



**INHERITANCE PATTERN OF SOME QUALITATIVE TRAITS IN
A CROSS BETWEEN CULTIVATED COWPEA (*Vigna unguiculata* (L.) Walp)
AND A WILD RELATIVE**

Awosanya, A. O.

Department of Biological Sciences, Tai Solarin University of Education, Ijagun, Ogun State, Nigeria
Corresponding Author's Email: awosanyaao@tasued.edu.ng, **GSM:** 08033892432

ABSTRACT

The study evaluated the inheritance patterns and segregation behaviour of five quantitative traits (flower weight, length/width ratio of terminal leaflet, number of days to first flowering, pod length and 100-seed weight) in populations derived from a cross between Ife BPC (Branched Peduncle Cowpea) and its wild relative (*Vigna unguiculata* subsp. *Protrata*). The cross was made at the screen house of the Department of Crop Protection and Environmental Biology, University of Ibadan, Ibadan, Nigeria. Each generation (P_1 , P_2 , F_1 , F_2) was grown in experimental pots with standard spacing using completely randomized design. In this cross, populations with significant phenotypic and genetic variability for important agronomic traits were generated. The presence of transgressive segregants highlighted opportunity to select superior genotypes that combine traits from both parents. The F_1 generation shows an intermediate mean pod length of 6.91cm, aligning closer to *protracta* than Ife BPC, suggesting partial dominance of the short-pod allele. The findings in this study are highly relevant for breeding programmes targeting traits associated with reproductive success, aesthetic value (e.g. in floriculture), or yield components in grain legumes where flower size may correlate with pod number or size. Future work should aim at confirming the genetic basis through molecular markers and mapping studies.

Keywords: *Vigna unguiculata*, Segregants, Inheritance, *protracta*, Heritability

INTRODUCTION

Cowpea (*Vigna unguiculata* [L.] Walp.) is an important grain legume widely grown in the tropics and subtropics, particularly in sub-Saharan Africa. As a dual-purpose crop, cowpea provides both high-protein food for humans and fodder for livestock. It is drought-tolerant, thrives in poor soils, and forms an essential component of traditional farming systems (Faye *et al.*, 2024). In Nigeria, cowpea is a staple food and an economic commodity, contributing significantly to household nutrition and income generation. Understanding the genetic basis of cowpea traits is crucial for improving yield, resistance to biotic and abiotic stresses, and adaptation to varying environments. In particular, hybridization with wild relatives such as *Vigna unguiculata* subsp. *protracta* offers opportunities to introduce novel traits and enhance genetic diversity (Timko & Singh, 2008). Cowpea is believed to have originated in Africa, with its center of origin located in the Sahelian region of West Africa, particularly in present-day Nigeria and Niger (Ketema *et al.*, 2020; Ba *et al.*, 2004 cited by Omondi *et al.*, 2016). From there, it spread to Asia, Europe, and the Americas through trade and migration. Today, it is cultivated in over 80 countries, with sub-Saharan Africa accounting for more than 80% of global production. Wild relatives of cowpea, including *Vigna unguiculata* subsp. *protracta*, are found across Africa and play a key role in the domestication history and gene pool enrichment of cultivated cowpea. Their genetic diversity is valuable for breeding efforts aimed at enhancing resistance to pests, diseases, and environmental stresses (Menssen *et al.*, 2017).

Globally, over 8 million hectares are planted to cowpea, with annual production exceeding 7 million metric tonnes. Nigeria is the largest producer and consumer of cowpea, with an annual output of over 3 million tonnes (FAO, 2022). Cowpea is an affordable source of plant-based protein, making it essential for food security, especially among low-income populations. In addition to its nutritional



benefits, cowpea fixes atmospheric nitrogen, improving soil fertility and reducing the need for synthetic fertilizers. This ecological service supports sustainable agriculture. The haulms and leaves are valuable livestock feed, especially during the dry season, making cowpea an integral component of mixed farming systems (Kamai *et al.*, 2023). Cowpea is an annual, herbaceous plant that exhibits considerable morphological variation. The plant varies in growth habit from erect, semi-erect, to trailing types. Leaves are trifoliate, and leaflets vary in shape from lanceolate to ovate. Flowers are typically white, purple, or pale yellow, and pods are cylindrical with varying lengths. Phenologically, cowpea is known for its short life cycle, maturing within 60 to 90 days depending on the variety and environment. Key phenological stages include seedling emergence, flowering, pod formation, and maturity. Traits such as flowering time and pod development are influenced by photoperiod, temperature, and water availability (Manggoel and Uguru, 2011).

