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# Character association and path analysis study of Soybean germplasm [*Glycine max* (L.) (Merrill)]

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#### **ABSTRACT**

An understanding of Soybean germplasm with check varieties can help in identifying germplasm in better adoption. The present investigation was carried out to access the genetic variation and morpho-metric characterization of Soybean germplasm. A set of 37 germplasm along with 3 checks were evaluated using randomized complete block design with 3 replications during kharif 2018 and 2019 in the experimental area of Instructional cum Research Farm, College of Agriculture, Assam Agricultural University, Jorhat, Assam. The performance of the genotypes was evaluated on the basis of ten characters. Selection was done for all characters which show direct association with yield. Significant difference was observed for most of the characters in all the genotypes. At genotypic level, seed yield/plant had significant and positive correlation with number of seed/pods, pod length, number of branches, pod/ plant, 100 Seed weight. At phenotypic level, seed yield/plant had significant and positive correlation with Number of seed/pods, pod length, pod/plant, number of branches, 100 seed weight, days to 50% flowering, days to maturity. Path analysis showed that the traits *viz.*, number of seed per pod and 100 seed weight were the most directly contributing traits to seed yield per plant and as such could be used as selection criteria in the present soybean breeding programme.

Key words: Correlation, Path analysis, Character association, Soybean, Genotypes

## Introduction

Soybean promises to be an important legume and oilseed crop as it has high protein, oil and is rich in lysine along with vitamins A, B and D. It is a rainy season crop in the rainfed agro-ecosystem of central and peninsular India (Agarwal *et al.*, 2013). There is considerable scope of cultivation of Soybean in Assam condition. A proper knowledge of yield and its attributing characters is very essential in order to develop some high yielding genotypes of Soybean. The present study was therefore undertaken to estimate phenotypic and genotypic associations between yield contributing characters along with path analysis for developing suitable selection criterion

for soybean improvement.

# **Materials and Methods**

A set of 37 genotypes along with 3 checks namely JS335, JS-9305 and BRAGG was obtained from All India Coordinated Research Project on Soybean. These were evaluated using Randomised complete Block design with three replications during Kharif 2018 and 2019 in the experimental area of Instructional cum Research Farm, college of Agriculture, Assam Agricultural University, Jorhat, Assam.

The genotypes and checks were accommodated in 3 blocks of 5m length representing the 3 replications. Blocks were separated from each other by 1 m.

The row to row spacing was maintained at 45cm apart while plant to plant spacing was 5 cm apart. Observations were recorded for characters namely days to 50% flowering, plant height, number of branches per plant, days to maturity, number of pods per plant, number of seeds per pod, 100 seed weight, pod length, seed yield per plant, percentage of oil. The data generated were subjected to correlation and path coefficient analysis to study the character association in Soybean. ANOVA was estimated based on the methodologies of Panse and Sukhatme (1978) while correlation and path coefficient analysis were evaluated as per Al-Jibouri *et al.* (1958) and Dewey and Lu (1959) respectively.

### **Results and Discussion**

Analysis of Variance clearly depicted that significant genetic variation was observed for all the characters under study (Table 1). Similar results were also obtained by Chandrawat *et al.* (2017).

The estimates of genotypic and phenotypic correlation coefficients between different characters of Soybean association are presented in Table 2 and 3. In general, here the values of Genotypic correlation

coefficients were found to be higher in magnitude than phenotypic correlation coefficients indicating a strong inherent association between these characters. Similar results between the pair of characters have been reported earlier also in soybean by Johnson *et al.* (1955) and Bhatt *et al.* (1968).

In the present study, phenotypic and genotypic correlation of seed yield was positive and significant with 100 seed weight, days to 50% flowering, days to maturity, number of branches, pod length, pods/plant, number of seeds/pod indicating the importance of these characters in determining seed yield. The results obtained from this study are in confirmation with the results of Parameshwar (2006).

The genotypic correlation coefficients were used for carrying out path coefficient analysis in 40 genotypes and the results revealed low residual value 0.00750 indicating most of the yield components were included in the study (Table 4 and 5).

Considering the direct effects of the component traits on seed yield in the germplasm it was observed that 100 seed weight and the number of seeds/pod exerted the highest direct positive effect on seed yield at both genotypic and phenotypic level Similar results were obtained by Muhammad *et al.* 

Table 1. Pooled analysis of variance

Sources of variation	df	Days to 50% flowering	Days to maturity	Plant height	No of branches	Pods/ plant	No of seed/pod	Pod length	100 seed weight	Oil%	Seed yield
Year	1	1,255.83**	2,106.33**	75,161.20*	*6,383.95*	*24,732.04**	0.08	0.00	226.56**	0.042	,242.74**
Rep within Year	4	7.00	12.35	10.34	0.05	0.18	0.04	0.00	0.12	0.01	1.48
Treatment	39	349.32**	412.53**	185.96**	14.71**	144.61**	2.20**	0.39**	25.79**	80.77**	151.13**
Year X Treatment	39	18.14**	45.03**	7.59	0.54**	18.76**	0.05	0.00	0.21	0.00	11.37**
Pooled Error	156	9.77	13.53	8.94	0.16	0.07	0.03	0.00	0.98	0.00	0.77

**Table 2.** Genotypic Correlation Coefficients fordifferent combinations of characters involving seed yield and its attributes

