Short communication

Bayesian estimation of genetic parameters for individual feed conversion and body weight gain in meat quail

Giovani da Costa Caetano[a], Rodrigo Reis Mota[b], Delvan Alves da Silva[a],
Hinayah Rojas de Oliveira[a], José Marcelo Soriano Viana[c], Otávio Henrique G.B.D. de Siqueira[a],
Pedro Henrique F. Freitas[a], Fabyano Fonseca e Silva[a],*

[a] Department of Animal Science, Universidade Federal de Viçosa, Av. P.H. Holfs, 36570-000 Viçosa, Brazil
[b] Department AGROBIOCHEM, Animal Science, University of Liege - Gembloux Agro-Bio Tech, Passage des Deportes, B-5030 Gembloux, Belgium
[c] Department of General Biology, Universidade Federal de Viçosa, Av. P.H. Holfs, 36570-000 Viçosa, Brazil

ARTICLE INFO

ABSTRACT

We estimated genetic correlations between partial and total body weight gain (BWG) and individual feed conversion (FC) aiming to identify possible partial traits as selection criteria in meat quail breeding programs. Data included 379 records from two different genetic lines (188 quails from UFV1 and 191 from UFV2). The following traits were evaluated: individual feed conversion from 21 to 28 (FC_{21-28}) and from 28 to 35 days of age (FC_{28-35}); body weight gain from 1 to 21 (BWG_{1-21}), 21–28 (BWG_{21-28}), 28–35 (BWG_{28-35}) and from 1 to 35 (BWG_{1-35}, full period) days of age. Genetic parameters (heritabilities and genetic correlations) were estimated through multi-trait models via Bayesian inference. For UFV1 line, genetic correlations estimates (with respective credible intervals) between BWG_{1-21} and BWG_{1-35}, BWG_{21-28} and BWG_{1-35}, BWG_{28-35} and BWG_{1-35}, FC_{21-28} and FC_{28-35}, FC_{21-28} and BWG_{1-35}, and FC_{28-35} and BWG_{1-35} were 0.62 0.15–0.90), 0.81 0.60–0.94), 0.69 0.35–0.88), 0.06 (−050 to 0.60), −0.87 (−0.97 to −0.63) and −0.51 (−0.84 to −0.01), respectively; and for UFV2 line, these estimates were 0.33 (−0.05 to 0.63), 0.79 0.59–0.92), 0.88 0.73–0.96), 0.35 (−0.30 to 0.78), −0.56 (−0.85 to −0.09) and −0.76 (−0.93 to −0.41), respectively. Additionally, for the UFV1 line heritability estimates for BWG_{21-28} and FC_{21-28} were 0.69 0.40–0.86) and 0.55 0.31–0.74), respectively; while for UFV2 line the heritabilities for BWG_{28-35} and FC_{28-35} were 0.68 0.47–0.83) and 0.37 0.17–0.63). Based on these results, we recommend as target traits BWG_{21-28} and FC_{21-28} for UFV1 line; and BWG_{28-35} for UFV2 line. Selecting for these indicated traits, we expect to reduce breeding program costs related mainly to feeding of non-selected animals and labor with phenotyping.

1. Introduction

In Brazil, the number of quails in the last few years have almost doubled (Silva et al., 2013), so that the meat production became an important activity to achieve a different range of the consumer market. Thus, breeding programs aiming to improve growth traits were prosed to ensure the future of this activity (Silva et al., 2013).

In general, the selection for meat quails have been based on body weight (BW) at specific ages (Barbieri et al., 2015) or body weight gain (BWG) between these ages (Aggrey et al., 2003). In general, the BWG has been of fundamental importance to reduce the slaughter age in quails (Case et al., 2012; Aggrey et al., 2003). Since the main part of the total production cost in meat quail is represented by feed costs, the inclusion of feed efficiency related traits in genetic breeding programs

is justified. According to Case et al. (2012), improving feed conversion (FC) by identifying animals that require the same amount of feed but have higher body weight gain (BWG) is valuable in the modern poultry breeding.

The majority of the studies involving genetic parameter estimates for FC and BWG were performed for Japanese quails based on group of animals (Varkoohi et al., 2010, 2011). Foomani et al. (2014) estimated genetic parameters for these traits using individual measures of Japanese quails; however results about these estimates for meat quails have not been yet reported. Furthermore, since FC and BWG are commonly measured later in the animals, if the genetic correlations between partial and final traits are high, partial traits can be used as selection criteria aiming to reduce breeding program costs (feeding of non-selected animals and labor cost with phenotyping).

