Variation components of fertility in Spanish Landrace pigs

L. Varona*, J.L. Noguera
Area de Produccio Animal, Centre UdL-IRTA, C/Rovira Roure 177, 25198 Lleida, Spain

Received 31 December 1999; received in revised form 23 May 2000; accepted 23 May 2000

Abstract

Fertility is a discrete trait with two categories (1, successful mating, 0, unsuccessful mating). A Bayesian analysis with a binary threshold animal model has been performed with 18,695 AI mating records from 1987 to 1997, concerning 4085 sows and 187 boars. The pedigree included all individuals genetically linked with data. The binary response was modeled under a probit approach. The model for liability includes paternal and maternal genetic and permanent environmental effects, 54 herd-year–season and seven order of parity effects. Posterior mean (and standard deviation) for paternal heritability was 0.028 (0.014), for maternal heritability 0.038 (0.014), and 0.028 (0.009) and 0.072 (0.017) for ratios of paternal and maternal permanent environmental effects. Posterior mean (and standard deviation) of genetic correlation between paternal and maternal genetic effects was −0.513 (0.264). Differences between parities suggest that fertility is bigger in second parity than in the first one, and decrease in subsequent parities. © 2001 Elsevier Science B.V. All rights reserved.

Keywords: Fertility; Threshold model; Bayesian analysis; Pigs

1. Introduction

In pig production, success in conception is a crucial economic task. Delays in pregnancy or failure to conceive lead to a substantial loss in efficiency of production (Legault, 1978; Jalvingh et al., 1992). In breeding schemes, for a long time, selection efforts have been concentrated on growth, feed conversion ratio and carcass quality (Haley et al., 1988). More recently, selection has also been focused on prolificacy (Bampton, 1992; Ducos et al., 1992; Estany et al., 1995). Success in conception, as a measure of fertility, has not been included as an objective in current selection programs. However, indirect selection in sows has been systematically carried out by culling (Dagorn and Aumaitre, 1979; Dijkhuizen et al., 1989).

Evidence of genetic variation in conception rate has been detected in cattle (Saloniemi et al., 1986; Mantysaari et al., 1993). However, Elbers et al. (1996) found a very small risk of recurrence of failure of conception along different parities in the same sow, suggesting a small genetic component in female fertility.

The conception rate depends on a great number of factors. Apart from female fertility, it also depends on male fertility. Boar selection according to their ability to fertilize sows in natural or artificial insemination may have an economic interest. Moreover, genetic evaluation of boars in traits based on female fertility can provide a useful tool to select progeny. For that reason, knowledge of the genetic relation-
ship between male and female fertility may be of substantial interest for breeding programs (Land, 1978).

Nevertheless, fertility is a complex trait, its expression is discrete (1, successful mating, 0, unsuccessful mating). Following Thompson (1979) and Gianola (1982), methods for continuous data are not appropriate for discrete data. In recent years, Markov Chain Monte Carlo methods (Albert and Chib, 1993; Sorensen et al., 1995; Moreno et al., 1997) allow the analysis of categorical traits with models that consider its particular structure of probability. Furthermore, models with more than one genetic effect have been also developed (Varona et al., 1999). In this case, fertility is suspected of having genetic and permanent boar and sow effects.

The objective of this study is to determine the sources of environmental and genetic variability of fertility, measured as success of conception, allowing its consideration for inclusion in selection programs.

2. Materials and methods

2.1. The data

18 695 artificial insemination mating records, 15 191 successful (y = 1) and 3504 unsuccessful (y = 0), from 1987 to 1997, concerning 4085 sows and 187 boars, from two purebreed Landrace herds were used. An artificial insemination was determined as a success when the sow got pregnant (farrowing or abort). A more detailed description of data for different orders of parity is presented in Table 1. The pedigree included 5067 individuals genetically linked with data. In all cases the reproduction is carried out using double artificial insemination, always under the same technical conditions. Estrus detection was performed twice daily by boar presence.

2.2. The model

The assumed model for the underlying distribution of the liability (I) was:

\[ I = X\beta + Z_u u_m + Z_p p_m + Z_s s + e \]

where \( \beta \) are the systematic effects (54 herd-year-season and seven order of parity effects); \( u_m \) and \( u_p \) are the vectors of maternal and paternal genetic effects; \( p_m \) and \( p_p \) are the vectors of maternal and paternal permanent effects; \( e \) is the residual vector, and \( X, Z_u, Z_p, Z_s \) and \( Z_e \) are the incidence matrices that link liability with systematic, genetic and permanent environmental effects.

