ESTIMATION OF HERITABILITY, GENETIC CORRELATION OF BODY WEIGHT, AND MODELING OF GROWTH CURVE IN TWO CHICKEN STRAINS

Walid S. Habashy[1*] ,Ibrahim A. Elkhaiat[2],Ghada M. Abd El-latif[3]
[1]Dep. of Anim. and Poult. Prod., Fac. of Agric., Damanhour
[2]Dep. of poult. Prod., Fac. of Agric.Kafrelsheikh Uni.,
[3]Dep. of Poult.Prod., Fac. of Agric., Alexandria Uni.
Corresponding author: Walid S. Habashy[1]Email:Walidh55@gmail.com

ABSTRACT: The purpose of this study was to use nonlinear models (NLN)to characterize the growth pattern and estimate the heritability (h^2), the genetic (r_g), and phenotypic(r_p) correlation of the body weight (BW) in two distinct genotypes of chicken raising under Egyptian conditions. A data set of 500 chickens with pedigree information was gathered for this study. For this purpose, the BW was measured at hatching (BW0),4 weeks (BW4), 8 weeks (BW8), and 12 weeks (BW 12) of age. Three NLN models (Logistic, Gompertz, and Von Bertalanffy) were used. Using Wombat software, a multi-trait animal model with a restricted maximum likelihood procedure was used to estimate h^2, r_g, and $r_p$for BW.The results showed that Golden Sabahi (GS) had a significantly higher weight than White Leghorn (WL). The growth curve parameters A (mature body weight), B (biological constant), and K (growth rate) were 3989.9, 0.7853, and 0.0624 for WL and 4332.6,0.7897, and 0.0642 for GS in the von Bertalanffy model, 2152.8, 3.8096, and 0.1322 for WL chickens and 2368, 3.8594, and 0.1350 for GS chickens in the Gompertz model, 1304.5, 19.0421, and 0.3382 for WL chickens and 1455.6, 19.6116, and 0.3411 for GS chickens in the logistic model. Three models represented the growth of the two breeds using goodness-of-fit metrics (R2, MSE, and AIC). Heritability estimates of BW at 0, 4, and 8 were higher in GS than WL, while the estimate of BW at 12 weeks of age was almost similar in the both strains GS and WL (0.1). Between BW0 and BW12, there were strong positive genetic and phenotypic correlations compared by the rest of growth traits**.** Based on the findings of this investigation, we recommend that the two strains can be utilized for selective breeding between the ages of 4 and 8 weeks to increase the overall genetic improvement of growth traits.

INTRODUCTION

Animal protein shortages are a problem in every city with a growing population, and modern poultry breeding could be a potential solution. Raising chickens for food and profit is a significant industry in many poor countries (Zaman et al. 2004). There would be benefits for both national economic growth and poultry biodiversity if traditional poultry breeding were encouraged and zootechnical performances were enhanced (Bouchardeau and Calet 1970; FAO 1998).

Native chickens are considered an important genetic resource for breeds with high yields. Native breeds are employed as breeding stock through a crossbreeding system with commercial breeds that takes use of heterosis. However, there needs to be more of a supply to satisfy customer demand because of their limitations, including their poor growth rate and limited egg production. Therefore, increasing our understanding of genetics is one approach to these issues and long-term success (Chomchuen et al.2022).

Golden Sabahiaconsists of 7/8 Lohman brown strain and 1/8 of four developed strains, according to Ghanem et al. (2017). This variety produces 219 eggs annually and has male and female weights of 1.02 kg and 0.850 kg at twelve weeks of age, respectively. At 6 months, a white leghorn is a lightweight fowl egg producing breed with a body weight of 3.4 kg for a roaster and 2.26 kg for a hen (Jeremy, 2021). For more than 20 years, this breed has been acclimated to Egyptian environmental circumstances (Hosny, 2006).

