Genetic Variability, Correlation Co-efficent and Path Analysis in Soybean (*Glycine max* L. Merr.) Genotypes

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Soybean (*Glycine max* L. Merr.) is an important oil seed and grain legume crop in the world and a perspective high potential crop in Bangladesh. It belongs to the family Leguminosae, sub-family papilionaceae and genus Glycine. An experiment was conducted with 14 genotypes of soybean (*Glycine max* L. Merr.) in a randomized complete block design (RCBD) to study the variability, correlation coefficient, and path analysis. Analysis of variance for each trait showed significant differences among the genotypes. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were close to each other for all the characters except the leaf area index, indicating the minor environmental influence on the expression of these characters. High heritability associated with high genetic advance in percent of mean was observed for leaf area index, number of seeds per plant, 100 seed weight, and yield, which pointed out that selection for these characters, would be effective. The significant positive correlation with seed yield was found in pod length and 100 seed weight which revealed that selection based on these traits would improve yield ultimately. Path coefficient analysis evidenced that 50% flowering, pod length, days

to 1st pod maturity, number of seed per plant and 100 seed weight had a positive direct effect on yield per plant. Therefore, importance must be given to these characters in further breeding programs to improve soybean yield.

1. INTRODUCTION

Soybean is a self-pollinated crop that is erect, bushy, leafy, and herbaceous, growing to a height of one to six feet and having a chromosome number of 2n=40. The crop can be cultivated in tropical, sub-tropical, and temperate climates, round all year.

The potential of soybean breeding is enormous since, currently, a small fraction of the existing accessions in germplasm collections contribute to the genetic base of the present cultivars. The expansion of the soybean genetic base may lead to the introduction of new favorable alleles for polygenic traits [1]. It is necessary to partition the observed variability into heritable and nonheritable components which are measured as genotypic and phenotypic coefficients of variation (GCV and PCV), heritability and genetic advance [2]. Traits with a higher range of genetic variability and high heritability would be effective tools to improve seed yield and quality in soybean. Many researchers [3] estimated the genetic variability, broad-sense heritability, and genetic advance parameters.

Phenotypic correlation coefficients between seed yield and yield determining characters have been estimated in soybeans [4]. The influence of the environment can be omitted by estimation of genetic correlations which has also been investigated in soybean [3], and there are just a few reported genetic correlations between seed yield and qualitative characters [4]. Correlation coefficients, although useful in quantifying the size and direction of trait associations, can be misleading if the high correlation between two traits is a consequence of the indirect effect of the traits [5,6]. In soybean, scientists used path analysis, which partitions the genotypic correlations into direct and indirect effects of the traits [7], whereas Arshad et al. [5] and Ghafoor et al. [8] have mentioned the worth of these techniques in other legumes also.

The lack of adequate soybean production in Bangladesh is due to the lack of high yielding and short duration varieties. So, there is an urgent need to develop high-yielding, short-duration varieties of soybean and select of suitable yield contributing characters for further breeding programs. Keeping this view in mind a study was conducted to evaluate the variability of agronomic traits, calculate the correlation between yield and yield contributing characters and assess the direct and indirect effects of traits on yield.

2. MATERIALS AND METHODS

Table 1. Name and origin of 14 soybean genotypes used in the present study

Sl. No.	Genotypes No.	Name/Acc No. (BD)	Origin
1	G1	BADC-SV$_1$	BADC
2	G2	GP: Sj-1	PGRC, BARI
3	G3	BR-13	PGRC, BARI
4	G4	GMOT-43	PGRC, BARI
5	G5	BR-33	PGRC, BARI
6	G6	BR-29	PGRC, BARI
7	G7	BS-29	PGRC, BARI
8	G8	BR-14	PGRC, BARI
9	G9	GP-Djs-9207	PGRC, BARI
10	G10	Asset-95	PGRC, BARI
11	G11	BINA Soybean-1	BADC
12	G12	BADC-SV$_2$	BADC
13	G13	MTD-453	PGRC, BARI
14	G14	BS-13	PGRC, BARI

PGRC=Plant Genetic Resources Centre, BADC = Bangladesh Agricultural Development Corporation, BARI=Bangladesh Agricultural Research Institute

2.1 Soybean Cultivation and Data Collection

Before sowing, seeds were soaked in water. Seedlings of all genotypes were raised to plastic bowls in the net house of Genetics. Recommended cultural practices were taken up before and after sowing the seeds.

