



Genetic evaluation of European quails by random regression models¹

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ABSTRACT - The objective of this study was to compare different random regression models, defined from different classes of heterogeneity of variance combined with different Legendre polynomial orders for the estimate of (co)variance of quails. The data came from 28,076 observations of 4,507 female meat quails of the LF1 lineage. Quail body weights were determined at birth and 1, 14, 21, 28, 35 and 42 days of age. Six different classes of residual variance were fitted to Legendre polynomial functions (orders ranging from 2 to 6) to determine which model had the best fit to describe the (co)variance structures as a function of time. According to the evaluated criteria (AIC, BIC and LRT), the model with six classes of residual variances and of sixth-order Legendre polynomial was the best fit. The estimated additive genetic variance increased from birth to 28 days of age, and dropped slightly from 35 to 42 days. The heritability estimates decreased along the growth curve and changed from 0.51 (1 day) to 0.16 (42 days). Animal genetic and permanent environmental correlation estimates between weights and age classes were always high and positive, except for birth weight. The sixth order Legendre polynomial, along with the residual variance divided into six classes was the best fit for the growth rate curve of meat quails; therefore, they should be considered for breeding evaluation processes by random regression models.

Key Words: *Coturnix coturnix coturnix*, genetic parameters, heterogeneity of variance

Introduction

The growing market for products of animal origin with high protein content and good acceptance by the consumer has caused the meat quail production to increase as well. However, meat quail production faces a lack of national genetic material. Currently, genetic material with less productive potential available in the market is used, which leaves the national market dependent on genetic material from other countries.

Therefore, breeding programs are important, since they estimate breeding parameters and establish selection strategies to renew the herds with animals of higher breeding potential at every new generation.

The main piece of information used in processes of genetic evaluation and selection is body weight during the growth period. Meat quail studies determine these weights at regular intervals, so the same animal has several weights determined during its life, thus characterizing repeated measurements or longitudinal data. This repeated measurement of the same animal over time has received

increasing interest of animal breeding researchers. Repeating traits have been studied using covariance functions. Among them, random regression models have received more attention from animal breeding researchers (Tholon & Queiroz, 2008).

Random regression models enable the prediction of breeding values for the interval at which measurements are taken and to estimate individual growth rate curves considering the relationship between animals, so they promote better use of the data and potential increase in the selection accuracy (Dionello et al., 2008).

According to El Faro & Albuquerque (2003), multiple regression analyses that use covariance functions also allow one to consider the heterogeneity of residual variances on the control day. Modeling can improve the partition of total variance, which increases accuracy of estimated genetic parameters, maximizing the response to selection.

Therefore, the objective of this study was to compare different random regression models defined from different classes of variance heterogeneity combined with different orders of Legendre polynomial for the genetic evaluation of meat quails.

Material and Methods

Female meat quails of the LF1 lineage (*Coturnix coturnix*) from Programa de Melhoramento Genético de Codornas of the Department of Animal Science, Universidade Federal dos Vales do Jequitinhonha e Mucuri, in Diamantina, MG, Brazil, were utilized in this experiment. For the analyses, a total of 28,076 records of body weights from 4,510 meat quails and 4,681 animals in the relationship matrix, taken every seven days (at birth, 7, 14, 21, 28, 35 and 42 days of age), collected from June 2010 to May 2011 were used. Three generations from the base population were studied; the first with 793 birds, the second with 2,189 and the third with 1,528 quails.

Quails with at least three weight records were considered for the analysis. They belonged to 174 contemporary groups, consisting of generation, hatching and sex. Quails were reared from birth to 42 days of age in pens with concrete floor and wood shaving beds, equipped with heating. Birds received feed and water *ad libitum*. From birth to 21 days of age, the diet supplied contained 25% CP and 2,900 kcal ME/kg, and from 22 to 42 days, the diet contained 24% CP and 2,925 kcal ME/kg, according to nutritional requirements specified in the literature (Oliveira et al., 2002; Fridrich et al., 2005; Corrêa et al., 2007; Veloso et al., 2010).

At birth, quails were identified, weighed and transferred to the pens. At 35 days of age, 210 females and 105 males were selected according to body weight and then transferred to individual cages to form the next generation on. The selected quails remained in the galvanized wire cage (95 cm long, 28.5 cm wide and 21.5 cm high) equipped with egg collector (15.5 cm in front of the cages), repeating the entire cycle every generation.