Weight-at-age predictions, and weights at which to select birds can be made using growth curves, which can help illustrate patterns of growth across time (Tzeng and Becker 1981; Aslam et al. 2011). Numerous models exist to help biologists explain the weight-age relationships of growing organisms. Bertalanffy's (Bertalanffy 1960), Gompertz's (France and Thornley 1984; Laird 1965), and Logistic (Grossman et al. 1985; Grossman and Bohren 1985; Mead et al. 1993) are growth models all account for S-shaped, asymptotic growth patterns.

Many mathematical functions like the Richards model logistic model (Grossman and Bohren1985) and Gompertz model (Barbato 1991; N'dri et al 2006)were used to describe poultry growth. To recapitulate the data in a few key parameters and critical points, a mathematical model has been developed that may characterize the weight distribution across different ages (Knizetova et al1997). Therefore, growth rate may be compared across animals at the same physiological stage, which is not achievable with atraditional body weight study (Mignon-Grasteau and Beaumont2000).

Accurate genetic parameter estimates, including heritability and correlation, play a major role in determining the actual response in economic features. For accurate estimations, to reduce error variance and avoid overweighting specific components, the variance needs to be divided and ascribed to as many sources as possible, as well as their interactions.

A crucial genetic statistic known as heritability describes the percentage of the additive variance that can be assigned to genetic influences, i.e., that which will be transferred from parents to their offspring (Visscher et al 2008; Awany and Chimusa 2021).Information regarding heritability estimates (h^2) is an

important tool in animal breeding that is used to predict probable response to or progress from selection (Visscher et al. 2008).

For BW traits at different ages, Busye et al. (2001) recorded a h^2 estimate ranging from 0.23 to 0.71. since the common environmental effect benefit greatly the h^2 estimates for BW characteristics, especially when the animals are young. Neglecting this effect would lead to an overestimated heritability estimate at an early age.

Therefore, the objectives of this study were (1) to use non-linear models to compare the average body weight growth curve with the mean of individual growth curves (2) to enhance poultry genetics in future generations, we used a multi-trait animal model to quantify heritability and genetic correlation.

MATERIAL AND METHODS

The research was conducted at Damanhour University, Faculty of Agriculture, Animal and Poultry Research Farm (EL-Bostan), Egypt. Damanhour University's Institutional Animal Care and Use Committee (IACUC) authorized all experimental techniques and approved the protocol for the animal research (DUFA-2021-11). The experiment began in December 2021 and lasted 5 months. In the current study, two pedigreed strains of chickens were used: White Leghorn (WL) and Golden Sabahi strain (GS). In this experiment, 500 chickens were used (n = 250 chickens per strain). The birds were bred from two strains in a pedigree of eight sires and 80 dams (four sires and forty dams for each strain), with each sire mated to ten dams. Each day, we gathered the eggs and labelled them with the pen number, so we could track their pedigree. Before being placed in the incubator for

21 days, the gathered eggs were sterilized with formaldehyde. After they hatched, each chick was weighed ((BW 0) after wings banded. They were weighed with digital balance with an accuracy of 0.1 g every four weeks of age, at hatch, 4 weeks (BW 4), 8 weeks (BW 8), and 12 weeks (BW12) of age, and Weight Gain (WG) was computed from hatch to 4 weeks of age (WG 0-4), from 4 to 8 weeks of age (WG 4-8), and from 8 to 12 weeks of age (WG 8-12).

Birds Husbandry:

All the chicks came from the same hatching batch and were fed the same diet with startingdiet (21% crude protein and 3050 kcal/kg metabolizable energy) for the first 4 weeks and with a pullet grower diet (18% crude protein and 3000 kcal/kg metabolizable energy) between 5-12 weeks. Chickens were kept in brooders on a litter floor with incandescent lighting, constant light, and no darkness from the time they were one to four weeks old. After four weeks of age, the chickens were housed in a slatted floor barn and fluorescent lighting was set up until they were 12 weeks old (20 hours of light and 4 hours of darkness) and become 15 hours of light during egg production. There was unlimited access to food and clean water.

