

Evaluation of Genetic Diversity in Soybean (*Glycine max* (L.) Merrill) Genotypes Based on Agronomic Traits

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ABSTRACT

Twenty-seven soybean genotypes were assessed for twelve morphological traits in a randomized complete block design with three replications throughout Rabi season, 2014 at field laboratory of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh. Significant variations were found among the genotypes for all the traits. Stover yield, seed yield, single pod weight per plant, 100-seed weight, number of branches per plant and number of pods per plant exhibited that they were governed by additive gene action and selection for the improvement of these characters would be fecund. The phenotypic variance was higher than the corresponding genotypic variance for all the characters. All the traits showed moderate to low phenotypic and genotypic coefficient of variation. The yield had significant positive correlations with number of branches per plant followed by stover yield and number of pod per plant. Number of branches per plant and stover yield had also the highest positive direct effect as well as significant and positively highest correlation with yield. Days to first flowering and number of pod per plant had negative direct effect on seed yield but they are significantly and positively correlated with yield. Considering genetic variability, correlation and path analysis emphasis should be given on the number of branches per plant, stover yield, number of pod per plant and single pod weight per plant during the breeding program to improve the seed yield of soybean.

Keywords: Soybean, Genetic diversity, Correlation, Path 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, 19% oil, 35% carbohydrate, 5% minerals and some other components with vitamins (Abady *et al.*, 2013). The current nutritional condition of the third world and some emerging countries like Bangladesh is a matter of great fear since most of the publics are suffering from malnutrition (Mahbub *et al.*, 2016). Soybean can show a significant role in this case and can aid to meet up the nutritional shortage difficulty. Furthermore, soybean also contains 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 (Kumar *et al.*, 2014). The low yield is the main constraint for growing of soybean. Therefore, breeders should highlight on yield enhancement of soybean. In order to improve yield, genetic variability is the preconditions meanwhile it is the cause of variation and raw factual for yield development effort (Mahbub *et al.*, 2015). Evaluation of genetic variability is also desirable for effective parent selection in the breeding program (Rahman *et al.*, 2011 and Khan *et al.*, 2016). Moreover, characters related with yield are to be resolute by correlation and path coefficient analysis to support selection in yield improvement work. Though correlation analysis specifies the connotation pattern of constituent traits with yield, they also represent the overall influence of a particular trait on yield rather than providing cause and effect association. The path coefficient analysis performance enables the partitioning of genotypic correlation into the direct and indirect effects of several characters on yield (Iqbal *et al.*, 2003). Such information would be of great worth in qualifying the breeder to definitely identify the vital constituent traits of yield and operate the genetic standards for improvement in a planned way. Therefore, the objective of the study is to see the genetic variability in twenty-seven promising soybean genotypes and carry out correlation and path analysis for yield and yield components to assists plant breeder for genetic improvement program.

MATERIALS AND METHODS

The experiment was carried out to evaluate the genetic diversity, correlation and path coefficient analysis for twenty-seven soybean genotypes (Table 1) during December, 2013 to April, 2014 at the research field 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. Soybean genotypes were sown in a randomized complete block design with three replications; every plot lied of a single row of 4m long with a row to row space of 1m preserving 10 plants per meter. Hand drill was used for sowing seeds in the field. Data were collected from ten randomly selected plants. The data were analysed by MSTAT program for ANOVA. Phenotypic, genotypic and error variances were estimated following Johnson *et al.*, 1955. Genotypic and phenotypic coefficients of variation were estimated according to Burton *et al.*, 1952]. Broad sense heritability, genetic advance (GA) and genetic advance in percent of mean (GAPM) were assessed by using the formula suggested by Johnson *et al.* (1955) and Hanson *et al.*, 1956. Genotypic and phenotypic correlation coefficient were carried out using formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956). The correlation coefficient was further partitioned into components of direct and indirect effects through path coefficient analysis established by Wright, (1934) and later described by Dewey and Lu, (1959).

