Expression of Metrical Traits on Yield and its Components in Different Accessions of Soybeans (*Glycine max* (L.) Merrill)

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***Abstract*—Low productivity in soybean (*Glycine max* L. Merrill) across Nigerian farming systems remains a persistent challenge, driven in part by the limited use of genetically diverse and locally adapted cultivars. This study evaluated the expression of yield-related traits among ten soybean accessions obtained from the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria, to identify superior genotypes and inform selection strategies for yield improvement. The experiment was conducted in a Randomized Complete Block Design (RCBD) with three replications at the research farm of Adekunle Ajasin University, Akungba-Akoko, Ondo State, Nigeria. Data were collected on nine quantitative traits: plant height, number of main branches, days to first flowering, days to maturity, pod length, pods per plant, seeds per pod, 100-seed weight, number of seeds per plant, and seed yield per plant. Analysis of variance revealed significant genotypic effects ($p \leq 0.05$) for most traits, except for the number of main branches and pods per plant. Accession V9 recorded the highest seed yield per plant (16.14 g), pods per plant (23.80), seeds per pod (3.53), and number of seeds per plant (84.71), while V5 produced the heaviest 100-seed weight (22.27 g). Genetic parameter estimates showed that days to first flowering had the highest broad-sense heritability (92.89%), followed by pod length (72.08%) and seeds per pod (70.58%), all with moderate to high genetic advance. Pearson's correlation analysis revealed highly significant positive associations between seeds per pod and number of seeds per plant ($r = 0.93$), number of seeds per plant and seed yield per plant ($r = 0.87$), and seeds per pod and seed yield per plant ($r = 0.78$). These findings identify V9 as the most promising accession for yield improvement and recommend seeds per pod and number of seeds per plant as the most reliable indirect selection criteria for advancing soybean yield within this germplasm.**

***Keywords*—quantitative traits, genetic parameters, correlation analysis, broad-sense heritability, indirect selection**

I. Introduction

Soybean (*Glycine max* L. Merrill), a member of the family Fabaceae, subfamily Papilionoideae, holds a central position in global agriculture owing to its exceptional nutritional profile, economic importance, and wide range of industrial applications. Its cultivation traces back more than 5000 years to East Asia, where it was domesticated from its wild progenitor Glycine soja, a process now understood to have involved considerable genomic restructuring and loss of rare alleles [1]. As a diploid short-day plant ($2n = 40$), soybeans have demonstrated remarkable adaptability across temperate and tropical agroecological zones, which explains much of their reach as a global crop [2]. Today, it sits at the intersection of food security and agricultural sustainability, contributing to human nutrition, livestock feed, and a diverse set of industrial products, including biofuels, adhesives, and pharmaceuticals [3].

The average protein content of soybeans falls between 35 and 40%, while oil content ranges from 18% to 22%, placing it well above most other legumes as a plant-based protein source [4]. Its amino acid profile is notable for high lysine concentration, and the seed additionally supplies unsaturated fatty acids, B-complex vitamins, and minerals including calcium, phosphorus, and iron [5]. Soybeans also contain isoflavones, bioactive compounds associated with reduced cardiovascular risk and improved bone health [3]. Beyond human consumption, soybean oil is among the most widely consumed edible oils in the world, while the protein-rich residual meal supports the poultry, swine, and aquaculture industries [4]. Global production has climbed steadily in response to this demand, reaching an estimated 406 million metric tons in 2023, with the United States, Brazil, and Argentina accounting for roughly 80% of the world's supply [6].

Within Africa, Nigeria leads soybean production, with cultivation concentrated in the Guinea and Sudan

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savannah belts across states including Benue, Kaduna, and Kano [7]. Despite this regional prominence, average yields at the farm level sit between 0.8 and 1.2 tons per hectare, a figure well below the global norm of 2.5 to 3.0 tons per hectare [8]. This yield gap reflects overlapping biotic and abiotic pressures. Pests such as the soybean aphid (*Aphis glycines*) and diseases, including soybean rust (*Phakopsora pachyrhizi*) and frogeye leaf spot (*Cercospora sojina*) can cause yield losses of up to 40% under field conditions [9]. Abiotic constraints, particularly drought and poor soil fertility in rainfed systems, compound these losses further, with drought alone capable of reducing yields by 20–50% depending on the growth stage affected [10].

