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Correlation and path analysis studies in soybean [*Glycine max* (L). Merrill]

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Abstract
The experiment "Correlation and Path analysis in Soybean [*Glycine max* (L). Merrill] "was carried out at the Post Graduate Research Farm, Botany Section, College of Agriculture, Dhule (Maharashtra) in the *Kharif* season of 2022. Total 42 different soybean genotypes were selected for this study. Ten distinct biometric characteristics were taken into account for this investigation of yield and its influencing factors. Analysis of variance proves that characteristics were shown to be statistically significant. The degree of association between significant plant traits is shown by correlation analysis. which also serves as a reliable indicator for forecasting how the yield will respond to changes in a given characteristic. From the experiment it can be stated that the characters like number of pods per plant, number of seeds per plant and 100 seed weight showed strong positive correlation with seed yield per plant and has also showed strong positive direct effect on seed yield. It indicates that direct selection based on this trait would help in identifying high yielding genotypes. Future crop development programs might benefit from selecting AMS19-01, RSC-11-42, AS-24, SL-1282, KDS -753, JS-9305, JS 20-34, and SL-1230.

Keywords: Soybean, characters, correlation, correlation analysis, significant, path analysis

Introduction

A large and frequently used oil seed crop, soybean is grown all over the world. Due to its numerous industrial, dietary, and agricultural benefits, it is often referred to as the "miracle bean" or the "golden bean." According to Carter *et al.* (2004) [10] and Kim *et al.* (2012) [11], the contemporary cultivated soybean (*Glycine max*) crop is thought to have originated from wild soybean (*Glycine soja*) in China between 6000 and 9000 years ago. After that, it spread to neighbouring nations via land and sea channels established for trade. It is a crop with a temperate origin, but from the 1960s, production of it spread to Asia's tropical and subtropical regions. Soybean has about 38-42% high-quality protein and 18-20% oil that has been supplemented with essential fatty acids. Additionally, it contains 5% minerals. Because of its high protein content and nutritional benefits, soybean is sometimes referred to as "poor man's meat". The direct and indirect effects of one variable on another are measured using the path coefficient method, which also allows the direct and indirect effects of the correlation coefficient to be separated (Dewey and Lu, 1959) [12].

Materials and Method

The present investigation entitled, "Correlation and Path analysis in Soybean [*Glycine max* (L). Merrill] conducted at Post Graduate Research Farm, Botany Section, College of Agriculture, Dhule (Maharashtra) during *Kharif* season 2022. The experimental material used for the study consisted of 42 genotypes of soybean were obtained from Agricultural Research Station (ARS), Kasbe Digraj, Sangali. The Post Graduate Research farm is situated in Agro climatic Zone-6 *viz.*, Scarcity Zone condition of Northern Maharashtra. It lies between 20.4 °N latitude and 74 °E longitudes. The altitude is 258 m above mean sea level. Climatologically, this area falls in the sub-tropical region at the North. Generally monsoon commences by third week of June and retreats at the end of September with the average annual rainfall of 1041.8 mm at College of Agriculture, Dhule. To explain the association between the characters, the genotypic and phenotypic correlation coefficients were calculated using Singh and Chaudhary's method (1979) [14]. Wright (1921) [13] proposed path analysis, which was further developed by Dewey and Lu (1959) [12]. Using path coefficient analysis, the genotypic correlation coefficient is separated into direct and indirect effects. It examines the direct and indirect effects of independent variables on the dependent variable. The list of genotypes used in the experiment is given in Table 1.

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Results and Discussion

In the present investigation, the experiments were undertaken to investigate the variability of 42 genotypes of soybean for 8 different morphological and 2 biochemical traits. The study examined at the relationship between the dependent and independent factors, as well as their direct and indirect effects on seed yield and genetic diversity across all genotypes. The yield of a crop depends on a number of qualitative factors that all interact with one another. That's why it's important to consider how all the other factors that affect yield interact with one another. Increasing the selective pressure on one trait that is linked to yield increases its effect on several other traits as well. Therefore, the plant breeder needs to have a firm grasp on the contribution made by both genetic and non-genetic elements in creating the link between character and yield in order to make improvements through selection. Characteristics such as days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, number of seeds per plant, 100 seed weight in (g), protein content(%), oil content (%), and seed yield per plant were all discussed in relation to each other in (Table 2 and 3) which also included the coefficients of phenotypic and genotypic correlation among these ten characters.

