

Full Length Research Paper

Genetic evaluation for calving ease trait using linear and threshold models in first parity dairy cows

Shahin Eghbalsaied^{1*}, Rohullah Abdullahpour² and Mahmood Honarvar³

¹Young Researchers Club, Khorasgan branch, Islamic Azad University, Isfahan, Iran.

²Department of Animal Science, Qaemshahr branch, Islamic Azad University, Qaemshahr, Iran.

³Department of Animal Science, Shahr-e-Qods Branch, Islamic Azad University, Tehran, Iran.

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Calving ease (CE) is a categorical trait which can be analyzed by both linear and threshold models. Though it has been assumed that threshold models qualify to be the best procedure for analyzing categorical traits, its efficiency with field data has not been clearly confirmed. This study was aimed at comparing linear and threshold models for estimation of CE genetic parameters. Data consisted of 10,575 first parturition CE records collected from 1985 to 2006 in Isfahan, Iran. CE scores were classified into 5 categories depending upon parturition situation. A sire-maternal grand sire model, consisting of birth herd-year-season and sex-age as fixed effects and parturition herd-season, sire and maternal grand sire additive genetic values as random effects, was applied in MATVEC software. Mean, standard deviation, coefficient of variation, skewness, and kurtosis for first parity CE records were 0.233, 0.644, 276.640, 2.950, and 8.097, respectively. CE scores varied from 0 (86%) to 4 (0.1%). CE means for males (0.285) and female calves (0.190) were significantly different. Parturitions during winter and summer were associated with the highest and lowest calving difficulties, respectively. Estimations for direct and maternal heritability were 0.1082, 0.0486 using linear model and 0.0689, 0.0100 using threshold model, respectively. Even though departure from normal distribution was expected to favour the threshold model, implementation of this model in field data analysis did not eventuate to better genetic estimations.

Key words: Calving ease, Holstein, Sire-MGS, threshold, genetic parameters.

INTRODUCTION

Two of the biggest concerns with which dairy producers are dealing, even in modern dairy farms, are calving difficulties and stillborn calves. Heifers and cows that suffer from a difficult calving tend to have impaired health, fertility, and production in the following lactation. Moreover, complicated parturition can also cause the death of the calf and/or its dam. On the other side, other sources like genetic disorders also cause stillbirth even when normal-sized calves are born without complications.

In Iranian dairy herds, involuntary culling of dairy cows is a common phenomenon, mainly due to fertility disabilities (Eghbalsaied, 2011). Problems at the time of parturition along side high milk production could enhance reproduction failure in these herds. Difficult calving is associated with post-parturition problems like retained placenta, increased open days, and non-return rate.

The threshold model approach has been supposed to be the best alternative for linear model in analysing categorical traits like CE. However, the efficiency of the procedure with field data sounds to be controversial and still remains to be confirmed (Luo et al., 2002; Wang et al., 2005; Matilainen et al., 2009; Eaglen and Bijma, 2009; Olson et al., 2009). Implementation of a scale with 4 or more CE scores tends to rank animals similarly based

*Corresponding author. E-mail: shahin.eghbal@khuisf.ac.ir. Tel: +98-311-5354015. Fax: +98-311-5354038.

Table 1. Calving ease classification.

Calving ease score	Degree of difficulty
0	Natural, no problem
1	Slight help, minor problem
2	Needed assistance, major problem
3	Considerable force, mechanical or labourer's assistance
4	Caesarean, very difficult

Table 2. Abundances of calving ease score in Holstein first parity cows for male and female calves.

Sex	Calving ease score					Least squares means (%)
	0	1	2	3	4	
Male	4136 (84.3)	340 (6.9)	246 (5.0)	180 (3.7)	6 (0.1)	0.285 (46.4 ^a)
Female	4962 (87.6)	412 (7.3)	217 (3.9)	72 (1.3)	4 (0.1)	0.190 (53.6 ^b)
Percentage	86.0	7.1	4.4	2.4	0.1	-
Sum	9098	752	463	252	10	100

^{a, b} superscripts indicates significant difference at $P < 0.05$.

based upon linear and threshold models (Ramirez-Valverde et al., 2001; Lee et al., 2002). Snell (1964) suggested a scaling procedure for ordered categorical data such as CE score, which makes the use of linear model more appealing. Even though threshold model is expected to estimate more accurate genetic parameters, the superiority has not been achieved with real dataset. Various factors have shown to be effective on CE phenotype including birth weight, gestation length, calf sex and twinning rate (Crews, 2006). Considering these factors as fixed effects in the model might lead to elimination of pleiotropic genes and subsequently under estimation of genetic parameters. The aim of this study was to compare estimated genetic parameters using threshold and linear model for calving ease in Holstein dairy cows.