An underlying constraint to breeding progress is the narrow genetic base of cultivated soybean. Research has demonstrated that domestication from Glycine soja caused the loss of approximately half of the available sequence diversity and more than 80% of rare alleles, a bottleneck that limits the raw genetic variation available for yield improvement [11]. This narrowing restricts the capacity of breeding programs to simultaneously address yield, stress tolerance, and environmental adaptability within the existing elite germplasm pool [12]. Landraces, wild relatives, and underutilized accessions represent potential reservoirs of novel alleles, particularly for traits related to drought tolerance, pest resistance, and nutrient use efficiency, yet their systematic utilization in Nigerian breeding programs remains limited.

Soybean yield is a polygenic trait expressed through the interaction of several components, most notably pods per plant, seeds per pod, seed weight, and plant height [13]. Each of these components responds to both genetic and environmental drivers, making systematic phenotypic evaluation across diverse accessions an essential step in any effort to identify superior genotypes for local production environments. The present study, therefore, evaluates yield trait expression across a range of soybean accessions under local agro-ecological conditions. Specifically, it seeks to assess phenotypic variation in yield-related traits, identify accessions with superior yield performance in the Guinea and Sudan savannah zones of Nigeria, and determine the relationships among key yield components across the accessions evaluated.

II. Materials and Methods

Soybean seeds of ten accessions were obtained from the International Institute of Tropical Agriculture (IITA), Ibadan, Oyo State, Nigeria (Table I). The study was conducted at the experimental field of the Department of Plant Science and Biotechnology, Adekunle Ajasin University, Akungba-Akoko, Ondo State, Nigeria. One hundred and fifty perforated plastic pots, each filled with 7 kg of topsoil, were used to ensure adequate drainage. The ten accessions were evaluated in a Randomized Complete Block Design (RCBD) with three replications. Two seeds were planted per pot and later thinned to one seedling per pot at two weeks after sowing. Weeds were removed by hand at regular intervals throughout the growing season. Cypermethrin insecticide was applied at recommended rates to control insect pest infestation.

TABLE I. Soybean Accessions and their Source

S/N	Accession ID	Source
1	TGM 1235	IITA
2	TGM 1244	IITA
3	TGM 1249	IITA
4	TGM 1254	IITA
5	TGM 4132	IITA
6	TGM 4134	IITA
7	TGM 4136	IITA
8	TGM 4336	IITA
9	TGM 4338	IITA
10	TGM 4398	IITA

III. Data Collection

Data were collected on nine quantitative traits beginning five weeks after sowing. The traits measured were days to first flowering, plant height (cm), number of primary branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight (g), seed yield per plant (g), and days to maturity. Data were collected from five selected plants from each accession in every plot, 14 days after the application of insecticide (cypermethrin). Measurements were taken using a measuring tape (cm), a weighing balance (g), a field notebook and a pen.

IV. Statistical Analysis

Data collected were subjected to analysis of variance (ANOVA) following the procedure of Singh and Chaudhary [14]. Treatment means were separated using Duncan's Multiple Range Test (DMRT) at $p \leq 0.05$ with SPSS version 22. Genetic parameters were estimated following the procedure of Osekita *et al.* [15].

Genotypic Variance (VG) and Phenotypic Variance (VP) were estimated according to Wricke and Weber [16]:

$$\mathrm{VG} = \left(\frac{MSg - MSe}{r}\right)$$

$$\mathrm{VP} = \mathrm{VG} + \mathrm{MSe}$$

where MSg = mean square for genotype, MSe = mean square for error, and r = number of replications.

The Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were computed following Osekita and Ajayi [17]:

$$\mathrm{PCV}\ (\%) = \left(\frac{\sqrt{VP}}{\bar{x}}\right) \times 100$$

$$\mathrm{GCV}\ (\%) = \left(\frac{\sqrt{VG}}{\bar{x}}\right) \times 100$$

where $\bar{x}$ is the grand mean. Values were classified according to Sivasubramanian and Madhavamenon [18] as

low (0–10%), moderate (10–20%), and high (>20%). The Coefficient of Variation (CV) was calculated as:

$$\text{CV}\ (\%)\ = \left(\frac{\sqrt{MSe}}{Gm}\right) \times 100$$

where Gm = grand mean.

Broad-sense heritability (H^2B) was estimated as the ratio of VG to VP and classified according to Robinson *et al*. [19], as low (0–30%), moderate (30–60%), and high (>60%). Genetic Advance (GA) and genetic advance as a percentage of the mean (GAM) were estimated following Johnson *et al.* [20]:

$$\text{GA}\ = \left(\frac{H^2B}{100}\right) \times K \times \sqrt{VP}$$

$$\text{GAM}\ (\%)\ = \left(\frac{GA}{GM}\right) \times 100$$

where $K = 2.06$ (selection intensity at 5%) and GM = grand mean. GAM was categorized as low (0–10%), moderate (10–20%), and high (>20%). Pearson's correlation coefficients among yield traits were computed using SPSS version 20, with significance assessed at $p \leq 0.05$ and $p \leq 0.01$, and degrees of freedom as $n - 2$.

V. Results and Discussion

A. Analysis of Variance and Genotypic Differences

The analysis of variance (Table II) revealed significant genotypic effects ($p \leq 0.05$) for most of the yield-related traits evaluated, including plant height, days to first flowering, days to maturity, pod length, seeds per pod, 100-seed weight, number of seeds per plant, and seed yield per plant. This pattern of significance indicates that the ten accessions carry meaningful genetic differences for these traits, and that selection among them could produce measurable improvements. The non-significance of genotype effects on the number of main branches and pods per plant suggests that environmental conditions and management factors more strongly influence these two traits than genetic background. This is broadly consistent with observations from earlier studies [21] working with soybean genotypes across Guinea Savannah environments, who similarly reported non-significant genotype effects for certain vegetative traits, while yield-defining traits showed clear significance. Addae-Frimpomaah *et al.* [22], evaluating 150 accessions from Ghana, Nigeria, the United States, and Colombia in alpha-lattice trials, also reported significant genotypic differences across all evaluated traits, affirming that the accessions carried sufficient genetic variability to sustain selection programmes.

Replication effects were non-significant for all traits, which confirms that the experimental blocks were homogeneous and that the RCBD was appropriately designed for this study. The Coefficient of Variation (CV) ranged from 1.60% for days to maturity to 28.82% for number of main branches. Low CV values for days to maturity and days to first flowering reflect the precision with which phenological traits were recorded, while the higher CV for branching reflects the inherently plastic nature of that trait in response to pot conditions and intra-plant competition. Singh and Chaudhary [14] note that CV values below 20% are generally considered acceptable for most agronomic experiments, and the majority of traits in this study fell within that boundary.

TABLE II. Mean Square Values from Analysis of Variance (ANOVA) for Quantitative Traits among Different Accessions of Soybeans

Source of variation	DF	PH (cm)	NMB	DFF	DTM	PDL (cm)	PDP	SPP	SW (g)	NSDPL	SDYPL (g)
Genotype	9	43.78*	20.04^{ns}	56.51*	22.48*	1.02*	20.46^{ns}	0.25*	10.12*	416.90*	14.91*
Replicate	2	3.73^{ns}	1.78^{ns}	0.26^{ns}	0.10^{ns}	0.12^{ns}	4.68^{ns}	0.01^{ns}	1.93^{ns}	66.77^{ns}	0.31^{ns}
Error	18	8.60	10.24	1.41	2.47	0.12	9.59	0.03	4.71	149.88	5.78
Coefficient of variation (%)		15.43	28.82	3.36	1.60	7.76	15.96	5.58	11.37	20.18	20.87

*: Significant at $p \leq 0.05$, ns: Not Significant. DF: Degree of freedom. PH: Plant height; NMB: Numbers of main branches; DFF: Days to first flowering: PDL; Pod length; PDP: Pod per plant; SPP: Seed per pod; SW; 100-seed weight; NSDPL: number of seed per plant; SDYPL: Seed yield per plant.

