

## Genetic Variability, Correlation and Path Analysis for Yield and Yield Components in Soybean

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**Abstract:** Twenty eight soybean genotypes were evaluated for eleven morphological characters during Robi season, 2011 at Sher-e-Bangla Agricultural University, Dhaka, Bangladesh. Analysis of variance revealed significant differences among the genotypes for all the traits. Plant height, seed yield per plant, branches per plant, number of seeds per pod, number of pods per plant and hundred seed weight exhibited that they were controlled by additive gene action and selection for the improvement of these traits would be rewarding. The phenotypic variance was higher than the corresponding genotypic variance for all the characters. All the characters showed moderate to low phenotypic and genotypic coefficient of variation. Genotypic coefficient of variation was the highest for seed yield per plant (31.45%) followed by number of branches per plant (29.9%) and plant height (27.42%). Days to maturity (99.93%) had the highest heritability. 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 genotypic and phenotypic correlation with seed yield. In path analysis, seeds per pod, hundred seed weight, pod length, days to maturity and plant height showed positive direct effect on yield. Considering genetic variability, correlation and path analysis, emphasis should be given on plant height, pod length, seeds per pod and hundred seed weight during breeding program to improve seed yield of soybean.

**Key words:** Soybean • Diversity • Correlation • Path coefficient analysis

### INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is a wonderful crop gifted by the nature to mankind which is one of the richest sources of oil as well as protein. It belongs to the family Leguminosae and is a self-pollinated crop having chromosome number of  $2n=40$ . Its seed 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. Soybean could be regarded as an ideal food for the people of poor and developing countries as it contains high quality protein and reasonable quantity of

oil as a source of energy [2]. 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 [3]. 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 [4]. 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 [5].

The low yield of soybean in these countries is the main constrain for growing of soybean. Therefore, breeders should emphasize on yield improvement of

soybean. In order to increase yield, genetic variability is the prerequisites since it is the source of variation and raw material for yield improvement work [6]. Assessment of genetic variability is also needed for efficient parent selection in breeding program [7], long term selection gain and exploitation of heterosis [6]. Furthermore, characters associated with yield are to be determined by correlation and path coefficient analysis to assist selection in yield improvement work.

Though correlation analysis indicates the association pattern of component traits with yield, they also represent the overall influence of a particular trait on yield rather than providing cause and effect relationship. The path coefficient analysis technique facilitates the partitioning of genotypic correlation into direct and indirect contribution of various characters on yield [6-9]. Such information would be of great value in enabling the breeder to specifically identify the important component traits of yield and utilize the genetic stock for improvement in a planned way.

Mention the objectives of the present study ??

### 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 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 a randomized complete block design with three replications; each plot consisted of a single row of 3 m long with row to row distance of 50 cm maintaining 10 plants per meter. Sowing was done with the help of a 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 cultural operations were carried out following standard procedures as described by Mondal *et al.* [10].

The data were analyzed by MSTAT program for ANOVA. Phenotypic variances, genotypic variances and error variances were estimated following Johnson *et al.*, [11]. Genotypic and phenotypic coefficients of variation were estimated according to Burton [12].

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

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

Source: Bangladesh Agricultural Research Institute (BARI)

Broad sense heritability, genetic advance (GA) and genetic advance in percent of mean (GAPM) were estimated using the formula suggested by Johnson *et al.*, [11] and Hanson *et al.*, [13]. Genotypic and phenotypic correlation coefficient were carried out using formula suggested by Miller *et al.*, [14], Johnson *et al.*, [11] and Hanson *et al.*, [13]. The correlation coefficients were further partitioned into components of direct and indirect effects by path coefficient analysis developed by Wright [15] and later described by Dewey and Lu [16].

### RESULTS AND DISCUSSION

**Genetic Variation:** All the morphological traits showed 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. High phenotypic and genotypic variances with low environmental variance for all the characters indicate that the expression of the genes controlling the characters are not markedly influenced by the environmental conditions [17]. Environmental variances were negligible for all the traits except plant height, number of pods per plant and seeds per pod. These three 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. The differences between GCV and PCV were very low for all characters studied, indicating that the environmental effects in the development of these parameters are very low. Environmental coefficient of variation was also low for branches per plant, number of pods per plant and number of seeds per pod and very low for other traits. Heritability was also higher for all traits which also indicate that genetic constituents are the main source of these traits. High genetic advance was found for plant height and seed per plant. Genetic advance was moderate for days to first flowering, days to 50% flowering, days to maturity and number of pods per plant and low for branches per plant, plant height, number of seeds per pod, hundred seed weight and seed yield per plant. Genetic advance (GA) in percent of mean for seed yield per plant, branches per plant, plant height, seeds per pod, number of pods per plant and hundred seed weight were high showing that these parameters could be improved in a large extent by plant selection improvement program. 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 or the improvement of these traits could be effective. This finding is comparable with the results previously published by Khan [18] and Iqbal *et al.* (2003) [8].

