NATIONAL AGRICULTURAL AND FOOD CENTRE
RESEARCH INSTITUTE FOR ANIMAL PRODUCTION NITRA

Slovak J. Anim. Sci., 58, 2025 (1): 3–12
ISSN 1337-9984, E-ISSN 1338-0095
SCICELL

RELATIONSHIP BETWEEN PITUITARY SPECIFIC TRANSCRIPTION FACTOR-1 (PIT-1) GENOTYPIC VARIANTS AND NON-LINEAR GROWTH CURVE PARAMETERS IN FUNAAB ALPHA CHICKENS

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ABSTRACT

This research was designed to identify genotypic variants in pituitary specific transcription factor-1 (PIT-1) gene and determine the relationship between PIT-1 genotypic variants and growth rate indices, with non-linear growth model parameters in FUNAAB Alpha chickens. Four non-linear growth models (Brody, Gompertz, Logistic and Bertalanffy) were fitted to measure the body weight of FUNAAB alpha chickens at 8 weeks of age. This analysis was conducted using the NLIN procedure of the SAS software (Version 9.2). The Akaike information criteria (AIC), Bayesian information criteria (BIC), Means Squared Error (MSE) and Root Mean Squared Error (RMSE) were used to determine the most appropriate model. Polymerase Chain Reaction-Restriction Fragment Length Polymorphism (PCR-RFLP) analysis was used to identify PIT-1 genotypic variants. The results revealed a significant effect of the PIT-1 genotypic variant on the relative growth rate (RGR). BB allele had the highest value (54.00), while AA and AB alleles had values of 44.13 and 52.11, respectively. A significant effect of chicken genotype was observed on body weight (BW), absolute growth rate (AGR) and RGR (relative growth rate). The mean values obtained for normal feather growth rate indices were higher than the mean values for frizzle feather (FF) and naked neck (NK). There was a high negative correlation between mature weight (A) and maturing index (k) in all the models for genotypic variants AA, AB and BB. AIC and BIC estimates were lowest in Gompertz for FF genotype and male sex of FUNAAB alpha chickens. This study found an association between PIT-1 genotypic variants and growth curve parameters; the Gompertz model was found to be the most appropriate non-linear model for describing growth in FUNAAB alpha chickens.

Key words: genotypic variants; pit-1; growth model; PCR-RFLP; FUNAAB alpha

INTRODUCTION

Poultry is one of the livestock and agricultural subsectors growing at the quickest rate, which also supplies a significant amount of the protein supplements from meat and eggs (Rama Rao, 2020). Poultry holds significant importance globally due to its contributions to nutrition, livelihoods and economic development. Poultry sector contributes significantly to economic expansion by generating jobs and supporting agribusiness (FAO, 2019). Nigeria is home to a variety of chicken breeds including FUNAAB alpha breed, an improved indigenous breed intended to close the disparity between the exotic and the indigenous chicken (Adebambo *et al.*, 2018). These birds were recognised as naked neck, normal feather and frizzled feather chickens. The enhanced growth performance of FUNAAB alpha chicken has resulted from intense crossbreeding and genomic improvement, leading to a lowering of the production cost and making it very competitive with its exotic counterparts (Adebambo *et al.*, 2011).

One of the essential qualities of all living things is growth and, according to Oleforuh-Okoleh *et al.* (2017), it entails dynamic physiological changes that commence

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Received: August 2, 2024
Accepted: December 12, 2024

https://doi.org/10.36547/sjas.930

at conception and continue until it reaches maturity. Kor *et al.* (2006) noted that growth is a complicated process regulated by both hereditary and non-genetic factors in all animals. Though animal's growth performance is a phenotypic trait that is impacted by its surroundings, and it is primarily a manifestation of its genetic makeup (Oleforuh-Okoleh *et al.*, 2017), mathematically, it is explained by a growth model, whose parameters have biological significance. These parameters are used to characterize the course of an animal's growth as well as to estimate an individual's predicted weight at a certain age (Yakupoglu and Atil, 2001). Growth is described by various growth functions, such as the logistic function, von Bertalanffy, Brody and Gompertz functions (Fitzhugh, 1976; France and Thornley, 1984; Maruyama *et al.*, 2001) and research have been done to forecast chicken growth in the future at any age using these functions (Raji *et al.*, 2014; Durosaro *et al.*, 2021). A crucial factor in the success of poultry enterprises is the capacity to predict growth, determine the periods of maximum growth rate and determine when the birds are ready for sale.

