



GENETIC VARIABILITY AND SELECTION INDICES FOR YIELD AND NUTRITIONAL QUALITY OF SOYBEAN (*Glycine max* L. Merrill) IN THE SOUTHERN GUINEA SAVANNA OF NIGERIA

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ABSTRACT

Genetic improvement of soybean (*Glycine max* L. Merrill) is essential for enhancing yield and nutritional security in sub-Saharan Africa. This study evaluated the genetic variability, heritability, and genetic advance of sixteen soybean genotypes at the National Cereals Research Institute, Badeggi, Nigeria, across the 2019 and 2020 rainy seasons. Observations were recorded on various yield and yield-contributing characters, namely: days to 50% flowering, days to maturity, plant height, first pod height, stand count per plot, number of branches per plant, number of pods per plant, 100-seed weight, fodder weight per plot, and grain yield per plot at the field level. Additionally, moisture, ash, oil content, protein content, crude fibre, and total carbohydrate content were evaluated in the laboratory. Analysis of variance (ANOVA) revealed highly significant variability for all the studied characters. High values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for characters such as fodder weight (31.86/32.06), yield per plot (25.16/25.38), number of pods per plant (23.23/27.31), crude fibre (21.75/25.07), and ash content (21.18/24.55), indicating the presence of high genetic variation. High broad-sense heritability (h^2) coupled with high genetic advance as percentage of means (GAM) was observed for traits including fodder weight ($h^2 = 99\%$; GAM = 65.2), and grain yield ($h^2 = 98\%$; GAM = 51.4). Furthermore, ash (74%/37.6) and crude fibre (75%/38.9) exhibited high estimates, suggesting that these traits are governed by additive gene action and can be improved through direct selection. These results suggest that genotypes with high yield and superior nutritional profiles can be effectively utilized in future soybean improvement programs in the Southern Guinea.

Keywords: Soybean, Genetic Variability, Heritability, Genetic Advance, Guinea Savanna.

INTRODUCTION

Remarkable progress has been achieved by plant breeders in developing and releasing improved soybean (*Glycine max* L. Merrill) varieties in Nigeria. This advancement is fundamentally rooted in the knowledge derived from the extensive genetic variation existing within soybean germplasm. Recent studies

emphasize that exploring this diversity is not only crucial for yield but also for enhancing climate resilience and nutritional density in sub-Saharan Africa (Khojely *et al.*, 2018 and Ojo *et al.*, 2012). Consequently, significant scientific effort has been dedicated to exploiting the diversity among various accessions to identify high-performing genotypes and select superior individuals for crop improvement programs. In any breeding exercise, the primary objective is the genetic enhancement of grain yield. However, yield is a complex, quantitative character influenced by numerous morpho-agronomic traits and environmental factors. Modern breeding perspectives suggest that understanding the genetic architecture of yield and its contributing variables is essential for transitioning from traditional selection to more precise genomic-assisted breeding (Teixeira *et al.*, 2017 & Abdelghany *et al.*, 2020). This selection process necessitates rigorous statistical procedures, as most yield-related traits are quantitative and exhibit continuous variation.

The success of such programs depends largely on the magnitude of genetic variability present in the source material and the extent to which these traits are heritable (Bisht *et al.*, 2018). Furthermore, the inheritance of quantitative traits is often influenced by correlations with other characters, which may arise due to pleiotropy or genetic linkage (Ghimir and Sah, 2019). Research by (Azevedo *et al.*, 2021) highlights that high broad-sense heritability (h^2) estimates, when coupled with high genetic advance, are more reliable predictors of the actual genetic gain than heritability alone. Where sufficient genetic variation exists, breeders can effectively exploit additive gene effects and transgressive segregation to improve traits of interest (Khangura *et al.*, 2024).

To achieve this, the use of genetic parameters specifically the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2), and genetic advance as a percentage of Mean (GAM) is of paramount importance for evaluating breeding populations (Ravindra *et al.*, 2017).

Against this backdrop, the present study was undertaken to evaluate the variability, heritability, and genetic advance of key agronomic and quality parameters in sixteen elite soybean genotypes, with the ultimate goal of identifying ideal plant types for yield and seed quality improvement in the Southern Guinea Savanna.

