The effect of selection and sex on genetic parameters of body weight at different ages in a commercial broiler chicken population

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ABSTRACT

Data from 54 selection rounds (SRs) for growth rate in a selection line from Cobb breeding company was used for analysis with the objective to investigate the extent of sex by genotype interaction for body weight (BW) in a commercial broiler chicken population, estimate genetic parameters of BW at three different ages, and study the development in genetic variance for BW over several generations of selection. BW was measured at three different ages (t, t-4 and t-7 days) in different birds of both sexes. For the first 39 SRs, BW was recorded at t days, however, as selection continued the birds reached desired BW earlier and the weighing age was changed to t-4 days for 7 SRs and then to t-7 days for the last 8 SRs. A bivariate random regression model regarding BW in each sex as different traits using segmented linear splines and heterogeneous residual variance was used to estimate genetic parameters of BW across the selection trajectory via Gibbs sampling. The genetic variance and the heritability estimates of BW in males and females were found to be different at all three ages. The genetic correlation between BW measured in males and females was less than unity and decreased further as age at weighing was increased. This illustrated that BW in the two sexes should be considered as different but correlated traits and models for BW should account for a decreasing genetic correlation as the distance between the weighing ages increased. An increased genetic variance of BW along the selection trajectory in the first period was observed and genetic correlations between BW measured in different SRs gradually decreased as the distance between SRs increased. Genetic correlations lower than unity between BW at early and late SRs in the first period indicated that the genetic background of BW has gradually changed along the selection trajectory. This change probably contributes significantly to maintaining large levels of genetic variance in highly selected broiler populations.

1. Introduction

In broilers body weight (BW) and carcass quality traits have been under intensive selection for more than half a century, and are considered the most important economic traits in broiler breeding programs (Nassar et al., 2012). Production traits in broilers are influenced not only by the genotype of the individual but also by maternal effects (Tomasz et al., 2010).

Considerable variation is found in the literature concerning estimates of heritabilities and genetic correlations for growth traits in broilers (Prado-González et al., 2003) due to differences in recording systems and age at recording.

Different authors have regarded BW in male and female turkeys as different traits with a genetic correlation different from unity (Nestor et al., 2008). This is the same as sex by genotype interaction and this interaction has been reported to be related to different hormonal

regulations in male and female broilers (Towne et al., 1997). Chapuis et al. (1996) found a larger genetic correlation for BW in turkey birds between males and females at early ages than at later ages which are consistent with increased differentiation between the sexes as the chicken get older. Therefore models used for estimation of genetic parameters of BW in broilers need careful consideration of sex differences and different ages at measuring BW.

Selection, generally, reduces the genetic variability of a trait due to change in gene frequencies in response to selection. The reduction in genetic variance is likely to be small during the first few generations because gene frequencies change slowly unless there are genes with large effects (Falconer and Mackay, 1996). The outcome of selection over a long period is unpredictable because the outcome depends on the properties of the individual genes contributing to the response and also due to new variation caused by mutation (Falconer and Mackay, 1996). Sørensen (1986) observed that the genetic variance for growth rate in

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broiler chickens were not significantly reduced after several generations of selection which was explained to be due to generation of new genetic variation (mutation and recombination) and due to epistatic effects.

Random regression models (RRMs) are reported to be more accurate than multiple trait models (MTM) in estimating genetic parameters especially when the data set is large. Meyer (2004) reported RRMs to be up to 9.5% more accurate than MTMs.

Bohmanova et al. (2005) also reported the accuracy of RRMs over MTMs. According to their report MTMs and RRMs have similar accuracy when records occur at standard points (ages). However MTMs lose accuracy while RRMs retain accuracy when records occur at non-standard points (outside the pre-adjusted age intervals). They also reported an increased accuracy of RRMs when additional records are incorporated.

BW growth is a longitudinal process and random regression models (RRMs) are useful for the analysis of longitudinal data (Schaeffer, 2004). RRMs can also be used to study changes in genetic parameters over time (Schaeffer, 2004). An appropriate way of dealing with traits that are measured over a trajectory is to fit a set of random coefficients of time or weight for each animal to allow for individual variation in the course of the trajectory (Meyer, 1998). Cognizant of this facts, RRMs should also be a model of choice to study development in genetic variance (genetic parameters) of a trait over several generations of selection.

