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Original Research Article

Selection of Soybean Genotypes (*Glycine max* (L.) Merrill) through Genetic Variability Analysis

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Abstract: The physiomorphological divergence was assessed in twenty-seven soybean genotypes by using cluster mean analysis, principal component and principal coordinate analysis and mean difference to identify parental genotypes for future breeding program in order to develop new high yielding varieties in randomized complete block design with three replications. Plant height, days to first flowering and days to 50% flowering have the highest percent of variations anomg the traits. The genotypes under the experiment were grouped into five clusters. The highest inter cluster distance was found between cluster I and IV followed by I and V. According to principal component scores F-85-11347 and ASSET-93-19-13 have the prominent influence towards varietal improvement. Selecting genotypes from distant clusters probably provide promising recombinants and better segregants for future breeding platform.
Keywords: Cluster, genotype, genetic variation, principal component analysis.

INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is a leguminous crop which is one of the richest sources of oil as well as protein. Soybean kernel contains 36% protein, 35% carbohydrate, 19% oil, 5% minerals and some other components with vitamins [1]. The current nutritional condition of third world and some emerging countries like Bangladesh is a matter of great fear since the most of the publics are suffering from malnutrition [2-4]. Soybean can show a significant role in this case and can aid to meet up the nutritional shortage difficulty. Furthermore soybean also contain frequent compounds that perform as antioxidant and are valuable to human fitness as they reduce the danger of cardiovascular syndromes, breast cancer, osteoporosis, diabetes and neurodegenerative sicknesses such as Alzheimer's and Parkinson's and decrease the menopausal signs [5].

Considering the potentiality of this crop, there is a need for improvement and to develop varieties suited to specific agro-ecological conditions and also for specific end use. Due to low soil fertility and stress condition [6] yield of soybean is poor in Bangladesh. Genetic diversity is a major factor that determines prospects of yield improvement in future. Knowledge of genetic diversity within a crop and correlation among the yield contributing characters is essential for the long-term success of a breeding program and maximizes the exploration of germplasm resources [2]. Moreover, evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm. Multivariate analysis acts as a useful tool to quantify the degree of divergence between the biological populations at genotypic level and to assess the relative contribution of different components to the total divergence both inter and intra cluster levels [7]. In the present study, genetic divergence of soybean has been assessed in the light of twelve important morphological and physiological traits to identify suitable genotypes for breeding program.

MATERIALS AND METHOD

The study was conducted to assess the morphogenetic divergence among twenty seven soybean genotypes. The experiment was carried out during December, 2013 to April, 2014 at the field laboratory of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh. Soybean genotypes were sown in randomized complete block design with three replications; each plot consisted of a single row of 4m long with row to row distance of 1m maintaining 10 plants per meter. Sowing was done with the help of hand drill. Ten random plants were used to take the data from field.

STATISTICAL ANALYSIS

The data were analyzed by Mahalanobi's D^2

statistics, principal component analysis, cluster mean analysis, principal coordinate analysis (PCA) and canonical variate analysis (CVA). Twenty seven soybean genotypes were grouped into cluster by using Genstat v 5.5, software.

RESULTS AND DISCUSSION

Analysis of variance

The results of analysis of variance regarding various plant traits are given in Table 1. From this table it is found that in replication only days to days to 80% maturity, number of branches per plant and stover yield showed 1% level of significant but treatments showed significant variation 5% level of significant for all twelve characters studied. So, emphasis should be given on these traits for future breeding program.

Table1: Analysis of variance of 12 yield and yield related character of soybean

Source	DF	Mean sum of square											
		PH	DFF	D50F	D80M	NBP	NPP	NSP	PL	TSW	SY	SPWP	YIELD
Replication	2	64.01	3.05	4.037	4.79*	4.23*	70.47	0.1	0.15	0.57	3.21*	0.1	5.16
Treatment	26	239.46**	38.61**	42.05**	72.42**	10.68**	931.30**	0.21**	0.66**	23.52**	47.89**	9.03**	314.23**
Error	52	26.23	1.33	1.47	1.17	1.07	82.63	0.06	0.06	0.26	0.88	0.43	5.11

** Significant at 1%

* Significant at 5%

DFF= Days to first flowering, PH= Plant height (cm), D50F= Days to 50% flowering, D80M= Days to 80% maturity, NBP= Number of branches per Plant, NPP= Number of pod per plant, NSP=Number of seeds per pod, PL= Pod lenght, HSW= Hundred seed weight (g), SY= Stover yield, SPWP= Single pod weight per plant, YIELD=Yield per plant.

Eigen values

The principle component analysis yielded five of the eigen values above unity accounted for 80.84% of the total variation and the last seven principle accounted for near about 20% of the total variation (Table 2).