	100 seed weight	Plant height	Days to 50% flowering	Days to maturity	Number of branches	Pod length	Pods/ plant	No. of seeds/	Oil%
100 seed weight									_
Plant height	0.34 **								
Days to 50% flowering	0.07	-0.20*							
Days to maturity	0.14	-0.08	0.88**						
Number of branches	0.01	-0.26**	0.12	0.12					
Pod length	-0.05	-0.23*	0.21*	0.19*	0.92**				
Pods/ plant	-0.02	-0.20*	0.19*	0.18*	0.92**	0.96**			
No. of seeds/ pod	-0.01	-0.15	0.19*	0.17	0.92**	0.97**	0.91**		
Oil%	-0.04	-0.07	0.00	0.03	0.28**	0.19*	0.26**	0.17	
Seed yield	0.32**	-0.06	0.20**	0.19*	0.88**	0.91**	0.87**	0.93**	0.17

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**Table 3.** Phenotypic Correlation Coefficients for different combinations of characters involving seed yield and its attributes

	100 seed weight	Plant height	Days to 50% flowering	Days to maturity	Number of branches	Pod length	Pods/ plant	No. of seeds/ pod	Oil%
100 seed weight									
Plant height	0.29**								
Days to 50% flowering	0.06	-0.19*							
Days to maturity	0.12	-0.08	0.81**						
Number of branches	0.02	-0.24**	0.11	0.10					
Pod length	-0.04	-0.21*	0.20*	0.18*	0.90**				
Pods/plant	-0.02	-0.19*	0.18*	0.17	0.91**	0.95**			
No. of seeds/ pod	-0.01	-0.15	0.19*	0.17NS	0.89**	0.95**	0.90**		
Oil%	-0.04	-0.06	0.00	0.03	0.27**	0.19*	0.26**	0.17	
Seed yield	0.32**	-0.06	0.19*	0.19*	0.86**	0.89**	0.86**	0.93**	0.17

Table 4. Path coefficient analysis at genotypic level of soybean

	100 seed weight	Plant height	Days to 50% flowering	maturity	Number of branches	Pod length	Pods/ plant	No. of seeds/pod	Oil%	Seed yield/ plant
100 seed weight	0.352	-0.001	0.002	-0.008	0.001	-0.012	0.000	-0.012	-0.001	0.321**
Plant height	0.119	-0.002	-0.008	0.005	-0.013	-0.057	0.003	-0.106	-0.001	-0.060
Days to 50% flowering	0.026	0.000	0.039	-0.051	0.006	0.052	-0.002	0.128	0.000	0.200**
Days to maturity	0.050	0.000	0.035	-0.058	0.006	0.047	-0.002	0.115	0.001	0.195*
Number of branches	0.005	0.000	0.005	-0.007	0.049	0.226	-0.012	0.615	0.005	0.888**
Pod length	-0.018	0.000	0.008	-0.011	0.046	0.245	-0.013	0.651	0.004	0.913**
Pods/plant	-0.007	0.000	0.008	-0.010	0.046	0.235	-0.013	0.611	0.005	0.876**
No. of seeds/ pod	-0.006	0.000	0.008	-0.010	0.046	0.239	-0.012	0.667	0.003	0.935**
Oil%	-0.015	0.000	0.000	-0.002	0.014	0.047	-0.003	0.119	0.019	0.179

Residual are 0.00750; \* significant at 5% probability, \*\* significant at 1% probability level

Table 5. Path coefficient analysis at phenotypic level of soybean

	100 seed weight	Plant height	Days to 50% flowerin	Days to maturity g	Number of branches	Pod length	Pods/ plant	No. of seeds/pod	Oil content plant	Seed yield/
100 seed weight	0.352	-0.001	0.002	-0.008	0.001	-0.012	0.000	-0.012	-0.001	0.321**
Plant height	0.119	-0.002	-0.008	0.005	-0.013	-0.057	0.003	-0.106	-0.001	-0.060
Days to 50% flowering	0.026	0.000	0.039	-0.051	0.006	0.052	-0.002	0.128	0.000	0.200**
Days to maturity	0.050	0.000	0.035	-0.058	0.006	0.047	-0.002	0.115	0.001	0.195*
Number of branches	0.005	0.000	0.005	-0.007	0.049	0.226	-0.012	0.615	0.005	0.888**
Pod length	-0.018	0.000	0.008	-0.011	0.046	0.245	-0.013	0.651	0.004	0.913**
Pods/ plant	-0.007	0.000	0.008	-0.010	0.046	0.235	-0.013	0.611	0.005	0.876**
No. of seeds/ pod	-0.006	0.000	0.008	-0.010	0.046	0.239	-0.012	0.667	0.003	0.935**
Oil content	-0.015	0.000	0.000	-0.002	0.014	0.047	-0.003	0.119	0.019	0.179

(2006) for 100 seed weight, and Mishra *et al.* (1994) for seeds/pod.

## Conclusion

The study of correlation and path analysis revealed

that Significant and positive genetic correlation coefficients were detected for almost all the characters except plant height and oil content which revealed importance of these characters in determining yield. Path analysis showed that the traits *viz.*, number of seed per pod and 100 seed weight were the most

directly contributing traits to seed yield per plant and as such could be used as selection criteria in the present soybean breeding programme.

Conflict of interest: None

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