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## ASSOCIATION ANALYSIS FOR YIELD CONTRIBUTING AND QUALITY PARAMETERS IN SOYBEAN

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## ABSTRACT

The present investigation aimed to study correlation and path analysis on various yield contributing and quality parameters in soybean. The experiment was conducted under randomized block design on forty six genotypes and five checks (two local viz., MAUS-71, MAUS-158 and three national viz., JS 335, JS 93-05, Bragg). Observations were recorded on five plants per treatment on eleven characters viz., days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, 100 seed weight, harvest index, oil content, protein content, trypsin inhibitor content and grain yield per plant. Analysis of variance showed the significant variability for all the studied characters. Harvest index (0.662, 0.582) and 100 seed weight (0.451, 0.363) were found positively and significantly correlated with grain yield at both genotypic and phenotypic level which shows ample opportunity for improvement of these traits along with grain yield. Path analysis studies revealed that harvest index has highest positive direct effect (1.871, 0.825) and days to 50% flowering (0.771), days to maturity (0.607), number of pods per plant (0.473) also showed positive and significant effect on grain yield per plant indicated the indirect selection for these traits will be useful for yield related breeding programmes.

## INTRODUCTION

Pulses are the important food crop of the world because it provides good source of vegetable dietary protein (Peerzada *et al.*, 2014). Taxonomically, soybean belongs to the genus *Glycine* which is divided into two subgenera, *Glycine* and *Soja*. The cultivated soybean, *G. max* (L.) Merrill (2n=40) comes under the subgenus *Soja* (Moench). Soybean (*Glycine max* (L.) Merrill.) is aptly called as "Golden Bean" or "Miracle Crop" of the 20th century and is one of the most important oilseed crop in the world (Adolaju *et al.*, 2009). Soybean has the highest protein content (30-45%) of all food crops and also contains a considerable oil content (15-24%) comprising high percent of unsaturated fatty acids (Akram *et al.*, 2011). Soybean also contains compounds which reduce the risk of cardiovascular diseases, breast cancer, osteoporosis, diabetes and reduces the menopausal symptoms (Kumar *et al.*, 2014).

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 which is helpful in designing effective utilization of germplasm. Furthermore, characters associated with yield are to be determined by association analysis choose the appropriate selection programme during breeding. Correlation studies enable breeder to know the relationship between various characters while the path coefficient analysis technique facilitates the partitioning of genotypic correlation into direct and indirect contribution of various characters on yield.

Previously, the study on association analysis between various yield and its related characters have done at broad level in soybean (Pandey and Torrie 1973, Akhter and Sneller 1996, Shukla *et al.*, 1998, Board *et al.*, 1999, Ball *et al.*, 2001, Malik *et al.*, 2006, Oz *et al.*, 2009, Akram *et al.*, 2011). The present study was planned to investigate correlation and path analysis to identify the best genotypes and the characters which are most suitable for yield improvement.

## MATERIALS AND METHODS

### Plant Material

The present investigation was undertaken during *kharif* 2013 at the experimental farm of AICRP on Soybean, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani. The experimental material comprised of 41 germplasm lines, three national checks (Bragg, JS-335 and JS-93-05) and two local checks (MAUS-71 and MAUS-158). The field experiment was conducted under randomised block design in two replications.

### Field observations

Observations were recorded on five randomly selected plants per treatment for

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eleven quantitative characters viz., days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, 100 seed weight, harvest index, oil content, protein content, trypsin inhibitor content and grain yield per plant.

### Laboratory observations

All the laboratory observations on biochemical traits (Oil, protein and trypsin inhibitor estimation) were conducted on matured soybean seeds at Department of Food Chemistry and Nutrition, College of Food Technology, VNMKV, Parbhani. Oil content of seed samples was estimated by solvent extraction using Soxhlet apparatus. The nitrogen content of the seed was determined by the Micro-Kjeldahl method (A.O.A.C., 1984) and the amount of total protein was calculated from percent nitrogen content using a conversion factor of 6.25. Trypsin and trypsin inhibitor assay. Trypsin activity was measured by using N-u-benzoyl OL-arginine p-nitroanilide (BAPNA) essentially according to the method described by Erlanger *et al.* (1961).

### Statistical methods

Significance of various observations was tested using standard statistical methods. The analysis of variance was done as suggested by Panse and Sukhatme (1967). Genotypic and phenotypic correlation coefficient were carried out using formula suggested by Johnson *et al.* (1955), Hanson *et al.* (1956) and Miller *et al.* (1958). The correlation coefficients were further partitioned into components of direct and indirect effects by path coefficient analysis developed by Wright (1921) and later described by Dewey and Lu (1959).