B. Mean Performance of Accessions for Yield Traits

Table III presents the mean performance of soybean genotype for various quantitative traits. Plant height varied from 12.28 cm in V4 to 25.77 cm in V5, with a grand mean of 19.01 cm. These values reflect the range expected from pot-grown plants under controlled conditions, where root volume and soil volume are constrained relative to field conditions. Studies conducted under field conditions typically report considerably greater plant heights; for instance, Chandrawat *et al*. [23] reported plant heights ranging from 40 to over 85 cm across soybean genotypes evaluated under field conditions in India, while Joshi *et al*. [24] similarly documented heights well above 50 cm in field-grown germplasm. However, the relative differences among accessions observed here remain informative for breeding selection, as the rank order of genotypes for plant height tends to be maintained across pot and field environments [2]. V5 and V6 consistently ranked among the tallest accessions, suggesting these lines carry alleles promoting greater internode elongation, a trait associated with improved light interception and biomass accumulation under high-density field conditions [25].

Days to first flowering ranged from 30.80 d in V1 to 43.93 d in V10, representing a span of approximately 13 days. This level of variation in flowering time is agronomically important because soybean is a short-day, photoperiod-sensitive crop, and the timing of floral initiation determines how long the vegetative period lasts

and how well the crop aligns its reproductive stages with the available moisture window [2]. V1 emerged as the earliest-flowering accession, a characteristic of potential value in environments with a short or unpredictable rainy season, such as the Sudan savannah zone of Nigeria. Studies conducted in northern Ghana by Addae-Frimpomaah *et al*. [22] showed that earlier-maturing genotypes flowered and matured ahead of their later counterparts, though early maturity did not always translate into higher grain yield due to adaptation effects. The present data suggest a similar pattern, with V10 recording both the latest first flowering (43.93 d) and the longest days to maturity (103.13 d), which could limit its suitability in short-season environments. Assfaw *et al*. [26], working with soybean genotypes across three agroecological zones in Nigeria, found highly significant genotypic effects for days to flowering, confirming that this trait is reliably heritable and responsive to selection across Nigerian growing environments.

Days to maturity across all accessions ranged from 94.40 days in V3 to 103 days in V10. These figures place all accessions within the medium-maturity category typically defined for tropical soybean. Khojely *et al*. [8] noted that maturity group differences are among the primary drivers of yield variation across sub-Saharan environments, and that varieties matching the length of the local rainy season tend to yield more reliably than those that mature prematurely or require a longer season than is available. Similar maturity ranges of 93 to 107 d have been reported by Mofokeng [27] and Jandong *et al*. [21] for tropical soybean accessions grown in comparable agroecological zones.

Pod length ranged from 3.35 cm in V4 to 5.13 cm in V6, with a grand mean of 4.40 cm. These values are consistent with published data for tropical soybean accessions. For instance, Joshi *et al*. [24] reported pod lengths between 3.80 and 5.60 cm in a germplasm study of 120 soybean genotypes, a similar range of longer pods, as observed in V2, V5, and V6, are generally associated with higher seed-filling capacity and are therefore desirable in breeding programmes targeting greater seed size and individual seed weight.

V9 stood out as the best-performing accession for several key yield components, recording the highest number of pods per plant (23.80), seeds per pod (3.53), seeds per plant (84.71), and seed yield per plant (16.14 g). V5 recorded the highest 100-seed weight at 22.27 g. These results are particularly instructive when viewed alongside each other, as they illustrate a common trade-off in soybean yield physiology: accessions with greater seed number per plant do not necessarily produce the heaviest individual seeds. This finding aligns with the broader soybean yield physiology literature, which consistently identifies seed number per unit area as the primary driver of yield variation, with seed weight playing a compensatory rather than additive role [25].

