Estimates of genetic parameters for monthly egg production traits in a commercial broiler female line

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Abstract

In this study, genetic parameters for monthly records of egg production, collected from weeks 24 to 55 on 16,830 hens during nine generations from a pedigreed commercial broiler female line, were estimated with single-trait, multiple-trait and repeated records animal models, using restricted maximum likelihood procedures. With and without age at sexual maturity as a covariate, two models were fitted to the data for each analysis. From the weekly productions, eight monthly records on a 28-day basis were created. The estimate of heritability from single-trait analysis for the first month’s record was relatively high (0.428), decreased to 0.150 and 0.092 in the second and third months, respectively, and then, with minor fluctuations, remained constant. Age at sexual maturity had a substantial influence only on heritability of the first month (0.192) and, to some extent, of the second month (0.103). Estimates of heritability and repeatability decreased from 0.067 and 0.379 to 0.029 and 0.251, respectively, owing to age at sexual maturity. Genetic correlations were generally positive, being relatively high to very high between adjacent monthly records, ranging from 0.725 (between the first and second month) to 0.986 (between the fourth and fifth month). These estimates between monthly records decreased as the time interval of the ages increased. The effect of age at sexual maturity on reduction of heritability of the first month’s record and of its genetic correlations with all other monthly records suggests that it is essentially necessary to be included in the model or that the analysis is carried out without the first month’s record.

Introduction

Many economically important traits, such as egg production in poultry species, are measured repeatedly over their reproductive lifetime. The pattern of genetic variations of these traits has been studied, using single-trait or multiple-trait analyses, treating each performance as different traits without or with covariance among them (Anang et al., 2000; Nurgiartiningsih et al., 2004), repeated-record analyses, considering each performance as repeated measurement of the same trait (Kranis et al., 2007; Wolc et al., 2007), fixed regression (Anang et al., 2001) and random regression analyses (Anang et al., 2002; Luo et al., 2007; Wolc and Szwaczkowski, 2009).

A considerable range in the estimates of heritabilities for the egg production traits has been reported in the literature. While Anang et al. (2000) found the estimates of heritabilities to be moderately low to relatively high (ranging from 0.18 to 0.49), Wolc et al. (2007) and Kranis et al. (2007) found them to be low (less than 0.12). Furthermore, most of these studies reported high estimates of heritability for the first two months of egg production traits, being more than 0.35 (Wolc et al., 2007; Nurgiartiningsih et al., 2004). The high estimates of heritability for these records have been attributed to the variation in age at sexual maturity (ASM) (Anang et al., 2000) and the rate of lay before peak (Nurgiartiningsih et al., 2004).

There is no published report related to the influence of ASM on the magnitude of genetic parameters, except for that of Luo et al. (2007), who fitted a single-trait random regression model with age at first egg and reported relatively low estimates for the heritabilities (less than 0.21) for monthly records of egg production. Therefore, the objective of our study was to estimate genetic parameters for monthly egg production records in a pedigreed broiler female line, under single-trait, repeated-records and multiple-trait analyses, without and with implementing ASM in the model.

Materials and methods

The data were collected from a commercial broiler female line, selected for nine generations (between 2000 and 2008), moderately for body weight and residual feed intake at seven weeks of age and mainly for the total number of chicks produced during 28 to 39 weeks of age, average egg weight at weeks 31 and 33 and ASM at 20 weeks of age. Body weight and residual feed intake were measured individually for each bird and taken from performance records of their half sibs and full sibs, respectively. Also, selection of the birds at 20 weeks of age was carried out based on information of their relatives collected for all previous generations.

Chicks were raised on full feed for the first seven weeks and then fed restricted amounts daily until 20 weeks. At 20 weeks of age, all selected birds (approximately 80 roosters and 720 to 880 hens per generation) were randomly assigned to floor pens, 9 to 11 hens plus 1 rooster per pen. The progeny of each generation were produced from up to four different hatches (weeks 43 to 50 for the first six generations and weeks 45 to 48 for the last three generations) through collecting hatching eggs over two consecutive weeks. For this line, weekly egg productions of 16,830 hens from approximately 1198 sires and 4564 dams were recorded individually in trap-nests for a period of 32 weeks, namely from 24 to 55 weeks of age. These productions were used to make eight monthly records, by summing each four consecutive weekly eggs (e.g. M1, the sum of the eggs produced from 24 to 27 weeks of age, to M8, the sum of the eggs produced from 52 to 55 weeks of age). For each weekly record, it was assumed that all missing
values are known and equal to zero. The structure of the data is shown in Table 1.

