

Genetic Evaluation of Some Newly Developed Soybean (*Glycine Max*) Genotypes at Badeggi in Niger State

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Abstract

A field experiment was conducted during 2024 at Badeggi in Niger state of Nigeria to evaluate 70 soybean (*Glycine max* L. Merrill) genotypes for genotypic and phenotypic variances, coefficient of variance, heritability, genetic advance for yield and its contributing traits. Significant variations among the genotypes, were observed for plant height (PH), days to 50 % flowering (DF), days to maturity (DM), lodging score, pod clearance (PClear), pod shattering (PShat), and 100-seed weight (SW100) and grain yield (GY). The foremost broad sense heritability values accompanied by high GA as percent of mean were demonstrated by lodging, plant height, pod clearance and 100 seeds weight, indicating that increase in these characters would improve soybeans yield. Genotypes with high pod number, large seed size, and early flowering (e.g., TGx_24_43NG-0115, TGx_24_36NG-0075, TGx_24_43NG-0120) should be prioritized as parents for crossing and further testing.

Keywords: Glycine max, genetic variability, heritability, genetic advance, soybean breeding

Introduction

Soybean (*Glycine max* (L.) Merrill) is an important leguminous crop, providing high-quality vegetable protein (approximately 40 %) and oil (approximately 20 %) for human consumption and animal feed. The United States is ranked as a leading producer, followed by Brazil, and Argentina (Abush *et al.*, 2017).

Despite the numerous benefits of the crop, its productivity remains low, averaging less than 1.5 t/ha compared to global averages of over 2.5 t/ha (FAOSTAT, 2018). The low yield is due in part to limited availability of well-adapted, high-yielding genotypes.

According to Shaahu *et al.*, 2012 the establishment and understanding of genetic variability, heritability and prediction of genetic advance are very valuable in all breeding stages or cycles, information on nature and magnitude of variability present in a population owing to genetic and non-genetic causes is an important prerequisite for a systematic breeding programme to improve the yield potential of genotypes. The need for collection of wide broad-spectrum material to form

a wide base from which selection could be made for introduction and choice of donor parents for further utilization in breeding programmes is highly important (Frankel, 1950).

As a means of increasing and ensuring reasonable high yield, the newly developed lines needed to be evaluated to identify high-yielding ones for genetic improvement of the crop (Shaahu *et al.*, 2012). To achieve a meaningful selection for improved agronomic traits, information on variability of the genotypes is therefore highly necessary. Hence, the objective of this study is to obtain information on the genetic variability existing among different maturity groups of soybean genotypes and to identify superior genotypes that will serve as parent in a systematic breeding programme.

Results and Discussion

The analysis of variance (ANOVA) for the 12 agronomic traits evaluated across 70 soybean genotypes is presented in Table 1. The mean squares revealed highly significant ($p < 0.01$) genotypic differences for plant height (PH), days to 50 % flowering (DF), days to maturity (DM), lodging score, pod clearance (PClear), pod shattering (PShat), and 100-seed weight (SW100). Grain yield (GY) showed significant genotypic differences at $p < 0.05$. However, non-significant genotypic differences were observed for nodulation (Nod), branches per plant, pods per plant, and seeds per pod, indicating limited genetic variability for these traits within the population under study. The coefficient of variation (CV) ranged from 3.588 % (days to maturity) to 62.011 % (grain yield). Low CV values for days to maturity (3.588 %), days to 50 % flowering (8.742 %), and 100-seed weight (11.933 %). Also, high CV values were recorded for pods per plant (50.874 %), and pod shattering (39.135 %) Table 2. The presence of highly significant genotypic differences ($p < 0.01$) for eight out of twelve traits indicates that substantial genetic variability exists among the 70 soybean genotypes for most agronomic characters. This finding is consistent with previous studies in soybean germplasm evaluation (Malik *et al.*, 2011; Sadeghi, 2009). The significant differences for plant height, flowering time, maturity, lodging, pod clearance, pod shattering, seed weight, and grain yield suggest that these traits have been effectively differentiated through the breeding process and provide scope for further selection. However, the non-significant genotypic differences for nodulation, branches per plant, pods per plant, and seeds per pod are concerning. These traits are important yield components, and their lack of genetic variation suggests a narrow genetic base for these characters within the population. This may be attributed to Environmental sensitivity masking genetic differences.