Table 1: List of forty genotypes of soybean used for the present study

Sr. No	Genotypes	Pedigree	Source
1	MAUS-818	-	VNMKV, Parbhani
2	AMS19-01	Mutant of JS 93-05	RRC, Amravati
3	DS-3124	DS-2615 × DS- 2709	IARI, Delhi
4	SL-1230	SL 905×{(G.soja×Ankur)×Sl(E)28}	PAU, Ludhiana
5	JS-335	JS 78-77×JS 17-05	JNKKV, Jabalpur
6	PS-1829	PS 1829 × KDS 344	GBPUAT, Pantnagar, U.K
7	JS-23-08	JS 20-29×JS 93-05	JNKKV, Jabalpur, M.P
8	KDS-344	JS 335× EC 241780	ARS, Digraj
9	DS-3163	DS-2205 × DS 12-13	IARI, Delhi
10	SL-1282	(SL525×JS 335) ×SL 525	PAU, Ludhiana
11	BAUS-116	JS 20-65 × JS 20-35	BAU, Ranchi, J.H
12	JS-23-05	SL 738 × JS 95-60	JNKKV, Jabalpur, M.P
13	NRC-189	Davis × Kaevi 651-6	ICAR-IISRI, Indore, M.P
14	KDS-726	JS 93-05 × EC 241780	ARS, Digraj
15	KBS-21-1	-	UAS, Dharwad
16	AS-40	G.Soy 1 × AMRS 472	JAU-CoA Amreli, G.J
17	KDS-753	JS 93-05 × EC 241780	ARS, Digraj
18	MAUS-791	-	VNMKV, Parbhani
19	VLS-103	VLS 63 × VLS 2007-24	VPKS, Almora, U.K
20	ACS-1735	-	ACS, PUNE
21	KDS-992	JS 93-05 × EC 241780	ARS, Digraj
22	HIMSO-1694	SL-679 × Harasoya	CSKKV, Palampur, H,P
23	DS-3163	DS-2205 × DS 12-13	IARI, Delhi
24	DLSB-3	Dsb-23 × SL 958	UAS, Darwad, K.A
25	AMS-115	AMS-MB5-18 × TAMS106	RRC, Amravati
26	DS-228	JS335 × Ankur	IARI, Delhi
27	AS-24	JS 335 × GJ 3	JAU-CoA Amreli, G.J
28	RVS-13-15	JS 20-88 × JSM 196	RVSKV, Sehore, M.P
29	KSS-204	-	Basant Agro Ltd. M..H
30	NRC-192	JS 97-52 × JS 335	ICAR-IISRI, Indore, M.P
31	PS-1682	PS 1583 × Bragg (F6-1)	GBPUAT, Pantnagar, U.K
32	RVSM-16-20	-	RVSKV, Morena, M.P
33	RVS-13-20	JS 20-29 × JS 93-05	RVSKV, Sehore, M.P
34	JS-93-05	Secondary selection from ps 73-22	JNKKV, Jabalpur, M.P
35	DS-1312	SL 688 × DS 3047	IARI, Delhi
36	VLS-102	VLS74 × EC 361360	VPKS, Almora, U.K
37	JS-20-34	-	JNKKV, Jabalpur, M.P
38	NRC128	JS 97-52 × (EC389148×PS 1042)	ICAR-IISRI, Indore, M.P
39	DLSB-4	Dsb-21 × SL 958	UAS, Dharwad, K.A
40	HIMSO-1693	Pb-1 × Himsoya	CSKKV, Palampur, H,P
41	DSb-39	JS 335 × EC 242104	UAS, Darwad, K.A
42	RSC-11-42	JS 97-52× JS93-05	IGKV, Raipur, C,G

