

DIVERSITY AND ASSOCIATION ANALYSIS FOR YIELD CONTRIBUTING AND MORPHOLOGICAL TRAITS IN SOYBEAN [*GLYCINE MAX* (L.) MERRILL]

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ABSTRACT

Information is derived from data on six yield-related morphological traits in sixty genotypes of soybean. All the genotypes showed considerable amount of variation in their mean performances with respect to the characters studied, indicates presence of sufficient variability and scope for further selection and breeding superior and desirable genotypes. PCV ranged from 15.38 (no. of nodes per plant) to 20.97 (no. of pods per node). High heritability (>60%) was recorded for no. of pods per node (82.29%), plant height (60 DAS) (65.96%), plant height (At maturity) (65.725) and no. of pods per plant (65.21%), indicating the additive type of gene action for these traits. Grain yield had significant and positive correlation with no. of pods per plant (0.39), no. of branches per plant (0.34) and plant height (60 DAS) (0.31), suggests that selection can be practiced for these traits to improve seed yield in soybean. Path coefficient analysis also confirmed that plant height (60 DAS) exhibited maximum positive direct effect (0.342) on grain yield along with no. of branches per plant (0.204) and no. of pods per plant (0.177), indicating importance of these characters.

INTRODUCTION

Legumes play a critical role in natural ecosystems, agriculture and agro forestry, where their ability to fix nitrogen in symbiosis makes them excellent colonizers of low-N environment, economic and environmentally friendly crop, pasture and tree species. Soybean is an economically important legume and called "miracle crop" of the 21st century and grows in tropical, subtropical and temperate climates. Taxonomically, soybean belongs to the genus *Glycine* which is divided into two subgenera, *Glycine* and *Soja*. The cultivated soybean (*Glycine max* (L.) Merrill) (2n=40) comes under the subgenus *Soja* (Moench). Soybean has the highest protein content (40 to 42%) of all other food crops and 18 to 22 per cent oil content, comprising high per cent of unsaturated fatty acids (Akram *et al.*, 2011) and rich in lycine and vitamins A, B and D. So it is highly desirable in the human diet (Antalina, 1999).

Soybean is a wonderful crop gifted by nature to mankind (Mahbub *et al.*, 2015) but often it faces the problem of low yield because of lodging, pod shattering and some other constraints (Ariyo, 1995). Seed yield is the primary objective of any crop improvement programme. Since seed yield is a polygenic character, it is influenced by a large number of other component characters (Ulaganathan and Nirmalakumari, 2014). For improvement in seed yield, it is essential to study of genetic variation, heritability and genetic advance of relative crop species for proper understanding and their manipulation in any crop improvement programme

(Dong *et al.*, 2001). Similarly, the correlation and path analysis studies are of great help in formulating efficient scheme of multiple traits selection, as they provide means for direct and indirect selection of component characters (Iqbal *et al.*, 2003 and Arshad *et al.*, 2006). Thus, knowledge of genetic variability, heritability, genetic advance, correlation and path coefficient is essential for a breeder to choose best genotypes and to decide the correct breeding methodology for crop improvement. With these objectives, the present study was undertaken for the genetic improvement on soybean.

MATERIALS AND METHODS

The research work was conducted during *kharif* 2013 at the Pulses Research area of Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana. The experimental material (Table 1) was sown in a randomized complete block design with three replications, each having three rows per genotype with row length of 3 meter and spacing of 45 cm between the rows and 5 cm within the rows. The recommended fertilizers and cultural practices were followed to raise the crop. Observations were recorded for plant height (60DAS) (cm), plant height (At maturity) (cm), number of branches per plant, number of nodes per plant, number of pods per plant, number of pods per node and seed yield (g/plant).

