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Genetic characterization of egg weight, egg production and age at first egg in quails

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ABSTRACT - The objective of this research was to estimate genetic parameters for the traits egg weight, egg production in 189 days and age at first egg in three laying quails and one meat line of quails. Data was analyzed by Bayesian procedures using Gibbs sampling. The heritability estimates for egg weight, egg production in 189 days and age at first egg, were, respectively, for yellow line, 0.31, 0.84 and 0.53; for blue line, 0.14, 0.82 and 0.60; for red line, 0.70, 0.96 and 0.75; and for meat line, 0.73, 0.96 and 0.72. Genetic correlation between egg weight and egg production in 189 days, egg weight and day at first egg and egg production in 189 days and day at first egg were for yellow line, 0.58, –0.77 and –0.90; for blue line, 0.09, –0.01 and –0.95; for red line, 0.09, 0.03 and –0.76 and for meat line, –0.18, 0.19 and –0.91, respectively. Based on the probabilities of posterior parameter distribution overlap, the lines are divided in two different groups: one group with the yellow and blue lines and another with the red and meat lines.

Key Words: genetic correlation, genetic variance, heritability, overlap probability, quails

Caracterização genética da idade ao primeiro ovo, da produção e do peso dos ovos em linhagens de codornas

RESUMO - O objetivo neste estudo foi obter estimativas de parâmetros genéticos para as características peso do ovo, produção de ovos em 189 dias de postura e dia do primeiro ovo em codornas de três linhagens de postura e uma de corte. Os dados foram analisados por meio de procedimentos bayesianos usando amostragem de Gibbs. As estimativas de herdabilidade para peso do ovo, produção de ovos em 189 dias de postura e dia do primeiro ovo foram, respectivamente, para a linhagem amarela, 0,31; 0,84 e 0,53; azul, 0,14; 0,82 e 0,60; vermelha, 0,70; 0,96 e 0,75; e de corte, 0,73; 0,96 e 0,72. As correlações genéticas entre peso do ovo e produção de ovos em 189 dias de postura, peso do ovo e dia do primeiro ovo e, produção de ovos em 189 dias de postura e dia do primeiro ovo foram, para amarela, 0,58; –0,77; e –0,90; azul, 0,09; –0,01; e –0,95; vermelha, 0,09; 0,03; e –0,76; e de corte, –0,18; 0,19 e –0,91. A partir das probabilidades de superposição das distribuições posteriories dos parâmetros, as linhagens dividem-se em dois grupos distintos: um com as linhagens amarela e azul e outro com as linhagens vermelha e de corte.

Palavras-chave: codornas, correlação genética, herdabilidade, probabilidade de superposição, variância genética

Introduction

Quails belong to the Gallinaceous order, Fasianidae family, Perdicinae subfamily and *Coturnix* genus. Among the many existing species of quails, the most appropriate one for breeding is *Coturnix coturnix japonica*, which is the result of several years of crosses made in China and Japan from the subspecies *Coturnix coturnix coturnix* (Murakami & Ariki, 1998).

Quail production has become an important segment in Brazilian poultry industry, which has significantly increased in recent years. According to IBGE (1990; 2007), the number of quails being raised in Brazil increased from 2,464,016 to 7,586,732 birds, showing an increase of 208%. The main factors contributing to this are: the meat, which has an exotic taste and is used in sophisticated delicacies; the egg, which tastes similar to chicken egg and is considered an aphrodisiac; better feed conversion into eggs, compared to chickens; the fast growth of the birds; early production and sexual maturity (after 35 days the birds begin oviposition), high yield (average of 300 eggs/bird/year); great longevity in high yield (14 - 18 months); low initial investment and cost

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to set up a small establishment, which may become a source of supplementary income to small farmers; the demand for little space for large populations; and the fast monetary circulation, as it provides a quick return of the invested money (Murakami & Ariki, 1998).

Development of genetic material in quails should follow the same procedure applied to laying hens and broilers, i.e. the development of lines through selection for complementary traits or not, aiming at the expression of additive genetic effects and subsequent crossover to exploit heterosis and recovery from the effects of a possible decay caused by inbreeding (Martins, 2002).

Thus, line development implies estimation of genetic and phenotypic parameters in order to guide selection decisions that will be taken from the genetic evaluations made based on data collected through performance tests.

The objective of this research was to estimate genetic parameters for egg weight, egg production in 189 days and age at first egg; in three laying and one meat line of quails.

