



Heritability estimate of body weight and linear body traits of F_1 progenies of local x exotic chicken strains

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Abstract

This study evaluated the heritability of body weight and linear body measurements in F_1 progenies of four chicken genotypes: R_1B_1 (Ross 308 × Brown dam), R_1B_2 (Ross 308 × Black dam), R_2B_1 (Arbor Acres × Brown dam), and R_2B_2 (Arbor Acres × Black dam). A total of 249 F_1 progenies were used for the study. Heritability estimates were obtained from sire (h^2_s), dam (h^2_d), and combined (h^2_s+d) components. Body weight exhibited moderate heritability across all genotypes ($h^2_s+d = 0.50-0.64$), while linear body traits such as body length, wing length, shank length, keel length, and breast width generally showed moderate to very high heritability (0.51–0.86). Maternal contributions were significant for several traits, particularly in crosses involving Black dams (R_1B_2 and R_2B_2). Traits with higher heritability, including wing length, shank length, and breast width, were identified as effective selection criteria for improving growth and carcass performance. Overall, the results indicate that crossbreeding exotic sires with local dam lines, especially Black dams, combined with selection based on linear traits, can enhance growth, skeletal development, and meat yield. These findings provide a strong genetic basis for designing effective poultry breeding programs in tropical environments.

Keywords: Heritability, Genotypes, Linear Body Traits, Crossbreeding, F_1 Progenies

Introduction

Poultry production is one of the most important components of animal agriculture worldwide, providing a rich source of protein, income, and employment, particularly in developing countries. The efficiency and profitability of poultry enterprises are largely determined by growth performance, which includes body weight, skeletal development, and carcass characteristics (Yakubu *et al.*, 2009). Among these, body weight and linear body measurements—such as body length, wing length, shank length, keel length, and breast width—serve as fundamental indicators of overall growth and meat yield. Linear traits are not only important for estimating body conformation but also provide indirect measures of carcass composition, enabling breeders to make informed selection decisions early in life (Olawunmi *et al.*, 2012; Musa *et al.*, 2015).

The genetic improvement of poultry relies on understanding the heritable variation of these traits. Heritability, defined as the proportion of phenotypic variation attributable to additive genetic factors, is a key parameter in breeding programs.

Traits with high heritability respond more effectively to selection, whereas traits with lower heritability are more influenced by environmental factors and require complementary management practices for improvement (Adeyinka *et al.*, 2006; Zerehdaran *et al.*, 2004). Knowledge of the relative contribution of sire and dam components to trait expression is critical for optimizing selection strategies, particularly in crossbreeding programs.

Crossbreeding exotic broiler sires with local dam lines is widely adopted to combine the rapid growth and high meat yield of commercial breeds with the adaptability and disease resistance of indigenous lines (Yakubu *et al.*, 2009; Olawunmi *et al.*, 2012). F_1 progenies from such crosses often display heterosis (hybrid vigor), exhibiting improved growth performance, survival, and feed efficiency compared to purebred lines (Musa *et al.*, 2015; Zerehdaran *et al.*, 2004). However, the extent of improvement depends on the heritable genetic potential of both sire and dam lines, making the evaluation of heritability in different F_1 genotypes a vital step for effective breeding (Adeyinka *et al.*, 2006).

Despite the economic importance of poultry in tropical regions, there is limited information on the genetic control of growth traits in crossbred chickens, particularly the contributions of sire and dam components (Olawunmi *et al.*, 2012; Musa *et al.*, 2015). Understanding these genetic parameters allows breeders to identify traits with high selection potential, design efficient breeding programs, and improve overall productivity and meat yield in both commercial and smallholder systems (Yakubu *et al.*, 2009; Adeleke *et al.*, 2011). This study, therefore, aimed to estimate the heritability of body weight and linear body traits in four F₁ chicken genotypes to provide a genetic basis for selection and crossbreeding programs targeting growth and carcass improvement in tropical poultry production systems (Zerehdaran *et al.*, 2004).

