

# Growth curves in meat-type and laying quail: a Bayesian perspective

## Curvas de crescimento em codornas de corte e postura: uma perspectiva Bayesiana

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### Abstract

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The aim of this study was to assess the goodness of fit for nonlinear models, using the best model to describe body growth curves, comparing the parameters obtained for gender and one meat-type (*Coturnix coturnix coturnix*) and two laying (*Coturnix coturnix japonica*) quail strains, as well as nesting via MCMC (Markov chain Monte Carlo processes) methods under a Bayesian approach. A total of 1,350 one-day-old mixed quail were used: 400 of meat-type, 450 of yellow laying, and 500 of red laying strains distributed in a completely randomized design with three treatments (each treatment corresponded to one strain) and five replications. The experimental period consisted of 1 to 42 days of age. At 21 days of age, quail sexing was performed by means of sexual dimorphism, being individually identified at one day of age with numbered rings, allowing determining growth curves by gender. Birds were reared in a conventional system, fed *ad libitum* with diets formulated to meet nutritional requirements. Body weight was determined weekly and assessed using nonlinear models: Logistic, Brody, Von Bertalanffy, and Gompertz. DIC (Deviance Information Criterion) criterion was used to select the best nonlinear model, i.e. the lower the DIC value is, the better the model goodness of fit to the data. Gompertz model was better adjusted to the data regardless the gender or strain. Meat-type quail had the highest asymptotic weights and the highest age at which growth rate was maximum, followed by red and yellow strains. All nestings presented significant differences ( $p < 0.05$ ) between gender for contrasted parameters. Meat-type, yellow, and red females presented values significantly ( $p < 0.05$ ) higher for asymptotic weight (370, 203, and 215 g, respectively) when compared to males (274, 131, and 143 g, respectively), which were earlier in body growth.

**Key words:** Deviance information criterion. Gompertz equation. Nonlinear models. Body weight.

### Resumo

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O objetivo deste trabalho foi avaliar a qualidade de ajuste dos modelos não lineares aos dados, utilizando o melhor modelo para descrever as curvas de crescimento corporal, comparando os parâmetros obtidos para gênero e uma linhagem de codornas de corte (*Coturnix coturnix coturnix*) e duas de postura (*Coturnix coturnix japonica*), bem como o aninhamento, via método MCMC (Cadeias de Markov em processos de Monte Carlo), sob o enfoque Bayesiano. Foram utilizadas 1.350 codornas mistas, com um dia de idade, sendo: 400 da linhagem de corte, 450 de postura amarela e 500 de postura vermelha, distribuídas por um delineamento inteiramente casualizado, com três tratamentos (cada tratamento corresponde a uma

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linhagem) e cinco repetições. O período experimental foi de 1 a 42 dias de idade. Aos 21 dias de idade foi realizada a sexagem por dimorfismo sexual, sendo que elas foram identificadas individualmente com um dia com anilhas numeradas, possibilitando a determinação das curvas de crescimento por gênero. As aves foram criadas em um sistema convencional, alimentadas *ad libitum* com rações formuladas para atender às exigências nutricionais. O peso corporal foi determinado semanalmente e avaliados por meio dos modelos não lineares: Logístico, Brody, Von Bertalanffy e Gompertz. Para a seleção do melhor modelo não linear utilizou-se o critério DIC (*Deviance Information Criterion*), em que quanto menor o valor de DIC, melhor é a qualidade do ajuste do modelo aos dados. Gompertz melhor se ajustou aos dados, independentemente do gênero ou linhagem. As codornas de corte tiveram os maiores pesos assintóticos e a maior idade em que a taxa de crescimento é máxima, seguido pela vermelha e amarela. Todos aninhamentos apresentaram diferenças significativas ( $p < 0,05$ ) entre gênero para os parâmetros contrastados. As fêmeas de corte, amarela e vermelha apresentaram valores significativamente ( $p < 0,05$ ) maiores para o peso assintótico (370, 203 e 215 g, respectivamente), comparados aos machos (274, 131 e 143 g, respectivamente), porém os machos foram mais precoces no crescimento corporal. **Palavras-chave:** *Deviance Information Criterion*. Equação de Gompertz. Modelos não lineares. Peso corporal.

## Introduction

Quail rearing has increased significantly in Brazil lately. However, genetic material available for both egg and meat production is of low quality, making the sector vulnerable and creating a need to import breeders to obtain a better performance and carcass conformation in meat-type quail and a greater egg production in laying quail, ideal for internal and external markets (TEIXEIRA et al., 2012). In order to improve Brazilian genetics, well-founded breeding programs based on precise and accurate parameters are needed (DIONELLO et al., 2008). In this sense, little is known about the productive potential of meat-type and laying quail in Brazil (MÓRI et al., 2005), one of the initial steps to be taken to improve productive indices and minimize the lack of uniformity of lots, one of the main rearing problems (GRIESER et al., 2015a).

Japanese quail (*Coturnix coturnix japonica*) reaches an adult weight between 120 and 175 g, depending on the strain, and their main purpose is the production of eggs for consumption. On the other hand, larger strains such as the European (*Coturnix coturnix coturnix*), whose quail reach between 200 and 300 g at 35 days of age, are used for slaughtering purposes (GRIESER et al., 2015a).

Quail strains present different body growth

curves, which implies changes in their nutritional requirements. In general, significant differences are observed when data are analyzed separately by gender (MARCATO et al., 2010), making the study of body development by genetic groups and gender relevant (GRIESER et al., 2015b).

Mathematical models can assist in describing body growth of birds (MARCATO et al., 2010). In this sense, the obtained data could corroborate with the improvement of productive indices of this activity, reducing production costs of eggs and meat of quail (GRIESER et al., 2015b). In addition, these models could allow predicting the nutritional requirements of birds, the best slaughter age, and production efficiency indices, providing data to develop a software for use by companies and producers to enhance understanding in regarding bird development, improved management, ambience of facilities, and nutrition to support the maximum expression of their genetic potential (MARCATO et al., 2010).

Various nonlinear mathematical models can be used to determine parameters of animal growth curves such as Brody, Von Bertalanffy, Gompertz, and Logistic, being the last two models considered as sigmoid by modeling S-shaped growth curves. In general, to make inferences in these models an

iterative process is considered to obtain parameter estimations. However, the obtained distributions from least squares estimators, maximum likelihood method, and construction of hypothesis tests or confidence intervals are based on usual asymptotic results, i.e. parameter distributions are approximate to the normal, requiring that sample number be high, assuming that the errors are also normal (KALBFLEISCH, 1985; BUZOLIN, 2005).

In this sense, the search for a methodology flexible, robust, and accurate in its estimations leads to improved procedures such as the Bayesian (PAULINO et al., 2003; ROSSI, 2011). The Bayesian approach avoids asymptotic inferences and allows the use of previous information regarding the parameters of interest, i.e. the incorporation of *a priori* knowledge through an *a priori* probability distribution that is informative, which can make *a posteriori* estimations more consistent with the reality of the variable of interest. If there is no *a priori* knowledge, *a priori* non informative densities are considered, which allows comparing the results of frequentist inference (ROSSI, 2011).

In this context, the aim of this study was to assess the goodness of fit for nonlinear models to the data using the best model to describe body growth curves, comparing the parameters obtained for gender and one meat-type (*Coturnix coturnix coturnix*) and two laying (*Coturnix coturnix japonica*) quail strains, as well as nesting by MCMC (Markov chain Monte Carlo processes) method under a Bayesian approach.

## Material and Methods

The experiment was carried out in accordance with the standards proposed by the Ethics Committee on Animal Experimentation of the State University of Maringá (UEM), Maringá, PR, Brazil under the protocol number 061/2012.

## Animals and diets

A total of 1,350 one-day-old mixed quail were used: 400 of meat-type (*Coturnix coturnix coturnix*), 450 of yellow laying (*Coturnix coturnix japonica*), and 500 of red laying (*Coturnix coturnix japonica*) strains. Yellow and red laying strains were originated from commercial strains that were genetically improved by the animal breeding program of the UEM. The meat-type, however, is a commercial strain.

Quail were reared in a conventional shed divided into boxes, each of them a replication or experimental unit. Mixed one-day-old quail were distributed in the replications by means of a completely randomized design with three treatments (each treatment corresponded of one quail strain), five replications, and 80, 90, and 100 quail per replication for meat-type, yellow, and red strains, respectively. The experimental period consisted of 1 to 42 days of age.

At 21 days of age, quail sexing was carried out by means of sexual dimorphism considering that males present red pigmentation in the region of throat and breast whereas females have dark spots. Quail were individually identified at one day of age with numbered plastic rings placed on the right foot, allowing the individual data collection and determining growth curves by gender from the first day of age. Therefore, a total of 238, 237, and 257 males and 162, 213, and 243 females were used in the experiment respectively for meat-type, yellow, and red strains. A necropsy was performed in birds that died before sexing (21 days of age) to verify the gender.

Throughout the experimental period, quail were reared in a conventional system, receiving feed and water *ad libitum*. Corn- and soybean meal-based diets were formulated using chemical and energetic composition values proposed by Rostagno et al. (2011), meeting the nutritional requirements of quail according to strain and growth phase (Table 1).

**Table 1.** Centesimal, chemical, and energetic composition of diets for meat-type quail at initial and final growth phases and for laying quail (yellow and red).

| Ingredient                             | Meat-type quail |             | Laying quail |
|--|-----------------|-------------|--------------|
|  | Initial phase   | Final phase |              |
|  | Amount (kg)     |             |              |
| Corn grain                             | 40.95           | 52.79       | 57.16        |
| Soybean meal (45%)                     | 49.75           | 39.31       | 38.05        |
| Soybean oil                            | 4.75            | 3.25        | 1.10         |
| Dicalcium phosphate                    | 1.56            | 1.60        | 1.41         |
| Common salt                            | 0.46            | 0.46        | 0.39         |
| Limestone                              | 0.36            | 0.28        | 1.16         |
| DL-Methionine                          | 0.67            | 0.66        | 0.19         |
| L-Lysine HCl                           | 0.68            | 0.80        | 0.05         |
| L-Threonine                            | 0.42            | 0.41        | 0.09         |
| L-Tryptophan                           | 0.006           | 0.04        | -            |
| Vitamin and mineral blend <sup>1</sup> | 0.40            | 0.40        | 0.40         |
| Total                                  | 100.00          | 100.00      | 100.00       |
| Calculated values                      |                 |             |              |
| Metabolizable energy (kcal/kg)         | 2,996           | 3,034       | 2,901        |
| Crude protein (%)                      | 27.49           | 23.51       | 22.01        |
| Calcium (%)                            | 0.64            | 0.61        | 0.90         |
| Available phosphorus (%)               | 0.41            | 0.41        | 0.37         |
| Sodium (%)                             | 0.20            | 0.20        | 0.18         |
| Potassium (%)                          | 1.02            | 0.86        | -            |
| Chlorine (%)                           | 0.31            | 0.31        | -            |
| Digestible methionine + cystine (%)    | 1.32            | 1.23        | 0.76         |
| Digestible lysine (%)                  | 1.87            | 1.73        | 1.12         |
| Digestible threonine (%)               | 1.25            | 1.11        | 0.79         |
| Digestible tryptophan (%)              | 0.30            | 0.28        | -            |

<sup>1</sup>Vitamin/mineral blend (guarantee levels per kg of product); vitamin A - 4,500,000 IU; vitamin D3 - 1250,000 IU; vitamin E - 4,000 mg; vitamin B1 - 278 mg; vitamin B2 - 2,000 mg; vitamin B6 - 525 mg; vitamin B12 - 5,000 mcg; vitamin K3 - 1.007 mg; calcium pantothenate - 4,000 mg; niacin - 10,000 mg; choline - 140,000 mg; antioxidant - 5,000 mg; zinc - 31,500 mg; iron - 24,500 mg; manganese - 38,750 mg; copper - 7,656 mg; cobalt - 100 mg; iodine - 484 mg; selenium - 127 mg.

## Body weight

Body growth of birds was determined according to the methodology described by Sakomura and Rostagno (2016). Weight was individually (birds identified with numbered rings) and weekly monitored with a precision balance (1,500 g × 0.01 g). This process allowed obtaining the empirically

observed growth curves of quail of different strains and gender in the period from 1 to 42 days of age.

## Statistical analysis

Data were analyzed by gender, treatment levels (strain), and gender within treatment levels

(nesting). Bayesian procedures were applied to nonlinear models presented in Table 2 for analyzing the obtained database.

From the growth models used (Table 2), the parameter  $\beta_1$  biologically represents the asymptotic value of the response variable,  $\beta_2$  is a constant that

is related to the initially observed value, indicating the proportion of the asymptotic value to be gained, and  $\beta_3$  is the growth rate of the response variable that indicates the velocity at which the observed value approaches the observed maximum value, i.e. determines the growth efficiency (CAMPOS, 2011).

**Table 2.** <sup>1</sup>Models used to express growth curves.

| Author                                      | Nonlinear model   |
|---|---|
| Brody (1945)                                | $Y_i = \beta_1(1 - \beta_2 e^{-\beta_3 x_i}) + \varepsilon_i$ [1]           |
| Gompertz (1825)                             | $Y_i = \beta_1 e^{-\beta_2 e^{-\beta_3 x_i}} + \varepsilon_i$ [2]           |
| Fialho (1999), adapted from Gompertz (1825) | $Y_i = \beta_1 e^{-e^{-\beta_3(x_i - \beta_2)}} + \varepsilon_i$ [3]        |
| Logistic (VERHULST, 1838)                   | $Y_i = \frac{\beta_1}{1 + e^{(\beta_2 - \beta_3 x_i)}} + \varepsilon_i$ [4] |
| Von Bertalanffy (1957)                      | $Y_i = \beta_1(1 - \beta_2 e^{-\beta_3 x_i})^3 + \varepsilon_i$ [5]         |

<sup>1</sup>Ratkowsky (1983).

Gompertz model [2] can be reparametrized to form [3] and obtain the parameter  $\beta_2^*$ , which has a special biological interpretation of interest in the study of animal growth curves. This is the time when the animal growth rate is maximum (FIALHO, 1999), which is given by the abscissa to the inflection point. A reparametrization of [2] should be carried out in terms of inflection point, i.e.  $\beta_2^* = \frac{\ln(\beta_2)}{\beta_3}$ , so that the form could be achieved.

In this interpellation, the effect of these six groups (gender with the respective strains) on parameter estimations of growth curves were determined by means of a Bayesian hierarchical model, which was adjusted separately for each of the four considered models (Brody, Gompertz, Logistic and Von Bertalanffy).

$$y_{ij}|x_{ij}, \beta, \sigma^2 \sim N(f(x_{ij}, \beta), \sigma^2) \quad (6)$$

with a priori distributions for the parameters  $\beta$  and  $\tau = \frac{1}{\sigma^2}$  (accuracy), being respectively  $\beta \sim N(0, 10^{-6})$  and  $\frac{1}{\sigma^2} \sim \text{Gamma}(10^{-3}, 10^{-3})$  non-informative.

The likelihood function (joint distribution of sample data) was obtained separately for each model:

$$L(\beta, \sigma^2) \propto \prod_{i=1}^n \prod_{j=1}^k \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left\{-\frac{[y_{ij} - f(x_{ij}, \beta)]^2}{2\sigma^2}\right\} \quad (7)$$

The presented model was performed in the software *R* (R DEVELOPMENT CORE TEAM, 2015) by using *BRugs* package, in which the algorithm for Gibbs Sampler was implemented. For all models, estimations close those frequentists obtained by means of *nls* package from *R* were considered as initial values. A total of 100,000 iterations, of which the first 10,000 were discarded, were used to avoid the effects of initial values since this period does not represent the balance of Markovian chain distribution. In addition, to eliminate the autocorrelation between consecutive iterations, thus ensuring sample independence, a spacing between sample points of size 10 was taken. Thus, a final chain with 9,000 observations was obtained for each parameter.

Convergence analysis of generated chains was performed by means of *coda* package from *R* using Heidelberger and Welch (1983) criteria. The selection of the best nonlinear model was performed using DIC (Deviance Information Criterion) criterion, in which lower DIC values indicate a model with the better goodness of fit to the data. DIC model was chosen since it is indicated to compare complex models with a preference for means based on parameterization that complies with the normality of approximate probability, in addition to its ease in calculations and availability in different statistical software (SPIEGELHALTER et al., 2002). According to Rossi (2011), when the models  $M_A$  and  $M_B$  are compared pairwise, the following criteria can be adopted:

$$D = |DIC_{M_A} - DIC_{M_B}| \quad (8)$$

If  $D < 5$ , then it is not significant; if  $5 \leq D \leq 10$ , then it is significant; and if  $D > 10$ , then it is highly significant.

For comparison of growth curves by gender, strain, and nesting (gender within strain), samples of posterior distributions were used considering the differences between averages of estimations of the parameters of interest. Thus, these differences are an additional parameter in the model and allow testing the hypothesis of equality of parameters through assessment of the credibility interval. If a zero value is contained within this interval, the parameters of both populations involved in the contrast are statistically the same at 5% significance level; if the differences of averages did not contemplate the zero value, then they are statistically different.

## Results and Discussion

Table 3 shows DIC values for each considered model for gender, strain, and nesting. Brody model significantly showed the highest DIC values, but not the best quality fit to body weight data. In the nesting factor conditioned to female, no guarantee of convergence of the generated chains was observed. In addition, this model significantly overestimated the asymptotic parameters, which could be observed through frequentist analyses and graphical inspection of fit, not presented in this paper. Other authors in the literature (RIBEIRO, 2014; MOTA et al., 2015; VELOSO et al., 2015; FINCO et al., 2016) also do not recommend the use of Brody model to describe bird growth since it does not have a good fit to the data. This model is not indicated to predict live weight at early phases because the inflection point of the growth curve coincides with the birth, resulting in a non-sigmoid curve without biological interpretation (BRODY, 1945).

Von Bertalanffy model showed values equal to or slightly lower than those found by Gompertz model for some factors. However, the difference between DIC values was not significant, in addition to overestimating the asymptotic parameters, as observed in Brody model. A similar result was obtained by Mazucheli et al. (2011), who studied 1 to 35-week-old meat-type quail and found that Von Bertalanffy model overestimated the average asymptotic weight of males and females. However, Mota et al. (2015), assessing 1 to 35 day-old meat-type and laying quail, recommended not only Gompertz model for describing body growth but also Von Bertalanffy and Logistic models. Similarly, Veloso et al. (2015) studied 1 to 84-day-old free-range chickens and concluded that Von Bertalanffy model showed the best fit for body weight data.

**Table 3.** Bayesian comparison of Brody, Gompertz, Logistic, and Von Bertalanffy models for each considered factor by DIC.

| Factor  |     | Nonlinear model |          |          |                 |
|---------|-----|-----------------|----------|----------|-----------------|
|         |     | Brody           | Gompertz | Logistic | Von Bertalanffy |
| Gender  | ♂   | 22.37           | 22.34    | 22.34    | 22.35           |
|         | ♀   | 17.55           | 17.54    | 17.56    | 17.54           |
| Strain  | 0   | 13.80           | 13.64    | 13.73    | 13.64           |
|         | 1   | 9.01            | 8.91     | 8.94     | 8.92            |
|         | 2   | 9.82            | 9.64     | 9.66     | 9.67            |
|         | ♂ 0 | 7.58            | 7.38     | 7.43     | 7.40            |
|         | ♀ 0 | –               | 5.85     | 5.91     | 5.85            |
| Nesting | ♂ 1 | 4.89            | 4.76     | 4.75     | 4.79            |
|         | ♀ 1 | –               | 3.82     | 3.85     | 3.82            |
|         | ♂ 2 | 5.22            | 4.99     | 4.94     | 5.02            |
|         | ♀ 2 | –               | 4.17     | 4.22     | 4.17            |

♂ = male and ♀ = female; 0 = meat-type, 1 = yellow, and 2 = red.

The logistic model presented similar or slightly higher values when compared to Gompertz model for DIC criterion adopted for model selection. However, although this difference was not significant, this model underestimated the values determined for the parameters and its use was not recommended due to a lower goodness of fit. This result was not in accordance with that found by Mota et al. (2015), who recommended the use of this model to determine body growth of meat-type and laying quail.

Gompertz model showed the best fit for body weight data of quail regardless gender and strain, according to DIC selection criterion. Therefore, Gompertz model [3] was chosen in MCMC simulation process due to its special parameterization and greater applicability. The parameterization in this model presents special interpretation since it expresses the age at which animal growth rate is maximum, which shows to be flexible and advantageous. The use of Bayesian procedures allowed obtaining accurate estimations, as well as results for comparison between genders and the analyzed genetic groups, which are extremely

important for animal production.

Similar to this study, Firat et al. (2016) worked with Japanese laying quail and applied to body weight data for growth description nonlinear models (Richards, Gompertz, and Logistic) under a Bayesian approach using DIC criterion to select the best model. DIC statistics of the above-mentioned models indicated that both Gompertz and Richards's functions presented a good fit to the data, being superior to the Logistic model considering the goodness of fit. Gompertz function has also been considered by many authors in the literature as the best option to describe bird growth, relating weight and age (MARCATO et al., 2010; MAZUCHELI et al., 2011; ROSSI; SANTOS, 2014; GRIESER et al., 2015b; MOTA et al., 2015; FINCO et al., 2016; ROCHA-SILVA et al., 2016).

Posterior summary measures and pairwise contrasts between parameters of Gompertz curve [3] for gender, strain, and nesting are shown in Table 4. All nestings presented significant differences between males and females for all tested parameters. Female quail, regardless the genetic group, presented significantly higher values for the asymptotic

weight of the response variable (272 g) and for age at which the growth rate is maximum (22 days) when compared to males. This pattern is repeated when the groups are analyzed in a nested way. In this modeling, nestings for meat-type, yellow, and red females presented significantly higher values for the asymptotic weight of the response variable, with values of 370, 203, and 215 g, respectively, when compared to males, with values of 274, 131, and 143 g, respectively. Although males had lower asymptotic weight, their maturity rates were higher (0.08), significantly differing from the values found for females, including the nestings.

High values of maturity rate for the same adult weight indicate that quail are earlier, concentrating the growth around the age at which the growth rate is maximum at a cost of a slower initial and final growth. However, smaller values for the maturity rate better distribute bird development over time, but

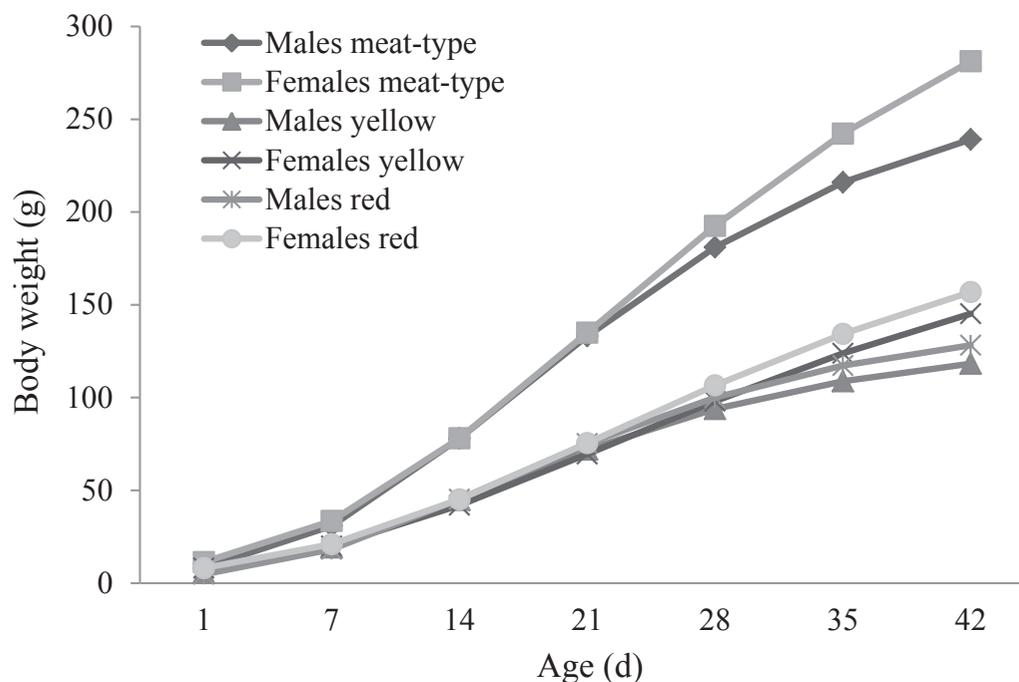
a later growth (FIALHO, 1999). Maturity rate, i.e. the velocity that quail reached the asymptotic weight, is an important variable to be used in breeding programs of quail since the faster the bird grows, the lower the time interval for reaching the slaughter age, reducing production costs and intervals between generations (DRUMOND et al., 2013).

Meat-type strain, regardless gender, presented a significantly higher asymptotic weight (319.5 g) and was later in the age at which the inflection point of the curve (18.5 days) occurred, followed by the red (168.9 g and 17.9, respectively) and yellow (155.9 g and 17.5, respectively) laying strains. No significant difference was observed for maturity rate between meat-type and red strains (0.071 and 0.070, respectively), which presented rates higher than that found for the yellow strain (0.069) (Table 4 and Figure 1).

**Table 4.** A posterior average and standard deviation (dp) of Bayesian estimations for curve parameters and  $\sigma$  and Gompertz [3] for gender, strain, and nesting.

| Factor  | Parameter |                             |                           |                            |              |
|---------|-----------|-----------------------------|---------------------------|----------------------------|--------------|
|         | $\beta_1$ | $\beta_2^*$                 | $\beta_3$                 | $\sigma$                   |              |
| Gender  | ♂         | 190.00 <sup>b</sup> (4.69)  | 16.21 <sup>b</sup> (0.44) | 0.080 <sup>a</sup> (0.004) | 37.13 (0.56) |
|         | ♀         | 271.50 <sup>a</sup> (13.79) | 21.60 <sup>a</sup> (1.07) | 0.059 <sup>b</sup> (0.004) | 41.04 (0.67) |
| Strain  | 0         | 309.50 <sup>a</sup> (4.49)  | 18.49 <sup>a</sup> (0.28) | 0.071 <sup>a</sup> (0.002) | 20.65 (0.37) |
|         | 1         | 155.90 <sup>c</sup> (2.86)  | 17.53 <sup>c</sup> (0.36) | 0.069 <sup>b</sup> (0.002) | 11.71 (0.25) |
|         | 2         | 168.90 <sup>b</sup> (2.17)  | 17.94 <sup>b</sup> (0.30) | 0.070 <sup>a</sup> (0.002) | 11.56 (0.23) |
|         | ♂ 0       | 274.50 <sup>b</sup> (3.45)  | 16.91 <sup>b</sup> (0.23) | 0.079 <sup>a</sup> (0.002) | 15.86 (0.38) |
|         | ♀ 0       | 370.00 <sup>a</sup> (10.55) | 21.13 <sup>a</sup> (0.56) | 0.062 <sup>b</sup> (0.002) | 21.55 (0.60) |
| Nesting | ♂ 1       | 131.40 <sup>b</sup> (2.02)  | 14.88 <sup>b</sup> (0.28) | 0.083 <sup>a</sup> (0.003) | 9.73 (0.27)  |
|         | ♀ 1       | 203.70 <sup>a</sup> (7.44)  | 22.31 <sup>a</sup> (0.81) | 0.055 <sup>b</sup> (0.002) | 10.66 (0.24) |
|         | ♂ 2       | 143.60 <sup>b</sup> (1.85)  | 15.75 <sup>b</sup> (0.23) | 0.083 <sup>a</sup> (0.002) | 8.83 (0.24)  |
|         | ♀ 2       | 215.40 <sup>a</sup> (6.43)  | 21.83 <sup>a</sup> (0.65) | 0.057 <sup>b</sup> (0.002) | 10.49 (0.32) |

dp = standard deviation of the mean; ♂ = male and ♀ = female; 0 = meat-type, 1 = yellow, and 2 = red;  $\beta_1$  = asymptotic value of the response variable;  $\beta_2^*$  = time at which the growth rate is maximum;  $\beta_3$  = growth rate of the response variable;  $\sigma$  = population standard deviation. <sup>a,b,c</sup> Different letters on the columns indicate significant differences ( $p < 0.05$ ) between the parameters involved in the contrast by means of Bayesian comparisons at a 95% credibility level.

