Livestock Science xxx (2011) xxx–xxx

Contents lists available at ScienceDirect

Livestock Science

journal homepage: www.elsevier.com/locate/livsci

Short communication

Genetic variance components for female fertility in Iranian Holstein cows

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ARTICLE INFO

Article history:
Received 4 November 2010
Received in revised form 28 January 2011
Accepted 28 January 2011
Available online xxxx

Keywords:
Genetic parameters
Fertility
Linear model
Threshold model
Bayesian
Iranian Holstein

ABSTRACT

Linear and threshold animal models were used to estimate genetic parameters for reproductive traits in Iranian Holstein cows. Reproductive traits included: days from calving to first service (DFS), number of inseminations to conception (INS), calving interval (CI), days open (DO), and interval between first and last insemination (IFL), pregnancy rate (PR), and success to first insemination (SF). A total of 72,124 records in parity 1 to 6 from 27,113 cows from 1981 to 2007 were used. Estimated heritabilities for reproductive traits were low (below 0.1); SF (0.029) had the lowest and DO and PR had the highest (0.076) heritability. Heritabilities obtained for interval traits were higher than those for categorical and binary traits. Strong genetic correlations were estimated between fertility traits. The results from current study show that fertility is a complex trait and several measurements related to fertility should be combined in a fertility index for selection purposes.

1. Introduction

Profitability of dairy herds strongly depends on reproductive performance (De Vries, 2006). Effects of undesirable reproductive performance include: increase in calving interval, involuntary culling rate, replacement cost and decreased milk production and therefore reduced net returns (Bagnato and Oltenacu, 1994). In the past decades, more attention has been placed on milk production in selection programs worldwide, which has caused a decline in female fertility due to the antagonistic genetic relationship between milk production and fertility (Liu et al., 2007). Therefore, it is necessary to include fertility traits in the breeding programs for improving fertility or stopping its downward genetic trend (Liu et al., 2007).

Fertility is a complex trait and different related measurements may be recorded in dairy herds, e.g. DFS, INS, CI or DO (Jorjani, 2007). Genetic evaluation of female fertility is implemented in different manners across countries. Some countries evaluate only one of the traits whereas other countries combine different fertility traits into a selection index (Weigel and Rekaya, 2000; VanRaden et al., 2004).

Genetic response for fertility traits is expected to be small due to low heritabilities as shown in many studies. Pryce and Veerkamp (2001) reviewed estimates of heritabilities for a wide range of fertility traits and found estimates from 0.4% for non return rates to 9.8% for CI, with average values under 5% for all traits in Holstein cows. Wall et al. (2003) estimated heritability of 3.3% for CI, 3.7% for DFS and 2% for INS. In Canada, Jamrozik et al. (2005) reported heritability estimates for 16 reproductive traits. Among reproductive traits in Canadian Holstein, non return rate to 56 d had the lowest (0.03) and age at first service had the highest (0.13) heritability. Although heritability estimated for fertility traits is low, these

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doi:10.1016/j.livsci.2011.01.020

traits have shown high genetic variation and therefore selection for fertility traits may be possible (Makgahlela et al., 2007).

The dairy cattle population in Iran has undergone a strong selection for milk production through the use of semen from high merit sires in the last decades and a decline in the fertility might also be expected. The use of selection indices that include fertility is foreseen. Most estimates of heritabilities and genetic correlations in Holstein animals have been obtained in Western countries under more intensive systems. Toghiani Pozveh et al. (2009) estimated genetic parameters for CI, DFS and DO in traits collected by the Animal Breeding Center of Iran from 1980 to 2004 on a data set including fertility records from 6000 cows. However, other economically important traits, such as INS, SF or IFL, were not investigated. Genetic variance may be reduced with selection (Bulmer, 1971); therefore a reduction in genetic variance of fertility traits may have occurred in Iranian Holstein cow due to intense selection on milk production. The objectives of the current study were to estimate genetic (co)variances among a comprehensive number of female fertility traits in Iranian Holstein cows.

2. Material and methods

2.1. Data

A total of 72,124 records of parities 1 to 6 from 27,113 cows collected from 1981 to 2007 in 15 large Iranian Holstein herds were used to estimate genetic (co)variances between female fertility traits. Only artificial insemination matings records were used. Heifer fertility records were removed from the data file. Reproductive traits in later parities were treated as repeated measurements. Fertility records were: DFS, INS, CI, DO, IFL, PR and SF. Data editing was based on Fatehi and Schaeffer (2003) and González-Recio and Alenda (2005). Cows were required to be 18 mor greater at first service. DO (date of pregnancy–date of calving) was required to be between 30 and 330 d, and DFS (date of first service–date of calving) ranged from 25 to 250 d. If INS was greater than 10, then INS was assigned to 10, and CI (date of current calving–date of previous calving) was required to be between 300 and 600 d. SF was a binary trait defined as 1 = successful if cow became pregnant at first insemination, 0 = failure. PR was calculated as PR = 0.25 × (233 − DO), as in VanRaden et al. (2004). Descriptive statistics for the edited data set used for analysis are shown in Table 1.