Cowpea is a diploid species ($2n = 2x = 22$) with a moderately sized genome (~620 Mb). Traditional breeding strategies have focused on selecting desirable phenotypes from landraces and improved varieties. Recent advances in molecular genetics, including the use of SSR, SNP, and QTL mapping, have enhanced the efficiency of cowpea breeding. Breeding objectives include yield improvement, resistance to pests (e.g., *Maruca vitrata*, aphids), diseases (e.g., *Fusarium* wilt), and tolerance to abiotic stresses such as drought and heat. Crossing cultivated varieties with wild relatives introduces new alleles for resistance and stress tolerance, although this may involve linkage drag and incompatibility challenges (Boukar *et al.*, 2020).

Merit and Demerit of Breeding Using Wild Relatives

Merits:

- Introduces novel genetic variation absent in cultivated gene pools.
- Enhances resistance to diseases, pests, and environmental stresses.
- Useful in broadening the genetic base and mitigating genetic erosion.

Demerits:

- May introduce undesirable traits such as small seed size or late maturity.
 - Cross-compatibility barriers and linkage drag complicate breeding.
 - Requires backcrossing and marker-assisted selection to recover elite traits.
- (Ahtisham, Obaid and Kisama, 2025).

Despite these challenges, the strategic use of wild relatives remains vital for the long-term sustainability of cowpea improvement programmes.

Quantitative traits such as yield, flowering time, and pod characteristics are governed by multiple genes and influenced by environmental conditions. Studies have demonstrated that these traits often exhibit additive, dominant, and epistatic gene actions (Falconer & Mackay, 2020). High heritability values suggest a strong genetic component, making such traits amenable to selection. Transgressive segregation in F_2 populations from interspecific crosses indicates the recombination of favorable alleles from both parents, a phenomenon that is crucial for generating superior phenotypes (Sunil and Lovely, 2025). Marker-assisted selection and genomic tools are increasingly employed to dissect the genetic architecture of such traits (Varshney *et al.*, 2021).

The narrowing genetic base of cultivated cowpea poses a risk to yield stability and adaptation under changing climates. Crosses involving wild relatives such as *protracta* can introduce desirable genes for early flowering, morphological diversity, and improved seed traits. However, understanding the inheritance patterns of these traits is essential to design effective selection strategies.

By evaluating five quantitative traits in progenies of Ife BPC \times *protracta*, this study contributes valuable information on trait heritability, segregation patterns, and selection potential. The findings will inform breeding programmes aiming to improve cowpea performance in diverse agroecologies.

Objectives of the study are to;

1. To assess the phenotypic variation of selected quantitative traits in F_1 and F_2 progeny of Ife BPC \times *Vigna unguiculata* subsp. *protracta*.



2. To estimate the heritability and genetic variability of flower weight, Terminal leaf length, days to flowering, pod length, and 100-seed weight.
3. To determine the inheritance patterns and segregation behavior of these traits in hybrid populations.
4. To provide recommendations for trait-based selection in cowpea improvement.

MATERIALS AND METHODS

Plant Material

The two parental lines used in the inheritance study are the Ife Branched Peduncle Cowpea (Ife BPC) and a variety of wild *Vigna unguiculata* subsp. *protracta*. Ife Branched Peduncle cowpea has an erect stem with light purple pigmentation on the wing petals. The terminal leaflet is subglobose in shape. Seeds are solid brown in coat colour with rough texture. The second parent was obtained as an off-type from plants grown to seeds of TVnu 1333, which belongs to the subspecies *stenophylla*. The stem has a semi-prostrate growth habit. Leaves are narrow, long and linear in shape. Flowers are small with deep purple pigmentation in both the standard and wing petals. Seeds are small with smooth texture and mottled coat colour.

Field Layout and Experimental Design

Experiments were conducted at the Department of Crop Protection and Environmental Biology, University of Ibadan, Ibadan, Nigeria. Each generation (P_1 , P_2 , F_1 , F_2) was grown in experimental pots with standard spacing. Complete randomized design was used in this study.

Trait Evaluation

Five traits evaluated are:

- Flower weight (g):
- Terminal leaflet length/width ratio.
- Number of Days to first flowering.
- Pod length (cm).
- 100-seed weight (g).

Data Analysis

Descriptive statistics and frequency distribution were performed using GenStat. Broad-sense heritability was estimated using variance components.

For these traits: means, variances, standard deviations, standard errors and coefficients of variation were computed for each generation of the cross. The computed variances were used to estimate heritability in the broad sense according to Matjetke *et al.*, (2025).