MATERIALS AND METHODS

The field experiment was conducted at the experimental farm of the National Cereals Research Institute (NCRI), Badeggi, Nigeria (Latitude 9°03' N and Longitude 6°09' E; 70.5 m above sea level) during the 2019 and 2020 rainy seasons. The sixteen soybean genotypes were laid out in a Randomized Complete Block Design (RCBD) with three replications. Each plot measured 3 m x 2 m (6 m²), consisting of four rows spaced 50 cm apart with 10 cm intra-row spacing. Fertilizer was applied at the rate of 20:40:20 kg ha⁻¹ of N: P: K during land preparation.

Table 1: Rainfall Distribution of Badeggi Station

Months	2019rainfall (mm)	2020rainfall (mm)	2019 Rainy Days	2020Rainy Days
January	0.00	0.00	0	0
February	10.20	0.00	1	0
March	2.00	6.00	1	1
April	14.90	69.00	2	4
May	176.40	256.00	11	14
June	179.60	207.00	13	12
July	186.80	167.00	14	11
August	324.50	63.00	18	7
September	309.20	495.10	20	23
October	130.40	155.80	9	10
November	2.10	12.50	0	1
Total	1,336.10	1,431.40	90	83

Source; (NAERLS, 2020)

Data Collection

Agronomic data were collected from the two central rows of each plot. Traits recorded included days to 50% flowering, days to maturity, plant height (cm), number of pods per plant, lowest pod heights (cm) pods/plant, number primary branching/plant, fodder weight, hundred seed weight.

Proximate Analysis Procedures

The nutritional composition of the seeds was determined using the methods described in (AOAC, 2006)

- Moisture Content: Determined by the air-oven method at 105°C until a constant weight was reached.
- Crude Protein: Determined using the micro-Kjeldahl method. Total nitrogen was digested and distilled, and the protein content was calculated using the nitrogen-to-protein conversion factor of 6.25.
- Crude Fat (Ether Extract): Extracted using a Soxhlet extractor with petroleum ether as the solvent for 6 hours.
- Crude Fibre: Determined by sequential acid and alkali digestion, followed by incineration of the residue in a muffle furnace.
- Ash Content: Determined by incinerating 2g of the sample in a muffle furnace at 550°C for 5 hours until a white/grey ash was obtained.
- Total Carbohydrates: Calculated by difference using the formula: $\% \text{ Carbohydrates} = 100 - (\% \text{ Moisture} + \% \text{ Protein} + \% \text{ Fat} + \% \text{ Ash} + \% \text{ Crude Fibre})$.

- vii. Energy content: Obtained by multiplying the mean values of crude protein, crude fat and total carbohydrate by the Atwater factors of 4, 9, 4 respectively, taking the sum of the products and expressing the result in kilocalories per 100 g sample (Etiosa *et al.*, 2017).

Statistical Analysis

The data were subjected to Analysis of Variance (ANOVA). Genetic parameters, including Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), Broad-sense Heritability (h^2), and Genetic Advance as percentage of Mean (GAM) were estimated using the formulas described by (Johnson *et al.*, 1955 & Burton and Davane, 1953). All calculations were performed using Crop Stat software version 7.2 (IRRI, 2007).

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) revealed highly significant differences ($P \leq 0.01$) among genotypes for most studied traits Table 2. Similar result was reported by (Baraskar *et al.*, 2014) where the analysis of variance revealed that mean squares due to genotypes were significant for all the characters indicating varietal differences for all the characters studied. This is an indication for the existence of considerable genetic variability among the genotypes for most of the traits and as such there is ample scope of selection for different quantitative traits for improvement of the crop. The highly significant 'Trial effect' in Table 2 confirms that the two seasons (2019 and 2020) were drastically different due to the recorded drought. In quantitative genetics, such environmental variation is common when field trials are subjected to abiotic stress. According to the National Agricultural Extension and Research Liaison Services (NAERLAS, 2020) wet season survey, the region experienced a significant mid-season dry spell which overlapped with the critical flowering and pod-filling stages. Oyeleke, *et al.*, 2018 noted that, such moisture stress in North-Central Nigeria increases phenotypic instability in soybean. However, despite this environmental static, the Genotype effect remained highly significant ($P < 0.01$) for all traits. Following the logic of (Johnson *et al.*, 1955) and when high heritability ($h^2 > 90\%$) persists alongside high CV, it indicates that the genetic variance (V_g) is so robust that it transcends environmental fluctuations.