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

Sl. No.	Genotypes No.	Name
1	G1	LG-92P-1176
2	G2	P1-4174-75
3	G3	KANH-33
4	G4	AGS-79
5	G5	MTD-452
6	G6	GMOT-17
7	G7	JOYAWAZA
8	G8	F-85-11347
9	G9	YESOY-4
10	G10	SHOHAG
11	G11	AUSTRALIA
12	G12	GC-82-332411
13	G13	PK-327
14	G14	ASSET-93-19-13
15	G15	PK-327
16	G16	AGS-95
17	G17	BARI SOYBEAN-6
18	G18	NS-1
19	G19	MTD-451
20	G20	GC-830059
21	G21	86017-66-6
22	G22	MTD-16
23	G23	LG-92P-12-18
24	G24	BS-33
25	G25	ASSET-95
26	G26	BS-13
27	G27	CHINA-1

Table 2. Estimatives of genetic parameters in twelve characters of twenty seven soybean genotypes

Parameters	Range	Mean	MS	CV (%)	σ^2P	σ^2g	σ^2e	PCV	GCV	ECV	Heritability	GA (5%)	GA (% mean)
PH	34.57-75.85	55.34	239.46**	9.25	97.31	71.08	26.23	17.82	15.23	9.25	73.05	14.84	26.82
DFE	74.00-90.33	82.10	38.61**	1.41	13.76	12.43	1.33	4.52	4.29	1.41	90.32	6.90	8.41
D50F	76.33-93.67	84.78	42.05**	1.43	15.00	13.53	1.47	4.57	4.34	1.43	90.18	7.19	8.49
D80M	116.33-157.00	127.32	218.42**	0.85	73.59	72.42	1.16	6.74	6.68	0.85	98.40	17.39	13.66
NBP	3.47-11.57	6.22	10.68**	16.63	4.27	3.20	1.07	33.23	28.77	16.63	74.96	3.19	51.32
NPP	28.33-95.00	49.51	931.31**	18.36	365.52	282.89	82.63	38.62	33.97	18.36	77.39	30.48	61.57
NSP	2.00-3.33	2.89	0.21**	8.33	0.11	0.05	0.06	11.48	7.90	8.33	47.40	0.32	11.21
PL	2.82-4.95	3.64	0.66**	6.87	0.26	0.20	0.06	14.06	12.26	6.87	76.09	0.80	22.04
HSW	5.13-14.70	9.06	23.52**	5.62	8.01	7.75	0.26	31.24	30.73	5.62	96.76	5.64	62.27
SY	2.90-19.83	7.84	47.89**	11.95	16.55	15.67	0.88	51.89	50.49	11.95	94.69	7.94	101.22
SPWP	1.47-9.74	4.37	9.03**	14.94	3.30	2.87	0.43	41.54	38.76	14.94	87.07	3.26	74.51
YIELD	8.37-49.81	18.54	314.23**	12.19	108.15	103.04	5.11	56.09	54.75	12.19	95.28	20.41	110.09

** Correlation is significant at the 0.01 level.

DFE= 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 length, HSW= Hundred seed weight (g), SY= Stover yield, SPWP= Single pod weight per plant, YIELD=Yield per plant, MS= Mean sum of square, CV(%)= Coefficient of variation, σ^2P = Phenotypic variance, σ^2g = Genotypic variance, σ^2e = Environmental variance, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, ECV= Environmental coefficient of variation, GA= Genetic advance.