RESULTS AND DISCUSSION

The result as presented in table 1 showed that, Ife BPC parental line displays a unimodal distribution and skewed toward higher flower weights. The highest frequency lies at the 0.40g class (18 individuals), indicating this genotype naturally produces heavier flowers. The mean flower weight is 0.36g with a negligible variance (0.00) and a standard deviation (δ) of 0.05g. The SEM of 0.01g suggests precise estimation of the mean due to the low variability. A co-efficient of variation of 13.88% indicates moderate variability around the mean, typical for a relatively homozygous inbred line. Notably, the broad-sense heritability ($h^2 = 72.4\%$) is very high, suggesting a large proportion of the phenotypic variance is due to genetic factors rather than environmental effects. This implies strong genetic control over flower weight in this line, making it a valuable donor for high-weight traits.

Table 1: Flower Weight (g) in Population Derived from the Cross of Ife BPC x *Vigna unguiculata* subsp. *protracta*

Traits	Number of Class per Midpoint							N	X	δ	δ^2	S.E.M	CV%	%h ² _{bs}
	0.10	0.15	0.20	0.25	0.30	0.35	0.40							
Ife BPC				1	2	4	10	18	0.36	0.05	0.00	0.01	13.88	72.4%
<i>Protracta</i>	3	11	4					18	0.15	0.03	0.00	0.01		
F_1			6	7	2			15	0.24	0.04	0.00	0.01		
F_2		6	38	92	32	7		174	0.25	0.04	0.00	0.00		



Conversely, *V. unguiculata* subsp. *protracta* shows a frequency peak at the 0.15g midpoint, with the majority of individuals concentrated between the 0.10g and 0.20g classes. The distribution is skewed toward lighter flower weights, indicating this parent produces significantly smaller flowers than Ife BPC. The mean value (0.15g) and low variance (0.00) suggest limited within-line variability, consistent with inbred status. The standard deviation of 0.03g and SEM of 0.01g confirm this low variability. The tight clustering of values around the mean implies high genetic fixation and minimal environmental influence.

The F_1 hybrid generation represents the first filial cross between the divergent parents. As expected, the flower weight distribution is intermediate between the two parents, centered around the 0.25g and 0.30g classes. The mean flower weight is 0.24g, which is closer to the mid-parent value (average of 0.36g and 0.15g = 0.255g), suggesting additive gene action. The small variance and standard deviation (0.04g) indicate that most F_1 individuals express similar phenotypes, and there is limited segregation due to their genetic uniformity. The standard error remains low (0.01g), consistent with expected homogeneity in F_1 hybrids.

This intermediate and relatively narrow distribution supports the assumption of partial dominance or additive inheritance for flower weight. The absence of extreme phenotypes (either very small or very large flowers) also points to a lack of transgressive segregation in F_1 , as alleles from both parents are still heterozygous and not yet recombined.

The F_2 population, derived by selfing the F_1 hybrids, displays a broad and almost continuous distribution of flower weight ranging from 0.20g to 0.40g. The highest frequencies occur at 0.25g (92 individuals) and 0.30g (38 individuals), forming a bell-shaped curve typical of polygenic traits following quantitative inheritance. The emergence of both parental-like and intermediate phenotypes confirms segregation and recombination of alleles at multiple loci.

With a population size of 175 individuals, the F_2 generation offers a comprehensive view of the genetic architecture of flower weight. The mean flower weight (0.25g) remains close to the mid-parent value, further reinforcing the role of additive gene action. However, the range of distribution suggests the involvement of multiple genes (polygenes) with small effects rather than a single major gene.

Although the variance is reported as 0.00 (which seems inconsistent with the spread observed), the standard deviation (0.04g) and the near-zero SEM indicate stable estimates due to the large sample size. This low SEM value highlights the power of large population sizes in reducing sampling error, thereby providing more reliable estimates of population parameters.

The coefficient of variation for Ife BPC is 13.88%, which is relatively high for a parental line. This suggests some degree of residual genetic or environmental variability despite the low variance.

The broad-sense heritability of 72.4% calculated signifies a strong genetic influence on flower weight. This high heritability implies that phenotypic selection for flower weight will likely be effective and that most of the trait variation can be passed to the next generation. Although h^2 for the F_2 is not listed, the observed phenotypic variability in this generation, combined with a stable mean and moderate standard deviation suggests moderately high heritability as well.

These results collectively support the hypothesis that flower weight in these *Vigna* accessions is governed by multiple genes exhibiting additive effects. The transgressive nature of F_2 individuals (e.g., some flowers heavier than F_1 but not as heavy as Ife BPC) hints at possible epistasis or complementary gene action, but more detailed genetic analyses, such as QTL mapping, would be required to confirm this.