The soil was treated with formaldehyde (45%) for 48 hours before filling the polybags and plastic pots to keep the soil free from pathogens. Pots were filled up two days before transplanting. Each pot was filled with 7 kg soil. The pot size was 20 cm in height, 30 cm in top diameter and 20 cm in bottom diameter. When the seedlings become 15 days old, they were transplanted into the polybag for hardening and when the seedlings become 30 days old, they were transplanted in the main plastic pot (1 plant per pot). Necessary watering and intercultural operations were provided as and when required. Experimental soybean plants were treated with Bavistin DF and Cupravit 50WP to prevent unwanted disease problems at 1 g/l respectively, to control insect Malathion 250 EC @ 0.5 ml/l is used.

Harvesting of soybean pods was done after the maturity stage when they turn brown in color. The pods per plant were allowed to ripen and then seeds were collected and stored at 4°C for future use.

2.2 Statistical Analysis

Multivariate analysis was performed on the mean data of the characters. Univariate analysis of the individual character was done for all characters under study using the mean values and was estimated using MSTAT-C computer program. 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 MSTAT-C.

3. RESULTS AND DISCUSSION

3.1 Genetic Variability, Heritability, and Genetic Advance

Presence of narrow gap between PCV and GCV for all the characters under this study, suggested that these traits studied has low environmental influence. The estimates of heritability alone fail to indicate the response to selection [9].

Therefore, the heritability estimates appear to be more meaningful when accompanied by estimates of genetic advancement. Genetic advancement as percent of mean (GAM) was also estimated. The extent of variation among the genotypes in respect of thirteen characters was studied and estimates of mean, range, genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic advance as percent mean for all the characters were studied and the results are interpreted in Table 2.

The Genotypic, phenotypic, and environmental variances observed were 314.011, 314.01 and 0.0001, respectively (Table 2) for days to 50% flowering. It was observed that there was no difference between the genotypic co-efficient of variation (25.84) and the phenotypic coefficient of variation (25.84) (Table 2) indicating minor environmental influence on this character. Therefore, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. Bangar et al. [10] reported that phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) which disagrees with the result of this experiment. The heritability (100%) estimates for this trait was very high, genetic advance (36.50) was at moderate level and genetic advance over percentage of mean (53.24) were found high, indicated that this trait was controlled by additive genes and selection of this character would be effective.

The mean for plant height was recorded 39.29 cm. It ranged from 20.00 cm to 60.33 cm (Table 2). The analysis of variance revealed highly significant differences among the genotypes with respect to plant height. The maximum plant height (60.33 cm) was recorded by the genotype 'Bs-29' and the lowest plant height (20 cm) was recorded by 'BADC SV1'. The genotypic and phenotypic variance was observed 152.442 and 158.68, respectively for plant height with low environmental influence. The phenotypic co-efficient of variation (32.06) was higher than the genotypic co-efficient of variation (31.42), which indicated presence of considerable variability among the genotypes for this trait. The heritability (96.07%) estimates for this trait was high, genetic advance (24.93) was low and genetic advance in per cent of mean (63.45) was found high, revealed that this trait was governed by additive gene. Therefore, selection for this trait will be effective. Plant height exhibited high heritability and high genetic

advance as percent mean in soybean which is similar to the earlier findings by Kumar et al. [11] and Ghodrati [2].

Considerable differences among the genotypes studied in case of number of branches per plant. The maximum number of branches recorded in ASSET-95 and BR-29 genotype showed the minimum number of main branches. The phenotypic variance (4.21) appeared to be higher than the genotypic variance (3.552) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 27.31 and 29.75, respectively which indicated the presence of considerable variability among the genotypes.

The heritability (84.31%) estimates for this trait was high, genetic advance (3.56) was low and genetic advance in per cent of mean (51.67) were found very high, revealed that this trait was governed by additive gene. Selection for this trait would be effective, which is coupled with the findings of Bangar et al. [10].

