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Character association and path coefficient analysis for seed yield and its contributing traits in soybean (*Glycine max* (L.) Merrill)

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Abstract

The present investigation consists of 40 Soybean genotypes used for studying genetic variability parameters, correlation and path analysis which was carried out at Field Experiment Centre, Department of Genetics and Plant Breeding during *Kharif* 2019 in Randomized Block Design with three replications. The data were recorded for 12 quantitative characters to study genetic variability, heritability, genetic advance, correlation and path analysis. Analysis of variance revealed highly significant differences among the genotypes for all the quantitative characters under study. Highest magnitudes coupled with a greater correspondence of the values of GCV with PCV for seed yield per plant. Seed yield per plant had significant positive association with days to 50% flowering, plant height, number of primary branches, nodes per plant, clusters per plant, pods per plant, pod length, 100 seed weight, biological yield and harvest index at genotypic and phenotypic level, whereas the seeds per pod showed positive significant correlation with seed yield at genotypic level only. Path analysis revealed that harvest index had highest magnitude of positive Significant direct effects on seed yield per plant. High estimates of heritability coupled with high genetic advance as per cent of mean were recorded for characters like 100-seed weight, plant height, nodes per plant, seed yield per plant, pods per plant, primary branches per plant, clusters per plant, biological yield per plant, days to 50% flowering, pod length and harvest index.

Keywords: Soybean (*Glycine max* (L.) Merrill), genetic variability, heritability, genetic advance, correlation, path analysis

Introduction

Soybean [*Glycine max* (L.) Merrill], a self-pollinated diploid ($2n = 2x = 40$) food legume belonging to family Leguminosae or Fabaceae, subfamily Papilionoideae is originated in north and central China. Soybean (*Glycine max* (L.) Merrill) is the most widely grown leguminous crop in the world and is an important source of protein and oil for food and feed. Soybean seeds are rich in proteins, unsaturated fatty acids, minerals (e.g. Ca and P) and vitamins (e.g. A, B, C and D), which meet the nutritional needs of humans and other animals (Malek *et al.*, 2014) [13]. Soybean seed is referred to the “protein hope” of the future, because of its high nutritive value, containing about 42-45% protein (Sathe *et al.*, 2009) [18].

India is a marginal player in the world soybean sector, with a production of just over 11.00 million tons in 2018-19, as against the world's estimated soybean production of 360.993 million metric tons. Our average productivity of around 1000 kilos per hectare is the lowest in the world, being less than one third of the world average. (Oilseeds -World Markets and Trade, USDA Publication). Hence large yield gap exist between India and other country in production and productivity. Narrowing this gap the production potential of soybean crop can be enhanced by developing high yielding genotypes through planned hybridization programme.

The germplasm possessing high genetic variability for quantitative traits is the basic material with plant breeder to initiate breeding programme. The yield potential of commercial varieties needs to be further upgraded under wide range of farming situation. For this, the knowledge of yield and quality attribute is essential to initiate the breeding work for development of genetically better soybean varieties, which can be adapted to wide range of diversified environment. A variety or genotype is considered to be more adaptive and stable one, if it has high mean yield but a low degree of fluctuation in yielding ability when grown over diverse environment (Eberheart and Russell, 1966) [19].

Existence of adequate genetic variability is a prerequisite for genetic improvement of any crop through breeding methods. Similarly, the correlation and path analysis studies are of great help in formulating efficient scheme for multiple traits selection as they provide means for direct and indirect selection of component characters. Thus, knowledge of genetic variability, genetic advance, correlation and path coefficient is essential for a breeder to choose best genotype and to decide the correct breeding methodology for crop improvement.

Therefore, it is essential to identify the contributing traits through which soybean seed yield can be improved further. Keeping this in view, the present study on “Character association and Path coefficient analysis for seed yield and its contributing traits in Soybean (*Glycine max* (L.) Merrill)” was carried out to formulate the selection strategies for improvement of seed yield in soybean.

Materials and Methods

The experimental material consisting 40 soybean genotypes received from Indian Institute of Soybean Research, Indore, Madhya Pradesh, during *Kharif* 2019. The experiment was laid out in a Randomized Block Design (RBD) with three

replications. The experimental material was planted in three replications. Each replication consisted of 40 genotypes randomized and replicated within each block. The experiment was laid down in Randomized Block Design with 40 genotypes including check variety. 12 yield component traits studied is presented in detail (table 1) viz. Days to 50% flowering Plant height (cm), Number of primary branches per plant, Number of nodes per plant, Number of clusters per plant, Number of pods per plant, Pod length (cm), Number of seeds per pod, 100 Seed Weight (g), Biological yield 2019. The experiment was laid out in a Randomized Block Design (RBD) with three replications. The experimental material was planted in three replications. Each replication consisted of 40 genotypes randomized and replicated within each block. The experiment was laid down in Randomized Block Design with 40 genotypes including check variety. 12 yield component traits studied is presented in detail (table 1) viz. Days to 50% flowering Plant height (cm), Number of primary branches per plant, Number of nodes per plant, Number of clusters per plant, Number of pods per plant, Pod length (cm), Number of seeds per pod, 100 Seed Weight (g), Biological yield (g), Harvest index (%), Seed yield per plant (g).

