



Evaluation of Genetic Diversity in Different Genotypes of Soybean (*Glycine max* (L.) Merrill)

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Abstract: Genotypic variations of twenty eight soybean genotypes were evaluated in a randomized complete block design during Rabi season, 2011 at Sher-e-Bangla Agricultural University, Bangladesh. The phenotypic variance was higher than the corresponding genotypic variance for most of the characters. High heritability coupled with high genetic advance was recorded for number of branches per plant, plant height, number of seeds per plant, number of pods per plant and 100-seed weight. This indicates the effectiveness of selection to improve these five characters. Plant height, pod length, number of seeds per pod, number of pods per plant, hundred seed weight, branches per plant, and number of seeds per pod showed significant positive correlation with seed yield. Based on inter genotypic distances F-85-11347, Australia, 86017-66-6, PK-327, MTD-452, Shohag, MTD-16, YESOY-4 are important for varietal improvement of soybean genotypes. Considering genetic variability, heritability and correlation analysis, emphasis should be given on traits during phenotypic selection and inter genotypic distances for genotypic selection for developing high yielding genotypes of soybean.

Keywords: Soybean, Heritability, Correlation, Genotypes

1. Introduction

Soybean (*Glycine max* L.) is a legume that grows in tropical, subtropical and temperate climates. Soybean is now cultivated throughout east and South East Asia where people depend on it for food, animal feed and medicine. It contains about 40 to 42% protein and 18 to 22% oil [1]. The present nutritional situation of third world and some developing countries like Bangladesh is a matter of great concern since the most of the people are suffering from malnutrition. Soybean can play an important role in this case and can help to meet up the nutritional deficiency problem [2]. Soybean could be regarded as an ideal food for the people of poor and developing countries as it contains high quality of protein and reasonable quantity of oil as a source of energy [3]. Because of a good source of protein, unsaturated fatty acids, minerals like Ca and P including vitamin A, B, C, and D, soybean can meet up different nutritional needs [4]. Soy protein products can be good substitutes for animal products because, soybean offers a 'complete' protein profile and can effectively replace animal-based health hazardous foods [5].

Moreover soybean also contain numerous compounds that act as antioxidant and are beneficial to human health as they diminish the risk of cardiovascular diseases, breast cancer, osteoporosis, diabetes and neurodegenerative diseases such as Alzheimer's and Parkinson's and reduce the menopausal symptoms [6]. Genetic diversity among the genotypes is important for effective breeding program as the genetically diverged parents are known to produce high heterotic effects and wide segregants for developing high yielding varieties. Assessment of genetic variability is also needed for efficient parent selection in breeding program [7], long term selection gain and exploitation of heterosis [8]. Furthermore, characters associated with yield are to be determined by correlation analysis to assist selection in yield improvement work.

In the present study, genetic divergence of soybean has been assessed in the light of eleven important morphological and physiological traits to identify suitable genotypes for breeding program.

2. Materials and Methods

The study was conducted to assess the genetic diversity, correlation and path coefficient analysis among twenty eight soybean genotypes (Table 1). The experiment was carried out during December, 2011 to April, 2012 at the field laboratory of Sher-e-Bangla Agricultural University, located at 23° 77' N latitude, 90° 33' E longitude at an altitude of 8.6 m above sea level in Dhaka, Bangladesh. Experimental material consisting of twenty eight genotypes were sown in randomized complete block design with three replications; each plot consisted of a single row of 3m long with row to row distance of 50cm maintaining 10 plants per meter. Sowing was done with the help of hand drill. Ten random plants were used to take the data on days to first flowering, days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per

plant, pod length, number of seeds per pod, seeds per plant, hundred seed weight and seed yield per plant from each plot of each replication. All intercultural operations were carried out following standard procedures as described by Mondal *et al.* [9].

The data were analyzed by MSTAT program for ANOVA. Phenotypic variances, genotypic variances and error variances were estimated following Johnson *et al.* [10]. Genotypic and phenotypic coefficients of variation were estimated according to Burton [11]. Graphical representation of the data was carried out using MS-Excel.

Heritability and Genetic advance in percent of mean (GAPM) were estimated using the formula suggested by Johnson *et al.* [10] and Hanson *et al.* [12]. Genotypic and phenotypic correlation coefficient was carried out using formula suggested by Miller *et al.* [13], Johnson *et al.* [10] and Hanson *et al.* [12].

Table 1. Name of twenty eight soybean genotypes used in the present study.

