



Genetic parameters of reproductive traits in Tunisian Holsteins

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Abstract. Multi-trait Bayesian procedure was used to estimate genetic parameters for reproductive traits in Tunisian Holstein cows. A total of 31 348 lactations of the calving years 2005 to 2012 were analyzed. Fertility traits were the calving interval (CI), days open (DO), days to first insemination (DFI), days from first insemination to conception (FIC), and number of inseminations per conception (NI). Posterior means of heritabilities of CI, DO, DFI, FIC, and NI were 0.047, 0.03, 0.025, 0.024, and 0.069, respectively. Posterior means of repeatabilities of the same respective traits were 0.106, 0.094, 0.051, 0.036, and 0.17. Genetic correlations among female fertility traits were also computed. Calving interval and DO had the highest genetic correlation estimate (0.85) because they have overlapping genetic meanings. The lowest genetic correlation estimate (–0.25) was found between DFI and NI. Genetic parameter estimates are low and are even lower than those reported in most literature, implying that more focus should be put upon improving the management of reproduction in dairy cattle herds in Tunisia.

1 Introduction

Female fertility is one of the major factors affecting longevity in dairy cattle. Nevertheless, dairy cattle breeding programs have focused on milk production traits for a long time. Numerous authors have reported antagonistic genetic relationships between reproductive traits and milk yield traits (Wall et al., 2003; Windig et al., 2006; Abe et al., 2009; Albarràñ-Portillo and Pollot, 2013; Yamazaki et al., 2014). For these reasons, the selection programs are often confronted with the challenge of maintaining satisfactory reproductive performances and high levels of milk production (Weigel and Rekaya, 2000). Therefore, it is necessary to include fertility traits in the selection programs in order to improve fertility or minimize the deterioration of these traits (Liu et al., 2008; Ghiasi et al., 2011). Heritability estimates of reproductive performance were low and ranged from zero to 0.1 (Muir et al., 2004; Sewalem et al., 2010; Ghiasi et al., 2011). Despite the low heritabilities of fertility traits, numerous studies showed an evident genetic variation revealed in fertility traits

and therefore genetic improvement of cow fertility may be possible (Weigel and Rekaya, 2000; Norman et al., 2009). In Tunisia, milk yield has traditionally been the most important breeding objective, with little or no focus on functional traits (Rekik and Ben Gara, 2004). Plans for the improvement of the national milk production have been developed in Tunisia since 1960 through the use of semen from high-merit sires and the importation of pregnant heifers from the United States and European countries such as Germany and the Netherlands (Djemali and Berger, 1992; Rekik and Ben Gara, 2004; Rekik et al., 2008). Reproductive data were included in the recording scheme in the late 1990s (Rekik et al., 2008). Estimates of genetic parameters for milk, fat, and protein yields from Tunisian data are reported in several publications (Ben Gara et al., 2006; Hammami et al., 2007, 2008). However, genetic parameters for fertility traits were rarely investigated (M'Hamdi et al., 2011). Most of the culling has consistently been explained with unsatisfactory fertility performances. Tunisian dairy herds are characterized by small sizes and low production levels. Furthermore, it is impor-

tant to note that Tunisia is characterized by constraining climatic conditions. The climate in Tunisia varies from arid in the south to humid in the north, and hot summers coupled with high humidity and cool winters are common (Djemali and Berger, 1992). Precipitation is variable from one year to another. The average maximum temperature varies from 16.2 °C in winter to 32.2 °C in summer. Average annual rainfall is less than 420 mm (Hammmami et al., 2008). The specific objective of this study was to estimate the genetic parameters of several reproductive traits and investigate the genetic correlations among these traits under Tunisian climatic conditions using Bayesian analysis with a multiple-trait animal model.

2 Materials and methods

2.1 Data

Data were obtained from the Tunisian Genetic Improvement Centre, Livestock and Pasture Office (OEP), Tunis, and included 37 994 records of one to six parities in 11 456 Tunisian Holstein cows which calved between 2005 and 2012 in 119 herds. All records used in the present study included the following five reproductive traits: calving interval (CI), days open (DO), days to first insemination (DFI), days from first insemination to conception (FIC), and number of inseminations per conception (NI). Data were edited based on González-Recio and Alenda (2005). Non-informative, erroneous, and records judged to be biologically unreasonable were discarded as follows.

