Estimation of Genetic Parameters and Breeding Values of Milk Traits for Simmental Cattle in Croatia Using a Lactation Animal Model

Miroslav KAPŠ¹ Marija ŠPEHAR²

SUMMARY

The objective of this study was to estimate genetic parameters and to predict breeding values for dairy traits in Simmental cattle in Croatia by developing an animal lactation model. Data consisted of 30761 first lactation records of cows born between 1985 and 2001. By including the pedigree there was a total of 48748 animals. The following effects were analyzed: age, season and year at first calving, days open, breeding organization, farm, animal, and genetic group. Adequacy of the models was tested by using F tests for fixed effects, and REML functions and 'Mendelian sampling' for the whole models. The best fit model was determined to have the following effects: age at first calving, days open, year x season interaction and breeding organization x year interaction as fixed, and animal and farm x year as random effects. By including genetic group the model was further improved. From this model, the following heritabilites were estimated: 0.34 ± 0.02 , 0.30 ± 0.02 , $0.29 \pm$ 0.03 for milk, milk fat and protein yield, respectively. Further, phenotypic and genetic trends were analyzed. The genetic gain in milk traits has been low so far, but by using an appropriate animal model, the breeding value prediction is expected to be improved in terms of accuracy and precision.

KEY WORDS

Cattle, Simmental, Milk, Animal model, Heritability, REML

¹Animal Science Department, Faculty of Agriculture, University of Zagreb Svetošimunska 25, 10000 Zagreb, Croatia ²Croatian Livestock Center, Ilica 101, 10000 Zagreb, Croatia E-mail: mkaps@agr.hr Received: November 15, 2004

INTRODUCTION

The development of an optimal animal model for estimation of genetic parameters and prediction of breeding values is not only important for a correct national genetic evaluation of animals, but also for a possible international evaluation and exchange of genetic material with other countries. Interbull, a nonprofit world organization responsible for development and standardization of national and international genetic cattle evaluation, gives a set of recommendations for national evaluations which will enable countries to participate in international evaluation (Interbull, 2001). However, Interbull emphasizes that there might be differences in defining an optimal model for each country. The model of choice must be based on an animal model which applies Best Linear Unbiased Prediction (BLUP, Henderson, 1973). Regarding the type of records the model can be lactation or test day model (Interbull, 2001). A lactation model uses records of whole lactation yield previously calculated, and a test day model uses daily records of cows. In the future, estimation of breeding value in Croatia will utilize a test day model, but in the interim a set of univariate lactation models will be used. The objective of this research is to develop a lactation animal model for parameter estimation and breeding value prediction for Simmental cattle in Croatia. This will be done by defining effects in the model, by estimating parameters and predicting breeding values using different models with subsequent comparison. For this purpose, the first lactation records will be used.

MATERIALS AND METHODS

Data utilized for this study consisted of first lactation records of 30761 Simmental cows born between 1985 and 2001. Including those in the pedigrees there were 48748 animals in the analysis. Standard lactation records of 305 days of milk were utilized. Lactations less than 305 days were not precorrected but adjustments were done in the evaluation model by using days open. Data were edited for unusually extreme values. Records of cows with: a) less than 1000 or more than 11000 kg of milk, b) less than 80 or more than 600 kg of milk fat or protein, c) less than 2 or more than 6 percent of milk fat or protein, d) less than 18 or more than 36 months for age at first calving, e) less than 30 or more than 150 days for days open were deleted. Also, records without calving date, beginning and ending of lactation, owner, breeding organization and district were not considered. The pedigree data were completely edited. Cows' records without known sire and dam or with dubious parentage information were deleted. Editing of data was done with a program written in SAS environment (SAS, 2000). Descriptive statistics was calculated by using the Univariate procedure (SAS, 2000).