Table 1: Mean sum of squares for different characters in soybean (*Glycine max* (L.)

S. No.	Characters	Mean sum of Squares		
		Replications (d.f.=2)	Treatment (d.f.=39)	Error (d.f.=78)
1	Days to 50% flowering	1.433	52.845**	2.501
2	Plant height (cm)	3.16	690.929**	4.79
3	No. of Primary Branches	0.01	2.448**	0.03
4	No. of Nodes per plant	0.026	11.122**	0.095
5	No of clusters per Plant	0.156	2.916**	0.117
6	No. of Pods per plant	5.001	915.768**	8.392
7	Pod length(cm)	0.005	0.11**	0.005
8	No. of seed per pod	0.009	0.115**	0.017
9	100 seed weight	0.173	16.069**	0.083
10	Biological yield	6.939	90.952**	3.953
11	Seed yield per plant	0.696	56.396**	0.498
12	Harvest index	22.397	510.362**	26.97

** Significant at P = 0.01

Observations for all traits were recorded on five randomly selected competitive plants from each replication. Reading from five plants was averaged replication wise and the mean data was used for statistical analysis, where observations were recorded on the plot basis.

Results and Discussion

The results of analysis of variance for Randomized Block Design for eleven characters of twenty soybean genotypes including two cheeks have been presented in Table 1. The mean sum of squares due to genotypes were showed highly significant difference for all the characters, it indicates that the sufficient variability present among the genotypes. Substantial variations in soybean have been also reported by Karad *et al.*, (2005)^[10], Reni and Rao (2007)^[16], Aditya *et al.*, (2011)^[1], Dilnesaw *et al.*, (2013)^[7] and Osekita and Olorunfemi (2014)^[14].

Among the genotypes, genotype TNAU 20051, MACS 128,

UPSM 57, PK 258 and KB -17 were found with high yield along with early flowering. These lines were found good for yield contributing traits also viz., pod length, 100-seed weight and harvest index.

Among all the characters, high GCV and PCV were observed for Seed yield per plant (g) (39.501 and 40.026), No. of pods per plant (35.375 and 35.862), Harvest index (%) (27.59 and 29.81), No. of primary branches per plant (25.78 and 26.268), Biological yield per plant(g) (22.665 and 24.161), 100-seed weight (g) (22.765 and 22.943) and Plant height (cm) (21.945 and 22.174). Moderate GCV and PCV were observed for No. of nodes per plant (16.07 and 16.081) and No. of clusters per plant (15.152 and 16.272) in comparison to other characters indicating the presence of high and medium amount of genetic variability for these characters.

Selection for these characters would be effective because the response to selection is directly proportional to the variability present in the experimental material.

Table 2: Variability parameters for different characters in soybean

S. No.	Characters	GCV	PCV	H ² (%)	GA (5%)	GA as % of mean (5%)
1	Days to 50% flowering	9.051	9.703	87.00	7.872	17.394
2	Plant height (cm)	21.945	22.174	98.00	30.833	44.741
3	No. of primary branches per plant	25.78	26.268	96.40	1.815	52.138
4	No. of nodes per plant	16.07	16.272	97.50	3.899	32.678
5	No. of clusters per plant	15.152	16.081	88.80	1.875	29.409
6	No. of pods per plant	35.375	35.862	97.30	35.339	71.881
7	Pod length (cm)	5.962	6.4	86.80	0.359	11.44
8	No. of Seeds per pod	7.499	9.305	65.00	0.299	12.451
9	100-seed weight (g)	22.765	22.943	98.50	4.718	46.531
10	Biological yield per plant(g)	22.665	24.161	88.00	10.407	43.8
11	Seed yield per plant (g)	39.501	40.026	97.4	8.776	80.306
12	Harvest index (%)	27.59	29.81	85.7	24.202	52.603

In the present investigation, high heritability along with high GCV was recorded for Seed yield per plant (g) (97.4 and 39.501), No. of pods per plant (97.30 and 35.375), Harvest index (%) (85.7 and 27.59), No. of primary branches per plant (96.40 and 25.78), Biological yield per plant(g) (88.00 and 22.665), 100-seed weight (g) (98.50 and 22.765), and Plant height (cm) (98.00 and 21.945). High heritability along with medium GCV was recorded for No. of nodes per plant (97.50 and 16.07) and No. of clusters per plant (88.80 and 15.152). This indicates closeness of respective σ_p and σ_g value thereby low environmental effect on expression of these characters. Thus phenotypic selection may be effective for these characters.

