



Use of Random Regression Models to Estimate the Heritability of Weight Growth in Meat Quails

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(Received 15-04-2024; Revised 06-07-2024; Accepted 12-07-2024)

ABSTRACT

The aim of this study was to estimate the best covariance function structure, by means of Legendre polynomials using random regression models (RRM) to describe the genetic variability of the weight growth trajectory of quails and to estimate the genetic parameters. Body weight records of animals at 7, 14, 21, 28, 35, and 42 days of age were used. The orders of fit of the polynomials were gradually increased in orders from 3 to 6 for comparison between the models the Akaike information criteria were used. The models included fixed effects of the contemporary group, the fixed regression coefficient of weight on the Legendre polynomial, random regression coefficients of the direct additive genetic, and the permanent environment effects of the animal, in addition to the residual random effect. The RRM with orders five for the additive genetic effect and six for the permanent environment effect, under the assumption of homogeneity, was the most suitable to describe the genetic variability of the birds' ponderal growth. There was greater expression of additive genetic variability after 21 days, resulting in distinct and increasing heritability estimates between two periods in ponderal development. Estimates of additive genetic correlations for weights between the ages evaluated indicated that genetic associations are more correlated between body weights at closer ages when compared to ages more distant along the growth trajectory. Thus, it is concluded that selection in birds is more efficient from 28 days of age due to the higher heritability values.

Keywords: *Coturnix coturnix coturnix*; genetic parameters; Legendre polynomials; longitudinal data

INTRODUCTION

Raising quails commercially aligned with the intensification of the use of genetically superior genotypes demonstrates profitability potential, especially for small producers, as it is an activity that allows a quick return on invested capital. Thus, it is important to implement and develop well-structured genetic improvement programs with constant monitoring of productive and economic data (Rossi & Gasparino, 2018), which allow the evaluation and identification of genetically superior animals that can be used in the breeding stock through the genetic selection process.

In the Midwest region of Brazil, there is a favorable scenario for the commercial exploitation of these birds, especially in family farming systems, promoting regional socio-economic development. However, research into the genetic selection of these birds is non-existent (Sousa *et al.*, 2014). In this light, the existing flock should be evaluated by estimating genetic parameters so that

the best selection strategies can be defined (Mota *et al.*, 2018; Mota *et al.*, 2015).

According to the literature, these traits have moderate to high heritability values, which imply significant genetic gains in the selection process (Sousa Júnior *et al.*, 2019; Karami *et al.*, 2017b). However, for these gains to be effective, the genetic parameters must be accurately estimated.

In this context, using more accurate methodologies to estimate variance components, such as random regression models (RRM), becomes attractive (Abou Khadiga *et al.*, 2017). RRM or infinite-dimensional models were initially described as a combination of the theory of using covariance functions (Ghosal & van der Vaart, 2017) combined with mixed models, with the objective of estimating variance components using restricted maximum likelihood for longitudinal data (Fonseca *et al.*, 2016, Fernandes Filho *et al.*, 2023, Farzin & Seraj, 2022).

In RRM, random curves of each individual are estimated as a deviation from a mean curve of the population or of a group of individuals by means of continuous functions, such as orthogonal polynomials (Peixoto *et al.*, 2014). In making this adjustment, it is implicitly assumed that there is a covariance structure between the regression coefficients estimated by the RRM, which are called covariance functions (Wang *et al.*, 2022). These covariance functions have the advantage of being able to describe gradual variations in covariances along the growth curve of the animals and predict variances and covariances for points on this trajectory, even if the information between them is restricted (Ribeiro *et al.*, 2021).

In this sense, the application of RRM for estimating genetic parameters becomes an efficient and advantageous tool in the genetic evaluation of weight development traits of broiler quails (Ribeiro *et al.*, 2020). Because they use all the information of the animals and their relatives to estimate genetic values, RRM allows more accurate predictions (Kheirabadi & Rashidi, 2016; Miranda *et al.*, 2016), thus promoting the increased selection accuracy and obtaining better genetic gains in the selection process and more efficient development of the genetic improvement program.

