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Longitudinal analysis of body weight, feed intake and residual feed intake in F_2 chickens

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ABSTRACT

The aim of this study was to estimate covariance functions, using B-spline random regression models for body weight (BW), feed intake (FI) and residual feed intake (RFI) in F_2 chickens. Feed intake and body weight were recorded on each bird every week from 2 to 10 weeks of age. The F_2 population was derived from a cross between a fast growing Arian broiler line and Iranian native fowl. Sex, hatch and age in week were fitted as fixed effects and additive genetic and permanent environment as random effects. Variance components were estimated by the means of a Bayesian analysis, using Gibbs sampling. Covariance components for cumulative FI and RFI were obtained as a function of week on test. The heritability estimates for BW ranged from 0.19 to 0.34 and were high at the early ages, decreases with age to a moderate value. A similar pattern was observed for FI, where the heritabilities decreased from 0.29 to 0.12 from the second week to 10th week of age. Estimates of heritabilities for RFI along the growth trajectory ranged from 0.10 to 0.29 and increased over the time. Cumulative FI and RFI had medium to high heritability (0.24 and 0.41, respectively). The posterior means of genetic correlations between BW at different age were moderate to high from 2 to 10 weeks of age, ranging from 0.26 to 0.99. These estimates for phenotypic correlations were lower than the corresponding genetic correlations for all the weeks. The posterior means of genetic correlations between different weeks of age ranged from 0.10 to 0.99 for FI and −0.15 to 0.96 for RFI. The genetic and phenotypic correlations consistently decreased as the time interval increased for all traits. However, for the cumulative FI and RFI traits were increased with increasing the age interval from 2 to 9 weeks of age. The genetic correlations and expected response to indirect selection showed that the optimum test length for FI and RFI can be reduced to 2 weeks without a large loss in overall genetic gain in FI or RFI. In general, spline model showed that there was genetic variation in the BW, FI and RFI curve of individual chicken. The results indicated that random regression models can provide a good description of the data and is recommended for genetic selection in chickens.

1. Introduction

Feed efficiency (FE, gain:feed) is one of the most important traits in breeding goals of poultry industry because the approximately 70% of the total cost of production (Arango, 2009) is due to feed. These costs can potentially be reduced by improving feed efficiency through genetic improvement. Furthermore, identifying and selecting chickens that are more efficient will lead to better use of limited feed resources.

A commonly used measure is feed conversion ratio (FCR, feed: gain), i.e. the inverse of FE. One problem with FCR measurement is its relatively high correlation with growth, feed intake and body composition (Carstens et al., 2003), therefore, selection on the basis of FCR may lead to chicken with greater maintenance requirements (Archer et al., 1999). In addition, selection based on ratio traits poses a challenge on the complex interdependence between the ratio and the component traits (Gunsett, 1984). Selection strategies for efficiency, therefore, in several animal species, have moved from FCR to residual feed intake (RFI). RFI is defined as the difference between actual feed intake and expected feed intake. The expectation is either based on standard feeding tables or from multiple regression models adjusting feed intake (FI) for maintenance and production requirements (Koch et al., 1963). Therefore, selection based on RFI will decrease feed intake and improves efficiency of energy utilization due to no reduction in the part intake required for production (Mrode and Kennedy

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1993, Herd et al., 2003).

Records on feed intake and body weight are necessary for determining feed efficiency in growing animals. The optimum length of test for these traits could be assessed in chicken. However, there is no information in the literature on the optimum period to evaluate residual feed intake. Sapp et al. (2004) considered optimal recording periods when selecting for feed efficiency in breeding programs for egg production.

Feed intake and growth are longitudinal processes and random regression model methodology (Henderson, 1982, Schaeffer and Dekkers, 1994) can be used for modeling such data that are represented as curves. Knowledge of genetic and environmental (co) variances of curve parameters are useful in assessing the optimum length of test, gain and also understanding the genetic effects on body weight, feed intake and residual feed intake.

Random regression models (RRM) have been successfully used in dairy cattle to model longitudinal traits at different ages or stages of lactation (Jensen, 2001). It has been increasingly used for genetic evaluation of longitudinal traits in poultry (Anang et al., 2000, Kranis et al., 2007, Luo et al., 2007, Venturini et al., 2012, Wolc and Szwaczkowski, 2009 and Wolc et al., 2013). Generally, polynomial random regression (PRR) is fitted in chicken. The advantages of polynomial random regression models are better definition of contemporary groups and better adjustment for environmental effects. However, a potential disadvantage of the LeGendre orthogonal polynomials is a need to use high order polynomials and often implausible estimates of genetic parameters and other variance components, especially towards the extremes of the time periods modeled (Jensen, 2001, Meyer, 2005). In PRR, the order of polynomial must be carefully optimized to fit the available data. An alternative is the use of segmented polynomials or spline functions (Bohmanova et al., 2008, Meyer, 2005, Silvestre et al., 2006). Splines are piecewise polynomials joined at knots such that the overall function is continuous, with the number of knots and their location selected by the user (Hastie et al., 2009).