Material and Methods

The data was collected from September 2007 to April 2008 in the quail sector in the Fazenda Experimental de Iguatemi – Universidade Estadual de Maringá.

At the end of the trial performance data was obtained from 628 birds (82 red line, 152 blue line and 212 yellow line, all laying lines) and 182 meat line birds. The performance data collected were mean egg weight (g) in two weighings, the first at 70 days and the second at 120 days; total egg production in 189 days; and age at first egg. Evaluations were performed using the software MTGSAM - *Multiple Trait Gibbs Sampling in Animal Models* (Van Tassel & Van Vleck, 1995), which proceeds from Bayesian estimation using the Gibbs sampling technique, applied to a three-trait animal model as follows.

$Y = X\beta + Za + e$

Which is equivalent to the model:

$$y=\begin{bmatrix} y_1\\ y_2\\ y_3\end{bmatrix}=\begin{bmatrix} X_1 & 0 & 0\\ 0 & X_2 & 0\\ 0 & 0 & X_3\end{bmatrix}\begin{bmatrix} \beta_1\\ \beta_2\\ \beta_3\end{bmatrix}+\begin{bmatrix} Z_1 & 0 & 0\\ 0 & Z_2 & 0\\ 0 & 0 & Z_3\end{bmatrix}\begin{bmatrix} a_1\\ a_2\\ a_3\end{bmatrix}+\begin{bmatrix} e_1\\ e_2\\ e_3\end{bmatrix}$$

in which: y_1, y_2 and y_3 = vectors of observations of the egg weights, egg production and age at first egg, respectively; X_1, X_2 and X_3 = incidence matrices for fixed effects contained in the β vector; Z_1, Z_2 and Z_3 = incidence matrices of genetic values contained in x vector; a_1, a_2 and a_3 = vectors of direct genetic effects associated with the y vector; e_1, e_2 and e_3 = vectors of random errors associated with the y vector.

The following joint distribution was assumed for y, a and e

$$\begin{bmatrix} y\\ a\\ e\end{bmatrix}\sim\left\{\begin{bmatrix} X\beta\\ 0\\ 0\end{bmatrix};\begin{bmatrix} V & ZG & R\\ GZ & G & \phi\\ R & \phi & R\end{bmatrix}\right\}$$

in which: V = matrix of variance and covariance of the observations given by ZGZ' + R; G = matrix of additive genetic variance and covariance given by $G = G_0 \otimes A$; in which A = numerator relationship matrix; $\otimes$ = Kronecker product; and G_0 = matrix of additive genetic variance and covariance between traits, as follows.

$$G_0=\begin{bmatrix} \sigma^2_{a_1} & \sigma_{a_2a_1} & \sigma_{a_3a_1}\\ \sigma_{a_1a_2} & \sigma^2_{a_2} & \sigma_{a_3a_2}\\ \sigma_{a_1a_3} & \sigma_{a_2a_3} & \sigma^2_{a_3}\end{bmatrix}$$

in which: $\sigma^2_{a_i}$ = additive genetic variances for the studied traits; $\sigma_{a_ia_j}$= genetic covariances between traits i and j; R = matrix of residual variance and covariance given by $R = R_0 \otimes I$; in which I = identity matrix and R_0 = matrix of residual variance and covariance among traits, given as follows.

$$R_0=\begin{bmatrix} \sigma^2_{e_1} & \sigma_{e_2e_1} & \sigma_{e_3e_1}\\ \sigma_{e_1e_2} & \sigma^2_{e_2} & \sigma_{e_3e_2}\\ \sigma_{e_1e_3} & \sigma_{e_2e_3} & \sigma^2_{e_3}\end{bmatrix}$$

in which: $\sigma^2_{e_i}$ = residual variances for the studied traits; $\sigma_{e_ie_j}$= residual covariances among traits i and j.

The Gibbs sampling procedure was applied under the assumption of a flat distribution of the y expected value and a normal distribution of the direct additive genetic and error effects. The Inverted Wishart (IW) distribution was assumed for the direct genetic and residual covariance matrices.

There was no formation of contemporary groups, because the animals were born on the same day, so the fixed effect was consisted only of the general mean.