The frequency distribution and descriptive statistics of flower weight in Ife BPC \times *V. unguiculata* subsp. *protracta* crosses provide robust evidence for quantitative inheritance. The F_2 generation, with its broader phenotypic range and intermediate mean, reveals the potential for selection of superior genotypes with improved flower weight.

High heritability suggests that selection for this trait will be effective in early generations. Ife BPC stands out as a donor parent for larger flower size, and crosses with lighter-flowered accessions like *protracta* can produce a range of intermediate and potentially elite lines through further breeding and selection.

These findings are highly relevant for breeding programs targeting traits associated with reproductive success, aesthetic value (e.g., in floriculture), or yield components in grain legumes where flower size may correlate with pod number or size. Future work should aim at confirming the genetic basis through molecular markers and mapping studies.

Table 2: Length/Width Ratio of Terminal Leaflet in Population Derived from the Cross of Ife BPC x *Vigna unguiculata* subsp. *protracta*

Traits	1.20	3.20	5.20	7.20	9.20	11.20	13.20	15.20	N	X	δ	δ^2	S.E.M	CV%	%h ² _{bs}
Ife BPC	15	3							18	1.53	0.77	0.59	0.18	50.32	95.2%
<i>Protracta</i>					5	8	4		17	11.08	1.50	2.25	0.36		
F ₁		4	5	3	2	2			16	6.33	2.73	7.45	0.68		
F ₂	23	42	35	33	26	12	2	1	174	5.73	3.13	9.81	0.24		

Ife BPC exhibits a narrow and strongly skewed distribution toward lower L/W ratios. The majority of its individuals (15 out of 18) fall within the 1.20 midpoint class, yielding a low mean value of 1.53. The low standard deviation (0.77) and variance (0.59) indicate minimal phenotypic variation, which is consistent with its likely homozygosity as an inbred line. The coefficient of variation (CV) is moderate at 50.32%, and the heritability is very high (95.2%), suggesting that most variation in this trait is genetically controlled in this background.

In contrast, *V. unguiculata* subsp. *protracta* displays a much higher mean L/W ratio of 11.08, showing a distribution skewed toward broader and narrower leaves. The majority of individuals fall in the 11.20 to 13.20 classes, and some extend to 15.20, suggesting long and narrow terminal leaflets. The variance (2.24) and standard deviation (1.50) are higher than in Ife BPC, and SEM is slightly elevated (0.36), indicating more variability in this parent. This trait difference between the parents establishes a strong foundation for studying inheritance in subsequent generations.

The F₁ population shows a wide distribution of leaf length/leaf width ratios with a mean of 6.33, clearly intermediate between the two parents. Individuals span from 3.20 to 13.20, suggesting partial dominance or additive inheritance for the trait. The relatively high standard deviation (2.73) and variance (7.45) reflect increased variability, possibly due to heterozygosity and segregation of alleles from both parents. The SEM of 0.68 indicates a modest estimation error due to the relatively small sample size (N = 16).

This distribution supports the hypothesis that multiple genes control the trait, and the intermediate mean reinforces the presence of additive genetic effects.

The F₂ generation exhibits a bell-shaped, continuous distribution typical of polygenic traits. It ranges from 1.20 to 19.20, encompassing and exceeding both parental extremes, which indicates transgressive segregation. This occurs when recombination in the F₂ produces novel allele combinations leading to extreme phenotypes not present in either parent.

The mean leaf length/leaf width ratio is 5.73, slightly below the F₁ mean, and closer to Ife BPC, suggesting partial dominance toward the shorter leaflet type. The highest frequencies are found around the 5.20 and 7.20 midpoints. The large standard deviation (3.13) and variance (9.81) reflect extensive phenotypic variation due to segregation of multiple alleles. However, the low SEM (0.24) due to a large sample size (N = 174) enhances the reliability of the mean.

The data suggests the leaf length/leaf width ratio of terminal leaflets is a polygenic trait influenced by additive gene action. The high heritability value in Ife BPC (95.2%) indicates that the trait is largely genetically determined, making it highly responsive to selection. Although heritability values for F₁ and F₂ were not specified, the broad phenotypic spread in F₂ suggests that selection for either narrow or broad leaflets can be effectively applied in segregating generations.

This frequency distribution analysis reveals significant phenotypic divergence between the parental lines and continuous variation in hybrid generations, indicating quantitative inheritance. The presence of transgressive segregants in F₂ offers opportunities for selecting novel genotypes with

desirable leaf architecture. Given the high heritability, especially in Ife BPC, the leaf length/leaf width ratio of terminal leaflets is a promising trait for breeding and genetic improvement in *Vigna* species.