Statistical analyses

An animal model was used to estimate variance and covariance components for eight monthly records. Three different analyses, namely single-trait, multiple-trait and repeated-record analyses, were implemented using restricted maximum likelihood (REML) procedures. Considering each monthly record as a different trait, the following model was used for single-trait and multiple-trait analyses:

$$y_{ijkl}=\mu+G_{i}+H_{j}+a_{k}+e_{ijkl}$$

where $y_{ijkl}$ is the monthly record of the hen, $\mu$ is the grand mean, $G_{i}$ is the fixed effect of generation (nine levels), $H_{j}$ is the fixed effect of hatching time (four levels for the first six generations and two levels for the last three generations), $a_{k}$ is the random additive genetic effect of the hen and $e_{ijkl}$ is the random residual effect. For single-trait analysis, direct additive genetic and residual effects were assumed to be normally and independently distributed with mean 0 and variances $a^2_s$ and $e^2$, respectively, where $A$ and $I$ are the numerator relationship matrix and identity matrix, and $\sigma_a^2$ and $\sigma_e^2$ are additive genetic and residual variances. For multiple-trait analyses, $\text{Cov}(a_i, a_j) = \sigma_a^2 \delta_{ij}$ and $\text{Cov}(e_i, e_j) = \sigma_e^2 \delta_{ij}$ were assumed, where $\sigma_{a_{ij}}$ and $\sigma_{e_{ij}}$ are direct additive genetic and residual covariances among monthly records, respectively.

Assuming the eight monthly records as the same traits, a repeated-records animal model was fitted as follows:

$$y_{ijkl}=\mu+G_{i}+H_{j}+a_{k}+pe_{k}+e_{ijkl}$$

where $y_{ijkl}$ is the repeated monthly records of each hen (M1-8), $\mu$ is the grand mean, $G_{i}$ is the fixed effect of generation (nine levels), $H_{j}$ is the fixed effect of hatching time (four levels for the first six generations and two levels for the last three generations), $a_{k}$ is the random additive genetic effect of the hen, $p_{k}$ is the random permanent environmental effect of the hen and $e_{ijkl}$ is the random residual effect. The assumptions for the mean and variances of the random direct additive and residual effects were identical to the single-trait animal model. For the permanent environmental effect, the variance was assumed to be $1\sigma_p^2$, where $\sigma_p^2$ is the permanent environmental effect.

To investigate the effect of ASM on (co)variance components and genetic parameters, the data were reanalysed by fitting this effect as a covariate in all the models. For the present population, the average ASM with its standard deviation was 178.8±10.8 days and ranged from 162 days to 226 days. Estimates of variance and covariance components and their respective parameters were carried out using the DFREML program (Meyer, 2001). For all analyses, convergence was considered to be achieved when the variance of the function values was less than $10^{-7}$.

Results and discussion

Estimates of variance components and direct heritabilities of monthly records of egg production using single-trait analyses are presented in Table 2. Among all monthly records, M1 indicated the highest heritability (0.428) without considering ASM as a covariate in the model. This estimate substantially decreased to 0.150 in M2, while remaining relatively stable from M3 to M8 records with values from 0.075 to 0.092. In general, the magnitude of the estimates of heritabilities in our study was different to that reported in the literature. However, the pattern of the heritability changes for the monthly records over the laying period was relatively similar to the results of Anang et al. (2000, 2002), Nurgiartiningisih et al. (2004), Kranis et al. (2007) and Wolc et al. (2007), who reported a high estimate of heritability at the beginning of the laying period, decreasing in the second period, but remaining constant for the rest of the time points.

