The Bioscan 11(2): 965-970, 2016 (Supplement on Genetics and Plant Breeding) www.thebioscan.com
AN INTERNATIONAL QUARTERLY JOURNAL OF LIFE SCIENCES

ASSESSMENT OF GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS FOR YIELD AND ITS COMPONENT IN SOYBEAN

J. M. JADEJA, D. A. PATEL, H. K. PARMAR* AND H. C. SISARA
Department of Genetics and Plant Breeding,
B. A. College of Agriculture, Anand Agricultural University, Anand - 388 110, Gujarat, INDIA
e-mail: hitiksha.parmar3010@gmail.com

KEYWORDS
Soybean
Variability
Heritability
Correlation
Path coefficient

Received on :
10.09.2015

Accepted on :
26.04.2016

***Corresponding author**

ABSTRACT
The genetic variability studies carried out on 50 soybean genotypes indicated that the estimate of phenotypic coefficient of variation were greater than those of the genotypic coefficient of variation for all the traits studied. The close proximity between PCV & GCV values for most of the characters indicated less influence of environment on the expression of the characters under study. Considering heritability, most of the characters showed high values. High heritability coupled with high genetic advance as per cent of mean were recorded for plant height (78.20, 27.87%), number of branches per plant (71.60, 23.09%), pods per plant (83.10, 57.71%), 100 seed weight (71.70, 21.82%), seed yield per plant (64.60,41.07%), germination percentage (92.80, 45.28%) indicating the scope of improvement through direct selection. Correlation analysis revealed that pods per plant (0.616**) and 100 seed weight (0.510**) were positively and significantly associated with seed yield per plant. Path coefficient analysis revealed that 100 seed weight (0.668) had maximum direct effect on seed yield per plant followed by seeds per pod (0.462), plant height (0.352) and pods per plant (0.251). Hence, these characters should be given more weightage in selection programme of high yielding soybean genotypes.

INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is a major oil seed crop in the world and is called as a golden bean or miracle bean because of its versatile nutritional qualities having 20% oil and 38 to 43 percent protein, which has biological value as meat and fish protein and rich in amino acids like lysine and tryptophan. The low yield of soybean in these countries is the main constrain for growing of soybean. Therefore, breeders should emphasize on yield improvement of soybean. Collection of genotypes and estimation of genetic variability is a basic step in each crop improvement program. Knowledge of variability in the germplasm will allow breeders to better understand the evolutionary relationships between germplasm, and to develop strategies to incorporate desirable traits in the breeding programs (Bretting and Widrlechner, 1995). Introgression of new genetic diversity through hybridization with introduced germplasm is one approach to increase genetic variation in breeding populations which progress and genetic advance in the program from selection depends on it (Guedira *et al.,* 2000). Khan *et al.* (2000) observed that seed yield of soybean was positively and significantly correlated with all yield components except pod height from the ground. Seed yield as a complex character is influenced by a number of attributes, controlled by polygenes, affected to components of yield, the environment and their interactions. Karad *et al.* (2005) distinguish high variability for plant yield, plant height and pods per plant, and moderate for seeds per pod and branches per plant, indicating that these traits have scope for improvement through hybridization and selection. Hence, it is necessary to partition the observed variability into heritable and non-heritable components measured as genotypic and phenotypic coefficients of variation (GCV and PCV), heritability and genetic advance. Traits with higher range of genetic variability and high heritability would be effective tools to improve seed yield and quality in soybean. The aim of this study finding the determination of suitable plant types available for further studies, seed yield improvement in soybean.

MATERIALS AND METHODS

The experimental material consists of 50 genotypes of soybean derived from different region. These genotypes of soybean were evaluated in randomized block design (RBD) with three replications at the Agronomy farm, B. A. College of Agriculture, Anand Agricultural University, Anand during *Kharif* 2014. Each genotypes accommodated in plot consisted of a two rows of 3m length with inter and intra row spacing of 45 cm and 10 cm, respectively. Observations on twelve characters i.e. days to 50% flowering, days to maturity, plant height, number of branches per plant, pod length, pods per plant, seeds per pod, 100 seed weight, seed yield per plant, protein content, oil content and germination percentage were recorded on randomly selected five plants from each genotypes and average value was used for statistical analysis. The data collected for all quantitative characters were subjected to analysis of variance according to the method suggested by Panse and Sukhatme (1985). Phenotypic and genotypic coefficients of variation were computed according to the method suggested by Burton (1952). Heritability in broad

sense was calculated as per the formula given by Allard (1960). Genetic advance was expressed as per cent of mean by using the formula suggested by Johnson *et al.* (1955). Correlation coefficients were worked out using the formula as suggested Hazel *et al.* (1943) using SPAR1 soft ware. The path coefficient analysis was carried-out according to the method suggested by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Analysis of variance worked out for seed yield and its component characters indicated that, the mean sum of squares due to genotypes were highly significant for all the characters except for days to 50% flowering. This suggested that the genotypes selected were genetically variable and considerable amount of variability existed among them (Table 1).