---

* Corresponding author.
  E-mail address: fabyanofonseca@ufv.br (F.F. e Silva).

Bayesian inference has been successfully applied to genetic parameter estimation in animal breeding. According to Sorensen and Gianola (2002), one important advantage of Bayesian inference is to obtain credible intervals for genetic parameters. It allows making inferences about the significance of genetic correlations in studies proposing new traits as selection criteria.

In this context, we aimed to estimate genetic parameters for partial and total BWG and individual FC through multi-trait models via Bayesian inference in order to verify the possibility of using partial traits as selection criteria in breeding programs for meat quails.

2. Material and methods

2.1. Population structure and animal management

All animal procedures were approved by the Animal Care and Use Committee of the Department of Animal Science from Universidade Federal de Viçosa (UFV), Brazil (73/2014-CEUAP).

Data used in this study were from an experiment carried out in 2014 and supported by the Breeding Program for Meat Quails of UFV. Individual observations of body weight gain and feed conversion from 188 (line UFV1) and 191 (line UFV2) animals were used. A total of 102 sires and 204 dams were matted under two females per each male rate. Eggs were collected during 10 days in each phase, incubated for 14 days and allocated in a hatcher for 3 days up to hatch. On hatching day, progenies received identification for pedigree information, and the body weight at birth was measured.

The birds were randomized and distributed in 24 screen pens (1.0 m × 0.8 m), in average of 20 and 10 animals from UFV1 and UFV2 lines, respectively. The pens had wood shavings provided as litter substrate with ad libitum access to food and water. During first 14 days a dish-type feeders and pressure cup drinker were used and were changed by tubular feeders and automatic nipple drinkers during the remaining period. Diet was formulated according to NRC (1994) nutritional recommendations. The temperature in each pen was maintained using infrared lamps until birds reached 15 days of age.

Each box received, in average, 20 and 10 animals from UFV1 and UFV2 lines, respectively. Animals were randomized allocated on each box and individually weighted at 1, 7, 14, 21, 28 and 35 days of age. These weight records were used for body weight gain calculation across the evaluated periods. At 21 days of age the animals were weighed and sexed; after was performed a random collect of 204 animals/line and they were moved to individual galvanized cages for feed intake control aiming to achieve more accurate measures (when compared with the measures in groups) of feed conversion. The number of animals collected is due to the limited number of individual cages available for each line. Cages had 0.15 m for sideboard egg and six divisions per cage in total and were equipped with galvanized sheet linear feeders, with subdivisions for each individual cage, and linear drinker, supplied with running water. Feed intake (FI) was recorded weekly, and feed conversions (FC) of each animal were calculated by the ratio between FI and BWG. However, feed conversion from the first phase (up to 21 days) were not used since it was a group measure and could lead to biased estimates of genetic parameters. Thus, only individual feed conversion data collected from 21 days were used.

The final dataset for each line was composed of animal identification, sire, dam, hatching number, sex, body weight gain in partial periods: 1–21 days ($BWG_{1–21}$), 21–28 days ($BWG_{21–28}$) and 28–35 days ($BWG_{28–35}$), body weight gain on full period: 1–35 days ($BWG_{1–35}$) and individuals feed conversion on partial periods: 21–28 days ($FC_{21–28}$) and 28–35 days ($FC_{28–35}$). Records with no sex and/or measures lower or higher than three standard deviations were removed. The final dataset presented 188 and 191 animals from UFV1 and UFV2 lines, respectively.

2.2. Statistical analysis

Two different analyses for each line (UFV1 and UFV2) were carried out according to the set of considered traits using multi-trait models. The first one involved only BWG traits ($BWG_{1–21}$, $BWG_{21–28}$, $BWG_{28–35}$ and $BWG_{1–35}$), which aimed to verify whether partial BWG measures are genetically correlated with the final trait ($BWG_{1–35}$). The second one involved the FC traits ($FC_{21–28}$ and $FC_{28–35}$) and $BWG_{1–35}$, which aimed to estimate the genetic correlation between an early and a late FC trait, as well as their correlations with the final BWG trait.