1. Cows without pedigree information were omitted.
2. Cows for which the days to first insemination were < 25 or > 160 were not considered.
3. Cows for which the interval between consecutive calvings was < 300 or > 600 were omitted.
4. Cows for which the days from Calving to conception were > 330 were excluded.

Limits were set for DFI, FIC, NI, DO, and CI in order to exclude from present analysis records that seemed out of range because of potential editing errors and/or that reflected serious management deficiencies. After editing, 31348 records remained. Heifer fertility records were discarded from the data file. The pedigree file used in this analysis included the cow's identification, the dam, the sire, the date of birth of each animal, and the herd origin for each animal. Descriptive statistics are given in Table 1.

2.2 Genetic analysis and statistical model

Genetic and environmental factors included in the model were designed to reflect data structure and were as inferred from the literature reporting on reproduction data analyses

Table 1. Number of records, mean, standard deviation (SD), minimum, and maximum for CI, DO, DFI, FIC, and NI.

| Trait | No. | Mean | SD | Min. | Max. |
|---------|--------|---------|--------|------|------|
| CI (d) | 31 348 | 405 600 | 63 612 | 301 | 587 |
| DO (d) | 31 348 | 127 186 | 63 519 | 31 | 299 |
| DFI (d) | 31 348 | 78 787 | 28 467 | 31 | 149 |
| FIC (d) | 31 348 | 48 416 | 59 920 | 0 | 264 |
| NI | 31 348 | 2058 | 1213 | 1 | 5 |

(Muir et al., 2004; Sewalem et al., 2010; Ghiasi et al., 2011, M'Hamdi et al., 2011). Data were analyzed with a five-trait animal model. The matrix notation of the model is as follows:

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{a} + \mathbf{W}\mathbf{p} + \mathbf{e},$$

where \mathbf{y} is the vector of reproductive traits, \mathbf{b} is the vector of fixed effects, \mathbf{a} is the vector of additive genetic effects, \mathbf{p} is the vector of random permanent environmental effects, and \mathbf{e} is the vector of residual effects. \mathbf{X} , \mathbf{Z} , and \mathbf{W} are the corresponding incidence matrices.

$$\mathbf{y} | \mathbf{b}, \mathbf{a}, \mathbf{p}, \mathbf{e} \sim N(\mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{a} + \mathbf{W}\mathbf{p}, \mathbf{R}),$$

and
$$\begin{bmatrix} \mathbf{a} \\ \mathbf{p} \\ \mathbf{e} \end{bmatrix} \sim N(\mathbf{0}, \mathbf{V}).$$

$$\mathbf{V} = \begin{bmatrix} \mathbf{G} \otimes \mathbf{A} & 0 & 0 \\ 0 & \mathbf{P} \otimes \mathbf{I} & 0 \\ 0 & 0 & \mathbf{R} \otimes \mathbf{I} \end{bmatrix},$$

where \mathbf{G} and \mathbf{P} are 5×5 genetic and permanent environmental var-covariance matrices, respectively. \mathbf{A} is the additive genetic relationship matrix among the animals; \otimes is the Kronecker product function. \mathbf{R} is a 5×5 residual covariance matrix. \mathbf{I} is the identity matrix of the order N . Vector \mathbf{b} of fixed effects includes herd \times year of first insemination, month of first insemination, and parity \times age at first insemination (age at first insemination nested within parity). A Bayesian approach was used to estimate genetic parameters for the five traits analyzed (Sorensen and Gianola, 2002) assuming that the multivariate normal prior distributions of the vector of additive genetic values (\mathbf{a}), the vector of the permanent environmental effects (\mathbf{p}), and the vector of the residual effects (\mathbf{e}) are

$$\mathbf{a} | \mathbf{G} \sim MVN(\mathbf{0}, \mathbf{G} \otimes \mathbf{A}),$$

$$\mathbf{p} | \mathbf{P} \sim MVN(\mathbf{0}, \mathbf{P} \otimes \mathbf{I}),$$

$$\mathbf{e} | \mathbf{R} \sim MVN(\mathbf{0}, \mathbf{R} \otimes \mathbf{I}).$$

The fully conditional posterior distributions of the additive, permanent environmental, and residual variances are inverse Wishart distributions (Sorensen and Gianola, 2002). The marginal distribution of each parameter was calculated