The magnitude of PCV was higher than that of GCV for all characters under study it indicated that apparent variation is not only due to genotypes but also due to the influence of environment (Table 2). Among the different yield attributing traits, pods per plant had the highest GCV (30.72 %) and PCV (33.69 %) followed by seed yield per plant (24.79 % and 30.85 %) and germination percentage (22.81 % and 23.68 %), which is an indicative of the substantial genetic variability exists in the soybean germplasm accessions. Similar findings were also reported by Karad *et al.* (2005) for pods per plant and seed yield per plant. Moderate GCV and PCV were observed for plant height (15.30% and 17.31%), number of branches per plant (13.23% and 15.64%) and 100 seed weight (12.48% and 14.74%). The similar result reported by Patil *et al.* (2011) for plant height; Karad *et al.* (2005) for number of seeds per pod and number of branches per plant. The lowest GCV and PCV were reported for pod length (9.01% and 10.04%), seeds per pod (6.99% and 10.61%), days to 50% flowering (2.55% and 6.68%), days to maturity (2.82% and 5.35%), protein content (5.10% and 7.55%) and oil content (3.82% and 7.14%) indicating that low variability was existed in studied material for these traits. Patil *et al.* (2011) reported low GCV and PCV for days to 50% flowering, days to maturity and protein content and Jain and Ramgiry (2000) also recorded similar result for seeds per pod.

Heritability determines the relative amount of heritable proportion of variability and important biometrical tool for adopting appropriate breeding procedure. It also acts as a predictive instrument in expressing the reliability of phenotypic value. Therefore, it helps the plant breeder to select a particular character when heritability is high. Wide range of variability was exhibited in the population according to estimates of heritability and genetic advance in percent of mean. Heritability in broad sense was classified as low (0-30), medium (30-60) and high (60 above). High heritability (92.80%) was observed for germination percentage followed by pods per plant (83.10%), pod length (80.50%), plant height (78.20%), 100 seed weight (71.70%), number of branches per plant (71.60%) and seed yield per plant (64.60%). Similar result was observed by Karad *et al.* (2005) for number of branches

Table 1: Analysis of variance (mean sum of squares) for different characters in soybean

Sr. No.	Characters	Mean Sum of Squares		
		Replications	Genotypes	Error
1	Days to 50 % flowering	2.328	9.717*	6.428
2	Days to maturity	21.437	44.465**	20.651
3	Plant height	7027.937**	426.589**	36.327
4	Number of branches per plant	28.859**	1.302**	0.152
5	Pod length	0.118**	0.326**	0.024
6	Pods per plant	823.125**	1208.314**	76.475
7	Seeds per pod	1.638**	0.136**	0.041
8	100 seed weight	5.289**	3.248**	0.377
9	Seed yield per plant	74.911**	35.359**	5.463
10	Protein content	20.304*	16.997**	4.832
11	Oil content	6.146*	3.480**	1.578
12	Germination percentage	2336.093**	767.384**	19.317

Table 2: The estimates of genotypic ($ó^2_g$) and phenotypic variance ($ó^2_p$) and other genetic parameters for different characters in soybean

Sr. No.	Characters	σ^2_g	σ^2_p	GCV (%)	PCV (%)	H^2_b (%)	GA % Mean
1	Days to 50 % flowering	1.10	7.52	2.55	6.68	14.60	1.99
2	Days to maturity	7.94	28.59	2.82	5.35	27.80	3.06
3	Plant height	130.09	166.41	15.30	17.31	78.20	27.87
4	Number of branches per plant	0.38	0.54	13.23	15.64	71.60	23.09
5	Pod length	0.10	0.12	9.01	10.04	80.50	16.77
6	Pods per plant	377.28	453.75	30.72	33.69	83.10	57.71
7	Seeds per pod	0.03	0.07	6.99	10.61	43.60	9.43
8	100 seed weight	0.96	1.33	12.48	14.74	71.70	21.82
9	Seed yield per plant	9.97	15.43	24.79	30.85	64.60	41.07
10	Protein content	4.06	8.89	5.10	7.55	45.60	7.17
11	Oil content	0.63	2.21	3.82	7.14	28.70	4.23
12	Germination percentage	249.36	268.67	22.81	23.68	92.80	45.28