Statistical analysis:

The NLIN procedure of SAS (SAS Institute Inc. 2016) was used to fit three growth models—Logistic, Gompertz, and Von Bertalanffy—to data for the evaluation of the growth parameters by using Marquardt methods (Narinc et al. 2010a) as follow:

Logistic equations are:

$$y = A * \left(1 + B^{(-k*t)}\right)^{-1}$$

Weight at inflection (IBW)= A/2

Time at point of inflection (IPT)= Ln(b)/k

Von Bertalanffy equations are:

$y = A * (1 - B^{(-K*t)})^3$

IBW= 8 A/27

IPT = Ln(3b)/k

Gompertz equations are:

$$Y = A * \exp\left(-B^{(-K*T)}\right)$$

IBW= A/e

IPT= Ln(b)/k

In all models, Y refers to live body weight (g) at age t (weeks), A is the mature body weight (g); b is the biological constant; k, is the growth rate (Sariyel et al., 2017). Adjusted coefficients of determination (R^2_{adj}), Mean square error (MSE), and Akaike information criterion (AIC) were used to determine the good fitness of the models in the present study using the following equation:

$$R^2_{Adj} = 1 - \left[\frac{(N-1)}{(N-P)}\right](1 - R^2)$$

Where R^2 is the multiple coefficients of determination ($R^2 = 1 - \frac{RSS}{TSS}$). TSS is total sum of squares, RSS is residual sum of squares, N is the number of observations and P is the number of parameters in the equation.

$$AIC = N * \ln(RSS) + 2P$$

Where RSS is residual sum of squares.

The UNIVARIATE function in SAS software was used to compute descriptive statistics for body weight attributes (SAS 2016). Significant differences were defined as p 0.05, and significant differences between means were assessed using Tukey. The statistical model was:

$Y_{ij=}$ μ + Si + eij

Individual trait observations were denoted by y_{ij}, the overall mean was represented by μ, the fixed effect of hatching batch with strain (i = 1, 2) was represented by S_i, and the random residual effect was denoted as e_{ij}~ NID (0, s^2 e). Pedigree and performance data were used to estimate the genetic (co) variance components. We employed genotype as the fixed effect while the residual and additive genetic effects as the random effects.

The Average Information Restricted Maximum Likelihood technique and the WOMBAT software (Meyer 2012) were used to determine the variance and covariance components (AI-REML; Johnson and Thompson 1995). The following equation illustrates the multi-trait mixed linear animal model.

y = Xβ + Zu + ƐFormula 1

Where y is the vector of traits to be observed, β is the vector of fixed effects consisting of strains (2 levels), X is the design matrix associated the appropriate fixed effects to each trait, u is the vector of the direct genetic effect of trait, Z is the design matrix correlating the appropriate random effect to each individual, and Ɛ is the vector of random residual effects. Formula 2 presents the mathematical model used in the two-trait analysis.

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} + \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} + \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} Ɛ_1 \\ Ɛ_2 \end{bmatrix}$$

Formula 2 Each y1 and y2 stands for a different characteristic. Both b_1 and b_2 have the identical fixed-effects vectors, as indicated for the univariate model. Random additive genetic effects are represented by the vectors a_1 and a_2, whereas residual effects are represented by e_1 and e_2. Elements of b_1 and b_2 were linked to corresponding records in y_1 and y_2 via the incidence matrices X_1 and X_2. Z_1 and Z_2 are incidence matrices that link a_1 and a_2 components. Estimates of heritability were derived from the variance components using the Falconer and Mackay equation (1996). The (co)variance components were then used

to determine genetic correlation and phenotypic correlation.

RESULTS AND DISCUSSION

The least-square means of body weight by strains are in Table 1. Results showed that GS strains had higher BW and GR than WL. Throughout the experiment, the GS strain had the highest BW and BWG compared to the WL strain (p ≤ 0.05). This could be due to genetic differences between the two strains. Kosba and Abd El-Halim (2008) and Debes (2017) both reported similar findings. A is a parameter that represents an estimation of asymptotic weights, or mature weight (Narinc et al. 2010b).