TABLE III. MEAN PERFORMANCE FOR QUANTITATIVE TRAITS OF DIFFERENT ACCESSIONS OF SOYBEANS

Genotype	PH (cm)	NMB	DFF	DTM	PDL (cm)	PDP	SPP	SW (g)	NSDPL	SDYPL (g)
V1	15.14±0.64^{ab}	8.73±0.18^{a}	30.80±0.20^{a}	97.33±0.59^{bc}	3.83±0.02^{ab}	17.47±1.69^{a}	3.13±0.07^{bc}	20.07±0.07^{abc}	54.76±5.68^{ab}	10.98±1.11^{ab}
V2	20.30±0.48^{bc}	10.00±0.20^{a}	31.53±0.13^{ab}	99.00±0.61^{cd}	4.97±0.07^{d}	21.80±1.96^{ab}	3.27±0.07^{cd}	17.33±1.50^{ab}	71.44±7.78^{bc}	12.47±1.89^{abc}
V3	20.13±1.47^{bc}	9.87±0.13^{a}	32.67±0.52^{ab}	94.40±1.27^{a}	4.62±0.26^{cd}	20.87±1.88^{ab}	3.07±0.13^{bc}	16.93±1.19^{b}	64.37±7.99^{abc}	11.08±2.13^{ab}
V4	12.28±0.29^{a}	11.87±0.64^{ab}	31.67±0.35^{ab}	97.27±1.17^{bc}	3.35±0.08^{a}	17.67±0.93^{a}	2.87±0.07^{b}	20.93±1.99^{cd}	50.63±2.70^{ab}	10.53±0.81^{ab}
V5	25.77±2.17^{d}	8.87±2.10^{a}	35.07±0.33^{cd}	95.73±0.48^{ab}	5.05±0.12^{d}	16.40±0.31^{a}	3.47±0.07^{d}	22.27±1.35^{c}	56.84±1.23^{ab}	12.69±1.03^{abc}
V6	22.73±3.95^{cd}	9.47±1.51^{a}	35.07±0.27^{cd}	96.80±0.20^{abc}	5.13±0.09^{d}	16.53±2.78^{a}	3.13±0.07^{bc}	16.53±0.48^{a}	52.11±9.57^{ab}	8.55±1.37^{a}
V7	17.67±0.78^{bc}	10.33±0.66^{a}	36.67±0.24^{d}	101.00±0.50^{de}	4.31±0.28^{bc}	20.20±1.91^{ab}	3.00±0.12^{bc}	18.13±0.41^{ab}	61.04±8.08^{ab}	11.04±1.42^{ab}
V8	17.33±1.16^{abc}	12.20±1.22^{ab}	33.60±0.23^{bc}	95.93±1.17^{ab}	4.23±0.39^{bc}	17.47±1.23^{a}	2.53±0.13^{a}	19.73±1.39^{abc}	43.92±0.97^{a}	8.65±0.49^{ab}
V9	20.73±1.28^{cd}	17.47±0.37^{b}	41.27±1.53^{e}	100.53±0.87^{de}	4.61±0.17^{cd}	23.80±2.36^{b}	3.53±0.13^{d}	19.33±1.45^{abc}	84.71±11.74^{c}	16.14±1.49^{c}
V10	18.01±0.51^{bc}	12.20±4.70^{ab}	43.93±1.10^{f}	103.13±1.05^{e}	3.93±0.18^{ab}	21.80±0.81^{ab}	3.07±0.07^{bc}	19.60±0.92^{abc}	66.89±3.29^{abc}	13.05±0.18^{bc}
Grand mean	**19.01±0.80**	**11.10±0.65**	**35.23±0.78**	**98.11±0.53**	**4.40±0.12**	**19.40±0.65**	**3.11±0.06**	**19.09±0.45**	**60.67±2.75**	**11.52±0.52**

Means with the same superscript within a column are not significantly different from one another at $p \leq 0.05$ using DMRT. PH: Plant height; NMB: Numbers of main branches; DFF: Days to first flowering: PDL; Pod length; PDP: Pod per plant; SPP: Seed per pod; SW; 100-seed weight; NSDPL: Number of seed per plant; SDYPL: Seed yield per plant.