Table 3: Genotypic and phenotypic correlations among different characters in soybean

Character		Seed yield/	Days to 50% plant	Days to maturity flowering	Plant height	Number of branches/ plant	Pod length	Pods/ plant	Seeds/ pod	100 seed weight	Protein content	Oil content	Germination percentage
Seed yield per plant	r_g	1.000	-0.556**	0.003	0.045	0.216	-0.229	0.616**	0.231	0.510**	-0.054**	-0.080	-0.040
	r_p	1.000	-0.148	0.050	0.024	0.112	-0.164	0.377**	0.114	0.395**	0.002	-0.071	-0.057
Days to 50% flowering	r_g		1.000	0.152	0184	0.188	-0.082	-0.310*	0.153	0.061	0.380**	-0.244**	0.215
	r_p		1.000	0.352**	0.010	0.107	-0.010	-0.077	0.062	-0.086	0.244**	-0.106	0.075
Days to maturity	r_g			1.000	0.480**	0.177	-0.026	- 0227	0.461**	0.361*	0.199	0.262	0.046
	r_p			1.000	0.244**	0.078	-0.005	-0.110	0.061	0.126	0.139	0.061	-0.007
Plant heihgt	r_g				1.000	0.017	0.018	-0.099	0.036	0.085	0.036	0.106	0.048
	r_p				1.000	-0.003	0.027	-0.108	-0.023	0.054	0.002	0.049	0.054
Number of branches	r_g					1.000	-0.346*	-0.072	0.232	0.180	0.018	-0.238	0.186
per plant	r_p					1.000	-0.263	-0.008	0.091	0.150	0.034	-0.085	0.160
Pod length	r_g						1.000	-0.237	0.127	0.037	-0.273	-0.017	-0.260
	r_p						1.000	-0.168	-0.020	0.038	-0.144	-0.023	-0.234**
Pods per plant	r_g							1.000	0.037	0.024	0.079	-0.062	0.138
	r_p							1.000	-0.043	-0.025	0.106	-0.005	0.112
Seeds per pod	r_g								1.000	0.158	0.064	0.160	-0.361*
	r_p								1.000	0.086	-0.031	0.161	-0.206
100 seed weight	r_g									1.000	0.196	-0.424**	0.061
	r_p									1.000	0.073	-0.148	0.042
Protein content	r_g										1.000	0.055	0.110
	r_p										1.000	-0.196*	0.045
Oil content	r_g											1.000	-0.038
	r_p											1.000	-0.007
Germination percentage	r_g												1.000
	r_p												1.000

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

Characters	Days to 50 % flowering	Days to maturity	Plant height	Number of branches per plant	Pod length	Pods per plant	Seeds per pod	100 seed weight	Protein content	Oil content	Germination percentage	Genotypic correlation with seed yield
Days to 50% flowering	-0.609	-0.083	0.065	0.026	0.020	-0.078	0.071	0.041	0.002	-0.033	0.023	-0.556**
Days to maturity	-0.093	-0.542	0.169	0.025	0.006	-0.057	0.213	0.241	0.001	0.035	0.005	0.003
Plant height	-0.112	0.260	0.352	0.002	-0.005	-0.025	0.017	0.056	0.000	0.014	0.005	0.045
Number of branches per plant	-0.115	-0.096	0.006	0.139	0.085	-0.018	0.107	0.120	0.000	-0.032	0.020	0.216
Pod length	0.050	0.014	0.006	-0.048	-0.244	-0.060	0.059	0.025	-0.001	-0.002	-0.027	-0.229
Pods per plant	0.189	0.123	-0.035	-0.010	0.058	0.251	0.017	0.016	0.000	-0.008	0.015	0.616**
Seeds per pod	-0.093	-0.250	0.013	0.032	-0.031	0.009	0.462	0.106	0.000	0.021	-0.038	0.231
100 seed weight	-0.037	-0.196	0.030	0.025	-0.009	0.006	0.073	0.668	0.001	-0.057	0.006	0.510**
Protein content	-0.232	-0.108	0.103	0.002	0.067	0.020	0.030	0.131	0.005	0.007	0.012	-0.054
Oil content	0.149	-0.142	0.037	-0.033	0.004	-0.016	0.074	-0.283	0.000	0.134	-0.004	-0.080
Germination percentage	-0.131	-0.025	0.017	0.026	0.064	0.035	-0.167	0.041	0.001	-0.005	0.105	-0.040

