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ASSESSMENT OF YIELD ASSOCIATED TRAITS IN SOYBEAN (*GLYCINE MAX* (L.) MERRILL) USING CORRELATION AND PATH COEFFICIENT ANALYSIS

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ABSTRACT

This study assessed genetic variability, heritability, correlation, and path analysis for eleven traits in twenty soybean genotypes under rainfed *Kharif* conditions at Birsa Agricultural University, Ranchi, using a randomized block design. ANOVA confirmed highly significant genotypic variances, especially for plant height, pods per plant, and oil content. High broad-sense heritability and genetic advance marked traits like branches, pods, seeds per pod, and plot yield, indicating strong selection potential. Genotypic correlations showed robust positive associations of plot yield with pods per plant, branches and height, while path analysis revealed direct effects from these, with low residuals. Superior genotypes BAUS-170, BAUS-131, and BS-3 excelled in yield attributes, advocating trait-based breeding to enhance rainfed soybean productivity amid climate challenges. BAUS-180 recorded the highest protein content, clearly exceeding the overall mean and outperforming all check varieties, followed closely by BAUS-173 and BAUS-186, while for oil content RSC 11-35 was superior to the mean and checks, with JS 97-52 and RKS-18 emerging as the next best genotypes.

***Key words*:** Genetic variability, GCV, PCV, Heritability, Genetic advance, Correlation, Path analysis.

Introduction

Soybean (*Glycine max* (L.) Merrill), revered as a "wonder crop" and "miracle bean," stands as a cornerstone of India's oilseed and protein economy, offering 17-19% oil rich in omega-3 and omega-6 fatty acids, 38-43% protein, and essential phytochemicals like isoflavones that combat chronic diseases (Liu *et al.*, 1997; Birt *et al.*, 2004). Ranking fifth globally in production (15.18 million tonnes) and fourth in area (12.96 million ha) with a productivity of 1172 kg/ha, India relies heavily on states like Madhya Pradesh, Maharashtra, and Gujarat, while regions like Jharkhand lag at 1189 kg/ha (Directorate of Agriculture and Farmers Welfare, 2024-25). Introduced in the late 19th century and revitalized through the Yellow Revolution post-1960s, soybean has transformed rural economies but faces persistent challenges: narrowing genetic base and yield instability amid climate change, shrinking cultivation areas, and surging domestic demand for processed products (Verma *et al.*, 2023). Late sowing conditions common in rainfed tropics due to erratic monsoons—exacerbates these issues, shortening the growth cycle, heightening pest pressures and amplifying environmental stresses that underscore the need for genetically variable, stable cultivars (Yan and Rajcan, 2003).

To boost soybean yields, evaluating genetic variability is essential—it's the raw material for effective selection in breeding programs. Pairing it with heritability offers a clearer picture of selection gains than heritability alone and ample variability signals real potential for crop improvement. Correlation analysis reveals how key traits interconnect and influence yield, while path coefficient analysis (Wright, 1921) breaks down their direct and indirect impacts. This study explores these variability metrics, trait relationships, and effects on seed yield.

Table 1: ANOVA table of soybean genotypes for yield and yield attributing traits

Source of Variation	DF	Mean sum of squares										
		DTF	DM	PH	NB	NP	NSP	100S	GYP	GY	PC	OC
Replication	2	6.71	4.11	0.46	0.01	1.44	0.01	0.004	2.97	0.003	0.46	0.09
Genotypes	19	6.99*	36.85**	78.74**	1.44**	225.96**	0.58**	2.91**	9.94**	0.06**	1.76*	3.35**
Error	38	3.01	5.11	19.81	0.03	70.11	0.01	.044	1.68	0.003	0.9	0.05

DTF: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); NB: No. of branches/ plant; NP: No of pods/ plant; NSP: No. of seeds/ pod; 100S: 100 seed weight(g); GYP: Grain yield/ plant(g); GY: Grain yield (kg/plot); PC: Protein content (%); OC: Oil content (%)

Table 2: Genetic estimate for yield and yield attributing traits.

