Random regression models for body weight from birth to 210 days of age in partridges (*Rhynchotus rufescens*)

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Abstract: *Rhynchotus rufescens* is a native bird spread out in South America. The adult reaches around 37 cm of height, 700 g of weight with the breast muscles representing 28.6 to 32.8% of the total body weight, traits that could allow raising this bird as a domestic species. Random regression models (RRM) fit random growth curves for each animal as a deviation from the population mean curve and also could be used to partition the phenotypic (co)variance into its genetic and environmental components. A total of 7,369 records of body weight measured from birth to 210 days of partridges born from 2000 to 2004 were used in this research. Data considered birds with at least 4 records of weight, sires with at least 5 progenies and groups of birth with at least 4 animals. The birds were raised in a commercial barn, grounded by grass hay litter. They received feed and water *ad libitum*. The eggs were hatched daily at 35.5 ºC and 70% of humidity. The chicks were sexed when reached around 250 g. The RRM applied to the data set considered the genetic additive direct (AD) and the permanent environment (PE) effects of the animal as random. It was not possible to include the maternal effects in the models. The residual variances were modelled using a variance function of order five. The population mean curve was fitted by a regression on Legendre polynomials of order six. AD and PE were modelled considering regression on Legendre polynomials ranging from order two to six. The RRM analyses were performed by the restricted maximum likelihood method. The models were compared by the likelihood ratio test (L), the Akaike's information criterion (AIC) and the Schwarz's Bayesian information criterion (BIC). Best results were showed by the models using the third order for AD and the sixth order for PE (AIC) and the third order for both AD and PE (BIC and L). Heritability estimates ranged from 0.02 to 0.57. The first eingenvalue were responsible for 94% and 90 % of AD and PE variation, respectively. Results showed selection in any age would be effective to improve growth.

Key words: heritability; Legendre polynomials; partridges (*Rhynchotus rufescens*); wild bird

Introduction

Measures of growth can be seen as a set of points in different ages that change gradually till get a plateau and it happens when the individual reaches the maturity. These points represent a set of correlated measures and, generally, repeated measures on the same animal are much more correlated than measures take on different animals.

Functions describing changes during a period of time can explain the variation of the trait during that period. Growth curve is a good example of the use of this kind of function in animal breeding. Records of weight (longitudinal data) can be study by using covariance functions that describe the joint variation of weight measures take in the same individual in different ages.

Recently, the random regression models have been applied in longitudinal data analysis in animal breeding. This method allows fitting random growth curves for each animal, expressed as deviation of an average curve of the population or individuals groups (Schaeffer, 1996). Since the random effects are described by continuous functions in the random regression models, Meyer and Hill (1997) and

Meyer (1998a) showed that random regression models (RRM) are a special case of covariance function (CF), and covariance function coefficients can be estimated directly from random regression models by restricted maximum likelihood in infinitive dimensional data (Meyer, 1998a).

The RRM allow to model random effects using polynomials functions and make possible to consider heterogeneous residual variance for each age.

The matrices of coefficients of the covariance functions (k) could be used to analyze inheritance patterns through the estimation of their eigenvalues and eigenfunctions (Kirkpatrick and Heckman, 1989). Eingenfunctions are continuous functions, whose coefficients are formed by the elements of the eigenvalues of the matrices of coefficients of the covariance functions. There is an eigenvalue for each eigenfunction and it represents the ratio of total variation that is explained by the eigenfunction (Sakaguti et al., 2003). The trajectories described by eigenfunctions could be used to define the best ages to apply selection (Sakaguti et al., 2003) and also to indicate the directions in which the average trajectory of the longitudinal trait could be modified.

This research aimed to estimate (co)variance components and genetic parameters of partridges (*Rhynchotus rufescens*) weights from birth to 210 days old using random regression models.

