Genetic parameters and evaluation of the Tunisian dairy cattle population for milk yield by Bayesian and BLUP analyses

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Abstract

A Markov Chain Monte Carlo Bayesian method and BLUP analyses were used on Tunisian dairy cattle data. Data included 92,106 lactation records collected on 37,536 animals over 19 freshening years, from 1983 to 2001. Each record was partitioned into the fixed effects of herd-year, month of calving, and age-parity, a permanent environmental effect, an additive genetic effect, and a residual effect.

Posterior conditional distributions were determined for variance components and model effects. Solutions (BLUE) and posterior means for levels of herd-year, month of calving, and age-parity showed similar patterns. Posterior means of heritability and repeatability were $0.17 \pm 18 \times 10^{-5}$ and $0.39 \pm 8 \times 10^{-5}$, respectively. Posterior means of bull's breeding values were compared to bull's BLUP solutions. BLUP solutions were obtained using 0.17 and 0.39, estimated from the data, and 0.25 and 0.40 estimates for heritability and repeatability, respectively. Rank correlations between bull's posterior means and BLUP breeding values were 0.998 and 0.994 using genetic parameters estimated from the data and from the literature, respectively. This correlation coefficient was 0.995 between bull's BLUP solutions using either of the two sets of genetic parameters. © 2005 Elsevier B.V. All rights reserved.

Keywords: Milk yield; Bayesian estimation; BLUP; Genetic evaluation

1. Introduction

Systematic selection for production traits in the Holstein population dates back to the 1940's when sires were selected using daughters' averages. Nowa-days, sires and cows are selected following their ranking on the animal model genetic evaluations in most countries (Wiggans et al., 1988). Prediction of BLUP breeding values requires known variance components. BLUP solutions were also proven to vary with the data quality (Winkelman and Schaeffer, 1988), the inclusion of all or part of the data, the use of pedigree information (Van Der Werf and De Boer, 1990), and the evaluation method (Henderson, 1988).

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A variety of factors may influence the estimation of co-variances and consequently affect genetic evaluations. Continuous selection was theoretically proven to reduce the genetic variance (Bulmer, 1971). Variance component estimates were also shown to depend on the level of production (Hill et al., 1983; Foulley et al., 1990; Meyer, 1991; Misztal et al., 1992; Short et al., 1990; Visscher, 1991). The effects of heterogeneous variances and selection on the BLUP breeding values were discussed in several works (Short et al., 1990; Wiggans and Van Raden, 1991).

Bayesian analysis is gaining popularity because of its more comprehensive assumptions than those of classical approaches and its flexibility in resolving a wide range of biological problems. Differences in bias and incorrectly ranking animals between BLUP and Bayesian estimates have been investigated (Gianola and Fernando, 1986; Sorensen et al., 1994; Schenkel et al., 2002).

There are 3 distinct production sectors in Tunisia, the state herds, the cooperative herds, and farmers' herds. These herds differ with respect to management and milk production levels. Mean yield in 305 days in milk ranged from 5456 kg in the cooperative herds to 8337 kg in the farmers' herds (Rekik et al., 2003). Breeding decisions are based on yield or on an intra-herd index in few herds for cows and proof of foreign bulls for sires. Artificial insemination is the usual type of breeding. Rations for cows are made of oat hey and silage and occasionally green forage feedings (Egyptian Glover, ray-grass, sorghum) in some farms. The objectives of this study were i) to estimate genetic parameters of dairy cattle population for milk yield in Tunisia by Bayesian analysis; and ii) estimate breeding values in a non-random mating population by Bayesian and BLUP procedures.

2. Materials and methods

2.1. Data

Database of the National Centre for Genetic Improvement at Sidi Thabet, Tunis was used in the analysis. Data consisted of 107,607 completed lactation records collected on Holstein–Friesian cows over 19 freshening years from 1983 to 2001. A completed lactation corresponds to the period from freshening till effective drying of the cow. Each record included the cow's identification number, herd code, lactation number, date of freshening, test-day dates and yields, and unadjusted total milk yield (the quantity of milk collected over the whole milking period). Milk records were standardised for times of milking and days in milk to 305-day and two times milking per day following Djemali and Berger (1992). Pedigree information included the date of birth, the sire, the dam, and the herd of origin for each animal. After editing for missing identification number and birth date, and unreasonable production (<1000 kg/lactation), 92,106 records remained (Table 1). These records were of 37,536 animals of which 1818 were sires (AI sires) with at least two progenies. There were 34,282 cows with production records in 137 herds (Table 1) and in 843 herd-year groups. A minimum of 5 records was required in each herd-year group for the analysis. Around three fourth (74.3%) of cows with production records had first lactations. Cows with missing first lactation records might be explained by the increase of the number of herds enrolled in data recording system in the 1990's (Table 1) and not all cows of those herds were in their first lactations when recording began.

2.2. BLUP analysis

The linear mixed model used for the analysis was:

$$\mathbf{y} = \mathbf{X}\boldsymbol{b} + \mathbf{Z}\boldsymbol{a} + \mathbf{ZQ}\boldsymbol{g} + \mathbf{W}\boldsymbol{p} + \boldsymbol{e}. \tag{1}$$

Where $\boldsymbol{y}$: is a vector of milk yield collected in 305 days with 2 times milking per day, $\boldsymbol{b}$: is a vector of fixed effects, $\boldsymbol{a}$: is a vector of additive genetic effects, $\boldsymbol{p}$: is a vector of permanent environmental effects, $\boldsymbol{g}$: is a vector of group effects, and $\boldsymbol{e}$: is a vector of random residual effects. Fixed effects included herd-year, month of freshening, and age-parity. $\mathbf{X}$, $\mathbf{Z}$, $\mathbf{W}$, and $\mathbf{ZQ}$ are incidence matrices relating a record to fixed environmental effects in $\boldsymbol{b}$, to a random animal effect in $\boldsymbol{a}$, to a random permanent environment in $\boldsymbol{p}$, and to a genetic group in $\boldsymbol{g}$, respectively. Unknown parents were replaced by genetic groups. The genetic groups were defined by sex and birth year of animals with