

SIRE EVALUATION FOR DIRECT EFFECTS ON DYSTOCIA
BY LINEAR AND THRESHOLD MODELS

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SUMMARY

Threshold (TM) and linear (LM) models have been compared in a data set of 10760 birth records from 89 AI charolais sires progeny tested for direct effects on dystocia. Two variables were defined: a calving score with 4 categories and dystocia (score 1-2 vs 3-4). Heritability under TM were higher than under LM and heritability of dystocia (.263) was higher than calving score (.089). In this progeny-testing program BLUP reaches comparable efficiency as TM evaluation to rank sires. However in reduced files superiority of TM becomes more evident.

INTRODUCTION

The main reason for the occurrence of dystocia is described as an incompatibility between the size of the calf and the pelvic opening of the dam (Ménissier *et al.*, 1981). Result of birth of a sire progeny depends on the size of the calves relatively to given characteristics of the population of the cows (breed, age etc...) which hold as thresholds and induce the discrete distribution of observation. In France breeders use to score birth from 1 (no assistance) to 4 (caesarian or fetotomy). Up to now, in spite of a discontinuous distribution of records, genetic evaluation on birth information has generally been analysed by mixed linear models. A more realistic model assuming an unobservable but continuous underlying variable and a set of thresholds has been first introduced by Wright (1934) and received further developments by Gianola and Foulley (1983), Harville and Mee (1984) and Gilmour *et al.* (1985).

In spite of their theoretical superiority, utilization of these threshold models has been limited by their computational complexity. Simulation studies and analysis of field data (Meijering, 1985, Meijering and Gianola, 1985, Djemali *et al.*, 1987, Weller *et al.*, 1988) have been done to test the conditions where the threshold model outperform the linear model. In this study the efficiency of the linear and threshold models will be compared for estimating the variance components and the sires breeding value in a population of AI Charolais sires progeny-tested for their direct effect on dystocia.

MATERIAL AND METHODS

Data were provided by an A.I. company (UCEF) that has progeny-tested 86 Charolais sires for direct effects on calving difficulties. These sires were tested in 7 different yearly batches of 10 to 19 sires each, simultaneously with 3 reference sires to ensure across years comparison. Progeny testing is performed in dairy herds with one calf per herd. Calving results are scored in four categories: 1) unassisted; 2) easy assistance; 3) hard pull; 4) caesarian or fetotomy. Two variables were defined: the preceding calving score and dystocia whose two categories correspond to easy (scores 1 and 2) or difficult calving (scores 3 and 4). Both variables were analysed under both linear (LM) and threshold (TM) models.

Analysing sire effects requires the following fixed effects to be included in the model: 28 year-seasons (where a season generally corresponds to a 2-month period), 2 regions, 3 dam breeds (Montbéliarde: 48%; Friesian: 45%; others: 7%), 4 dam-age groups defined after a preliminary analysis (heifers: 3%; young cows from 2d to 5th parity: 74%; mature cows from 6th to 8th parity: 18%; old cows after the 8th parity: 5%) and 2 sex of the calf. Records from twins were eliminated as well as records with incomplete information or with erroneous gestation length. The data file includes 10760 records with an average progeny group size of

102 for each young sire and 97 for each reference sire in each yearly batch. Sires have between 75 and 125 records.

A preliminary study was realized only on fixed effects to define the adequate model of analysis, testing all fixed effects and two-term interactions. Under both LM and TM, all main effects appeared to be highly significant. A significant interaction has been detected between sex and age of dam in the ordinary least squares analysis under the linear model while none could be detected in a maximum likelihood analysis under a multinomial logit model (SAS-CATMOD procedure). Similar discrepancies between LM and TM have already been shown by Quaas *et al.* (1988) with data of the American Simmental Association. They result of the inadequacy of the linear model to eliminate scale interactions due to the discrete distribution of the observed variable.

