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Estimation of genetic parameters, interrelation and path coefficient analysis for seed yield and its component traits in soybean

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Abstract

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Selection criteria is very crucial to pick up promising genotypes in a breeding program. An experiment was conducted with twenty soybean genotypes following a randomized complete block design to study the inheritable agronomic traits, their interrelation and partitioning of genotypic correlation into direct and indirect effects to identify the traits responsible for higher seed yield. Results indicated that phenotypic variance was higher than that of genotypic variance for all the characters. The highest PCV was found for the trait seed yield per plant (39.03%) followed by yield per plot (32.85%). The higher GCV was also found for the same traits- seed yield per plant (37.36%), yield per plot (27.23%). PCV and GCV was the lowest for trait days to maturity (6.28%, 4.16%) and days to flowering (3.20%, 2.24%). Estimated broad sense heritability was ranged from days to flowering (44.05%) to seed yield per plant (91.62%). Higher estimate of heritability was also observed for yield per plot (88.65%) followed by hundred seed weight (85.39%) whereas; heritability was moderate for plant height (76.75%) and pod per plant (70.17%). The genetic advance was the highest for plant height (19.39%). On the other hand, primary branch per plant, days to flowering and days to maturity showed low heritability with low GA depicts the influence of non-additive gene effect. Pod per plant, hundred seed weight, days to maturity and plant height is positively and significantly correlated with yield. Pod per plant (0.908) and hundred seed weight (0.907) showed highest direct positive effect on seed yield at genotypic level. Path analysis also confirmed highest positive direct effect of hundred seed weight (0.701). So, the present study suggests that, higher hundred seed weight and pod per plant can be effective selection measure for improvement of soybean yield.

Keywords: Genetic variability; heritability; Genetic advance; correlation; path analysis

Introduction

Soybean (*Glycine max* L. Merrill) is the leading oilseed crop in the world. It contains about 40-45% protein and 18-20% oil and provide around 60% of world's supply of vegetable protein and 30% of the oil (Fehr, 1989). Average yield of soybean in Bangladesh is much lower compared to other soybean growing countries. Report says, the total annual demand for edible oil is around 3 million tons in Bangladesh. In 2020, around 2.73 million tons of oils and fat were imported, out of which palm oil import was 1.33 million tons and soybean oil were 0.80 million tons (The Daily Star, 2022). In Bangladesh, Soybean is being cultivated as minor crop where locally available low yielding varieties are cultivated.

Replacement of old variety will be effective for increasing growing area as well as production in Bangladesh.

Genetic diversity is considered as the base for survival of plants in nature and for crop improvement. Furthermore, heritability allows establishing an estimate of the genetic gain to be obtained and defines the best strategy to be used in the breeding program (Baldissera et al., 2014). Only the idea about heritability is not appropriate in selection of traits but heritability with genetic advance is more judicious (Johnson et al., 1955).

In soybean, grain yield is a complex trait like other crops because it results from the expression and association of different components (El-Mohsen et al., 2013). Therefore, details information about the traits that influence yield is essential. Correlation between traits allows establishing criteria for an efficient selection (Silva et al., 2015). Path coefficient analysis provides an effective means to partition correlation coefficients into unidirectional and alternative pathways, thus permitting a critical examination of the specific factors that produce a given correlation; this can then be employed to formulate an effective selection program (Jain et al., 2015). The present study was therefore conducted to determine the variability using genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), heritability and genetic advance along with interrelation between characters and their effect in soybean yield which will be useful for future hybridization program.