RESULTS AND DISCUSSION

Genetic variation

All the morphological characters exhibited highly significant variations among the genotypes (Table 2). The phenotypic variance was slightly higher than the corresponding genotypic variance for all the characters and showed moderate to low phenotypic and genotypic coefficient of variation (Figure 1). High phenotypic and genotypic variances with a low environmental variance for all the characters indicate that the expression of the genes controlling the characters is not markedly influenced by the environmental conditions (Rahman *et al.*, 2014). Environmental variances were negligible for all the traits except plant height and number of pods per plant. These traits may not be subject to environmental causes. The expressions of other trait were mainly due to the genetic constituents rather than environmental influences. The differences between GCV and PCV were very low for all characters studied which showed that the environmental effects on these traits are very low. The environmental coefficient of variation was also low for number of branches per plant, number of pods per plant and single pod weight per plant but very low for other traits. Heritability estimates were also high for all traits which also confirmed that genetic constituents are the main source of variation for these traits. A high genetic advance was found for number of pod per plant and yield. The genetic advance was moderate for plant height, days to first flowering, days to 50% flowering, days to 80% maturity and stover yield but low for number of seeds per pod, pod length, hundred seed weight and single pod weight per plant. Genetic advance (GA) in percent of a mean for stover yield, grain yield, single pod weight per plant, hundred seed weight, number of branches per plant and number of pods per plant were high (Figure 2) which showed that these parameters could be improved to a large extent by plant improvement program. High heritability and high genetic advance in percent

of the mean of these traits showed that these traits were under the control of additive gene action and selection for the improvement of these characters could be effective. This conclusion is similar to the results before published by Mahbub *et al.*, 2015.

Correlation among the traits

Yield showed significant positive correlation with days to 50% flowering, days to 80% maturity, a number of branches per plant, number of pod per plant, single pod weight per plant and grain yield per plant (Table 3). The highest positive correlation was absorbed between grain yield number of branches per plant followed by stover yield and number of pod per plant. Such result indicated that the increase of one character will increase in the positively correlated character. Mahbub and Shirazy, (2016) highlighted the significance of number of pods per plant in determining seed yield in soybean. Therefore, to improve yield of soybean importance should be given to the correlated characters based on the strength of their correlation. It is evident from Table 4 and Figure 2 that the phenotypic correlation coefficients were larger in values as compared to their respective genotypic correlation coefficients. This indicates a greater contribution of the phenotypic factor in the development of the association.