C. Estimates of Genetic Parameters

The estimates of phenotypic (PCV) and genotypic (GCV) coefficients of variation presented in Table IV provide an initial indication of the extent of variability present and its genetic basis. PCV values were consistently higher than GCV values for all traits, which reflects the contribution of environmental factors to total phenotypic variation. This pattern has been widely reported in soybean germplasm studies [24, 26] and confirms that the environment modulates trait expression even when genetic differences among genotypes are real and significant.

Plant height recorded a high PCV (23.72%) and moderately high GCV (18.01%), coupled with moderate broad-sense heritability (H^2B = 57.69%) and a high genetic advance as a percentage of the mean (GAM = 28.19%). The combination of moderate-to-high heritability and high genetic advance suggests that additive gene effects contribute substantially to plant height variation in this germplasm, making phenotypic selection a viable approach for modifying this trait. Jandong *et al*. [21] reported high PCV and GCV for plant height in soybean accessions evaluated in Nigeria's Guinea Savannah, along with high heritability, and similarly concluded that selection for plant height would be effective. Other studies, including those of Chandrawat *et al*. [23], have consistently reported high heritability for plant height in soybean, supporting the present findings.

TABLE IV. ESTIMATES OF GENETIC PARAMETERS OF QUANTITATIVE TRAITS AMONG DIFFERENT ACCESSIONS OF SOYBEANS

Parameter	GV	PV	PCV (%)	GCV (%)	H^2B (%)	GA	GAM (%)
PH (cm)	11.73	20.33	23.72	18.01	57.69	5.36	28.19
NMB	3.27	13.50	33.11	16.29	24.20	1.83	16.50
DFF	18.37	19.77	12.62	12.17	92.89	8.51	24.16
DTM	6.67	9.14	3.08	2.63	72.94	4.54	4.63
PDL (cm)	0.30	0.42	14.68	12.47	72.08	0.96	21.80
PDP	3.62	13.21	18.74	9.81	27.42	2.05	10.58
SPP	0.07	0.10	10.29	8.65	70.58	0.46	14.96
SW (g)	1.81	6.51	13.37	7.04	27.73	1.46	7.64
NSDPL	89.00	238.89	25.48	15.55	37.26	11.86	19.55
SDYPL (g)	3.04	8.82	25.79	15.15	34.50	2.11	18.33

GV: Genotypic variance; PV: Phenotypic variance; PCV: Phenotypic coefficient of variation; GCV: Genotypic coefficient of variation; H2B: Broad sense heritability; GAM: Genetic advance as percent of the mean; PH: Plant height; NMB: Numbers of main branches; DFF: Days to first flowering: PDL; Pod length; PDP: Pod per plant; SPP: Seed per pod; SW; 100-seed weight; NSDPL: Number of seed per plant; SDYPL: Seed yield per plant.

Days to first flowering showed moderate PCV (12.62%) and GCV (12.17%) but very high heritability (H^2B = 92.89%), the highest recorded among all traits in this study. The near-identical PCV and GCV values indicate that environmental variance contributed minimally to the total phenotypic variance for this trait, and that most of the observed variation was genetically determined. Very high heritability estimates for days to first flowering have been documented in multiple studies; it was also reported that heritability of 95.3% for this trait, and a PLOS ONE study on IITA soybean breeding lines evaluated across three agroecological zones in Nigeria found highly significant genotypic effects for days to 50% flowering across all environments [26]. The moderate GAM (24.16%) for this trait further suggests that gains in selecting for earlier or later flowering would accumulate at a reasonable pace over selection cycles, a finding of direct relevance to breeding for phenological adaptation.