Methods and Materials

Twenty genotypes of Soybean were used in the experiment (Table 1). The experiment was laid out in Randomized complete block design (RCBD) with three replications in the research field of Sher-e-Bangla Agricultural University in 2017. The twenty genotypes of the experiment were assigned at random into plots of each replication. Plot size was 3 m x 2 m with row to distance 25 cm and plant to plant distance 5 cm. Plant populations were similar in all the plots. The manures and fertilizers were applied as per recommended doses. Several intercultural operations like thinning, weeding, irrigation and insecticide spraying were done as per requirement. Pods were picked on the basis of horticultural maturity, size, color and age being determined for the purpose of consumption throughout the harvesting period. Date was recorded on yield and yield attributing characters viz, days to 50% flowering, plant height (cm), primary branches per plant, pods per plant, hundred seed weight (gm), days to maturity and yield per plot (kg). All the data were taken as average of 5 plants and yield was measured as yield of 6 m^2 plot.

Table 1. List of twenty soybean genotypes used in the study

Sl. no.	Genotypic Name	Sl. no.	Genotypic Name	Sl. no.	Genotypic Name
1.	Tas-4	8	GMOT-13	15	BINA SOYBEAN 1
2	Djs-9207	9	AGS-205	16	SOHAGH
3	AGS- 95	10	BARI SOYBEAN 5	17	BARI SOYBEAN 6
4	K-16	11	FV-4PL-NICE-7	18	BINA SOYBEAN 3
5	GMOT-95	12	BOSS	19	BINA SOYBEAN 2
6	ASSET-93	13	AGS-79	20	LOCAL
7	ASOMEME	14	BINA SOYBEAN 4		

Source: BARI = Bangladesh Agricultural Research Institute BINA=Bangladesh Institute of Nuclear Agriculture.

Mean data of the characters were subjected to multivariate analysis. Univariate analysis of the individual character was done for all characters under study using the mean values (Singh & Chaudhury, 1985) and was estimated using R software. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean range and co-efficient of variation (CV %) were also estimated using R software. Genotypic and phenotypic variances were estimated according to the formula given by Johnson et al. (1955).

Genotypic variances (s^2_g) were obtained by subtracting Error MS from Genotypic MS and dividing by the number of replications.

$$\text{Genotypic variance } (s^2_g) = \frac{\text{GMS} - \text{EMS}}{\text{r}},$$

where GMS = Genotypic mean sum of square, EMS = Error mean sum of square, r = number of replications.

The phenotypic variance (σ^2_p) were derived by adding genotypic variance (σ^2_g) with error variance (σ^2_e).

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e,$$

where,σ^2_g = Genotypic variance, σ^2_e = Error variance.

Genotypic and phenotypic co-efficient of variation were calculated by the formula suggested by Burton et al. (1952).

$$\text{Genotypic co-efficient of variation (GCV \%)} = \frac{\sigma_g}{\bar{X}} \times 100,$$

where σ_g = Genotypic standard deviation, $\bar{X}$ = Population mean

$$\text{Phenotypic co-efficient variation (PCV)} = \frac{\sigma_p}{\bar{X}} \times 100,$$

where σ_p = Phenotypic standard deviation, $\bar{X}$ = Population mean.

Broad sense heritability (Lush, 1943) was estimated by the following formula, suggested by Johnson et al. (1955).

$$\text{Heritability } (H_b\%)\ \frac{\sigma^2_g}{\sigma^2_p} = \times\ 100,$$

where H_b = Heritability in broad sense, σ^2_g = Genotypic variance, σ^2_p = Phenotypic variance.

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1943) and Johnson et al. (1955).

$$\text{Genetic advance (GA)} = K \times \frac{\sigma^2_g}{\sigma^2_p} \times \sigma_p,$$

where K= Selection differential, the value which is 2.06 at 5% selection intensity, σ_p = Phenotypic standard deviation, σ^2_g = Genotypic variance, σ^2_p = Phenotypic variance.