RRMs using Legendre polynomials have been widely used following Kirkpatrick et al. (1990), Meyer (2005). Legendre polynomials are able to model a variety of curves along a trajectory but they may have undesirable properties such as poor fit at the extremes of the trajectory and at points of the trajectory with few records (Misztal et al., 2000). However, poor fits in splines are more obvious than with Legendre polynomials and they can be better controlled by changing the number and positions of knots. Such models usually have good fit at the knots but may have poorer fit between the knots (Misztal, 2006). In addition a number of authors have reported RRMs with splines to have better numerical properties than Legendre polynomials since each coefficient in splines affect only a portion of the trajectory and only co-variables associated with two adjacent knots are non-zero while in Legendre polynomials of order n all co-variables are generally non-zero (Robbins et al., 2005). Splines are also advantageous in offering greater flexibility than the functions typically used in RRMs and are often used for smoothing data (Jensen, 2001).

Thus the objectives of the present study were to (i) investigate the extent of sex by genotype interaction for BW in a commercial broiler chicken population (ii) estimate the genetic parameters of BW at three different ages and (iii) study the development in genetic variance for BW over several generations of selection.

2. Materials and methods

2.1. Simulation study

A small simulation study was performed to test that if the complex random regression model we have used for the real body weight data can handle a continuous change in variance over time. Data on 30,000 birds were generated, so that each bird had 3 observations recorded at different ages according to the following model.

$$y_{ijk} = \mu + a_{oi} + a_{1i}(L_{1j}) + a_{2i}(L_{2k}) + e_{ijk}$$

Where, y_{ijk} is the trait of interest for bird i recorded at time point j and age k. a_{0i} is the intercept, a_{1i} and a_{2i} are breeding values of bird i for intercept, time effects and age effects, respectively. L_1 and L_2 are co (variables) for across bird time effects and within bird age effects, respectively, and e_{ijk} is the random residual. Co (variables) L_1 and L_2 were generated as follows:

$L_{1i} = ID_i/na$, where ID_i is the individual bird and na is the total

number of birds. The ID of individual birds were ordered by time t and this means that time effects gradually change over from the first bird to the last bird.

$L_{2k} = j_k/n_j$, where j_k is the kth record number (age) and n_j is the total number of records (ages). I.e. these effects gradually change with age of the birds. The birds were assumed to be independent and breeding values were assumed to be trivariate normal, with a 3 × 3 identity matrix as co (variance) matrix. The residuals were assumed to be normally distributed with unit variance. After the generation of the data, co (variance) components were estimated using the same model as used for simulation. Estimation of variance components were carried out using DMU software package (Madsen and Jensen, 2013). The simulation was replicated 150 times and the mean, standard deviation (SD) and standard error of the mean (SEM) of all co (variance) components estimated are reported.

2.2. Data

Data from 54 selection rounds (SRs) for growth rate in a selection line from Cobb breeding company was used for analysis. The number of broilers with BW and pedigree data was 646,703 and 649,483, respectively, and the pedigree covers about 8 generations back from the youngest animals. BW was measured at three different ages (t, t-4 and t-7 days) in different animals of both sexes. For the first 39 SRs BW was recorded at t days of age, however, as selection continued the birds reached desired BW earlier and the weighing age was changed to t-4 days for 7 SRs and then changed again to t-7 days for the last 8 SRs.

2.3. Statistical model

The statistical model in this study is explained in two parts. First initial multivariate animal models which lead to the final model are briefly explained and then the final bivariate random regression model in which the results are based is explained in detail. The initial model was used to test whether BW in the two sexes as well as BW in the three different weighing ages (periods) should be considered as the same trait or as different traits while the final model was used to meet the three objectives of the study as well as to confirm the two results found from the initial analysis.

The initial multivariate (6 trait) animal model included fixed effect SRH (1502 levels), which is an effect of hatch within selection round of the individual chicken, each SR containing 28 hatch batches. This was included in the model after testing significance of its effect using the generalized linear model of SAS. Direct genetic effect of the animal, maternal permanent environmental effect (pe) and residual environmental effects were included as random effects in the model. BW in each of the three ages was treated as different traits for both males and females. Therefore two traits in each of the three weighing ages resulted in a multivariate model with six traits included. Covariance components were estimated by REML using the AIREML module in the DMU software package (Madsen and Jensen, 2013).

The results of the multivariate analysis showed different heritability estimates of BW in the two sexes and genetic correlations of BW between the two sexes to be different from unity. The results of the analysis also showed that BW in the three weighing ages have different heritability estimates and genetic correlations of BW between the three different ages to be different from unity with decreased genetic correlation as the distance between the ages increased. Therefore, the initial model illustrated that BW in the two sexes as well as BW in the three different ages should not be considered as same trait in the subsequent analysis.

Based on the results from the initial model, a bivariate random regression model with piece-wise (segmented) linear splines which are not continuous across segments were used to estimate genetic parameters of BW along the trajectory of SRs using Gibbs sampling. Such a model can accommodate different parameters for each sex and different