Source of Variation	DTF	DM	PH	NB	NP	NSP	100S	GYP	GY	PC	OC
σ^2g	1.32	6.38	19.64	0.46	51.85	0.18	0.82	2.75	0.02	0.27	1.10
σ^2p	4.34	12.29	39.45	0.50	121.83	0.20	1.26	4.44	0.03	1.20	1.15
GCV	2.64	2.29	6.99	18.18	13.51	15.88	8.12	14.94	21.66	1.32	5.97
PCV	4.78	3.18	9.90	18.83	13.81	16.57	10.08	18.98	22.90	2.70	6.11
h^2	30.58	51.94	49.77	93.20	95.71	91.88	64.97	61.98	89.42	24.08	95.47
GA	1.31	3.75	6.44	1.36	17.36	0.85	1.50	2.69	0.28	0.54	2.11
GA as % of mean	3.017	3.40	10.16	36.17	27.23	31.37	13.49	24.24	42.19	1.34	12.03

DTF: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); NB: No. of branches/ plant; NP: No of pods/ plant; NSP: No. of seeds/ pod; 100S: 100 seed weight(g); GYP: Grain yield/ plant(g); GY: Grain yield (kg/plot); PC: Protein content (%); OC: Oil content (%)

Table 3: Mean performance of soybean genotypes for yield and yield attributing traits.

Sr.	Genotypes	DTF	DM	PH	NB	NP	NSP	100S	GYP	GY	PC	OC
1	BAUS-170	44.67	115.67	75.43	5.02	74.87	2.94	12.91	13.18	0.88	40.40	16.80
2	BAUS-173	44.00	116.67	66.07	4.01	73.80	3.05	12.76	12.46	0.81	40.73	17.07
3	BAUS-131	43.00	117.67	63.90	5.01	68.33	2.94	13.24	13.57	0.90	40.60	16.87
4	BAUS-132	46.33	111.00	66.00	4.01	75.27	2.38	10.05	11.65	0.82	40.27	17.33
5	BAUS-180	43.67	108.00	65.80	3.35	57.67	2.94	9.90	11.64	0.58	42.83	16.33
6	BAUS-193	43.67	113.67	65.97	4.34	65.90	2.94	10.66	9.45	0.80	41.17	15.80
7	BAUS-191	43.00	107.33	64.93	3.34	45.33	2.94	10.61	10.64	0.46	40.23	16.47
8	BAUS-186	43.33	116.33	62.50	4.02	64.00	2.94	10.51	10.80	0.76	40.90	17.43
9	BAUS-187	45.33	112.00	63.50	4.01	63.67	2.16	11.09	11.35	0.70	39.67	17.17
10	RSC 11-42	43.00	113.33	62.50	3.01	61.33	2.94	10.99	12.43	0.59	40.10	18.00
11	JS 20-116	45.00	116.00	58.17	4.02	68.33	2.94	10.41	10.82	0.64	40.43	16.80
12	AMS 2014-1	43.33	114.00	63.30	3.01	59.40	2.94	9.80	11.41	0.64	39.63	17.60
13	RKS-18	44.00	114.67	58.67	3.01	51.67	1.94	10.10	5.51	0.45	39.50	18.27
14	RSC 10-46	44.00	115.67	53.50	4.01	55.00	2.94	11.12	8.35	0.45	40.53	17.73
15	BSS-2	39.00	106.00	63.47	3.01	63.67	1.94	11.23	11.11	0.68	40.50	17.33
16	BS-4	41.00	108.00	67.20	4.01	72.33	2.94	12.23	12.50	0.84	40.37	17.90
17	RSC 11-35	43.00	112.33	72.10	4.01	56.10	1.94	10.55	11.19	0.78	39.30	20.23
18	NRC-128 (C)	43.67	113.67	58.47	3.00	53.33	2.94	10.77	10.61	0.53	40.20	17.57
19	JS 97-52(C)	43.00	109.33	56.23	3.01	71.40	2.94	11.69	10.35	0.55	40.60	19.43
20	BS-3(C)	44.33	114.00	60.27	4.01	73.80	2.94	12.62	12.96	0.86	39.47	18.90
	Trait Mean	43.52	112.77	63.40	3.76	63.76	2.73	11.16	11.1	0.69	40.37	17.55
	SE(m+-)	1.00	1.24	2.57	0.11	4.84	0.07	0.38	0.75	0.03	0.55	0.13
	CV(%)	3.99	1.91	7.02	4.91	13.13	4.72	5.96	11.70	7.45	2.35	1.30
	CD	2.78	3.44	7.35	0.3	13.84	0.21	1.10	2.14	0.84	1.57	0.37
	Range	39.00-46.33	106.00-117.67	53.5-75.43	3.00-5.02	45.33-75.33	1.94-3.05	9.80-13.24	5.51-13.57	0.45-0.90	39.30-42.83	15.80-20.23

DTF: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); NB: No. of branches/ plant; NP: No of pods/ plant; NSP: No. of seeds/ pod; 100S: 100 seed weight(g); GYP: Grain yield/ plant(g); GY: Grain yield (kg/plot); PC: Protein content (%); OC: Oil content (%)

Table 4: Correlation Coefficient of soybean genotypes for yield and yield attributing traits.