Materials and methods

The information used in this paper was taken from birds of the Wild Animal Section of the Faculdade de Ciências Agrárias e Veterinárias (UNESP), at Jaboticabal, São Paulo State, Brazil. The birds were raised in reproduction wired boxes, with concreted floor, covered by a bed lid of Coast-cross (*Cynodon dactylon*) hay, whose dimensions were 1.0 x 2.0 x 2.0 m, placed inside an avian barn. The proportion of females per males ranged from 1:1 to 6:1. The water supply and feeding were *ad libtum* with peletized ration in tubular hods and hanging fountains.

Eggs were colected daily and identified individualy for pedigree control. After 15 days of incubation at 35.5 ºC and 70% of humidity, they were transfered to the birth place. The newborn chicks received temporary markers and were transfered to the breeding boxes, being the maximum allotment of 20 animals per box. The sex verification was made by cloaca reversion, when the birds weighted around 250 g and they received a definitive numered metal marker placed on the right wing when they reached around 90g of weight. The healthy management included the checking for endo and ectoparasites and the bed lid change every two months. The daily hatch procedure caused little synchronized births, originating heterogeneous groups of animals.

Records came from 408 animals born from 2000 to 2004 totaling 7369 observations. The animals were weighed weekly on digital balance (Filizola) from birth to 210 days of age. Data set included records on 67 sires, 17 dams and 27 grandsires, animals with at least 4 records on weight and sires with at least 5 progenies.

Random regression models using an animal model were performed to analyze the data set. Fixed effects included contemporary groups (formed by year and fortnight of birth), sex of bird and age of the animal at weighting effects. The last one was considered as covariates. This effect was modeled using quintic regression on Legendre polynomials.

The random effects included in the models considered the additive genetic direct and animal permanent environmental effects. These effects were modeled by regressions from 2^{nd} to 6^{th} order on Legendre polynomials. The additive genetic maternal effect was not included in the models because very few females could be identified on the maternal side of pedigree. Heterogeneous residual variances using variance function of order 5^{th} was applied to model the temporary environmental effect.

The number of parameters estimated for each model was $k(k+1)/2$ coefficients for additive genetic direct and animal permanent environmental (with k being the order of polynomial fitted) besides residual variances.

The variance components were estimated by REML using the DXMRR option of the DFREML program (Meyer, 1998b).

The residual variances (σ^2_e) using variance function was estimated by regression coefficients of the variance function, represented as follows:

$$\sigma^2_{e_i} = \sigma^2_{e_o}\left(1+\sum_{r=1}^{q}\beta_r t_{ij}^r\right)$$

Where: σ^2_{eo} is the intercept variance, β_r are the r regression coefficients from variance function of order q and t_{ij} are the ages i for each animal j.

The models could be represented by:

$$Y_{ij} = F + \sum_{m=0}^{k_b-1}\beta_m\phi_m(t_{ij}) + \sum_{m=0}^{k_A-1}\alpha_{im}\phi_m(t_{ij}) + \sum_{m=0}^{k_R-1}\gamma_{im}\phi_m(t_{ij}) + \varepsilon_{ij}$$

where:

Y_{ij} is the ith age from the jth animal;

F is a set of fixed effects;

β_m are the fixed regression coefficients to model the population mean;

$\phi_m(t_{ij})$ is the mth Legendre polynomial of age;

t_{ij} is the standardized (-1 to +1) age at recording;

α_{jm} and γ_{jm} are the random regression coefficients for additive genetic direct and animal permanent environmental effects for each animal j; and

ε_{ij} is the temporary environmental effect.

The models were compared by likelihood ratio test (LRT). LRT allows comparisons between nested models and tends to favor models with higher number of parameters. Akaike's information criterion (AIC) and Schwarz's Bayesian information criterion (BIC) (Wolfinger, 1993) were also applied. These favored more parsimonious models imposing penalties according to the number of parameters to be estimated.