Note ; *, ** significant at 5% and 1% levels, respectively; Residual effect = -0.261

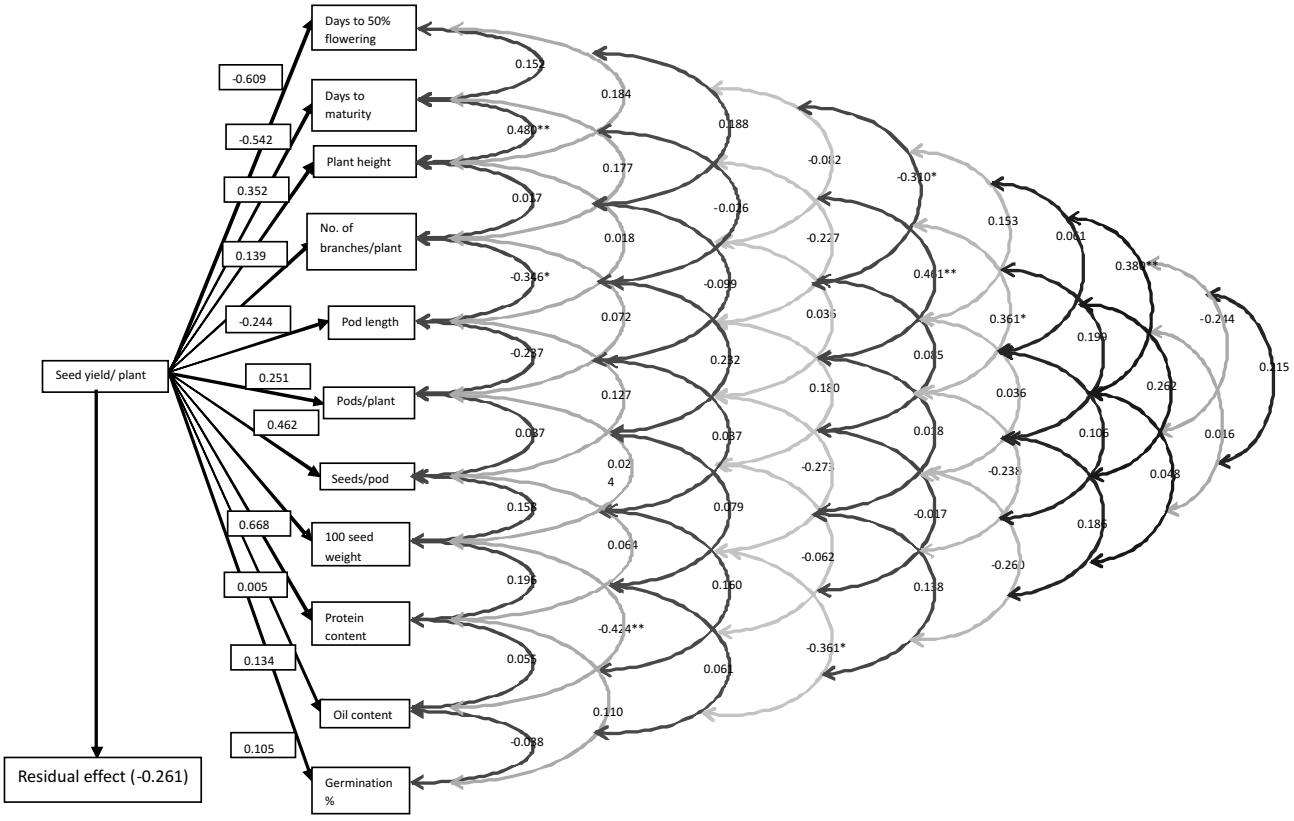

Figure 1: Path diagram showing direct and indirect effect of various traits on seed yield

per plant. Chettri *et al*. (2005) reported that the seed yield per plant and 100 seed weight was highly potential trait for selection in soybean; however the environmental influence was considerable for this trait which could be observed from the difference between genotypic coefficient of variation and phenotypic coefficient of variation. Genetic advance is indicative of the expected genetic progress for a particular trait under selection procedure. High heritability values coupled with high percentage of genetic advance were recorded for pods per plant, germination percentage and seed yield per plant which indicated more numbers of additive factors for this character for which improvement is feasible through selection based on phenotypic observations. These results are in agreement with the findings of Sharma and Abraham (1988) in soybean.