Numerous genes influence growth, but the most significant one is a pituitary specific transcription factor-1 (PIT-1). It functions as a transcription factor for the genes that control growth in chickens including prolactin, growth hormone and transforming growth factor-β (Cohen *et al.*, 1996; Miyai *et al.*, 2005). The anterior pituitary gland development (Li *et al.*, 1990) and the initiation of hepatic progenitor cell differentiation into prolactin-producing cells have been associated with the PIT-1 gene (Lee *et al.*, 2005). This gene also regulates mammalian development. The expression of this gene and its association has been investigated in pigs to indicate the PIT-1 gene in relation to growth variation (Song *et al.*, 2005; Xue *et al.*, 2006) and in cattle – for growth and carcass traits (Zhao *et al.*, 2004), while the expression of this gene and its relationship with growth parameters has been studied in some chicken breeds (Adeleke *et al.*, 2011). Understanding, how chicken growth is influenced by genes, is limited to quantitative trait loci (QTLs) identification associated with body weights at a particular age (Ai *et al.*, 2012; Yoo *et al.*, 2014). Growth traits linked to non-linear growth parameters are vital for proper genetic evaluation and selection of important traits, as they have a substantial impact on the profitability of chicken production enterprises. The exon 6 of the PIT-1 gene has been shown by Jiang *et al.* (2004) to positively correlate with growth improvement in chicken, especially with growth rate in chicken at early stage. Hence, there is a need to identify polymorphisms in PIT-1 (exon 6) gene in FUNAAB alpha chickens and to determine its relationship with non-linear growth model parameters.

MATERIALS AND METHODS

Experimental site

The experiment was carried out at the Federal University of Agriculture (FUNAAB), Abeokuta, Ogun State, in the Poultry Breeding Unit of the Directorate of University Farms (DUFARMS).

Experimental birds and management

The chickens used for the experiment were purchased form the University's hatchery. For the experiment, 250 FUNAAB Alpha dual-purpose birds comprising 66 naked neck chickens, 26 frizzle feather and 158 normal feather chickens were used. A deep litter pen was used to raise the chicks. At the 1 day old, the chicks had their wings tagged for identification; they were also subjected to similar management practices throughout the whole experiment. Starter diets (M.E: 2900 kcal/kg and C.P: 23 %) were fed to the birds from 1-day old until they were 4 weeks of age and finisher diets (M.E.: 3000 kcal/kg and C.P: 21 %) for the remaining 4 – 8 weeks of age. The birds were also given unrestricted access to clean, fresh water. Adequate sanitation was practised, and biosecurity measures were put in place to prevent outbreak of diseases.

Data collection

Early in the morning before feeding, the weight of individual birds was recorded, at day old and then fortnightly until the age of 8 weeks. The body weights were measured in grams using a sensitive weighing scale. At 8 weeks of age blood samples were collected from 97 selected chickens (50 normal feather, 25 naked neck and 22 frizzle feather chickens). From each chicken, 0.2 ml of blood was withdrawn aseptically through the jugular vein with needle and syringe and put on the Flinders Technology Associates (FTA) card. The samples were air-dried at room temperature away from sunlight, labelled accordingly and kept safe for further analysis.

Estimation of growth curve parameters

The parameters of growth curves were estimated using a non-linear function including Gompertz, Brody,

Logistic and von Bertanlanffy models implemented within the NLIN procedure of SAS.