Statistical methods

Significance of various observations was tested using standard statistical methods. Analysis of variance was calculated by Panse and Sukhatme (1985). The GCV and PCV were estimated by the formula suggested by Burton and Devane (1953). Heritability in broad sense was calculated by the formula given by Lush (1949) and genetic advance was computed by the formula used by Miller *et al.* (1958). The statistical analyses were carried out on the basis of mean of five competitive plants. The phenotypic and genotypic correlation coefficients and path coefficients were worked out by the formula described by Dewey and Lu (1959). The estimated values were compared with table values of correlation coefficient to test the significance of correlation coefficient prescribed by Fisher and Yates (1963).

RESULTS AND DISCUSSION

The analysis of variances indicated the existence of significant differences among the genotypes studied revealing that sufficient variability is present for the different characters and selection would be effective to develop the varieties with desired forms of crop plants.

The development of an effective plant breeding programme depends on the existence of genetic variability. According to Agawane and Parhe (2015), seed priming also influenced the seed yield and yield contributing characters of soybean. They exhibited that seeds primed with GA3 recorded significantly higher germination percentage over the untreated control.

Choudhary *et al.* (2014) demonstrated that application of 60 ppm S and 5 ppm Zn should be used for improvement of yield and quality traits of soybean grain. Similarly, Meena and Ghasolia (2013) reported that application of FYM in the field@ 5 t/ha are better to increase microbial population as well as yield attributes of soybean in the field. In the present study, the estimates of coefficients of phenotypic variation were higher than their respective genotypic coefficients for all the characters studied indicate the role of environment in expression of characters (Table 2). Genotypic coefficients of variation ranged from 11.63 to 18.61 whereas phenotypic coefficient of variation ranged from 15.38 to 20.97 among various parameters studied. The maximum extent of PCV and GCV was exhibited by grain yield (26.93 and 25.38) and among morphological traits, highest value was shown by number of pods per node (20.97 and 18.61) followed by number of branches per plant (20.52 and 16.20) and number of pods per plant (20.01 and 16.15). The high magnitude of phenotypic variation were composed of high genotypic coefficient of variations and less of the environment variations, which indicated high genetic variability for different traits and less influence of environment. This suggests that selection can be effective on the basis of phenotype alone with equal probability of success. Bhat and Basavaraja (2011) reported moderate values of GCV and PCV for plant height. Shivakumar (2008) also reported moderate PCV and GCV estimates for plant height and high values for seed yield per plant. Similar findings for seed yield per plant were also reported by Aditya *et al.* (2011).

Table 1: List of genotypes studied

S. No.	Genotype	S. No.	Genotype	S. No.	Genotype
1	SL1096	21	SL1152	41	SL1172
2	SL1104	22	SL1153	42	SL1173
3	SL1113	23	SL1154	43	SL1174
4	SL1116	24	SL1155	44	SL1175
5	SL1117	25	SL1156	45	SL1176
6	SL1119	26	SL1157	46	SL1177
7	SL1120	27	SL1158	47	SL1178
8	SL1121	28	SL1159	48	SL1179
9	SL1122	29	SL1160	49	SL1180
10	SL1123	30	SL1161	50	SL1181
11	SL1124	31	SL1162	51	SL1182
12	SL1143	32	SL1163	52	DS15-2
13	SL1144	33	SL1164	53	DS12-13
14	SL1145	34	SL1165	54	PS1477
15	SL1146	35	SL1166	55	SL295
16	SL1147	36	SL1167	56	SL525
17	SL1148	37	SL1168	57	SL744
18	SL1149	38	SL1169	58	SL900
19	SL1150	39	SL1170	59	SL955
20	SL1151	40	SL1171	60	SL958

Table 2 : Genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability (h^2) and genetic advance (GA) estimated for different characters