Days to maturity had low PCV (3.08%) and GCV (2.63%), indicating minimal genetic variation for this trait within the tested accessions. Heritability was high at 72.94%, but GAM was low (4.63%), a combination that points to non-additive 1genetic control. When heritability is high but genetic advance is low, the likely explanation is that dominance or epistatic gene action is driving the high heritability estimate, making straightforward phenotypic selection inefficient for this trait. This interpretation aligns with earlier reports by Ghodrati [28] and Chandrawat *et al*. [23], both of whom found that high heritability coupled with low genetic advance for maturity-related traits indicated a greater role for non-additive effects, and recommended progeny testing or heterosis breeding as more appropriate improvement strategies for such traits.

Pod length showed moderate PCV (14.68%) and GCV (12.47%), high heritability (72.08%), and a high GAM (21.80%). This combination is widely regarded as the most favourable scenario for selection, because it indicates that the trait is heritable and that meaningful genetic gains can be expected per selection cycle. The high heritability of pod length in the present study, combined with its significant correlation with seeds per pod (r = 0.45, though non-significant), suggests that selecting for longer pods may have a secondary positive effect on seed number within pods.

Seeds per pod recorded moderate PCV (10.29%) and GCV (8.65%), high heritability (70.58%), and moderate GAM (14.96%). These estimates, taken together, indicate that additive genetic variance is the dominant component driving variation in seeds per pod within this germplasm set. A similar pattern was found by Dangi and Sharma [29] and Chandrawat *et al*. [23], both of whom reported high heritability and moderate genetic advance for this trait. The high heritability confirms that selection among the tested accessions for seeds per pod would produce a predictable genetic response, making this trait useful as a secondary selection criterion in yield improvement programmes targeting V9-type performance.

100-seed weight showed moderate PCV (13.37%) but low GCV (7.04%), low heritability (27.73%), and low GAM (7.64%). The large gap between PCV and GCV for this trait confirms a strong environmental contribution to its expression, which reduces the effectiveness of phenotypic selection. This finding is consistent with observations from Jandong *et al*. [21], who also noted that 100-seed weight in soybean tends to be more sensitive to environmental conditions, particularly those prevailing during the seed-filling period, than to genetic differences among genotypes. Despite this, V5 recorded the highest 100-seed weight (22.27 g) among all accessions, a value comparable to those reported for the best-performing genotypes in Indian germplasm studies [27], indicating that this accession carries alleles worth exploring for seed size improvement under more stable field conditions.

Seed yield per plant and number of seeds per plant both showed high PCV (25.79% and 25.48% respectively) and moderate GCV (15.15% and 15.55% respectively), with moderate heritability (34.50% and 37.26%) and moderate GAM (18.33% and 19.55%). The discrepancy between PCV and GCV for both traits confirms that environmental influences account for a substantial portion of the observed variation, which is a commonly reported feature of direct yield measurements in legume crops [24, 35]. Despite this, the moderate GAM values indicate that some genetic gain from selection remains achievable. These estimates are broadly comparable to those reported by Mofokeng [30], who found moderate heritability and GAM for seed yield per plant across soybean genotypes evaluated in South Africa, and similarly concluded that indirect selection

through highly heritable component traits would be more efficient than direct selection for yield itself.

Pods per plant presented a more challenging breeding scenario, with moderate PCV (18.74%) but low GCV (9.81%), low heritability (27.42%), and low GAM (10.58%). The dominance of environmental over genetic variance for this trait, combined with the absence of a significant genotype effect in the ANOVA, means that direct selection for pod number within this accession set is unlikely to yield consistent genetic progress. Xavier and Rainey [30], working with the SoyNAM population, similarly reported that pod number had low heritability and a weak genetic correlation with yield across environments, suggesting that its expression is highly dependent on canopy conditions, solar radiation, and reproductive period length rather than fixed genetic differences.

D. Pearson's Correlation Analysis

The correlation analysis presented in Table V revealed three statistically significant associations among the yield traits evaluated. Seeds per pod showed a highly significant positive correlation with number of seeds per plant (r = 0.93, $p \leq 0.01$), indicating that accessions producing more seeds per pod also tend to accumulate more seeds across the entire plant. This strong relationship is mechanistically logical: in the absence of a compensatory reduction in pod number, any increase in the number of seeds filled per pod directly translates into a greater total seed count per plant. Painkra *et al*. [31], evaluating 273 soybean germplasm accessions, reported a highly significant positive correlation between seeds per pod and seeds per plant of comparable magnitude, and concluded that selecting for seeds per pod would reliably improve total seed count at the plant level.