Table 1
Descriptive statistics (number of records, mean, and standard deviation (SD)) for the edited data set used for analysis.

Trait [a]	No. of records	Mean	SD	Maximum	Minimum
INS (no)	72,124	2.13	1.39	9	1
CI (d)	72,124	393.85	62.70	600	300
DFS (d)	72,124	72.93	35.01	250	25
IFL (d)	72,124	44.76	57.22	289	0
DO (d)	72,124	117.67	63.60	330	30
PR (%)	72,124	28.93	15.94	51	−24
SF (%)	72,124	0.42	0.0018	1	0

[a] Number of inseminations to conception (INS), calving interval (CI), days from calving to first service (DFS), interval between first and last insemination (IFL), days open (DO), pregnancy rate (PR) and success to first insemination (SF).

2.2. Genetic analysis and statistical model

The following statistical model was applied to estimate genetic parameters:

$$\boldsymbol{y} = \boldsymbol{X}\boldsymbol{b} + \boldsymbol{Z}\boldsymbol{u} + \boldsymbol{W}\boldsymbol{p} + \boldsymbol{e}$$

where **y** was the trait of interest; **b** were fixed effects of parity (6 levels) and age at previous calving for all traits (20 levels), herd (15 levels), year (27 levels), season (4 levels) of calving for DO, CI, INS, IFL and SF, herd-year of calving for DFS and PR, months of first insemination (12 levels) for DO, INS, IFL, and SF, and previous month of calving (12 levels) for DFS and PR; **u** was the additive genetic effect; **p** was the cow permanent environmental effect for all traits and a random effect of service sire at first insemination for SF; **e** was the residual term; and **X**, **Z** and **W** were incidence matrices relating data to the corresponding period effect.

Bivariate Bayesian threshold–threshold and linear–threshold models were applied to estimate genetic parameter for binary (SF) and categorical (INS) and genetic correlation between binary and categorical traits with interval traits (CI, DFS, IFL and DO) using Gibbs sampling by TM software (available in http://snp.toulouse.inra.fr/~alegarra). For threshold models probit distribution was used. Gibbs sampling consisted of 50,000 iteration and the first 10,000 samples were discarded as burn-in period. Means and standard deviations of marginal posterior distribution of each parameter were calculated by Bayesian output analysis package (available in http://www.public-health.uiowa.edu/boa). Bivariate linear models in the REML method with the ASREML software (Gilmour et al., 2002) were used to estimate genetic parameters for interval traits (CI, DFS, IFL and DO).

3. Results and discussion

3.1. Heritabilities

Estimates of heritability, phenotypic and genetic correlations between fertility traits are shown in Table 2. Heritability estimates for all fertility traits were low, ranging from 0.029 for SF to 0.076 for PR and DO. Heritability estimated for other fertility traits were 0.046 for INS, 0.074 for CI, 0.058 for DFS and 0.044 for IFL. These estimates are in agreement with the results obtained by González-Recio and Alenda (2005) and Gredler et al. (2007) in Holstein cows. Liu et al. (2007) reported lower heritability for IFL, DFS and DO. Heritability estimates obtained in this study were larger than the ones obtained by Toghiani Pozveh et al. (2009) for CI, DFS and DO in the previous study of Iranian Holsteins. The heritability estimates obtained for interval traits (DO, CI, IFL and DFS) were higher than those obtained for categorical (INS) or binary traits (SF). However interval traits may be affected by management decisions such as the length of the voluntary waiting period or estrus synchronization applied in some farms.

3.2. Genetic correlations

In general, strong genetic correlation estimates were obtained between fertility traits. Three groups of traits could be defined according to the estimated genetic correlations. The

Table 2
Heritabilities (bold), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) with their standard errors in parentheses for all reproductive traits.