The three hatchings of the first generation totaled 793 birds; the five hatchings of the second generation totaled 2,189 birds, while the four hatchings of the third generation totaled 1,528 birds. The hatches of the same generation were collected every seven days and the quails were reared under the same management practices described before.

Body weights were analyzed by random regression models. The fixed and random regression models were represented by continuous functions, whose ages were described by the Legendre orthogonal polynomials. The different order (2nd, 3rd, 4th, 5th and 6th order) models adjusted for the random effects can be represented as follows:

$$y_{ij} = F + \sum_{m=1}^{k_{\beta}-1} \beta_m \phi_m + \sum_{m=1}^{k_{\alpha}-1} \alpha_{im} \phi_m + \sum_{m=1}^{k_p-1} \rho_{im} \phi_m + \varepsilon_{ij}$$

in which y_{ij} = body weight on day j of quail i ; F = set of fixed effects, constituted by the contemporary group (174 subclasses); β_m = fixed regression weight coefficient of the Legendre polynomial m ; k_{β} = polynomial order for the mean curve, varying from two to six ($k_{\beta} = 2, 3, \dots, 6$) to obtain the average growth rate curve of the quail population; α_{im} and ρ_{im} are animal additive genetic and permanent environmental regression coefficients, respectively, for quail i ; k_{α} and k_p = Legendre adjusted polynomial orders; ϕ_m = Legendre polynomial function of the standardized age m ($-1 < \text{age} < 1$); and ε_{ij} = residual random effect.

The model above can be described by the following matrix:

$$y = X\beta + Z_1a + Z_2p + e$$

$$E \begin{bmatrix} y \\ a \\ p \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \\ 0 \end{bmatrix};$$

$$\text{Var}(a) = k_a \otimes A; \text{Var}(p) = k_p \otimes I_{N_d}; \text{Var}(e) = R$$

in which y = vector of N observations on 4,510 animals; β = fixed effect vector that includes the fixed regression coefficients used to model the mean trajectory of the population; a = vector $k_{\alpha} \times N_d$ of additive genetic random regression coefficients, in which N_d = total number of animals in the relationship matrix (4,681); p = vector $k_p \times N$ of permanent environmental random regression coefficient; e = random error vector; X , Z_1 and Z_2 = incident matrices of fixed regression coefficients, animal additive genetic and permanent environmental random regression coefficients, respectively; k_a and k_p = covariance matrices between the random regression coefficients for animal additive genetic and permanent environmental effects, respectively. A is the matrix of numerators of coefficient of relationship between individuals; I_{N_d} = size identity matrix N_d ; \otimes = direct product operator; and R = diagonal matrix containing the residual variances.

The residual variance model considered classes of residual variance from homogeneous to heterogeneous, according to different ages: class 1, homogeneous residual variance (1 to 42 days of age); class 2, heterogeneous variances in two different periods (1 to 7 days and 8 to 42 days of age); class 3, heterogeneous variances in three periods (1 to 7, 8 to 14 and 15 to 42 days of age); class 4, heterogeneous variances in four periods (1 to 7, 8 to 14, 15 to 21 and 22 to 42 days of age); class 5, heterogeneous variances in five periods (1 to 7, 8 to 14, 15 to 21, 22 to 28 and 29 to 42 days of age); and, class 6: heterogeneous variances in six periods (1 to 7, 8 to 14, 15 to 21, 22 to 28, 29 to 35 and 36 to 42 days of age), totaling six different classes of variance heterogeneity to be used in the data analysis.

Each of the six classes combined with the different orders of Legendre polynomial (2nd, 3rd, 4th, 5th and 6th order) resulted in 30 models to be tested.