Table 2. Summary of marginal distributions of the heritability of CI, DO, DFI, FIC, and NI. HPD: high posterior density region.

| Traits | Mean | Mode | Median | SD | HPD (95 %) |
|--------|-------|-------|--------|-------|----------------|
| CI | 0.047 | 0.047 | 0.045 | 0.013 | [0.019, 0.094] |
| DO | 0.030 | 0.030 | 0.031 | 0.010 | [0.010, 0.063] |
| DFI | 0.025 | 0.025 | 0.024 | 0.009 | [0.007, 0.043] |
| FIC | 0.024 | 0.024 | 0.023 | 0.007 | [0.014, 0.041] |
| NI | 0.069 | 0.070 | 0.070 | 0.010 | [0.037, 0.123] |

Table 3. Summary of marginal distributions of the repeatability of CI, DO, DFI, FIC, and NI.

| Traits | Mean | Mode | Median | SD | HPD (95 %) |
|--------|-------|-------|--------|-------|----------------|
| CI | 0.106 | 0.112 | 0.106 | 0.026 | [0.039, 0.191] |
| DO | 0.094 | 0.094 | 0.096 | 0.023 | [0.023, 0.187] |
| DFI | 0.051 | 0.050 | 0.051 | 0.013 | [0.017, 0.185] |
| FIC | 0.036 | 0.035 | 0.036 | 0.009 | [0.020, 0.058] |
| NI | 0.170 | 0.163 | 0.170 | 0.026 | [0.104, 0.191] |

using a Gibbs sampling scheme as implemented by Misztal et al. (2002). Gibbs Sampling consisted of 50 000 iterations, and the first 5000 samples were discarded as burn-in period.

3 Results

3.1 Heritability and repeatability estimates

Summary statistics (mean, mode, median, standard deviation, and 95 % highest-probability density interval) are shown in Table 2. Heritability estimates for all traits were lower than 0.1 and ranged from 0.024 for FIC to 0.069 for NI. Both traits, i.e., DFI and FIC, had comparable heritability estimates close to 0.025. The heritability estimate was 0.047 for CI and was 0.03 for DO. Estimates of repeatability are given in Table 3. All fertility traits in this study had quite low repeatability estimates, ranging from 0.036 to 0.17. The CI and DO traits had similar repeatability values (0.1). The FIC had the lowest repeatability (0.036) among all traits. The repeatability estimates of all traits were almost double those of corresponding heritability values.

3.2 Genetic correlations

Table 4 shows genetic and permanent environmental correlations among fertility traits. Most of the genetic correlations obtained in the current study were high and positive. The approximate genetic correlation between CI and DO was 0.85 ± 0.021 , whereas the genetic correlations of DFI with FIC and NI were moderate and negative, estimates were -0.13 and -0.25 , respectively. The CI was genetically correlated to all traits with high correlation estimates, ranging from 0.77 with NI to 0.85 with DO. Permanent envi-

ronmental correlations among fertility traits were comparable in sign and in magnitude as genetic correlations among the same traits, but the permanent environmental values estimated are associated with a relatively high SD (Table 4). Permanent environmental correlation estimates were above 0.6 with the exception of the negative correlation of DFI with FIC (-0.09) and NI (-0.19). Permanent environmental correlation estimates associated with DFI were consistently higher than estimates of genetic correlations for DFI with CI (0.77 vs. 0.67) and for DFI with DO (0.76 vs. 0.67).