S. No.	Character	Mean of genotypes	Range	GCV	PCV	h^2 (%)	GA (% of mean)
1	Plant height (60DAS) (cm)	47.70	32.7-63.0	12.77	15.73	65.96	21.37
2	Plant height (At maturity) (cm)	64.00	41.5-85.7	14.39	17.74	65.72	24.02
3	No. of branches per plant	8.20	4.7-12.4	16.20	20.52	59.68	25.77
4	No. of nodes per plant	13.90	10.2-18.1	11.63	15.38	57.21	18.13
5	No. of pods per plant	71.90	45.8-101.2	16.15	20.01	65.21	26.87
6	No. of pods per node	5.20	2.70-7.36	18.61	20.97	82.29	34.78
7	Seed yield (g/plant)	12.45	4.92-20.60	25.38	26.93	88.84	49.28

Table 3 : Correlation coefficients for all possible pair of characters

S. No.	Character	Plant height(60DAS)(cm)	Plant height (At maturity) (cm)	No. of branches/plant	No. of nodes/plant	No. of pods/plant	No. of pods/node	Seed yield (g/plant)
1	Plant height (60DAS) (cm)	-	0.06	0.03	-0.14	-0.11	0.30	-0.70
2	Plant height (At maturity) (cm)	0.66**	-	-0.21	-0.18	-0.12	-0.04	0.05
3	No. of branches per plant	0.03	0.06	-	0.07	-0.17	0.44	0.07
4	No. of nodes per plant	0.05	0.32**	0.26**	-0.99	0.20	0.17	
5	No. of pods per plant	0.24**	0.03	0.20**	0.16*	-	0.17	0.48
6	No. of pods per node	0.30**	-0.10	-0.01	-0.35**	0.57**	-	-0.17
7	Seed yield (g/plant)	0.31**	0.05	0.34**	0.14	0.39**	0.22**	-

Critical value of $\geq 5\% \geq 0.15^*$ and that at $1\% \geq 0.19^{**}$; The values above diagonal are genotypic correlations and below are phenotypic correlation

Table 4a : Path analysis for seed yield based on phenotypic correlations among different traits in 60 soybean genotypes

S. No.	Character	Plant height (60 DAS) (cm)	Plant height (At Maturity) (cm)	No. of branches per plant	No. of nodes per plant	No. of pods per plant	No. of pods per node	Correlation with seed yield
1	Plant height (60DAS) (cm)	0.342	-0.048	0.006	0.001	0.043	0.007	0.31**
2	Plant height (At maturity) (cm)	0.224	-0.074	0.012	0.006	0.006	-0.002	0.05
3	No. of branches per plant	0.011	-0.004	0.204	0.005	0.036	0	0.34**
4	No. of nodes per plant	0.017	-0.024	0.053	0.017	0.029	-0.008	0.14
5	No. of pods per plant	0.084	-0.002	0.041	0.003	0.177	0.013	0.39**
6	No. of pods per node	0.103	0.007	-0.002	-0.006	0.1	0.022	0.22**

Table 4b: Path analysis for seed yield based on genotypic correlations among different traits in 60 soybean genotypes

S. No.	Character	Plant height (60 DAS) (cm)	Plant height (At Maturity) (cm)	No. of branches per plant	No. of nodes per plant	No. of pods per plant	No. of pods per node	Correlation with seed yield
1	Plant height (60DAS) (cm)	0.547	-0.187	0.008	-0.024	0.012	0.072	-0.7
2	Plant height (At maturity) (cm)	0.408	-0.25	0.015	0.124	0.001	-0.036	0.05
3	No. of branches per plant	0.02	-0.016	0.232	0.113	0.016	0.007	0.07
4	No. of nodes per plant	-0.042	-0.099	0.084	0.041	0.008	-0.106	0.17
5	No. of pods per plant	0.168	-0.005	0.093	0.06	0.314	0.164	0.48
6	No. of pods per node	0.185	0.043	0.008	-0.157	0.031	0.213	-0.17

The coefficient of variation indicates only the extent of variability existing for various characters, but does not give any information about the heritable portion of it. Therefore, it is essential to know about the heritability. In the present investigation, heritability in broad sense was calculated for all characters under study and is presented in table 2. Heritability is classified as high (above 60%) and low (below 60%). High estimate of heritability were exhibited for grain yield (88.84%) followed by number of pods per node (82.29%), plant height (60 DAS) (65.96%), plant height (At maturity) (65.72%) and number of pods per plant (65.21%). This suggests that selection can be practiced by using these traits to improve grain yield in soybean. In a similar study, Karasu *et al.* (2009) observed moderate to low heritability estimates for plant height and number of pods per plant. Results of present study confirm the findings of Malik *et al.* (2006) and Ramteke *et al.* (2010) who reported high heritability for seed yield per plant.