In the present study genetic advance as % of mean varied from 11.44 to 80.306. High genetic advance as % mean (>20%) was recorded for Seed yield per plant (g) (80.306), No. of pods per plant (71.881), Harvest index (%) (52.603), No. of primary branches per plant (52.138), 100-seed weight (g) (46.531), Plant height (cm) (44.741), Biological yield per plant(g) (43.8), No. of nodes per plant (32.678), and No. of clusters per plant (29.409) along with high heritability and high to moderate GCV. Such values may be attributed to the additive gene effects and direct selection for these traits would be fruitful.

Phenotypic Correlation coefficient analysis revealed that seed yield per plant exhibited positive and significant correlation with almost all the characters except No. of Seeds per pod at phenotypic level only. Seed yield per plant exhibited positive and significant correlation with No. of pods per plant (0.8174**), Harvest index (%) (0.7848**), No. of clusters per plant (0.7424**), Biological yield per plant (g) (0.5926**), 100-seed weight (g) (0.5003**), No. of primary branches per plant (0.3926**), Pod length (cm) (0.3736**), Days to 50 % flowering (0.2834**), No. of nodes per plant (0.2726**) and Plant height (cm) (0.1987*). Seed yield per plant exhibited positive and non significant correlation with No. of Seeds per pod (0.1739).

Genotypic correlation coefficient analysis revealed that seed yield per plant exhibited positive and significant correlation with all the characters under study viz., No. of pods per plant (0.8455**), Harvest index (%) (0.8129**), No. of clusters per plant (0.7950**), Biological yield per plant(g) (0.6560**), 100-seed weight (g) (0.5107**), Pod length (cm) (0.4088**), No. of primary branches per plant (0.3981**), Days to 50 %

flowering (0.3031**), No. of nodes per plant (0.2812**), No. of Seeds per pod (0.2141*) and Plant height (cm) (0.2059*).

Similar results exhibiting highly significant and positive correlation between grain yield and other traits as obtained in the present investigation were in accordance with earlier findings of several workers viz., Ali *et al.*, (2015) [3], Ekka *et al.*, (2016) [8], Baig *et al.*, (2017) [4], Balla and Ibrahim (2017) [6], Paikra *et al.*, (2018) [15] and Lal *et al.*, (2018) [5].

Path coefficients which are worked out from phenotypic correlation coefficient are referred to as phenotypic path coefficient analysis. It splits the phenotypic correlation coefficient into the measures of direct and indirect effects. Maximum positive direct effects was depicted by Harvest index (%) (0.6418) followed by Biological yield per plant(g) (0.492), No. of pods per plant (0.1995), Pod length (cm) (0.0713), 100-seed weight (g) (0.0398), Plant height (cm) (0.0346), No. of primary branches per plant (0.0171), No. of Seeds per pod (-0.0027), Days to 50 % flowering (-0.0085), No. of clusters per plant (-0.0209), and No. of nodes per plant (-0.0744).

Genotypic maximum positive direct effects was depicted by Harvest index (%) (1.742) followed by Biological yield per plant (g) (1.0821), No. of primary branches per plant (0.162), No. of nodes per plant (0.0916), Days to 50 % flowering (0.0717), Pod length (cm) (0.0474), plant height (cm) (-0.1698), No. of Seeds per pod (-0.308), No. of clusters per plant (-0.4519), No. of pods per plant (-0.5897) and 100-seed weight (g) (-0.6312).

In the present investigation, both at phenotypic and genotypic level, the positive direct effect on grain yield was depicted by Harvest index (%), Biological yield per plant (g), No. of primary branches per plant and Pod length (cm). The residual component of phenotypic and genotypic path analysis indicated that 86 and 85% of variability of seed yield was accounted for by these twelve characters. The positive direct effect on grain yield was reported by Karnwal and Singh (2009) [11] for primary branches/plant, Jain *et al.*, (2015) [9] for biological yield per plant, Mahbub *et al.*, (2015) [12] for pod length, and Akram *et al.*, (2016) [2] for Number of branches per plant. Showkat and Tyagi (2010) [17] revealed that biological yield and harvest index were major characters influencing seed yield directly and indirectly. The results indicated that biological yield is responsible for manipulation of seed yield in soybean.

