Preliminary studies on genetic backgrounds for fertility and hatchability in laying hens

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Segregation of single loci affecting reproduction traits of number of livestock species has been exhibited in literature. Hence, the mixed inheritance model (polygenes plus major gene) can be hypothesized for these fertility and hatchability in laying hens. To our knowledge, no Bayesian detection of single loci has been reported for these layer traits. The aim of this contribution was to verify the hypothesis about segregation of a major gene for fertility and hatchability by the use of the Gibbs sampling procedure. The data included 3070 pedigreed birds (2040 and 2015 recorded layers for fertility and hatchability, respectively) from one strain Rhode Island Red (R33) located on pedigree farm in Poland. Fertility (checked at 8-th day of incubation) and hatchability were registered only for dams. Hence, the number of observations per generation was limited. Binary data of single eggs has been summarized to proportion of fertilized egg (PFE) and proportion of hatched of set eggs (PHC). The analysis is based on two single linear animal models (including single locus effects and without). Relative large single gene variance and hypothetical genotype effects indicate mixed inheritance model for PFE. By contrast to PFE, the results for the second trait studied indicate no segregation of the major gene. As expected, these heritability estimates of both traits studied were low.

Key words: laying hens; reproduction ability; Bayesian analysis; major gene

Introduction

Long term selection focused on production traits affected depression of the so-called functional traits, including reproduction ones. A number of characters of the reproductive ability of poultry have been considered in literature to analyze final hatching efficiency (VAN KREY, 1993; LIPTOI and HIDAS, 2006). The first one is fertility. From the biological perspective it is both the sire and dam trait. In practice, fertility for single eggs is usually checked by candling on the 8-th day of incubation. JASSIM et al. (1996) reported that about 65% of embryonic mortality occurs in two phases with peaks at 4-th and 19-th day of incubation. Hence, the fertility is probably underestimated. Another very important trait is hatchability, summarized as fertility and incubation process. So, these traits are determined by many genetic and environmental effects.

On the other hand, segregation of single loci that affects the reproduction traits of a number of livestock species has been exhibited in literature (CASSADY et al., 2001; COBANOGLU et al. 2005). Hence, the mixed inheritance model (polygenes plus major gene) can be hypothesized for fertility and hatchability in laying hens. To our knowledge, no Bayesian detection of single loci has been reported for these layer traits.

The aim of this contribution was to verify the hypothesis about segregation of a major gene for fertility and hatchability by the use of the Gibbs sampling procedure.
Material and methods

The data included 3070 pedigreed birds (2040 and 2015 recorded layers for fertility and hatchability, respectively) from one strain Rhode Island Red (R33) located on a pedigree farm in Poland. A brief description of the data set is given in Table 1. Within-strain selection was based on the classical selection index, which included initial egg production, average egg weight, body weight and age at sexual maturity.

Fertility (checked at 8th day of incubation) and hatchability were registered only for dams. Hence, the number of observations per generation was limited. Binary data of single eggs have been summarized to proportion of fertilized egg (PFE) and proportion of hatched of set eggs (PHC).

Table 1. Population means and standard deviations of the traits studied

<table>
<thead>
<tr>
<th></th>
<th>PFE</th>
<th>PHC</th>
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<tbody>
<tr>
<td>average</td>
<td>0.87</td>
<td>0.69</td>
</tr>
<tr>
<td>SD</td>
<td>0.18</td>
<td>0.20</td>
</tr>
</tbody>
</table>

The Bayesian analysis is based on two single linear animal models. The main model (denoted as I) is as follows:

\[ y = X\beta + ZMw + Za + e, \]

where: \( y \) is the \((n \times 1)\) vector of observations, \( \beta \) is the \((p \times 1)\) vector of fixed effects (eight generations and four hatch periods), \( w \) is the \((3 \times 1)\) vector of random effects of single locus; it was assumed: \( w_{AA} = 0 \) and \( w_{aA} = -w_{AA} \); \( a \) is the \((q \times 1)\) vector of random additive polygenic effects; \( e \) is the \((n \times 1)\) vector of residuals; \( X \) and \( Z \) are design matrices relating fixed and genetic effects; \( M \) is a \((n \times 3)\) random matrix containing information on the genotype of each individual; each row of \( M \) has one of the following forms: \([1, 0, 0]\), \([0, 1, 0]\) or \([0, 0, 1]\) corresponding to genotypes AA, Aa or aa, respectively. Thus, \( Mw \) is the vector of single genotype effects.