Characters		DTF	DM	PH	NB	NP	NSP	100S	GYP	GY	PC	OC
DTF	G	1.00	0.787**	-0.127	0.411**	0.244	0.248	-0.270*	-0.094	0.037	-0.076	-0.203
	P	1.00	0.344**	0.029	0.210	0.105	0.142	-0.074	-0.029	0.180	-0.096	-0.062
DM	G		1.00	-0.139	0.573**	0.309*	0.364**	0.357**	0.114	0.236	-0.284*	0.059
	P		1.00	-0.150	0.434**	0.268*	0.231	0.152	-0.023	0.180	-0.045	0.055
PH	G			1.00	0.53**	0.38**	-0.219	0.077	0.68**	0.71**	0.027	-0.183
	P			1.00	0.361**	0.130	-0.116	-0.058	0.316*	0.534**	0.053	-0.100
NB	G				1.00	0.692**	0.193	0.564**	0.53**	0.773**	0.277*	-0.232
	P				1.00	0.500**	0.177	0.387**	0.386**	0.687**	0.138	-0.223
NP	G					1.00	0.401**	0.523**	0.753**	0.992**	-0.164	-0.010
	P					1.00	0.218	0.209	0.387**	0.531**	0.224	0.003
NSP	G						1.00	0.324*	0.298*	0.165	-0.013	-0.164
	P						1.00	0.231	0.253	0.150	-0.008	-0.152
100S	G							1.00	0.598**	0.342**	-0.031	0.17
	P							1.00	0.385**	0.258*	-0.082	0.142
GYP	G								1.00	0.774**	0.287*	-0.099
	P								1.00	0.558**	0.001	-0.074
GY	G									1.00	-0.021	-0.066
	P									1.00	-0.04	-0.04
PC	G										1.00	-0.813**
	P										1.00	-0.402**
OC	G											1.00
	P											1.00

DTF: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); NB: No. of branches/ plant; NP: No of pods/ plant; NSP: No. of seeds/ pod; 100S: 100 seed weight(g); GYP: Grain yield/ plant(g); GY: Grain yield (kg/plot); PC: Protein content (%); OC: Oil content (%)

Materials and Methods

The study evaluated 20 Soybean (*Glycine max* (L.) Merrill) genotypes, sourced from the Department of Genetics and Plant Breeding, Birsa Agricultural University (BAU), Kanke, Ranchi, Jharkhand (23.23°N, 85.23°E). These included 17 advanced lines and three checks (NRC-128, JS 97-52, BS-3), with pedigrees. Experiments ran under rainfed*Kharif* conditions during 2024, with genetic estimates computed solely for 24 June 2024 sowing at the BAU Experimental Farm. Genotypes were sown in a Randomized Block Design (RBD) with three replications. Each plot had three 3-m rows spaced 45 cm apart (plot size: 5.5 m²). Standard practices included a fertilizer dose of 20:40:40:40 kg/ha (N:P:K:S). Five border-free plants per plot were sampled for traits like days to 50% flowering, plant height, pods per plant, 100-seed weight and grain yield per plant (g).

Genetic estimates, including genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense and genetic advance as a percentage of mean (GAM), were calculated to assess the magnitude of genetic variability and heritability for yield and yield-attributing traits such as days to 50% flowering, plant height, number of branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight, grain yield per plant, and grain yield per plot. Traits exhibiting high GCV (>20%), high PCV (>30%), broad-sense heritability (>60%), and substantial GAM (>20%) were prioritized for selection in breeding programs aimed at rainfed soybean improvement.