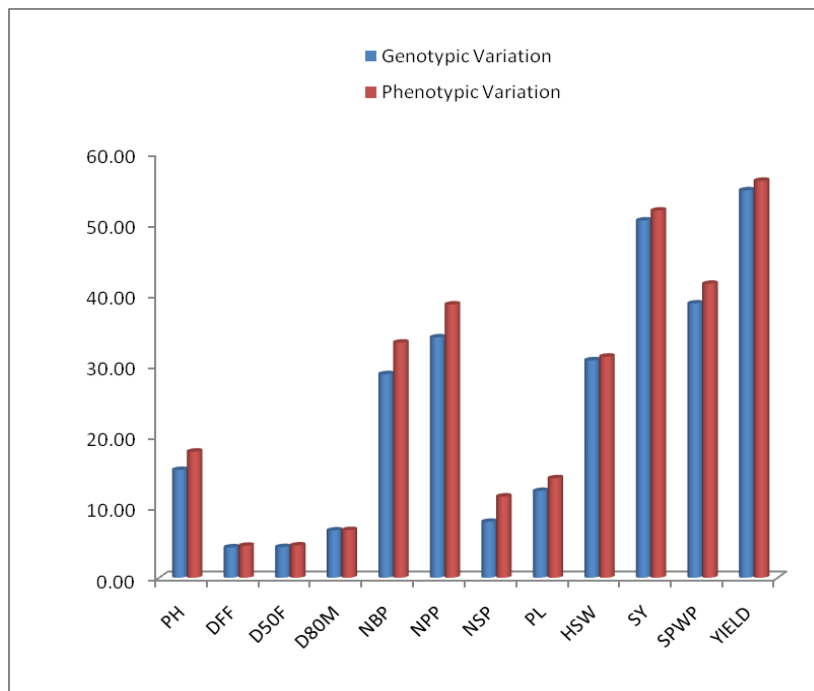


Figure 1. Genotypic and phenotypic variations in soybean genotypes

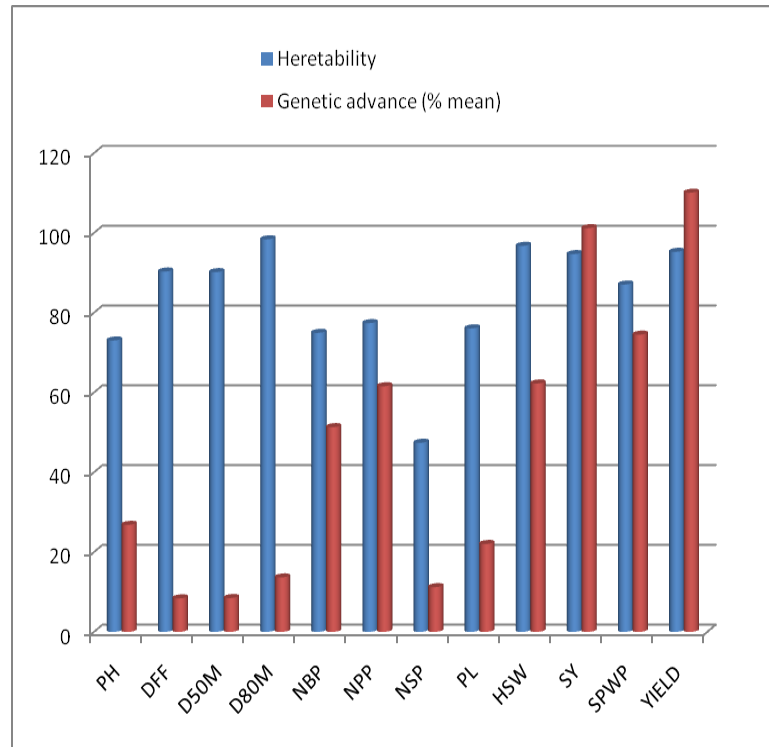


Figure 2. Heritability estimates and genetic advance over mean in soybean genotypes

Path analysis

The data presented in Table 4 showed that number of branches per plant have the maximum positive direct effect on seed yield (0.665) followed by stover yield (0.557), pod length (0.270), days to 80% maturity (0.186), days to 50% flowering (0.135), single pod weight per plant (0.120) and hundred seed weight (0.035). Days to first flowering, plant height, number of pod per plant and number of seeds per pod showed a negative direct effect on seed yield. Days to first flowering and number of pod per plant had a negative direct effect but they were significantly and positively correlated with yield. Number of branches per plant and stover yield had the highest positive direct effect as well as significant and positively highest correlation with yield. Hence these traits could consider for yield improvement.

Table 3. Pearson correlation coefficients among different pairs of yield and yield contributing character for different genotypes of soybean.

Character	DFE	D50F	D80M	NBP	NPP	NSP	PL	HSW	SY	SPWP	YIELD
PH	0.40*	0.39*	-0.09	0.48*	0.63**	0.05	0.03	-0.15	0.32	0.19	0.36
DFE		0.98**	0.06	0.34	0.41*	0.12	0.21	-0.08	0.34	0.28	0.43*
D50F			0.06	0.28	0.44*	0.15	0.19	-0.09	0.31	0.31	0.42*
D80M				-0.07	0.16	0.25	0.18	0.49**	0.20	0.33	0.21
NBP					0.50**	0.15	0.11	-0.18	0.29	0.11	0.65**
NPP						0.25	0.09	-0.03	0.66**	0.52**	0.57**
NSP							0.56**	0.11	0.19	0.35	0.23
PL								0.38*	0.38	0.41*	0.30
HSW									0.00	0.48*	-0.04
SY										0.52**	0.63**
SPWP											0.43*

** Significant at 1%

* Significant at 5%

DFE= 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 length, HSW= Hundred seed weight (g), SY= Stover yield, SPWP= Single pod weight per plant, YIELD=Yield per plant

CONCLUSION

All the morphological traits that showed highly significant variations among the genotypes and which were controlled by additive gene action as well as had significant positive correlation with yield and direct effect should be considered during selection in the breeding program in order to increase yield.