Table 3: Phenotypic correlation coefficient of soybean genotypes

	Days to 50% flowering	Plant height	Primary Branches	Nodes per plant	Clusters per plant	Pods per plant	Pod length	Seed per pod	100 seed weight	Biological yield	Harvest index	Seed yield
Days to 50% flowering	1.00	0.5773**	0.4006**	0.3514**	0.3223**	0.4379**	-0.1282	-0.1142	-0.0911	0.4579**	-0.0034	0.2834**
Plant height		1.00	0.6981**	0.5436**	0.2424**	0.2924**	-0.1847*	-0.1520	-0.0698	0.4107**	-0.0658	0.1987*
Primary Branches			1.00	0.5231**	0.4309**	0.4849**	-0.0340	0.0074	-0.0298	0.5112**	0.0905	0.3926**
Nodes per plant				1.00	0.5035**	0.5182**	-0.1000	-0.1719	-0.2003*	0.6874**	-0.1468	0.2726**
Clusters per plant					1.00	0.8075**	0.1361	-0.0446	0.1146	0.5999**	0.4941**	0.7424**
Pods per plant						1.00	0.1318	0.0144	0.0105	0.7268**	0.4539**	0.8174**
Pod length							1.00	0.2172*	0.3845**	-0.0225	0.4265**	0.3736**
Seed per pod								1.00	0.0601	-0.0943	0.3003**	0.1739
100 seed weight									1.00	0.0705	0.6015**	0.5003**
Biological yield										1.00	-0.0020	0.5926**
Harvest index,											1.00	0.7848**
Seed yield per plant												1.00

* Significant at P = 0.05, ** Significant at P = 0.01

Table 4: Genotypic correlation coefficient of soybean genotypes

	Days to 50% flowering	Plant height	Primary Branches	Nodes per plant	Clusters per plant	Pods per plant	Pod length	Seed per pod	100 seed weight	Biological yield	Harvest index	Seed yield
Days to 50% flowering	1.00	0.6243**	0.353**	0.3680**	0.3727**	0.4705**	-0.1401	0.2344**	-0.929	0.5193**	-0.0041	0.3031**
Plant height		1.00	0.7200**	0.5592**	0.2544**	0.3049**	-0.1966*	-0.1958*	-0.0683	0.4367**	-0.0625	0.2059*
Primary Branches			1.00	0.5376**	0.4534**	0.5125**	-0.0404	-0.0339	-0.0315	0.5554**	0.0893	0.3981**
Nodes per plant				1.00	0.5375**	0.5288	-0.1124	-0.2316*	-0.2078*	0.7358**	-0.1536	0.2812**
Clusters per plant					1.00	0.8851**	0.1688	-0.0627	0.1114	0.6614**	0.5683**	0.7950**
Pods per plant						1.00	0.1343	0.0172	0.0129	0.7725**	0.5126**	0.8455**
Pod length							1.00	0.2595**	0.4119**	-0.0515	0.5201**	0.4088**
Seed per pod								1.00	0.0765	-0.1294	0.3962**	0.2141*
100 seed weight									1.00	0.0688	0.6594**	0.5107**
Biological yield										1.00	0.1228	0.6560**
Harvest index											1.00	0.8129**
Seed yield per plant												1.00

* Significant at P = 0.05, ** Significant at P = 0.01

Table 5: Phenotypic path coefficient of soybean genotypes

	Days to 50% flowering	Plant height	Primary Branches	Nodes per plant	Clusters per plant	Pods per plant	Pod length	Seed per pod	100 seed weight	Biological yield	Harvest index
Days to 50% flowering	-0.0085	-0.0049	-0.0034	-0.0030	-0.0028	-0.0037	0.0011	0.0010	0.0008	-0.0039	0.0000
Plant height (cm)	0.0200	0.0346	0.0241	0.0188	0.0084	0.0101	-0.0064	-0.0053	-0.0024	0.0142	-0.0023
Primary Branches	0.0069	0.0120	0.0171	0.0090	0.0074	0.0083	-0.0006	0.0001	-0.0005	0.0088	0.0016
Nodes per plant	-0.0262	-0.0405	-0.0389	-0.0744	-0.0375	-0.0386	0.0074	0.0128	0.0149	-0.0512	0.0109
Clusters per plant	-0.0067	-0.0051	-0.0090	-0.0105	-0.0209	-0.0169	-0.0028	0.0009	-0.0024	-0.0125	-0.0103
Pods per plant	0.0874	0.0583	0.0968	0.1034	0.1611	0.1995	0.0263	0.0029	0.0021	0.1450	0.0906
Pod length	-0.0091	-0.0132	-0.0024	-0.0071	0.0097	0.0094	0.0713	0.0155	0.0274	-0.0016	0.0304
Seed per pod	0.0003	0.0004	0.0000	0.0005	0.0001	0.0000	-0.0006	-0.0027	-0.0002	0.0003	-0.0008
100 seed weight	-0.0036	-0.0028	-0.0012	-0.0080	0.0046	0.0004	0.0153	0.0024	0.0398	0.0028	0.0239
Biological yield	0.2253	0.2020	0.2515	0.3382	0.2951	0.3576	-0.0111	-0.0464	0.0347	0.4920	-0.0010
Harvest index	-0.0022	-0.0422	0.0581	-0.0942	0.3171	0.2913	0.2737	0.1927	0.3861	-0.0013	0.6418
Seed yield per plant	0.2834**	0.1987*	0.3926**	0.2726**	0.7424**	0.8174**	0.3736**	0.1739	0.5003**	0.5926**	0.7848**
Residual effect=	0.1421										

* Significant at P = 0.05, ** Significant at P = 0.01

Table 6: Genotypic path coefficient of soybean genotypes

	Days to 50% flowering	Plant height	Primary Branches	Nodes per plant	Clusters per plant	Pods per plant	Pod length	Seed per pod	100 seed weight	Biological yield	Harvest index
Days to 50% flowering	0.0717	0.0448	0.0312	0.0264	0.0267	0.0337	-0.0100	-0.0168	-0.0067	0.0372	-0.0003
Plant height (cm)	-0.1060	-0.1698	-0.1223	-0.0950	-0.0432	-0.0518	0.0334	0.0333	0.0116	-0.0741	0.0106
Primary Branches	0.0705	0.1167	0.1620	0.0871	0.0735	0.0830	-0.0065	-0.0055	-0.0051	0.0900	0.0146
Nodes per plant	0.0337	0.0512	0.0493	0.0916	0.0492	0.0485	-0.0103	-0.0212	-0.0190	0.0674	-0.0141
Clusters per plant	-0.1684	-0.1149	-0.2049	-0.2429	-0.4519	-0.4000	-0.0763	0.0283	-0.0504	-0.2989	-0.2568
Pods per plant	-0.2775	-0.1798	-0.3022	-0.3118	-0.5219	-0.5897	-0.0792	-0.0101	-0.0076	-0.4555	-0.3023
Pod length	-0.0066	-0.0093	-0.0019	-0.0053	0.0080	0.0064	0.0474	0.0123	0.0195	-0.0024	0.0247
Seed per pod	0.0722	0.0603	0.0104	0.0713	0.0193	-0.0053	-0.0799	-0.3080	-0.0236	0.0399	-0.1220
100 seed weight	0.0586	0.0431	0.0199	0.1312	-0.0703	-0.0081	-0.2600	-0.0483	-0.6312	-0.0434	-0.4162
Biological yield	0.5619	0.4725	0.6010	0.7962	0.7157	0.8359	-0.0557	-0.1401	0.0744	1.0821	0.1326
Harvest index	-0.0071	-0.1088	0.1556	-0.2676	0.9900	0.8929	0.9059	0.6902	1.1487	0.2138	1.7420
Seed yield per plant	0.3031**	0.2059*	0.3981**	0.2812**	0.7950**	0.8455**	0.4088**	0.2141*	0.5107**	0.6560**	0.8129**
Residual effect=	0.1544										

* Significant at P = 0.05, ** Significant at P = 0.01

Conclusion

The analysis of variance showed significant differences among the genotypes for all the twelve characters under study. Among the genotypes, genotype TNAU 20051, MACS 128, UPSM 57, PK 258 and KB -17 were found with high yield along with early flowering. High genetic advance as % mean along with high heritability and high to moderate GCV was recorded for Seed yield per plant (g), No. of pods per plant, Harvest index (%), No. of primary branches per plant, 100-seed weight (g), Plant height (cm), Biological yield per plant(g), No. of nodes per plant, and No. of clusters per plant. Phenotypic and genotypic correlation coefficient analysis revealed that seed yield per plant exhibited positive and significant correlation with almost all the characters. All the characters were positively and significantly correlated with seed yield per plant except No. of Seeds per pod. High Positive direct effect on grain yield was depicted by Harvest index (%), Biological yield per plant (g), No. of primary branches per plant and Pod length (cm).

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