Seeds per pod also showed a significant positive correlation with seed yield per plant (r = 0.78, $p \leq 0.05$), further confirming that filling more seeds per pod contributes meaningfully to final yield. This finding reinforces observations by Tayade *et al*. [25], which identified seeds per pod and pod number as the two yield components most consistently correlated with total seed yield across a broad range of soybean studies. Vu *et al*. [32], reported a positive correlation of seeds per pod with yield of r = 0.93 across a set of soybean genotypes evaluated in field conditions, a value strikingly close to the present observation, suggesting that this relationship is robust across environments and germplasm types.

Seeds per plant showed a highly significant positive correlation with seed yield per plant (r = 0.87, $p \leq 0.01$). This is perhaps the most practically useful association identified in this study, as it suggests that screening for total seed count per plant can serve as a reliable and observable proxy for seed yield per plant, which itself is a more time-consuming measurement. Painkra *et al*. [31] reported an almost identical coefficient (r = 0.898) between these two traits, and Correlation and Path Analysis studies in soybean by Baraskar [33] consistently ranked seeds per plant among the top contributors to seed yield per plant in path analysis, confirming its central role in yield determination.

TABLE V. PEARSON'S CORRELATION ANALYSIS OF QUANTITATIVE TRAITS AMONG DIFFERENT ACCESSIONS OF SOYBEANS

Traits	PH	NMB	DFF	DTM	PDL	PDP	SPP	SW	NSDPL	SDYPL
PH (cm)	1	0.03	0.23	-0.17	0.63	0.08	0.44	-0.10	0.22	0.18
NMB		1	0.36	0.27	-0.17	0.35	0.11	0.12	0.34	0.37
DFF			1	0.62	0.01	0.33	0.22	0.05	0.34	0.38
DTM				1	-0.13	0.41	0.18	0.05	0.39	0.39
PDL (cm)					1	0.19	0.45	-0.26	0.32	0.20
PDP						1	0.38	-0.22	0.93**	0.78*
SPP							1	0.03	0.69	0.68
SW (g)								1	-0.17	0.33
NSDPL									1	0.87**
SDYPL (g)										1

*: Significant at $p \leq 0.05$; **: Significant at P ≤ 0.01. PH: Plant height; NMB: Numbers of main branches; DFF: Days to first flowering: PDL; Pod length; PDP: Pod per plant; SPP: Seed per pod; SW; 100-seed weight; NSDPL: Number of seed per plant; SDYPL: Seed yield per plant.

VI. CONCLUSION

The ten soybean accessions evaluated in this study showed clear and exploitable genetic variation for most yield-related traits. Accession V9 was the outstanding performer, recording the highest seed yield per plant, seeds per pod, number of seeds per plant, and pods per plant, while V5 produced the heaviest 100-seed weight. Days to first flowering, pod length, and seeds per pod returned the highest heritability estimates, confirming that these traits are under strong additive genetic control and can be selected for reliably in early breeding generations. Traits such as 100-seed weight and pods per plant showed low heritability and low genetic advance, making them poor targets for direct early generation selection.

Seeds per pod and seeds per plant were the strongest indirect predictors of seed yield per plant, with correlation coefficients of 0.78 and 0.87 respectively, and are recommended as primary selection criteria for yield improvement within this germplasm. A cross between V9 and V5 is proposed as the most promising hybridization strategy, with the potential to combine high seed number with superior seed size in derived progeny. Field evaluation of a wider range of accessions, including local landraces, remains necessary to develop cultivars suited to the diverse agro-ecological zones of Nigeria.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

AUTHOR CONTRIBUTIONS

O.S.O. conceived the research idea and wrote the paper; A.T.A. analysed the data and interpret the results; V.B.A. conducted the research; E.I.O. conducted the research; O.A.O. wrote and read the manuscript; all authors had approved the final version.

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