Revising the Genetic Evaluation for Calving Ease in the Italian Holstein Friesian

***Fabiola Canavesi*[1]*, S. Biffani*[1]*, A.B. Samorè*[1]**

1 – ANAFI, Cremona, Italy

Abstract

The present procedure of genetic evaluation for calving ease dates back at beginning to the nineties. It is a simple sire linear model with no relationship matrix that analyses data collected on calving difficulty linear transformed on a scale from 0 to 100. The value zero corresponds to an easy calving and value of 100 to a very difficult calving with stillbirth. Its revision was planned many years ago and never carried out up to now. New tools available and the relevance of the trait for the profit of a dairy farm allow now to set up a new procedure for calving ease genetic proofs computation.

The new model is an heteroskedastic threshold sire maternal grand sire model with relationship matrix as proposed by Foulley and Gianola (1996) and as applied in genetic evaluation for calving ease in France (Ducrocq, 2000). Calving ease scores (1 = easy calving, no assistance, 2 = easy calving, assistance of one person, 3 = difficult calving) were analysed taking into account the interaction effect of province by year, sex by parity-age classes, year by month as fixed effect, herd-year effect and considering heterogeneity of residual for province, sex and year. Random effects in the model were herd-year, sire and maternal grand sire.

Parameter estimated on a sample of the national data base with few representative provinces were: 0.07 for direct heritability and 0.027 for maternal effect. Further analysis will investigate sire proofs results in comparison with the official bulls proofs published every six months in order to define the final model and the timeframe for its application to routine evaluation of calving ease in Italy.

Introduction

Reduction of dystocia is indeed of great economic importance for dairy farmers . It is very important to be able to correctly identify bulls that should not be used on heifers to avoid economic losses in terms of increased mortality, decreased fertility and labour costs.

An accurate genetic evaluation for calving ease is highly dependent on data quality.

Calving difficulty scores are collected by milk recording people each month as recorded by the farmers on a scale of 5 classes. A is for easy calving requiring no assistance, B is for calving assisted by one person only, C is for cesarean birth, D for difficult calving and E for embriotomy.

The current model for genetic evaluation of calving difficulty scores has been developed very long ago. Its revision has been planned long time ago but never realized.

The present model in place for routine genetic evaluation analyses with a sire model the linear transformation of those classes on a linear scale ranging from 0 for easy calving to 100 for very difficult calving. The linear transformation is a combination of the scores with the calf being born alive or dead. No relationship matrix is used and fixed effects in the model are: sex-parity-month and herd year.

It has been suggested by many studies that a proper analysis of calving conditions recorded on a subjective scale like this should take into account the nature of the measurement as well as the complex genetic background behind it, combining not only the direct effect of the calf with the maternal effect of the dam (Ducrocq, 2000). Result from studies conducted in France have shown the feasibility of a genetic evaluation based on a threshold sire maternal grandsire model also for large populations (Manfredi et al, 1991; Foulley and Manfredi, 1991). Manfredi also stressed the importance of data quality. The recent extension of the model developed by Foulley and Gianola (1996) to incorporate heteroskedastic residual variance helps in dealing with quality of data that is not constant across provinces, years, and often sexes (Ducrocq, 2000).

The objective of this study was to assess the feasibility of a routine genetic evaluation for dystocia based on a threshold model accounting for heterogeneity of residual variances.

Material and Methods

For computational reasons a sample of the national data base of calving scores, grouping six different provinces, representative of the Italian situation were used for the model definition and for the parameters estimation. Table 1 shows some general yearly statistics of the national data base.

Table 1. Distribution of calving conditions by year.

	Year		
	1999	**2000**	**2001**
N. records	504,950	510,293	532,672
Scores	%	%	%
A	72.07	71.91	72.41
B	25.94	26.00	25.45
C	0.13	0.13	0.14
D	1.85	1.96	2.00
E	0.01	0.01	0.00
Alive/Dead			
D	11.23	12.06	10.48
A	88.77	87.94	89.52
Sex			
1 (M)	51.23	51.00	51.22
2 (F)	48.77	49.00	48.78

Given the very low incidence of the last three categories they were grouped together for the analysis for a total of three classes: 1 for easy calving coded as A, 2 for assisted calving coded as B, and 3 for difficult calving coded as C, D and E.