The estimates of heritability for the first and second monthly records decreased by about 55.14% (from 0.428 to 0.192) and 31.33% (from 0.150 to 0.103), respectively, through including ASM in the model (Table 2). The similarity of the overall pattern of the results, from excluding or including ASM in the model for heritability estimates, of M3 to M8 clearly indicated that such reduction in M1 and M2 may be attributed to the large influence of ASM on the magnitude of direct additive genetic, residual and phenotypic variances, for these two monthly records. Although similar conclusions have been drawn by Anang et al. (2000) and Nurgiartiningisih et al. (2004), no comparable estimate of heritability with and without fitting ASM was found in the literature. However, the pattern of reduction in the results of our study can be confirmed by the reports of Luo et al. (2007), who fitted age at first egg in a random regression model and obtained a very low estimate of heritability (0.06) for the first month’s egg production in a broiler dam line.

Table 1. Structure of data.

| Traits | n   | Mean ± SD | Min | Max | CV, % |
|--------|-----|-----------|-----|-----|------|
| M1     | 16830 | 8.98±6.28 | 0   | 27  | 69.96 |
| M2     | 16830 | 20.50±6.38 | 0   | 28  | 31.10 |
| M3     | 16830 | 18.97±6.46 | 0   | 28  | 34.06 |
| M4     | 16830 | 17.50±6.52 | 0   | 28  | 37.24 |
| M5     | 16830 | 15.87±6.90 | 0   | 28  | 43.44 |
| M6     | 16830 | 14.46±7.10 | 0   | 28  | 48.87 |
| M7     | 16830 | 13.73±7.37 | 0   | 26  | 65.09 |

M, monthly egg production; n, number of records; SD, standard deviation; CV, coefficient of variation.

Table 2. Estimates of variance components and heritabilities for monthly records using a single-trait animal model without and with age at sexual maturity.

| Traits | Without ASM | With ASM |
|--------|-------------|---------|
|        | $\sigma^2_a$ | $\sigma^2_e$ | $\sigma^2_p$ | $h^2±SE$ | $\sigma^2_a$ | $\sigma^2_e$ | $\sigma^2_p$ | $h^2±SE$ |
| M1     | 15.95       | 21.33    | 37.28      | 0.428±0.019 | 2.65       | 11.19       | 13.84       | 0.192±0.018 |
| M2     | 7.03        | 39.89    | 46.92      | 0.150±0.016 | 3.08       | 26.99       | 30.08       | 0.103±0.014 |
| M3     | 4.30        | 42.60    | 46.90      | 0.092±0.012 | 3.59       | 34.60       | 38.19       | 0.094±0.014 |
| M4     | 4.36        | 43.04    | 47.39      | 0.092±0.012 | 3.86       | 36.28       | 40.14       | 0.096±0.014 |
| M5     | 3.77        | 43.24    | 47.01      | 0.080±0.013 | 3.34       | 37.56       | 40.90       | 0.082±0.013 |
| M6     | 4.52        | 45.04    | 49.56      | 0.091±0.014 | 3.95       | 40.57       | 44.52       | 0.089±0.013 |
| M7     | 4.09        | 46.00    | 50.09      | 0.082±0.012 | 3.72       | 42.28       | 46.00       | 0.081±0.012 |
| M8     | 3.07        | 37.78    | 40.85      | 0.075±0.011 | 2.77       | 35.78       | 38.54       | 0.072±0.011 |

ASM, age at sexual maturity; M, monthly egg production; $\sigma^2_a$, direct additive genetic variance; $\sigma^2_e$, residual variance; $\sigma^2_p$, phenotypic variance; $h^2$, heritability; SE, standard error.
Table 3 indicates the estimates of variance components, heritability and repeatability of monthly egg production records from the repeatability animal model. Without ASM, direct additive genetic and permanent environmental effects of the hen accounted for 6.7% and 31.2% of phenotypic variation, respectively. By incorporating ASM in the model, these two components accounted for 2.9% and 22.2% of the phenotypic variance. Estimates of genetic and phenotypic variances, using a repeatability animal model, have rarely been reported for monthly records of egg production. Also, results for these estimates in the literature are, to some extent, inconsistent owing to differences in the definition of the trait, number of records available for analysis and population. Using a similar model (without ASM as a covariate) to that in our study, Wolc et al. (2007) reported repeatability estimates ranging from 0.04 to 0.22 for three lines of laying hens. Bennewitz et al. (2007) analyzed the liability to fertile eggs of eggs set by a Bayesian animal threshold model and reported values of 0.07 and 0.22 for heritability and repeatability, respectively. These estimates were found to be 7% and 24% for heritability and repeatability, respectively, for one week’s set of eggs averaged over the laying period (Wolc et al., 2009).