The models were compared by the logarithm of the likelihood function ($\text{Log}_e L$), the likelihood ratio, Akaike Information Criterion ($\text{AIC} = -2\text{Log}_e L + 2p$) and the Schwarz's Bayesian Information Criterion ($\text{BIC} = -2\text{Log}_e L + p\text{Log}_e(N-r)$) tests, in which: p = number of model parameters; N = total number of observations; r = rank of the incidence matrix for the fixed effects; and $\text{Log}_e L$ = logarithm of the likelihood function. For the likelihood ratio test (LRT), 1% probability was adopted and the statistics was given by the equation: $\text{LRT}_{ij} = 2\text{Log}_e L_i - 2\text{Log}_e L_j$, in which $\text{Log}_e L_i$ = maximum likelihood function for the complete model i and $\text{Log}_e L_j$ is the maximum likelihood function for the reduced model. The LRT estimate was compared to the given Chi-square value with d degrees of freedom at 1% significance level, in which d is the difference between the number of parameters estimated by the complete and reduced models.

The AIC and BIC tests allow to compare non-nested models and both penalize models with more parameters, but BIC is the most stringent and tends to favor more parsimonious models (Wolfinger, 1993; Nunez-Antón & Zimmerman, 2000). Low values for AIC and BIC and high values for $\text{Log}_e L$ indicate good fit.

The covariances between random regression coefficients for animal additive genetic and permanent environmental effects, according to the best fit model by the chosen criteria, were estimated by restricted maximum likelihood (REML) using the software Wombat (Meyer, 2006).

After estimating the covariance components necessary to obtain the solutions of the system of equations of the mixed model, the estimates of the matrices G and P, both 6×6 , became known and therefore possible to represent the covariance structure effects throughout the studied interval using the covariance functions. After structuring the covariances, one can estimate the variance or covariance values for any point or combination points within the age range considered, to determine heritability and correlations as well.

The estimates of covariances for animal additive genetic and permanent environmental effects for animal weight on day t were obtained by:

$$\hat{\sigma}_{a_{t_i}}^2 = Z'_{t_i} \hat{K}_a Z_{t_i}; \quad \hat{\sigma}_{p_{t_i}}^2 = Z'_{t_i} \hat{K}_p Z_{t_i}; \quad \hat{\sigma}_{a_{t_i}t_j} = Z'_{t_i} \hat{K}_a Z_{t_j} \quad \text{and} \\ \hat{\sigma}_{p_{t_i}t_j} = Z'_{t_i} \hat{K}_p Z_{t_j}.$$

Weight heritability of the birds can be estimated at any age within the range of the interval studied. Direct heritability represents the fraction of phenotypic variance explained by variance of the additive genetic value of studied birds and was obtained as follows:

$$h_{t_i}^2 = \frac{\hat{\sigma}_{a_{t_i}}^2}{\hat{\sigma}_{a_{t_i}}^2 + \hat{\sigma}_{p_{t_i}}^2 + \hat{\sigma}_{e_i}^2}$$

The genetic and permanent environmental correlations with weights of the different weighing days, t_i and t_j , were estimated by:

$$r_{a_{t_i}t_j} = \frac{\hat{\sigma}_{a_{t_i}t_j}}{\sqrt{\hat{\sigma}_{a_{t_i}}^2 \times \hat{\sigma}_{a_{t_j}}^2}} \quad \text{and} \quad r_{p_{t_i}t_j} = \frac{\hat{\sigma}_{p_{t_i}t_j}}{\sqrt{\hat{\sigma}_{p_{t_i}}^2 \times \hat{\sigma}_{p_{t_j}}^2}}$$

The genetic value for each animal was obtained as follows:

$$VG = b_0 + b_1 t + b_2 t^2 + b_3 t^3 + b_4 t^4 + b_5 t^5$$

in which b_0 is the regression coefficient of the intercept and b_1, b_2, b_3, b_4 and b_5 are the regression coefficients of the n -order polynomial regression model, and t is the bird age represented by the Legendre polynomial.

The genetic trend of additive effect for generations was estimated by the linear regression coefficient of mean genetic values of birds in the year of birth, using PROC REG of the software SAS (Statistical Analysis System, version 9.0).

Results and Discussion

Random regression modeling using Legendre polynomial requires the definition of the best fit order for each random effect considered in the analysis model. Thus, the polynomial order was gradually increased (ranging from 2 to 6) in order to determine the minimum order able to describe the covariance structures as a function of time (Table 1).

