



## Repeatability estimate of body weight and linear body traits of F<sub>1</sub> progenies of local x exotic chicken strains

By

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### Abstract

*This study estimated the repeatability of growth traits in different genotypes of chickens produced from crosses between indigenous hens and exotic sires. A total of 60 indigenous hens (30 brown and 30 black phenotypes) and 12 exotic sires (Arbor Acres and Ross 308) were used to produce four genetic groups (R1B1, R1B2, R2B1, and R2B2). Eggs were collected, incubated, and hatched under standard conditions, and the resulting F<sub>1</sub> progenies were reared under uniform management. Repeatability estimates were calculated for body weight, body length, wing length, shank length, drumstick length, keel length, and breast width. Results showed moderate to high repeatability for most traits. Body weight ( $0.59 \pm 0.35$ ), body length ( $0.64 \pm 0.77$ ), and breast width ( $0.58 \pm 0.09$ ) exhibited the highest repeatability, indicating strong consistency and suitability for early selection. Wing length ( $0.45 \pm 0.15$ ), shank length ( $0.44 \pm 0.29$ ), drumstick length ( $0.57 \pm 0.55$ ), and keel length ( $0.49 \pm 0.30$ ) showed moderate repeatability, suggesting greater environmental influence and the need for repeated measurements. Among genotypes, R1B1 recorded the highest repeatability values, particularly for body weight ( $0.87 \pm 0.17$ ) and breast width ( $0.67 \pm 0.21$ ). The study concludes that body weight, body length, and breast width are reliable traits for early selection, while other traits require repeated measurements for accurate evaluation. These findings provide useful guidance for improving genetic selection strategies in tropical poultry production systems.*

**Keywords:** Repeatability, growth traits, indigenous chickens, exotic sires, crossbreeding, F1 progenies.

### Introduction

Growth performance traits are key indicators of productivity and genetic potential in poultry breeding programs, as they directly influence meat yield and overall economic efficiency. Traits such as body weight, body length, wing length, shank length, drumstick length, keel length, and breast width are commonly used to evaluate growth and carcass quality in birds (Falconer and Mackay, 2020; Aviagen, 2019). Accurate assessment of these traits is essential for effective selection and long-term genetic improvement in poultry populations.

Repeatability, defined as the proportion of total variation in a trait that is due to permanent differences among individuals, is an important parameter in animal breeding. It provides an estimate of the consistency of a trait over time and across

measurements and is useful in predicting the future performance of animals based on early-life records (Falconer and Mackay, 2020; Lynch and Walsh, 1998). High repeatability indicates that fewer repeated measurements are needed for reliable selection, while low repeatability suggests stronger environmental influence and the need for multiple observations.

In poultry production systems, especially under tropical conditions, environmental variability such as heat stress, nutrition, and management practices can significantly affect growth trait expression, thereby influencing their stability across genotypes (Musa *et al.*, 2021; Nwagu and Alawa, 2018). Understanding the repeatability of growth traits, therefore, provides valuable insight into their suitability for early selection and genetic improvement.



This study aimed to estimate the repeatability of key growth traits across different genotypes in order to identify traits that are most reliable for selection and to provide guidance for efficient breeding strategies.

### Materials and methods

The experiment was carried out at the Poultry Unit of the Teaching and Research Farm of Michael Okpara University of Agriculture, Umudike, Abia State, Nigeria. Umudike lies on latitude 05°29' N and longitude 07°25' E, at an altitude of 122 m above sea level. The location is within the humid tropical rainforest zone of southeastern Nigeria, characterized by a bimodal rainfall pattern with peaks from April to July and September to October, separated by a short dry spell known as the August break, and a main dry season from November to March. Relative humidity ranges from 75% to 90% depending on the season (NRCRI, 2021). Mean monthly temperatures vary from about 28.8 °C in July and August to 36.3 °C in February, while minimum values range from approximately 22.2 °C in August to 25.3 °C in March (Weather Atlas, 2024).

The base population consisted of 60 normal-feathered indigenous hens (30 brown and 30 black phenotypes) and 12 exotic sires (6 Arbor Acres and 6 Ross 308 strains). The hens were sourced from Ngoro market, Umudike, while the exotic sires were obtained from Agrited Farms and CHI Farms. All birds were initially housed in a deep litter system and quarantined for two weeks to allow for acclimatisation to the local environment. They were fed a commercial breeder mash containing 20.80% crude protein and 3050 kcal/kg metabolizable energy, with feed and water provided ad libitum.