For each of the traits evaluated, the descriptive statistics including the extreme genotype mean values which formed the range and their means together with their standard errors obtained on the basis of average data are summarized in Table 3. The analysis showed wide range of variability for most of the characters and all the traits exhibited broad spectrum of ranges between the maximum and minimum mean values. For instance, days to 50%flowering ranged from 32 to 46 with a mean of 40.57 days while, days to maturity ranging from 88 to 131 with a mean of 104 days. Similarly, plant height and first pod height ranged from (33.2 to 56.6) cm and (7.6 to 13.4) cm, respectively. Branches of the tested genotypes varied from 1.6 to 7.5 with mean of 4.64 branches per plants. Grain yielding ability ranged from 160-675g (equivalent to 0.27 to 1.13 t ha⁻¹) while, weight of 100 seeds weight ranged from 10g to 23g with a mean of 13.71g. In respect to these mean values for all evaluated characters, the existence

of required diversity for breeding purposes is established and it is possible to succeed in improving yield through selection. The mean values obtained for agronomic parameters are in agreement with previous findings by several authors.

Table 2: Analysis of variance for agronomic and proximate traits of 16 soybean genotypes

Traits	Mean sum of square					
	Trial (df=1)	Block (df=4)	Genotype (df=15)	Trial: Genotype (df=15)	Pooled Error (df= 60)	(CV)
D50F	58.5938**	2.3333 ^{ns}	63.5771**	46.0382**	1.5556	3.07
DTM	7245.375**	11.271 ^{ns}	408.397**	240.953**	10.837	3.16
PHAM	1230.518**	5.5004 ^{ns}	52.511**	61.853**	7.021	5.91
FPH	3.190 ^{ns}	1.815 ^{ns}	3.3145**	3.498**	0.776	8.18
NPPP	488.704*	27.303 ^{ns}	284.634**	315.418**	32.0848	14.34
NBPP	5.876*	0.632 ^{ns}	1.547*	3.159**	0.712	18.19
YPP	386715.1**	73.8646 ^{ns}	23921.11**	46100.58**	140.542	3.35
FWPP	49868.17**	89.4792 ^{ns}	33138.42**	46973.63**	141.268	3.61
100SW	0.107	1.564	13.124**	4.0518*	1.444	8.77
MC			1.932*		0.126	6.28
ASH			6.106**		0.627	12.41
CFA			27.615*		0.305	3.03
CP			14.662**		2.707	5.05
CFB			2.7781*		0.274	12.45
CHO			46.024**		8.452	8.84
EV			1023.745**		18.453	1.01

*Significant at $P=0.05$ level, ** Significant at $P=0.01$ level. ^{ns} not significant where; D50F=days to 50% flowering, DTM=days to 95% maturity, PHAM= plant height at maturity (cm), FPH=first pod height (cm), NPPP= number of pod/plant, NBPP= number of branches /plant, YPP= yield/plot (g), FWPP= fodder weight /plot (g), 100SW= weight of 100 seeds (g), MC= moisture content (%), ASH= ash content (%), CFA= crude fat (%), CP= crude protein (%), CFB= crude fibre (%), CHO=Total carbohydrate (%) and EV= energy value (K/cal).

Note: Proximate traits were analyzed on pooled samples; degrees of freedom for Trial and Block do not apply.

For example, (Chandrawat *et al.*, 2017) observed that weight of 100 seed of soybean can reach up to 26g. Other parameters that can be associated to his findings include, days to 50% flowering, number of branches per plant and oil content. The extreme values obtained for days to 95% maturity can be justified by maximum value observed by (Ali *et al.*, 2016) and the minimum value recorded by (Ravindra *et al.*, 2017). The latter also support the values obtained for plant height and possible number of pods per plant.

Table 3: Summary of Means Performance of 16 soybean genotypes

Variable	Min	Max	Mean	SE Mean
D50F	32	46	40.57	0.44
DTM	88	131	104.27	1.39
PHAM	33.2	56.6	44.82	0.61
FPH	7.6	13.4	10.77	0.13
NPPP	20.6	73.2	39.49	1.12
NBPP	1.6	7.5	4.64	0.12
YPP	160	675	353.93	12.59
FWPP	89	540	329.23	11.76
100SW	10	23	13.71	0.2
MC	4.75	6.47	5.65	0.06
ASH	4.87	8.42	6.38	0.12
CFA	15.9	23.79	18.19	0.22
CP	28.11	36	32.57	0.21
CFB	2.85	5.55	4.2	0.08
CHO	27.16	37.83	32.87	0.36
EV	404.46	465.93	424.88	1.34

where; D50F=days to 50% flowering, DTM=days to 95% maturity, PHAM= plant height at maturity (cm), FPH=first pod height (cm), NPPP= number of pod/plants, NBPP= number of branches/plant, YPP= yield/plot (g), FWPP= fodder weight/plot (g), 100SW= weight of 100 seeds (g), MC=moisture content (%), ASH= ash content (%), CFA= crude fat (%), CP= crude protein (%), CFB= crude fibre (%), CHO=Total carbohydrate (%) and EV= energy value (K/cal).