Estimates of genetic and phenotypic correlations among monthly records of egg production, derived from a multiple-trait animal model without and with ASM, are presented in Tables 4 and 5, respectively. In general, the genetic and phenotypic correlations between monthly records decreased as the time interval of the ages increased. Also, later ages indicated higher estimates for these correlations than early ages. These results are in agreement with the results of Luo et al. (2007), who used a random regression model and showed a lower correlation between the initial weeks of production with later stages of production in a broiler dam line. Without considering ASM in the model, all genetic correlations were positive and substantially high between adjacent records, being 0.725 (between M1 and M2), increasing to 0.986 (between M4 and M5) and then, with minor reduction, changing to 0.958 (between M7 and M8). This trend is similar to the estimates of genetic correlations between egg numbers of five different periods based on a random regression model, reported by Kranis et al. (2007), and between 12 monthly records based on a multivariate animal model, reported by Anang et al. (2000). For non-adjacent records, the genetic correlation of M1 with all other records was moderate, ranging from 0.358 with M7 to 0.406 with M3. These estimates were moderately high to very high, ranging from 0.614 (between M2 and M7) to 0.957 (between M4 and M6). The corresponding estimates of phenotypic correlations were lower than the genetic correlations, ranging from 0.183 (between M1 and M8) to 0.839 (between M6 and M7). While the estimates of genetic correlations are the greatest departure from the results of Nurjatiartiningi et al. (2004), in which the early part of the record tended to have a negative genetic correlation with production in later periods, they were consistent in direction and somewhat in magnitude with those reported by Anang et al. (2000) and Luo et al. (2007). For our study, the relatively low estimates of genetic correlations between M1, M2 and, to some extent, M3 and all other monthly records indicates that these performances are not influenced by the same genes and, therefore, considering each performance as the same record and fitting a repeatability animal model, seem to be invalid.

The estimates of genetic and phenotypic correlations between M1 and all other monthly records decreased largely (ranging from -0.024 to 0.137) and then, with minor reduction, changing to 0.958 (between M7 and M8). This trend is similar to the estimates of genetic correlations between egg numbers of five different periods based on a random regression model, reported by Kranis et al. (2007), and between 12 monthly records based on a multivariate animal model, reported by Anang et al. (2000). For non-adjacent records, the genetic correlation of M1 with all other records was moderate, ranging from 0.358 with M7 to 0.406 with M3. These estimates were moderately high to very high, ranging from 0.614 (between M2 and M7) to 0.957 (between M4 and M6). The corresponding estimates of phenotypic correlations were lower than the genetic correlations, ranging from 0.183 (between M1 and M8) to 0.839 (between M6 and M7). While the estimates of genetic correlations are the greatest departure from the results of Nurjatiartiningi et al. (2004), in which the early part of the record tended to have a negative genetic correlation with production in later periods, they were consistent in direction and somewhat in magnitude with those reported by Anang et al. (2000) and Luo et al. (2007). For our study, the relatively low estimates of genetic correlations between M1, M2 and, to some extent, M3 and all other monthly records indicates that these performances are not influenced by the same genes and, therefore, considering each performance as the same record and fitting a repeatability animal model, seem to be invalid.

The estimates of genetic and phenotypic correlations between M1 and all other monthly records decreased largely (ranging from -0.024 to 0.137 and 0.073 to 0.101, respectively) when ASM was included in the model. These changes among all M2 to M8 records were minor, suggesting that ASM is a main source of variation for the first month’s egg production record. However, no studies have been found to confirm the influence of ASM on genetic and phenotypic correlations in the literature.
Conclusions

The results of our study indicated that exclusion of ASM from the analysis of monthly records of egg production, especially for the first and, to some extent, second month’s egg production records after initiation of laying, resulted in overestimation of variance components and their corresponding parameters. Estimates of heritability from different analyses were generally low. The corresponding estimates for genetic correlations among all monthly records after the peak of the laying period were very high, which suggested that improvement of egg production is feasible through selection according to each monthly record from the third month onward.

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