Sl. No.	Genotypes No.	Name
1	G ₁	AGS-79
2	G ₂	BS-13
3	G ₃	JOYAWAZA
4	G ₄	F-85-11347
5	G ₅	AGS-95
6	G ₆	GC-82-332411
7	G ₇	BOAS-5
8	G ₈	LG-92P-12-18
9	G ₉	BS-33
10	G ₁₀	GC-830059
11	G ₁₁	ASSET-95
12	G ₁₂	BARI SOYBEAN-6
13	G ₁₃	KANH-33
14	G ₁₄	NS-1
15	G ₁₅	GMOT-17
16	G ₁₆	LG-92P-1176
17	G ₁₇	CHINA-1
18	G ₁₈	MTD-16
19	G ₁₉	SHOHAG
20	G ₂₀	PK-327
21	G ₂₁	AUSTRALIA
22	G ₂₂	YESOY-4
23	G ₂₃	PI-4174-75
24	G ₂₄	MTD-452
25	G ₂₅	86017-66-6
26	G ₂₆	ASSET-93-19-13
27	G ₂₇	BARI SOYBEAN-5
28	G ₂₈	MTD-451

Source: Bangladesh Agricultural Research Institute (BARI)

3. Results and Discussion

3.1. Genetic Variation

The phenotypic variance was slightly higher than the corresponding genotypic variance for most of the characters and showed moderate to low phenotypic and genotypic coefficient of variation (Fig 1). Genetic advance (% mean) was negligible for all the traits except number of branches

per plant, plant height, number of seeds per plant, number of pods per plant and 100-seed weight (Fig 2). These traits might be influenced in a small extent by the environmental factors. The expressions of other traits are mainly due to the genetic constituents rather than environmental influence. Heritability was also higher for all traits which also supplemented that genetic constituents are the main source of these traits. High heritability and high genetic advance in percent of mean of these traits showed

that these traits were under the control of additive gene and selection for the improvement of these traits could be effective. This finding is comparable with the results

previously published by Khan, [14] and Iqbal *et al.* [15] and mahbub *et al.* [16].

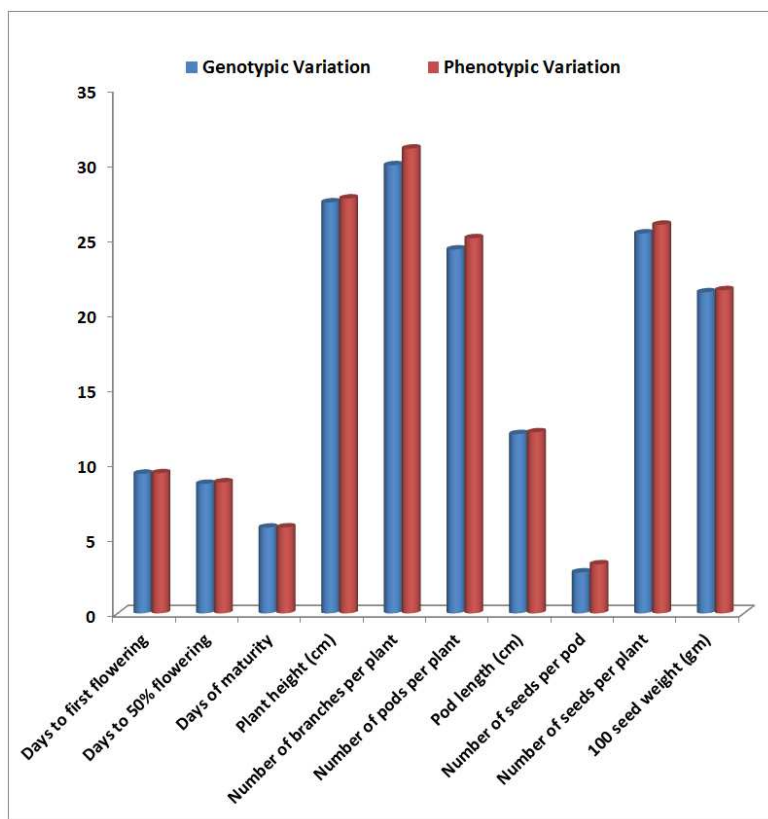


Fig. 1. Genotypic and phenotypic variability in soybean.