Genetic advance as percentage of mean was calculated from the following formula as proposed by Comstock & Robinson (1952).

$$\text{Genetic advance (\% mean)} = \frac{\text{Genetic advance (GA)}}{\text{Population mean}} \times 100$$

Results and Discussion

The genetic parameter along with coefficient of variation, heritability and genetic advanced of the characters studied are presented in Table 2. The PCV was higher than the corresponding GCV for all the studied traits indicating that, the environmental factors influencing the expression of these characters. The highest PCV was found for seed yield per plant (39.03%) followed by yield per plot (32.85%), pod per plant (28.89%) and plant height (28.22%). The GCV was also found high for the same traits i.e., seed yield per plant (37.36%), yield per plot (27.23%), pod per plant (24.20%) and plant height (24.72%). Guleria et al., (2018) and Barh et al., (2014) reported high GCV and PCV for these traits.

Differences between PCV and GCV were smaller for the trait seed yield per plant, hundred seed weight, days to maturity and days to flowering. Similar results for these characters were obtained by Guleria et al. (2018), Sawale & Vikram (2014), Malek et al. (2014) and Mahbub et al. (2015). Less difference between PCV and GCV denotes that, the environmental effect is less in that trait. The highest difference between PCV and GCV were found for the traits primary branch per plant, plant height and pod per plant indicates that these traits are strongly influenced by environment compared to genotypic effect. Coefficient of variation is an indicator of variability within a population. According to Deshmukh et al. (1986), CV higher than 20% indicates highest diversity, CV between 10 to 20% indicates moderate diversity and less than 10% indicates low diversity. In our findings, greatest diversity was found for the all the studied traits except for days to flowering and days to maturity. This result defines that, all the traits with higher CV retain the sufficient variability for these traits among the studied genotypes. These genotypes could be used for future breeding program for improvement of soybean. The lowest CV of the trait days to flowering and days to maturity indicates that, studied genotypes will not be effective for improvement of these two traits. Phenotypic variance is constituted of two variances: genotypic variance which is heritable and environmental variance (non-heritable).

The magnitude of genotypic variance was found higher than environmental variance for the traits plant height, pod per plant, hundred seed weight and seed yield per plant. It indicates that, genotypic variance is the main contributor to total variation in these traits of the studied genotypes. On the other hand, magnitude of higher environmental variance compared to genotypic variance was observed for the trait days to flowering, days to maturity and primary branch per

Table 2. Estimation of components of variance of the studied traits

Parameters	Range	σ^2p	σ^2g	σ^2e	σ^2g/σ^2e	PCV	GCV
DF	39-48	6.92	3.05	3.87	0.79	6.28	4.16
DM	84-91	7.91	3.86	4.05	0.95	3.20	2.24
PH	21.33-63.33	150.46	115.48	34.98	3.30	28.22	24.72
PBP	2.33-4.65	0.81	0.37	0.44	0.84	25.64	17.38
PPP	10.67-28.67	29.87	20.96	8.91	2.35	28.89	24.20
HSW (g)	8.67-16.33	8.91	7.61	1.3	5.85	24.60	22.73
SYP (g)	4.35-12.10	7.93	7.26	0.67	10.84	39.03	37.36
YP (kg)	2.08-5.80	2.09	1.29	0.80	1.61	22.85	17.23

σ^2p = Phenotypic variance, σ^2g = Genotypic variance and σ^2 e = Environmental variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation. DF = Days of 50% flowering, PH = Plant height (cm), PBP = Primary branches per plant, PPP = Pods per plant, HSW = 100 seed weight (g), DM = Days to maturity and YP = Yield per plot (kg).

plant depicts that, environmental variance plays role for the variation in these traits.

Heritability is an indicator of transferability of particular traits to its progeny. In this study, highest heritability was observed for the trait seed yield per plant (91%) followed by yield per plot (88.65) and hundred seed weight (85.39%); moderate high plant height (76.75%) and pods per plant (70.17%) (Table 3). Low heritability was observed for the traits days to flowering (44.05), days to maturity (48.78) and primary branch per plant (45.95). Teixeira et al. (2017) also reported high heritability for yield and hundred seed weight. Barh et al. (2014) also reported similar magnitude of heritability for these traits.