MATERIALS AND METHODS

Data consisted of 10,575 first parity calving ease records which were collected from 1985 to 2006 in Isfahan Province of Iran. Calving ease was classified into 5 categories depending on parturition situation (Table 1). For genetic analysis, cows in categories 3 and 4 were mixed into one class because there were few observations in these two classes. Animals with no sire and dam were excluded. Animals with twinning were also eliminated from genetic analysis. Genetic analysis was performed using the following model in MATVEC software:

$$CE = \mu + BHYS + PHS + GA + MGS + S + e$$

Where μ , BHYS, and GA were CE mean, birth herd-year-season, and gender-age at parturition as fixed effects, respectively. PHS, S, MGS, and e indicate parturition herd-season, sire, maternal grand

sire, and residual as random effects, respectively. (Co)variance components for direct (σ_d^2) and maternal (σ_m^2) effect obtained from those due to sire (σ_s^2) and maternal grandsire (σ_{Mgs}^2) with the following equation:

$$\begin{pmatrix} \sigma_d^2 \\ \sigma_{d-m} \\ \sigma_m^2 \end{pmatrix} = \begin{pmatrix} 4 & 0 & 0 \\ -2 & 4 & 0 \\ 1 & -4 & 4 \end{pmatrix} \begin{pmatrix} \sigma_s^2 \\ \sigma_{S-Mgs} \\ \sigma_{Mgs}^2 \end{pmatrix}$$

The same model and dataset were used for estimation of genetic parameters and variance components using linear and threshold models.

RESULTS

Descriptive statistics

Calving ease score varied from 0 to 4 with 86 and 0.1% frequency, respectively. Mean, standard deviation, coefficient of variation, skewness, and kurtosis for first parity calving ease records were 0.23, 0.64, 276.64%, 2.95, and 8.10, respectively. As shown in Table 2, female calves were more abundant (53.6%) than male calves (46.4%), while least squares mean of calving ease in female calves (0.190) was significantly lower than in males (0.285).

Moreover, parturitions in summer (0.202) and winter (0.275) were associated with the lowest and highest CE score (Table 3). Parturitions in springs and falls were quite similar from CE scope. However, their difference from both summer and winter CE was considerable.

Table 3. Calving ease score of Holstein first parity cows in seasons.

Season	Calving ease score					Lease square means
	0	1	2	3	4	
Spring	2271	201	106	59	2	0.227 ^b
Summer	2144	166	108	38	0	0.202 ^c
Fall	2379	157	118	69	6	0.229 ^b
Winter	2304	228	131	86	2	0.275 ^a

^{a, b} Superscripts with different letters indicate the means are significantly different at $P < 0.05$.

Table 4. Variance-covariance components, standard errors (in brackets) and genetic parameters estimated for calving ease using sire-maternal grand sire linear and threshold models.

Model	σ_s^2	σ_{smgs}	σ_{mgs}^2	$\sigma_{H,Y}^2$	σ_e^2	h_d^2	h_m^2	r_{dm}	r_{S-MGS}
Linear	0.00991 (0.00202)	0.00194 (0.00129)	0.00392 (0.00112)	0.09281 (0.10010)	0.25597 (0.00369)	0.1082	0.0486	-0.4536	0.3126
Threshold	0.019331 (0.00992)	0.002587 (0.00604)	0.000559 (0.00386)	0.096493 (0.01265)	1.0 (0.00390)	0.06894	0.0100	-0.9613	0.7870

σ_s^2 ; variance due to sire effect, σ_{s-mgs} ; covariance between sire and maternal sire effects, σ_{mgs}^2 ; variance due to maternal grand sire effect, $\sigma_{H,Y}^2$; variance due to herd-year effect, σ_e^2 ; residual variance, h_d^2 ; direct heritability, h_m^2 ; maternal heritability, r_{dm} ; genetic correlation between direct and maternal effects.

Genetic evaluation

As presented in Table 4, estimates of CE variance-covariance components using linear model were 0.00991, 0.00392, and 0.00194 for sire, MGS, and sire-MGS covariance, respectively. Direct additive genetic (0.03964), maternal additive genetic (0.01783), and their covariance (-0.01206) were estimated from their compartments based on the mentioned formula. Estimated herd-year and residual random variances were 0.09281 and 0.25597, respectively. Direct and maternal heritabilities were 0.1082 and 0.0486, respectively. Additive genetic correlation for direct-maternal sources and sire –MGS were -0.4536 and 0.3126, respectively.

Implementation of threshold model for CE showed that (co)variance estimates including sire, MGS, and sire-MGS were 0.019331, 0.000559, and 0.002587, respectively. Direct additive genetic (0.077323), maternal additive genetic (0.011219), and their covariance (-0.02831) were estimated from their compartments based on the mentioned formula. Predicted herd-year and residual random variances were 0.096493 and 1.0, respectively. Direct and maternal heritabilities were 0.06894 and 0.01000, respectively. Additive genetic correlation for direct-maternal sources and sire –MGS were -0.96126 and 0.7870, respectively.