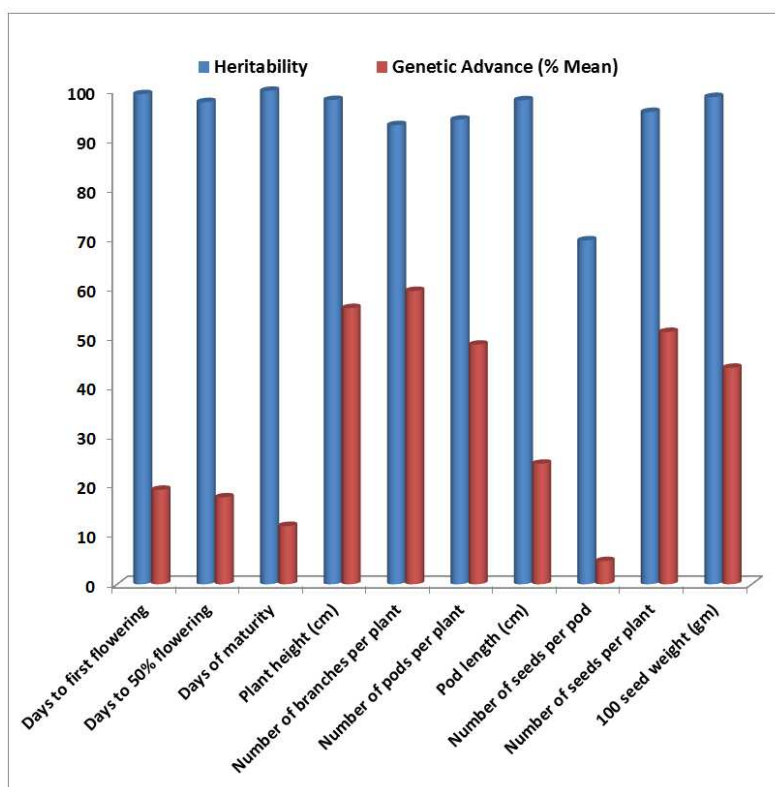


Fig. 2. Heritability and genetic advance over mean in soybean.

3.2. Correlation Among the Traits

Genotypic correlation coefficients were larger in values as compared to their respective phenotypic correlation coefficient (Table 2). This indicates greater contribution of genetic factor in the development of the association. Seed yield per plant showed the highest significant positive correlation with pod length followed by number of seeds per pod, number of pods per plant, hundred seed weight, branches per plant, plant height and number of seeds per plant similar result observed by Ghodrati *et al.* [17]. Such result indicated that the increase of one character will increase in the correlated character. For example, plant height was positively and significantly correlated with number of pods per plant, hence taller plants are more likely to produce greater number of branches and number of pods per plant. Chand, [18] and Rajanna *et al.* [19] observed similar results and showed positive and significant correlations of plant height with

number of pods and number of branches. Significant positive correlation was found between days to first flowering with days to 50% flowering, days to maturity, plant height, number of branches per plant and pod length. Days to maturity showed significant positive correlation with pod length and branches per plant. Plant height has significant positive correlation with branches per plant, number of pods per plant and pod length. On the other side, hundred seed weight showed significant negative correlation with plant height. It means increase of plant height decreased the seed weight in soybean. Khanghah & Sohani, [20], Rajanna *et al.* [19], Singh & Yadava, [21] and Arshed *et al.* [22] also reported similar findings for different parameters in soybean. Therefore, to improve yield of soybean, emphasis should be given on the correlated traits (pod length, number of seeds per pod, number of pods per plant, hundred seed weight, branches per plant, plant height

Table 2. Pearson correlation coefficients among different pairs of yield and yield contributing characters for different genotypes of soybean.

	D50%F	DM	PH	BPP	NPP	PL	NSP	SPP	HSW	SYP
DFF	0.98**	0.91**	0.45**	0.50**	0.18	0.26**	0.02	0.20	-0.03	0.17
D50%F		0.90**	0.46**	0.51**	0.19	0.28**	-0.01	0.21*	-0.02	0.18
DM			0.40**	0.43**	0.146	0.19	-0.03	0.15	-0.07	0.11
PH				0.83**	0.63**	0.32**	0.01	0.66**	-0.28**	0.37**
BPP					0.53**	0.46**	0.06	0.55**	-0.11	0.39**
NPP						0.25*	0.29**	0.98**	-0.22	0.66**
PL							0.25**	0.32**	0.62**	0.72**
NSP								0.34**	0.07	0.33**
SPP									-0.16	0.72**
HSW										0.55**

** = Significant at 1%.

* = Significant at 5%.

DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), BPP = Branches per plant, NPP = Number of pods per plant, PL = Pod length (cm), NSP = Number of seeds per pod, SPP = Seeds per plant, HSW = Hundred seed weight (g), SYP = Seed yield per plant (g).

and number of seeds per plant) based on the strength of their correlation like genotypic correlation coefficient was higher than phenotypic correlation coefficient (Fig 3).

