

Heritability, Genetic Advance and Path Coefficient Analysis for Grain Yield and its Component Characters in Soybean (*Glycine max* L. Merrill)

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Abstract: *Twenty two promising new and three checks of Soybean (*Glycine max* L. Merrill) genotypes were grown in two successive seasons of 2014/2015 and 2015/2016 to assess the presence of variability for desired traits and amount of variation for different parameters. Genetic parameters, correlations, and partial regressions were estimated for all the traits. Analysis of variance showed significant differences among entries for all the characters. The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for grain yield per plant, biological yield and number of seeds per pod. Broad sense heritability estimates for various traits ranged from 74.62 to 99.73%. Grain yield per plant showed high significant positive genetic and phenotypic correlation with number of pods per plant and number of seeds per pod. Multiple correlations of characters (0.36), via, number of pods per plant, number of primary branches and number of seeds per pod which were significant with grain yield were far from the multiple correlations of all characters (0.96). The total variability calculated through multiple correlation in the population for yield improvement accounted by number of pods per plant, number of primary branches and number of seeds per pod was 36 % compared to 96 % accounted by all other characters. It was concluded that more number of pods per plant, number of primary branches and number of seeds per pod are major yield contributing factors in selecting high yielding soybean cultivars. Highly significant positive correlations, with the highest positive direct effect were observed for the number of pods per plant followed by the number of primary branches per plant. Therefore, the number of pods per plant and number of primary branches per plant can be considered as critical criteria for improving yield.*

Keywords: *Phenotypic, Genotypic, Coefficient, Variation, Genetic advance, Heritability, Path Coefficient, Soybean.*

1. INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is the most important vegetable food sources in the world. In Ethiopia, soybean is an introduced crop and had a higher expansion of cultivated area in recent years, with crop production of 636531 quintal of harvest with average of productivity 19.98 quintal per hectare in 2013/2014 cropping season [1]. National average yield is very low compared with its potential and yields obtained in other soybean producing countries. It is largely grown in the lowlands of the country and constitutes roughly 2-3% of the annual pulse production and plays an appreciable role in human nutrition and health, edible oil, livestock feed and many other industrial and pharmaceutical applications [2].

Understanding the magnitude of existing variability, proper characterization of the most important physiological traits and their interrelationships with yield and yield components would be extremely helpful in the synthesis of most efficient and highly productive genotypes [3]. So, soybean improvement depends on the continuous supply of new germplasm as donors of various genes of agronomic importance. The development of high yielding-cultivars is the main objective of any breeding programs in the world [4]. One of the main objectives of any breeding program is to produce high-yielding and better-quality lines for release as cultivars to farmers. The prerequisite to achieve this goal is to find sufficient amount of variability, in which desired lines are to be selected for further manipulation to achieve the target. Introduction of new populations can be made from one region to the other easily and may be used for further manipulation to develop new breeding lines [5].

Identification of better genotypes with desirable traits and their subsequent use in breeding program and establishment of suitable selection criteria can be helpful for successful varieties improvement program. Analysis of variability among the traits and the association of a particular character in relation to other traits contributing to yield of a crop would be of great importance in planning a successful breeding program [6][7]. Development of high-yielding cultivars requires a thorough knowledge of the existing genetic variation for yield and its components. The observed variability is a combined estimate of genetic and environmental causes, of which only the former one is heritable. However, estimates of heritability alone do not provide an idea about the expected gain in the next generation, but have to be considered in conjunction with estimates of genetic advance, the change in mean value among successive generations [8]. A survey of genetic variability with the help of suitable parameters such as genetic coefficient of variation, heritability estimates and genetic advance are absolutely necessary to start an efficient breeding program [9]. Assessment of the extent of genetic variability within soybean, is fundamental for soybean breeding programs and the conservation of genetic resources, and is particularly useful as a general guide in the choice of parents for breeding hybrids. The objectives of the present study were to assess and evaluate genetic variability of soybean germplasm based on agro-morphological traits.