Consequently, the investigation of heritability estimates in meat quails is crucial for the identification of optimal characteristics following their genetic and phenotypic correlations to implement genetic selection in breeding programs (Zerehdaran *et al.*, 2012; Silva *et al.*, 2021; Ribeiro *et al.*, 2017; Ahmed *et al.*, 2019; Paiva *et al.*, 2018; Bhowmik & Khan, 2021).

Thus, we aimed to estimate the best covariance function structure by applying Legendre polynomials using random regression models, which describe the weight growth trajectory of broiler quails and, consequently, estimate the heritability for the body weights of the animals.

MATERIALS AND METHODS

The experiment was approved by the Research Ethics Committee of the Centro Universitário da Amazônia (UNAMA), protocol nº 0003-87/2023 (CEUA).

We used information on the body weight records of broiler quails (*Coturnix coturnix japonica*) weighed at 7, 14, 21, 28, 35, and 42 days of age for 579 males and 581 females. The animals came from an experiment carried out at the Laboratório de Nutrição de Monogástricos, belonging to the Federal University of Mato Grosso, Sinop Campus, in Mato Grosso State.

During the incubation period, the eggs were numbered according to the identification code of their parents and stored separately to keep track of their genealogy. The eggs were collected for 7 days before incubation, and the incubation date was set according to the date of hatching. After 15 days, the eggs were transferred from the incubator to the hatcher. These were placed in perforated bags and identified according to family, where they remained for 3 days, completing 18 days of hatching. After hatching, the birds were weighed and identified with numbered rings and distributed to the

aviaries; individual body weights were obtained after the first week of life. The animals were kept in small-scale aviaries with concrete floors and heated rice husk bedding

The birds were given free water and feed throughout the experimental period and were fed diets consisting of 2950 Kcal of metabolizable energy, 23% crude protein, 1.14% digestible lysine, 4.02% crude fiber, 0.89% digestible methionine and cystine, 0.75% calcium, 0.29% available phosphorus, and 0.16% sodium.

The descriptive statistics for the body weights of the birds at each age and subjected to the different diets are shown in Table 1. The age of the birds was standardized between -1 and 1, using the expression presented by Kirkpatrick *et al.* in Ziadi *et al.* (2021):

$$a_i^* = u + [(v - u) / (a_{max} - a_{min})] (a_i - a_{min})$$

where a_i^* is the standardized age; and u and v are defined as $u = -1$ and $v = 1$; a_{max} and a_{min} are the highest and lowest age at which the animals were measured, respectively.

The birds' body weights were analyzed by means of an animal model using random regression using the Wombat software (Nasirifar *et al.*, 2021), in which the covariance functions in the description of the fixed and random regressions were represented by continuous functions using Legendre's orthogonal polynomials in the random regression model (RRM).

The j -th orthogonalized Legendre polynomial, P_j , is given by the expression:

$$\varphi_j(a_i^*) = \frac{1}{2^j} \sqrt{\frac{2j+1}{2}} \sum_{m=0}^{j/2} (-1)^m \binom{j}{m} \binom{2j-2m}{j} x^{j-2m}$$

The orders of fit of the continuous functions adopted in RRM, were gradually increased in orders from 3 to 6. In order to determine the minimum order necessary to describe the covariance structures as a function of bird age, Akaike's information criterion was used to compare the different RRM (Júnior *et al.*, 2023a). Akaike information criteria (AIC) allows the comparison of non-nested models and penalizes more parameterized ones (Mrode *et al.*, 2021). The AIC is defined as $AIC = -2\text{Log}(L) + 2p$, where p is the number of model parameters and L is the model's likelihood value. In this sense, the RRM can be represented as follows:

$$y_{ij} = Gc + \sum_{m=1}^{k_{ij}} \beta_m \varphi_m + \sum_{m=1}^{k_a} \alpha_{im} \varphi_m + \sum_{m=1}^{k_c} \rho_{im} \varphi_m + \varepsilon_{ij}$$

where y_{ij} represents the weight on day j of quail i ; Gc is the fixed effect of the contemporary group (generation-hatchling-sex); β_m is the fixed regression coefficient of the weight on the Legendre polynomial m used to

Table 1. Mean and standard deviation (SD) for body weight (g) of broiler quails at different ages (days) and sex