The objectives of the current study was: (1) to fit spline models for BW, FI and RFI along the trajectory (2) to provide an understanding of dynamics of genetic and environmental control of BW, FI and RFI in different parts of growth period, and (3) to determine the optimum recording period for FI and RFI in chicken.

2. Materials and methods

2.1. Experimental design and data collection

The F_2 resource population of chickens originated from a cross between a fast growing broiler male Arian line (AA) and Orumieh Iranian native fowl (NN). Arian broiler line was established in 1990 in Babol-Kenar, Babol, Iran, through importing four different lines, namely A, B, C and D, from the Netherlands (Shariatmadari, 2000). The male lines (A and B) have been selected for growth performance, feed conversion ratio and body conformation traits. For the female lines (C and D), the selection has been mainly carried out based on the reproductive traits and moderately on growth traits. All lines have been under selection for about 23 generations. Also, in 9 recent generations, the feed conversion ratio has been replaced by the residual feed intake in breeding program. The Orumieh chick is an Iranian native fowl with slow growth and high immune capacity that are distributed in the northwestern part of Iran. These birds are classified as dual-purpose breed and used for both egg and meat production. The F_1 birds were generated from the mating of AA ♂ × NN ♀ and NN ♂ × AA ♀ birds. The F_1 males from each reciprocal cross were each mated to 4–8 females from other families. A total of 450 F_2 chicken, produced in six different hatches, were available for the experiment.

Chicks were placed on the floor for 1 week with a photoperiod of 22 h of light and 2 h of darkness. Then, all chicks were transferred to individual cages. Birds were fed starter diet (22.8% CP and 3025 kcal of ME/kg) for the first two weeks, a crumbled grower diet (20% CP and 2960 kcal of ME/kg) between 3 and 7 weeks; and a crumbled finisher diet (18% CP and 3070 kcal of ME/kg) from 8 to 10 weeks of age. The chickens were not vaccinated against any disease. Feed and water were provided ad libitum. Individual performances of feed intake and body weight were measured weekly from week 2 to week 10.

2.2. Statistical analyses

The data were analyzed with a random regression models using B-spline functions. The following model was fitted for body weight and feed intake traits, respectively:

$$y_{ijkl} = Sex_j + Hatch_k + Week_l + \sum_{m=1}^{q} \alpha_{im}\phi(l) + \sum_{m=1}^{q} \beta_{im}\phi(l) + \sum_{m=1}^{q} \gamma_{im}\phi(l) + e_{ijkl}$$

$$y_{ijkl} = Sex_j + Hatch_k + Week_l + \sum_{m=1}^{q} \alpha_{im}\phi(l) + \sum_{m=1}^{q} \gamma_{im}\phi(l) + e_{ijkl}$$

For the RFI, the model was as follows:

$$y_{ijkl} = Sex_j + Hatch_k + Week_l + b_1(mbw) + b_2(wg) + \sum_{m=1}^{q} \alpha_{im}\phi(l) + \sum_{m=1}^{q} \gamma_{im}\phi(l) + e_{ijkl}$$

where, y_{ijkl} was body weight and feed intake of ith chicken, in sex j, born in hatch class k and in week l. Sex, hatch and week were considered to be fixed effects. The hatch was adjusted for the common environment influencing a group of birds hatched on the same date and managed in the same contemporary group. Using week as fixed effect ensures maximum flexibility of modeling in the general growth trajectory. The *mbw* and *wg* were metabolic body weight ($BW^{0.75}$) and body weight gain per week (g) and b_1 and b_2 represent the regression coefficients on metabolic body weight and weight gain, respectively. The $\varphi(l)$ was a β-spline function defined as a function of week (l), with q was a number of regression coefficient for each animal (3 for BW and FI and 5 for RFI trait) and α_{im}, β_{im} and γ_{im} were the random regression coefficients related to the additive direct, maternal permanent and permanent environmental effects of animal i, respectively. The residual (e_{ijkl}) of the models fitted for all traits with heterogeneous variance in 9 classes for each week that traits were recorded. The preliminary analysis indicated no significant effect of original parents on all traits and thus was removed from the final analysis.

Random regression was fitted with linear spline using 3 knots for body weight and feed intake. The knots were located at 2, 5 and 10 weeks for body weight and 2, 6 and 10 weeks for FI, based on preliminary results of multiple trait analysis that showed variance and covariance components change more after 5 and 6 weeks for BW and FI, respectively.

For RFI, a quadratic spline model was created with 4 knots at 2, 5, 7 and 10 weeks. The position of knots was determined correspond to the pattern of changes along the trajectory defined in the multi-traits animal models. A larger number of knots were placed in time periods with rapid changes in variances and in time periods with small changes in variance components a sparser distribution of knots were used. The number of parameters was, 21 for BW and FI, and 39 for RFI, respectively.

In matrix notation, the model can be described as:

$$\mathbf{y} = \mathbf{X}\,\mathbf{b} + \mathbf{Z_1 a} + \mathbf{Z_2 c} + \mathbf{Z_3 pe} + \mathbf{e}$$

Where, **y** is a vector of observations; **b** is the vector of fixed effects, **a** is the vector of random regression coefficients for the additive direct genetic effects; **c** is the vector of random regression