigenvalues more than 1 and explained 44.9%, 19.2% and 11.5% of total variation individually and 75.6% together (Table 5). HAMID *et al.* (2011) observed that the first four PCs of PCA explained 76.2% of the total variations of pigeon pea genotypes. In this study, plant height, yield attributes, and seed yield had a high positive

contribution but the DW of reproductive plant parts, SPAD value and seed weight had a remarkable negative contribution to PC 1 (Table 4). These characters separated the genotypes from other group members along the PC 1. Leaf area and dry weight of the stem, leaf, and petiole separated the genotypes to PC 2. The parameters that associated with PC 3 were the number of branches and days to maturity. Many researchers evaluated genotypic variation and pattern of diversity among plant population through PCA (MEIJER *et al.*, 1996; BISHT *et al.*, 1999; MANNAN *et al.*, 2010; HAMID *et al.*, 2011).

Table 5. Extracted Eigenvalues and Eigenvectors associated with the first three principal components

Plant characters	Principal components		
	1st	2nd	3rd
Extracted Eigenvalue	7.18	3.07	1.83
% of variation	44.86	19.17	11.46
	Eigenvectors		
Plant height (cm)	0.84	0.15	0.02
Number of leaf	0.64	-0.42	0.47
Branch plant <sup>-1</sup>	0.51	-0.24	0.63
Leaf area (dm <sup>2</sup> )	0.76	0.59	0.04
Stem DW (g)	0.72	0.65	-0.05
Leaf DW (g)	0.40	0.85	0.17
Petiole DW (g)	0.63	0.73	-0.08
Reproductive parts DW (g)	-0.50	0.31	-0.60
Days to flowering	0.64	-0.03	0.01
Days to maturity	0.47	-0.04	0.54
SPAD value	-0.80	-0.04	0.26
Pods plant	0.84	-0.42	-0.19
Pod weight (g)	0.80	-0.29	-0.33
Seeds pod	0.69	-0.45	-0.41
100-seed weight (g)	-0.39	0.37	0.06
Seed yield (g)	0.83	-0.30	-0.34

#### ***Discriminant function analysis***

Stepwise discriminant function analysis (DFA) was done to determine the set of discriminatory functions contributed in separating 80 genotypes into six distinct clusters. Moreover, it provides a graphical view illustrating the existence of groups (SINGH *et al.*, 1991). The five discriminant functions that differentiated among clusters were obtained by the stepwise procedure. Table 6 summarizes the contribution of each of 5 canonical discriminant functions for explaining the variance along with their Eigenvalues (Latent root) and canonical correlation coefficient. Function 1 alone explained 77.2% of total variance and function 2 explained 11.5% of the total variance. Hence, the function 1 and function 2 accounted for a cumulative 88.7% of total variance. Table 7 summarizes the variables mostly contributed to the discriminatory functions along with their coefficient under each function. The result shows that plant height, days to maturity, pods plant<sup>-1</sup> and seed yield mostly contributed in grouping 80 genotypes and explained the genotypic variation under function 1 and function 2. There showed the highest coefficient of

Pods plant<sup>-1</sup> (0.89) in function 1, which indicates that pods plant<sup>-1</sup> mostly explained the 77.2% of the total variance in function 1. The coefficient of days to maturity (0.84) was the highest in function 2 indicating the higher contribution of this variable in explaining 11.5% of the total variance in function 2. The variation that explained in function 3 is absolutely for days to flowering.

*Table 6. Discriminant functions that distinguish between clusters of 80 soybean genotypes*

Function	Latent root	Variance %		r <sup>2</sup> coefficient	p
		Function	Cumulative		
1	13.99	77.2	77.2	0.97	0.000
2	2.09	11.5	88.7	0.82	0.000
3	1.22	6.7	95.4	0.74	0.000
4	0.73	4.0	99.4	0.65	0.000
5	0.11	0.6	100.0	0.31	0.007

*Table 7. Coefficients of the plant characteristics mostly contributed in grouping 80 soybean genotypes*