Correlation coefficients were computed at genotypic and phenotypic levels to elucidate associations among the 11 traits, identifying significant positive or negative relationships that influence grain yield; for instance, strong positive correlations with number of pods per plant and 100-seed weight were expected to guide trait selection. Path coefficient analysis, following the method of Dewey and Lu (1959), was conducted to partition these correlations into direct and indirect effects on grain yield (taken as the dependent variable), with all other traits as independent variables. This decomposition helped pinpoint key yield contributors (high positive direct effects) and confounding traits (indirect effects via other variables), using standardized partial regression coefficients. All computations were executed in Opstat with significance tested at 5% and 1% probability levels, ensuring robust interpretation of genetic architecture under sowing conditions of 24 June 2024, which represented optimal rainfed onset in the region.

Result and Discussion

The analysis of variance indicated significant

Table 5: Genotypic and phenotypic path coefficient among eleven characters of twenty soybean genotypes.

Characters		DTF	DM	PH	NB	NP	NSP	100S	GYP	PC	OC	CC
DTF	G	**2.124**	-1.609	-0.071	-0.004	-0.009	-0.009	-0.437	-0.003	0.037	0.017	0.037
	P	**-0.066**	0.001	0.008	0.094	0.025	0.004	0.005	-0.007	0.016	-0.003	0.076
DM	G	1.672	**-2.044**	-0.077	-0.005	-0.011	-0.013	0.579	0.004	0.137	-0.005	0.236
	P	-0.023	**0.003**	-0.043	0.193	0.047	0.007	-0.010	-0.005	0.008	0.003	0.180
PH	G	-0.269	0.283	**0.556**	-0.005	-0.014	0.008	0.124	0.023	-0.013	0.016	0.710**
	P	-0.002	-0.001	**0.286**	0.161	0.031	-0.003	0.004	0.071	-0.009	-0.005	0.534**
NB	G	0.873	-1.171	0.295	**-0.009**	-0.026	-0.007	0.913	0.018	-0.134	0.020	0.773**
	P	-0.014	0.001	0.104	**0.445**	0.118	0.005	-0.025	0.087	-0.023	-0.010	0.687**
NP	G	0.518	-0.631	0.211	-0.006	**-0.037**	-0.014	0.846	0.026	0.079	0.001	0.992**
	P	-0.007	0.001	0.037	0.223	**0.235**	0.006	-0.013	0.087	-0.037	0.000	0.531**
NSP	G	0.527	-0.743	-0.122	-0.002	-0.015	**-0.036**	0.525	0.010	0.006	0.014	0.165
	P	-0.009	0.001	-0.033	0.079	0.051	**0.026**	-0.015	0.057	0.001	-0.007	0.150
100S	G	-0.574	-0.731	0.043	-0.005	-0.019	-0.012	**1.619**	0.020	0.015	-0.015	0.342**
	P	0.005	0.001	-0.017	0.172	0.049	0.006	**-0.064**	0.086	0.014	0.007	0.258*
GYP	G	-0.199	-0.234	0.379	-0.005	-0.028	-0.011	0.968	**0.034**	-0.139	0.008	0.774**
	P	0.002	0.000	0.091	0.172	0.091	0.006	-0.025	**0.224**	0.000	-0.003	0.558**
PC	G	-0.161	0.581	0.015	-0.002	0.006	0.000	-0.050	0.010	**-0.483**	0.069	-0.016
	P	0.006	0.000	0.015	0.061	0.053	0.000	0.005	0.000	**-0.165**	-0.018	-0.043
OC	G	-0.431	-0.120	-0.102	0.002	0.000	0.006	0.276	-0.003	0.391	**-0.085**	-0.066
	P	0.004	0.000	-0.029	-0.100	0.001	-0.004	-0.009	-0.016	0.066	**0.046**	-0.040

DTF: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); NB: No. of branches/ plant; NP: No of pods/ plant; NSP: No. of seeds/ pod; 100S: 100 seed weight(g); GYP: Grain yield/ plant(g); CC: Correlation coefficient; PC: Protein content (%); OC: Oil content (%)

differences among genotypes for most of the traits studied, demonstrating the existence of considerable genetic variability. Genotypic mean sum of squares was highly significant for days to maturity, plant height, number of branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight, grain yield per plant, grain yield per plot and oil content, while days to 50% flowering and protein content were significant at 5%. Replication effects were non-significant for all characters, indicating uniform experimental conditions. The relatively low error mean squares for most traits suggested good experimental precision. Khumukcham *et al.,* (2023), Tandekar *et al.,* (2022) and Jain *et al.,* (2018) observed similar trends.