The analyses of Gibbs chains were set between 5,500,000 and 7,500,000 cycles, and the first 500,000 cycles (*burn-in*) were discarded to reduce the influence of the initial prior, by sampling every 1,000 cycles (*thinning interval*). Thus, from 5,000 to 7,000 samples were obtained for all parameters to be estimated, allowing the verification of convergence and the establishment of credibility intervals. The convergence of Gibbs chains for stationary distributions was tested by the Geweke and the Heidelberger & Welch diagnostic, available in the package CODA (*Convergence Diagnosis and Output Analysis*), implemented in the software R (2004), and all the chains converged.

The overlap of the chain of the samples of the generated parameters for each trait was evaluated by the probability of simultaneous occurrence of a given parameter in two lines in the area common to the two posterior distributions.

Results and Discussion

The four lines showed high potential for response to selection for the studied traits, except for egg weight in the yellow and blue lines, whereas the estimates of heritability for this trait were shown to be moderate and low, respectively (Table 1).

Baungartner (1994) reported a heritability value for egg weight of 0.35, while Saatci et al. (2006) found heritability of 0.25. Heritability values of 0.39 for egg production until 13 weeks of age were observed by Minvielle et al. (1997). Micheli et al. (2007) reported values of heritability for egg weight at 70, 100 and 130 days of age in three lines of laying quails of 0.39; 0.51; and 0.51 for the first line, 0.32; 0.54; and 0.46 for the second one and 0.43; 0.40; and 0.44 for the third line. Minvielle (1998), in his review of genetic breeding in quails for production, presented heritability values indicated by the collected data from 0.32 to 0.39 for egg production and from 0.35 to 0.62 for egg weight. More recently, Mielenz et al. (2004) used two lines of Japanese quails — the first selected for high body weight and low egg weight and the second selected only for high egg weight — and found heritability for egg production and egg weight of 0.35 and 0.66 for the first line and 0.21 and 0.58 for the second line, respectively. Paiva (2004), using the same lines of quails studied in the present work, found heritability values of 0.73; 0.13; and 0.17 for the yellow line; 0.19; 0.15; and 0.19 for the blue line; and 0.22; 0.25; and 0.15 for the red line for age at first egg, egg weight at 60 and 90 days, respectively. Georg (2007) studied the same lines of quails and estimated heritabilities for egg weight at 70, 100 and 130 days of age of 0.40; 0.51; and 0.51 for the yellow line, 0.32; 0.55; and 0.46 for the red line and, 0.43; 0.40; and 0.45 for the blue line, while for total egg production after 90 days the heritability in all three lines were virtually null. In the present study, heritabilities for total egg production differed from those obtained by Georg (2007) because the production period in the present study was 189 days.

Table 1 - Heritability (main diagonal), genetic correlation (below the diagonal) and phenotypic (above the diagonal), genetic variances and credibility intervals* for age at first egg, egg production and egg weight in quail lines

	Egg weight	Egg production	Age at first egg	Genetic variance
		Yellow line		
Egg weight	0.31 (0.14; 0.51)	0.18 (0.03; 0.32)	–0.04 (–0.18; 0.09)	0.18931 (0.08379; 0.32505)
Egg production	0.58 (0.17; 0.87)	0.84 (0.73; 0.92)	0.50 (–0.59; –0.40)	359.596 (274.007; 454.680)
Age at first egg	–0.77 (–0.95; –0.44)	–0.90 (–0.97; –0.80)	0.53 (0.39; 0.65)	49.497 (33.451; 67.999)
		Blue line		
Egg weight	0.14 (0.05; 0.32)	0.09 (–0.05; 0.23)	0.02 (0.17; 0.12)	0.08163 (0.02614; 0.18539)
Egg production	0.09 (–0.64; 0.74)	0.82 (0.73; 0.89)	-0.49 (0.60; 0.38)	433.897 (328.704; 553.789)
Age at first egg	–0.01 (–0.67; 0.69)	–0.95 (–0.99; –0.88)	0.60 (0.49; 0.70)	81.5503 (56.8590; 109.1231)
		Red line		
Egg weight	0.70 (0.58; 0.81)	0.10 (–0.11; 0.29)	0.09 (–0.11; 0.28)	1.89034 (1.34653; 2.5803)
Egg production	0.09 (–0.16; 0.33)	0.96 (0.92; 1.00)	0.53 (–0.70; –0.32)	863.817 (626.329; 1,165.004)
Age at first egg	0.03 (–0.23; 0.29)	–0.76 (–0.96; –0.41)	0.75 (0.47; 0.98)	94.4389 (45.5095; 153.8139)
		Meat line		
Egg weight	0.73 (0.64; 0.82)	–0.16 (–0.30; –0.01)	0.12 (–0.01; 0.25)	1.3915 (1.07315; 1.76178)
Egg production	–0.18 (–0.34; 0.00)	0.96 (0.95; 0.97)	–0.65 (–0.73; –0.57)	628.567 (512.314; 761.425)
Age at first egg	0.19 (0.01; 0.37)	–0.91 (–0.96; -0.82)	0.72 (0.47; 0.98)	64.6872 (47.2069; 85.8243)

*Values in parentheses.