The range of variation was also wide for Ash content, fibre, protein, crude fats and carbon content. All the mean values obtained for each proximate variables evaluated have similarity with the values revealed by (Etiosa, *et al.*, 2017). The wide range of variation observed for traits such as grain yield (equivalent to 0.27 to 1.13 t ha⁻¹) and protein content (28.11 – 36%) suggests that these genotypes can be effectively utilized for both yield enhancement and nutritional bio-fortification.

Table 4: Estimate of Variance Components, Heritability and Genetic Advance as Percentage of Means

Traits	Mean	σ^2_g	σ^2_p	h^2	GCV	PCV	GAM
D50F	40.57	20.67	22.23	0.93	11.21	11.62	22.26
DTM	104.27	132.52	143.36	0.92	11.04	11.48	21.87
PHAM	44.82	15.16	22.18	0.68	8.69	10.51	14.80
FPH	10.77	0.85	1.62	0.52	8.54	11.83	12.71
NPPP	39.49	84.18	116.27	0.72	23.23	27.31	40.73
NBPP	4.64	0.28	0.99	0.28	11.37	21.45	12.41

Traits	Mean	σ^2_g	σ^2_p	h^2	GCV	PCV	GAM
YPP	353.93	7926.86	8067.40	0.98	25.16	25.38	51.37
FWPP	329.23	10999.05	11140.32	0.99	31.86	32.06	65.20
100SW	13.71	3.89	5.34	0.73	14.39	16.85	25.32
MC	5.65	0.60	0.73	0.83	13.73	15.10	25.73
ASH	6.38	1.83	2.45	0.74	21.18	24.55	37.65
CFA	18.19	9.10	9.41	0.97	16.59	16.86	33.61
CP	32.57	3.99	6.69	0.60	6.13	7.94	9.74
CFB	4.2	0.83	1.11	0.75	21.75	25.07	38.88
CHO	32.87	12.52	20.98	0.60	10.77	13.93	17.14
E.V	424.88	335.10	353.55	0.95	4.31	4.43	8.64

Where, σ^2_g : genotypic variance, σ^2_p : phenotypic variance GCV: genetic co-efficient of variation, PCV: phenotypic co-efficient of variation, h^2 : heritability, GAM: genetic advance as percent of mean; D50F=days to 50% flowering, DTM=days to 95% maturity, PHAM= plant height at maturity (cm), FPH=first pod height (cm), NPPP= number of pod/plant, NBPP= number of branches/plant, YPP= yield/plot (g), FWPP= fodder weight/plot (g), 100SW= weight of 100 seeds (g), MC=moisture content (%), ASH= ash content (%), CFA= crude fat (%), CP= crude protein (%), CFB= crude fibre (%), CHO=Total carbohydrate (%) and EV= energy value (K/cal).

In the present study, most characters showed moderate GCV and PCV values. Although, the estimated values of PCV were slightly higher than GCV for all the characters studied indicating role of environment on the performance of soybean genotypes. A noteworthy difference between GCV and PCV was observed for plant height and first pod height where the differential values consequently changed the classifications of the individual PCV from low to moderate. Another noticeable difference in partitioning was exhibited for number of branches per plant where the GCV value was moderate but the corresponding PCV was high. These discrepancies in portioning for one trait or the other were also observed in the study carried out by (Ali *et al.*, 2016) for pod formation, (Bairwa *et al.*, 2020) for yield and (Jandong 2020) for number of branches per plant. However, high values of GCV and PCV were revealed for fodder weight (31.86/32.06), yield per plot (25.16/25.38), number of pods per plant (23.23/27.31), Fibre (21.75/25.07) and Ash (21.18/24.55). Similar trend of high GCV and PCV was reported for yield, fodder weight and number of pods per plant by (Bisht *et al.*, 2018). On the other hand, low GCV and PCV values (6.13/7.94) and (4.31/4.43) were observed for crude protein and energy value respectively. Comparable values were recorded for protein in the study conducted by (Neelima *et al.*, 2018). The coefficient of variation indicates only the extent of variability existing for various characters, but does not give any information regarding heritable proportion of it. Hence, amount of heritability permits greater effectiveness of selection by separating out the environmental influence from the total variability and to indicate accuracy with which a genotype can be identified phenotypically.