As the order of the Legendre polynomial increased, the values of Log L, BIC and AIC decreased. For all the studied residual variance classes, the sixth order Legendre polynomial yielded the lowest values of BIC and AIC (Table 1). According to Log L, the highest polynomial order of the model yielded significant values ($P < 0.01$) for the likelihood ratio test (LRT), which indicates that the model with the most parameters (model 66 with 48 parameters), in which $K_a = 6$ and $K_p = 6$ for additive genetic and permanent environmental effects, respectively, was the best fit for the experimental data. Therefore, it is recommended to use six classes of variance heterogeneity (one for each week of life) and to adopt the sixth order Legendre polynomial (model 66) when studying the growth rate curves of meat quail when considering a total of seven weight data.

Similar results were reported by Bonafé et al. (2011), who also reported the sixth order Legendre polynomial as the best fit for growth rate curves of meat quail. Akbas et al. (2004), when assessing the weight of meat quails, also

reported best fit for the sixth order Legendre polynomial for random effects and constant residual variance at all ages.

The comparison of the fitting residue model between the six classes of variance residual heterogeneity showed increased Log L significantly ($P < 0,01$) for the likelihood ratio test (LRT) as the number of heterogeneous classes increased. All Heterogeneous Variance Models had better fit compared with the Homogeneous models (Class 1), given the lower values of BIC and AIC. The values of Log L, BIC and AIC changed considerably and significantly ($P < 0,01$) for LRT up to Class 6 model, thus suggesting this to be the best fit.

Sarmiento (2007), while studying the growth rate curve of Santa Inês sheep, found that the Homogeneous Residual Variance model was inadequate, while the Residual Variance model in five classes was a good fit for the data. Other authors also emphasized the need to consider Heterogeneous Residual Variance models to assess growth rate curves (Meyer, 2000; Sousa et al., 2008), for milk production on the control day (El faro & Albuquerque, 2003;

Sarmiento et al., 2008) and sensitivity studies of genotypes in meat quails (Felipe, 2010).

The random regression coefficient of the intercept (b_0) displays the largest variance of all random effects. For all other coefficients, variance decreased as the function order increased (Table 2). The correlations between intercept and linear coefficient were positive and high for all random effects. The correlations between intercept and the quadratic and cubic coefficients were always negative. For other coefficients, the correlations changed between positive and negative, with small values close to one.

The intercept justifies the high variance for the random effects in the model (Table 2). Despite being the model with the most parameters (model 66) and the best fit according the criteria adopted in the study (LRT, BIC and AIC), this result demonstrates that the regression coefficients of higher order tend to add less variance to the random effects.

Additive genetic variance increased up to 28 days of age and decreased slightly up to 42 days (Table 3). It should

Table 1 - Comparison of models by likelihood logarithm (Log L), Bayesian Information Criterion (BIC), Akaike Information Criterion (AIC) and likelihood ratio test (LRT) for meat quails

Heter. residual var.	Model	NP	Log L	BIC	AIC	LRT	
						Model	LRT _{ij}
Class 1	12	7	-94,681.79	189,435.291	189,377.59	13 - 12	4,218.12**
	13	13	-90,463.66	181,060.491	180,953.34	14 - 13	8,844.40**
	14	21	-81,619.29	163,453.676	163,280.58	15 - 14	1,971.50**
	15	31	-79,647.76	159,613.059	159,357.54	16 - 15	496.50**
	16	43	-79,151.22	158,742.893	158,388.46	26 - 16	7,614.58**
Class 2	22	8	-93,606.00	187,293.999	187,228.06	23 - 22	11,314.40**
	23	14	-82,291.60	164,726.605	164,611.21	24 - 23	9,737.20**
	24	22	-72,554.43	145,334.201	145,152.86	25 - 24	754.40**
	25	32	-71,800.07	143,927.917	143,664.15	26 - 25	263.40**
	26	44	-71,536.64	143,523.959	143,161.28	36 - 26	71.95**
Class 3	32	9	-93,603.69	187,299.574	187,225.39	33 - 32	12,874.02**
	33	15	-80,729.60	161,612.984	161,489.34	34 - 33	8,357.95**
	34	23	-72,371.72	144,979.025	144,789.44	35 - 34	-268.94**
	35	33	-72,640.66	145,619.332	145,347.32	36 - 35	1,175.97**
	36	45	-71,464.68	143,390.288	143,019.37	46 - 36	33.68**
Class 4	42	10	-93,596.08	187,294.597	187,212.17	43 - 42	13,014.49**
	43	16	-80,581.58	161,327.057	161,195.17	44 - 43	8,266.07**
	44	24	-72,315.51	144,876.844	144,679.02	45 - 44	751.39**
	45	34	-71,564.12	143,476.491	143,196.24	46 - 45	133.12**
	46	46	-71,431.00	143,333.163	142,954.00	56 - 46	1.40**
Class 5	52	11	-93,513.73	187,140.139	187,049.47	52 - 53	12,945.13**
	53	17	-80,568.59	161,311.321	161,171.20	53 - 54	8,387.24**
	54	25	-72,181.35	144,618.767	144,412.70	54 - 55	622.42**
	55	35	-71,558.92	143,476.335	143,187.84	55 - 56	129.32**
	56	47	-71,429.59	143,340.59	142,953.18	66 - 56	11.73**
Class 6	62	12	-93,468.27	187,059.464	186,960.55	62 - 63	14,458.23**
	63	18	-79,010.04	158,204.456	158,056.09	63 - 64	6,833.13**
	64	26	-72,176.91	144,620.131	144,405.82	64 - 65	624.38**
	65	36	-71,552.52	143,473.792	143,177.06	65 - 66	134.67**
	66	48	-71,417.85	143,327.354	142,931.71	-	-

