Estimation of genetic parameters for body weight and feed efficiency traits in a broiler chicken population using genomic information.

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Summary

In this study, data from an experimental broiler chicken population from Cobb-Vantress were obtained for analysis. A total of 1000 broilers were tested in a feed efficiency (FE) experiment. Genetic parameters of body weight (BW) and FE traits were estimated using genomic information. The heritability estimates of BW and FE traits for this line were found to be lower than those reported in other studies, which are estimated based on pedigree relations. The observed low estimates in this study might be due to pre-selection of the broilers for BW before the FE experiment, weak relationship between broilers in the data and use of only genomic information to enable estimation of genetic parameters since there was no available pedigree information for this population.

Key words: Feed conversion ratio, body weight, broiler chicken, heritability, genomic information.

Introduction

Body weight (BW) and feed efficiency (FE) traits are economically important traits in broiler breeding programs. In animal breeding, knowledge of the genetic properties of the traits we are interested in is the first pre-requisite in establishing an efficient selection programme (Meyer, 1989a). Different studies reported estimates of genetic parameters for BW (Mebratie et al., 2017; Case et al., 2012; Aggrey et al., 2010; Khaldari et al., 2010) and FE traits (Case et al., 2012; Aggrey et al., 2010; Zhang et al., 2003) in different poultry populations. However, most studies estimated genetic parameters using pedigree relations, and, there is only limited information on genetic parameter estimates that are based only on genomic relations in poultry. The objective of this study is to estimate genetic parameters for BW and FE traits in an experimental broiler chicken population using genomic information.

Materials and Methods

A total of 5000 male broilers were fed from hatch to t days of age. At the age of t+1 days (BW t+1), broilers were weighed and the heaviest 1000 were selected for FE experiment. At the age of
t+4 days (BWt+4) broilers started the FE experiment for a duration of 7-days and final body weight (BWt+11) were recorded at the end of the experiment. After quality control, there were 852 broilers with BW and FE records. The genotypic data consists of 57636 SNPs that are distributed across 28 autosomes, two linkage groups, and the sex chromosome. Plink software was used for quality control of the genotypic data (Purcell et al., 2007). Finally, 45938 SNPs passed the quality control and retained for further analysis. More detailed information about the experimental set up is reported in, Reyer et al (2015). Genetic parameters of BW and FE traits were estimated using GCTA software (Yang et al., 2011). After calculating the genetic relationship matrix (GRM) between all pairs of samples using all the autosomal SNPs, genetic parameters were estimated with a univariate REML analysis using the following linear mixed model.

Where is the observation of individual i, \( \mu \) is the overall mean for each trait, is the random additive effect of SNP k, and is the random residual effect and, \( \sum \) denotes summation of all SNPs.

**Results and Discussion**

Descriptive statistics of the data and genetic parameters of BW and FE traits are presented in Table 1. The heritability estimates for BW traits in this study are found to be low, in the range from 0.00-0.18 with considerably high standard errors (Table 1) which is not in line with previous estimates, which are based on pedigree relations. Different authors have reported BW in broiler chickens at different ages to be moderately heritable in the range from 0.30-0.53 (Mebratie et al., 2017; Aggrey et al., 2010). The heritability estimates of FE traits in this study are low (0.03-0.09) with high standard errors, which might partly be due to the small sample size used for analysis (Table 1). The estimates are lower than pedigree based estimates reported in the previous studies. Aggrey et al. (2010) reported moderate heritability estimates for feed intake (0.48), body weight gain (0.51) and FCR (0.49) in broiler chickens. Case et al. (2011) also reported moderate heritability estimates for FCR (0.16) and feed intake (0.25) in turkeys.

The observed low estimates of genetic parameters in this study might be related to the data set used for analysis. In this study, broilers were pre-selected for BW and; only the heaviest 1000 entered the FE experiment. This might partly explain the observed low genetic variance and heritability estimates of the traits since selection generally results decrease in genetic variance (Falconer and Mackay, 1996). The other reason for the low heritability estimates might be the weak relationship between broilers in the data (Figure 1), with average and standard deviation of the off diagonal elements of the GRM, -0.001(0.03). I.e. there are only few half sibs and full sibs in the data. Reyer et al (2015) have identified QTL associated with BW and FE traits in this population. However, the weak relationship between individuals in the population circumvent accurate estimation of genetic variance. Therefore, genetic variance may be biased downwards and the high standard error of the estimates might reflect this bias. Yang et al. (2011) reported that, estimates of heritability using genomic relatedness in nominally unrelated individuals are typically substantially lower than known heritabilities, due to imperfect LD between causal and marker loci. Furthermore, this broiler population does not have known pedigree therefore only genomic information is used to enable estimation of the parameters, which only captures the contribution from causal variants that are in LD with the genotyped SNPs, while a pedigree-based
estimator, captures the contribution from all causal variants (Yang et al., 2011). This might also explain lower estimates and high standard errors of the parameters in our study compared to the estimates in the cited literatures, which are all pedigree-based estimates.

Conclusions

The heritability estimates of BW and FE traits in this study are found to be lower than those reported in previous studies, which are estimated based on pedigree relations. The observed very low heritability estimates in this study might be related to pre-selection of the broilers for BW before the FE experiment, weak relationship between broilers in the data and the use of only genomic information to enable estimation of the parameters since there is no known pedigree information for this broiler line.

Acknowledgments

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List of References

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Reyer, H., Hawken, R., Murani, E., Ponsuksili, S., Wimmers, K., 2015. The genetics of FE traits in a commercial broiler line, scientific reports. 5,16387.
Table 1. Descriptive statistics of the data and estimated genetic parameters for BW and FE traits.

<table>
<thead>
<tr>
<th>Traits</th>
<th>N</th>
<th>Mean (Kg)</th>
<th>SD</th>
<th>0.178 (0.075)</th>
<th>0.005 (0.002)</th>
<th>0.022 (0.002)</th>
</tr>
</thead>
<tbody>
<tr>
<td>BWt+1 days</td>
<td>852</td>
<td>2.27</td>
<td>0.16</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>BWt+4 days</td>
<td>852</td>
<td>2.59</td>
<td>0.19</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BWt+11 days</td>
<td>852</td>
<td>3.41</td>
<td>0.31</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Weight gain</td>
<td>852</td>
<td>1.41</td>
<td>0.26</td>
<td>0.027 (0.066)</td>
<td>0.001 (0.003)</td>
<td>0.037 (0.003)</td>
</tr>
<tr>
<td>Feed intake</td>
<td>852</td>
<td>0.82</td>
<td>0.20</td>
<td>0.090 (0.069)</td>
<td>0.006 (0.005)</td>
<td>0.061 (0.005)</td>
</tr>
<tr>
<td>FCR</td>
<td>852</td>
<td>1.75 Kg/Kg</td>
<td>0.28</td>
<td>0.051 (0.065)</td>
<td>0.004 (0.005)</td>
<td>0.075 (0.006)</td>
</tr>
</tbody>
</table>

FCR: Feed conversion ratio, : Heritability, Genetic variance, : residual variance.

Figure 1. Histogram of the off-diagonal elements of the genetic relationship matrix.