Genetic correlation estimates between egg weight and total egg production were positive and moderate for the yellow line, while for the other lines they were low, but positive for the blue and red lines and negative in the meat line. This indicated that in the yellow line, genetic gains may be obtained for one of these traits if the selection is based on another trait. However, the same cannot be said about the other three lines, in which simultaneous gains in both traits will be obtained only if the selection includes both traits.

Between egg weight and age (days) at first egg, genetic correlation estimates were negative and of high magnitude in the yellow line and of little importance in the other three lines. This result allows the same interpretation about the achievement of simultaneous genetic gain for egg weight and total egg production.

Genetic correlation estimates between total egg production and age at first egg were negative and of high magnitude in the four lines indicating that selection based on only one of the traits would produce correlated genetic gain.

All this information indicated that selection on the yellow line could be based on only one trait and it would lead to genetic gains in the other traits as correlated response. However, in the other three lines, the use of a selection index would be recommended.

Micheli et al. (2007) reported values from 0.48 to 0.60 for genetic correlation of egg production and egg weight. Minvielle (1998), in a review about genetic improvement in quails, found genetic correlation for egg production and egg weight ranging from –0.55 to –0.19. Mielenz et al. (2004) when studying two quail lines, observed values for genetic correlation between total egg production and egg weight of –0.36 and 0.07 in lines 1 and 2, respectively. Paiva (2004), using the same genetic material, found estimates of genetic correlation between age at first egg and egg weight at 60 and 90 days, respectively, of 0.04 and -0.36 for the yellow line; –0.32 and –0.09 for the blue line; and –0.01 and –0.19 for the red line. Also, Georg (2007), in the same lines, observed values of genetic correlation between total egg production after 90 days and egg weight at 70, 100 and 130 days of 0.54, 0.54 and 0.48 for the yellow line; 0.61, 0.63 and 0.61 for the red line; and 0.55, 0.54 and 0.53 for the blue line.

The yellow and blue lines showed a high coincidence in the posterior distributions of heritability, genetic correlations and genetic variances of the three studied traits, indicating great genetic similarity between these two lines (Table 2). Among the yellow, red and meat lines, there was a low coincidence in the posterior distributions of heritabilities and genetic variances for egg weight and total egg production. In the posterior distributions of genetic correlations, there was low coincidence for egg weight and age at first egg between these lines, while for egg weight

Table 2 - Overlap probability (%) of posterior distributions of heritabilities, genetic correlations and additive genetic variance of production traits in quail lines

		Yellow line × Blue line	Yellow line × Red line	Yellow line × Meat line
	Egg weight	0.9638	0.1490	0.0730
Heritability	Egg production	0.9960	0.2333	0.0102
	Age at first egg	0.9997	0.6154	0.4863
	Egg weight × egg production	0.8526	0.5299	0.0891
Genetic correlation	Egg weight × age at first egg	0.7386	0.0840	0.0180
	Egg production × age at first egg	0.9769	0.7555	1.0000
	Egg weight	0.9394	0.0000	0.0000
Genetic variance	Egg production	0.9855	0.0032	0.0641
	Age at first egg	0.8413	0.5596	0.9564
		Blue line × Red line	Blue line × Meat line	Meat line × Red line
	Egg weight	0.0100	0.0049	0.9981
Heritability	Egg production	0.0636	0.0000	0.9394
	Age at first egg	0.6323	0.0158	0.9619
	Egg weight × egg production	0.8964	0.6071	0.8646
Genetic correlation	Egg weight × age at first egg	0.8670	0.7013	1.0000
	Egg production × age at first egg	0.7457	0.9466	0.9194
	Egg weight	0.0000	0.0000	0.8524
Genetic variance	Egg production	0.1181	0.5399	0.8017
	Age at first egg	0.9584	0.9936	0.8441

and total egg production, the coincidence was low only between the yellow and meat lines. These results indicated significant genetic difference between the yellow line and the red and meat lines.