Results and discussion

Table 1 presents the values of LRT (nested models), AIC and BIC for the models studied. The AIC criterion indicated the model fitting the order six to genetic effect and the order three to the permanent environmental effect (G_6_6_3_FV5), as the best. Criteria LRT and BIC indicated the most feasible model the one that fitted order 3 for both the genetic and environmental effects (G633FV5). The best model pointed out by LRT and BIC criteria was more parsimonious than the one picked by AIC. Parsimonious models are better choices because they diminish the time need to carry out the statistical analysis and also the requirement for computer features.

Table 2 shows the estimates of (co)variance and the correlation between the random regression coefficients of the coefficients matrix and also the eingenvalues for the additive genetic and permanent environment effects. Both animal genetic additive and animal permanent environment effects showed higher estimates of variance associated to the intercept. The correlation between intercept and linear and quadratic coefficients of the additive genetic effect were positive and high. For animal permanent environment effect, the correlation estimated between intercept and the linear coefficient was also positive and high, and those between linear and quadratic coefficients and between intercept and quadratic coefficients were high (-0,805) and low (-0,148), respectively, and negative (Table 2).

Estimates of phenotypic, genetic direct, animal permanent environmental and residual standard deviations (SD) for the G633VF5 model are presented in Figure 1. Gradual increase on standard deviations was observed for all effects and probably it was due to the decrease in the number of weighting information in posterior ages and also because the increase in individual differences between animals. Permanent environment standard deviation presented intense increase until 17th week of age (119 days) which was coincident with the beginning of the puberty for these birds.

The estimates of heritability followed the same trend of animal genetic standard deviation, presenting higher values from the 14th week of age (98 days) on (Figure 2).

Table 1. Number of parameters (p), value of maximum likelihood function (Log L), Akaike's information criterion (AIC), Schwarz's Bayesian information criterion (BIC) and likelihood ratio test (LRT) to models using different orders of fitting to genetic and permanent environment effects of the animal and residual variance function of 5th order.

	Models	p	LOG L	AIC	BIC	LRT	
(1)	G_6_3_3_VF5	18	**-24123.313313**	48182.626626	**48306.917297**		-
(2)	G_6_4_3_VF5	22	-24596.672076	49237.344152	49389.254973	(2-1)	473.359**
(3)	G_6_5_3_VF5	37	-24747.038110	49548.076221	49734.512228	(3-2)	150.366**
(4)	G_6_5_4_VF5	31	-25414.942185	50891.884257	51105.940413	(4-3)	667.904**
(5)	G_6_5_5_VF5	36	-24786.315891	49644.631781	49893.213123	(5-4)	628.6263**
(6)	G_6_5_6_VF5	42	-24917.941680	49919.883361	50209.894927	(6-5)	231.626**
(7)	G_6_6_3_VF5	33	-24152.162494	**48170.324989**	48398.191220	(7-6)	865.7792**
(8)	G_6_6_4_VF5	37	-24726.019353	49526.038707	49781.525087	(8-7)	673.857**
(9)	G_6_6_5_VF5	42	-24959.164052	50002.328105	50292.339671	(9-8	233.145**
(10)	G_6_6_6_VF5	48	-24196.543818	48489.087637	48820.529427	(10-9)	762.6202**

VF5 = residual variance function of fifth order; G_6_5_3_VF5 = order of fitting 6 to the fixed effect of population mean, 5 to genetic additive effect and 3 to animal permanent environment effect, respectively; ** P<0.01.

Table 2. Estimates of variances (diagonal), (co) variances (lower diagonal) and correlations (upper diagonal) between random regression coefficients of coefficients matrix and their eingenvalues (λ), to genetic and permanent environment effects of the animal. Model G_6_3_3_FV5.

		1	2	3	λ
Additive	1	**2733.520**	0.919	0.413	4271.820
Genetic	2	1960.780	**1664.900**	0.738	259.125
	3	248.871	346.954	**132.670**	0.140
Permanent	1	**5379.560**	0.706	-0.805	6229.220
Environment	2	1578.930	**929.709**	-0.148	666.603
	3	-1429.920	-109.460	**586.661**	0.110

1 = intercept; 2 = linear coefficient e 3 = quadratic coefficient.