NP - number of parameters.

** Significant at 1% probability.

be noted that animal permanent environmental variance increased with time and dropped slightly in the last week.

Similar behavior was reported by Bonafé (2008), whose estimates considering heterogeneous variance ranged from 0.33 to 290.30 for the UFV1 meat quail and 0.33 to 288.30 for the lineage UFV2. Similar results were also reported by Akbas et al. (2004), while studying meat quails considering homogeneous residual variance, in which permanent environment variance also increased with age.

The phenotypic and animal permanent environmental variances displayed similar behavior, increased in the first week, decreased from 7 to 14 days and increased again until 35 days of age due to scale effect, since the weights increased with age. However, animal permanent environmental variance displayed lower values (Figure 1).

Similar results were reported by Akbas et al. (2004), Dionello et al. (2008) and Bonafé et al. (2011), while studying meat quails, in which both variances also increased with age.

Additive genetic variance increased from birth to 35 days of age and dropped slightly in the last week. The

residual variance also decreased at 21 and 35 days of age; however, it increased up to 42 days of age. The drop of additive genetic variance at 42 days of age may be related to animal behavior patterns, since they become more agitated in the last rearing stages, females reach sexual maturity and males develop competitive behavior to determine patterns of social dominance, such as competition for territory, food and water. These factors may lead to an increase in residual variance that possibly reflects on the declining additive genetic variance.

Heritability decreased along the growth rate curve, ranging from 0.51 (1 day) to 0.16 (42 days of age). These results contradict Bonafé et al. (2011), who reported that heritability decreased up to 14 days, increased from 14 to 35 days and decreased again after 35 days (Figure 2).

According to Akbas et al. (2004), the heritability estimated for body weight of meat quails increased until the 5th week (0.61), with a slight drop during the last week (0.44), but remained high. Dionello et al. (2008) reported increasing heritability from birth (0.01) to 42 days of age (0.50) for the EV1 lineage, but low values (0.01 to 0.10) for the EV2 lineage.

Silva et al. (2010), while studying meat quails using multiple trait model, also reported that estimates decreased as age increased, varying from 0.43 at 28 days to 0.27 at 147 days of age.

The downward trend in heritability from 35 to 42 days may be related to the increase of the residual variance in the last two weeks, in which caused a steeper decrease of the additive genetic variance.