2. MATERIAL AND METHODS

Twenty two promising new and three checks of Soybean (*Glycine max* L. merrill) genotypes from IITA/Nigeria were used. Gisham, Awassa-95 and Belessa-95 were the checks. Entry number, genotype, seed source, and year are presented in Table 1. The experiment was conducted at Pawe Agricultural Research Center (PARC), North West of Ethiopia from 2014/2015 to 2015/2016 rainfed season in a randomized complete block design (RCBD) with three replications, each plot with four rows of 0.40m width and 5 m row length. Sowing was done by hand drilling at a seed rate of 70 kg/ha. The spacing between plots and replication were 0.40m and 1 m, respectively. Di ammonium phosphate (DAP) fertilizer was applied at the rate of 100 kg/ha. All the cultural practices were performed as recommended. The plant data during the cropping season and after harvesting were recorded. The seed yield per plot and biological yield per plot were measured by taking a net plot of 0.8 m x 5 m or 4 m² and this was used to determine harvest index. All other characters were recorded on a single plant basis by randomly taking five plants from each experimental plot.

Table 1. Entry number, genotype, seed source, and year

Entry No	Genotype	Source	Year	Entry No	Genotype	Source	Year
1	TGX 1987-35F	IITA/Nigeria	2007	14	TGX 1987-40F	IITA/Nigeria	2011
2	TGX 1987-11F	IITA/Nigeria	2007	15	TGX 1987-38F	IITA/Nigeria	2007
3	TGX 1740-2F	IITA/Nigeria	2006	16	TGX 1987-37F	IITA/Nigeria	2007
4	TGX 1987-9F	IITA/Nigeria	2007	17	TGX 1987-14F	IITA/Nigeria	2011
5	TGX 1987-23F	IITA/Nigeria	2007	18	TGX 1987-10F	IITA/Nigeria	2007
6	TGX1987-64F	IITA/Nigeria	2011	19	TGX 1987-65F	IITA/Nigeria	2011
7	TGX 1987-62F	IITA/Nigeria	2011	20	TGX 1989-59F	IITA/Nigeria	2007
8	TGX1987-15F	IITA/Nigeria	2006	21	TGX 1987-18F	IITA/Nigeria	2007
9	TGX 1986-3F	IITA/Nigeria	2005	22	TGX 1987-20F	IITA/Nigeria	2007
10	TGX 1987-36F	IITA/Nigeria	2011	23	GISHAMA	IITA/Nigeria	2005
11	TGX 1987-19F	IITA/Nigeria	2011	24	AWASSA95	IITA/Nigeria	2004
12	TGX 1935-10E	IITA/Nigeria	2005	25	BELESSA95	IITA/Nigeria	2005
13	TGX 1987-34F	IITA/Nigeria	2007				

2.1. Weather Condition

The precipitation and average temperature for the 2014/2015 and 2015/2016 cropping seasons in Pawe Agricultural Research Center farm field are presented in Table 2. Total precipitation in 2014/2015 was 1242.2 mm, while it was 1351.9 mm in 2015/2016.

Table 2. Distribution of rainfall and temperature regimes during the seasons.

Month	Rainfall (mm)		Temperature °C	
	2014/2015	2015/2016	2014/2015	2015/2016
May	181.6	68.7	27.1	27.85
June	132.3	270.3	24.9	24.7

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July	231.2	340.1	23.25	22.95
August	367.8	338.1	22.6	22.9
September	248.6	242.4	23.4	23.3
October	80.5	85.9	24.15	24.5
November	0.2	6.4	23.35	23.6
Total	1242.2	1351.9		

2.2. Character Studied

The characters measured included biological yield per plant (g) (BY), grain yield per plant (g) (GY), plant height (cm) (PH), number of primary branches (NPRB), number of pods per plant (NPP), number of seeds per pod (NSP), Hundred seed weight (g) (HSW), number of days to flower (DF), number of days to maturity (DM), grain filling period (GFP) and harvest index (HI).

2.3. Statistical Analysis

Analysis of variance, using randomized complete block design, was computed for all the characters evaluated using the computer software system of SAS (SAS Institute, 2002).

3. RESULTS

3.1. Phenotypic Variation

The results from analyses of variance over two years for the investigated characteristics are presented in Table 3. Grain yield and some yield component characteristics of the twenty two promising new soybean genotypes and three check cultivars which were introduced from IITA were assessed in a two year study and a high significant variability among the promising soybean genotypes were determined with respect to the studied parameters (Table 4). Effects of cultivar (V) and year (Y) were found to be significant for all the parameters, except for the effect of year of grain yield per plant, biological yield, harvest index, and hundred seed weight. However, the interaction of Y × V was not significant. The mean values of the characteristics studied are shown in Table 5.