Table 2 illustrates the distribution of records in the data set resulting by grouping the six provinces used for genetic parameter estimation.

Data were edited. Only bulls with at least 20 records and mgs with at least 20 daughters were considered, hy classes with less than 15 observations were discarded.

Herd-year classes were edited for quality: classes with more than 95% of 1 codes, or more than 95% of 2 codes and more than 50% C codes were deleted.

Table 2. Characteristic of the data file analysed.

Records	1,069,296
Sires	22,959
Maternal grand sires	22,959
Herd-year	23,095
% code 1	67.0
% code 2	31.6
% code 3	1.4

The model used was a Threshold model of S. Wright as described by Foulley, Gianola, Harville and Mee. It assumes the existence of n underlying non observable, normally distributed variable y_i controlling the observed variable Y_i through a set of J-1 threshold τ_j (for J categories, in this case 3).

For a more detailed description of the model, included the added flexibility of heterogeneous residual variances see Ducrocq (2000).

The model included the fixed effects of year by month, region by year, sex by parity-age. Heterogeneity of residual was modelled based on the effects of year, province and sex. This model was the second best according to evaluation of Log likelihood and AIC assessment criterion. The random part of the model included the effect of the i^{th} herd-year level, the sire and the maternal grand-sire effect.

Results and Discussion

Table 3 presents estimates of variance components. Heritability for the direct effect was comparable with the estimate found by Manfredi (1991) for the Holstein breed in France. Maternal effect heritability was much lower than estimated in the French population and lower than the direct heritability. A lower heritability for the maternal effect compared to the direct heritability was also found for the Normande and the Montbeliarde breed by Ducrocq (2000).

Table 3. Estimates of variance components.

Component	Estimate
σ^2 (sire)	0.0331
σ^2 (mgs)	0.0074
σ^2 (hy)	0.8303
Cov (sire-mgs)	0.0032
Total σ^2	1.8701
h^2 direct (%)	7
h^2 maternal (%)	2.7
ρ sire-mgs	0.20
ρ direct-maternal	-0.53

Figure 1 presents solution estimates for sex and parity-age classes. As in Manfredi (1991) and Ducrocq (2000) it was found that solutions for male calves and first parity cows are much higher than for females and later parity cows. The difference was almost constant across parities.

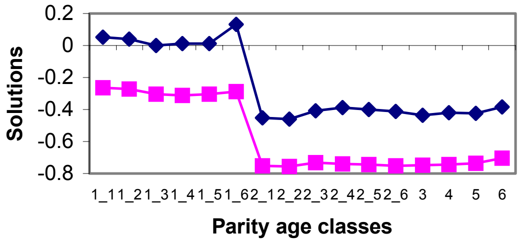

Figure 1. Solutions for sex x parity age class.

Figure 2 shows solutions for three of the provinces analysed x year. The variability across provinces was not very large but not constant over years. Differences between provinces were not larger than the differences observed between sex and parities, except for the years from 1998 to 2001. The high variability in these year may be due to changes in regulations regarding animal identification.

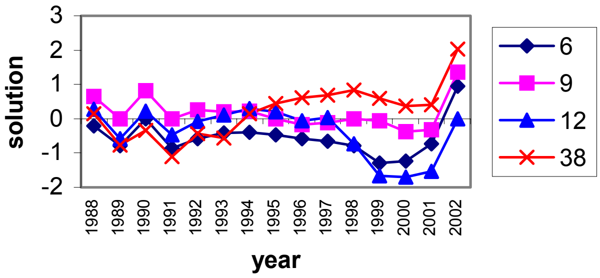

Figure 2. Solutions for year by province.

Figure 3 displays the solution for the effect of month by year. Differences were very large across years. The size of differences was larger on average than the differences found for sex and parity and for province by year.