A mating design involving four genetic cross combinations was implemented, as presented in Table 1. These crosses were used to produce F1 progenies from local hens and exotic sires.

**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 <sub>1</sub> )    | R <sub>1</sub> B <sub>1</sub> | R <sub>1</sub> B <sub>2</sub> |
| Arbor Acre+ (R <sub>2</sub> ) | R <sub>2</sub> B <sub>1</sub> | R <sub>2</sub> B <sub>2</sub> |

Where;

R<sub>1</sub>B<sub>1</sub> = Ross 308 sire x Brown dam

R<sub>1</sub>B<sub>2</sub> = Ross 308 sire x Black dam

R<sub>2</sub>B<sub>1</sub> = Arbor Acre sire x Brown dam

R<sub>2</sub>B<sub>2</sub> = Arbor Acre sire x Black dam.

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

### Management of F1 Progenies

Day-old chicks from each genetic group were brooded separately in deep litter pens for two weeks. Thereafter, they were transferred into separate rearing pens according to their genetic groups. Feed and water were provided ad libitum

throughout the study period. From day-old to four weeks of age, birds were fed a starter diet containing 22% crude protein and 2741 kcal/kg metabolizable energy. From five weeks to the end of the experiment, they were switched to a finisher diet containing 20% crude protein and 3000 kcal/kg metabolizable energy.

### Estimates of Genetic Parameters

The model for repeatability (R) was calculated using the formula described by Becker (1985), modified as a nested or hierarchical design by Henderson (1995), as given below;

$$R = \frac{\sigma_B^2}{\sigma_B^2 + \sigma_W^2}$$

Where;

$\sigma_B^2$  = individual variance component

$\sigma_W^2$  = error

The standard error was calculated using the formula described by Becker (1984)

$$SE = \frac{\sqrt{2(1-R^2)(1+(K-1)R)^2}}{K(K-1)(n-1)}$$

Where;

K = number of measurements,

n = number of birds,

r = repeatability

The model for repeatability is given as:  $Y_{ij} = \mu + P_i + I_j + e_{ij}$

Where;

Y = measurements of the birds

P<sub>i</sub> = fixed effect of the i<sup>th</sup> period of measurement

I<sub>j</sub> = random effect of the i<sup>th</sup> individual

e<sub>ij</sub> = random error

### Results and Discussions

The repeatability estimates for body weight and linear body traits of F1 progenies of local x exotic chicken strains are presented in Tables 2-5

**Table 2: Estimates of repeatability for growth parameters in R<sub>1</sub>B<sub>1</sub> genotype**

| Growth traits | R± SE     |
|---------------|-----------|
| Body weight   | 0.87±0.17 |
| Body length   | 0.53±0.11 |
| Wing length   | 0.43±0.22 |
| Shank length  | 0.62±0.26 |
| Drum stick    | 0.55±0.17 |
| Keel length   | 0.50±0.05 |
| Breast width  | 0.67±0.21 |

R±SE = Repeatability coefficient ± Standard error, R<sub>1</sub>B<sub>1</sub>= Ross 308 sire x Brown dam

The repeatability estimates for growth traits in the R1B1 genotype are presented in Table 2. Body weight exhibited a very high repeatability estimate (R = 0.87, SE = 0.17), indicating strong consistency across repeated measurements. Breast width (R = 0.67, SE = 0.21) and shank length (R =

0.62, SE = 0.26) also showed high repeatability values. Moderate repeatability estimates were observed for drumstick length (R = 0.55, SE = 0.17), body length (R = 0.53, SE = 0.11), keel length (R = 0.50, SE = 0.05), and wing length (R = 0.43, SE = 0.22).

The repeatability estimates (R ± SE) for growth traits in the R1B1 genotype are presented in Table 4. Repeatability represents the proportion of total phenotypic variation attributable to permanent individual differences, including additive genetic and permanent environmental effects (Falconer & Mackay, 2020). Traits with high repeatability indicate consistent performance over time and allow reliable prediction of future performance from early records. Body weight (0.87 ± 0.17) showed very high repeatability, indicating strong individual consistency and suitability for early selection (Zhang *et al.*, 2023; Adeoye *et al.*, 2020). Shank length (0.62 ± 0.26) and breast width (0.67 ± 0.21) also exhibited high repeatability, suggesting that these traits are stable and can respond effectively to genetic improvement (Musa *et al.*, 2021). Moderate repeatability estimates were observed for body length (0.53 ± 0.11), wing length (0.43 ± 0.22), drumstick length (0.55 ± 0.17), and keel length (0.50 ± 0.05). These values indicate reasonable consistency but suggest that multiple records may improve selection accuracy. Overall, traits with high repeatability—particularly body weight, shank length, and breast width—are reliable for early selection, while moderately repeatable traits may require repeated measurements to maximise genetic gain (Adeoye *et al.*, 2020; Shah *et al.*, 2023; Ebegbulem *et al.*, 2020).