Table 3. Analysis of variance form applied for combined data of two seasons

Source of variation	df	MS	Expected MS
Season (s)	s-1	-	-
Rep. within season	s(r-1)	-	-
Cultivars (V)	g-1	MS1	$\sigma^2_e + \sigma^2_{gs} + sr \sigma^2_g$
V × S	(s-1)(g-1)	MS2	$\sigma^2_e + r \sigma^2_{gs}$
Pooled error	S(r-1)(g-1)	MS3	σ^2_e

Table 4. Analysis of variance for biological yield per plant (BY), grain yield per plant (GY), harvest index per plant (HI), Number of primary branches (PRBP), number of pods per plant (NPP), Number of seeds per pod (NSP), hundred seed weight (HSW), plant height (PH), flowering date (DF), maturity date (DM) and grain filling period (GFP) of 25 soybean genotypes grown under field conditions

Source of variance	Mean square										
	BY	GY	HI	PRBP	NPP	NSP	HSW	PH	DF	DM	GFP
Season (S)	0.01	0.47	318.34	2.08**	648.88**	333.75**	16.52	449.31**	187.91**	848.88**	238.01**
Rep. within season	34.68**	7.68**	716.41**	3.32**	144.26**	6.03	4.35	40.61**	22.11**	164.26**	84.86**
Cultivars (V)	15.76**	3.77**	209.58**	1.30**	1053.52**	661.52**	330.25**	635.93**	138.06**	253.52**	177.33**
V × S	0.75	0.01	39.88	0.33	11.70	7.92	17.67	11.46	3.68	13.70	13.51
Pooled error	1.91	0.80	101.07	0.31	6.14	10.10	20.23	11.57	3.65	11.14	13.70

*, ** Significant at 0.05 and 0.01 level, respectively.

Table 5. Variation for 11 characters in 25 soybean genotypes and mean values of check cultivars.

Variable	Range	Mean±SE	Std Dev	F.values for genotype	LSD (P-0.05)	Check cultivars		
						GISHAMA	AWASSA95	BELESSA95
BY	2.00-14.25	6.92±0.79	02.06	08.24**	01.57	6.66	6.32	7.59
GY	0.58-7.65	3.04±0.51	01.09	04.72**	01.02	2.99	2.78	3.41
HI	9.5-84.4	44.23±5.80	10.65	00.39**	11.42	44.88	44.35	45.94
PRBP	1-5	02.47±0.32	00.71	04.28**	00.63	02.17	02.75	02.38
NPP	79-97	79.11±1.96	10.76	4.95**	03.87	65.25	63.33	67.83
NSP	3-4	2.9±0.83	0.86	3.45**	0.61	3.71	2.51	2.9
HSW	24.97-79.20	48.34±2.59	08.42	16.33**	05.11	50.79	51.44	45.44
PH	39-91	64.11±1.96	10.76	54.95**	03.87	62.25	66.33	61.83
DF	106-139	116.12±1.10	05.13	37.80**	02.17	116.75	112.25	119.04
DM	123-178	143.05±1.92	07.36	22.74**	03.79	141.92	140.79	148.17
GFP	12-48	26.93±2.14	06.44	13.74**	04.21	25.71	28.54	29.13

3.2. Promising Soybean Genotypes Vs Standard Cultivars

Comparisons between the promising soybean genotypes and the improved cultivars showed that, in general, promising soybean genotypes were similar to the check cultivars except for number of seed per pod and flowering date. Check cultivar (GISHAMA) has greater number of seed per pod than the promising soybean genotypes. Also, BELESSA95 check was later in flowering than other promising soybean genotypes. The mean values of other characters compared to the check cultivars are presented in Table 5. There was one promising soybean genotype TGX1987-40F that was superior to the check GISHAMA for grain yield per plant. The grain yield and other characters of the superior plant and check cultivars are presented in Table 6. Among yield components, this genotype TGX1987-40F was better than the check in number pods per plant, number seed per pod and number of primary branches.

Table 6. Mean values of grain yield components of examined genotypes of soybean

No.	Genotype	BY	GY	HI	PRBP	NPP	NSP	HSW	PH	DF	DM	GFP
1	TGX 1987-35F	06.12	1.83	29.87	1.67	79.00	2.1	38.51	47.00	131.67	158.67	27.00
2	TGX 1987-11F	05.45	1.85	33.96	2.17	80.50	1.7	39.66	45.50	136.83	160.83	24.00
3	TGX 1740-2F	04.31	01.72	39.95	1.67	84.00	1.7	28.63	44.00	135.67	163.00	27.33
4	TGX 1987-9F	06.85	03.06	44.68	2.67	81.00	2.5	29.06	51.00	113.00	142.33	29.33
5	TGX 1987-23F	05.62	02.34	41.53	2.33	83.50	2.0	32.55	43.50	120.00	134.83	14.83
6	TGX1987-64F	05.87	2.77	47.18	2.50	86.17	2.8	32.49	56.17	115.17	136.67	21.50
7	TGX 1987-62F	05.73	2.94	51.34	3.33	86.33	2.4	38.80	56.33	113.33	134.50	21.17
8	TGX1987-15F	05.21	2.12	40.59	2.33	82.67	2.3	37.54	52.67	113.83	133.50	19.67
9	TGX 1986-3F	04.79	2.37	49.46	2.00	81.50	2.1	44.03	61.50	110.58	137.50	26.92
10	TGX 1987-36F	07.51	2.74	36.43	3.00	88.50	2.2	41.46	58.50	131.33	148.83	17.50
11	TGX 1987-19F	07.07	3.02	42.68	3.50	89.17	2.0	43.15	69.17	116.83	144.27	27.43
12	TGX 1935-10E	11.34	4.95	43.69	2.83	86.17	3.5	46.78	66.17	113.67	150.67	37.00
13	TGX 1987-34F	08.57	03.83	44.68	2.67	69.33	3.5	43.41	69.33	116.83	141.50	24.67
14	TGX 1987-40F	09.62	05.07	52.66	3.50	97.00	4.0	51.68	72.00	113.33	142.50	29.17
15	TGX 1987-38F	06.79	03.41	50.20	2.67	93.33	3.4	46.24	69.33	113.83	140.00	26.17
16	TGX 1987-37F	09.69	04.36	45.00	3.33	93.83	3.7	45.59	63.83	116.50	144.50	28.00
17	TGX 1987-14F	10.69	04.97	46.53	2.17	96.33	3.5	42.80	76.33	114.67	144.33	29.67
18	TGX 1987-10F	10.30	4.42	42.92	2.50	89.33	3.6	40.80	69.33	116.83	141.50	24.67
19	TGX 1987-65F	07.35	02.31	31.40	1.50	92.00	3.2	47.94	72.00	113.33	142.50	29.17
20	TGX 1989-59F	08.71	4.93	56.58	3.17	89.33	2.9	42.71	69.33	113.83	140.00	26.17
21	TGX 1987-18F	09.15	4.73	51.70	3.00	93.83	2.6	46.17	63.83	116.50	144.50	28.00
22	TGX 1987-20F	09.60	4.72	49.22	2.83	86.33	2.8	46.52	76.33	114.67	144.33	29.67
23	GISHAMA	05.77	2.75	47.58	1.50	65.25	3.6	48.19	57.17	118.00	135.00	17.00
24	AWASSA 95	05.31	2.62	49.39	2.67	63.33	1.8	48.72	56.00	109.00	137.83	28.83
25	BELESSA 95	03.97	2.11	53.15	1.67	67.83	3.0	41.66	58.17	125.33	142.67	17.33

3.3. Genetic Variability

In trying to determine the extent to which variation in yield components are responsible for differences in yield among various cultivars, it must be borne in mind that overall variability depends on heritable and non-heritable components. While coefficients of variation measure the magnitude

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of variability present in a population, estimates of heritability and genetic advances are important preliminary steps in any breeding program as they provide information needed in designing the most effective breeding program and the relative practicability of selection. Genotypic variance, phenotypic variance, genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), broad sense heritability, genetic advance and genetic advance expressed as percentage of mean for 11 characters are presented in Table 7.

Table 7. Genetic parameters for some characteristics in soybean genotypes grown during two seasons 2014/15 and 2015/16 under field conditions.

Source of variance	BY	GY	HI	PRBP	NPP	NSP	HSW	PH	DF	DM	GFP
σ_g^2	2.50	0.63	28.28	0.16	107.22	108.93	52.10	104.08	22.40	39.97	27.30
σ_p^2	2.63	0.632	34.93	0.22	114.82	110.25	55.04	105.9	23.01	42.25	29.56
Heritability%	95.24	99.73	80.97	74.62	93.38	98.80	94.65	98.20	97.33	94.60	92.38
GCV (%)	22.86	26.04	12.02	16.28	21.24	35.24	14.93	15.91	4.08	4.42	19.40
PCV (%)	23.42	26.07	13.36	18.85	21.98	35.45	15.35	16.06	4.13	4.54	20.19
GA	3.18	1.63	9.86	0.72	20.61	21.37	14.47	20.83	9.62	12.67	10.35
GAM	45.95	53.57	22.29	28.97	42.28	72.15	29.92	32.48	8.28	8.85	38.42
* Significant at the 0.05 probability level.											

3.4. Estimates of Heritability

The results showed considerable phenotypic and genotypic variances among the genotypes for the traits under consideration. In all traits a large portion of the phenotypic variance was accounted for by the genetic component and the contributions of genetic variance to phenotypic variance were more than 74% (Table 7). The estimates of GCV were high for number of seeds per pod (35.24), grain yield per plant (26.04), biological yield per plant (22.86), number of pods per plant (21.24), grain filling period (19.40), number of primary branches (16.28), and plant height (15.91). The remaining traits recorded moderate to low GCV estimates. The PCV values were higher than GCV values for all the traits which reflect the influence of environment on the expression of traits. The results of heritability indicated that moderate heritability values were recorded for number of primary branches per plant, while high heritability estimates for other yield components (Table 8).

Table 8. Genotypic (*Bold*) and phenotypic correlations among different quantitative characters in soybean.

	BY	GY	HI	PRBP	NPP	NSP	HSW	PH	DF	DM	GFP
BY	1	0.92 **	-0.22 **	0.60 **	-0.63**	0.71 **	0.18 **	0.71 **	-0.16 **	0.42 **	0.66 **
GY	0.98**	1	0.17 **	0.68 **	0.88**	0.77 **	0.27 **	0.55 **	-0.30 **	0.26 **	0.60 **
HI	-0.11 **	0.49 **	1	0.14 **	0.45	0.14 **	0.29 **	-0.34 **	-0.51 **	-0.53 **	-0.18 **
PRBP	0.31 **	0.33 **	0.08 *	1	-0.831**	0.12 **	0.10 **	0.29 **	-0.20 **	-0.05 **	0.24 **
NPP	-0.7.1**	0.91**	-0.78**	0.851**	1	-0.239	0.541	-0.556	-0.091	-0.074	0.56**
NSP	0.53 **	0.52 **	0.08	0.07	0.39	1	-0.06 **	0.42 **	-0.13 **	0.40 **	0.60 **
HSW	0.15 **	0.33 **	0.15 **	0.03	0.67	-0.04	1	0.27 **	-0.41 **	-0.16 **	0.17 **
PH	0.50 **	0.35 **	-0.11 **	0.18 **	-0.53**	0.38 **	0.22 **	1	-0.34 **	0.20 **	0.56 **
DF	-0.12 **	0.15 **	-0.18 **	-0.09 **	0.32**	-0.10 **	-0.33 **	-0.28 **	1	0.59 **	-0.19
DM	0.28 **	0.15 **	-0.20 **	0.006	0.41**	0.33 **	-0.13 **	0.17 **	0.51 **	1	0.68 **
GFP	0.41 **	0.31 **	-0.09 **	0.08	0.73**	0.46 **	0.12 **	0.42 **	-0.21	0.73 **	1
*, ** Significant at 0.05 and 0.01 level, respectively											

3.5. Estimates of Expected Genetic Advance

The expected genetic advance values for 11 characters of the genotypes evaluated is presented in Table 7. These values are also expressed as percentage of the genotypes mean for each character so that comparison could be made among various characters, which had different units of measurement. High heritability along with high genetic advance is an important factor for predicting the resultant effect for selecting the best individuals. Number of seeds per pod, grain yield per plant, biological yield, number of pods per plant, grain filling period, plant height, and hundred seed weight had high

heritability accompanied with high genetic advance, while maturity date, flowering date and harvest index had high heritability coupled with low genetic advance.