## RESULTS AND DISCUSSION

### Correlation analysis

The analysis of variance revealed that, prevalence of significant differences among the genotypes for all the eleven characters studied. The genotypic correlations were generally higher than the phenotypic correlations (Nagarajan *et al.*, 2015) indicating the greater contribution of genetic factor in development of the dependent trait *i.e.* yield. Phenotypic and genotypic correlation of seed yield was positive and significant with harvest index and 100 seed weight (Table 1). The results obtained from this study are in confirmation with the results of Yao *et al.* (1987), Bhardwaj *et al.* (1990), Ramgiry and Raha (1997), Mehtre *et al.* (1997) and Mukhekar *et al.* (2004), Nagarajan *et al.* (2015) for harvest index and for 100 seed weight it is in confirmation with Dixit and Patil (1982), Harer and Deshmukh (1992), Mehtre *et al.* (1997), Sunil Kumar *et al.* (1997), Banger *et al.* (2003), Mukhekar *et al.* (2004), Parmeshwar (2006), Malik *et al.* (2011), Ghodrati *et al.* (2013), Jain *et al.* (2015). However, seed yield per plant showed significant and negative association with protein content in both genotypic and phenotypic correlation studies which is in confirmation with the results of Maharaddi (1996).

The characters viz., days to 50% flowering, days to maturity and number of branches per plant showed positive but non-significant association with seed yield per plant (Table 1). Similar results obtained by Mahajan *et al.* (1990), Ramana *et al.* (2000), Bangar *et al.* (2003), Arshad *et al.* (2014), Ali *et al.*

Table 1: Estimates of genotypic and phenotypic correlation coefficients among grain yield and yield contributing characters in soybean

Characters	Level of correlation	Days to 50% flowering	Days to Maturity	Plant height	No. of branches/plant	No. of pods/plant	100 seeds weight	Harvest Index	Oil content	Protein content	Trypsin inhibitor content	Grain yield/plant
Days to 50% Flowering	Genotypic	1.000	0.537**	0.518**	0.208*	0.675**	0.329**	-0.543**	0.116	0.345**	-0.045	0.071
	Phenotypic	1.000	0.312**	0.345**	0.138	0.458**	0.129	-0.321**	0.065	0.192	-0.030	-0.030
Days to Maturity	Genotypic	1.000	1.000	0.301**	0.252*	0.553**	0.269**	-0.494**	0.111	0.165	-0.035	0.128
	Phenotypic	1.000	1.000	0.159	0.153	0.292**	0.150	-0.213*	-0.010	-0.023	0.010	-0.005
Plant height (cm)	Genotypic	1.000	1.000	1.000	0.146	0.592**	-0.274**	-0.512**	0.011	-0.189	0.052	-0.082
	Phenotypic	1.000	1.000	1.000	0.101	0.466**	-0.230*	-0.396**	0.002	-0.136	0.021	-0.072
Number of branches per plant	Genotypic	1.000	1.000	1.000	1.000	0.472**	-0.192	-0.312**	-0.072	0.230*	0.187	0.053
	Phenotypic	1.000	1.000	1.000	1.000	0.421**	-0.155	-0.135	0.021	0.145	0.169	0.062
Number of pods per plant	Genotypic	1.000	1.000	1.000	1.000	1.000	-0.311**	-0.832**	0.107	0.286**	-0.027	-0.184
	Phenotypic	1.000	1.000	1.000	1.000	1.000	-0.177	-0.630**	0.055	0.185	0.010	-0.088
100 seeds weight	Genotypic	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.125	0.196	-0.113	0.451**
	Phenotypic	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.131	0.165	-0.134	0.363**
Harvest Index	Genotypic	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.048	-0.305**	0.067	0.662**
	Phenotypic	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.054	-0.185	0.053	0.582**
Oil content	Genotypic	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.025	-0.370	-0.095
	Phenotypic	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.016	-0.228	-0.043
Protein content	Genotypic	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.071	-0.268**
	Phenotypic	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.119	-0.205
Trypsin Inhibitor content	Genotypic	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.074
	Phenotypic	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.044
Grain yield per plant	Genotypic	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	Phenotypic	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000

**Table 2: Estimates of genotypic and phenotypic path analysis for direct and indirect effects of yield components on grain yield per plant in soybean**