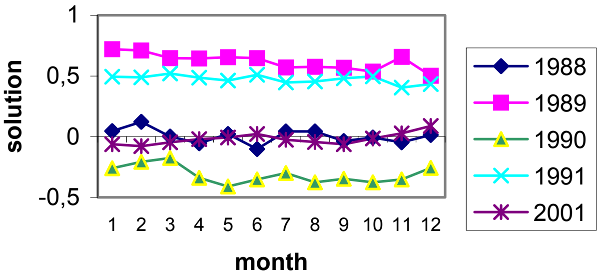

Figure 3. Solutions for month by year.

Residual variability was higher for males (σ_i=1.027) than for females (σ_i=1). Figures 4 and 5 show the residual standard deviation as a function of the province and the year. The reference(σ_i=1) are the females born in 2002. Residual variability as in Ducrocq (2000) was low in region that had large region by year effect (province 38 in figure 2 and 4).

Residual variability did show a trend across year that was comparable with the trend observed in the different provinces by year (see Figure 2). Higher variability was associated with smaller fixed effect solution once again.

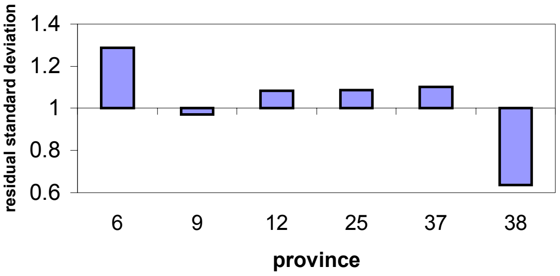

Figure 4. Residual standard deviation as a function of the province, for the six provinces analysed.

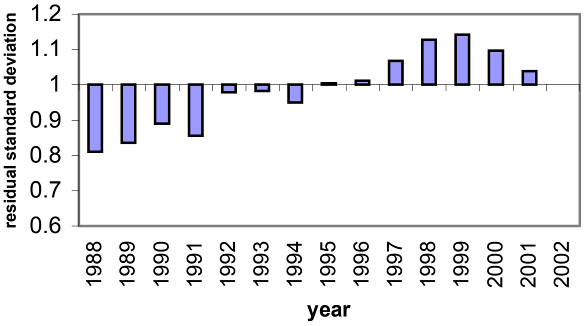

Figure 5. Residual standard deviation as a function of the year, from 1988 to 2002.

Conclusion

The results of this research show that the application of a genetic evaluation based on a threshold model with heterogeneity of residual variance is feasible. The model allows a more complete and exhaustive analysis of the data compared to the one actually used for routine genetic evaluation. The ability of this model to take into account heterogeneity of data quality across time and provinces and its flexibility is particularly appealing. Further analysis of some preliminary results on the entire data set of calving score will help define the final model, genetic parameters and criteria for publication of proofs. Upon those results the next national technical committee of the breed will decide when it will be implemented for routine genetic evaluation in Italy.

Acknowledgments

The work of Pilar Schneider and the assistance of V. Ducrocq throughout the development of this research is greatly appreciated.

References

Ducrocq, V. 2000. Calving ease evaluation of French dairy bulls with a heteroskedastic threshold model with direct and maternal effects. *Interbull Bulletin 25,* 123- 130.

Foulley, J.L. & Gianola, D. 1996. Statistical analysis of ordered categorical data via a structural heteroskedastic threshold model. *Genet. Sel. Evol. 28,* 249-273.

Foulley, J.L. & Manfredi, E. 1991. Approches statistiques de l'évaluation génétique des reproducteurs pour des caractères binaries à seuils. *Genet. Sel. Evol. 23,* 309-338.

Harville, D.A. & Mee, R.W. 1984. A mixed model procedure for analysing ordered categorical traits. *Biometrics 40,* 393-408.

Manfredi, E., Ducrocq, V. & Foulley, J.L. 1991. Genetic analysis of dystocia in cattle. *J. Dairy Sci. 74,* 1715-1723.