3.6. Genotypic and Phenotypic Correlations among Characters

The phenotypic and genotypic correlations for morpho-agronomic traits are presented in Table 8. Number of pods per plant and number of seeds per pod which are the main component of grain yield gave the highest positive significant phenotypic and genotypic association with grain yield per plant implying that improving these characters could result in high grain yield. Since yield of grain is the product of number of pods per plant, number of seeds per pod, and hundred seed weight, all assume importance in efforts to attain new levels of productivity in soybean. Number of primary branches per plant had a highly significant genotypic correlation with grain yield but had low phenotypic correlation. The significant positive correlation of primary branches per plant with yield per plant has been reported by Arshad [10] and that of number of pods per plant and number of seeds per pod by Baraskar [11]. Physio-morphological trait, i.e. plant height ranked second after yield components (Number of pods per plant, number of seeds per pod and number of primary branches per plant) in their positive associations with grain yield. A positive association between grain yield and grain filling period was obtained. On the contrary, grain yield had strong negative correlation ($P < 0.01$) with days to flowering.

3.7. Multiple Correlation and Regression Analysis

In order to determine the effect of morphological traits on grain yield, multiple correlation analyses were carried out (Table 9). The joint association through multiple correlations of all characters studied with yield was highly significant. Multiple correlations of characters (0.36), *via* number of pods per plant, number of primary branches and number of seeds per pod, which were significant with grain yield were far from the multiple correlation of all characters (0.96).

The significance of partial regression coefficients was also tested (Table 10). Partial regression analysis of grain yield on the basis of all yield components are given in Table 10. Yield showed a significant partial regression coefficient with number of pods per plant, number of primary branches and flowering date. The selection of best regression equation done through backward elimination procedure showed that number of pods per plant, number of primary branches, number of seeds per pod and flowering date were the most effective variables contributing to the grain yield. The partial regression coefficients of number of pods per plant (0.584), number of primary branches (0.47) and number of seeds per pod (0.05) were significant (Table 10).

Table 9. Multiple correlation analysis of grain yield per plant on the basis of all yield components (Col. 1) and on the basis of number of primary branches and number of seeds per pod (Col. 2)

	Col. 1	Col. 2
Multiple correlation		
Coefficient of determination (R^2)	0.9635	0.3638
Adjusted R-square	0.9629	0.3616
Standard error	0.2214	0.8773

** Significant at 0.01 Level

Table 10a. Partial regression analysis of grain yield with its components in soybean genotypes

Yield component	Partial regression coefficient (B)	S.E (B)	"t"
Number of Primary branches	0.0584 **	0.01534	3.81
Number of pods per plant	0.0362**	0.01301	2.72
Number of seed per pod	0.00244*	0.00109	2.24
Hundred seed weight	0.00004	0.00115	0.41
Plant height	-0.0008	0.0010	-0.81
Flowering date	0.0038 *	0.0016	2.32
Maturity date	0.0030	0.0023	1.27

*, ** Significant at 0.05 and 0.01 level, respectively

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Table 10b. Partial regression analysis of grain yield with Number of primary branches and number of seeds per pod in soybean genotypes

Yield component	Partial regression coefficient (B)	S.E (B)	“ t”
Number of pods per plant	0.584*	0.0301	2.72
Number of primary branches	0.470**	0.0514	9.15
Number of seeds per pod	0.050* **	0.003	15.13

*, ** Significant at 0.05 and 0.01 level respectively

3.8. Path coefficient Analysis

Partitioning path correlation coefficients into direct and indirect effects provides information on the actual contribution of independent variables with respect to a dependent variable. The present study showed a maximum direct effect on yield for the number of pods per plant (NPP), which influences grain yield per plant (GY) directly in a positive direction, followed by number of branches per plant (NPRB), hundred seed weight (HSW), plant height (PH), harvest index (HI) and grain filling period (GFP) (Table 11).

Days to flowering (DF) was negatively correlated with yield per plant (GY). Again, biological yield (BY), number of seed per pod (NSP), days to flowering (DF) and days to maturity (DM) had direct negative effects on yield.