In present study, broad sense heritability, which includes both additive and non-additive gene effects, was estimated. The estimate of heritability acts as predictive instrument in expressing the reliability of phenotypic value. These estimated values were classified as low ($< 30\%$), medium ($30\text{--}60\%$) and high as ($>60\%$) in accordance to the (Johnson *et al.*, 1955) recommendations. In general, high estimates of heritability were found for most traits except for NBPP which showed the least heritability estimates (28%). Low heritability estimate for this trait was reported by (Kuswantoro *et al.*, 2017). Thus, phenotypic selection for this character in subsequent generations will be ineffective.

Moderate heritability was observed for CP (60%) and FPH (52%). Similar results were reported by (Lyima *et al.*, 2017 & Azevedo *et al.*, 2021) respectively. Even though these traits had less environmental influence on account of low environmental variances, improvement of these traits by selection will not be possible as the heritable variation among genotypes was meager.

Characters with highest heritability values were; FWPP (99%), YPP (98%), CF (97%), EV (95%), D50F (93%) and DTM (92%). These values were comparable to the value recorded in (Baiwa *et al.*, 2020) for fodder weight, while the values for days 50% flowering and days to maturity reported in the results of (Teixeira, *et al.*, 2017). The value for crude fats (oil) here matched that reported by (Ali *et al.*, 2016). High heritability values indicated that, these traits were less influenced by the environment in their expressions. As such, selection can be safely made on the basis of phenotypic expressions.

Yield being a complex character is influenced by many factors. In the present study, high heritability coupled with high genetic advance as percent mean was observed for most variables. These included; fodder weight (99%/65.2), seed yield per plot (98%/51.4), crude fat (97%/33.6), days to 50% flowering (93%/22.3), days to maturity (92%/21.9), number of pods per plant (72%/40.7), Ash (74%/37.6), 100 seed weight (73%/25.3), and fibre (75%/38.9). Similar observations were made by (Bairwa *et al.*, 2020) for number of pods plant, (Vikram *et al.*, 2014) for fodder weight, (Datta *et al.*, 2005) for 100 seed weight, (Ghimire and Sah, 2019) for yield and days to 50% flowering. This result indicates the lesser influence of environments in expression of characters and prevalence of additive gene action in their inheritance.

High heritability with moderate genetic advance as percent of mean was recorded for plant height at maturity (68%/14.8) only. The results indicate that these characters were less influenced by environment but governed by additive and non-additive gene action.

The character, Energy Value exhibited (95%/8.6) high heritability with low genetic advance as percent of mean. It only implies that expression of this character may be due to non-additive gene action.

CONCLUSIONS

This study provides a comprehensive assessment of the genetic architecture governing yield and nutritional quality in soybean genotypes within the Southern Guinea Savanna of Nigeria. The analysis of variance revealed extensive phenotypic variability across all sixteen genotypes, confirming a rich genetic reservoir for future breeding efforts. While environmental factors, including a recorded mid-season

drought in 2020, influenced performance as evidenced by phenotypic coefficients of variation (PCV) consistently exceeding genotypic coefficients (GCV) the underlying genetic variance remained robust for several critical traits.

The most significant finding of this research is the identification of traits governed by additive gene action, characterized by high broad-sense heritability coupled with high genetic advance. Specifically, fodder weight per plot ($h^2 = 99\%$; GAM = 65.2) and grain yield per plot ($h^2 = 98\%$; GAM = 51.4) emerged as the most reliable selection markers. Furthermore, the high heritability and genetic gain observed for ash (74%) and crude fibre (75%) indicate that nutritional bio-fortification can be effectively pursued alongside yield enhancement.

In contrast, the low heritability observed for the number of branches per plant (28%) suggests that phenotypic selection for this character will be largely ineffective. Consequently, future improvement programs should prioritize genotypes that combine high grain yield with optimal proximate compositions, utilizing the identified high-gain traits as primary selection indices. These findings offer a clear strategic pathway for developing high-performing, resilient soybean varieties tailored to enhance food and nutritional security in the Southern Guinea Savanna region.

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