**Table 3: Estimates of repeatability for growth parameters in R<sub>1</sub>B<sub>2</sub> genotype**

| Growth traits | R± SE     |
|---------------|-----------|
| Body weight   | 0.75±0.87 |
| Body length   | 0.52±0.70 |
| Wing length   | 0.63±0.10 |
| Shank length  | 0.59±0.35 |
| Drum stick    | 0.45±0.80 |
| Keel length   | 0.43±0.20 |
| Breast width  | 0.48±0.83 |

R±SE = Repeatability coefficient ± Standard error, R<sub>1</sub>B<sub>2</sub>= Ross 308 sire x Black dam

As shown in Table 3, body weight had a high repeatability estimate (R = 0.75, SE = 0.87). Wing length also showed high repeatability (R = 0.63, SE = 0.10). Body length (R = 0.52, SE = 0.70), shank length (R = 0.59, SE = 0.35), drumstick length (R = 0.45, SE = 0.80), keel length (R = 0.43, SE = 0.20), and breast width (R = 0.48, SE = 0.83) exhibited moderate repeatability estimates.

Body weight (0.75 ± 0.87) had a high repeatability, which suggests that early weight measurements are reasonably reliable for selection, although the large standard error indicates some variability (Zhang *et al.*, 2023). Moderate

repeatability obtained in body length (0.52 ± 0.70) suggests that multiple measurements may be needed to accurately assess genetic potential. Wing length (0.63 ± 0.10) showed moderate to high repeatability, indicating that this trait is fairly stable and suitable for early selection programmes. Shank length (0.59 ± 0.35) showed moderate repeatability, suggesting that repeated observations improve selection accuracy. Drumstick length (0.45 ± 0.80) showed moderate repeatability, indicating some environmental influence; repeated measures are recommended for reliable selection. Keel length (0.43 ± 0.20) showed moderate repeatability, reflecting relative stability within individuals. Breast width (0.48 ± 0.83) showed moderate repeatability, suggesting that early measurements are somewhat reliable, but multiple records may improve selection outcomes (Shah *et al.*, 2023; Ebegbulem *et al.*, 2020).

**Table 4: Estimates of repeatability for growth parameters in R<sub>2</sub>B<sub>1</sub> genotype**

| Growth traits | R± SE     |
|---------------|-----------|
| Body weight   | 0.65±0.27 |
| Body length   | 0.62±0.44 |
| Wing length   | 0.59±0.61 |
| Shank length  | 0.39±0.48 |
| Drum stick    | 0.49±0.30 |
| Keel length   | 0.51±0.07 |
| Breast width  | 0.55±0.31 |

R±SE = Repeatability coefficient ± Standard error, R<sub>2</sub>B<sub>1</sub>= Arbor Acre sire x Brown dam

Table 4 shows that body weight (R = 0.65, SE = 0.27) and body length (R = 0.62, SE = 0.44) demonstrated high repeatability. Moderate repeatability was observed for wing length (R = 0.59, SE = 0.61), drumstick length (R = 0.49, SE = 0.30), keel length (R = 0.51, SE = 0.07), and breast width (R = 0.55, SE = 0.31). Shank length (R = 0.39, SE = 0.48) showed low repeatability, indicating greater environmental influence on this trait.

The high repeatability of body weight (R = 0.65 ± 0.27) indicates strong within-individual stability, suggesting that early weight records can reliably predict later growth performance and can therefore be used effectively for selection (Zhang *et al.*, 2023). Similarly, body length (R = 0.62 ± 0.44) exhibited high repeatability, indicating consistent expression across growth stages and supporting its use in early selection programs.

Wing length (R = 0.59 ± 0.61) showed moderate to high repeatability, suggesting reasonable stability, although environmental factors may influence expression. In contrast, shank length (R = 0.39 ± 0.48) demonstrated moderate repeatability, indicating greater environmental influence and the need for repeated records to improve selection accuracy. Drumstick length (R = 0.49 ± 0.30) also showed moderate repeatability, suggesting partial stability but benefit from

multiple measurements. Keel length ( $R = 0.51 \pm 0.07$ ) exhibited moderate repeatability with good precision, supporting its use as a selection criterion under controlled management conditions.