4 Discussion

Mean heritability estimates were in the same range as those found in several studies from various populations (Hansen et al., 1983; Campos et al., 1994; González-Recio and Alenda, 2005; Liu et al., 2008; Sewalem et al., 2010; Ghiasi et al., 2011). Ghiasi et al. (2011) reported 0.074 ± 0.004 , 0.076 ± 0.004 , 0.044 ± 0.004 , 0.058 ± 0.005 , and 0.046 ± 0.004 for CI, DO, FIC, DFI, and NI, respectively, using the same model. They included also categorical and binary traits for female fertility in Iranian Holsteins. Heritability estimates obtained for reproductive traits in the current analysis are comparable to those reported by M'Hamdi et al. (2011). These authors reported 0.032, 0.041, and 0.063 estimates for DFI, DO, and CI, respectively, using a multiple-trait animal model. However, results from the current study on heritability estimates are smaller than those found by Sewalem et al. (2010). Running bivariate analyses they found heritability estimates of 0.08 ± 0.02 and 0.05 ± 0.01 for DFI and FIC, respectively. Yamazaki et al. (2014) analyzed the reproductive traits of Japanese Holstein cows using a multiple-trait linear model and found heritability values for DO of 0.07 ± 0.01 for the first lactation, 0.06 ± 0.01 for the second lactation, and 0.12 ± 0.01 for the third lactation. Our study indicates that CI had the highest heritability estimate among the interval traits 0.047 ± 0.013 and therefore has the potential to be included in genetic improvement programs. However, CI is strongly influenced by management systems. Furthermore, several studies reported that the heritability of fertility traits in hot climates was lower than in temperate climates. Hansen et al. (2011) also found that heat stress was the major cause of the decrease in reproductive performances through physiological adaptations ensuring a better thermoregulatory ability. The repeatability estimates of all traits were twice as high as heritability estimates, indicating an important effect of the permanent environmental components on each of the studied trait. The results of the present study on repeatability estimates were in agreement with the repeatability values estimated by Yagüe et al. (2009) for fertility traits in beef cows using the Bayesian methodology. Most of the genetic correlations among fertility traits obtained in the current study were high and positive, in agreement with those found by other researchers for similar traits (Campos et al., 1993; González-

Table 4. Genetic (above diagonal) and permanent (below diagonal) correlations among fertility traits with standard errors in parentheses.

| | CI | DO | DFI | FIC | NI |
|-----|--------------|--------------|---------------|---------------|---------------|
| CI | | 0.85 (0.021) | 0.67 (0.020) | 0.79 (0.011) | 0.77 (0.013) |
| DO | 0.81 (0.023) | | 0.67 (0.013) | 0.85 (0.020) | 0.21 (0.023) |
| DFI | 0.77 (0.010) | 0.76 (0.020) | | -0.13 (0.018) | -0.25 (0.016) |
| FIC | 0.81 (0.026) | 0.83 (0.028) | -0.09 (0.021) | | 0.83 (0.022) |
| NI | 0.83 (0.033) | 0.47 (0.032) | -0.19 (0.011) | 0.83 (0.010) | |

Recio and Alenda, 2005; Jamrozik et al., 2005; Ghiasi et al., 2011). The strongest genetic correlation was observed between CI and DO (0.85 ± 0.021) because these two traits may be considered as the same trait (González-Recio and Alenda, 2005). Conversely, a few studies, such as Toghiani Pozveh et al. (2009) found no genetic relationships among fertility traits. Toghiani Pozveh et al. (2009) using a multiple-trait analysis reported low genetic correlation estimates of DO with CI and DFI of 0.111 and 0.004, respectively, and suggested that these fertility traits are genetically independent. Large permanent environmental correlation estimates (0.6–0.83) were found among fertility traits, except for DFI with FIC and NI, where estimates were low and negative. However, permanent environmental correlation estimates of DFI with CI and DO were high, ranging from 0.76 to 0.77. These estimates are comparable to those found by Yagü et al. (2009) and may be explained by the fact that DFI were greatly dependent on herd management (health care, estrus synchronization, etc.). There are several studies regarding the detrimental impact of the health status and increased production levels on fertility. Rekik et al. (2008) documented that both intervals DFI and FIC increased by 1.3 to 2 days for each unit increase in somatic cell score in Tunisian Holsteins. Melenendez and Pinedo (2007) reported that for each 100 kg increase in a 305-day milk yield, the DO increased by 0.6 and the conception rate at first insemination decreased by 0.9 %.

5 Conclusions

Genetic parameters for female fertility traits were estimated by Bayesian analysis in the Tunisian Holstein population. Heritability and repeatability estimates were low but comparable to most previously reported research results, especially those found in the same population. The improvement of reproductive performances of the Tunisian Holsteins should focus not only on putting more emphasis on fertility traits in selection but also on upgrading the management of the reproduction of cows.

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