The blue and yellow lines showed low coincidence with the red and meat lines, for the posterior distributions of heritabilities of egg weight and total egg production, and also for age at first egg for the meat line. Also, in the posterior distributions of genetic variances for egg weight and total egg production, the blue line differed from the red line, but from the meat line, it differed only for the posterior distribution of genetic variance of egg weight. In the posterior distributions of genetic correlations, there was a high coincidence among the blue, red and meat lines.

These results indicated that the blue line, similar to the yellow one, also differed from the red and meat lines, except for genetic correlations. The red and meat lines showed high coincidence in the posterior distributions for all the studied parameters, which indicated a strong similarity between these two lines.

Genetic parameter estimates obtained and submitted for comparison indicated genetic similarity between the yellow and blue lines and between the red and meat lines.

Conclusions

Quail lines show a high potential for response to selection for the production traits considered in this study and formed two distinct groups based on similarities among the estimated genetic parameters: one formed by the yellow and blue lines and the other by the red and meat lines.

References

BAUNGARTNER, J. *Japanese quail production* breeding and genetics. **World's Poultry Science**, v.50, n.3, p.228-235, 1994.

GEORG, P.C. **Caracterização de três linhagens de codornas de postura alimentadas com rações de alto e baixo nível de energia metabolizável**. 2007. 60f. Dissertação (Mestrado em Zootecnia) – Universidade Estadual de Maringá, Maringá.

INSTITUTO BRASILEIRO DE GEOGRAFIA E ESTATÍSTICA - IBGE. [2008] **Pesquisa Pecuária Municipal** (PPM). Disponível em: <http://www.ibge.gov.br.> Acesso em: 18/10/2009.

MARTINS, E.N. Perspectivas do melhoramento genético de codornas no Brasil. In: SIMPÓSIO INTERNACIONAL DE COTURNICULTURA, 1., 2002, Lavras. **Anais...** Lavras: UFLA, 2002. p.109-112.

MICHELI, A.; GEORG, P.C.; TOLEDO, J.B. et al. Parâmetros genéticos para peso do ovo e produção de ovos em três linhagens de codornas de postura. In: ENCONTRO ANUAL DE INICIAÇÃO CIENTÍFICA, 16., 2007, Maringá. **Anais...** Maringá: UEM [2007]. (CD-ROM).

MIELENZ, N.; NOOR, R.R.; SCHUELLER, L. Estimation of additive and non-additive genetic variances of body weight, egg weight and egg production in quail, using animal models. In: WORLD'S POULTRY CONGRESS, 22., 2004, Istanbul. **Proceedings...** Istanbul: World's Poultry Congress & Exhibition, [2004]. (CD-ROM).

MINVIELLE, F.; MONVOISIN, J.L.; COSTA J. et al. Quail lines selected on egg number either on pure line or on crossbred performance. In: INTERNATIONAL SYMPOSIUM, 12., 1997, Pruhonice. **Proceedings...** Pruhonice, 1997.

MINVIELLE, F. Genetics and breeding of Japanese quail for production around the world. In: ASIAN PACIFIC POULTRY CONGRESS, 6., Nagoia, 1998. **Proceedings...** Nagoia: Poultry Science Association, 1998. p.122-127.

MURAKAMI, A.E.; ARIKI, J. **Produção de codornas japonesas**. Jaboticabal: Funep, 1998. 79p.

PAIVA, E. **Parâmetros genéticos e fenotípicos para peso aos 28 dias, idade ao primeiro ovo e peso do ovo, em codornas**. 2004. 12f. Trabalho de conclusão de curso (Graduação em Zootecnia) – Universidade Estadual de Maringá, Maringá.

R Development Core Team [2004]. **R**: A language and environment for statistical computing. R Foundation for Statistical Computing. Disponível em: <http://www.R-project.org> Acesso em: 10/10/2009.

SAATCI, M.; OMED, H.; AP DEWI, I. Genetic parameters from univariate and bivariate analyses of egg and weight traits in japanese quail. **Poultry Science**, v.85, 2006. p.185-190.

Van TASSEL, C.P.; Van VLECK, L.D. **A manual for use of MTGSAM. A set of fortran programs to apply Gibbs sampling to animal models for variance components estimation.** (Draft). Lincoln: Departament of Agriculture/ Agriculture Research Service, 1995. 86p.