For estimation of parameters and prediction of breeding values a set of single trait animal models were used, shown in the general form:

$$y = X\beta + Z_a a + Z_c c + \varepsilon$$

where **y** is a vector of milk, fat and protein measurements, β is a vector of fixed effects, **a** is a random vector of additive genetic effects, **c** is a vector of additional random effects, **X**, **Z**_a and **Z**_c are incidence matrices relating β , **a** and **c** to **y**, and ε is a vector of error effects. The model has the following distributional assumptions:

$$E[\mathbf{y}] = X\boldsymbol{\beta}, E[\mathbf{a}] = \mathbf{0}, E[\mathbf{c}] = \mathbf{0} \text{ and } E[\boldsymbol{\varepsilon}] = \mathbf{0}$$

Variances and covariances are:

$$Var[\mathbf{y}] = \mathbf{Z}_{\mathbf{a}}\mathbf{A}\mathbf{Z}_{\mathbf{a}}^{*}\sigma_{\mathbf{a}}^{*} + \mathbf{Z}_{\mathbf{c}}\mathbf{Z}_{\mathbf{c}}^{*}\sigma_{\mathbf{c}}^{*} + \mathbf{I}\sigma^{2}, Var[\mathbf{a}] = \mathbf{A}\sigma_{\mathbf{a}}^{2},$$

$$Var[\mathbf{c}] = \mathbf{I}\sigma^{2}_{\mathbf{c}}, Var[\mathbf{\epsilon}] = \mathbf{I}\sigma^{2}$$

where σ_a^2 is the additive genetic variance, σ_c^2 is the variance not correlated with the additive genetic variance, σ^2 is the error (environmental) variance, **A** is the additive genetic relationship matrix and **I** is the identity matrix.

The following effects were considered: age, season and year at first calving, days open, breeding organization (as a regional effect), farm and animal. Also, genetic groups were defined by bulls' birth year and country of origin. Variances and covariances were estimated by using restricted maximum likelihood (REML) and computer programs MTDFREML (Boldman et al., 1993) and DFREML (Meyer, 1998). The model fit was analyzed by F tests, REML functions and by estimation of 'Mendelian sampling'. 'Mendelian sampling' is calculated as the difference between the average breeding value of offspring and the average breeding values of their parents. The expectation of those values should be equal to zero and with no trend. Thus, possible changes of 'Mendelian sampling' averages per year were verified. Using the best model, phenotypic and genetic trends were estimated.

RESULTS AND DISCUSSION

Descriptive statistics for milk, fat and protein yield of first lactations are presented in Table 1. The phenotypic trend for milk yield average per year is shown in Figure 1. Evidently, the average increase of milk yield per year is only 49.6 kg. In an evaluation for Simmental herdbook cows in Germany in the years from 1990 to 2001, increase of milk yield was 92 kg per year (Röhrmoser and Pichler, 2002). Also, average milk production in Germany was higher. For example, the averages in the years 1990 and 2000 were 5400 and 6300 kg, respectively (comparing to data from this study in which the average milk production for cows under milk recording was 3300

Table 1. Descriptive statistics for milk, fat and	protein yield
in 305 days first lactation in Simmental cattle	(period 1985
- 2000)	

Trait	Number of records	Mean	Std. dev	CV(%)
Milk yield (kg)	30761	3612	730	20.23
Fat yield (kg)	30610	139	32.22	23.14
Protein yield (kg)	15005	127	26.68	23.30

Table 2. F test for fixed effects for 305 days first lactation milk yield in Simmental cattle

Source	F value	P value
Age at first calving	7.46	<.0001
Days open	60.13	<.0001
Year x season at first calving	5.81	<.0001
Breeding organization x year at first calving	20.22	<.0001

kg in 1990 and 4100 kg in 2000). Although, Croatian results are about first lactations and German for all lactations, evidently the potential milk yield in Croatia has not been achieved.