Age	Males Mean (SD)	Females Mean (SD)	General Mean (SD)
7	28.99 (6.50)	30.00 (6.61)	29.44 (6.58)
14	73.74 (13.31)	71.91 (13.91)	75.81 (13.76)
21	122.63 (25.62)	129.93 (27.41)	126.25 (26.76)
28	181.10 (23.33)	191.25 (25.74)	186.16 (25.07)
35	224.06 (20.82)	219.43 (27.13)	232.21 (26.28)
42	247.56 (22.03)	283.70 (29.31)	265.47 (31.57)

model the average growth curve of the population; α_{im} and ρ_{im} represent the regression coefficients of the direct additive genetic and permanent environment effects of the animal, respectively, for quail i ; k_a and k_c are the orders of adjustment of the corresponding Legendre polynomials, which ranged from 1 to 6; ϕ_m represents the Legendre polynomial function of standardized age m ; and ϵ_{ij} is the residual random effect.

The RRM were processed under two assumptions about the residuals; in the first, residual homogeneity was considered, and in the second, classes of residual variances were tested, defined as 2 classes: from 7 to 21 and from 28 to 42 days of age; 3 classes: from 1 to 7; from 14 to 21 and from 28 to 42 days of age; 4 classes: 1 day, 7 days, from 14 to 21 days and from 28 to 42 days of age.

The additive genetic variances and covariances (G) were obtained as $G=M(K_a)M'$, where M is a matrix of dimension 6 rows with 5 columns and represents the six standardized ages (between -1 and 1) associated with the first five Legendre polynomials, K_a is the matrix, of order five, of the covariance function estimated by the RMM and M' represents the transpose of the matrix M . Similarly, the variance matrix of the permanent environment effect (P) was obtained as $P=W(K_p)W'$, where W is the matrix of order six, referring to the six standardized ages associated with the first six Legendre polynomials and K_p is the matrix of order six of the covariance function associated with this effect. Thus the heritability estimates (h^2) at each age were obtained

as: $h^2 = \frac{\sigma_a^2}{\sigma_p^2}$, where σ_a^2 is the variance component of the additive genetic effect and σ_p^2 represents the phenotypic variance component.

Subsequently, in an additional step, the Gompertz non-linear regression model was fitted to describe the inflection point and the absolute growth rate of the birds in order to help discuss the genetic variability described by the random regression model. The Gompertz non-linear model is described as: $y_t = A + e^{-B(-(k+kt)t)}$, where Y_t is the bird's body weight (in grams) at age " t " (in days); where " A " is the asymptotic weight parameter at maturity; " B " is an integration constant with no biological interpretation and " K " is a parameter related to the rate of maturity.

Covariance functions for the additive genetic and permanent environmental effects were estimated by random regression models using the restricted maximum likelihood method using the program WOMBAT.

RESULTS

Comparisons between random regression models with different Legendre polynomial orders when adjusting the covariance functions for the random effects of the linear mixed model, according to the AIC and BIC, indicated that the model that used Legendre polynomials of order five for the additive genetic effect and six for the permanent environment effect, as well as both the condition of homogeneity of variance and the heterosce-

dastic model with two classes of residual variances, were the best suited to describing the variability of quail body weight (Table 2).

The permanent environment correlations estimated between the weights of the various ages tended to be higher between closer ages; however, this was not verified between birth weight and the weights obtained from 7 to 14 days, i.e., the correlations between these characteristics were very low. These two models had the same likelihood function values and the Akaike and Schwarz Bayesian information criteria were close, so the simplest model was chosen with the assumption of homogeneity of variances.

Thus, with the information on the most suitable model for describing the genetic variability of body weight in birds, the variance components were obtained, as well as the estimates of heritability using the covariance function obtained by the chosen model (Table 3).

By predicting the animal's weight growth curve using the non-linear Gompertz function, obtained as $\hat{y}_i = 336.2 \exp(-3.8172 \exp(-0.0661x_i))$, where \hat{y}_i is predicted value of weight body and x_i is the age (in days) of animals. The correlation between the observed weight and the predicted weight (\hat{y}_i) was equal to 0.96, we obtained the absolute growth rate of the animals, which is the first derivative of the growth curve (Figure 1).

It can be seen that the maximum growth rate increases up to 20 days of age (approximately 8.11 g/day), with growth slowing down after this age, a result that coincides with the greater genetic variability observed after 21 days of age. With the absolute growth rate on the rise, greater deposition of protein and water in the carcass is expected. After reaching maximum growth, the growth rate decreases and weight gain begins to have a progressively diminishing return, with an increase in fat deposition in the viscera.

The birds showed an increase of approximately 4.3 and 9.0 times their body weight at 21 and 42 days of age, respectively, compared to their weight at seven days of

Table 2. Random regression models used to describe body weight variability in quails, with different orders of the covariance function fit for the random effects, values of the logarithm of the likelihood function, and the Akaike Information Criterion (AIC) and the Bayesian Schwarz Information Criterion (BIC)

Models	Log (L)	(-0.5) AIC	(-0.5) BIC
K3K3 e1	-16577.47	-16590.47	-16633.49
K4K4 e1	-16507.05	-16528.05	-16597.55
K5K5 e1	-16154.62	-16185.62	-16288.20
K5K6 e1	-15713.04	-15750.04	-15872.48
K6K5 e1	-15840.06	-15877.06	-15999.49
K5K6 e2	-15713.04	-15751.04	-15876.79
K5K6 e3	-15713.04	-15752.04	-15881.10
K5K6 e4	-15713.04	-15755.04	-15894.03
K6K6 e1	-15708.57	-15751.57	-15893.86

Note: The number in the first and second letter 'K' are the orders of the covariance functions for the additive genetic and permanent environment effects of the animal, respectively. The number in the letter 'e' represents the number of residual variance classes.

Table 3. Estimates of residual, additive genetic, animal permanent environment, and phenotypic variance components and heritability with standard error (SE) for body weights (g) of quails at different ages (days)

Age (day)	Variance components				Estimate of Heritability \pm SE
	Residual	Additive	Permanent	Phenotypic	
7	8.73	5.90	15.18	29.81	0.20 \pm 0.05
14	8.73	33.80	134.23	176.76	0.05 \pm 0.05
21	8.73	112.77	564.24	685.74	0.16 \pm 0.04
28	8.73	169.40	433.69	611.82	0.28 \pm 0.06
35	8.73	205.12	472.25	686.10	0.30 \pm 0.06
42	8.73	337.58	639.00	985.30	0.34 \pm 0.07

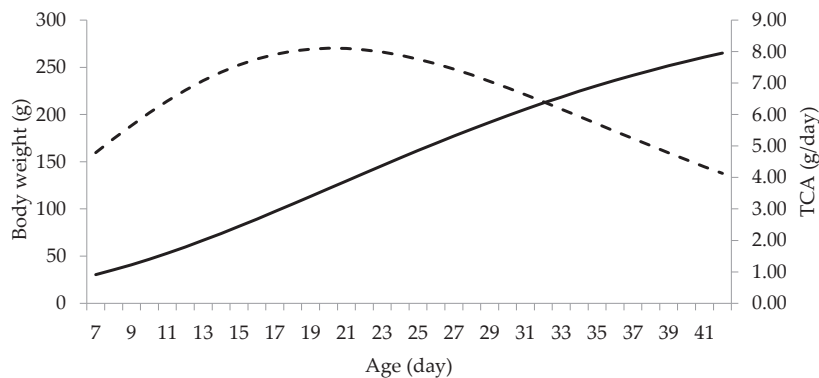


Figure 1. Growth curve and absolute growth rate predicted (Pred) for broiler quails using the non-linear Gompertz function. — = Pred; - - - = TCA.

age. In addition, the females became heavier than the males after 21 days of age, due to the high weight of the reproductive system, which can represent 10% of their live weight.

The quail's final growth phase begins after 21 days of age, with sexual dimorphism starting at 15 days of age, with females showing a larger abdomen and a wider chest and, consequently, being heavier. Thus, greater phenotypic differentiation between individuals is expected at this stage due to the increased expression of additive genetic variability and, consequently, an increase in heritability estimates at this stage, resulting in different heritability estimates and between two periods of the birds' weight development, the first coinciding with the bird initial growth phase, from 7 to 21 days of age, and the second, from 28 to 42 days of age, characterized by the final growth phase.

DISCUSSION

Several studies that compared random regression models observed that the values of the log-likelihood function, AIC, and BIC pointed to the selection of models with higher orders (Cho *et al.*, 2016; Li *et al.*, 2020; Tırnık *et al.*, 2022; Ferreira *et al.*, 2017). The correlations between weights at different ages were similar to those already reported in other studies. Bonafé *et al.* (2011) and NarinÇ & Aydemir (2022) observed, for both models, medium and high positive correlations between weights at different ages, except for birth weight. This low genetic correlation involving two adjacent characteristics, one of which is birth weight, was also reported by Barbieri *et al.* (2015).

These results indicate that body weight is a very important factor in selection studies, capable of increasing the efficiency of these programs, especially when associated with other selection features (Júnior *et al.*, 2023b; Taskin *et al.*, 2017). The inclusion of slaughter weight or other body weight traits at older ages adjacent to slaughter weight are examples of this, and for this reason, they were also included in breeding programs as correlated traits (Jahan *et al.*, 2020; Akbarnejad *et al.*, 2015). From an alternative perspective, Ebrahimi *et al.* (2019) and Karami *et al.* (2017a) observed that the estimated correlations for the permanent environment between weights at different ages exhibited higher values for those closer in age.

The estimated heritability in this research varied from medium to high, decreasing in the first 14 days of life and then increasing until 35 days. Analogous to what was found by Hussain *et al.* (2014), Felipe *et al.* (2012), Nasiri Foomani *et al.* (2014), and El-Attrouny *et al.* (2020), who also showed that this parameter is increasing. In another analysis, Sarvari-Kalouti *et al.* (2023) reported moderate direct heritability for body weight and weight gain when studying early growth traits in quail.

Mohammadi-Tighsiah *et al.* (2018) also reported instability in the values found for estimating heritability with increasing age for the body weight characteristic, with the estimated heritability for birth weight being approximately twice as high as that found for other ages. The results obtained for the additive genetic correlations and phenotypic correlation (Table 4) for body weights between the ages evaluated in the birds were all significant at 0.05. The results indicated that the genetic

Table 4. Estimated additive genetic correlation (above the diagonal) and phenotypic correlation (below the diagonal) for the birds' body weight (g) at each age evaluated

Age (days)	Age (days)					
	7	14	21	28	35	42
7	1.00	0.93	0.80	0.79	0.74	0.55
14	0.79	1.00	0.92	0.90	0.79	0.57
21	0.66	0.87	1.00	0.98	0.80	0.61
28	0.64	0.84	0.90	1.00	0.90	0.76
35	0.54	0.73	0.76	0.90	1.00	0.95
42	0.36	0.50	0.52	0.66	0.80	1.00

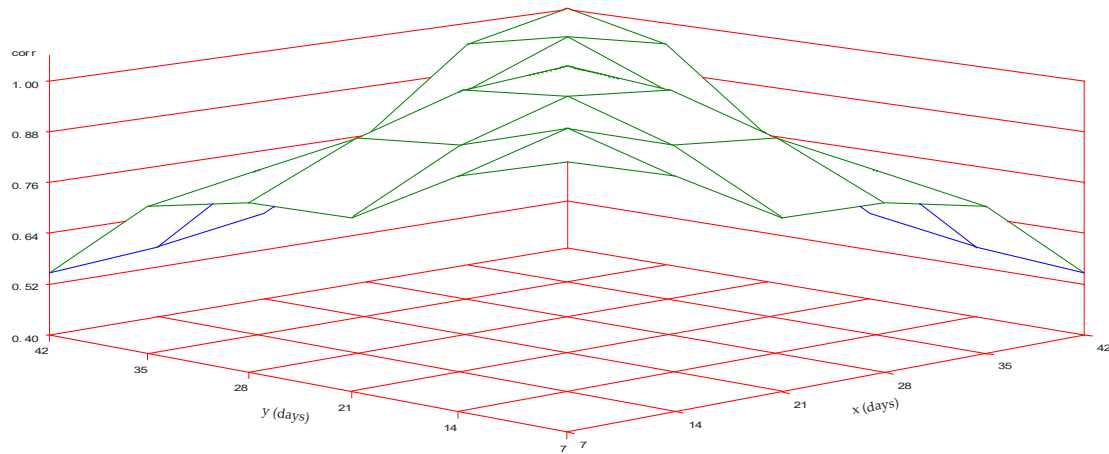


Figure 2. Estimates of genetic correlations between body weights of broiler quails at different ages, each line on the three-dimensional axis represents age (7 to 42 days) on the scale in weeks, using random regression models. The genetic associations are more correlated between body weights at closer ages when compared to more distant ages (green lines).