Table 11. Estimation of path coefficients by partitioning phenotypic correlations into direct and indirect effects (bold values indicate the direct effect)

TRAIT	BY	HI	PBRP	NPP	NSP	HSW	PH	DF	DM	GFP	GY
BY	-0.277	-0.0120	0.472	-0.128	-0.0401	-0.0399	0.0495	0.2756	0.0692	-0.0120	0.92**
HI	0.3065	0.0455	-0.1322	-0.4131	-0.094	0.0610	0.0214	-0.001	-0.052	0.0249	0.17**
PRBP	0.0218	0.0249	1.973	2.387	0.0661	0.0728	-0.0112	0.1592	0.0966	0.0029	0.68**
NPP	0.0661	0.0246	1.640	2.848	0.0661	0.0605	-0.0049	0.0905	0.0694	0.0019	0.88**
NSP	0.0401	-0.0227	0.472	0.4131	-0.277	0.00575	0.00732	-0.0427	0.0032	0.00166	0.77**
HSW	0.1381	0.0232	1.067	1.452	0.1381	0.0728	0.00154	0.3065	0.0327	0.00166	0.27**
PH	-0.302	0.0010	-0.1461	-0.1310	-0.0303	-0.0122	0.067	-0.749	-0.0398	0.00004	0.55**
DF	-0.0119	-0.014	-0.1796	-0.0119	-0.0119	-0.0116	0.0505	-0.995	-0.0502	-0.00135	-0.30**
DM	0.0072	-0.0119	1.097	-1.581	0.0072	0.0563	0.0214	-0.4001	-0.125	-0.0031	0.26**
GFP	0.0155	0.1381	-0.1461	0.0072	-0.0174	0.0655	-0.0112	-0.0726	0.0779	0.0049	0.60**

Residual effect = 0.274

Note: * and ** indicates significant at 5% and 1% probability level, respectively, biological yield per plant (g) (BY), grain yield per plant (g) (GY), plant height (cm) (PH), number of primary branches (NPRB), number of pods per plant (NPP), number of seeds per pod (NSP), Hundred seed weight (g) (HSW), number of days to flower (DF), number of days to maturity (DM), grain filling period (GFP) and harvest index (HI).

4. DISCUSSION

The significant differences among soybean genotypes in the investigation indicate the presence of genetic variability in the material used and provide a good opportunity for yield improvement. Grain yield and other characters exhibited stability across the seasons since the significance of genotype × environment interaction was not detected and the differences among genotypes were obvious (Table 4). This appears to show that further improvement through selection for all characters studied could be effective. High ratios of the genotypic variance to phenotypic variance for biological yield, grain yield per plant, number of pods per plant, number of seeds per pod, hundred seed weight, plant height, flowering date, maturity date and grain filling period indicate the existence of immense inherent variability that remains unaltered by environmental conditions among the genotypes, which in turn is more useful for exploitation in selection and hybridization programs.

Although the genotypic coefficient of variation showed the extent of genetic variability present in the genotypes for various traits, it does not provide full scope to assess the variation that is heritable. Heritable variation is useful for permanent genetic improvement [12]. The most important function of the heritability in the genetic study of quantitative characters is its predictive role to indicate the reliability of the phenotypic value as a guide to breeding value [13][14]. The genotypic coefficient of variation along with heritability estimates provide reliable estimates of the amount of genetic advance to be expected through phenotypic selection [15]. High heritability estimates for grain

yield, number of seeds per pod, plant height and hundred seed weight indicate a high response to selection in these traits [16] and this results were also reported by Dhanwani [17] and Rashid [18] which support the present findings. Heritability and genetic advance are important selection parameters. The estimate of genetic advance is more useful as a selection tool when considered jointly with heritability estimates [19]. The estimates of genetic advance help in understanding the type of gene action involved in the expression of various polygenic characters. High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action [19]. Thus the heritability estimates will be reliable if accompanied by high genetic advance.

High heritability accompanied with high genetic advance as percent of the mean in case of grain yield per plant, number of seeds per pod, biological yield, plant height, grain filling period, hundred seed weight and number of primary branches indicate that these are simply inherited traits and most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. Similar findings have been reported by some authors [18]. However, maturity date, flowering date and harvest index had high heritability coupled with low genetic advance indicates non-additive gene effects.