**Correlation among the Traits:** It is evident from Table 3 that the genotypic correlation coefficients were larger in values as compared to their respective phenotypic correlation coefficient. This indicates greater contribution of genetic factor in the development of the association.

Significant positive genotypic and phenotypic correlations were found between days to first flowering, days to 50% flowering, days to maturity, plant height, number of branches per plant and pod length. Number of pods per plant showed significant positive correlations with plant height, branches per plant, number of seeds per pod, seeds per plant and seed yield. Seed yield showed the highest significant positive genotypic and phenotypic 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 results were recorded by Ghodrati *et al.*, [19]. Such results 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.

Table 2: Estimation of genetic parameters in eleven characters of 28 genotypes in soybean

Traits	Range	Mean	MS	CV (%)	$\sigma^2_p$	$\sigma^2_g$	$\sigma^2_e$	PCV%	GCV%	ECV%	Heritability	GA (5%)	GA (%mean)
DFE	51.67-76.33	66.15	395.46**	0.81	38.26	37.97	0.29	9.35	9.31	0.81	99.25	12.65	19.12
D50%F	55.33-79.00	69.6	125.79**	1.34	37.02	36.15	0.87	8.74	8.64	1.34	97.65	12.24	17.59
DM	105.33-132.00	124.29	4,101.14**	0.15	50.66	50.62	0.04	5.73	5.72	0.15	99.93	14.65	11.79
PH	21.90-79.87	56.89	153.98**	3.84	248.03	243.26	4.77	27.68	27.42	3.84	98.08	31.82	55.93
BPP	1.80-5.87	4.12	40.76**	8.21	1.63	1.52	0.11	31.01	29.9	8.21	92.98	2.45	59.4
NPP	24.62-59.57	38.83	48.76**	6.09	94.46	88.88	5.58	25.03	24.28	6.09	94.09	18.84	48.52
PL	2.53-4.19	3.03	150.46**	1.69	0.13	0.13	0	12.08	11.96	1.69	98.03	0.74	24.4
NSP	2.37-2.66	2.51	7.88**	1.8	0.01	0	0	3.27	2.73	1.8	69.63	0.12	4.69
SPP	60.70-158.37	97.55	66.76**	5.42	639.6	611.69	27.91	25.93	25.35	5.42	95.64	49.82	51.08
HSW	6.27-16.57	10.49	224.84**	2.48	5.12	5.05	0.07	21.56	21.42	2.48	98.68	4.6	43.83
SYP	5.73-17.40	10.16	78.98**	6.17	10.6	10.21	0.39	32.05	31.45	6.17	96.3	6.46	63.57

\*\* means correlation is significant at the 0.01 level.

[DFE = 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), MS = mean sum of square, CV (%) = Coefficient of variation,  $\sigma^2_p$  = Phenotypic variance,  $\sigma^2_g$  = Genotypic variance,  $\sigma^2_e$  = Environmental variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation]

Table 3: Genotypic (G) and phenotypic (P) correlation coefficient 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
DFD	G	0.999**	0.917**	0.464**	0.527**	0.185	0.268**	0.015	0.206	-0.033	0.174
	P	0.985**	0.913**	0.460**	0.509**	0.003	0.265**	0.016	0.202	-0.033	0.170
D50%F	G		0.916**	0.480**	0.543**	0.207	0.294**	0.034	0.224*	-0.026	0.194
	P		0.905**	0.467**	0.518**	0.200	0.285**	-0.009	0.203	-0.025	0.186
DM	G			0.411**	0.451**	0.149	0.200	-0.042	0.161	-0.070	0.119
	P			0.408**	0.435**	0.146	0.198	-0.036	0.159	-0.070	0.117
PH	G				0.865**	0.666**	0.326**	0.023	0.684**	-0.284**	0.389**
	P				0.838**	0.640**	0.326**	0.017	0.662**	-0.282**	0.380**
BPP	G					0.556**	0.490**	0.109	0.585**	-0.121	0.413**
	P					0.530**	0.465**	0.067	0.558**	-0.113	0.397**
NPP	G						0.266**	0.347**	0.991**	-0.232*	0.664**
	P						0.255**	0.291**	0.984**	-0.226*	0.662**
PL	G							0.300**	0.336**	0.635**	0.749**
	P							0.256**	0.325**	0.626**	0.727**
NSP	G								0.388**	0.100	0.380**
	P								0.340**	0.078	0.332**
SPP	G									-0.165	0.719**
	P									-0.163	0.722**
HSW	G										0.558**
	P										0.551**

\*\* = Significant at 1%.