Table 2: Genotypic correlation coefficients among different yield components of ten characters of 42 soybean genotypes

Genotypic correlation	Days to 50 percent flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of pods per plant	Number of seeds per plant	100 seed weight (g)	Protein content (%)	Oil content (%)	Seed yield per plant
Days to 50 percent flowering	1	0.4863**	0.0933	0.2756*	-0.1557	-0.0842	0.2124	0.1516	-0.2667*	0.0093
Days to maturity		1	-0.1429	-0.2103	-0.2912**	-0.2313	0.0085	0.0979	-0.2871**	-0.23
Plant height(cm)			1	0.3161**	0.119	0.1756	0.07	-0.0347	0.2119	0.1682
Number of primary branches per plant				1	0.3626**	0.4047**	0.036	0.0159	0.0554	0.2762**
Number of pods per plant					1	0.9583**	-0.1033	-0.0348	0.1079	0.6994**
Number of seeds per plant						1	-0.1636	-0.0475	0.13	0.6953**
100 seed weight(g)							1	0.0062	0.0054	0.3207**
Protein content(%)								1	-0.6629**	-0.1181
Oil content(%)									1	0.1256
Seed yield per plant										1

*, ** significant at 5 and 1 percent, respectively

Table 3: Phenotype correlation coefficients among different yield components of ten characters of 42 soybean genotypes

Phenotypic correlation	Days to 50 percent flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of pods per plant	Number of seeds per plant	100 seed weight (g)	Protein content (%)	Oil content (%)	Seed yield per plant
Days to 50 percent flowering	1	0.445**	0.0875	0.132	-0.144	-0.0835	0.2074	0.1555	-0.2635*	-0.004
Days to maturity		1	-0.113	-0.074	-0.246*	-0.176	0.020	0.091	-0.276*	-0.153
Plant height(cm)			1	0.1784	0.1111	0.1607	0.0704	-0.0433	0.1905	0.1485
Number of primary branches per plant				1	0.1775	0.148	0.026	-0.0018	0.0548	0.0651
Number of pods per plant					1	0.9411**	-0.100	-0.0311	0.1078	0.6895**
Number of seeds per plant						1	-0.1595	-0.0286	0.1251	0.7155**
100 seed weight(g)							1	0.008	-0.0026	0.2946**
Protein content(%)								1	-0.621**	-0.0903
Oil content(%)									1	0.119
Seed yield per plant										1

*, **significant at 5 and 1 percent, respectively

Table 4: Partitioning of genotypic correlation coefficient into direct and indirect effects of morphological characters of 42 Soybean genotypes by path coefficient analysis

Traits	Days to 50 percent flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of pods per plant	Number of seeds per plant	100 seed weight (gm)	Protein content (%)	Oil content (%)	Correlation with Seed yield plant
Days to 50 percent flowering	0.061	0.0300	0.0058	0.0170	-0.0096	-0.0052	0.0131	0.0094	-0.0165	0.0093
Days to maturity	-0.0500	-0.102	0.0147	0.0216	0.0299	0.0238	-0.0009	-0.0101	0.0295	-0.2300
Plant height(cm)	0.0024	-0.0036	0.025	0.0080	0.0030	0.0045	0.0018	-0.0009	0.0054	0.1682
Number of primary branches per plant	-0.0264	0.0202	-0.0303	-0.095	-0.0348	-0.0388	-0.0035	-0.0015	-0.0053	0.2762**
Number of pods per plant	-0.0119	-0.0223	0.0091	0.0278	0.076	0.0734	-0.0079	-0.0027	0.0083	0.6994**
Number of seeds per pod	-0.0600	-0.1649	0.1252	0.2885	0.6832	0.712	-0.1166	-0.0339	0.0927	0.6953**
100 seed weight(g)	0.0926	0.0037	0.0305	0.0157	-0.0450	-0.0713	0.435	0.0027	0.0023	0.3207**
Protein content(%)	-0.0203	-0.0131	0.0047	-0.0021	0.0047	0.0064	-0.0008	-0.134	0.0888	-0.1181
Oil content(%)	0.0212	0.0229	-0.0169	-0.0044	-0.0086	-0.0104	-0.0004	0.0528	0.079	0.1256