The genetic architecture of the population can be measured by the idea of estimates of heritability along with genetic advance (Baraskar et al., 2014). High heritability does not mean a high genetic advance for a particular quantitative character. Genetic advance measures the expected genetic progress that would result from selecting the best performance genotypes for a given characters (Allard et al., 1960). Johnson et al. (1955) reported that heritability estimates along with genetic gain would be more rewarding than heritability alone in predicting the consequential effect of selection to choose the best individual. According to Baraskar et al. (2014), genetic advance estimates can be divided into three classes which are high (>20%), moderate (10-19%) and low (<10%). In this study, genetic advance was found high in plant height (19.39). All the other traits showed lower genetic advance ranged from 0.85 to 7.90 (Table 3). Similarly, Desissa (2017) estimated high GA for plant height. Dilnesaw et al. (2013) also observed moderate to low GA for days to flowering, days to maturity and hundred seed weight. High heritability with high genetic advance indicates additive gene effects and high heritability with low genetics advance indicates non-additive gene effects for that considered trait.

In our study, additive gene effect has been observed only for the trait plant height and it indicates the possibility of an effective selection of genotypes by phenotype in early generations. Low genetic advance with low heritability was observed for the trait primary branch per plant, days to flowering and days to maturity also indicates non-additive gene effect for these traits and selection based on this trait will not be effective.

Table 3. Estimation of genetic parameters of different characters of twenty soybean genotypes

Parameters	Heritability (Broad Sense)	Genetic Advance (GA)
DF	44.05	2.39
DM	48.78	2.83
PH	76.75	19.39
PBP	45.95	0.85
PPP	70.17	7.90
HSW (g)	85.39	5.25
SYP (g)	91.62	5.31
YP (kg)	88.65	6.24

Relationship between yield and its component traits

Correlation analyses among the eight characters are presented in Table 4. The phenotypic correlation between traits can be achieved directly through measurements or evaluation between two traits. Despite having genetic and environmental causes, the genetic correlations are heritable and can be used in breeding programs (Cruz et al., 2012). In most of the cases the genotypic correlations were higher than phenotypic correlation, indicating a fairly strong inherent relationship among the traits. Higher genotypic correlation was also reported by Bisinotto et al. (2017).

In this present investigation, days to flowering showed negative correlation with plant height, hundred seed weight and yield per plot whereas correlation was positive with primary branch per plant, pod per plant and days to maturity (Table 4). Khadka et al. (2022) reported positive inter-relation of days to flowering with number of pods, days to maturity and number of branches per plant. Shekhar et al. (2018) also reported positive correlation of days to flowering with days to maturity and negative interrelation with seed yield. This finding is almost parallel with Sulistyo et al. (2018). Similar kinds of results were also reported by others (Baig et al., 2017; Ghiday et al., 2017 and Chavan et al., 2016).

Plant height revealed strong negative correlation with primary branch per plant. Negative inter relation with primary branch per plant also reported by Sulistyo et al. (2018). On the other hand, it has significant positive correlation hundred seed weight and seed yield per plant. This result is in resemblance with Chavan et al. (2016) and Guleria et al. (2018). The positive significant inter relation with yield per plot and plant height indicates that selection for yield through plant height would be effective. Primary branch plant showed strong negative correlation with pod per plant, hundred seed weight, days to maturity and yield per plot. Pod per plant showed strong positive correlation with hundred seed weight, days to maturity and yield per plot. Shekhar et al. (2018) and Chavan et al. (2016) also reported similar kind of result for pod per plant. Interrelation of hundred seed weight was also significantly strong with days to maturity and yield per plot. Days to maturity and yield per plot revealed strong positive correlation. This result is in parallel with Shekhar et al. (2018).