In case of number of leaves per plant mean sum of square significant (66.742) in soybean indicated a considerable difference among the genotypes studied (Table 2). Maximum number of leaves recorded in BR-13 (76.33) and BR-29 genotype showed the minimum number of leaves (23.33). The phenotypic variance (33.92) appeared to be higher than the genotypic variance (32.819) suggested considerable influence of environment on the expression of the genes controlling this trait. The heritability (96.74%) estimates for this trait was high, genetic advance (11.51) was low and genetic advance in per cent of mean (27.62) were also found low, revealed that this trait was governed by non-additive gene. Therefore, selection would be effective for this trait.

In soybean, a significant mean sum of squares for leaf area index (0.003) indicated a significant difference among the genotypes studied (Table 2). The value ranged from 0.03 to 0.13 with a mean of 0.07. The genotype 'GMOT-43' had highest (0.13) and lowest (0.03) in the genotype 'BADC SV1'. The genotypic variance (0.002) appeared to be higher than the phenotypic variance (0.00) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of

variation and phenotypic co-efficient of variation were 56.24 and 58.03, respectively which were close to each other (Table 2). There was a very little difference between phenotypic and genotypic co-efficient of variation, indicating minor environmental influence on this character. The heritability (93.94%) estimates for this trait was also high, genetic advance (0.08) very low and genetic advance in per cent of mean (112.29) was very high, revealed that this trait was governed by additive gene. So, selection of this trait would be effective.

From the current study we observed that the maximum range for number of flowers per plant was found 43.00 and the minimum was recorded as 19.00 (Table 2) in soybean. The difference between genotypic (91.044) and phenotypic (97.68) variances indicate high environmental influence (Table 2). The difference between phenotypic coefficient of variation (30.64) and genotypic coefficient of variation (29.58) was low, which indicated presence of low variability among the genotypes. The heritability (93.20) estimates for this trait was high, genetic advance (18.98) was low on the other hand, genetic advance in per cent of mean (58.82) were found moderate, revealed that this character was governed by additive gene and selection for this character would be effective. Agarwal et al. [12] also found high heritability and high genetic advance in soybean.

Significant mean sum of square for pods per plant (181.804) indicated that considerable variation for this trait exists in soybean (Table 2). The number of pods per plant was ranged from 11.67 to 37.67 with mean of 24.07. The minimum number of pods per plant was observed in genotype BADC SV1 while maximum number of pods per plant was found in the genotype BINA Soybean-1. The phenotypic variance (92.77) appeared to be higher than the genotypic variance (89.030) suggested considerable influence of environment on the expression of the genes controlling this trait. The heritability (95.96%) estimates for this trait was high, genetic advance (19.04) was low and genetic advance in per cent of mean (79.11) was found very high, revealed that this trait was governed by additive gene. Pods per plant showed high heritability with high genetic advance in soybean which is similar to the earlier findings by Chandel et al. [13].

Table 2. Estimation of genetic parameters in thirteen characters of fourteen genotypes in soybean

Traits	Range	Mean	MS	CV (%)	σ^2_g	σ^2_e	σ^2_P	GCV	ECV	PCV	h^2_b	GA (5%)	GA(% mean)
D50F	47.00-89.00	68.57	628.022**	0.015	314.011	0.0001	314.01	25.84	0.01	25.84	100.00	36.50	53.24
PH	20.00-60.33	39.29	311.121**	6.356	152.442	6.2363	158.68	31.42	6.36	32.06	96.07	24.93	63.45
NMB/P	4.00-10.33	6.90	7.766**	11.785	3.552	0.6612	4.21	27.31	11.78	29.75	84.31	3.56	51.67
NSB/P	7.00-23.33	13.64	66.742**	7.705	32.819	1.1044	33.92	42.00	7.70	42.70	96.74	11.61	85.10
NL/P	23.33-76.33	42.02	66.742**	2.501	32.819	1.1044	33.92	13.63	2.50	13.86	96.74	11.61	27.62
LAI	0.03-0.13	0.07	0.003**	14.286	0.002	0.0001	0.00	56.24	14.29	58.03	93.94	0.08	112.29
NF/P	19.00-43.00	32.26	188.727**	7.987	91.044	6.6392	97.68	29.58	7.99	30.64	93.20	18.98	58.82
NP/P	11.67-37.67	24.07	181.804**	8.038	89.030	3.7436	92.77	39.20	8.04	40.02	95.96	19.04	79.11
PL	3.59-4.85	4.14	0.413**	2.021	0.203	0.0070	0.21	10.89	2.02	11.07	96.67	0.91	22.05
DFPM	49.00-157.00	116.93	4318.368**	0.009	2159.184	0.0001	2159.18	39.74	0.01	39.74	100.00	95.72	81.86
NS/P	23.33-113.00	63.38	2319.890**	5.234	1154.442	11.0055	1165.45	53.61	5.23	53.86	99.06	69.66	109.91
WHS	3.00-10.40	6.78	18.065**	0.147	9.033	0.0001	9.03	44.33	0.15	44.33	100.00	6.19	91.32
YIELD	0.54-1.74	0.96	0.419**	8.590	0.206	0.0068	0.21	47.29	8.59	48.06	96.81	0.92	95.85