Materials and Methods

The experiment was conducted at the poultry unit of the Teaching and Research farm of Michael Okpara University of Agriculture, Umudike, Abia State, Nigeria. Umudike is situated at a latitude of 05°29' N, longitude 07°25' E, at 122 metres above sea level. The area falls within the humid tropical rainforest zone of southeastern Nigeria, characterised by a bimodal rainfall pattern with peaks from April to October and September to October, along with a short dry period in August known as the August break, and a dry season occurring roughly from November to March. Relative humidity fluctuates between 75% and 90%, depending on the season (NRCRI, 2021). The average monthly high temperature ranges from approximately 28.8 °C in July and August to 36.3 °C in February, while the average monthly low temperature varies between about 22.2 °C in August and 25.3 °C in March (Weather Atlas, 2024).

The base population constitutes a total of 60 normal feathered local hens, 30 each of brown and black phenotype, as well as 12 exotic sires comprising 6 each of Arbor Acre and Ross 308 strains. The hens were procured from Ndoro market, Umudike, while the exotic strain was purchased from Agrited farms and CHI farms. The birds were housed separately in deep litter and quarantined for 2 weeks to allow them to acclimatise to the environment. They were fed with commercial breeder mash comprising 20.80% CP and 3050 Kcal/kgME. Feed and water were given *ad libitum*.

The mating scheme consists of 4 genetic main crosses as shown in Table 1 below.

Table 1: Mating procedure of the base population for the production of F₁ progenies from crosses between local and exotic sires.

Exotic sire	Brown local hen (B1)	Black local hen (B2)
Ross 308 (R ₁)	R ₁ B ₁	R ₁ B ₂
Arbor Acre+ (R ₂)	R ₂ B ₁	R ₂ B ₂

Where;

R₁B₁ = Ross 308 sire x Brown dam

R₁B₂ = Ross 308 sire x Black dam

R₂B₁ = Arbor Acre sire x Brown dam

R₂B₂ = Arbor Acre sire x Black dam.

Each genetic group was replicated 3 times with a mating ratio of 1 sire: 5 hens per replicate

The number of F₁ progenies hatched is as indicated in Table 2.

Table 2: Distribution of chicks hatched in 6 batches

Mating type	Batch						Class total
	1	2	3	4	5	6	
R ₁ B ₁	7	9	10	7	11	12	56
R ₁ B ₂	11	10	8	8	11	15	63
R ₂ B ₁	9	8	12	11	9	13	62
R ₂ B ₁	12	10	10	13	12	11	68
						Tot al	249

Egg setting

Eggs from each genetic group were collected 2-3 times daily to prevent the cracking of the egg shell, and were allowed to stay more than 7 days before they were incubated to avoid reduced hatchability due to prolonged storage. The eggs to be hatched were covered with polyethene to prevent the drying of the egg content and incubated with an automated cabinet-type incubator at a temperature of 37.7 °C and about 70% humidity. The eggs in the incubator were turned a minimum of 3 times daily to prevent adhesion, and on the 9th day, the eggs were candled to evaluate the percentage fertility index of the eggs. On the 14th day of incubation, the eggs were re-candled to determine the percentage dead-in-germ. The incubated eggs hatched between the 19th and 21st day. Each genetic group were properly marked for proper identification.

Management of F₁ Progenies

Upon collection of day-old chicks from the hatchery, each genetic group was brooded separately in different deep litter pens for two (2) weeks, after which they were transferred to different rearing pens according to their groups. Adequate feed and water were supplied to the birds *ad libitum*. From day old to 4 weeks of age, the birds were fed with starter diets of 2741 Kcal/kg ME and 22 % CP, and from the 5th week to the end of the study, the birds were fed with finisher diets of 3000 kcal/kg ME and 20 % CP.