Traits [a]	INS	CI	DFS	IFL	DO	PR	SF
INS	**0.046** (0.004)	0.69 (0.032)	0.10 (0.069)	0.92 (0.030)	0.72 (0.030)	−0.73 (0.026)	Ne [b]
CI	0.70 (0.002)	**0.074** (0.005)	0.77 (0.032)	0.92 (0.018)	0.99 (0.002)	−0.99 (0.002)	−0.81 (0.033)
DFS	−0.09 (0.003)	0.42 (0.003)	**0.058** (0.005)	0.58 (0.081)	0.76 (0.032)	−0.76 (0.032)	−0.18 (0.080)
IFL	0.87 (0.001)	0.80 (0.001) (0.002)	−0.007 (0.002) (0.005)	**0.044** (0.004)	0.94 (0.013)	−0.94 (0.012)	Ne [b]
DO	0.73 (0.001)	0.95 (0.004)	0.45 (0.003)	0.87 (0.001)	**0.076** (0.005)	−0.99 (0.0001)	−0.83 (0.031)
PR	−0.73 (0.001)	−0.95 (0.004)	−0.45 (0.003)	−0.87 (0.001)	−0.98 (0.0001)	**0.076** (0.005)	0.83 (0.031)
SF	−0.70 (0.0001)	−0.53 (0.002)	0.08 (0.003)	−0.67 (0.0001)	−0.55 (0.002)	0.55 (0.002)	**0.029** (0.003)

[a] INS = number of inseminations to conception, CI = calving interval, DFS = days from calving to first service, IFL = interval between first and last insemination, DO = days open, PR = pregnancy rate, and SF = success to first insemination.
[b] Ne = not converged.

first one is formed by the traits that measure overall fertility of the cow (i.e. CI, DO and PR) which can be obtained directly from calving dates. In particular, DO and PR showed phenotypic and genetic correlation estimates around −0.98 and the same correlation but of opposite sign with the rest of the traits, which indicates that these two traits are genetically the same as expected because PR is a linear function of DO. The same results were found by VanRaden et al. (2004) and González-Recio and Alenda (2005). Note that PR is calculated from a linear function of DO. Estimated correlations between these traits and CI were also very high (>0.95). These traits measure the same aspects of reproductive performance in cows. Hence, recording only one of them would be sufficient in the Iranian Holstein population. However, Toghiani Pozveh et al. (2009) reported very low (0.11) genetic correlation between CI and DO in the previous study on Iranian Holstein cows. The second group of traits includes DFS, which showed large estimated correlations with the overall fertility traits but close to zero with INS and SF. This indicates that a weak genetic relationship exists between cow's ability to recover reproductive function and the ability to conceive after showing heat. Therefore, different fertility traits should be combined into a fertility index to genetically improve female fertility. A third group of traits includes IFL, INS and SF. INS presented a genetic correlation estimate close to one with IFL. Despite of the fact that IFL is measured in a continuous scale and it would be more suitable for estimation of variance components under linear models with REML, heritability estimates and their standard error were very similar for both INS and IFL. Both traits would therefore be interchangeable in this population in a selection index that considers ability to conceive after showing heat signs. Traits like INS and SF are usually more difficult and expensive to register in a recording scheme than interval traits like CI, because CI can be calculated simply from date records that are recorded in milking recording scheme but recording INS is not common in many herds. Recording of these traits leads to higher labour costs for farmers. In those cases where INS cannot be directly recorded, interval traits may be used as alternatives. Large estimates of genetic correlations between CI and IFL were obtained in this study. However, it is worth mentioning that using CI rather than IFL can increase generation interval because IFL are recorded earlier than CI. Similar results for genetic parameters estimated were reported by González-Recio and Alenda (2005) and Gredler et al. (2007). Higher genetic correlation between INS and IFL, DO and CI were also reported by González-Recio and Alenda (2005). However, genetic correlation estimated by Gredler et al. (2007) between INS and DO or CI in Austrian dual purpose Simmental (Fleckvieh) cows was between 0.42 and 0.22, respectively. Genetic correlations of SF with INS and IFL were not estimated because mathematical artifacts appeared when the phenotypic value of SF is one and the corresponding phenotypic value for IFL and INS was zero and one, respectively. Thus, residual and genetic correlations tend to be estimated at one and convergence cannot be reached using REML estimation, as happened in González-Recio and Alenda (2005).

4. Conclusions

Estimated heritability for fertility traits was low as expected, ranging from 0.029 (SF) to 0.076 (DO and PR). Heritabilities obtained for interval traits were higher than those obtained for binary and categorical traits. A strong genetic correlation exists between traits. Fertility traits in this study can be classified into three groups: SF, IFL and INS measure the ability of cows to become pregnant, DFS is related to the ability of cow to re-cycle after calving. Traits in the third group, CI and DO or PR combine the two former groups. This classification of reproductive performance traits indicates that several fertility traits need to be used to explain fertility performance. It is important to determine which of these traits should be included in the total merit index.

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Please cite this article as: Ghiasi, H., et al., Genetic variance components for female fertility in Iranian Holstein cows, Livestock Science (2011), doi:10.1016/j.livsci.2011.01.020

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Please cite this article as: Ghiasi, H., et al., Genetic variance components for female fertility in Iranian Holstein cows, Livestock Science (2011), doi:10.1016/j.livsci.2011.01.020