Table 3: Number of Days to First Flowering in the Population Derived from the Cross of Ife BPC x *Vigna unguiculata* subsp. *protracta*

Traits	Number of Class per Midpoint									N	X	δ^2	Δ	S.E.M	CV%	%h ² _{bs}
	40	50	60	70	80	90	100	110	120							
Ife BPC		2	11	3						16	60.63	32.92	5.74	1.43	9.51	96.6%
<i>Protracta</i>	2	14	1							17	49.41	18.38	4.29	1.04		
F ₁		13	3							16	51.88	16.25	4.03	1.01		
F ₂	18	47	28	26	21	17	4	2	1	164	64.54	353.62	18.80	1.47		

Number of days to first flowering is a critical phenological trait in crop plants, affecting yield potential, adaptability, and overall growth cycle. Table 3 summarizes the frequency distribution of days to first flowering in different generations - *Ife BPC*, *Vigna unguiculata* subsp. *protracta*, F₁, and F₂—derived from their hybridization.

Ife BPC shows a mean flowering time of 60.63 days, with most individuals concentrated in the 60–70 day classes (11 individuals), indicating a relatively late flowering genotype. The variance (32.92) and standard deviation (5.74) are moderate, reflecting limited intra-population variability. The low SEM (1.43) indicates that the population mean is reliable despite a small sample size (N = 16). The CV of 9.51% shows modest variability around the mean. Notably, the heritability estimate is extremely high (96.6%), suggesting that most of the variation observed in flowering time within this genotype is genetically determined and not significantly influenced by environmental factors.

In contrast, *V. unguiculata* subsp. *protracta* flowers earlier, with a mean of 49.41 days. The highest number of individuals are found in the 50-day class (14 individuals), confirming it as an early-flowering genotype. It has a lower variance (18.38) and standard deviation (4.29) than Ife BPC, signifying slightly more uniformity. SEM is also lower (1.04), reinforcing the reliability of the mean estimate. This early flowering behavior indicates a major genetic difference between the two parental lines regarding this trait.

The F₁ generation, resulting from the hybridization of the two parental genotypes, has a mean flowering time of 51.88 days—closer to *protracta*, suggesting partial dominance of early flowering. The variance (16.25) and standard deviation (4.03) are slightly lower than in both parents, which may be due to genetic uniformity in the F₁ hybrids. This reduction in variability is expected due to the heterozygous but genetically stable nature of the F₁ generation. With 13 of the 16 individuals concentrated in the 100-day class (which appears to be a mislabel—likely meant to represent 50–60 days), the distribution confirms relatively early flowering, reinforcing the influence of *protracta* alleles.

The F₂ population exhibits a broad, continuous distribution of days to first flowering, ranging from 40 to over 120 days, and a population size of 164. The mean flowering time increases to 64.54 days, skewing toward later flowering, possibly due to segregation of recessive alleles from the late-flowering Ife BPC parent. The distribution is unimodal but right-skewed, with most individuals clustered around 50–80 days. The presence of individuals in both early (40–50 days) and very late (100–120 days) classes indicates transgressive segregation, where new allele combinations create phenotypes more extreme than either parent.

The variance is very high (353.62), and the standard deviation (18.80) reflects substantial phenotypic variation due to segregation and recombination of multiple genes controlling flowering time. However, despite this large variation, the SEM remains low (1.47) due to the large sample size, which makes the population mean highly reliable.

The extremely high heritability (96.6%) reported for days to first flowering indicates that genetic factors overwhelmingly control the trait in that background. The extensive phenotypic variation observed suggests that selection for flowering time in segregating generations will be

effective, particularly in early breeding cycles. The continuous variation and presence of transgressive segregants in F_2 suggest polygenic inheritance with additive gene effects.

The analysis of days to first flowering in the hybrid population derived from Ife BPC \times *V. unguiculata* subsp. *protracta* reveals that this trait is quantitatively inherited and exhibits high genetic variability in segregating generations. The wide range of flowering times in the F_2 population reflects the contributions of both parental alleles and indicates opportunities for selecting early- or late-flowering genotypes. The high heritability observed supports the feasibility of effective phenotypic selection. These findings are important for breeding programs aiming to tailor flowering time to specific agroecological zones or cropping systems.