Estimates of Genetic Parameters

The data were subjected to analysis of variance (ANOVA) in a nested or hierarchical design and in a paternal half-sib analysis. All data generated was analysed using the SAS (2004) statistical procedure. The model fitted was a nested or hierarchical design (Henderson, 1995) as given below;

$$Y_{ijk} = \mu + S_i + D_j + e_{ijk}$$

Where;

Y_{ijk} = record on individual progeny of jth dam mated to ith sire;

μ = overall mean;

S_i = random effect of ith sire

D_j = effect of the j^{th} dam mated to the i^{th} sire
 e_{ijk} = random error, assumed to be independently, identically and normally distributed with zero mean and constant variance (iid 0, σ^2)

The variance component obtained from the ANOVA was used to analyse the genetic parameters as follows;

Heritability of sire component

$$h^2_s = \frac{4\sigma^2_s}{\sigma^2_p}$$

where;

σ^2_s sire variance

σ^2_p phenotypic variance

Heritability of the dam component

$$h^2_D = \frac{4\sigma^2_D}{\sigma^2_p}$$

where;

σ^2_D = dam variance

σ^2_p = phenotypic variance

Heritability of sire and dam components

$$h^2_{s+d} = \frac{2(\sigma^2_S + \sigma^2_D)}{\sigma^2_p}$$

where;

σ^2_S = Sire variance

σ^2_D = dam variance

σ^2_p = phenotypic variance

Results and Discussions

The heritability for body weight and linear body traits of F_1 progenies of local x exotic chicken strains is presented in Tables 3, 4, 5 and 6.

Table 3: Heritability estimates for growth parameters in R_1B_1 genotype

Growth Traits	h^2_s	h^2_d	h^2_{s+d}
Body weight	0.40±0.04	0.52±0.08	0.56±0.08
Body length	0.37±0.08	0.42±0.26	0.53±0.20
Wing length	0.54±0.25	0.68±0.02	0.77±0.09
Shank length	0.50±0.03	0.67±0.51	0.62±0.09
Drum stick	0.28±0.01	0.38±0.43	0.42±0.06
Keel length	0.55±0.05	0.49±0.05	0.58±0.01
Breast width	0.39±0.19	0.48±0.16	0.62±0.01

h^2_s = heritability due from sire component; h^2_d = heritability due from dam component; h^2_{s+d} = heritability due from both sire and dam components, R_1B_1 = Ross 308 sire x Brown dam

Table 3 presents the heritability estimates for body weight and linear body measurements of F_1 progenies derived from a cross between Ross 308 sire and Brown dam (R_1B_1 genotype). Estimates were partitioned into sire (h^2_s), dam (h^2_d), and combined sire and dam (h^2_{s+d}) components.

Body weight had moderate heritability ($h^2_s = 0.40$, $h^2_d = 0.52$, $h^2_{s+d} = 0.56$), indicating a substantial contribution of additive genetic factors and maternal effects. This suggests that

selection for body weight in this cross is feasible, though environmental influences may also affect growth. Body length showed moderate heritability ($h^2_{s+d} = 0.53$), suggesting that skeletal growth is under genetic control from both sire and dam. This trait can serve as a reliable indicator of overall growth. Wing length exhibited high heritability ($h^2_{s+d} = 0.77$), particularly due to maternal influence ($h^2_d = 0.68$). This indicates strong genetic determination and minimal environmental impact, making wing length an effective trait for selection. Shank length had moderate to high heritability ($h^2_{s+d} = 0.62$), with a higher dam contribution. This highlights maternal effects and confirms the trait as a good selection criterion for skeletal development. Drumstick length recorded lower heritability ($h^2_{s+d} = 0.42$), suggesting greater environmental or non-additive genetic influence. Selection progress for this trait may be slower. Keel length had high heritability ($h^2_{s+d} = 0.58$), indicating strong additive genetic control. Its association with breast muscle development makes it an important trait for carcass improvement. Breast width showed moderate to high heritability ($h^2_{s+d} = 0.62$), indicating a strong genetic component, supporting its use as a selection trait for meat yield.

The heritability estimates for the R_1B_1 genotype indicate that most growth traits are moderately to highly heritable. Body weight exhibited moderate heritability ($h^2_{s+d} = 0.56$), suggesting that genetic improvement through selection is feasible, though environmental factors also play a role (Adeyinka *et al.*, 2006; Yakubu *et al.*, 2009). Linear body measurements, including wing length ($h^2_{s+d} = 0.77$), shank length (0.62), keel length (0.58), and breast width (0.62), had higher heritability than body weight, indicating strong additive genetic control and low environmental influence (Olawunmi *et al.*, 2012; Adebambo *et al.*, 2010). The higher dam contribution for traits such as wing and shank length highlights the importance of maternal effects in early growth and skeletal development (Musa *et al.*, 2015). These findings suggest that selection based on linear body traits in R_1B_1 crosses can effectively improve growth and carcass characteristics.