$R^2 = 0.6968$, Residual effect (R) = 0.55006 (*, ** significant at 5 and 1 percent, respectively)

Table 5: Partitioning of phenotypic correlation coefficient into direct and indirect effects of morphological characters of 42 Soybean genotypes by path coefficient analysis.

Traits	Days to 50 percent flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of pods per plant	Number of seeds per plant	100 seed weight (gm)	Protein content (%)	Oil content (%)	Correlation with Seed yield Per plant
Days to 50 percent flowering	0.0268	0.0119	0.0023	0.0035	-0.0039	-0.0022	0.0056	0.0047	-0.0085	-0.0040
Days to maturity	-0.0277	-0.0621	0.0070	0.0046	0.0153	0.0110	-0.0012	0.0026	0.0123	-0.1533
Plant height(cm)	-0.0023	0.0029	-0.0259	-0.0046	-0.0029	-0.0042	-0.0018	0.0033	-0.0029	0.1485
Number of primary branches per plant	-0.0036	0.0021	-0.0049	-0.0276	-0.0049	-0.0041	-0.0007	-0.0077	0.0062	0.0651
Number of pods per plant	-0.0076	-0.0129	0.0058	0.0093	0.0523	0.0493	-0.0052	0.0041	0.0054	0.6895**
Number of seeds per plant	-0.0621	-0.1315	0.1194	0.1100	0.6997	0.7435	-0.1186	0.0147	0.0862	0.7155**
100 seed weight(g)	0.0807	0.0078	0.0274	0.0101	-0.0389	-0.0620	0.3890	-0.0446	-0.0086	0.2946**
Protein content(%)	-0.0391	0.0092	0.0283	-0.0621	-0.0173	-0.0044	0.0255	-0.2225	0.1382	-0.0903
Oil content(%)	0.0309	0.0194	-0.0110	0.0218	-0.0101	-0.0113	0.0022	0.0605	-0.0974	0.119

$R^2 = 0.7148$, Residual effect (R) = 0.5340 (*, ** significant at 5 and 1 percent, respectively)

Path coefficient analysis is a standardized partial regression coefficient which divides the correlation coefficient into the measures of direct and indirect effects. The relative value of each yield component's direct and indirect influence may not be accurately reflected by the association of character defined by correlation co-efficient. Path analysis at both genotypic and phenotypic level was used to determine the direct and indirect effects between yield per plant and other yield parameters, as well as the relative relevance of each component. Table 4 and 5 displays the results of a path co-

efficient study used to estimate the direct and indirect effects of soybean production.

Conclusion
At both the genotypic and phenotypic levels, traits such as number of pods per plant, 100 seed weight and number of primary branches per plant showed a significant and positive correlation with seed yield per plant. The strongest correlation at the genotypic and phenotypic level was found between number of pods per plant and seed yield per plant, which was followed by the days to 50 percent flowering and days to maturity.

Path analysis was used to examine the associations between 42 different soybean genotypes. According to the path coefficient analysis, the traits' days to 50% flowering, number of pods per plant, number of seeds per plant, 100 seeds weight all had a positive direct effect on the amount of seeds yield per plant. Selection of these traits directly can result in an increase in crop output. While number of seeds per plant showed high direct positive effect on seed yield per plant via, 100 seed weight. The traits such as days to maturity, plant height, oil content protein content, number of primary branches showed negative direct impact on seed yield per plant.

The characters number of pods per plant, number of seeds per plant and 100 seed weight showed strong positive correlation with seed yield per plant and has also showed strong positive direct effect on seed yield. It indicates that direct selection based on this trait would help in identifying high yielding genotypes.

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