The mean performance of 20 soybean genotypes, including three checks (NRC-128, JS 97-52, BS-3), revealed considerable variability across agronomic and quality traits (Table 3). BAUS-170 exhibited superior grain yield/plant (13.18 g) and plot yield (0.90 kg), alongwith high plant height (75.43 cm), branches/plant (5.02) and pods/plant (74.87), while BAUS-131 and BS-3 having 13.57 g and 12.96 g grain yield/plant, respectively. Early flowering (39.00 days) and maturity (106.00 days) were recorded in BSS-2, and RSC 11-35 showed the highest oil content (20.23%). Overall trait means were 43.52 days to 50% flowering, 112.77 days to maturity, 63.40 cm plant height, 3.76 branches/plant, 63.76 pods/plant, 2.73 seeds/ pod, 11.16 g 100-seed weight, 11.10 g grain yield/plant, 0.69 kg plot yield, 40.37% protein, and 17.55% oil, reflecting substantial variability for quality traits among the genotypes evaluated.BAUS-180 had the highest protein level at 42.83% above the average of 40.37% and more than all check varieties like NRC-128 (40.20%), JS 97-52 (40.60%), and BS-3 (39.47%) followed by BAUS-173 (40.73%) and BAUS-186 (40.90%). RSC 11-35 showed high oil content of 20.23% with 17.55% trait mean and checks such as JS 97-52 (19.43%) and BS-3 (18.90%), followed by JS 97-52 and RKS-18 (18.27%).These findings were comparable to that found by Li *et al.,* (2012) and Choi *et al.,* (2021).

Genotypic variance exceeded environmental components for most traits, yielding high broad-sense heritability above 90% for branches per plant (93.20%), pods per plant (95.71%), seeds per pod (91.88%), grain yield per plot (89.42%), and oil content (95.47%) (Table 2). PCV surpassed GCV marginally, e.g., grain yield per plot (PCV 22.90%, GCV 21.66%), reflecting moderate environmental influence. Genetic advance% mean was impressive for branches (36.17%), pods (27.23%), seeds (31.37%) and plot yield (42.19%), showing strong response to selection for these yield-attributing traits. These patterns aligned with Tandekae *et al.,* (2023) and Nayak *et al.,* (2024).

Genotypic correlations were predominantly positive and significant for yield with pods per plant (0.992**), branches per plant (0.773**), plant height (0.710**), and plant yield (0.774**) (Table 4). Days to maturity positively linked to branches (0.573**) and seeds per pod (0.364**), while oil content showed a strong negative tie to protein (-0.813**). Phenotypic correlations mirrored genotypic trends but were weaker; pods and plot yield (0.531**), highlighting heritable associations ideal for indirect yield selection. These results were similar to Kalamkhede *et al.,* (2025), Ragade *et al.,* (2025), emphasising pods/plant and branches as reliable yield boosters in early sowings.

Path analysis for plot yield confirmed strong direct effects from pods per plant (0.992), plant yield (0.774), branches (0.773), and height (0.710), aligning with high correlations (Table 5). Indirect positive effects via pods bolstered branches (0.846) and height (0.211), while 100-seed weight contributed moderately (0.342) directly. Negative indirect paths, like flowering via maturity (-1.609), were minimal; residual effect was low (0.066), indicating most yield variation was accounted for, prioritizing pods and branches for breeding focus. High direct effects in yield components were consistent with that found by Conte *et al.*, (2020), Ragade *et al.*, (2025) and Thorat *et al*., (2023).

Conclusion

This study underscores the rich genetic variability among twenty soybean genotypes under rainfed *Kharif* conditions, with ANOVA confirming highly significant differences across traits like plant height, pods per plant, and oil content, paving the way for targeted selection. High heritability for key yield attributes—branches per plant, pods per plant, seeds per pod, plot yield, and oil content—paired with substantial genetic advance for plot yield, branches, pods, and seeds, signals strong additive gene action and reliable breeding progress. Genotypic correlations highlighted robust positive links between plot yield and pods per plant, branches, height and plant yield, while path analysis affirmed direct positive effects from these traits, notably pods per plant, minimizing residual influence. Top performers like BAUS-171, BAUS-131, and BS-3 excelled in yield and components, ideal for rainfed cultivation in eastern India. BAUS-180 showed superior protein content, while RSC 11-35 excelled in oil among genotypes. These insights advocate prioritizing pods and branches in selection indices to develop stable, high-yielding cultivars, addressing yield gaps amid climate variability and bolstering soybean's role in nutritional security.

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