For both analyzes, the following multi-trait Bayesian model was fitted:

$$\mathbf{y} = X\boldsymbol{\beta} + \mathbf{Za} + \mathbf{e},$$

where:

$\mathbf{y}$ is the vector of phenotypic observations, assumed as $\mathbf{y}|\boldsymbol{\beta}, \mathbf{a}, \mathbf{G_0}, \mathbf{R_0} \sim N(X\boldsymbol{\beta} + \mathbf{Za}, \mathbf{R_0} \otimes \mathbf{I})$; $\boldsymbol{\beta}$ is the vector of systematic effects (sex and hatching), assumed as $\boldsymbol{\beta} \sim N(\mathbf{0}, \sum_{\beta} \otimes \mathbf{I})$, being $\sum_{\beta}$ a known diagonal matrix with values $1e + 10$ (large variances) to represent vague prior knowledge; $\mathbf{a}$ is the vector of random additive genetic effects, assumed as: $\mathbf{a}|\mathbf{G_0}, A \sim N(\mathbf{0}, \mathbf{G_0} \otimes \mathbf{A})$, being $\mathbf{A}$ the additive relationship matrix among the animals and $\mathbf{G_0}$ the additive genetic (co)variance matrix. Furthermore, it was assumed that $\mathbf{G_0}$ follows an inverted Wishart distribution, WI (v_a, $\mathbf{V_a}$), with hyperparameters $v_a = 2$ and $\mathbf{V_a}$; $\mathbf{X}$ and $\mathbf{Z}$ are the incidence matrices of systematic and random additive genetic effects, respectively; $\mathbf{e}$ is the vector of random errors, assumed as $\mathbf{e}|\mathbf{R_0} \sim N(\mathbf{0}, \mathbf{R_0} \otimes \mathbf{I})$, where $\mathbf{I}$ and $\mathbf{R_0}$ are, respectively, an identity and residual covariance matrices. Similarly as assumed for $\mathbf{G_0}$, $\mathbf{R_0} \sim WI(v_e, \mathbf{V_e})$, with hyperparameters $v_e = 2$ and $\mathbf{V_e}$. The matrices $\mathbf{V_a}$ and $\mathbf{V}e$ represent a pool (approximated average values) obtained empirically from literature (Varkoohi et al., 2011; Case et al., 2012; Aggrey et al., 2003). The degrees of freedom, $va = ve = 2$, were chosen to provide non-informative priors, since the "previous knowledge" about the parameters to be estimated can be considered "week" given the small number of studies for the considered traits. The covariance matrices ($\mathbf{G_0}$ and $\mathbf{R_0}$) assumed the dimensions 4×4 and 3×3, respectively to the first (involving $BWG_{1–21}$, $BWG_{21–28}$, $BWG_{28–35}$ and $BWG_{1–35}$ traits) and second (involving $FC_{21–28}$, $FC_{28–35}$ and $BWG_{1–35}$ traits) multi-trait analyses.

The (co)variance components and genetic parameters were estimated through Gibbs sampler algorithm by using the GIBBSF90 software (Misztal et al., 2002). The posterior marginal distribution samples for heritability of a trait i (h_i^2) and genetic correlations between traits i and j (r_{ij}) were obtained from the (co)variance components samples generated in each Gibbs sampler iteration (k) as follow: $h_i^{2(k)} = \sigma_{a_i}^{2(k)}/(\sigma_{a_i}^{2(k)} + \sigma_{e_i}^{2(k)})$ and $r_{ij}^{(k)} = \sigma_{a_{ij}}^{(k)}/\sqrt{\left(\sigma_{a_i}^{2(k)}\sigma_{a_j}^{2(k)}\right)}$. The genetic variances ($\sigma_{a_i}^2$) and covariances ($\sigma_{a_{ij}}$) were obtained from $\mathbf{G_0}$, and the residual variance ($\sigma_{e_i}^2$) from $\mathbf{R_0}$. A total of 500,000 samples were generated, assuming a burn-in period of 50,000 iterations. The convergence was assessed by Geweke test using POSTGIBBSF90 software (Misztal et al., 2002).

3. Results

Descriptive statistics for all traits in each one of these lines are shown in Table 1.

Estimates of additive genetic and residual (co)variances, heritabilities and genetic correlations for BWG traits are shown in Table 2. For the line UFV1, heritability estimates for $BWG_{1–21}$, $BWG_{21–28}$, $BWG_{28–35}$ and $BWG_{1–35}$ were 0.17, 0.69, 0.24 and 0.56, respectively. Except for $BWG_{21–28}$ ($h^2 = 0.49$), the line UFV2 showed higher heritability estimates (0.24, 0.68 and 0.73, respectively for $BWG_{1–21}$, $BWG_{28–35}$ and $BWG_{1–35}$). The largest genetic correlation estimate for the line UFV1 was between $BWG_{21–28}$ and $BWG_{1–35}$ (0.81), while for the line UFV2,