3.3. Cluster Analysis

There was much variation among the clusters compared

to inter-cluster variations (Table 3). The inter-cluster distance was maximum between cluster II and IV (11.19) followed by cluster II and V (9.36) and cluster III and IV (8.74) and the lowest inter-cluster distance was obtained between cluster II and III (4.04) (Table 3). It is expected from the above results that the genotypes belonged to the cluster II and IV and cluster II and V having greater inter cluster distance could be effective for future breeding program to produce high yielding soybean varieties. Because the genotypes from diverge cluster may be recommended for inclusion in hybridization program as they are expected to produce good segregants [23].

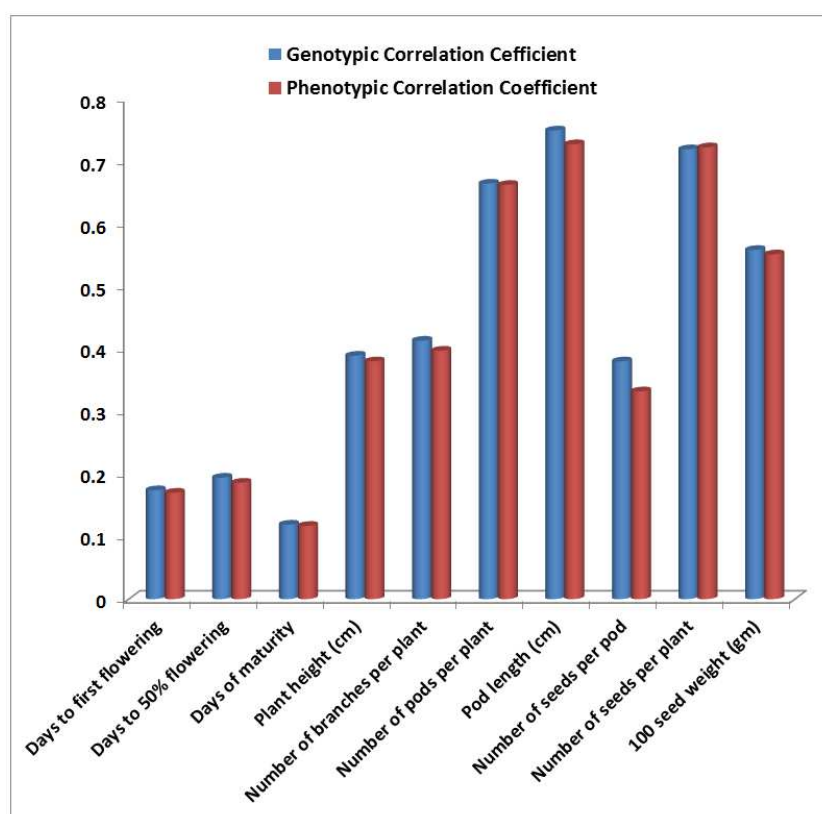


Fig. 3. Genotypic and phenotypic correlation coefficient of different character with yield.

On the other hand highest inter genotypic distance observed in between G4 and G21 (117.27) followed by in G4 and G25 (108.31) and in G4 and G20 (107.62), and the lowest inter genotypic distance in between G8 and G28 (0.532) (Table 4). So if crossing between these distant genotypes is possible there could be finding some interesting results which can be beneficial for mankind.

Table 3. The nearest and farthest clusters from each cluster between D^2 values in soybean.

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	I	III (4.32)	IV (6.56)
2	II	III (4.04)	IV (11.19)
3	III	II (4.04)	IV (8.74)
4	IV	V (5.04)	II (11.19)
5	V	I (4.73)	II (9.36)

Table 4. Ten highest and ten lowest inter genotypic distance among the 28 genotypes of soybean.

Highest distance				Lowest distance			
Sl No.	Genotype	Distance		Sl No.	Genotype	Distance	
01	G4	G21	117.27	01	G8	G28	0.532
02	G4	G25	108.31	02	G1	G9	1.074
03	G4	G20	107.62	03	G10	G13	1.140
04	G4	G24	103.93	04	G2	G3	1.298
05	G4	G19	103.06	05	G1	G17	2.362
06	G4	G18	102.48	06	G22	G24	2.970
07	G4	G22	101.01	07	G9	G17	3.436
08	G21	G28	96.35	08	G5	G16	4.480
09	G8	G21	95.98	09	G16	G17	4.899
10	G12	G21	84.97	10	G14	G15	5.546

4. Conclusions

High heritability coupled with high genetic advance as percent of mean recorded for number of branches per plant, plant height, number of seeds per plant, number of pods per plant and 100-seed weight. These conditions indicate that there is good opportunity to improve these characters using the tested genotypes. Therefore, emphasis should be given on correlated characters with yield contributing characters and inter genotypic distance with these traits during selection in breeding program in order to increase soybean production.

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