D50F = Days to 50% flowering, PH = Plant height (cm), NMBP/P = Number of main Branches per plant, NSB/P = Number of secondary branches per plant, NL/P= Number of leaf/plant, L.A.I= Leaf Area Index, NF/P= Number of flower/plant, NP/P= Number of pod/plant, PL= Pod length (cm), DFPM= Days to 1st pod maturity, NS/P= Number of seed/plant, WHS= Weight of 100 seed (g) and YIELD= Yield ton/ha, MS = mean sum of square, $\sigma^2 p$ = Phenotypic variance, $\sigma^2 g$ = Genotypic variance, $\sigma^2 e$ = Environmental variance, PCV = Phenotypic Coefficient of Variation, GCV= Genotypic Coefficient of Variation and ECV= Environmental Coefficient of Variation

Highly significant mean sum of square (0.413) for pod length in soybean indicated considerable difference among the genotypes studied (Table 2). It ranged from 3.59 to 4.85 cm with a mean of 4.14 cm. The minimum pod length was recorded by the genotype BINA soybean-1 and Genotype BS-29 showed the maximum pod length. The difference between phenotypic variance (0.21) and genotypic variance (0.203) was very low which, suggested that there was no influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 10.89 and 11.07, respectively which indicated presence of considerable variability among the genotypes. The heritability (96.67%) estimates for this trait was high, genetic advance (0.91) was very low and genetic advance in per cent of mean (22.05) was found low, revealed that this trait was governed by non-additive gene. Therefore, selection based on this trait would take long time.

Significant mean sum of square (4318.368) for 1st pod maturity in soybean indicated considerable difference among the genotypes studied (Table 2). It ranged from 49.00 DAS to 157 DAS with a mean of 116.93 DAS. The difference between phenotypic variance (2159.18) and genotypic variance (2159.184) was very low which, suggested that there was no influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 39.74 and 39.74, respectively which were close to each other (Table 2). There was a very little difference between phenotypic and genotypic co-efficient of variation, which also indicating minor environmental influence on this character. The heritability (100%) estimates for this trait was high, genetic advance (95.72) very high and genetic advance in per cent of mean (81.86) was also found very high, revealed that this trait was governed by additive gene. So, selection based on this trait can be done. Iqbal et al. [7] and Bhandarkar (1999) observed that high heritability and high genetic advance in percent of mean for days to maturity which is similar with the findings of the present study.

Significant mean sum of square for number of seeds per plant (2319.890) in soybean indicated existence of considerable variation for this trait (Table 2). The germplasm genotypes differed significantly for this character. The values ranged from 23.33 to 113.00 with a mean of 63.38. The genotype BR-13 had highest number of seeds per plant while it was lowest in the genotype BADC SV1. The phenotypic variance (1165.45) appeared to be higher than the genotypic variance (1154.442) suggested considerable influence of environment on the expression of the of variation genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 53.61 and 53.86, respectively which were close to each other (Table 2). The heritability (99.06%) estimates for this trait was high, genetic advance (69.66) and genetic advance in percent of mean (109.91) was found very high (Table 2), revealed that this trait was governed by additive gene. Therefore, selection for this trait would be effective. Similar findings were reported by Chandel et al. [13].