**Figure 1.** Gompertz joint curves [3] adjusted to the data of body weight (g) for different strains and gender.

The asymptotic weight value (319.5 g) obtained for meat-type quail in this study is lower and the maturity rate is higher (0.071) when compared to those mentioned in the literature by Mota et al. (2015), who assessed seven different 1 to 35-day-old meat-type quail strains (EV1, EV2, UFV1, UFV2, UFV3, LF1, and LF2) and obtained values of 357.5, 361.4, 361.4, 365.4, 381.6, 409.7 and 410.5 g for asymptotic weight and 0.070, 0.070, 0.070, 0.070, 0.068 and 0.068 for maturity rate, respectively. This difference in parameter estimations of Gompertz equation estimated to describe body growth is due to differences in the genetic potential of the assessed strains. Furthermore, an average variation in asymptotic weight values of 53 g of the strain with higher and lower values can be observed, which is normal when it comes to different strains that have passed through different breeding programs with different selection criteria and priorities. Considering the maturity rates, the meat-type strain studied here was earlier, with a higher growth rate.

Comparing the asymptotic weight of mixed Japanese laying quail of yellow and red strains (155.9 and 168.9 g, respectively) and maturity rate (0.070 and 0.069, respectively) with the results found in the literature, lower values were observed in relation to those found by Firat et al. (2016) for asymptotic weight and maturity rate for mixed Japanese quail, which presented values of 222.1 g and 0.080, respectively. The values for asymptotic weight and maturity rate found by Mota et al. (2015) for mixed laying quail were similar to those found in this study, whose estimations were 166.39 g and 0.072, respectively. These differences in values of growth parameters estimated by Gompertz model are due to differences in genetic and environmental conditions.

Assessing the growth of 1 to 119-day-old Japanese laying quail, Finco et al. (2016) observed lower values for asymptotic weight and age of the inflection point of the growth curve (158.8 g and 16.27 days, respectively) and higher for maturity rate (0.063) when compared to those found in this

study for yellow (203.7 g, 22.31 days, and 0.055, respectively) and red (215.4 g, 21.83 days, and 0.057, respectively) females. The strain assessed by Finco et al. (2016) is lighter, earlier in body development, and has a higher maturity rate and lower age to reach maximum growth, being the most indicated when compared to the yellow and red laying strains studied here in relation to body weight since these strains require a smaller amount of food for growth and maintenance.

Meat-type and laying quail growth is characterized by a rapid body development up to about 18 and 17 days of age, respectively, when it starts decreasing (Table 4). However, when analyzed for gender, the age of the inflection point of the growth curve was 21.6 days for females and 16.21 days for males, which is a significant difference, indicating that females of quail are later in body growth rate. When analyzed separately by strain, the age of the inflection point of the growth curve was similar between genders for the three strains.

From the age at which the growth rate is maximum, the differences presented for body weight and rates of nutrient deposition in the carcass start being generally significant between genders due to the marked sexual dimorphism (DU PREEZ; SALES, 1997). The same can be observed in this study, in which females of the three strains presented higher weights at maturity when compared to males of their respective strains. Males are heavier than females in most poultry species, but for quail, females are heavier than males and the difference start being relevant from 21 to 28 days of age, when the ovaries grow and the liver increases in size (OGUZ et al., 1996). This difference in body development between genders results in changes in nutritional requirements, demanding a different management regarding gender and strain for the improvement of zootechnical indices and an increased production profitability (GRIESER, 2012).

For model fit improvement, further studies can

be performed assuming heterogeneity of variances (CAMPOS, 2011; MAZUCHELI et al., 2011) with a Bayesian approach since the variances are not constant over time for the data analyzed in this study. When studying body weight of males and females of 1 to 35-week-old meat-type quail, Mazucheli et al. (2011) reported that the model adjusted by MCMC methods under the assumption of homogeneity of variances seemed to overestimate the true asymptotic mean weight of birds, which did not occur when the model with heteroscedastic errors was considered. Campos (2011) also observed in tree growth studies (*Eucalyptus sp.*) that the fit of the best nonlinear model (Brody) among those tested (Gompertz, Richards and Von Bertalanffy) was inferior under the hypothesis of homoscedasticity when compared to heteroscedasticity.

## Conclusion

Gompertz model was better adjusted to body weight data of quail regardless the gender or strain and the Bayesian approach allowed obtaining accurate estimations. Meat-type strain presented the highest body asymptotic weight, followed by red and yellow laying strains. Females presented higher asymptotic weight than that found for males of their respective strains but were later in growth.

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