The importance of including particular fixed effects in the model is presented by using F tests (Table 2). For milk yield, the effects age at first calving, days open, year x season interaction and breeding organization x year interaction F tests were highly significant (P < 0.001), so they have to be included in the model. Those effects proved to be important for milk fat and protein yield as well. Descriptions of the analyzed models together with estimated heritabilities and criteria of goodness of fit are presented in Table 3.

The best fit model should have highest log likelihood and smallest 'Mendelian sampling' standard deviation. Thus, the model was defined with the following



Figure 1. Phenotypic trend of first lactation milk yield in Simmental cattle



Figure 2. 'Mendelian sampling' per year for 305 days first lactation milk yield in Simmental cattle

effects: age at first calving, days open, year x season interaction, breeding organization x year interaction as fixed and animal and farm x year interaction as random effects. The interaction of farm x year was defined as random due to the large number of small farms. Validity of the model was confirmed by plotting 'Mendelian sampling' changes per year (Figure 2). No trend is apparent and deviations from zero are relatively small.

Effects in the model Heritability Log Likelihood Mendelian Sampling Fixed Random Mean Std.dev Age at first calving, Days open, Year x Animal, Error 0.66 ± 0.015 -1808.52-0.42261.5 season Age at first calving, Year x season, Animal, Error 0.54 ± 0.017 654.62 -0.15181.9 Breeding organization x year Age at first calving, Days open, Year x Animal, Error 0.55 ± 0.017 608.75 -0.14183.0 season, Breeding organization x year Age at first calving, Days open, Year x Animal, Error, 1643.08 120.4 0.35 ± 0.017 -0.13season, Breeding organization x year Farm x year Age at first calving, Days open, Year x Animal, Error, 113.6 0.34 ± 0.017 1680.83 -0.72season, Breeding organization x year, Farm x year Genetic groups

Table 3. Description of the models, heritabilities and model validity criteria for 305 days first lactation milk yield in Simmental cattle

Trait	Milk yield (kg)	Milk fat yield (kg)	Protein yield (kg)
Additive genetic variance	119850 ± 21189	194.8 ± 11.8	181.8 ± 17.8
Temporary environmental variance	117650 ± 15412	216.2 ± 8.6	179.1 ± 12.9
Heritability	0.34 ± 0.02	0.30 ± 0.02	0.29 ± 0.03
Heritability (Austria and Germany) ^a	0.36	0.31	0.27
Heritability (Switzerland) ^a	0.31	0.26	0.25

Table 4. Estimated heritability for 305 days first lactation milk yield for Simmental cattle in Croatia and comparison with the estimates from Austria, Germany and Switzerland

^a Source Interbull (2000)

The estimated heritabilities for milk, fat and protein yield in this study using the best fit model (Table 4) are similar to the estimated values for Simmental cattle in Germany, Austria and Switzerland (Interbull, 2000). In Germany and Austria (joint evaluation) the estimates ranged from 0.27 to 0.36, and in Switzerland the estimates ranged from 0.25 to 0.31.



Figure 3. Genetic trend for 305 days first lactation milk yield in Simmental bulls



Figure 4. Genetic trend for 305 days first lactation milk yield in Simmental cows

Genetic trend for bulls (Figure 3) and for cows (Figure 4) for milk yield shows very small genetic increase. The average increase for bulls is 12.2 kg per year and the average increase for cows is 8.0 kg per year. In comparison, the evaluation in Germany bulls shows an increase of genetic value of about 65.0 kg per year (Röhrmoser and Pichler, 2002). Again, Croatian results are about first lactations and German for all lactations, but it illustrated low genetic progress in Croatia.

CONCLUSION

The development of an animal model implies correct and precise breeding value prediction of Simmental cattle in Croatia; that was demonstrated by comparison of different proposed models. The best fit model was determined to base upon the following effects: age at first calving, days open, year x season interaction, breeding organization x year interaction as fixed, and animal and farm x year interaction as random effects. By including genetic groups the model was further improved. In future, to develop a test day model and multiple trait approach, it is essential to improve data quality.

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