From the above discussion, hundred seed weight, grain yield per plant, number of seeds per pod, biological yield, and plant height were shown to have high to moderate genotypic variance, high to moderate heritability and greater genetic gain. Selection can therefore be based on these characters and their phenotypic expression would be a good indicator of their genotypic potentiality. The remaining traits recorded lower scores in the three genetic parameters considered in this study and therefore offered less scope for selection as they were much more under the influence of the environment. An understanding of inter-character correlation is essential to successful selection of useful genotypes from the whole population but intensive selection for any characteristic might result in losses in others [19]. The magnitude of the genotypic and phenotypic correlations and their utilization in the selection had been stated by a number of researchers [20] [21]. Genotypic correlation coefficient offers a measure of the genetic association between characteristics and may provide an important criterion of the selection procedures [22]. Genotypic correlation coefficient values were greater for most of the characters than their corresponding phenotypic correlation coefficient values, indicating inherent association of the characters. Positive significant associations were obtained between grain yield and plant height because these tall lines generally excelled in their capacity to support seed growth by stem reserve mobilization [23]. Therefore, selection for tall plants tends to increase grain yield per plant. The present study suggests that a positive association between grain yield and grain filling period and a negative association with days to flowering were obtained. Previous studies have confirmed this result by Dilnesaw [20] and Sureshrao [24], which means that early flowering genotypes with adequate grain filling period escape terminal moisture stress and, thus give better grain yield. The yield components exhibited varying trends of association among themselves. Plant height showed positive significant correlations with number of seed per pod. The significant positive correlation of plant height with number of seed per pod has been reported by Islam [22]. To evaluate the correlation between variables, it is important to number of seed per pod this "magnitude" or "strength" as well as the significance of the correlation. It expresses the amount of common variation between the two variables. The estimate of determination (R^2) indicates that the total variability accounted by all the characters considered together was 96 %, whereas 36 % of the total variability for yield per plant could be accounted if selection was based only on number of pods per plant, number of primary branches and number of seeds per pod indicating that more emphasis should be laid on the improvement of these two components for increasing the grain yield in soybean.

Partitioning path correlation coefficients into direct and indirect effects provides information on the actual contribution of independent variables with respect to a dependent variable. The present study showed a maximum direct effect on yield for the number of pods per plant (NPP), which influences grain yield per plant (GY) directly in a positive direction, followed by number of branches per plant (NPRB), hundred seed weight (HSW), plant height (PH), harvest index (HI) and grain filling period (GFP) (Table 11). These characters have direct positive effects on yield per plant (GY), indicating that these are the main contributors to yield for soybean plants. Therefore, during phenotypic selection the main emphasis should be given to these traits for producing high yielding soybean genotypes. These results are in agreement with other studies of Malik [25] and Jain [26].

Days to flowering (DF) was negatively correlated with yield per plant (GY). Again, biological yield (BY), number of seed per pod (NSP), days to flowering (DF) and days to maturity (DM) had direct negative effects on yield. This result demonstrates that for soybean selection on the basis of these traits might lead to a yield compromise [27]. Sharma [28] reported that days to maturity and days to flowering contributed mostly to the seed yield. Differences between studies might be due to the influence of environmental factors [27]. Biological yield (BY), number of seed per pod (NSP) and days to maturity (DM) were positively correlated with yield per plant (GY), but the direct effect on yield per plant (GY) was positive. This negative effect could be due to the fact that any negative indirect effects nullified any direct positive effects that biological yield (BY), number of seed per pod (NSP) and days to maturity (DM) might have on yield. The residual effect on seed yield/plant was low and this indicates that the traits under study could be used to determine any effects on seed yield [29]. The above information suggests that a highly significant positive correlation, with the highest positive direct effect were observed for the number of pods per plant (NPP) followed by the number of primary branches per plant (NPBP). Therefore, the number of pods per plant (NPP) and number of primary branches per plant (NPBP) can be considered as critical criteria for improving yield. Similar conclusions were found in other studies [25] [26].

5. CONCLUSION

The present study showed that grain yield per plant had strong and positive genotypic correlation with number of pods per plant, number of primary branches and number of seeds per pod. Multiple correlations indicated that the total variability accounted by these traits was 36.38 %. Regression analysis also indicated number of pods per plant, number of primary branches and number of seeds per pod as the most effective variables contributing to the grain yield. So, it is concluded that these three traits may be considered as the selection criteria for the improvement of grain soybean.

Yield in soybeans is a complex polygenic character, so direct selection based on yield might not give positive results without giving due consideration to genetic background. Importantly, correlation analysis can help when examining selection criteria for improving yield through indirect selection of its component traits, which are highly correlated. Considering the inter-relationships studied and path analysis of the various component characters with seed yield and among themselves, it is clear that number of pods per plant (NPP), number of branches per plant (NPRB), hundred seed weight (HSW), plant height (PH), harvest index (HI) and grain filling period (GFP) are important traits to be considered when breeding to improve the yield of soybean.

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