The models were specified as follows:

Gompertz: yt = Ae–b exp(–kt) + εt

Logistic: yt = A /(1 + e–kt) + εt

Brody: yt = A (1–be–kt) + εt

Von Bertalanffy: yt = A (1–be–kt)3 + εt,

where:

- yt: the animal's weight at an exact age (t); parameter A was the asymptomatic weight at age t approaching infinity
- b: scaling point
- k: function of the maturation rate (Gbangboche *et al.*, 2008)
- e: Euler's number/constant
- t: time observed
- ε: the residue error

DNA extraction and PCR amplification

Samples of chicken's blood were utilized for DNA extraction. Utilizing a 1 mm Harris p-punch on a cutting mat, five discs of 1 mm were punched out of 97 FTA cards. After inserting the discs into the 1.5 ml Eppendorf tube and adding 200 µl of FTA purification reagent to each tube, the tubes were agitated for 30 minutes, during which the excess solution was removed by tipping off. After a 10-minute shake-free repetition of the wash procedure using 200 µl of distilled water, the washed solution was tipped off. When the DNA was ready for use, each tube received 50 µl of distilled water and heated in a water bath at 90 °C for 15 minutes.

The PCR mixture with a total reaction volume of 25 µl contained 12.5 µl of master mix (2x JENA Ruby hot start pol), 1 µl of each forward and reverse primer pair (10 pmol) targeting the PIT-1 gene, 1 µl of DNA template and 9.5 µl of sterile nuclease-free water resulting. The PCR amplification was done in an Applied Biosystem 2720 Thermocycler. The reaction mixture underwent initial denaturation at 94 °C for 2 min, followed by 34 cycles of denaturation at 94 °C for 60 sec, annealing at 67 °C for 2 min and extension at 72 °C for 3 min. A final extension step was performed at 72 °C for 8 min. A 2 % agarose gel with ethidium bromide in 0.5x Tris-borate buffer (pH 8.0) was used to visualize the PCR products.

Primer Information

The following primer sequences were used for the amplification of FUNAAB alpha chicken PIT-1 gene: F: 5'-TGGGAAGAACAGTTTATGGC-3'; R: 5'-TGGCTAGCTTGTAAGGGAATC-3' (Nie *et al.*, 2008).

Amplicon digestion by BspH1 restriction enzyme using RFLP

RFLP analysis with the BspH1 restriction enzyme was used to genotype the SNP. Each of the reaction mixture with a total volume of 15 µl consisted of 10 µl of PCR products, 1.5 µl of 10x NE buffer, 0.1 µl of BspH1 restriction enzyme and 3.4 µl of nuclease-free water. The mixtures were incubated for 15 min at 37 °C, followed by inactivation of the enzyme for 20 min at 80 °C. A 2 % agarose gel with ethidium bromide in 0.5x Tris-borate buffer (pH 8.0) and a 100 bp molecular marker (Jena Biosciences) were used to visualize the digested PCR products.

Analysis of association between growth curve parameters and PIT-1 polymorphism

A preliminary analysis was done, and the non-significant interactions effects were removed. Analysis of association between PIT-1 genotypic variants and growth curve parameters was used in quantifying body weight in FUNAAB alpha chickens. This was done using the nonlinear procedure of the SAS V.9.2 statistical software (SAS Institute Inc., Cary, NC, USA).

$Y_{ijkl} = \mu + C_i + S_j + G_k + \varepsilon_{jkl}$,

where:

- Y_{ijkl} – the observed value of the dependent variables (Body weight and Growth rate indices),
- µ – the populations mean
- C_i – the fixed effect of i^{th} chicken genotypes, (i = Naked, Frizzle, Normal)
- S_j – the fixed effect of j^{th} sex, (j = Male and Female)
- G_k – the effect of k^{th} PIT-1 gene variants, (k = AA, AB, BB)
- ε – the random residual error.

Assessment of goodness-of-fit

Each of the model goodness-of-fit was calculated using Akaike's information criterion (AIC), Bayesian Information Criterion (BIC), Mean Squared Error (MSE) and Root Mean Squared Error (RMSE), as delineated by Lambe *et al.* (2006).