DISCUSSION

The mean calving ease of first parity Holstein dairy cows in Isfahan district of Iran of 0.26 was lower than Netherland's

average of 1.57 (Eaglen and Bijma, 2009). Bull calves are usually larger and more problematic at the time of parturition than heifer calves. In agreement with previous reports (Manfredi et al., 1991; Steinbock et al., 2003; Eaglen and Bijma, 2009;), present survey also showed that male calves have significantly greater calving difficulty than female calves. This could be attributable to differences in body size and shape between calf sexes (Hickey et al., 2007). Moreover, parturitions during summer were significantly easier than other seasons particularly winter, a phenomenon which agrees with previous findings (Manfredi et al., 1991; Steinbock et al., 2003; Eaglen and Bijma, 2009). The highest rate of fetal weight gain is achieved during the last months of pregnancy. Since calves in summer parturitions suffer more heat stress, it is most likely that they have relatively lower gestation length and birth weight. Normal distribution indicators that is skewness, and kurtosis showed that CE data deviated very much from normal distribution. However, linear models have been routinely used to evaluate categorical traits using an animal model. Categorical traits are often supposed to be the result of an underlying normally distributed liability factor. In threshold models phenotypes are the result of the position of the underlying liability with respect to some thresholds determining the phenotypic categories.

In the present study, we used both linear and threshold models from the same dataset and model equation to compare their estimations from field data. Estimates of heritability and genetic variance for CE using both models were in a good agreement with other reports (Manfredi et

al., 1991; Luo et al., 2002; Matilainen et al., 2009; Eaglen and Bijma, 2009; Olson et al., 2009). Estimated direct heritability (0.11 vs. 0.07) and maternal heritability (0.05 vs. 0.01) using linear model was considerably higher than threshold model. However, higher negative genetic association between direct and maternal genetic sources was estimated via threshold model. Estimated direct and maternal genetic correlation has been in the range of -0.07 and -0.47 (Wiggans et al., 2003; Hickey et al., 2007; Eaglen and Bijma, 2009). The only exception is for the positive genetic correlation which could be attributed to the Bayesian estimation (Luo et al., 2002). It seems that linear model estimation for direct-maternal genetic correlation is closer to other estimates. Previously, Luo et al. (2002) reported positive direct and maternal genetic correlation using threshold model. They postulated that threshold animal models have some problems with convergence, which could lead to biased estimates (Luo et al., 2002). It would appear that, for parameter estimation with categorical traits, threshold models perform better because linear models applied to an underlying scale seem to underestimate the parameters (Abdel-Azim and Berger, 1999; Steinbock et al., 2003; Hossein-Zadeh et al., 2007). However, the comparative advantages of threshold models over linear models in terms of genetic parameter estimations and sire ranking were negligible for field data (Luo et al., 2002; Phocas and Laloe, 2003; Wang et al., 2005; Matilainen et al., 2009; Eaglen and Bijma, 2009). Implementation of threshold models has been considered to be complicated and computationally expensive and not easily extended to multiple categorical traits within the same analysis (Misztal et al., 1989; Abdel-Azim and Berger, 1999; Ramirez-Valverde et al., 2001; Lee et al., 2002; Wang et al., 2005). It seems that calving ease trait might not qualify threshold model assumptions. CE truncation points are influenced by several factors in which extreme phenotypes for each factor, like pelvic cavity, calf size and orientation can produce a difficult calving *per se* without aggregation of other factors.

Another strategy to improve estimates of CE genetic parameters might be data transformation. Even though transformation of CE data to Snell scores provides quite normal distributional properties, estimated genetic parameters coupled with animal ranking were similar in original and transformed data (Jamrozik et al., 2005).

Transformation of observations to a liability scale did not affect the estimated genetic parameters and sire ranking (Eaglen and Bijma, 2009). However, estimation of multi-trait models and greater dataset might provide more desirable and accurate genetic estimation.

Conclusion

In this study, we estimated genetic parameters of calving

ease trait using linear and threshold models from the same Holstein dairy cow dataset. Estimates of heritability via linear and threshold models were 0.11 and 0.07 (direct heritability) and 0.05 and 0.01 (maternal heritability), respectively. Direct and maternal additive genetic correlation was -0.45 and -0.96 using linear and threshold model, respectively.

In conclusion, linear model analysis of CE dataset in Isfahan Province of Iran using linear model led to higher heritability estimates (direct and maternal) while lower estimations for additive genetic correlation (direct-maternal and sire –MGS) than that of threshold models.

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