The following complete model of analysis was therefore defined:

$$y_{ijklmno} = Y-S_i + REG_j + D-BREED_k + D-AGE_l + SEX_m + sire_n + e_{ijklmno}$$

Where :

$y_{ijklmno}$	= observed or underlying variable for the calf $ijklmno$
$Y-S_i$	= fixed effect of the year-season i
REG_j	= fixed effect of the region j
$D-BREED_k$	= fixed effect of the dam-breed k
$D-AGE_l$	= fixed effect of the dam-age group l
SEX_m	= fixed effect of the sex m
$sire_n$	= random effect of the sire n of the calf $ijklmno$, sires are unrelated.
$e_{ijklmno}$	= random residual.

Under the linear model (LM) sire effects were estimated as BLUP (Henderson, 1973) after variance components had been estimated with REML (Patterson and Thompson, 1971). Under the threshold model (TM) sire evaluations were obtained with the GFCAT method (Gianola and Foulley, 1983) and the variance components by a Marginal Maximum Likelihood method using a EM algorithm (Höschel *et al.*, 1987). All these methods are available in a computing program developed by Misztal *et al.*, 1989.

Methods were compared through the estimated heritability coefficients and the rank correlation between sire evaluations. A first comparison was realized on the whole data and a second one in 4 reduced files where only an average of 20% (12 to 28%) of the progeny per sire had been randomly selected.

RESULTS AND DISCUSSION

Estimated mean frequencies by the threshold model are 33.4% of unassisted birth, 56.0% easy assistance, 9.3% hard pull and 1.4% caesarian that gives a 10.7% dystocia.

Heritability coefficients and rank correlations between sire evaluations by both TM and LM are reported in table 1. In good agreement with the equations of Dempster and Lerner (1950) for dichotomous traits and Gianola (1982) for polychotomous traits, heritability coefficients are higher when estimated under a threshold model as compared with a linear model. Although calving score contains more information than dystocia owing to a better description of birth results, its heritability is inferior, when estimated under TM. We investigated this problem and estimated heritability of different traits corresponding to all possible combinations of scores in 2, 3 or 4 categories. Heritability was always lower when scores 1 and 2 were separated in two different categories suggesting that the main reason for these differences in heritability is due to an unclear definition of these two scores that leads to misclassification by breeders on the observed scale.

Table 1 Heritability and sire rank correlation coefficients

	Complete file		mean of 4 reduced files
	h^2 calving score	h^2 dystocia	h^2 calving score
Linear Model (LM)	.127	.089	.133
Threshold Model (TM)	.159	.263	.178
rank correlation LM vs TM	.999	.992	.970

In spite of higher heritability, threshold models do not significantly outperform the linear model in ranking sires in our complete file. For dystocia with a rank correlation of .992, an average of 1.4 sires will not be selected by truncature on BLUP as compared to a selection on TM evaluation: that corresponds to 5% of the selected sires when 1/3 of sires are selected. These close correlations between TM and LM have already been obtained in Holstein sire evaluations in the Netherlands (Meijering, 1985) and Israël (Weller *et al.*, 1988). Although the incidence of dystocia is low enough and heritability high enough to correspond to the most favorable situation described by Meijering and Gianola (1985) for higher efficiency of the TM over LM, the progeny testing procedures in our data set provide a relatively high and homogeneous progeny group size, while TM is better adapted to very unbalanced data. In the 4 reduced files with an average group size of 20, the rank correlation between LM and TM sire evaluation on calving score decreased to 0.970. In that case misranking occurs more frequently with 17% of error when selecting 1/3 of the sires on their BLUP evaluation. Djemali *et al.* (1987) found the same features with Holstein data in US where the effective number of progeny per sire averaged 23.3.

Therefore it can be concluded that the threshold model, in spite that it is more realistic, does not increase significantly the efficiency of sire selection in the condition where AI sires are progeny tested in France. However it has been clearly shown that with more reduced information, as in genetic evaluation of cows or natural service bulls using field data the threshold model has to be preferred to linear models. However computation requirements may lead to evaluations limited within-herd, and improvement in computing facilities is needed for a national evaluation of beef cattle on dystocia.

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