Table 4: Heritability estimates for growth parameters in R_1B_2 genotype

Growth Traits	h^2_s	h^2_d	h^2_{s+d}
Body weight	0.43±0.15	0.32±0.15	0.50±0.00
Body length	0.60±0.11	0.71±0.15	0.64±0.00
Wing length	0.54±0.10	0.57±0.16	0.60±0.42
Shank length	0.54±0.02	0.31±0.22	0.88±0.08
Drum stick	0.70±0.17	0.40±0.58	0.35±0.17
Keel length	0.41±0.18	0.55±0.05	0.51±0.03
Breast width	0.71±0.16	0.96±0.14	0.86±0.03

h^2_s = heritability due from sire component; h^2_d = heritability due from dam component; h^2_{s+d} = heritability due from both sire and dam components, R_1B_2 = Ross 308 sire x Black dam

Table 4 presents heritability estimates for F₁ progenies derived from Ross 308 sire × Black dam (R₁B₂). Body weight had moderate heritability ($h^2_s = 0.43$, $h^2_d = 0.32$, $h^2_{s+d} = 0.50$), indicating a balance between sire additive effects and environmental influence, with a lower maternal contribution than in R₁B₁. Selection for body weight is feasible but may progress more slowly. Body length recorded high heritability ($h^2_{s+d} = 0.64$), with strong contributions from both sire and dam. This suggests skeletal growth is strongly controlled genetically and can respond well to selection. Wing length showed moderate to high heritability ($h^2_{s+d} = 0.60$), indicating a considerable genetic component, though the larger standard error suggests some variability in expression. Shank length exhibited exceptionally high combined heritability ($h^2_{s+d} = 0.88$), despite a lower dam component. This indicates strong additive genetic control and high potential for rapid improvement through selection. Drumstick length had variable heritability ($h^2_{s+d} = 0.35$), suggesting a strong influence of environmental or non-additive genetic factors. Improvement through direct selection may be limited. Keel length had moderate heritability ($h^2_{s+d} = 0.51$), with stronger maternal influence, indicating potential for genetic improvement of breast muscle development. Breast width recorded very high heritability ($h^2_{s+d} = 0.86$), with an exceptionally high dam component (0.96). This indicates strong genetic control and highlights the importance of the Black dam line for carcass traits.

Heritability estimates for the R₁B₂ genotype were generally higher than in R₁B₁, particularly for skeletal and carcass traits. Shank length ($h^2_{s+d} = 0.88$) and breast width (0.86) exhibited exceptionally high heritability, indicating strong additive genetic control and high potential for rapid genetic improvement through selection (Zerehdaran *et al.*, 2004; Olawunmi *et al.*, 2012). Body weight ($h^2_{s+d} = 0.50$) showed moderate heritability, suggesting that environmental factors still influence growth (Yakubu *et al.*, 2009). The very high dam contribution for breast width (0.96) highlights the role of the Black dam line in enhancing carcass traits (Adeleke *et al.*, 2011). Overall, these results indicate that the R₁B₂ cross is particularly suitable for selection programs targeting skeletal growth and meat yield, with linear body traits serving as effective selection criteria.

Table 5: Heritability estimates for growth parameters R₂B₁ genotype

Growth Traits	h^2_s	h^2_d	H^2_{s+d}
Body weight	0.43±0.15	0.32±0.15	0.50±0.00
Body length	0.28±0.11	0.51±0.15	0.64±0.00
Wing length	0.54±0.10	0.63±0.16	0.77±0.42
Shank length	0.31±0.02	0.54±0.22	0.68±0.08
Drum stick	0.30±0.17	0.50±0.58	0.63±0.17
Keel length	0.41±0.18	0.55±0.05	0.51±0.03