Table 4: Pod Length (cm) in Population Derived from the Cross of Ife BPC \times *Vigna unguiculata* subsp. *protracta*

Traits	Number of Class per Midpoint							N	X	δ^2	Δ	S.E.M	CV%	%h ² _{bs}
	4.30	5.32	6.34	7.36	8.38	9.00	10.02							
Ife BPC							2	4	9	15	11.53	0.60	0.77	0.20
<i>Protracta</i>		2	11	1						14	6.27	0.23	0.48	0.13
F_1		1	6	8	1					16	6.91	0.55	0.74	0.19
F_2	1	5	13	42	40	46	17	6		170	8.28	1.57	1.25	0.10

Pod length is a key morphological trait in legumes that influences yield potential, harvest efficiency, and market preference. Ife BPC shows a high mean pod length of 11.53 cm, with most individuals distributed across higher midpoint classes—10.02 cm (4 individuals), 11.04 cm (9 individuals), and 12.06 cm (2 individuals). The distribution is tightly clustered, indicating high uniformity. The variance (0.60) and standard deviation (0.77) are low, reflecting limited variability. The standard error of the mean (0.20) confirms reliability despite a small sample size ($N = 15$). A low CV (6.67%) further underscores phenotypic stability. The broad-sense heritability is high (87.2%), suggesting strong genetic control over pod length in this genotype.

In contrast, *V. unguiculata* subsp. *protracta* exhibits a much shorter pod length, with a mean of 6.27 cm. The majority of individuals fall within the 5.32 cm and 6.34 cm classes. The variance (0.23) and standard deviation (0.48) are lower than in Ife BPC, consistent with a genetically uniform population. SEM is minimal (0.13), affirming the precision of the estimated mean. This stark contrast with Ife BPC establishes the potential for segregating phenotypes in the hybrid generations.

The F_1 generation shows an intermediate mean pod length of 6.91 cm, aligning closer to *protracta* than Ife BPC, suggesting partial dominance of the short-pod allele. The majority of F_1 individuals are clustered in the 8.38 cm to 10.02 cm range. The variance (0.55) and standard deviation (0.74) are higher than either parent, which is expected due to the heterozygous nature of the F_1 hybrids. The SEM (0.19) is acceptably low, given the sample size ($N = 16$). The distribution pattern indicates a mix of alleles, with additive and possibly dominance effects influencing the trait.

The F_2 population ($N = 170$) exhibits a wide range of pod lengths from approximately 5.32 cm to 12.06 cm. The mean pod length is 8.28 cm, intermediate between both parents and F_1 , indicating segregation and recombination of genetic factors. The largest frequencies are in the mid classes—7.36 cm (42 individuals), 8.38 cm (40), and 9.00 cm (46)—resulting in a bell-shaped distribution typical of quantitative traits.

The high variance (1.57) and standard deviation (1.25) reflect extensive phenotypic diversity, likely due to polygenic control and environmental interactions. Despite this variability, the SEM is low (0.10), due to the large sample size, indicating a reliable mean estimate. The appearance of transgressive segregants (individuals with longer or shorter pods than either parent) highlights the recombination of complementary alleles in the F_2 , a valuable feature in plant breeding.

The data reveals that pod length is a quantitatively inherited trait with significant additive genetic variation. The high broad-sense heritability (87.2%) reported in Ife BPC suggests that most of the phenotypic variation is heritable, making pod length highly amenable to selection. Though not

explicitly given for F_2 , the observed spread supports a high genetic component. The presence of transgressive segregants in F_2 implies that recombination has produced genotypes superior to the parents, which breeders can exploit.

The frequency distribution and statistical analysis of pod length in populations derived from *Ife BPC* \times *V. unguiculata* subsp. *protracta* confirm that this trait is under polygenic, additive genetic control. The distinct differences between parents, intermediate expression in F_1 , and broad segregation in F_2 support quantitative inheritance. High heritability indicates strong genetic influence, and the presence of transgressive segregants in F_2 suggests potential for selecting elite genotypes with improved pod traits. This makes pod length a suitable target for selection in breeding programs aimed at yield enhancement or adaptation.

Table 5: 100-Seed Weight (g) in Population Derived from the Cross of *Ife BPC* \times *Vigna unguiculata* subsp. *protracta*

Traits	Number of Class per Midpoint									N	X	δ^2	Δ	S.E.M	CV%	%h ² _{bs}
	2.40	4.60	6.80	9.00	11.20	13.40	15.60	17.80	20.00							
Ife BPC							1	11	3	15	18.09	1.29	1.14	0.29	6.30	94.6%
<i>Protracta</i>	14									14	2.40	0.00	0.00	0.00		
F_1			11	1						12	4.78	0.40	0.64	0.18		
F_2	6	86	62	8						163	5.59	2.11	1.45	0.11		

Ife BPC exhibits significantly high seed weight with a mean of 18.09 g per 100 seeds. The majority of individuals fall in the 15.60 g to 20.00 g classes, indicating a consistently large-seeded phenotype. The variance (1.29) and standard deviation (1.14) are low, suggesting homogeneity typical of an inbred line. The SEM is also minimal (0.29), implying a precise estimate of the population mean despite the small sample size ($N = 15$). The CV (6.30%) reflects moderate phenotypic variability. Notably, the heritability is very high at 94.6%, indicating that seed weight in this genotype is strongly under genetic control and that selection for this trait would be highly effective.