Discriminating variables	Discriminant Function		
	1	2	3
Plant height (cm)	0.51	0.38	-0.38
Days to flowering	-0.05	-0.07	1.00
Days to maturity	0.37	0.84	0.09
Pods plant <sup>-1</sup>	0.89	-0.56	0.12
Seed yield (g plant <sup>-1</sup> )	0.06	0.32	-0.46

Table 8 describes the correlation of coefficient between discriminatory variables and discriminatory functions. It is important to note that pods plant<sup>-1</sup> was placed at the top of the list of discriminatory variables with the correlation coefficient of 0.82 followed by seed yield under function 1. It indicates that pods plant<sup>-1</sup> played the most dominant role in explaining the maximum variance in function 1. Similarly, days to maturity contributed to maximum variability in function 2. Figure 2 graphically showed the orientation of genotypes into different clusters according to discriminant function 1 and 2. Genotypes situated at the right side of the diagram produced highest pods plant<sup>-1</sup> and that of the left side produced lowest pods plant<sup>-1</sup> based on X ordinate. Therefore, function 1 separated cluster 2 and 6 very clearly from group 5 and 4 based on pods plant<sup>-1</sup>. Cluster 1 and 3 were intermediate in producing pods. On the other hand, the genotypes scattered on the upper part of the diagram required more days to maturity and that of the lower part required lesser days to maturity based on Y ordinate. Therefore, function 2 separated cluster 3 and 4 very clearly from cluster 5, and 1 based on the days required to maturity. Group 3 and group 4 were early maturing and others were late maturing.

*Table 8. Correlations between discriminating variables mostly contributed in grouping 80 soybean genotypes*

Discriminating variables	Discriminant Function		
	1	2	3
Pods plant <sup>-1</sup>	0.82*	-0.49	0.05
Days to maturity	0.23	0.80*	0.22
Days to flowering	0.23	0.01	0.86*
Seed yield (g plant <sup>-1</sup> )	0.48	-0.20	-0.14
Plant height (cm)	0.35	0.30	-0.14

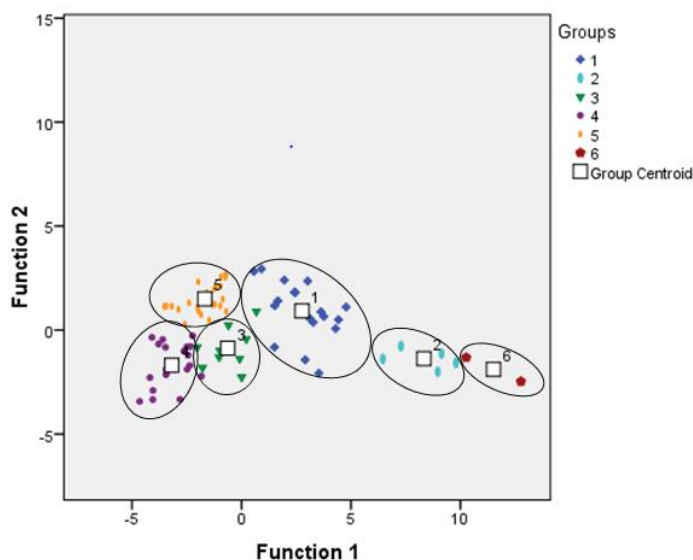


Figure 2. Discriminant function analysis ordination of 80 soybean genotypes. The encircled accessions indicate the groups (clusters) obtained through cluster analysis

### ***Representative genotypes***

Figure 3 showed the orientation of genotypes under each of 6 clusters. The relative position of genotypes indicated the cumulative response of variables representing of function 1 and function 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 the response of discriminating variables was very close to the group centroid and might be considered as the most representative of that group. Accordingly, the genotype G00125 in cluster 1, the genotype GMD2093 in cluster 2, the genotype G00163 in cluster 3, the genotype G00113 in cluster 4, the genotype G00161 in cluster 5 and the genotype G00209 in cluster 6 might be considered as more representative of their respective groups.