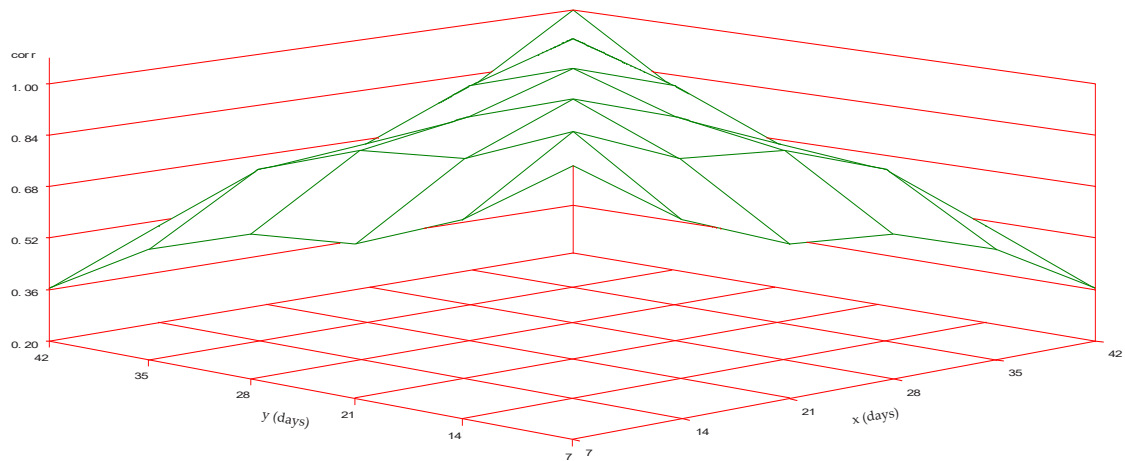


Figure 3. Estimates of phenotypic correlations between body weights of broiler quails at different ages, each line on the three-dimensional axis represents age (7 to 42 days) on the scale in weeks, using random regression models.

associations are more correlated between body weights at closer ages when compared to more distant ages along the growth trajectory (Figure 2). The behavior of the phenotypic correlations (Figure 3) was very similar to the correlations of the additive genetic effect but with lower estimated values.

In the study carried out by Caetano *et al.* (2017), when estimating partial and total body weight gain to identify possible partial characteristics as selection criteria in meat quail genetic improvement programs,

it was also recommended to use similar body weights for the two genetic lines studied, rather than total body weight.

Genetic correlations between body weight at 42 days and the other ages ranged from 0.55 to 0.95, with weight at 7 and 35 days of age, respectively. Like what Barbieri *et al.* (2015) reported when studying genetic parameters for body weight in meat quails at different ages, they found heritability ranging from 0.03 to 0.23 and genetic correlations mainly high and positive. In

this context, the genetic selection of birds should be carried out after 21 days of age, when heritability estimates are higher and at more correlated ages.

CONCLUSION

Random regression models with orders five for the additive genetic effect and six for the permanent environment effect with the assumption of homogeneity of residual variance are sufficient to describe the genetic variability of weight growth in broiler quails. The higher heritability estimates from the age of 28 days onwards indicate greater success in selecting birds in this period since closer ages are highly correlated.

CONFLICT OF INTEREST

We certify that there is no conflict of interest with any financial, personal, or other relationships with other people or organization related to the material discussed in the manuscript.

ACKNOWLEDGEMENT

This study was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) – Finance Code 001, year 2023. The authors gratefully acknowledge the Ministério Público do Estado de Mato Grosso (MPMT, Sinop, Brazil), especially Dr. Pompílio Paulo Azevedo Silva Neto, for supporting the Project BAPRE “Produção de proteína animal de baixo carbono no estado de Mato Grosso”.

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