RESULTS AND DISCUSSION

RFLP Genotyping of PIT-1 gene of FUNAAB alpha chicken

Following the digestion of the PCR products, PIT-1 gene produced a single band of 236 bp for the AA allele, 236 and 455 – for the AB allele and 455 bp – for the BB allele, as presented in Figure 1. In the PIT-1 gene

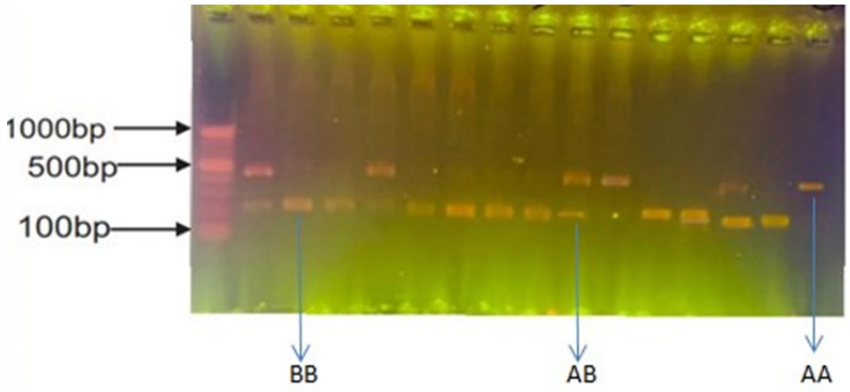

Figure 1. PIT-1 PCR RFLP genotyping of FUNAAB alpha chickens

locus, the frequencies of A and B alleles were 0.40 and 0.60, respectively. B allele was identified as a dominant allele in the PIT-1 locus due to the highest frequency. The frequency of AB heterozygous genotype was the lowest among all loci (0.16), whereas BB genotype had the highest frequency of 0.52, while AA allele had a genotype frequency of 0.32.

Effect of sex, chicken genotype and PIT-1 genotypic variants on body weight and growth rate indices in FUNAAB alpha chickens at week 8

Table 1 presents the mean values of growth rate indices, including absolute growth rate (AGR), relative growth rate (RGR) and body weight (BW). There was no significant impact of sex on BW, AGR and RGR. However, a significant ($P < 0.05$) effect of the genotype was observed on BW and GR indices. Though the effect of sex was not significant, males consistently showed higher mean values for BW, AGR and RGR than females. This result agrees with the report of Rizzi *et al.* (2013) and Eleroglu *et al.* (2014), who showed that male chickens had higher values in BW parameter than females, and Oyeleye *et al.* (2023), who reported higher values in AGR for males. For the body weight, the naked neck genotype had higher mean value than the observed mean value for normal feather genotype. For the growth rate indices, the mean values obtained for normal feather genotype were higher than mean values obtained for frizzle feather genotype. This indicates that genetic factors influence muscle fibre growth and overall metabolic efficiency (Deeb and Lamont, 2002). This also suggests that the normal feather genotype could be preferrable for breeding programs. A significant effect of PIT-1 genotypic variants on RGR was also observed. The mean value for BB was higher than the values obtained for AA and AB alleles. However, Oyeleye *et al.* (2023) found no significant difference in the genotype variant, used in their study. This could be due to differences in the chicken genotypes, or the gene studied. The superior RGR of the BB genotypic variant suggests enhanced growth hormone activity and better growth efficiency underscoring the importance of genetic marker in poultry breeding.

Means of non-linear growth model parameters in each of PIT-1 genotypic variants of FUNAAB alpha chicken at week 8

Means of non-linear growth model parameters in each of PIT-1 genotypic variants of FUNAAB alpha chicken at week 8 are shown in Table 2. This table shows association between the PIT-1 genotypic variants (AA, AB, BB) and the growth curve parameters (A: asymptotic limit of the weight; b: folding point; k: maturing rate; the rate at which weight approaches A) for the Brody, Gompertz, Logistics and Von Bertalanffy model. There was a significant ($p < 0.01$) effect of genotypic variants for Gompertz and Logistics. The parameters A, b and k for the Brody model show no association for the observed genotypic variant and in BB for Von Bertalanffy. A significant effect of genotypic variant on A was observed for Gompertz, Logistic and Von Bertalanffy (AA and AB). The highest value of A was observed at AA (2307.8) in von Bertalanffy followed by the BB (2253.8) in Gompertz. The least value of A (0.78) was observed in the Brody model at AA, followed by AB with value of 1.68. Gompertz and Logistic models showed a significant effect of

Table 1. Effect of sex, chicken genotype and PIT-1 genotypic variants on body weight and growth rate indices on FUNAAB alpha chicken at week 8