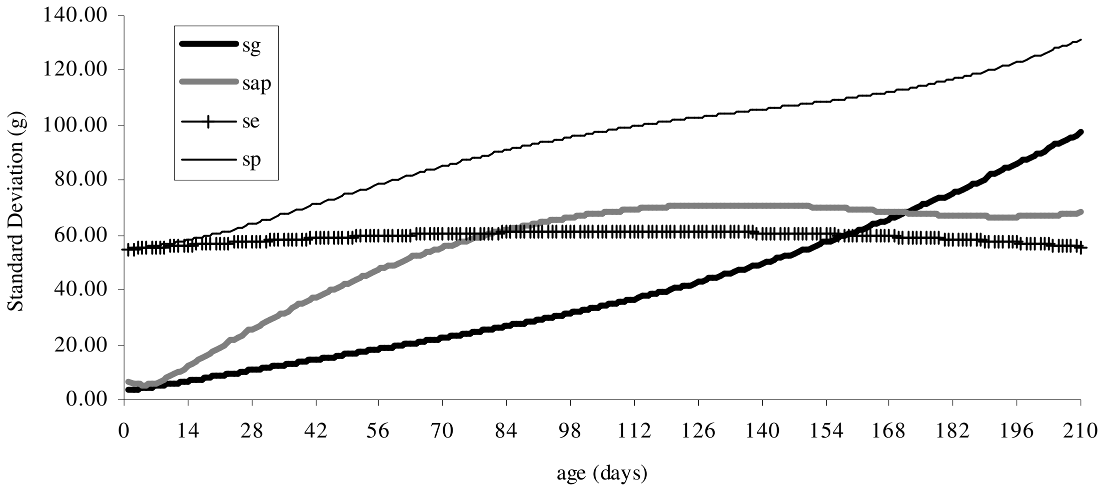

Figure 1. Estimates of phenotypic (sp), genetic additive direct (sg), animal permanent environment (sap) and residual (se) standard deviation using model with variance function of order five and order of fitting 6 to fixed effect, 3 to additive direct and 3 to animal permanent environment random effects (G_6_3_3_FV5) of partridges (*Rhynchotus rufescens*) body weight.

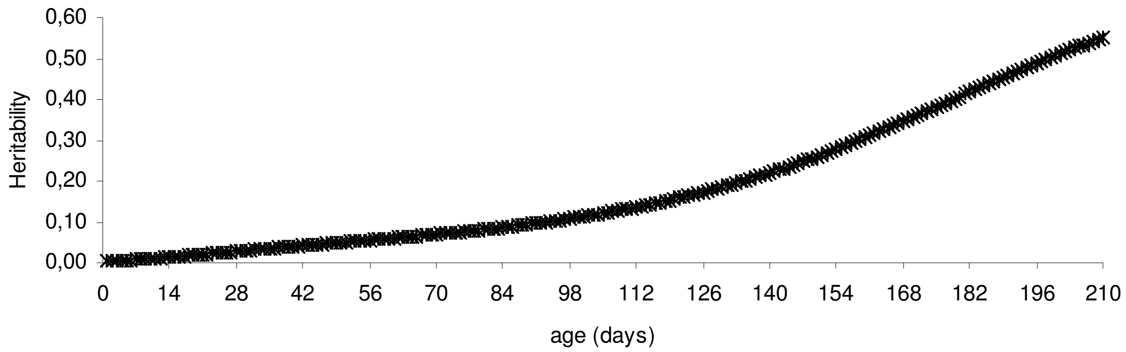

Figure 2. Estimates of direct heritability using model with variance function of order five and fitting order 6 to fixed effect, 3 to additive direct and 3 to animal permanent environment random effects (G_6_3_3_FV5) of partridges (*Rhynchotus rufescens*) body weight.