Response in fertility is modeled with a probit approach:

\[ f(y|I) = \prod_{i=1}^{n} f(y_i|t) \]

\[ = \prod_{i=1}^{n} [1(t_i < t)I(y_i = 0) + 1(t_i > t)I(y_i = 1)] \]

and

\[ f(I'|\beta, u_m, u_p, p_m, p_p, \sigma_e^2) = N(X\beta + Z_u u_m + Z_p p_m + Z_s s + \sigma_e^2) \]

where \( t \) is the threshold that defines the categories of response, \( n \) is the total number of data, \( \beta \) are the systematic effects (54 herd-year-season and seven order of parity effects); \( u_m \) and \( u_p \) are the vectors of maternal and paternal genetic effects; \( p_m \) and \( p_p \) are the vectors of maternal and paternal permanent effects; \( \sigma_e^2 \) is the residual variance (set to 1), and \( X, Z_u, Z_p, Z_s \) and \( Z_e \) are the incidence matrices that link liability with systematic, genetic and permanent environmental effects.

The following prior distributions were assumed:

\[ f(\beta) = U(-5,5) \]

\[ f(u_m, u_p | G) = N(0, A \otimes G) \]

\[ f(p_m | \sigma_m^2) = N(0, I \sigma_m^2) \]
and
\[ f(p_i | \sigma^2_p) = N(0, 1\sigma^2_p) \]
where \( A \) is the numerator relationship matrix and \( G \) is the matrix of (co)variance components, \( \sigma^2_m \) and \( \sigma^2_p \) are the permanent environmental variances for sows and boars, respectively.

Moreover, prior distributions of \( G, \sigma^2_m \) and \( \sigma^2_p \) where the following vague proper distributions
\[ f(G) = IW(SG, 5) \]
\[ f(\sigma^2_m) = \chi^{-2}(sm, 5) \]
\[ f(\sigma^2_p) = \chi^{-2}(sp, 5) \]
where \( sm = 0.1 \), \( sp = 0.1 \) and
\[ SG = \begin{bmatrix} 0.1 & 0 \\ 0 & 0.1 \end{bmatrix} \]

2.3. The Gibbs sampler

Bayesian analysis of the univariate and bivariate models were carried out with the Gibbs sampler algorithm (Geman and Geman, 1984; Gelfand and Smith, 1990; Tanner, 1993) to obtain autocorrelated samples from the joint posterior density and subsequently from the marginal posterior densities of all the unknowns in the model. The Gibbs sampler consists of an iterative sampling scheme of updated full posterior conditional distributions. The full posterior conditional distributions for the locations parameters (herd-year-season; parity effects; paternal and maternal breeding values and permanent environmental effects) were univariate normal distributions, the posterior distribution of the genetic (co)variance component is an inverted Wishart, and the posterior distributions of paternal and maternal permanent environmental variances were inverted chi-squares. Moreover, the posterior conditional distributions of augmented underlying variables are censored normal as described by Sorensen et al. (1995). A more detailed description of the distributions involved can also be found in previous studies (Wang et al., 1993, 1994; Sorensen et al., 1995).

The Gibbs sampler analysis was carried out through a simple chain of 700 000 iterations, after discarding the first 50 000. The analysis of convergence and the calculation of effective sample size followed the algorithms by Geyer (1992) and Raftery and Lewis (1992). All iterations of the analysis were used to compute posterior means and standard deviations so that all the available information from the output of the Gibbs sampler could be considered. Densities of marginal posterior distributions were calculated using the algorithms of Silverman (1986).

3. Results and discussion

3.1. Analysis of convergence of the Gibbs sampler

Convergence and effective sample size results for heritabilities, ratios of permanent environmental effects and genetic correlation between male and female fertility are presented in Table 2. The number of iterations to discard ranged from 2412 to 11 484 and the effective sample size (EFS) ranged from 52.8 to 357.4.

The number of iterations discarded in this analysis (50 000) were substantially greater than every value proposed by the algorithm of Raftery and Lewis (1992). The effective sample size computed by the algorithm proposed by Geyer (1992) was relatively high, with the exception of genetic correlation between maternal and paternal genetic effects. However, summaries of marginal posterior distributions can be estimated with a low Monte Carlo error.

3.2. Heritabilities and correlations

A summary of marginal posterior distributions for maternal and paternal heritabilities, ratios of permanent environmental effects and genetic correlation between paternal and maternal effects is presented in Table 3. As can be observed in this table, posterior means of paternal heritability and ratio of environmental permanent variation are low (0.028 and 0.028). Posterior mean of maternal heritability was

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Burn in</th>
<th>EFS</th>
</tr>
</thead>
<tbody>
<tr>
<td>( h^2_m )</td>
<td>8426</td>
<td>139.7</td>
</tr>
<tr>
<td>( h^2_p )</td>
<td>11 187</td>
<td>163.4</td>
</tr>
<tr>
<td>( p_{m} )</td>
<td>2412</td>
<td>289.8</td>
</tr>
<tr>
<td>( p_{p} )</td>
<td>4920</td>
<td>357.4</td>
</tr>
<tr>
<td>( r_{mp} )</td>
<td>11 484</td>
<td>52.8</td>
</tr>
</tbody>
</table>
also low (0.038), but the ratio of maternal permanent effects was slightly higher (0.072). These results show that 17% of variation of liability assuming a probit threshold model are determined by paternal and maternal sources of variation. Another 83% of variation in the underlying variable can be attributed to unknown sources of variation. As previously shown by Elbers et al. (1996), the female-based source of variation was small, and most of the causes for failure in AI can be attributed to external factors not based on the sow. These results are also in agreement with the ones obtained by Boichard and Manfredi (1994) in conception rate of dairy cattle. A non-reported analysis of sensitivity shows minor changes when different priors were assumed, as expected from the size of the database and the low amount of information provided by the selected priors.

A high negative genetic correlation between maternal and paternal genetic effects is obtained (posterior mean of −0.513) with 95.24% of posterior probability of genetic correlation smaller than 0. This result is surprising, because several studies in dairy cattle suggest very low genetic correlation (Hansen, 1979; Boichard and Manfredi, 1994). As pointed out by Boichard and Manfredi (1994), the estimate of this genetic correlation is very sensitive to extreme males. It must be noticed that, due to semen quality control, extreme sterile sires are not included. Moreover, it must be considered that only 187 boars are included in the analysis. However, this strong negative genetic correlation resembles the ones obtained by the maternal animal model (Meyer, 1992; Robinson, 1996), which also includes two genetic effects in the model. However, none of the physiological explanations of negative genetic correlations in the maternal animal model can be adapted in this case.

Moreover, a non-presented simulation study confirms the ability of the statistical procedure to recover the simulated parameters. Further research will be necessary to investigate the source of the strong estimated genetic correlation.

Results for order of parity in the underlying scale are presented in Table 4. Differences between parities suggest that fertility is greater in second parity than the first one, and decrease in subsequent ones. These results are in complete agreement with the direct observation of data (Table 1). Aging effects of the sire were not considered, because sires was kept in the insemination center for only about 8 to 10 months.

As a major consequence, the low heritability implies that efficiency of selection for these traits will be small. Genetic correlation with other traits of economic importance must be carried out to determine some alternatives for indirect selection.

**Table 3**  
Summary of marginal posterior distributions of heritabilities, percentage of permanent environmental variation and genetic correlation (mean, mode, posterior standard deviation (PSD), and percentiles at 1, 5, 50, 95 and 99%)

<table>
<thead>
<tr>
<th></th>
<th>Mean</th>
<th>Mode</th>
<th>PSD</th>
<th>1%</th>
<th>5%</th>
<th>50%</th>
<th>95%</th>
<th>99%</th>
</tr>
</thead>
<tbody>
<tr>
<td>$h^2$</td>
<td>0.028</td>
<td>0.025</td>
<td>0.014</td>
<td>0.005</td>
<td>0.007</td>
<td>0.025</td>
<td>0.053</td>
<td>0.069</td>
</tr>
<tr>
<td>$h^2$</td>
<td>0.038</td>
<td>0.036</td>
<td>0.014</td>
<td>0.007</td>
<td>0.016</td>
<td>0.036</td>
<td>0.064</td>
<td>0.074</td>
</tr>
<tr>
<td>$p^2$</td>
<td>0.028</td>
<td>0.026</td>
<td>0.009</td>
<td>0.010</td>
<td>0.013</td>
<td>0.026</td>
<td>0.043</td>
<td>0.053</td>
</tr>
<tr>
<td>$p^2$</td>
<td>0.072</td>
<td>0.071</td>
<td>0.017</td>
<td>0.026</td>
<td>0.050</td>
<td>0.071</td>
<td>0.099</td>
<td>0.112</td>
</tr>
<tr>
<td>$r_p^2$</td>
<td>−0.513</td>
<td>−0.560</td>
<td>0.264</td>
<td>−0.917</td>
<td>−0.867</td>
<td>−0.560</td>
<td>−0.010</td>
<td>0.261</td>
</tr>
</tbody>
</table>

**Table 4**  
Summary of marginal posterior distributions of differences with first parity

<table>
<thead>
<tr>
<th>Parity</th>
<th>Mean</th>
<th>Mode</th>
<th>Median</th>
<th>PSD</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>0.193</td>
<td>0.196</td>
<td>0.192</td>
<td>0.037</td>
</tr>
<tr>
<td>3</td>
<td>0.083</td>
<td>0.080</td>
<td>0.082</td>
<td>0.041</td>
</tr>
<tr>
<td>4</td>
<td>0.107</td>
<td>0.108</td>
<td>0.107</td>
<td>0.045</td>
</tr>
<tr>
<td>5</td>
<td>0.049</td>
<td>0.048</td>
<td>0.048</td>
<td>0.049</td>
</tr>
<tr>
<td>6</td>
<td>−0.009</td>
<td>−0.009</td>
<td>−0.010</td>
<td>0.054</td>
</tr>
<tr>
<td>&gt;6</td>
<td>−0.033</td>
<td>−0.035</td>
<td>−0.033</td>
<td>0.048</td>
</tr>
</tbody>
</table>

**Acknowledgements**

The authors wish to thank Joan Estany for his collaboration. This study has been funded by the IRTA (grant 21022).
References