Estimates of genetic correlations (Table 4) between weights at different ages were high and positive, except for the correlation between birth weight and life weight, thus suggesting that selection should not be based on birth weight. From 7 days of age, all genetic correlations between body weights were high and positive, indicating that selection can start at this age. The highest genetic correlation (0.972) was observed between 21 and 28 days of age, suggesting that selection at 28 days of age can be effective, considering that correlation between 28 and 35

Table 2 - Estimates of variances (diagonal), covariances (below the diagonal) and correlations (above the diagonal) among random regression coefficients (b0 to b5) and the eigenvalues of the coefficient matrix for model 66

	b ₀	b ₁	b ₂	b ₃	b ₄	b ₅	Eigenvalues (%)
Additive genetic effect K _a = 6							
b ₀	204.57	0.89	-0.69	-0.59	0.35	0.65	92.26
b ₁	92.42	52.51	-0.40	-0.74	0.03	0.64	5.65
b ₂	-40.07	-11.82	16.12	0.52	-0.88	0.59	2.01
b ₃	-20.01	-12.70	4.94	5.53	-0.27	-0.78	0.06
b ₄	3.42	0.14	-2.39	-0.44	0.45	0.37	0.02
b ₅	4.03	2.07	-1.03	-0.80	0.10	0.19	0.01
Permanent environmental effect K _p = 6							
b ₀	562.13	0.92	-0.55	-0.95	0.15	0.46	91.24
b ₁	330.26	226.95	-0.24	-0.94	-0.13	0.15	7.99
b ₂	-94.82	-26.03	53.08	0.52	-0.88	-0.88	0.69
b ₃	-90.64	-56.70	15.33	16.01	-0.19	-0.41	0.06
b ₄	10.94	-5.90	-19.08	-2.28	8.78	0.84	0.02
b ₅	14.27	2.96	-8.460	-2.15	3.26	1.72	0.00

Table 3 - Estimates of heterogeneous residual variance components (model 66) for meat quails

Variance component	Model	Age (days)						
		1	7	14	21	28	35	42
$\hat{\sigma}_a^2$	66	0.39	15.45	62.72	156.52	246.22	240.37	189.09
$\hat{\sigma}_p^2$	66	0.17	16.87	100.38	432.43	779.74	876.52	580.68
$\hat{\sigma}_e^2$	66	0.19	0.19	42.92	33.40	95.34	21.33	347.60
$\hat{\sigma}_f^2$	66	0.75	32.52	206.03	622.36	1,121.31	1,138.23	1,117.37

$\hat{\sigma}_a^2$ - additive genetic variance; $\hat{\sigma}_p^2$ - permanent environment variance; $\hat{\sigma}_e^2$ - phenotypic variance; $\hat{\sigma}_f^2$ - residual variance.

days of age (selection age) was also high (0.965). These results are consistent with those reported by Dionello et al. (2008) and Bonafé et al. (2011), who also reported high genetic correlation from 7 days of age.

The permanent environmental correlations were, in general, similar to the genetic correlations, which highlights the importance of strong permanent effect on body weight, indicating that environmental factors may influence body weight at all ages.

The genetic trend (Figure 3) displayed an increasing pattern over generations (1.2586 g/generation) for the genetic value for body weight at 35 days of age.

A fact that may explain the low breeding value of the second generation is the high number of birds that were born from the five hatchings. As a consequence, the higher number of birds per lot accentuated the competitive behavior among them. With increasing age, the birds became more agitated, tending to establish hierarchy for food and territory, which increased the residual variance, causing the breeding value of the animals to drop. This shows that animals raised out of an ideal condition can express their genetic potential differently; it would be a classic case of genotype × environment interaction.

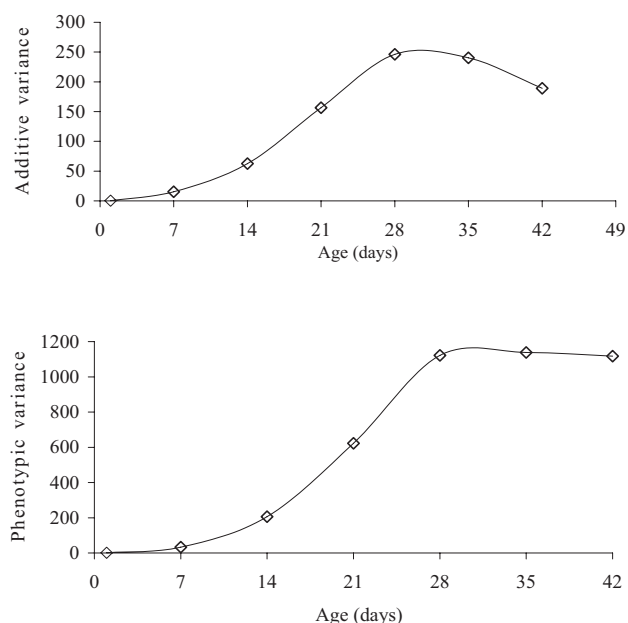


Figure 1 - Components of additive genetic ($\hat{\sigma}_a^2$), permanent environment ($\hat{\sigma}_p^2$), phenotypic ($\hat{\sigma}_p^2$) and residual ($\hat{\sigma}_r^2$) variances for weight versus age for meat quails.