Parameters	Subclass	BW	AGR	RGR
Sex	Male	915.16 ± 5.02	628.03 ± 11.31	50.89 ± 2.75
	Female	873.52 ± 4.31	419.02 ± 95.64	45.13 ± 2.36
Genotype	FR	999.71 ± 7.47^{ab}	245.13 ± 16.58^{b}	37.81 ± 4.10^{b}
	NK	1022.93 ± 5.27^{a}	595.42 ± 21.11^{b}	51.27 ± 2.89^{ab}
	NM	1020.38 ± 3.84^{b}	851.11 ± 85.27^{a}	54.96 ± 2.10^{a}
PIT-1	AA	1100.80 ± 5.68	448.41 ± 12.62	44.13 ± 3.22^{b}
	AB	1221.89 ± 6.42	624.32 ± 14.22	52.11 ± 3.65^{b}
	BB	1119.90 ± 3.93	683.33 ± 88.01	54.00 ± 2.23^{a}

^{ab} Means within the same column with different superscripts differ significantly (P < 0.05); BW: body weight; AGR: absolute growth rate; RGR: relative growth rate; FR: Frizzle feather; NK: Naked neck; NM: Normal feather

genotypic variant on b parameter. The highest value of b was observed at AB (36.67) in Gompertz, followed by the AA (32.70) in Gompertz. The least value of b was observed in von Bertalanffy model at BB (-252.5). For k parameter, there were significant association for Gompertz and Logistic models. For Gompertz, AB had values higher than AA and BB, while for Logistics, the value obtained for AB was higher than the AA genotype. Non-linear growth model parameters are used to calculate the predicted weight of animals at specific ages and to describe the pattern of growth over time (Selvaggi *et al.*, 2015). The growth curve parameters can also be used in selection of appropriate growth models. Oyeleye *et al.* (2023) noted that mature weight (A) offered the best opportunity to make comparison among models. According to Narinc *et al.* (2010), matured body weight parameter represents the maximum growth response of the birds. Generally, a small estimate of k often corresponds to the biggest estimated value of A. This was true for the Gompertz, Logistics and Von Bertanlaffy, except for the Brody, as the smallest mature weight observed also has the smallest k value. This, according to Durosaro *et al.* (2021), could be as a result of gene and environmental influence on the slope of the weight-curve.

Table 2. Means of non-linear growth model parameters in each of PIT-1 genotypic allele of FUNAAB alpha chicken at week 8

Model	Genotypic variant	A	b	k
Brody	AA	0.78 ± 158.7	-11.45 ± 2356.5	-0.47 ± 0.56
	AB	1.68 ± 144.8	-8.13 ± 712.3	-0.50 ± 0.29
	BB	222.6 ± 583.4	0.99 ± 0.82	0.0022 ± 57.97
Gompertz	AA	1679.6 ± 439.2^{ab}	4.86 ± 0.82^{b}	0.28 ± 57.97^{b}
	AB	1606.1 ± 355.3^{b}	5.25 ± 1.31^{a}	0.34 ± 0.10^{a}
	BB	2253.8 ± 472.8^{a}	4.76 ± 0.43^{b}	0.25 ± 0.05^{b}
Logistics	AA	1226.4 ± 141.3^{b}	32.70 ± 11.71^{ab}	0.63 ± 0.10^{b}
	AB	1276.5 ± 134.4^{ab}	36.67 ± 17.63^{a}	0.69 ± 0.13^{a}
	BB	1541.6 ± 140.1^{a}	31.60 ± 6.50^{b}	0.59 ± 0.06^{ab}
Von Bertanlaffy	AA	2307.8 ± 1042.6^{a}	-0.90 ± 0.10	0.16 ± 0.07
	AB	2001.3 ± 708.2^{b}	-0.95 ± 0.17	0.21 ± 0.09
	BB	811.7 ± 36.61	-252.5 ± 337.8	3.52 ± 66.87

A = asymptotic weight or mature weight; b = scaling parameter (constant of integration); k = maturity index

Table 3. Correlation among the growth model parameters based on PIT- 1 genotypic alleles