Characters	Level of path analysis	Days to 50% flowering	Days to Maturity	Plant height	No. of branches per plant	No. of pods per plant	100 seeds weight	Harvest index	Oil content	Protein content	Trypsin Inhibitor content	Grain yield per plant
Days to 50% Flowering	Genotypic	0.7712**	0.414**	0.399**	0.16	0.52**	0.254*	-0.419**	0.089	0.266*	-0.035	0.071
	Phenotypic	-0.012	-0.003	-0.004	-0.001	-0.005	-0.001	0.003	-0.000	-0.002	0.000	-0.030
Days to Maturity	Genotypic	0.326**	0.607**	0.183	0.153	0.336**	0.163	-0.300**	0.067	0.100	-0.021	0.128
	Phenotypic	-0.014	-0.047	-0.007	-0.007	-0.014	-0.007	0.010	0.000	0.001	-0.000	0.005
Plant height (cm)	Genotypic	-0.082	-0.048	-0.159	-0.023	-0.094	0.043	-0.081	-0.001	0.0302	-0.008	-0.082
	Phenotypic	0.028	0.013	0.082	0.008	0.038	-0.018	-0.032	0.000	-0.011	0.001	-0.072
Number of branches per plant	Genotypic	0.019	0.023	0.013	0.094	0.044	-0.018	-0.029	-0.006	0.021	0.017	0.053
	Phenotypic	0.010	0.011	0.007	0.022	0.030	-0.011	-0.009	0.001	0.010	0.012	0.062
Number of pods per plant	Genotypic	0.319**	0.262*	0.280**	0.223*	0.473**	-0.147	-0.394**	0.051	0.135	-0.012	-0.184
	Phenotypic	0.224*	0.142	0.227*	0.205*	0.488**	-0.086	-0.307**	0.027	0.090	0.005	-0.088
100 seeds weight	Genotypic	-0.181	-0.148	0.151	0.105	0.171	-0.55	-0.189	0.068	-0.108	0.062	0.451**
	Phenotypic	0.043	0.050	-0.077	-0.052	-0.059	0.334*	0.065	-0.043	0.055	-0.044	0.363**
Harvest Index	Genotypic	-1.017**	-0.925**	-0.957**	-0.585**	-1.558**	0.644**	1.871**	-0.091	-0.572**	0.126	0.662**
	Phenotypic	-0.265*	-0.176	-0.327**	-0.111	-0.520**	0.161	0.825**	0.045	-0.152	0.044	-0.582**
Oil content	Genotypic	-0.046	-0.044	-0.004	0.029	-0.043	0.0504	0.019	-0.403**	-0.0104	0.149	-0.095
	Phenotypic	-0.006	0.001	-0.000	-0.002	-0.005	0.013	-0.005	-0.101	0.001	0.023	-0.043
Protein content	Genotypic	-0.054	-0.026	0.03	-0.036	-0.045	-0.031	0.048	-0.004	-0.157	0.011	-0.268**
	Phenotypic	-0.040	0.005	0.028	-0.030	-0.039	-0.035	0.039	0.003	-0.211*	0.025	-0.205
Trypsin Inhibitor content	Genotypic	0.016	0.012	-0.019	-0.068	0.009	0.041	-0.024	0.134	0.025	-0.036	-0.074
	Phenotypic	0.003	-0.001	-0.002	-0.018	-0.001	0.014	-0.005	0.025	0.013	-0.111	-0.044

(2015) for days to 50% flowering, Lakhani *et al.* (1993), Mukhekar *et al.* (2004) for days to maturity and Jadhav *et al.*, (1995), Maharaddi *et al.* (1996), Singh and Singh (1996), Hina Kausar (2005), Parmeshwar (2006), Bekele and Alemahu (2011), Ghodrati *et al.* (2013) for number of branches per plant. This suggests while selection of traits for improvement in seed yield, these characters can be kept in mind and it should show high variability, which is basis for selection. In addition, oil content didn't showed any significant positive correlation with other characters but it showed a significantly negative association with trypsin inhibitor content which indicates that oil content can be increased by lowering the trypsin inhibitor content which will also improve the quality of soybean and soy-products.

Protein content was found to be significantly negatively correlated (Sonawane *et al.*, 2006) and trypsin inhibitor content negatively correlated with grain yield per plant which means while selecting traits for grain yield it wouldn't be necessary to get the increased protein content too. 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.

Characters showing positive association may be raised through the indirect selection for the respective trait in breeding programmes while, the traits showing negative association were seems to be independently associated with each others and could be improved independently. In terms of the present investigation plants with more harvest index and 100 seed weight likely to produce more yield as they are positively associated with seed yield while, plants with low protein content and TI content will produce greater yield as they are negatively associated with yield. Similarly indirect selection for low trypsin inhibitor content will also provide the plants with high oil content which will be a helpful step for quality improvement in soybean.

#### Path analysis

The path coefficient analysis takes into account the cause and effect relation between the variables is unique in partitioning the association into direct and indirect effect through other independent variables. The path coefficient analysis also measures the relative importance of causal factors involved. The path analysis indicated that harvest index has highest positive direct effect and highest positive indirect effect on grain yield per plant at genotypic and phenotypic level (Table-2). Ghodrati *et al.* (2013) found the highest positive effect of total dry matter followed by harvest index on grain yield per plant. Showkat and Tyagi (2010), Dubey *et al.* (2015), Nagarajan *et al.* (2015) also found harvest index with a direct effect on grain yield per plant.

The characters *viz.*, days to 50% flowering, days to maturity, number of pods per plant also showed positive and significant effect on grain yield per plant (Table 2). Lal and Haque (1971), Tanaka (1978), Rajanna *et al.* (2000), Iqbal (2003), Datt (2011), Kobraee and Shamsi (2011), Machikowa and Laosuwan (2011), Patil (2011) and Li *et al.* (2013) found that pods per plant have the maximum direct effect on seed yield per plant. Significant and positive correlation of days to maturity with grain yield could be explained by its positive direct effect.

Taware (1995) reported indirect effect on yield via days to 50% flowering and 100 grain weight. These characters may be considered as the most important yield contributing characters and due emphasis should be placed on these characters while breeding for high grain yield in soybean.

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