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

Characters		PH	PBP	PPP	HSW	DM	YP
DF	r_g	-0.540**	0.582**	0.112	- 0.297*	0.189	- 0.143
	r_p	-0.198	0.370**	0.060	-0.172	0.004	- 0.084
PH	r_g		- 0.632**	0.188	0.617**	- 0.035	0.464**
	r_p		-0.376**	0.189	0.493**	0.020	0.397**
PBP	r_g			-0.299*	-0.357**	-0.121	-0.422**
	r_p			-0.113	-0.227	-0.021	-0.276*
PPP	r_g				0.631**	0.292*	0.908**
	r_p				0.488**	0.167	0.733**
HSW	r_g					0.597**	0.907**
	r_p					0.396**	0.885**
DM	r_g						0.535**
	r_p						0.383**

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

DF = Days of 50% flowering, PH = Plant height (cm), PBP = Primary branches per plant, PPP = Pods per plant, HSW = 100 seed weight (g), DM = Days to maturity and YP = Yield per plot (kg).

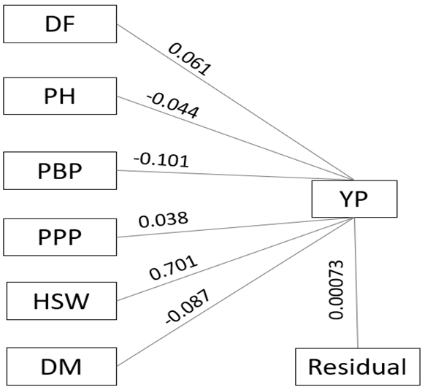

Fig. 1. Direct effect of six important characters on yield

DF = Days of 50% flowering, PH = Plant height (cm), PBP = Primary branches per plant, PPP = Pods per plant, HSW = 100 seed weight (g), DM = Days to maturity and YP = Yield per plot (kg).

In order to find out a clear picture of the inter-relationship of yield and its components direct (Figure 1) and indirect effects were formulated using path coefficients (Table 5). The path coefficient was analyzed using the genotypic correlation only.

Path coefficient analysis revealed that hundred seed weight showed the highest positive direct effect on seed yield followed by pods per plant and days to flowering. Neelima et al. (2017) also reported positive effect of pods per plant on seed yield. Plant height, primary branch per plant and days to maturity showed negative effect on yield. This finding is similar with Baig et al. (2017) and Chavan et al. (2016).

Additionally, the number of pods per plant and 100 seed weight could be the next components to be considered for attaining high response in improvement in soybean. The residual effect observed in the path analysis was 0.00073 indicating that the characters studied contributed 99% of the yield.

Table 5. Indirect effects of six important characters of soybean by path analysis

	Effect Via						Genotypic correlation with yield
	DF	PH	PBP	PPP	HSW	DM	
DF	–	0.024	-0.059	0.004	-0.208	-0.017	-0.143
PH	-0.033	–	0.064	0.007	0.433	0.003	0.464**
PBP	0.036	0.028	–	-0.011	-0.250	0.011	-0.422**
PPP	0.007	-0.008	0.030	–	0.442	-0.025	0.908**
HSW	-0.018	-0.027	0.036	0.024	–	-0.052	0.907**
DM	0.012	0.002	0.012	0.011	0.418	–	0.535**

Residual effect: 0.00073; *and ** indicates significant at 5% and 1% level of probability, DF = Days of 50% flowering, PH = Plant height (cm), PBP = Primary branches per plant, PPP = Pods per plant, HSW = 100 seed weight (g), DM = Days to maturity

Conclusion

Phenotypic coefficient of variation was higher for all the studied traits compared to their corresponding GCV with less difference which indicates environment has less effect on the traits studied. All the characters showed low genetic advance except plant height. Heritability was higher to moderate for all the traits except days to flowering, days to maturity and primary branch per plant. Significant positive genotypic correlations between seed yield and all other characters studied except days to flowering and primary branch per plant. Hundred seed weight and pod per plant would be effective selection criteria because these traits have direct genotypic effect on yield.

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