Table 2 shows the estimated parameter, IPT, and IPW of three NLINs for chickens. The Von Bertalanffy function had the highest values of asymptotic weight parameter (A) (3989.9 g for WL and 4332.6 g for GS), while Gompertz had 2152.8 g for WL and 2368 g for GS and the Logistic model had 1304.5 g for WL and 1455.6 g for GS. The GS breed arrived at IPT earlier than the WL. The differences for the Gompertz, Logistic, and von Bertalanffy models were 0.12, 0.01, and 0.3 weeks, respectively. The mature BW estimated for GS was greater than that estimated for WL. The A value for the chicken under study in the Von Bertalanffy and Gompertz models was higher than previously reported (Boonkum et al. 2021). The A value depends on genetic and environmental factors (Raji et al. 2014), so strains with different genotypes and environments can expect different A values. Another important feature to consider is the parameter k, which represents the maturation rate and indicates the growth rate required to reach the asymptotic weight. In the current study, GS chickens had higher values for this parameter than WL chickens.

The estimates of coefficients of determination (adjusted R^2), Mean square errors (MSE), and Akaike information criteria (AIC) statistics for the three growth curves using Bertalanffy, Gompertz, and Logistic models, by strains are in Table 3.

To sum up, the Von Bertalanffy model provided the best fit to the data for both strains according to the goodness-of-fit criteria (R^2, MSE, and AIC). Understanding the growth parameters of both strains could aid in the development of nutritional feeding programs from hatching to the age of maximum growth, as well as marketing and reproduction strategies. Using genetic parameters, we can predict that the two breeds can be used for selective breeding between the ages of 4 and 8 weeks to further advance the genetic improvement of growth performance attributes. To enable growth parameter selection, it is recommended that future research estimate the genetic parameters of the WL and GS growth curves.

The growth curves for WL and GS can be accurately described by Bertalanffy, Gompertz, and Logistic models, according to the curve fitting results for each strain. The coefficients of determinations were 90 % and lower AIC. Bertalanffy, Gompertz, and logical models were in the order that provided the best fit. Figure 1 shows predicted growth curves and observed data using the Bertalanffy, Gompertz, and logistic models, for strains of WL and GS, respectively.

The highest relative growth rate and exponential growth rate anticipated in this study were equivalent to those reported in in Japanese QuailbyNarinc et al. (2010b)

using the Von Bertalanffy model and in local Italian chickens by Rizzi et al. (2013) using the logistic model. Nonetheless, they were lower than those found with fast-growing chickens (Ross PM3), as reported by Topal and Bolukbasi (2008). The lack of a genetic improvement program and inadequate sanitary management may be the reasons why WL chickens' relative growth is slower than that of GS chickens. Our results are consistent with those of Yang et al. (2006) and Adenaike et al. (2017), who also concluded that the Von Bertalanffy growth model best explains the development of native chicken. However, Zhao et al. (2015) discovered that the Gompertz-Laird model better described the growth of native Chinese chickens.

Table 4 displays the heritability of growth traits. The estimated body weight heritability ranged from 0.55 (BW0) to 0.10 (BW12) in WL chickens and ranged from 0.68 (bw0) to 0.10 (bw12) in GS chickens. Estimates of h^2 for the traits in this research varied from 0.1 to 0.68, were comparable to the findings of previous studies on Thai native synthetic chickens (Chomchuen et al. 2022) and Mazandaran native chickens (Niknafs et al. 2012). Except for the day of hatching, the heritability of body weight peaked at 4 weeks of age and then declined with advancing age, suggesting that identifying genetic variation for BW might be more challenging at 12 weeks of age than at 4 weeks. Intense selection for economic qualities was not used in the development of these breeds, which may

account for the higher h^2 estimates for GS growth traits. Therefore, using BW4 as a selection criterion appeared more effective than using BW12. Similar results were mentioned by Dana et al. (2011) and Manjula et al. (2018). The high h^2 for body weight at hatch is due to the incorporation of the maternal genetic effect (Niknafs et al. 2012, Mookprom et al. 2017).