In plant breeding, correlation coefficient analysis measures the mutual relationship between various characters and determines the component characters on which selection can be made for genetic improvement in yield. Association analysis measures the natural relationship between various plant characters and determines the components on which selection could be based on improvement. The association of character may be due to either genetic linkage or pleiotrophy. Knowledge of correlation that exists among important character may facilitate proper interpretation of results and provide basis for planning more efficient breeding programmes. Interpretation of data on correlations showed that most of the correlation coefficients at genotypic level were

greater than the corresponding phenotypic correlation coefficients. This suggested the predominance of genotypic effects over environmental factors. Genotypic correlation of twelve yield and yield attributing characters presented in Table 3 indicated that seed yield was positively and significantly associated with pods per plant (0.616), 100 seed weight (0.510) and days to 50% flowering (-0.556). These results are agreement with similar finding of Dineshkumar *et al*. (2015) and Shruti *et al*. (2015) for pods per plant and 100 seed weight while Mehetre *et al*. (1995) for days to 50% flowering. The days to 50% flowering had positive and significant correlation with protein content (0.380 and 0.244) at both genotypic and phenotypic levels, while positive and significantly correlated with days to maturity (0.352) at phenotypic level. The positive and significant correlation of days to maturity observed with plant height (0.480) and seeds per pod (0.461). Ngon *et al*. (2006) reported that any increase in duration of crop will increase in plant height. The number of branches per plant was negative and significantly correlated with pod length (-0.346); while seeds per pod had significant and negative correlation with germination percentage (-0.361) and likewise 100seed weight also negatively and significantly correlated with oil content (-0.424). The negative and significant correlation of oil content with protein content (-0.196) and it was earlier reported by Manjaya *et al*. (2007).

While correlation values clarifies the inter-relationship between different characters, path coefficient splits the amount of inter relationship into components, direct and indirect effects as exerted on dependent character. Therefore, in the present investigation the direct and indirect effect of different component characters as exerted on seed yield per plant were estimated and presented in Table 4 and Figure 1. Path coefficient analysis was based on correlation coefficient using seed yield as the dependent factor (effect) and fix other quantitative characters viz., days to 50% flowering, days to maturity, plant height, number of branches per plant, pod length, pods per plant, seeds per pod, 100 seed weight, protein content, oil content and germination percentage as independent factor (causes). Correlation coefficient of each independent quantitative character was segmented into direct and indirect effect towards seed yield. As the residual effect was found low, it could be suggested that the number of characters chosen in the investigation was appropriate. Direct effects of 100 seed weight (0.668), seeds per pod (0.462), plant height (0.352), pods per plant (0.251), number of branches per plant (0.139), oil content (0.134) and protein content (0.005) were positive and days to 50% flowering (-0.609), days to maturity (-0.542), pod length (-0.244) exerted negative direct effect on seed yield per plant. 100 seed weight followed by seeds per pod, plant height and pods per plant showed maximum positive direct effect on seed yield per plant.

Other direct positive influences as exerted by rest of the characters were found to be marginal. The characters contributing maximum for seed yield like 100 seed weight and pods per plant were also found to be correlated with the dependent character. Similar results were reported by Gohil *et al*. (2003) who observed highest contribution towards seed yield per plant with 100 seed weight, likewise, Shaikh *et al*. (2010) for seeds per pod. The days to 50% flowering had highest negative direct effect towards seed yield per plant and negatively correlated with seed yield and similar result was reported by Malik *et al*. (2006).

Hence, this investigation conclude that 100 seed weight, pods per plant and days to 50% flowering can be used as selection indices in soybean to bring about the improvement in yield.

REFERENCES

Allard, R. W. 1960. Quantitative inheritance. In: "Principle of Plant Breeding" *J. Willey and Sons. Inc*, New York. pp. 75-88.