The heritability estimate along with genetic advance is more useful than the heritability alone in predicting the resultant effect of selecting the best individual genotype as it suggests the presence of additive gene effects (Johnson *et al.* 1955). High heritability coupled with high genetic advance as per cent of mean was recorded for seed yield per plant, number of pods per node, number of pods per plant and plant height, indicating the presence of additive type of genetic variability for these traits. These types of characters could be improved

by mass selection and breeding methods based on progeny testing. These results are in conformity with the reports of Dixit *et al.* (2002), Bangar *et al.* (2003) and Iqbal *et al.* (2003) for seed yield per plant.

Phenotypic and genotypic correlations among all characters studied were estimated and are shown in table 3. The estimates of genotypic correlation coefficients were generally higher than the phenotypic correlation coefficients (Nagarajan *et al.* 2015) indicating the greater contribution of genetic factor in development of the dependent trait *i.e.* yield. Therefore, results have been discussed only on the basis of phenotypic correlation coefficients. The grain yield had significant and positive correlation with number of pods per plant (0.39), number of branches per plant (0.34), plant height (60 DAS) (0.31) and number of pods per node (0.22). Positive correlation of grain yield with plant height was supported by the study of Ramana *et al.* (2000), Mukhekar *et al.* (2004), Cicek *et al.* (2006) and Malik *et al.* (2007). In addition, significant and negative association was observed number of nodes per plant with number of pods per node (-0.35). The negative correlation is hypothesized to be due to either tight gene linkages or pleiotropy or both (Brim and Burton, 1979). However, the genetic linkages can be broken by large population of segregants. According to NeWall and Eberhart (1961) when two characters show negative phenotypic and genotypic correlation it would be difficult to exercise simultaneous

selection for these characters in the development of a variety. Hence, under such situations, judicious selection programme might be formulated for simultaneous improvement of such important developmental and component characters. In terms of the present investigation, plants with more number of pods per plant, more number of branches per plant, average plant height (60 DAS) and more number of pods per node likely to produce more yield as they are positively associated with seed yield.

Correlation studies reveal only the general relationship between any two variables without unfolding the underlying cause of such association. As many variables are included in correlation studies, the indirect effects of other variable become confounded. In such a situation, path coefficient analysis is useful in finding out direct and indirect causes of associations and allows a precise perception of specific forces acting to produce a given correlation. The path coefficient analysis on phenotypic basis (Table 4a) and genotypic basis (Table 4b) revealed that plant height (60 DAS) exhibited maximum positive direct effect (0.342 and 0.547) on grain yield followed by number of branches per plant (0.204 and 0.232), number of pods per plant (0.177 and 0.314) and number of pods per node (0.022 and 0.213), respectively. Ghodrati *et al.* (2013) found the highest positive effect of total dry matter on grain yield per plant. Malik *et al.* (2007) and Karnwal and Singh (2009) also found direct effect of number of pods per plant and plant height on grain yield per plant. On the other hand, plant height (At maturity) exhibited negative direct effect on grain yield with a value of -0.074 (on phenotypic basis) and -0.250 (on genotypic basis), showed minimal negative direct effect on grain yield. Path analysis revealed that plant height (60 DAS), number of branches per plant, number of pods per plant and number of pods per node are the important yield component traits which can be strategically used to improve the yield of soybean grains.

Thus, the soybean lines, which are diverse at genetic level and have significant correlation with seed yield and have direct effect on seed yield, should be used for future breeding programme.

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