Table 5 displays the genetic and phenotypic correlations among growth traits. They ranged from moderate to high. Strongly positive genetic correlations were found between body weight (BW0, BW4, BW8, and BW12), ranging from 0.854 to 0.995. Lower than the genetic correlations, the phenotypic correlations between growth traits ranged from (0.234 to 0.782). These current findings are consistent with those published by Niknafs et al. (2012), El-Attrouny et al. (2017), and Tongsiri et al (2019). Studies in KM1 and Esfahan native chickens found a similar low genetic correlation between BW0 and other traits (Promwatee et al. 2013 and Zonuz et al. 2013). High estimates of genetic correlations were found between BW4 and BW8 or BW12(0.89 and 0.71), as reported by Abd El-Ghany and Abd El-Ghany (2011). This indicates that, even when there is a high heritability for body weight at day hatch, BW0 may not be used to properly forecast whether a chicken has the genetic potential for healthy growth at rising ages. Given the association, we propose that growth between the ages of 4 and 8 weeks be considered in a selection programme.

Egyptian; Growth curve; Genetic parameter; Nonlinear models; Productive

Table (1): least square means ± S.E. of body weight traits in two strains

Traits	White Leghorn	Golden Sabahia	P value
Body weight at hatch	29.4±0.436[b]	37.5±0.461[a]	0.0001
Body weight at 4 weeks	245±2.84[b]	256.±2.99[a]	0.0073
Body weight at 8 weeks	574±7.49[b]	635±7.91[a]	0.0001
Body weight at 12 weeks	987±13.2[b]	1108±14.09[a]	0.0001
Growth rate 0-4	216±2.70	219±2.85	0.4374
Growth rate 4-8	328±5.51[b]	378±5.83[a]	0.0001
Growth rate 8-12	413±7.62[b]	473±8.12[a]	0.0001
Growth rate 0-12	958±13.1[b]	1070±13.9[a]	0.0001

[ab]Means with different letters in a row differ significantly (p>0.05)

Table (2): Estimated parameters ± SE of growth models for both strains of chickens.

Strain	Growth Model	A	B	K	IPT (week)	IPW(g)
White Leghorn	Von Bertalanffy	3989.9±570.2	0.7853±0.006	0.0624±0.006	13.73	1182.19
	Gompertz	2152.8±146.4	3.8096±0.047	0.1322±0.007	10.12	791.97
	Logistic	1304.5±35.49	19.0421±0.679	0.3382±0.009	8.71	652.25
Golden Sabahia	Von Bertalanffy	4332.6±636	0.7897±0.006	0.0642±0.006	13.4	1283.7
	Gompertz	2368.0±166.6	3.8594±0.051	0.1350±0.0073	10.00	871.14
	Logistic	1455.6±41.95	19.6116±0.755	0.3411±0.009	8.72	727.8

IPT: age at inflection point; IPW: weight at inflection point

Table (3): The goodness of fit criteria for fitted growth function

Strain	Growth Model	R^2	MSE	AIC
White Leghorn	Von Bertalanffy	0.902	11595	16669.2
	Gompertz	0.901	11619	16672.9
	Logistic	0.900	11765	16695.1
Golden Sabahia	Von Bertalanffy	0.902	14466	15204.8
	Gompertz	0.902	14504	15208.9
	Logistic	0.900	14754	15236.1

R^2: multiple coefficients of determination; MSE: Mean square error; AIC: Akaike information criterion.