Breast width 0.66±0.14 0.71±0.16 0.83±0.03

h^2_s = heritability due from sire component; h^2_d = heritability due from dam component; h^2_{s+d} = heritability due from both sire and dam components, R₂B₁= Arbor Acre sire x Brown dam

Table 5 presents heritability estimates for body weight and linear body measurements in F₁ progenies of Arbor Acres sire × Brown dam (R₂B₁). Body weight had moderate heritability ($h^2_s = 0.43$, $h^2_d = 0.32$, $h^2_{s+d} = 0.50$), suggesting that additive genetic effects, primarily from the sire, influence growth, while environmental factors also contribute. This indicates that selection for body weight is feasible, but progress may be moderate. Body length recorded moderate to high heritability ($h^2_{s+d} = 0.64$), with a larger maternal contribution ($h^2_d = 0.51$). This suggests that skeletal growth is strongly influenced by dam genetics, making body length a useful trait for indirect selection. Wing length exhibited high heritability ($h^2_{s+d} = 0.77$), indicating strong additive genetic control with minimal environmental influence. High maternal contribution ($h^2_d = 0.63$) further emphasises the importance of dam genetics in skeletal development. Shank length had moderate to high heritability ($h^2_{s+d} = 0.68$), with a larger maternal component, suggesting that maternal effects significantly contribute to limb development and overall structural growth. Drumstick length showed moderate heritability ($h^2_{s+d} = 0.63$), with a balanced contribution from sire and dam components, indicating that both parental lines influence the trait. Environmental factors may also play a role, as reflected in the variability of the dam component. Keel length recorded moderate heritability ($h^2_{s+d} = 0.51$), highlighting additive genetic control and potential for improvement in carcass traits, particularly breast muscle development. Breast width exhibited very high heritability ($h^2_{s+d} = 0.83$), with substantial contributions from both sire and dam. This indicates strong genetic determination and confirms its value as a key selection trait for meat yield.

The heritability estimates for the R₂B₁ genotype indicate that most growth traits are moderately to highly heritable, suggesting substantial additive genetic control and potential for genetic improvement through selection. Body weight showed moderate heritability ($h^2_{s+d} = 0.50$), indicating that both sire and environmental effects contribute to growth, with the maternal influence slightly lower. These results are consistent with previous reports in broiler and crossbred chickens, which show moderate heritability for body weight (Adeyinka *et al.*, 2006; Yakubu *et al.*, 2009).

Linear body measurements generally exhibited higher heritability than body weight. Wing length ($h^2_{s+d} = 0.77$), shank length (0.68), and breast width (0.83) recorded high heritability, indicating strong additive genetic control and minimal environmental influence. The high dam contributions for wing length, shank length, and body length highlight the importance of maternal genetics in skeletal growth, as reported by Musa *et al.* (2015) and Olawunmi *et al.* (2012).

Drumstick length and keel length showed moderate heritability (0.63 and 0.51, respectively), suggesting that environmental factors may also influence these traits. The high heritability of breast width confirms its suitability as a key selection criterion for improving carcass yield, in agreement with studies by Adeleke *et al.* (2011) and Zerehdaran *et al.* (2004).

Table 6: Heritability estimates for growth parameters
R₂B₂ genotype

Growth Traits	h ² s	h ² d	H ² s+d
Body weight	0.42±0.01	0.59±0.30	0.64±0.25
Body length	0.67±0.07	0.70±0.01	0.86±0.02
Wing length	0.62±0.11	0.83±0.06	0.77±0.03
Shank length	0.51±0.23	0.64±0.04	0.60±0.03
Drum stick	0.53±0.33	0.65±0.10	0.73±0.06
Keel length	0.60±0.06	0.71±0.21	0.68±0.02
Breast width	0.28±0.02	0.41±0.09	0.38±0.07

h²s = heritability due from sire component; h² d = heritability due from dam component; h²s+d = heritability due from both sire and dam components, R₂B₂= Arbor Acre sire x Black dam