Genotypic variant	Model	A and b	A and k	b and k
AA	Brody	1.00	-0.89	-0.89
	Gomperz	-0.75	-0.97	0.88
	Logistic	-0.60	-0.88	0.90
	Von-Bertalanffy	0.83	-0.99	-0.90
AB	Brody	1.00	-0.88	-0.88
	Gompertz	-0.78	-0.96	0.92
	Logistic	-0.61	-0.84	0.92
	Von-Bertalanffy	0.85	-0.98	-0.93
BB	Brody	1.00	-1.00	-1.00
	Gompertz	-0.72	-0.98	0.84
	Logistic	-0.58	-0.90	0.86
	Von-Bertalanffy	0.58	-0.58	-1.00

A = asymptotic weight or mature weight; b = scaling parameter (constant of integration); k = maturity index

Correlation among the growth model parameters based on PIT-1 genotypic variants

Correlation among the growth curve parameters based on PIT-1 genotypic variants is presented in Table 3. In this study, negative correlation coefficients were observed between A and b in the three genotypic variants for Gompertz and Logistics, while Brody model had estimated values of 1.00 for all genotypic variants and Von Bertalanffy model had estimated values of 0.83, 0.85 and 0.58 for AA, AB and BB, respectively. Negative correlation was estimated for all the genotypic variants (AA, AB, BB) between A and k in all four non-linear growth models used in this study. Positive correlation was observed between b and k parameters in AA, AB and BB for Gompertz and Logistic models, while other models were negatively correlated.

The negative correlations between mature weight and maturity index observed in this study indicated that increase in asymptotic weight due to selection will have negative indirect selection effect on maturity index, and k will be decreasing. Generally, fast early growth, low age and size at maturity are associated with high k value (Karkach, 2006). The high negative correlation also indicated that FUNAAB alpha chicken genotypes with faster growth do not attain a large mature weight compared to those that mature slowly in early life. According to Mignon-Grasteau *et al.* (2000), negative correlation between A and k can be related to a rapid decrease in growth rate after inflection resulting in a lower asymptotic body weight. Therefore, chicken with higher maturity index attained point of inflection faster, as observed in Von Bertanlaffy model, which had the highest k value. Aggrey (2002) noted that the position of inflection point greatly impacts the growth rate and the mature body weight. Hence, the faster the inflection point was attained the lower the mature body weight value.

Comparison of four non-linear growth models goodness-of-fit measure for FUNAAB alpha chicken based on genotype and sex

The goodness-of-fit measure of four non-linear growth model for FUNAAB Alpha chicken based on genotype and sex are presented in Table 4. The results showed that FUNAAB alpha normal feather genotype had the highest Akaike information criterion (AIC) and Bayelsian information criterion in both Logistics and Gompertz models, respectively. Logistic and Gompertz observed to converge for all FUNAAB alpha chicken genotypes (Frizzle feather, Naked neck and Normal feather chicken). The Frizzle feather chicken had the lowest AIC estimates for Gompertz models followed by von Bertalanffly and Logistic among all the genotypes. Bayelsian information criterion estimates also followed the same pattern as the AIC estimates, where the lowest BIC estimates were recorded for Frizzle feather chicken in Gompertz, followed by von Bertalanffly and Logistic model. The highest values for MSE and RMSE were observed in the Brody model for frizzle feather chicken, while the least MSE and RMSE were observed in the Brody model for normal feather chicken. For the sexes, Brody had the highest Akaike information criterion (AIC) and Bayelsian information criterion in

Table 4. Comparison of four non-linear growth model goodness of fit measure for FUNAAB alpha chicken based on chicken genotype and sex