The high CV values for grain yield (62.01 %), pod shattering (39.135 %) and pods per plant (50.87 %) indicate substantial variability but also high environmental influence. The relatively low CV for days to maturity (3.59 %) suggests that most genotypes matured within a narrow window, which may be desirable for mechanical harvesting but limits the identification of early-maturing types for drought-prone areas

Genetic Parameters

The partitioning of variances (Table 3) revealed that high heritability was recorded in lodging, plant height, days to 50% flowering, pod shattering and pod clearance. Moderate was recorded on days to maturity and 100 seeds weight. This result indicates the presence of additive type of genes action and also the possibility of selection based on the phenotypic performance of these characters. These results are comparable to the results reported by various scientists including Shaahu *et al.* (2012), Khumukchametal. (2022), kumar *et al.* (2018) and Admasu *et al.* (2025).

Genotypic and Phenotypic Coefficients of Variation

The extent of genetic and environmental influence in the expression of a character is discerned through the phenotypic and GCV. Notably, from the on-going study, the magnitude of the PCV surpassed that of the GCV across all characters scrutinized implies that the environment significantly influenced the expression of these traits and direct selection alone may not be effective enough. Thus, opting for indirect selection is preferable for enhancing these characteristics (Abrar *et al.*, 2020). It was revealed from the current research (Table 3) that for all traits, PCV exceeded GCV, confirming that environmental factors played a substantial role in trait expression. The difference between PCV and GCV (PCV – GCV) was smallest for Days to 50 % flowering (PCV = 9.24 %, GCV = 7.73 %, difference = 1.51 %), 100-seed weight (PCV = 15.66 %, GCV = 12.21 %, difference = 3.45 %), Plant height (PCV = 30.27 %, GCV = 26.77 %, difference = 3.50 %). These traits are under relatively stronger genetic control and the result aligns with the work of (Admasu *et al.*, 2025) and (Shaahu *et al.*, 2012). The largest differences were observed for grain yield (PCV = 62.01 %, GCV = 21.36 %, difference = 40.65 %) and pods per plant (PCV = 50.87 %, GCV = 0%, difference = 50.87 %), indicating strong environmental modulation.

The heritability estimates obtained in this study range from 0 % (pods per plant, seeds per pod) to 82 % (lodging). High values of heritability were observed for Lodging (82 %), Plant height (78 %), Days to 50 % flowering (70 %), Pod clearance (68 %), Pod shattering (65 %), and 100-seed weight (60 %) table 3. These findings align with previous reports (Malek *et al.*, 2014; Pandey *et al.*, 2014; Admasu *et al.*, 2025). On the other hand, moderate heritability was recorded for Days to maturity (53 %) whereas, low heritability was recorded for Grain yield (12 %) which is a common challenge in soybean breeding (Burton, 1987) which could be due to polygenic inheritance. Nodulation (12 %) and branches per plant (7 %) also showed low heritability, likely due to the subjective scoring scales and environmental sensitivity of nodulation (influenced by soil rhizobia population). Similar results were reported (Shaahu *et al.*, 2012).

Genetic Advance (GA) and Genetic Advance as Percent of Mean (GAM)

Genetic advance as percent of mean (GAM) estimates the expected gain from selecting the top 5 % of genotypes. The highest GAM values were observed for plant height, lodging and pod clearance. Selection for these traits might be more effective than for other traits. This is also similar to the findings of Vange *et al.* (1995).

Higher heritability values, coupled with increased GA as percent of mean, typically denote more significant improvements in traits undergoing selection than relying solely on heritability (Abrar *et al.*, 2020; Johnson *et al.*, 1955). Accordingly, pertaining to the data reflected in Table 3 specifies high heritability accomplished with high GA as percent of mean for the traits, namely, lodging, plant height and pod clearance. Similar results were reported by Chandel *et al.* (2013) and Khumukcham *et al.* (2022) for 100 seed weight. This indicates that these traits are believed to be primarily controlled by additive genes and environmental factors have minimal influence on such traits. Hence, selection would be effective in the significant enhancement for these traits.