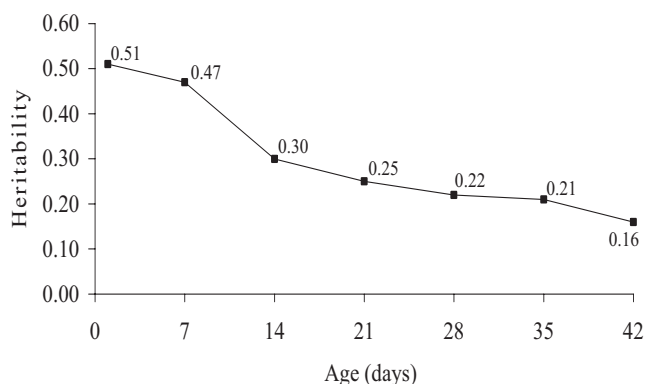


Figure 2 - Heritability versus age for LF1 meat quails.

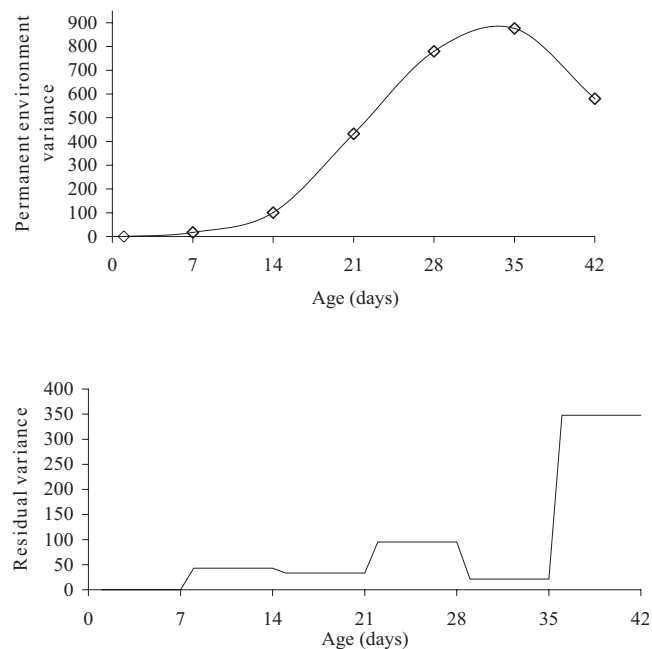


Figure 3 - Genetic trend of breeding values for weight at 35 days of age versus generations for the growth rate curve of LF1 lineage meat quails.

Table 4 - Estimates of genetic (above the diagonal) and permanent environmental (below the diagonal) correlations between weights at the studied ages for meat quails (model 66)

Age	Age (days)						
	1	7	14	21	28	32	42
1	-	0.35	0.32	0.32	0.35	0.39	0.44
7	0.27	-	0.91	0.76	0.65	0.60	0.64
14	0.34	0.64	-	0.94	0.85	0.77	0.69
21	0.26	0.46	0.96	-	0.97	0.89	0.75
28	0.22	0.42	0.90	0.96	-	0.96	0.83
35	0.19	0.36	0.70	0.79	0.92	-	0.93
42	0.19	0.36	0.69	0.78	0.91	0.99	-

Conclusions

The use of sixth order Legendre polynomial along with residual variance divided into six periods was the best fit for the growth rate curve of female LF1 meat quails, and they should be considered for breeding evaluation processes by random regression models. Heritability estimates decreased along the growth rate curves; therefore, genetic gains are higher when younger birds are selected. The genetic trend of breeding values increased over generations, thus symbolizing genetic progress of the studied population.

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