V. unguiculata subsp. *protracta* displays extremely low seed weight, with all 14 individuals concentrated at the 2.40 g midpoint class. The mean is exactly 2.40 g, and both variance and standard deviation are zero, signifying no intra-population variation. This complete uniformity suggests a highly homozygous genotype and confirms that *protracta* is a true small-seeded line.

The F_1 generation shows a mean seed weight of 4.78 g—much closer to *protracta* than *Ife BPC*—indicating partial dominance of the small-seed allele. Most individuals fall in the 9.00 g class, with a few extending into 11.20 g. This intermediate expression is consistent with additive or partial dominance inheritance. The variance (0.40) and standard deviation (0.64) are low, as expected in genetically uniform F_1 hybrids. The SEM is 0.18, indicating precision in the mean estimation with a sample size of 12. The distribution indicates reduced variability due to heterozygosity, but also confirms the trait's responsiveness to recombination in subsequent generations.

The F_2 generation exhibits a much broader distribution, ranging from 4.60 g to 13.40 g, with the majority of individuals in the 6.80 g (86 individuals) and 9.00 g (62 individuals) classes. This creates a bell-shaped, continuous frequency curve typical of polygenic traits governed by multiple loci. The mean (5.59 g) is higher than F_1 but still substantially lower than *Ife BPC*, suggesting segregation and partial expression of alleles from both parents.

The variance (2.11) and standard deviation (1.45) are the highest among all generations, highlighting extensive genetic variation due to segregation and recombination in F_2 . Despite the high variability, the SEM is low (0.11), owing to the large sample size ($N = 163$), which ensures a reliable population mean. The emergence of intermediate and transgressive individuals (those with seed weights higher than F_1 but lower than *Ife BPC*) supports the hypothesis of additive gene action and the presence of minor genes with cumulative effects.

The contrasting parental phenotypes and intermediate F_1 mean suggest that 100-seed weight is a quantitative trait influenced by additive and partially dominant genes. The high heritability in *Ife*



BPC (94.6%) signifies strong genetic control, and the wide segregation in the F₂ generation implies that selection can be effectively applied in early breeding generations. The presence of F₂ individuals with seed weights approaching the Ife BPC parent shows that favorable alleles from both parents can be recombined to enhance seed weight.

The frequency distribution and statistical metrics of 100-seed weight in the cross between *Ife BPC* and *Vigna unguiculata* subsp. *protracta* clearly indicate quantitative inheritance. The trait exhibits significant additive genetic variation, with high heritability, making it highly responsive to selection. The wide range of phenotypes in the F₂ population offers opportunities to select for genotypes with improved seed size, which is critical for grain quality and yield improvement in cowpea breeding programs.

The evaluation of quantitative traits such as flower weight, terminal leaflet length-to-width ratio, days to first flowering, pod length, and 100-seed weight in populations derived from the cross between Ife BPC and *Vigna unguiculata* subsp. *protracta* reveals critical insights into the genetic basis of these agronomically important characters. Each trait demonstrated measurable phenotypic variation, transgressive segregation, and inheritance patterns indicative of quantitative genetic control. The combined findings from the five traits provide a comprehensive understanding of the inheritance, genetic variability, and potential for selection in cowpea (*Vigna unguiculata*) breeding programs.

Flower weight exhibited a continuous range of variation across the generations. Ife BPC displayed significantly heavier flowers ($\bar{X} = 0.36$ g), while *protracta* had lighter flowers ($\bar{X} = 0.15$ g). The F₁ generation showed intermediate flower weight ($\bar{X} = 0.24$ g), and the F₂ generation displayed a broad phenotypic range (0.20–0.40 g), supporting the hypothesis of polygenic inheritance. High heritability ($h^2 = 72.4\%$) in Ife BPC suggests strong genetic control, indicating that flower weight is a promising target for selection in segregating generations. The bell-shaped distribution in F₂ and appearance of parental-like individuals indicates additive genetic effects with potential contributions from minor genes and complementary epistasis (Kang *et al.*, 2020; Hill, 2010).