Table 4. Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotypes of soybean

Character		DFF	D50F	D80M	NBP	NPP	NSP	PL	HSW	SY	SPWP	YIELD
PH	G	0.418*	0.410*	-0.083	0.554*	0.672**	0.087	0.060	-0.153	0.331	0.201	0.388
	P	0.400*	0.395*	-0.086	0.482*	0.627**	0.049	0.029	-0.150	0.315	0.194	0.359
DFF	G		0.988**	0.071	0.350	0.425*	0.155	0.224	-0.086	0.348	0.296	0.436*
	P		0.978**	0.055	0.341	0.406*	0.124	0.211	-0.084	0.340	0.282	0.430*
D50F	G			0.068	0.291	0.465*	0.166	0.201	-0.084	0.312	0.320	0.433*
	P			0.063	0.277	0.441*	0.147	0.192	-0.086	0.307	0.307	0.424*
D80M	G				-0.075	0.162	0.286	0.190	0.496**	0.200	0.337	0.211
	P				-0.070	0.155	0.247	0.181	0.493**	0.197	0.325	0.210
NBP	G					0.546**	0.179	0.107	-0.189	0.311	0.130	0.683**
	P					0.501**	0.153	0.105	-0.176	0.291	0.112	0.648**
NPP	G						0.356	0.137	-0.033	0.701**	0.544**	0.614**
	P						0.246	0.093	-0.034	0.663**	0.518**	0.575**
NSP	G							0.658**	0.110	0.218	0.428	0.258
	P							0.564**	0.106	0.185	0.349	0.228
PL	G								0.413*	0.404	0.452*	0.306
	P								0.384*	0.376	0.412*	0.299
HSW	G									0.003	0.494*	-0.035
	P									0.004	0.484*	-0.036
SY	G										0.527**	0.641**
	P										0.519**	0.630**
SPWP	G											0.454*
	P											0.431*

*and ** Significant at 5 and 1% Probability levels .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 length, HSW= Hundred seed weight (g), SY= Stover yield, SPWP= Single pod weight per plant, YIELD=Yield per plant.

Table 5. Path coefficient analysis showing direct and indirect effects of different characters on yield of soybean

Characters	Direct effect	Indirect effects											Pearson Correlation with Yield
		PH	DFE	D50F	D80M	NBP	NPP	NSP	PL	HSW	SY	SPWP	
PH	-0.024	-0.024	-0.489	0.528	0.380	0.319	-0.169	-0.001	0.085	-0.005	0.178	0.022	0.36
DFE	-0.122	-0.009	-0.122	0.132	-0.011	0.226	-0.110	-0.001	0.057	-0.002	0.189	0.033	0.43*
D50F	0.135	-0.009	-1.197	0.135	0.011	0.186	-0.118	-0.001	0.051	-0.003	0.172	0.037	0.42*
D80M	0.186	-0.001	0.076	0.083	0.186	-0.048	-0.049	-0.011	0.049	-0.029	0.010	0.049	0.21
NBP	0.665	-0.011	-0.415	0.379	-0.013	0.665	-0.134	-0.001	0.029	-0.006	0.161	0.013	0.65**
NPP	-0.268	-0.015	-0.501	0.595	0.029	0.332	-0.268	-0.002	0.024	-0.001	0.367	0.006	0.57**
NSP	-0.009	-0.001	-0.146	0.203	-0.046	0.099	-0.067	-0.009	0.152	0.003	0.105	0.042	0.23
PL	0.270	0.006	-0.010	0.018	0.049	0.062	0.005	-0.106	0.270	-0.110	0.004	0.127	0.3
HSW	0.035	0.003	0.097	-0.121	0.091	-0.119	0.008	-0.001	0.103	0.035	0.000	0.057	-0.04
SY	0.557	-0.007	-0.415	0.419	0.037	0.193	-0.177	-0.001	0.073	0.000	0.557	0.062	0.63**
SPWP	0.120	-0.004	-0.342	0.419	0.061	0.073	-0.139	-0.003	0.111	0.017	0.289	0.120	0.43*