Model	Genotype	Convergence	Iteration	AIC	BIC	MSE	RMSE
Brody	FF	Not converge	100	700.25	706.32	255843.74	492.07
	Nk	Not converge	100	1224.21	1232.15	125851.94	349.60
	Nm	Not converge	100	-4629.40	-4619.55	6.1E-11	7.77E-06
Gompertz	FF	Converge	17	547.74	553.81	16796.25	126.08
	Nk	Converge	16	1303.42	1109.35	38642.84	193.72
	Nm	Converge	19	2425.12	2046.97	30503.58	173.32
Logistic	FF	Converge	16	653.95	554.03	16861.98	126.33
	Nk	Converge	17	1467.47	1273.41	187137.47	426.31
	Nm	Converge	13	2795.48	2417.33	199907.57	443.69
Von-Bertalanffy	FF	Converge	26	653.77	553.84	16806.42	126.12
	Nk	Converge	67	1303.53	1109.46	38684.07	193.83
	Nm	Not converge	100	2697.73	2319.58	121713.86	346.21
	Sex						
Brody	Male	Not converge	100	-3661.79	-4001.79	5.98E-11	7.73E-06
	Female	Not converge	100	2671.50	2313.19	220195.04	465.47
Gompertz	Male	Converge	17	2111.29	1786.70	34103.67	183.04
	Female	Converge	20	2312.25	1953.94	32245.05	178.12
Logistic	Male	Converge	13	2112.58	1787.99	34363.39	183.73
	Female	Converge	12	2312.34	1954.04	32262	178.17
Von-Bertalanffy	Male	Not converge	100	2361.36	2036.77	148473.17	381.91
	Female	Converge	27	2312.69	1954.38	32321.96	178.34

AIC: Akaike Information Criteria; BIC: Bayelsian Information Criteria; MSE: Mean Squared of Error; RMSE: Root Mean Squared of Error

female and failed to converge. The highest values for MSE and RMSE were recorded in female sex for the Brody model. Gompertz was observed to converge and had the least AIC and BIC for male and female, followed by Logistic model for male and female with low number of iterations across the sexes for growth models used. According to Brown *et al.* (1976), in modelling growth, the degree to which a technique accurately describes the observed body weight determines its value. Kaps and Lamberson (2004) stated that the lower the values of AIC, BIC and MSE, the better it fits the data. Following the fitting of the growth data, the best fit model(s) are required, which is based on goodness-of-fit test.

The Brody model was unable to converge for the frizzle feather and naked neck and normal feather chickens and for both sexes, as well as Von Bertanlaffy for normal feather genotype and males. This may be an indication that these two models may not be useful for these genotypes and male chicken in our study. However, this is not in line with the report of Durosaro *et al.* (2021) on FUNAAB alpha chickens. In their study, Logistics and Gompertz models were found not to converge, which could be because of sample size differences. The lowest AIC, BIC and MSE were observed in the Gompertz model, and was adjudged the best fit model for frizzle feather, naked neck and normal feather chickens. This was followed by Von Bertanlaffy and Logistics. For both sexes, the AIC and BIC values for the Gompertz model were the lowest. This result was not in agreement with the report of Bashiru *et al.* (2020), who reported Von Bertanlaffy as the best fit non-linear model for FUNAAB alpha, and Durosaro *et al.* (2021), who reported the Brody model as best fit for frizzle feather chicken and Von Bertanlaffy for male chickens. The difference may be attributed to the degree of selection pressure on FUNAAB alpha or sample size. This result, however, is corroborated by the report of Barbato (1991) and Mignon-Grasteau *et al.* (1999), that the growth parameters estimated by Gompertz model are adjudged to be appropriate for inclusion into genetic enhancement programmes

in chickens based on their medium-high values of heritability.

CONCLUSION

From the study it can be concluded that the PIT-1 gene is polymorphic and that there is a relationship between PIT-1 genotypic variants and growth curve parameters. The BB variant had the best RGR. Based on goodness-of-fit, the Gompertz model was found to be the most appropriate non-linear model for describing growth in FUNAAB alpha chickens.

ETHICAL APPROVAL

All procedures were approved by the Animal Care and Use committee of the Federal University of Agriculture, abeokuta, Ogun state, Nigeria.

AUTHOR'S CONTRIBUTIONS

Conceptualization: AKPAN, U.

Methodology: AKPAN, U., OLOWOOKERE, V. O.

Investigation: OLOWOOKERE, V. O.

Data curation and supervision: OLOWOOKERE, V. O.

Writing-original draft preparation: OLOWOOKERE, V. O.

Writing-review and editing: AKPAN, U., IKEOBI, C. O. N

Project administration: AKPAN, U., IKEOBI, C. O. N

All authors have read and agreed to the published version of the manuscript.

DATA AVAILABILITY STATEMENT

The data presented in this study are available on request from the corresponding author.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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