\* = Significant at 5%.

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

Table 4: Path coefficient analysis showing direct and indirect effects of different characters on yield of soybean

Characters	Direct effect	Indirect effect										Pearson Correlation with yield
		DFD	D50%F	DM	PH	BPP	NPP	PL	NSP	SPP	HSW	
DFD	-0.010	-	-0.008	0.057	0.019	-0.031	-0.017	0.019	0.000	0.180	-0.019	0.17
D50%F	-0.001	-0.030	-	0.056	0.020	-0.031	-0.018	0.020	0.000	0.189	-0.013	0.18
DM	0.062	-0.028	-0.008	-	0.017	-0.026	-0.014	0.014	0.000	0.135	-0.045	0.11
PH	0.043	-0.014	-0.004	0.025	-	-0.051	-0.058	0.023	0.000	0.595	-0.179	0.37**
BPP	-0.031	-0.015	-0.004	0.027	0.036	-	-0.049	0.033	-0.001	0.496	-0.070	0.39**
NPP	-0.040	-0.006	-0.002	0.009	0.027	-0.033	-	0.018	-0.002	0.883	-0.141	0.66**
PL	0.072	-0.008	-0.002	0.012	0.014	-0.028	-0.023	-	-0.002	0.288	0.397	0.72**
NSP	-0.004	-0.001	0.000	-0.002	0.000	-0.004	-0.027	0.018	-	0.306	0.045	0.33**
SPP	1.200	-0.006	-0.002	0.009	0.028	-0.034	-0.091	0.023	-0.003	-	-0.102	0.72**
HSW	0.739	0.001	0.000	-0.004	-0.012	0.007	0.020	0.045	-0.001	-0.144	-	0.55**

Residual effect: 0.395

\*\* indicates significant at 1% and \* indicates significant at 5% level of probability.

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

Chand [20] and Rajanna *et al.*, [21] reported similar results and showed positive and significant correlations of plant height with number of pods and number of branches. 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 and number of seeds per plant) based on the

strength of their correlation. On the other side, hundred seed weight showed significant negative genotypic and phenotypic correlation with plant height and number of pods per plant. It means that increase of plant height and number of pods per plant decreased the seed weight. Khanghah and Sohani [22], Rajanna *et al.*, [21], Singh and Yadava [23] and Arshed *et al.*, [24] also reported similar findings for different parameters in soybean.

**Path Analysis of the Traits:** The data presented in Table 4 showed that seeds per pod had the maximum positive direct effect on yield (1.20) followed by hundred seed weight (0.739), pod length (0.072), days to maturity (0.062) and plant height (0.043). Similar results were reported by Malek *et al.*, [25]. Number of pods per plant showed the highest negative direct effect on yield (-0.040) followed by branches per plant (-0.031), days to first flowering (-0.010), number of seeds per pod (-0.004) and days to 50% flowering (-0.001).

Branches per plant, number of pods per plant and number of seeds per pod had negative direct effect but significant positive correlation with yield. Though number of branches per plant, number of pods per plant and number of seeds per pod showed highly significant positive correlation with seed yield, but they showed negative direct effect on yield. Number of seeds per pod showed very little negative direct effect on yield but showed positive indirect effect on days to 50% flowering, plant height, pod length, seeds per pod and hundred seed weight along with highly significant positive correlation with seed yield. Therefore, this trait could consider for yield improvement.

## CONCLUSIONS

All the morphological traits showed highly significant variations among the genotypes and the variations could be used in plant improvement program. Seed yield per plant, branches per plant, plant height, seeds per pod, number of pods per plant and hundred seed weight were controlled by additive gene action and selection for the improvement of these traits could be effective. Furthermore, among studied traits, four traits viz, plant height, pod length, seeds per pod and hundred seed weight showed highly positive correlation and positive direct effect on seed yield. Therefore, emphasis should be given on these traits during selection in breeding program in order to increase seed yield.

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