Residual effect= 0.287

*and** :Significant at 5% probability levels

* Significant at 5%

DFE= 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 length, HSW= Hundred seed weight (g), SY= Stover yield, SPWP= Single pod weight per plant, YIELD=Yield per plant

REFERENCES

- Abady S, Merkeb F, Dilnesaw Z. 2013. Heritability and path-coefficient analysis in soybean (*Glycine Max* L. Merrill) genotypes at Pawe, North Western Ethiopia. *Journal Environment Science Water Resources*, 2(8): 270 – 276.
- Burton GW. 1952. Quantitative interaction in grasses. In: *Proc. 6th International Grassland Congress*, 1(2): 77-283.
- Dewey JR, Lu KH. 1959. A correlation and path co-efficient analysis of components of crested wheat seed production. *Agronomy Journal*, 51 : 515-518.
- Hanson CH, Robinson HF, Comstock RE. 1956. Biometric studies of yield segregating population in Korean lespedeza. *Agronomy Journal*, 48: 268-272.
- Iqbal S, Mahmood T, Tahira, Ali M, Anwar M, Sarwar M. 2003. Path-coefficient analysis in different genotypes of soybean [*Glycine max* (L) Merrill]. *Pakistan Journal of Biological Science*, 6(12): 1085-1087.
- Johnson HW, Robinson HF, Comstock RE. 1955. Estimation of genetic and environmental variability in soybean. *Agronomy Journal*, 47(7): 314-317.
- Khan MRA, Mahbub MM, Reza MA, Shirazy BJ, Mahmud F. 2016. Selection of Field Pea (*Pisum sativum* L.) Genotypes through Multivariate Analysis. *Scientia Agriculturae*, 16 (3): 98-103.
- Kumar A, Kumar A, Lal SK, Jolly M, Sachdev A. 2014. Influence of gamma rays and ethyl methane sulphonate (EMS) on the levels of phytic acid, raffinose family oligosaccharides and antioxidants in soybean seeds of different genotypes. *Journal of Plant Biochemistry and Biotechnology*, Pp: 1-6.
- Mahbub MM, Rahman MM, Hossain MS, Mahmud F, Kabir MMM. 2015. Genetic Variability, Correlation and Path Analysis for Yield and Yield Components in Soybean. *American-Eurasian Journal of Agricultural and Environmental Sciences*, 15 (2): 231-236.
- Mahbub MM, Rahman MM, Hossain MS, Nahar L, Shirazy BJ. 2016. Morphophysiological Variation in Soybean (*Glycine max* (L.) Merrill). *American-Eurasian Journal of Agricultural and Environmental Sciences*, 16(2): 234-238.
- Mahbub MM, Shirazy BJ. 2016. Evaluation of Genetic Diversity in Different Genotypes of Soybean (*Glycine max* (L.) Merrill). *American Journal of Plant Biology*, 1(1): 24-29.
- Millar PA, Williams JC, Robinson HF, Comstock RE. 1958. Estimates of genotypic and environmental variance and covariance and their implication in selection. *Agronomy Journal*, 50:126-131.
- Rahman MM, Rasul MG, Bashir MK, Syed MA, Islam MR. 2011. Parent selection for transplanted Aman rice breeding by morphological, physiological and molecular diversity analysis. *Libyan Agriculture Research Center Journal International*, 2(1): 29-35.
- Rahman MM, Syed MA, Akter A, Alam MM, Ahsan MM. 2014. Genetic variability, correlation and path coefficient analysis of morphological traits in transplanted Aman rice. *American-Eurasian Journal of Agricultural and Environmental Sciences*, 14(5) : 387-91.
- Wright S. 1934. The method of path coefficients. *The Annals of Mathematical Statistics*, 5(3): 161-215.