Table 2: Eigen values and yield percent contribution of twelve characters of twenty seven genotypes

Characters	Eigen values	Percent variation	Cumulative % of percent variation
Plant height	4.37	36.45	36.45
Days to first flowering	2.24	18.69	55.14
Days to 50% flowering	1.22	10.2	65.34
Days to 80% maturity	1.07	8.92	74.26
Number of branches per plant	0.75	6.22	80.48
Number of pod per plant	0.72	5.98	86.46
Number of seeds per pod	0.66	5.46	91.92
Pod length	0.45	3.73	95.65
100 seed weight	0.24	2.03	97.68
Stover yield	0.15	1.27	98.95
Single pod weight per plant	0.11	0.96	99.91
Yield per plant	0.01	0.09	100

Cluster analysis

Twenty seven genotypes were grouped in five clusters (Table 3). From cluster I nearest cluster was III (5.32) and farthest cluster was IV (15.10). Cluster V (2.93) is the nearest cluster from cluster II and the farthest cluster was IV (11.07). Highest cluster distance found in between cluster I and cluster IV. Whereas lowest cluster distance found between cluster II and cluster V. [8, 9] also grouped soybean genotypes in to different clusters. Because the genotypes from diverge cluster may be recommended for inclusion in hybridization program as they are expected to produce good segregants.

Table 3: The nearest and farthest cluster from cluster between D^2 values in soybean genotypes

Sl	Cluster	Nearest cluster with D^2 values	Farthest cluster with D^2 values
1	I	III (5.32)	IV (15.10)
2	II	V (2.93)	IV (11.07)
3	III	I (5.32)	IV (10.01)
4	IV	III (10.01)	I (15.10)
5	V	II (2.93)	I (12.89)

Performance of different traits

Means regarding different plant traits and their comparison are given in Table 4. Plant height is an important trait in erect type soybean and usually positively correlated with yield [10]. The present result revealed that height of plant was highly significant affected due to various soybean genotypes. The plant height ranged from 34.57 to 75.85. The line Australia was found lowest plant height, whereas genotype PK-327 had highest plant height. Some earlier reports [11, 12] also showed highly significant variability in plant height in various soybean genotypes. BS-33 showed the early flowering and F-85-11347 showed the late flowering. Similar results found in case of line BS-33 for days to 50% flowering but days to 80% flowering required minimum 116.33 days for LG-92P-1176.In case of line F-85-11347 for days to 50% flowering maximum 93.67 days, whereas days to 80% flowering required maximum 157 days for Australia.

The number of branches is the most important yield component in soybean. The effective and fruit bearing branches play important role in enhancing the final yield. The number of branches varies from genotype to genotype depending upon genetic potential of a variety. In present study the number of branches was significantly affected by the various genotypes. The highest branches (11.57) were produced by ASSET-93-19-13 followed by GC-82-332411 (10.53) and F-85-11347 (8.27). Similarly AGS-79 and P1-4174-75 had shown very poor performance by showing only 3.47 and 4.07, branches per plant respectively. These results are in harmony with the findings of [13] and [14] that number of branches showed significant variation in different soybean genotypes.

Table 4: Mean performance of various growth parameter and yield components

Genotype	PH	DFF	D50F	D80F	NBP	NPP	NSP	PL	HSW	SY	SPWP	YIELD
LG-92P-1176	50.4	85	87.33	116.33	5	48.67	2.33	3.35	11	8.07	4.37	12.35
P1-4174-75	54.11	82.67	85.33	127.33	4.07	30.47	3	4.95	11.67	12.6	4.87	15.13
KANH-33	64.11	84	87	120.67	4.87	39.27	3	3.57	5.2	6.73	4.81	15.15
AGS-79	47.25	77.33	81.33	118.33	3.47	48.53	2.8	3.03	7.1	3.99	1.98	9.22
MTD-452	50.07	81.33	84.33	120.33	5.73	50	3.07	4.22	8.23	8.23	4.9	19.67
GMOT-17	55.31	81.33	83.67	119	5.43	37.4	3	3.65	5.13	5.78	3.61	13.57
JOYAWAZA	60.48	82.33	86.33	117.33	7.83	44.73	2.8	3.11	6.47	5.85	3.47	38.48
F-85-11347	59.65	90.33	93.67	137	8.27	95	3	4.19	10.1	19.83	9.74	49.81
YESOY-4	60.69	82.67	84.33	131.67	5.67	58.33	3	3.09	8.23	10.19	4.51	16.07
SHOHAG	54.05	77.67	80.33	131	5.6	28.33	2	2.82	8.37	4.2	2.97	10.67
AUSTRALIA	34.57	77.67	81	157	4.47	38.27	3.33	3.95	12.37	8.21	4.72	22.59
GC-82-332411	58.97	81.33	82.67	120.33	10.53	43.2	3	3.53	6.13	6.1	1.47	18.28
PK-327	66.42	82	84.33	131.33	5.4	55.87	3	3.95	8.13	7.27	3.16	19.79
ASSET-93-19-13	74.21	85	87	131.33	11.57	88.93	3	3.75	8.63	14.97	6.47	43.36
PK-327	75.85	84.67	89.33	132	7.3	92.67	3	3.43	8.07	8.29	4.75	14.01
AGS-95	52.35	79	80.67	130.67	6.7	40.93	2.47	3.47	10.13	4.93	2.45	17.34
BARI SOYBEAN-6	46.22	84	86.33	130.33	4.33	28.4	2.63	3.01	6.87	4.33	3.23	10.34
NS-1	52.3	83.67	85.67	128	7.67	38.67	3	4.23	9.03	7.53	3	28.3
MTD-451	42.43	85.67	89	119	7	37.33	3	3.47	5.3	2.9	2.77	12.07
GC-830059	55.53	81.33	83.33	119.67	8	63.33	3	3.83	5.5	12.07	3.77	21.13
86017-66-6	54.41	77.67	80.67	131.67	4.67	53.67	3	3.57	13.13	6.33	5.85	14.08
MTD-16	52.47	81	83.67	129	4.8	46.64	3	3.43	8.83	6.37	6.17	8.37
LG-92P-12-18	55.59	81	83	131.33	6.2	37.73	3	3.7	14.7	4.83	5.71	14.57
BS-33	43.97	74	76.33	119.67	6.13	43.13	3	3.78	12.1	6.87	6.35	10.51
ASSET-95	54.8	81.33	83.67	125.33	4.67	53.67	2.67	3.23	7.63	15.33	2.68	14.63
BS-13	55.45	89.67	92.33	135.67	6.47	46.33	3	3.79	13.4	4.71	4.65	14.79
CHINA-1	62.61	83	86.33	126.33	6.13	47.27	3	4.17	13.13	5.13	5.5	16.21
Mean	55.34	82.1	84.78	127.32	6.22	49.51	2.89	3.64	9.06	7.84	4.37	18.54
Min.	34.57	74	76.33	116.33	3.47	28.33	2	2.82	5.13	2.9	1.47	8.37
Max.	75.85	90.33	93.67	157	11.57	95	3.33	4.95	14.7	19.83	9.74	49.81
CV (%)	9.25	1.41	1.43	0.85	16.63	18.36	8.33	6.87	5.62	11.95	14.94	12.19