Table (4): Heritability estimates of growth traits in two strains of chicken

Traits	White Leghorn	Golden Sabahia
Body weight at hatch	0.55	0.68
Body weight at 4 weeks	0.48	0.62
Body weight at 8 weeks	0.10	0.46
Body weight at 12 weeks	0.10	0.10

Table (5): Genetic (above diagonal), and phenotypic (below diagonal) correlations of growth traits (±SE)

	BW0	BW4	BW8	BW12
Bw0		0.854 ± 0.235	0.949 ± 0.605	0.914 ± 0.515
Bw4	0.379 ± 0.069		0.975 ± 0.166	0.989 ± 0.389
Bw8	0.355 ± 0.069	0.782 ± 0.023		0.995 ± 0.360
Bw12	0.234 ± 0.064	0.585 ± 0.039	0.702 ± 0.030	

BW0 body weight at hatch, BW4 body weight at 4 weeks, BW8 body weight at 8 weeks, BW12 bodyweight at 12 weeks.
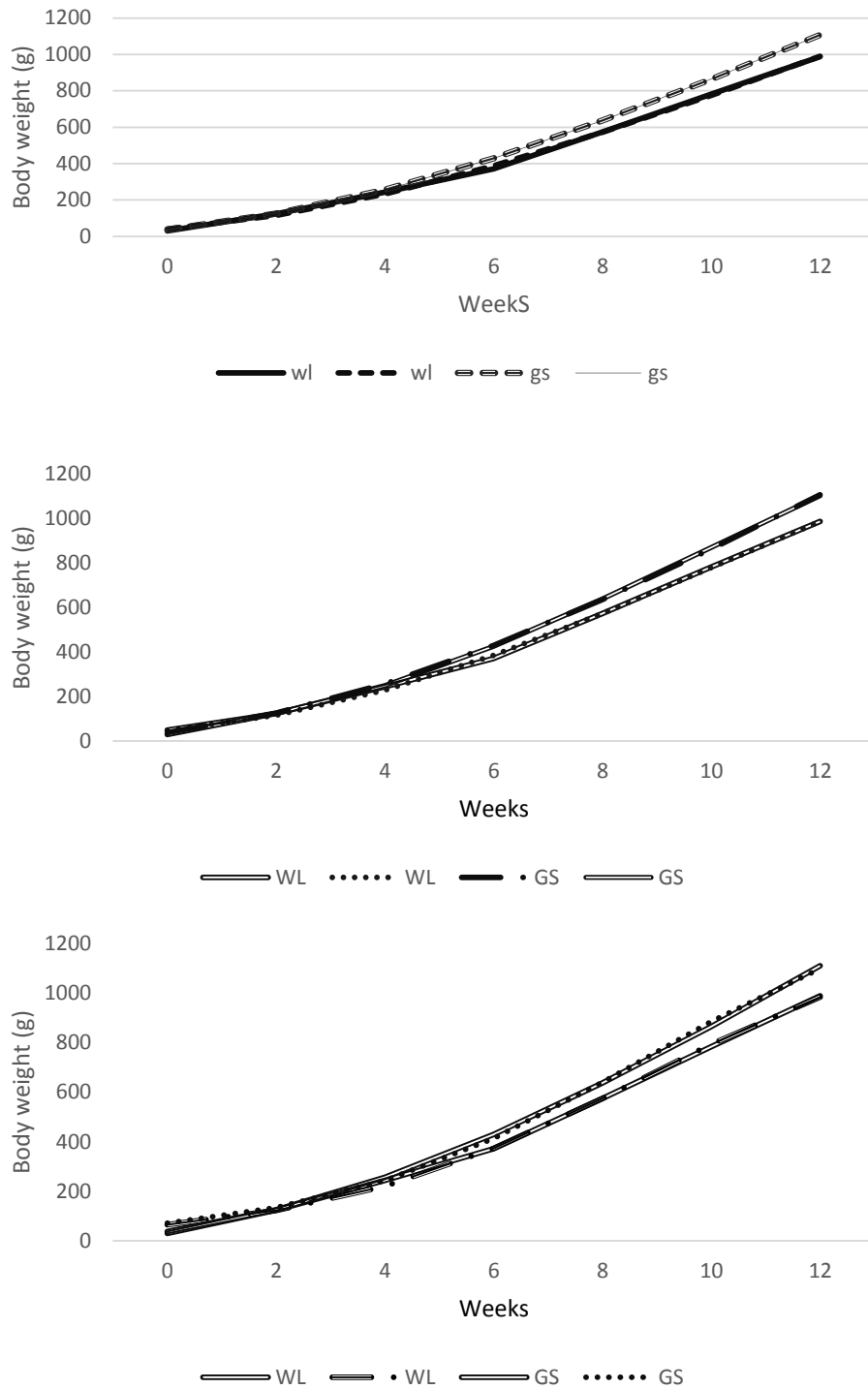
Figure (1): Modelling of growth curve in White Leghorn (WL) and Golden Sabahia (GS) chickens