Table 6 presents heritability estimates for body weight and linear body measurements in F₁ progenies of Arbor Acres sire x Black dam (R₂B₂). Body weight showed moderate to high heritability (h²_s+d = 0.64), with a higher maternal contribution (h²_d = 0.59) than paternal (h²_s = 0.42), indicating that maternal genetics strongly influence growth and that selection for body weight could be effective in this cross. Body length recorded very high heritability (h²_s+d = 0.86), suggesting strong additive genetic control from both parents (h²_s = 0.67; h²_d = 0.70). This implies skeletal growth is highly heritable and can respond rapidly to selection. Wing length also exhibited high heritability (h²_s+d = 0.77), with a dominant maternal component (h²_d = 0.83), indicating that wing development is strongly influenced by dam genetics. Shank length showed moderate to high heritability (h²_s+d = 0.60), suggesting both sire and dam contribute to limb development and structural growth. Drumstick length recorded high heritability (h²_s+d = 0.73), highlighting strong genetic control from both parents. Keel length had high heritability (h²_s+d = 0.68), reflecting additive genetic control and suitability for improving carcass traits. Breast width recorded moderate heritability (h²_s+d = 0.38), lower than other skeletal traits, suggesting that environmental effects may play a larger role in this trait.

The heritability estimates for the R₂B₂ genotype indicate strong genetic control for most growth traits, particularly linear body measurements, which generally exhibited higher heritability than body weight. Body weight (h²_s+d = 0.64) showed moderate to high heritability, consistent with findings in other broiler and crossbred chicken populations (Adeyinka *et al.*, 2006; Yakubu *et al.*, 2009).

Skeletal traits, such as body length (h²_s+d = 0.86), wing length (0.77), shank length (0.60), and drumstick length (0.73), were highly heritable, suggesting strong additive genetic influence and minimal environmental interference (Olawunmi *et al.*, 2012; Musa *et al.*, 2015). The higher maternal contributions for wing length and body length indicate that dam genetics play a key role in early skeletal development and growth.

Breast width exhibited moderate heritability (h²_s+d = 0.38), indicating greater environmental influence compared to other skeletal traits. This aligns with previous studies showing that carcass traits like breast width can be more sensitive to management and nutritional factors (Adeleke *et al.*, 2011; Zerehdaran *et al.*, 2004).

Overall, the R₂B₂ cross (Arbor Acres x Black dam) demonstrates high potential for genetic improvement of skeletal and carcass traits, particularly when selection is based on linear body measurements. Maternal genetic contribution plays a significant role in the expression of most traits, reinforcing the importance of dam line selection in crossbreeding programs.

Conclusion

Heritability estimates for growth traits in the four F₁ genotypes—R₁B₁ (Ross 308 x Brown dam), R₁B₂ (Ross 308 x Black dam), R₂B₁ (Arbor Acres x Brown dam), and R₂B₂ (Arbor Acres x Black dam)—indicate that most traits are moderately to highly heritable, with linear body measurements generally more heritable than body weight. Body weight showed moderate heritability (h²_s+d = 0.50–0.64), suggesting that both additive genetic effects and maternal contributions influence growth, while environmental factors also play a role.

Linear traits such as body length, wing length, shank length, keel length, and breast width exhibited moderate to very high heritability, highlighting their strong genetic control. Among these, wing length, shank length, and breast width were particularly heritable, making them reliable selection criteria for improving growth and carcass performance. Maternal effects were significant for several traits, emphasising the contribution of dam genetics to early growth and skeletal development.

Overall, crosses involving the Black dam line (R₁B₂ and R₂B₂) generally showed higher heritability for skeletal and carcass traits, suggesting greater genetic potential for improvement. These results demonstrate that selection based on linear body traits is highly effective and provide a strong genetic basis for designing breeding programs aimed at enhancing growth and meat yield in crossbred chickens.

Recommendations

Selection for growth improvement in these crossbred chickens should focus on linear body traits such as wing length, shank length, keel length, and breast width, which demonstrate high heritability. Utilising superior dam lines, particularly Black dams, can maximise maternal genetic contribution. Crosses involving exotic sires and Black dams (R₁B₂, R₂B₂) are

recommended for improved skeletal and carcass traits. Adequate nutrition and management are essential to unlock the full genetic potential.

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