TABLE 1: Analysis of variance for 12 characters of soybean

Source of Variation	Df	PH	DF	DM	Nod	Lodging	PClear	PShat	Branches	Pods	SeedsPod	SW100	GY
Genotype	69	200.659**	35.071**	30.899**	0.280ns	0.073**	17.200**	2.555**	1.091ns	680.481ns	0.135ns	4.079**	406576.796*
Replication	2	1219.431	40.533	7.148	0.284	0.076	8.309	2.033	5.269	9477.095	0.870	2.502	5280321.349
Error	137	59.990	12.461	7.143	0.206	0.033	7.756	0.971	0.902	622.331	0.870	0.741	289808.488
CV (%)		27.956	8.742	3.588	13.918	20.748	32.433	39.135	37.122	50.874	14.025	11.933	62.011

Table 2. Basic Statistic Parameters for yield and yield components of soybean grown at Baddegi, Nigeria

Trait	Mean	SE	CV	Minimum	Maximum	Range
PH	38.758	0.749	27.96	4	89.02	85.02
DF	51.405	0.31	8.74	39	60	21
DM	107.88	0.267	3.59	95	129	34
Nod	3.4533	0.0332	13.92	2.2	4.8	2.6
Lodging	1.0381	0.0149	20.75	1	3	2
PClear	10.17	0.228	32.43	4	23	19
PShat	3.1333	0.0846	39.14	1	5	4
Branches	2.7019	0.0692	37.12	1	7.4	6.4
Pods	52.97	1.86	50.87	9.4	193.2	183.8
SeedsPod	2.6219	0.0254	14.02	2	3	1
SW100	11.446	0.0945	11.93	8.3	15.8	7.5
GY	994.1	42.5	61.9	103	3675.5	3572.5

Table 3. Genetic Parameters for 12 Agronomic Traits in 70 Soybean Genotypes

Trait	σ^2g	σ^2e	σ^2p	h^2	GCV (%)	PCV (%)	GA	GAM (%)
PH (cm)	46.89	59.99	106.88	0.78	26.77	30.27	12.92	42.28
DF (days)	7.54	12.46	20.00	0.70	7.73	9.24	4.82	12.62
DM (days)	7.92	7.14	15.06	0.53	2.65	3.09	4.22	3.98
Nod (1-5)	0.02	0.21	0.23	0.12	4.65	13.57	0.11	3.39
Lodging (1-5)	0.01	0.03	0.04	0.82	8.62	20.29	0.21	32.40
PClear (cm)	3.15	7.76	10.91	0.68	15.16	24.64	3.12	24.58
PShat (1-5)	0.53	0.97	1.50	0.65	22.22	36.02	1.22	10.18
Branches	0.06	0.90	0.96	0.07	9.17	35.24	0.14	5.20
Pods	0.00	622.33	622.33	0.00	0.00	50.87	0.00	0.00
SeedsPod	0.00	0.87	0.87	0.00	0.00	14.03	0.00	0.00
SW100 (g)	1.11	0.74	1.85	0.60	12.21	15.66	1.68	12.48
GY (kg/ha)	38922.77	289808.49	328731.26	0.12	21.36	62.01	158.46	5.48

σ^2g = Genotypic variance; σ^2e = Environmental variance; σ^2p = Phenotypic variance; h^2 = Broad-sense heritability (σ^2g/σ^2p); GCV = Genotypic coefficient of variation; PCV = Phenotypic coefficient of variation; GA = Genetic advance; GAM = Genetic advance as percent of mean

Conclusion

ANOVA highlighted adequate variances among the 70 genotypes across all the traits studied, emphasizing intensive genetic variability between the tested soybean varieties. The difference between PCV and GCV (PCV – GCV) was smallest for Days to 50% flowering, 100-seed weight and Plant height, featuring their potential importance in selecting promising soybean cultivars. The foremost broad sense heritability values accompanied by high GA as percent of mean were demonstrated by lodging, plant height and pod clearance. Thus, focusing on enhancing these traits is likely to lead to simultaneous improvements in the soy bean breeding programmes by magnifying the productivity as well as production of the crop. Genotypes with high pod number, large seed size, and early flowering (e.g., TGx_24_43NG-0115, TGx_24_36NG-0075, TGx_24_43NG-0120) should be prioritized as parents for crossing and further testing.

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