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الملخص العربى

تقديرالمكافئ الوراثي والارتباط الوراثي لوزن الجسم ونمذجة منحنى النموفي سلالتين
من الدجاج
وليد شعبان حبشي[1]ـ ابراهيم عرفه الخياط[2]ـ غاده محمد عبداللطيف[3]
[1] قسم الأنتاج الحيواني والداجني ـكلية الزراعة – جامعة دمنهور
[2] قسم انتاج الدواجن – كلية الزراعةـ جامعة كفر الشيخ
[3] قسم أنتاج الدواجن – كلية الزراعة – جامعة الأسكندرية

كان الغرض من هذه الدراسة هو استخدام النماذج غير الخطية (NLN) لتوصيف منحنى النمو وتقدير العلاقة بين المكافئ الوراثي (h^2) والارتباط الوراثي (r_g) والظاهري (r_p) لوزن الجسم (BW) في نمطين وراثيين متميزين للدجاج تحت الظروف المصرية. حيث تم استخدام 500 كتكوت معلوم النسب في هذه الدراسة ولهذا الغرض تم قياس وزن الجسم BW عند الفقس (BW0)، 4 أسابيع (BW4)، 8 أسابيع (BW8) ، و 12 أسبوعا (BW 12) من العمر، تم وصف منحني النمو باستخدام ثلاثة نماذج غير خطية (Logistic, Gompertz, and Von NLN (Bertalferny). باستخدام برنامج Wombat ، تم استخدام نموذج الحيوان المتعدد الصفات لتقدير المكافئ الوراثي والارتباط الوراثي والمظهري لوزن الجسم. أظهرت النتائج أن سلالة الصبحية الذهبي (GS) كانت لها وزن أعلى معنويا من اللجهورن الابيض(WL) . وكانت مقاييس منحني النمو (وزن الجسم الناضج ، الثابت البيولوجي حول شكل المنحنى ، معدل النمو) 3989.9 ، 0.7853 ، 0.0624 لسلالة اللجهورن وكان 4332.6 ، 0.7897 ، 0.0642 لسلالة الصبحية الذهبي في نموذج von Bertalanffy، 0.1322 ، 3.8096 ، 2152.8، لسلالة اللجهورن الأبيض ، 2368، 3.8594 ، 0.1350 لسلالة الصبحية الذهبي في نموذج Gompertz، 1304.5 ، 19.0421 ، 0.3382 لسلالة اللجهورن الأبيض ، 1455.6 ، 19.6116 ، 0.3411 لسلالة الصبحية الذهبي في نموذج Logistic. كانت تقديرات المكافئ الوراثي لوزن الجسم عند الفقس و 4 و 8 أسابيع أعلي في سلالة الصبحية مقارنة بسلالة اللجهورن الأبيض ، ولكن عند عمر 12 أسبوع كان المكافئ الوراثي في كلتا السلالتين متشابه تقريبا (0.1) وكان هناك ارتباط وراثي ومظهري قوي وموجب بين وزن الجسم عن الفقس وعند عمر 12 أسبوع مقارنة بباقي صفات النمو. بناء على نتائج هذه الدراسة ، نوصي باستخدام السلالتين بين عمر 4 و 8 أسابيع في برامج الانتخاب لزيادة التحسين الوراثي العام لصفات النمو.