The animal genetic additive effect eigenvalues were lower than the animal permanent environment ones and these results can be seen on Table 3. The first eigenvalues concentrated most of the variation for both effects. This result indicates the first eigenfunction as the best choice for modifying the growth curve through selection.

Figure 3 picturizes the first three eigenfunctions trends. The first eigenfuntion indicates increasing in weight from the second week of age (14 days) on and it was responsible for 94.28% of the genetic variation. The second eigenfuntion would bring reduction in the weight until 112 days of age and increase in growth in posterior ages. It explained only 5.72% of the genetic variation. The third eigenfuntion presented similar trend to the second, however the decrease in weight would occur only until 70 days of age, explaining a very little proportion of the animal additive genetic variation.

Table 3. Eingenvalues (λ) for genetic additive direct and permanent environment effects of body weight of partridges (*Rhynchotus rufescens*).

	Intercept	Linear Coefficient	Quadratic Coefficient
λ Additive Genetic	4271.8200	259.1250	0.1400
%	94.278100	5.71880	0.0030
λ Permanent Environment	6229.2200	666.6030	0.1100
%	90.3318	9.6667	0.0001

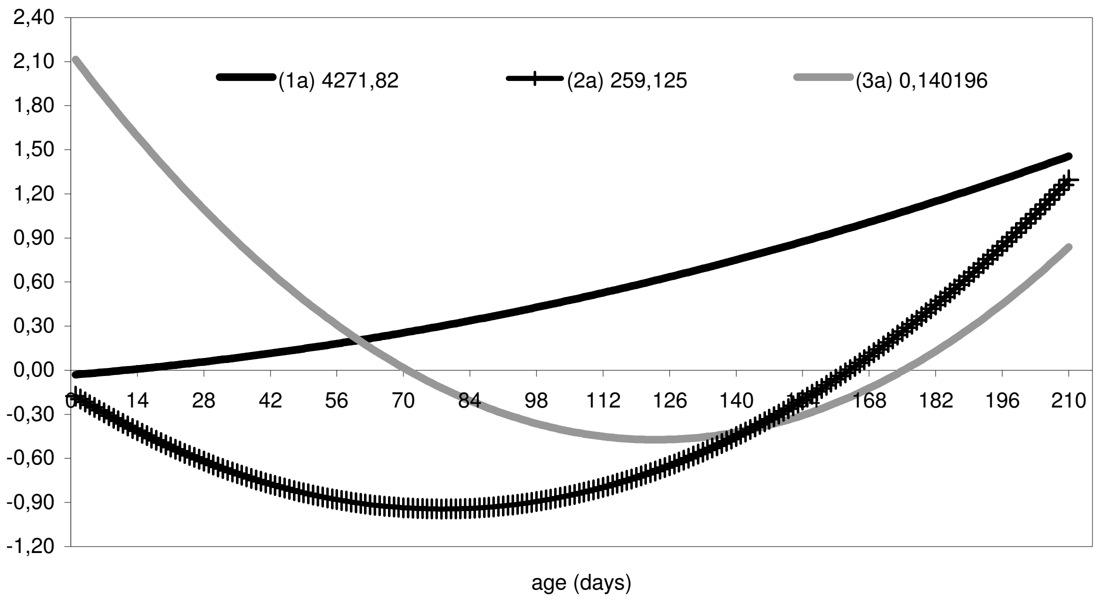

Figure 3. Eingenfunctions estimated by model with order of fitting 6 for fixed effects, 3 for genetic additive direct and permanent environment effects of the animal, and residual variance function of fifth order (G_6_3_3_FV5) of body weight of partridges (*Rhynchotus rufescens*).

In conclusion, the identification of the individuals showing better performance in body weight would be more effective from 120 days of age on and the results showed the possibility of applying selection to the shape of growth curve. The first eingenfunction would be useful to direct this kind of selection.

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