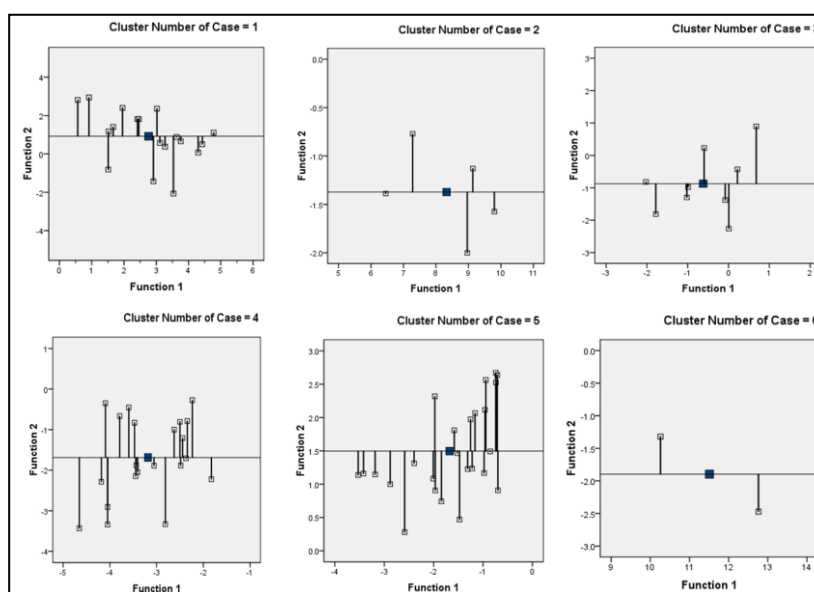


Figure 3. Graphical illustration of soybean genotypes under each cluster by DFA based on 16 plant characters

### CONCLUSION

There exists a wide range of variation in morpho-physiological and phenotypic characters and yield performance of 80 soybean genotypes. These genotypes can be used as breeding materials for improving the crop. Of the 16 quantitative plant traits, days to flowering, days to maturity, plant height, the number of pods plant<sup>-1</sup> and seed yield mostly contributed in classifying 80 genotypes into different groups. These characters are important for selecting desirable genotypes. Genotypes under cluster 3 and 4 were comparatively early maturing, although cluster 3 genotypes gave better seed yield compared to cluster 4. The genotypes can be useful for cultivating in the rice-based cropping system. Genotypes under cluster 2 and cluster 6 were long stature, late maturing and produced higher seed yield. The genotype G00003 is the best in regards to seed yield (15.64 g plant<sup>-1</sup>).

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**MORFO-FIZIOLOŠKA KARAKTERIZACIJA GENOTIPOVA SOJE U SUBTROPŠKIM USLOVIMA**

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**Izvod**

Soja je uljana biljna vrsta koja sve više dobija na značaju u Južnoj i Jugoistočnoj Aziji. Uprkos ogromnom značaju, ovaj usev još uvek nije popularan kod farmera, prvenstveno zbog malih prinosa postojećih sorata. Zbog toga je u ovom radu izučavano 80 genotipova soje, u cilju izdvajanja onih koji imaju poželjne morfo-fiziološke osobine i visok potencijal za prinos. Korišćenjem multivariacionih metoda, genotipovi su klasifikovani u različite grupe na osnovu 16 kvantitativnih osobina. Širok opseg variranja je utvrđen kod skoro svih osobina. Prve tri komponente u okviru PCA analize objašnjavaju 75% ukupne varijabilnosti genotipova soje. Klaster analiza je grupisala genotipove u 6 klastera, a najveći broj je bio u klasteru 5. Fenologija, visina biljke, broj mahuna i prinos zrna su značajne diskriminatorne varijable za grupisanje genotipova. Broj mahuna po biljci ima najznačajniju ulogu u determinisanju maksimalne varijabilnosti genotipova. Genotip G00003 u klasteru 2 dao je najviši prinos zrna, dok bi u klasteru 6, genotip G00209 bio bolji izbor za ostvarivanje višeg prinosa. Može se zaključiti da genotipovi unutar klastera 2, 6 i 3 mogu biti značajni izvori za dobijanje visoko prinosa genotipova soje za subtropske uslove gajenja.

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