The L/W ratio of terminal leaflets is another trait exhibiting polygenic inheritance. Ife BPC showed very low ratios ($\bar{X} = 1.53$), indicative of broad leaflets, while *protracta* had narrow, elongated leaflets ($\bar{X} = 11.08$). The F₁ population ($\bar{X} = 6.33$) and F₂ generation ($\bar{X} = 5.73$) presented continuous variation, with transgressive segregants extending beyond the parental range. A wide phenotypic variance and standard deviation in F₂ ($\delta^2 = 9.81$) suggest the influence of multiple segregating loci. The high heritability in Ife BPC ($h^2 = 95.2\%$) again affirms the genetic basis of this trait, aligning with findings in similar studies that describe leaf morphology as a heritable polygenic trait (Ren *et al.*, 2020).

Time to first flowering is a critical adaptive trait influencing crop duration and environmental fitness. The early-flowering *protracta* ($\bar{X} = 49.41$ days) contrasted strongly with the late-flowering Ife BPC ($\bar{X} = 60.63$ days). F₁ hybrids exhibited early flowering ($\bar{X} = 51.88$ days), suggesting partial dominance of early-flowering alleles. The F₂ population showed a wide range (40–120 days), with a mean of 64.54 days and a large variance ($\delta^2 = 353.62$), indicating polygenic segregation and quantitative inheritance. The exceptionally high heritability (96.6%) in Ife BPC suggests that flowering time is under strong genetic regulation, making it highly responsive to selection. Early-flowering cultivars are desirable in drought-prone or short-season environments, making this a valuable trait for breeding (Alidu, 2018;).

Pod length is a key yield-related trait. Ife BPC, with long pods ($\bar{X} = 11.53$ cm), contrasted with *protracta* ($\bar{X} = 6.27$ cm). F₁ and F₂ generations showed intermediate means (6.91 and 8.28 cm respectively), and the F₂ distribution exhibited transgressive segregants exceeding both parents, indicating the expression of recombined favorable alleles. The F₂ variance ($\delta^2 = 1.57$) and heritability in Ife BPC (87.2%) support the notion that pod length is governed by multiple genes with additive effects. Similar inheritance patterns have been reported in cowpea and other legumes, emphasizing the feasibility of selecting for longer pods in early generations.

Seed weight is a primary yield determinant. Ife BPC exhibited large seed size ($\bar{X} = 18.09$ g), while *protracta* had the smallest seeds ($\bar{X} = 2.40$ g). F₁ ($\bar{X} = 4.78$ g) and F₂ ($\bar{X} = 5.59$ g) populations demonstrated intermediate and broad distributions. The presence of transgressive segregants in F₂, as



well as the high variance ($\delta^2 = 2.11$), implies polygenic inheritance with the opportunity for favorable recombination. The high heritability (94.6%) further supports the role of genetics over environment in determining seed weight, validating findings from earlier studies on cowpea (Owusu, *et al.*, 2021).

DISCUSSION

General Patterns and Genetic Implications

Across all traits, certain key patterns emerged:

Additive Gene Action and Polygenic Inheritance: Traits exhibited continuous variation and intermediate F_1 means, consistent with additive gene action. This is typical for quantitative traits controlled by multiple genes with small effects (Falconer & Mackay, 2020).

Transgressive Segregation: F_2 populations showed individuals with trait values beyond both parents, particularly in pod length, seed weight, and flowering time. This suggests recombination of complementary alleles from both parents, a desirable outcome for generating superior phenotypes (Sunil and Lovely, 2025).

High Heritability Estimates: Traits such as seed weight, flowering time, pod length, and leaflet shape had heritability values above 70%, indicating that environmental influence is minimal and phenotypic selection would be effective.

Potential for Genetic Improvement: The presence of wide segregation, coupled with high heritability and transgressive segregants, implies that hybrid populations derived from Ife BPC \times *protracta* harbor substantial genetic variability that can be exploited through selection (Nwosu and Nwadike, 2021).

CONCLUSION AND RECOMMENDATION

The cross between Ife BPC and *Vigna unguiculata* subsp. *protracta* generated populations with significant phenotypic and genetic variability for key agronomic traits. The patterns observed—intermediate F_1 means, continuous variation in F_2 , and high heritability—support the hypothesis of polygenic control with predominantly additive gene action. The presence of transgressive segregants further highlights the opportunity to select superior genotypes that combine favorable traits from both parents.

From a breeding perspective, traits such as flower weight, pod length, and seed weight are particularly promising due to their high heritability and ease of phenotypic assessment. Early flowering, as observed in *protracta*, offers adaptive advantage under time-constrained or drought-prone conditions.

Leaf morphology and pod characteristics provide additional selection indices for varietal differentiation and adaptation.

Future breeding efforts can benefit from marker-assisted selection (MAS) or genomic selection (GS) to further dissect the genetic architecture underlying these traits. The results provide a foundation for developing elite lines that combine yield potential, early maturity, and morphological diversity.

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