DFF= Days to first flowering, PH= Plant height (cm), D50F= Days to 50% flowering, D80M= Days to 80% maturity, NBP= Number of branches per Plant, NPP= Number of pod per plant, NSP=Number of seeds per pod, PL= Pod lenght, HSW= Hundred seed weight (g), SY= Stover yield, SPWP= Single pod weight per plant, YIELD=Yield per plant.

Pod length (cm) and number of seeds per pod are very important yield parameters for soybean. Both pod length and number of seeds per pod were highly significantly affected due to various soybean genotypes. The range for pod length was recorded from 2.82 to 4.95 cm. The longest pods were found at genotype PI-4174-75. It was followed by some genotypes namely NS-1, MTD-452 and F-85-11347 with a pod length of 4.23, 4.22 and 4.19 cm, respectively. Similarly, the highest number of seeds per pod was recorded in genotypes AUSTRALIA with an average 3.33 seeds per pod while the lines SHOHAG were observed with less number of seeds 2.00 in individual pods. Earlier findings of [15] also showed significant variability in pod length and number of seeds per pod in various soybean genotypes.

In present study the range for number of pod per plant were recorded from 28.33to 95. The highest number of pod per plant were noticed at F-85-11347 and followed by PK-327 and ASSET-93-19-13 with an average 92.67, 136.07, and 88.93, respectively. The lowest number of pod per plant was found at SHOHAG.

Grain weight is an important yield parameter and is vary from genotype to genotype. In the present study 100 seed weight (g) ranged from 5.13 to 14.7 g. Genotype LG-92P-12-18 showed maximum weight for 100 seeds (14.7 g) while GMOT-17 was noticed with minimum 100 grain weight (5.13 g). The highest stover yield was noticed in F-85-11347 (19.83 g) and lowest in MTD-451 (2.9). Genotype F-85-11347 showed the highest single pod weight per plant, whereas GC-82-332411 showed the lowest.

Grain yield being complex trait is highly influenced by various environmental factors including biotic and a biotic factors. It is also interplay of various morphological characters which either favor or worsen the final yield. In present investigations grain yield per plant in grams were measured. Grain yield was found to be highly significantly different due to different soybean genotypes. The genotype F-85-11347 superseded all the genotypes with highest yield of 49.81 g per plant. It was closely followed by another high yielding line ASSET-93-19-13 with grain yield of 43.36 g per plant. The genotype MTD-16 and AGS-79 showed poor performance in this experiment producing only 8.37 and 9.22 g of grain yield per plant respectively. It was further observed that the lines with highest grain weight and more pod numbers had produced higher yield. The findings of Malik *et al*., Sirohi *et al*. and Oz *et al*. are in accordance with these results.

CONCLUSION

Most of the genotypes showed highly significant variations among the traits and the variations could be used in plant improvement program. Based on the results of this experiment, it may be concluded that breeding program can be undertaken selecting F-85-11347 and ASSET-93-19-13 as parental genotypes following by selection of superior segregants from the successive generations. Because these genotypes bearing most of the desirable characters including highest yield per plant. Therefore, emphasis should be given on these genotypes during selection in breeding program in order to increase yield.

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