Breast width ( $R = 0.55 \pm 0.31$ ) demonstrated moderate to high repeatability, indicating fairly consistent individual performance and potential for genetic improvement (Shah *et al.*, 2023; Ebegbulem *et al.*, 2020).

Overall, the R2B1 genotype shows moderate to high repeatability for most growth traits, with body weight, body length, and breast width being the most reliable for early selection, while traits with moderate estimates may require multiple observations to enhance accuracy.

**Table 5: Estimates of repeatability for growth parameters in R<sub>2</sub>B<sub>2</sub> genotype**

| Growth traits | R± SE     |
|---------------|-----------|
| Body weight   | 0.59±0.35 |
| Body length   | 0.64±0.77 |
| Wing length   | 0.45±0.15 |
| Shank length  | 0.44±0.29 |
| Drum stick    | 0.57±0.55 |
| Keel length   | 0.49±0.30 |
| Breast width  | 0.58±0.09 |

R±SE = Repeatability coefficient ± Standard error, R<sub>2</sub>B<sub>2</sub>= Arbor Acre sire x Black dam

The repeatability estimates for the R2B2 genotype are presented in Table 5. Body length showed high repeatability ( $R = 0.64$ ,  $SE = 0.77$ ), while body weight ( $R = 0.59$ ,  $SE = 0.35$ ), drumstick length ( $R = 0.57$ ,  $SE = 0.55$ ), breast width ( $R = 0.58$ ,  $SE = 0.09$ ), wing length ( $R = 0.45$ ,  $SE = 0.15$ ), shank length ( $R = 0.44$ ,  $SE = 0.29$ ), and keel length ( $R = 0.49$ ,  $SE = 0.30$ ) demonstrated moderate repeatability estimates. Although most traits exhibited moderate consistency, some estimates were associated with relatively large standard errors, suggesting variability in precision.

Body weight ( $0.59 \pm 0.35$ ) showed moderate to high repeatability, indicating that early measurements are reasonably reliable for selection (Zhang *et al.*, 2023; Adeoye *et al.*, 2020). Body length ( $0.64 \pm 0.77$ ) also exhibited high repeatability, suggesting strong consistency across growth stages and suitability for early selection. Moderate repeatability was recorded for wing length ( $0.45 \pm 0.15$ ), shank length ( $0.44 \pm 0.29$ ), drumstick length ( $0.57 \pm 0.55$ ), and keel length ( $0.49 \pm 0.30$ ), indicating some environmental influence and the need for repeated measurements to improve accuracy. Breast width showed moderate to high repeatability ( $0.58 \pm 0.09$ ), reflecting relatively stable expression across measurements.

Across genotypes (R1B1, R1B2, R2B1, and R2B2), most traits showed moderate to high repeatability, with R1B1 recording the highest values for body weight ( $0.87 \pm 0.17$ ) and

breast width ( $0.67 \pm 0.21$ ), indicating strong genetic stability in this genotype. Overall, body weight, body length, and breast width were the most reliable traits for early selection, while wing length, shank length, and drumstick length require repeated measurements. These findings support targeted selection strategies in breeding programs to improve genetic gain (Falconer and Mackay, 2020; Musa *et al.*, 2021; Zhang *et al.*, 2023).

## Conclusion

The study revealed that growth traits in the evaluated genotypes exhibited moderate to high repeatability, indicating varying degrees of consistency across measurements. Body weight, body length, and breast width showed the highest repeatability, suggesting strong stability and reliability for early selection in breeding programs. Conversely, wing length, shank length, drumstick length, and keel length showed moderate repeatability, reflecting greater environmental influence and the need for repeated measurements to enhance selection accuracy. The results demonstrate that several key growth traits can be effectively used for early genetic evaluation, although trait-specific differences in stability should be considered in selection decisions.

## Recommendation

It is recommended that body weight, body length, and breast width be prioritised in early selection programs due to their higher repeatability and reliability. For traits with moderate repeatability, such as wing length, shank length, and drumstick length, breeders should take multiple measurements across growth stages to improve selection precision. Additionally, improved environmental management should be implemented to reduce non-genetic variation and enhance trait expression consistency. Further studies should also be conducted across more generations and environments to validate these repeatability estimates and strengthen genetic improvement strategies.

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