Model II:

\[ y = X\beta + Za + e \]

where: \( y, \beta, a, e, X \) and \( Z \) – as above.

Parameters of both models were estimated by the Gibbs sampling, using the algorithm described by JANSS et al. (1995) and DOBEK et al. (1999). The following parameter estimates were analysed:

- polygenic additive genetic variance \( \sigma_a^2 \),
- residual variance \( \sigma_e^2 \),
- single genotype variance \( \sigma_w^2 = 2p_Ap_a w_{AA}^2 \),
- polygenic heritability \( h_a^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_e^2} \),
- total heritability \( h_t^2 = \frac{\sigma_a^2 + \sigma_w^2}{\sigma_a^2 + \sigma_w^2 + \sigma_e^2} \),
- single genotype effects \( w_{AA}, w_{aA} \),
- frequencies of alleles \( p_A, p_a \).
These estimates were obtained from averages of each ten step of 200000 samples. Based on initial trials, a burn-in-period of 50000 was used for all estimated parameters. The point and 95% interval estimates of heritabilities were based on the samples collected.

**Results and discussion**

The marginal posterior distribution of additive polygenic variance for PFE obtained via both models is shown in Figures 1a-1b, respectively. Larger polygenic variance was estimated from the second model. It likely resulted from overestimation of the variance due to omission of the single gene effect. The hypothesis is confirmed by a relatively large variance of single locus as shown in Table 2 by comparison of polygenic and total heritabilities for this trait. The posterior distribution of frequency of recessive allele is presented in Figure 3a whereas the respective distribution for genotype effects (AA) is given in Figure 4a. In general, the effects of genotypes correspond with the hypothesis of a mixed inheritance model for this trait. It must be recalled that PFE is measured as proportion, therefore the additive genotype effect equal 0.28 seems to be relatively large.

By contrast to PFE, the results for the second trait studied indicate no segregation of the major gene. It corresponds with the obtained estimates of additive polygenic variance (see Figures 2a-2b) and, first of all, with the small effect of AA genotype visualised in Figure 4b. So far, the polygenic and total heritability estimates of PHC are very similar (Table 2).

From a practical perspective, the reproductive characters are very difficult to include in genetic improvement programs because of their low heritability (see e.g. BRAH et al., 1999, SZWACZKOWSKI et al., 2000). On the other hand, hitherto existing approaches were usually based on the linear model, which may lead to underestimation of heritability. By the way, it must be recalled that similar tendencies have been observed in other livestock species (KARLSEN et al., 2000). However, methodology based on Bayesian estimation of parameters by threshold model often yields higher estimates of genetic parameters (DOBEK et al., 2003). Both fertility and hatchability have a simple binary phenotypic expression. They are called threshold traits. However, classical statistical methodology for threshold traits is based on the polygenic model with a normal distribution of unobserved liability. Unfortunately, this assumption does not hold in the case of segregation of a major gene. Therefore direct application of the threshold model methodology seems to be troublesome.
Figure 1a. Histogram of additive polygenic variance ($\sigma_a^2$) for PFE in model I.

Figure 1b. Histogram of additive polygenic variance ($\sigma_a^2$) for PFE in model II.

Figure 2a. Histogram of additive polygenic variance ($\sigma_a^2$) for PHC in model I.

Figure 2b. Histogram of additive polygenic variance ($\sigma_a^2$) for PHC in model II.

Figure 3a. Histogram of allele frequency ($p_a$) for PFE.

Figure 3b. Histogram of allele frequency ($p_a$) for PHC.
Table 2 The polygenic and total heritability estimates – marginal posterior means, lower and upper cutoffs for 95% credible sets

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Trait/model</th>
<th>Mean</th>
<th>Lower cutoff</th>
<th>Upper cutoff</th>
</tr>
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<tbody>
<tr>
<td>$h^2_{AA}$</td>
<td>PFE/I</td>
<td>0.203</td>
<td>0.118</td>
<td>0.303</td>
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<tr>
<td></td>
<td>PFE/II</td>
<td>0.141</td>
<td>0.073</td>
<td>0.237</td>
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<tr>
<td></td>
<td>PHC/I</td>
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<tr>
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<td>0.317</td>
<td>0.543</td>
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<tr>
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<td>PHC/I</td>
<td>0.281</td>
<td>0.145</td>
<td>0.436</td>
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References:


