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Estimation of genetic and phenotypic parameters for bacteriological status of the udder, somatic cell score, and milk yield in dairy sheep using a threshold animal model

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ABSTRACT

The objective of this study was to estimate the genetic parameters for infection status (INF), as indicator of mastitis, SCS (i.e., log-transformed SCC), and milk yield (MY), by using a Gibbs sampling algorithm. The data comprised 17,843 test-day records of 2040 ewes. The pedigree file included 2948 animals. A bivariate variance component analysis was performed using the TM software. Fixed effects considered in the analysis were litter size, parity, flock by test-day interaction, year by season of lambing interaction, and stage of lactation; whereas the animal, and the permanent environmental effect within and across lactations were considered as random as well as the error. Flat priors were used for both fixed effects and variance components. Parameters were drawn from the posterior conditional distributions. The posterior means of heritability for MY, SCS and INF were equal to 0.14, 0.09, and 0.09, respectively; whereas the repeatability within lactation was around 0.30 for the three traits, and ranged between 0.29 and 0.41 across lactations. The genetic correlation between INF and SCS was equal to 0.93, suggesting that selection for low SCS would also lead to a reduced incidence of mastitis. On the other hand, the positive and moderate genetic correlation between mastitis and milk yield (0.59) confirms the antagonistic association between udder health and milk yield. Therefore, in breeding programs that emphasize milk yield, the unfavorable genetic correlation between milk yield and mastitis, may result in an increased incidence of the latter.

1. Introduction

Mastitis is one of the major diseases in dairy ewes and cows, which leads to economic losses, mainly due to discarded milk, reduced milk production and quality, early culling, and increased health care costs in both dairy ewes (Leitner et al., 2003, 2004) and cows (i.e., Bennett et al., 1999; Wellenberg et al., 2002). Mastitis has therefore motivated extensive research towards improved udder sanitation and mastitis control (El-Saied et al., 1998). However, genetic evaluation of mastitis is particularly difficult because of the low heritability and the categorical nature of the trait. As a consequence, correlated traits have been suggested to increase the efficiency of selection for mastitis resistance. In particular, SCC has been promoted as an indirect method of predicting mammary infections (Boettcher, 2005) and as a selection criterion to improve mastitis resistance (Gonzalo et al., 2003). It has been indeed demonstrated that mastitis causes an increase in SCC in small ruminants (Leitner et al., 2004; Sanchez et al., 1999; Zeng et al., 1997) and cattle

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(e.g., Heringstad et al., 2006; Olde Riekerink et al., 2007). Moreover, mastitis data are difficult and expensive to collect, whereas SCC is currently recorded in several milk recording schemes in both dairy sheep (Astruc et al., 2004) and cattle (Boettcher, 2005).

Estimates of genetic correlations between infection status (i.e., mastitis), SCC, and production traits are essential for the calculation of optimal selection indices. However, one problem in this sense is that the categorical nature of mastitis is usually ignored and genetic parameters have been often estimated using methodologies developed to analyze normally distributed traits, which is considered to be not optimal for categorical traits (e.g., Gianola and Foulley, 1983). The definition of mastitis as a binary trait, however, does not fully use all information provided by the data, because some animals can have more than one case of mastitis (Hinrichs et al., 2005). Rekaya et al. (1998) suggested the development of test-day models for longitudinal binary response for the analysis of mastitis field data in cattle. Test-day models should in fact allow considering the dynamic nature of mastitis, which is usually ignored by lactation models.

Whereas several estimates of genetic correlation between mastitis and SCC and production traits are available in cattle (Carlen et al., 2004; Koivula et al., 2005; Rupp and Boichard, 2003); such an information is lacking in sheep. Therefore, the objective of this study was to estimate the genetic parameters for infection status (INF), as indicator of mastitis, SCS (i.e., log-transformed SCC), and milk yield (MY), by using a test-day model implemented with a Gibbs sampling algorithm.

2. Materials and methods

All procedures involving animals were performed according to the principles and specific guidelines on animal care and welfare as required by Italian law.

2.1. Data and trait definitions

The original data consisted of 17,923 test-day records from 3406 lactations of 2046 ewes. Test-day records for MY and SCC were collected at approximately 1-month intervals, following an A4 recording scheme (ICAR, 2003), by the University of Palermo in four Valle del Belice flocks between 2004 and 2011. At milking time, cases of clinical mastitis were identified by the technicians and test-day weights and milk samples of those ewes were not considered. Clinical mastitis was reported for the evident signs of udder inflammation, or abnormal milk, or both.

All ewes were milked twice daily, and the milk of both daily milkings was analyzed; SCC were calculated as the weighted average of the morning and evening milking, where weighting is according to the corresponding milk yield. SCC was log-transformed to SCS, using Ali and Shook (1980) formula.

At the same time, milk samples were collected aseptically from each animal for bacteriological analyses, which were performed by conventional techniques, on 5% sheep blood agar plates, incubated at 37 °C, and examined after 10–24 h and 36–48 h incubation. Several bacteriological colonies were considered, mainly of genera *Staphylococcus*, *Streptococcus*, *Pasteurella*, *Escherichia*, and *Pseudomonas*. The information on the presence/absence of mastitis-causing pathogens was used to create an infection status variable, i.e. 0 if no pathogens were isolated, 1 otherwise, without considering the different pathogenicity of these bacteria. Ewes were considered infected if >5 colony forming units (CFU) per 10 μl of milk of one species of bacteria were isolated.

All test-day records used in the analysis were required to have information regarding MY, SCS, and INF. After editing, the data comprised 17,843 test-day records from 3000 lactations of 2040 ewes. The average number of test-day records per ewe per lactation was 4.84 ± 3.36. The pedigree file included 2948 animals. In addition to the 2040 animals with records, 158 sires and 750 dams were included.

2.2. Model

Bivariate variance component analyses were performed, in which the binary variable (i.e., INF) was analyzed with each of the two continuous traits (i.e., SCS and MY). For the infection status, the threshold concept was applied. The threshold model postulates an underlying continuous random variable, liability (λ), such that an observed binary response takes the value of 1 if λ is larger than a fixed threshold (τ), and 0 otherwise. Given the mean and the variance, liability was assumed to be normally distributed. Since with binary data the threshold (τ) and the residual variance (σ^2_e) are not identifiable, these parameters are usually set to arbitrary values: $\tau=0$ such that INF$=1$ if $\tau>0$ and 0 otherwise and $\sigma^2_e=1$. The model was formulated in a Bayesian context, in which the data vector was augmented with the unobservable liabilities. Liabilities were later integrated out of the joint posterior distribution, using Gibbs sampling.

The model for the observable continuous traits (either MY or SCS), denoted as y_1 and the augmented underlying liability for the INF, denoted as y_2, was as follows:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} Z_{\text{pew1}} & 0 \\ 0 & Z_{\text{pew2}} \end{bmatrix} \begin{bmatrix} \text{pe}_{\text{w1}} \\ \text{pe}_{\text{w2}} \end{bmatrix} + \\ + \begin{bmatrix} Z_{\text{pea1}} & 0 \\ 0 & Z_{\text{pea2}} \end{bmatrix} \begin{bmatrix} \text{pe}_{\text{a1}} \\ \text{pe}_{\text{a2}} \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

where X_1 and X_2 are the design matrices relating fixed effects in β_1 and β_2 to y_1 and y_2, respectively. The β's included effects of litter size (2 levels: single or multiple born lambs), parity (three levels: first, second, and third or higher parity), flock by test-day interaction (187 levels), year by season of lambing interaction (14 levels), where the season of lambing was coded as 1 if a ewe gave birth in the period January through June, otherwise it was coded as 2 (according to Riggio et al., 2007), and stage of lactation (9 levels, each of thirty days in milk, from weaning – i.e., ~30 days after lambing – to the end of lactation). The design matrices Z_{pew1} and Z_{pew2} are related to the random permanent environmental effect within lactation (indicated as pe_{w1} and pe_{w2}, respectively),

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