The mean sum of square for hundred seed weight was found 18.065 in soybean which significantly indicated considerable differences among the genotypes studied (Table 2). The mean hundred seed weight noticed was 6.78 with a range of 3.00-10.40 g. The genotype GMOT-43 showed the minimum hundred seed weight, and the maximum hundred seed weight was recorded in the genotype BADC SV2. The genotypic variance appeared (9.033) to be higher than the phenotypic variance (9.03) suggested considerable influence of environment on the expression of the genes controlling this trait. There was a very little difference between phenotypic 48.06 and genotypic co-efficient of variation 47.29, indicating minor environmental influence on this character. Heritability (100%) estimates for this trait was very high, genetic advance (6.19) was low and genetic advance in per cent of mean (91.32) was found very high, revealed that this trait was governed by additive gene. Selection performed based on this trait would be effective which is coupled with the earlier findings of Kumar et al. [11] and Nooghab et al. [14].

Significant mean sum of square for yield (0.419) in soybean indicated existence of considerable variation for this trait (Table 2). For this trait, the germplasm genotypes differed significantly. The values ranged from 0.54 to 1.74 ton with a mean of 0.96 ton. The genotype BS-29 had highest yield while it was lowest in the genotype MTD-453. The phenotypic variance (0.21) appeared to be higher than the genotypic variance (0.206) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient and phenotypic co-efficient of variation were 47.29 and 48.06, respectively indicating presence of considerable

variability among the genotypes. The heritability (96.81%) estimates for this trait is high, genetic advance (0.92) was very low but genetic advance in percent of mean (95.85) was found very high (Table 2), revealed that this trait was governed by additive gene. Similarly high heritability and high genetic advance was observed in the findings of Swapnil et al. [15].

3.2 Correlation and Path Analysis

Correlation studies along with path analysis provide a better understanding of the association of different characters with fruit yield. So, selection may not be effective unless the other contributing components influence the yield directly or indirectly. Pearson correlation analysis among yield and its contributing characters are shown in Table 3. For clear understanding correlation coefficients are separated into genotypic and phenotypic level in Table 4. The genotypic correlation coefficients in most cases were higher than their phenotypic correlation coefficients indicating the genetic reason of association.

A highly significant and positive association of plant height with days to 50% flowering (0.811 and 0.766) at both the genotypic and phenotypic levels was observed. The correlation of days to 50% flowering with leaf area index (0.763 and 0.712), number of flowers per plant (0.670 and 0.620), number of pods per plant (0.592 and 0.568) and number of seed per plant (0.561 and 0.536) was positive and significant at both the genotypic and phenotypic levels (Table 3). A highly significant and positive association of number of main branches per plant at both the genotypic and phenotypic levels was observed with number of main branches per plant. Similar significant and positive association of number of secondary branches per plant at both the genotypic and phenotypic levels was observed with number of secondary branches per plant (0.935 and 0.905). The number of branches per plant had positive and highly significant correlation with number of branches per plant (0.847 and 0.833) and number of secondary branches per plant (0.983 and 0.972) both at genotypic and phenotypic levels (Table 3). Leaf area index (L.A.I) had also highly significant and positive association with days to 50% flowering (0.763 and 0.712), single pod weight per plant (0.544 and 0.518) and plant height (0.621 and 0.612) (Table 3). Moreover, Number of flowers per plant showed a highly positive association with days to 50% flowering (0.670 and 0.620),

number of secondary branches per plant (0.621 and 0.612) and number of leaves per plant (0.589 and 0.573) at both the genotypic and phenotypic levels (Table 3). Pod length had significant and positive association with number of numbers of secondary branches (0.712 and 0.694), number of leaves per plant (0.717 and 0.697) and number of flowers per plant (0.951 and 0.933) at both the genotypic and phenotypic levels (Table 3). Pod length had significantly positive association with weight of 100 seed (0.637 and 0.27) and yield (0.661 and 0.647) at both genotypic and phenotypic levels (Table 3). Days to 1st pod maturity had highly significant positive association with number of main branches per plant (0.579 and 0.572) and leaf area index (0.603 and 0.590) at both the genotypic and phenotypic levels (Table 3). A highly significant and positive association of number of seed per plant at both the genotypic and phenotypic levels was observed with number of main branches per plant (0.594 and 00.584), number of secondary branches per plant (0.764 and 0.751), number of leaves per plant (0.765 and 0.752), leaf area index (0.621 and 0.604), number of flowers per plant (0.844 and 0.832) and number of pods per plant (0.921 and 0.909). A highly significant and negative association of weight of 100 seed at both the genotypic and phenotypic levels was observed with number of secondary branches per plant (-0.669 and -0.658), number of leaves per plant (-0.669 and -0.652), number of flowers per plant (-0.688 and -0.672) number of pods per plant (-0.793 and -0.781), number of seed per plant (-0.604 and -0.594). For pod length (0.637 and 0.627) and yield (0.567 and 550), however, significant positive associations were found at both the genotypic and phenotypic levels.

A highly significant and positive association of yield at both the genotypic and phenotypic levels was observed with pod length (0.661 and 0.647) and weight of 100 (0.567 and 0.550).

Though correlation analysis indicates the association pattern of components traits with yield, they simply represent the overall influence of a particular trait on yield rather than providing cause and effect relationship. The path coefficient analysis technique was developed by Wright [16] and demonstrated by Deway and Lu [6] facilitates the portioning of correlation coefficients into direct and indirect contribution of various characters on yield. It is standardized partial regression coefficient analysis. As such, it measures the direct influence of one variable

Table 3. Pearson correlation coefficients among different pairs of yield and yield contributing characters for different genotype of soybean

Traits	D50F	PH	NMB/P	NSB/P	NL/P	LAI	NF/P	NP/P	PL	DFPM	NS/P	WHS
PH	0.77**											
NMB/P	0.51	0.27										
NSB/P	0.47	0.19	0.91**									
NL/P	0.44	0.23	0.83**	0.97**								
LAI	0.71**	0.61*	0.59*	0.49	0.43							
NF/P	0.62*	0.45	0.42	0.61*	0.57*	0.51						
NP/P	0.57*	0.50	0.49	0.69**	0.70**	0.50	0.93**					
PL	-0.16	-0.04	-0.17	-0.29	-0.35	0.18	-0.27	-0.31				
DFPM	0.23	0.23	0.57*	0.49	0.48	0.59*	0.33	0.36	0.05			
NS/P	0.54*	0.40	0.58*	0.75**	0.75**	0.60*	0.83**	0.91**	-0.07	0.53		
WHS	-0.35	-0.27	-0.481	-0.66*	-0.65*	-0.23	-0.67**	-0.78**	0.63*	-0.15	-0.59*	
YIELD	0.16	0.17	-0.07	-0.10	-0.09	0.32	0.14	0.04	0.65*	0.38	0.30	0.55*

D50F= Days to 50% flowering, PH= Plant Height (cm), NMB/P= Number of main branch/plant, NSB/P= Number of secondary branch/plant, NL/P= Number of leaf/plant, AI= Leaf area index., NF/P= Number of flower/plant, NP/P= Number of pod/plant, PL= Pod length (cm), DFPM= Days to 1st pod maturity, NS/P= Number of seed/plant, WHS= Weight of 100 seed (g) and YIELD= Yield (ton/ha)

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

Characters	Direct effect	Indirect effect									Genotypic correlation with Yield
		D50F	PH	NMB/P	LAI	NP/P	PL	DFPM	NS/P	WHS	
D50F	0.754	-	0.611	0.426	0.575	0.446	-0.122	0.174	0.422	-0.276	0.163
PH	-0.163	-0.132	-	-0.048	-0.101	-0.083	0.007	-0.037	-0.067	-0.044	0.175
NMB/P	-0.460	-0.260	-0.134	-	-0.274	-0.227	0.081	-0.267	-0.273	0.230	-0.079
LAI	-0.561	-0.428	-0.348	-0.334	-	-0.283	-0.104	0.338	-0.348	0.132	0.333
NP/P	-0.087	-0.052	-0.045	-0.043	-0.044	-	0.028	-0.032	-0.080	0.069	0.051
PL	0.307	-0.049	-0.014	-0.054	0.057	-0.098	-	0.017	-0.025	0.195	0.661
DFPM	0.519	0.120	0.119	0.301	0.313	0.191	0.029	-	0.278	-0.084	0.388
NS/P	0.894	0.502	0.366	0.531	0.555	0.824	-0.072	0.479	-	-0.540	0.321
WHS	0.796	-0.291	-0.217	-0.397	-0.187	-0.631	0.507	-0.128	-0.480	-	0.567

Residual effect: 0.286 D50F= Days to 50% flowering, PH= Plant Height (cm), NMB/P= Number of main branch/plants, LAI= Leaf area index, NP/P= Number of pod/plants, PL= Pod length (cm), DFPM= Days to 1st pod maturity, NS/P= Number of seed/plants, WHS= Weight of 100 seed (g) and YIELD= Yield (ton/ha

upon other. 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.

In path coefficient analysis, the direct effect of a trait on yield of plant and its indirect effect through other characters were computed and the results are presented in Table 4.

Path analysis revealed that days to 50% flowering had positive direct effect (0.754) on yield. Plant height had negative direct effect (-0.163) on yield. Pod length (0.007) influenced the yield per plant indirectly (Table 4). It had a negative indirect effect through day to 50% flowering (-0.132), number of main branches per plant (-0.048), number of seed per pod (-0.101), number of pods per plant (0.083), days to 1st pod maturity (0.037), number of seed per plant (-0.067) and weight of 100 seed (0.044).

Number of branches per plant had negative direct effect (-0.460) on yield. It had a negative indirect effect through day to days to 50% flowering (-0.260), plant height (-0.134), leaf area index (-0.274), number of pods per plant (-0.227), days to 1st pod maturity (-0.267) and number of seed per plant (-0.273). Path analysis revealed that leaf area index had negative direct effect (-0.567) on yield. The leaf area index had an indirect positive influence on the number of days until the first pod matured (0.338) and the weight of 100 seeds (0.132).

The number of pods per plant had a negative direct effect on yield (-0.087), but a positive indirect effect via pod length (0.028) and weight of 100 seeds (0.069) (Table 4).

However, it had indirect negative effects through days to 50% flowering (-0.052), pod length (0.045), number of main branches per plant (-0.043), leaf area index (0.044), days to 1st pod maturity (-0.032) and number of seed per plant (-0.080) (Table 4).

Path analysis revealed that pod length had positive direct effect (0.307) on yield whereas, it showed indirect positive effects on seed yield by leaf area index (0.057), days to 1st pod maturity (0.017) and weight of 100 seed (0.195) showed in (Table 4). Negative indirect effect on seed yield was observed through days to 50% flowering (-0.049), plant height (-0.014), number of main branches per plant (-0.054), number of

pods per plant (-0.098) and number of seeds per plant (-0.025). Harpreet et al. (2007) observed that pod length can serve as reliable variable for selection. Days to 1st pod maturity had the positive direct effect on yield (0.519) and it had positive and indirect influence on seed yield through days to 50% flowering (0.120), plant height (0.119), number of main branches per plant (0.301), leaf area index (0.313), number of pods per plant (0.191), pod length (0.029) and number of seeds per plant (0.278) (Table 4). However, it showed negative indirect effect with yield through weight of 100 seed (-0.084). Path analysis evidenced that Number of seeds per plant had positive direct effect (0.894) on yield whereas, it showed indirect positive effects on seed yield by days to 50% flowering (0.502), plant height (0.366), number of main branches per plant (0.301), leaf area index (0.555), number of pods per plant (0.824) and days to 1st pod maturity (0.479) (Table 4). It showed indirect negative effect on seed yield through pod length (-0.072) and weight of 100 seed (-0.540) showed in (Table 4). Weight of 100 seeds had a direct positive effect on yield (0.796) and an indirect positive effect via pod length (0.507) (Table 4). However, it had indirect negative effects through days to 50% flowering (-0.291), plant height (-0.217), number of main branches per plant (-0.397), leaf area index (-0.187), number of pods per plant (-0.631), days to 1st pod maturity (-0.128) and number of seeds per plant (-0.480) (Table 4). 100 seed weight had positive direct effect on grain yield which is coupled with the earlier findings by Inderjit et al. [17].

4. CONCLUSION

The analysis of variance showed significant differences among the genotypes for all the characters. High heritability coupled with high genetic advance in percent of mean was observed in plant height, number of main branches per plant, leaf area index, number of flowers per plant, pod length, hundred seed weight, branches per plant, number of seed per plant, weight of 100 seed and yield per hectare. Hence, yield improvement in soybean would be achieved through selection of these characters.

● Pod length and weight of 100 seed showed a significant and positive correlation with yield at both genotypic and phenotypic levels. These results suggested that seed yield per plant can be increased by improving these characters. Days to 50% flowering, pod length, days to 1st pod

maturity, seeds per plant, weight of 100 seed showed positive direct effect on yield. So, yield improvement was associated with these characters.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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