Bretting, P. K. and Widrlechner, M. P. 1995. Genetic markers and plant genetic resource management. In: Plant Breeding Reviews. (Ed.): J. Janick. *J. Wiley and Sons, Inc.*, New York. **13:** 11-87.

Burton, G. W. 1952. Quantitative inheritance in grasses. *Proc. of 6th International Grassland Congress*. **1:** 277-283.

Chettri, M., Mondal, S. and Nath, R. 2005. Studies on genetic variability in soybean (*Glycine max* (L.)Merril) in the mid hills of Darjeeling District. *J. Interacademicia*. **9(2):** 175-178.

Dewey, J. R. and Lu, K. H. 1959. A correlation and path co-efficient analysis of components of crested wheat seed production. *Agron. J.* **51:** 515-8.

Dineshkumar, T., Sunil kumar, N., Tuleshkumar, G. and Rakesh kumar, P. 2015. Character association and path coefficient analysis for seed yield and its contributing traits in soybean [*Glycine max* (L.) Merrill.]. *The Bioscan*. **10(4):** 1947-1950.

Gohil, V. N., Pandya, H. M. and Mehta, D. R. 2003. Genetic association and path analysis for seed yield, its components and quality attributes in soybean. *GAU Res. J.* **28(1-20):** 9-11.

Guedira, G. L. B., Thompson, J. A., Nelson, R. L., Warburton, M. L., 2000. Evaluation of genetic diversity of soybean introductions and North American ancestors using RAPD and SSR markers.*Crop Science*. **40:** 815-823.

Hazel, L. N., Baker, M. L. and Reinmiller, C. F. 1943. Genetic and environmental correlations between the growth rates of pigs at different ages. *J. Animal Sci*. **2:** 118.

Jain, P. K. and Ramgiry, S. R. 2000. Genetic variability of metric traits in Indian germplasm of soybean (*Glycine max* (L.) Merrill). *Advances Pl. Sci.* **13(1):** 127-131.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955. Estimates of genetic and environmental variability in soybeans. *Agronomy J*. **47:** 314-18.

Karad, S. R., Harer, P. N., Kadam, D. D. and Shinde, R. B. 2005. Genotypic and phenotypic variability in soybean (*Glycine max* (L.) Merrill). *J. Maharashtra Agric. Univ*. **30(3):** 365-367.

Khan, A., Hatam, M. and Khan, A. 2000. Heritability and interrelationship among yield determining components of soybean varieties. *Pakistan J. Agricultural Research*.**16:** 5-8.

Malik, M. F. A., Qureshi, A. S., Muhammad, A. and Ghafoor, A. 2006. Genetic Variability of the Main Yield Related Characters in Soybean. *Int. J. Agri. Biol*. **8(3):** 815-819.

Manjaya, J. G., Gopalkrishna, T., Pawar, S. E. and Bapat, V. A. 2007. Genetic variability for trypsin inhibitor content with oil and protein.*Indian J.Genet*. **67(1):** 51-55.

Mehetre, S. S., Mahajan, C. R., Desai, N. S. and Shinde, R. B. 1995. Variability, heritability and character association in M3 families of gamma irradiated soybean. *Soybean Genetics News letter*. **22:** 126-131.

Ngon, T. T., Van, K., Kim, M. Y. and Lee, S. H. 2006. Genetic variation in flowering time and maturity and its relationship among agronomic characters in soybean.*Korean Crop Sci*. **51(2):** 163-168.

Panse, V. G. and Sukhatme, P. V. 1985. Statistical methods for Agricultural Workers. *ICAR,* New Delhi, 4th Edition.

Patil, S. S., Naik, M. R., Patil, P. P. and Shinde, D. A. 2011. Genetic variability, correlation and path analysis in soybean.*NavsariAgril. Uni*. **34(1):** 36-40.

Shaikh, M. M., Wadikar, P. B. and Ghodke, M. K. 2010. Path coefficient analysis for some quantitative traits in soybean. *Ann. Plant Physio*. **24(1):** 44-46.

Sharma, S. K. and Abraham, M. J. 1988. Genetic Variability in indigenous soybean [*Glycine max* (L.) Merrill.] of north eastern hills region. *India. J. Oilseeds Res*. **5(2):** 93-100.

Shruti, K., Basavaraja, G. T., Sobha, I. and Vijayakumar, A. G. 2015. Correlation and path coefficient analysis for yield and its component in soybean (*Glycine max* L. Merrill.). *The Bioscan*. **10(4):** 2065-2067.