

APPLICATION OF AN ANIMAL MODEL  
ON A NATIONAL BASIS IN THE FRENCH BEEF CATTLE INDUSTRY

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SUMMARY

A first application of an animal model on french field recorded performance is presented. The data used in analysis are 210 day-weight of animals from the Limousine reference sire testing program of natural service bulls. The solving method of the mixed model equations used is an iterative on data method. Future improvements of the evaluation procedure are discussed.

INTRODUCTION

Up to now, the French genetic evaluation of beef cattle, based on field performance recording is done separately for males and females (Ménissier, 1988) :

- Maternal abilities of cows are estimated from their calves performance as dam traits. Evaluations are carried out by the contemporary comparison method as detailed by Marguin (1988). This evaluation includes four traits: birth weight, 120 day-weight, skeleton and fleshiness scores at weaning.

- Natural service bulls are progeny tested using planned matings in a reference sire program. Bulls are evaluated by a sire model and a BLUP procedure. A connexion index is computed in order to quantify degrees of comparison between sires of different herds (Foulley and Sapa, 1982). The four same traits as above are evaluated, except the 120 day-weight replaced by the 210 day-weight.

In the future, these two evaluations will be replaced by a simultaneous evaluation of all animals according to an animal model in order to take advantage of the well known properties of this model and to discriminate between direct and maternal genetic effects for the maternal influenced preweaning traits like weaning weight (Benyshek *et al.*, 1988). The aim of this paper is to show models and solving methods used for a first application of an animal model on french field data, including an example of the Limousine breed for the 210 day-weight.

MATERIAL AND METHODS

The statistical model includes :

- as fixed effects : herd-year, sex-management, parity of the dam and season of birth,

- as random effects : additive direct and maternal genetic effects, and maternal permanent environment.

It can be written as :

$$y = Xb + Wc + Za + M_1m + M_2p + e$$

where : y is the vector of observations,

b is the vector of fixed herd-year effects,

c is the vector of other fixed environmental effects,

a is the vector of direct additive genetic effects,

m is the vector of maternal additive genetic effects,

p is the vector of maternal permanent environmental effect,

e is the vector of residuals,

and X, W, Z,  $M_1$  and  $M_2$  are the corresponding incidence matrices.

The expectations and variance-covariance matrices of the random variables of the model are assumed to be :

$$E \begin{pmatrix} d \\ m \\ p \\ e \end{pmatrix} = \begin{pmatrix} 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} \quad V \begin{pmatrix} d \\ m \\ p \\ e \end{pmatrix} = \begin{pmatrix} A s_a & A s_{am} & 0 & 0 \\ A s_{am} & A s_m & 0 & 0 \\ 0 & 0 & I s_p & 0 \\ 0 & 0 & 0 & I s_e \end{pmatrix}$$

where the  $s$  are the values of the variances and covariances of the effects and are taken from Bertrand and Benyshek (1987) : The direct genetic variance ( $s_a$ ), the direct by maternal genetic covariance ( $s_{am}$ ), the maternal genetic variance ( $s_m$ ), the permanent environmental variance ( $s_p$ ) and the residual variance ( $s_e$ ) are respectively 63.94, -18.65,

61.67, 23.70 and 269.58 kg<sup>2</sup>. The other covariances, including permanent environmental and residual effects, are assumed to be zero.  $A$  is the additive genetic relationship matrix.

The mixed model equations are written as :

$$\begin{pmatrix} X'X & X'W & X'Z & X'M_1 & X'M_2 \\ W'X & W'W & W'Z & W'M_1 & W'M_2 \\ Z'X & Z'W & Z'Z+k_{11}A^{-1} & Z'M_1+k_{12}A^{-1} & Z'M_2 \\ M_1'X & M_1'W & M_1'Z+k_{12}A^{-1} & M_1'M_1+k_{22}A^{-1} & M_1'M_2 \\ M_2'X & M_2'W & M_2'Z & M_2'M_1 & M_2'M_2+k_{33}I \end{pmatrix} \begin{pmatrix} \hat{b} \\ \hat{c} \\ \hat{a} \\ \hat{m} \\ \hat{p} \end{pmatrix} = \begin{pmatrix} X'y \\ W'y \\ Z'y \\ M_1'y \\ M_2'y \end{pmatrix}$$

The parameters  $k_{11}$  to  $k_{33}$  are functions of the variances and covariances between random effects.

The chosen solving method is the so called "iterative on data" method (Schaeffer and Kennedy, 1986), that avoids explicit computation of the coefficient matrix, but requires reading as many copies of data files as there are fixed factors in the model. An additional file, containing an expanded pedigree file, must be read in order to apply Henderson's rules for computing the inverse of the relationship matrix (Henderson, 1976). This strategy performs Gauss-Seidel or successive overrelaxation type iterations.

Moreover, in order to minimize the number of data files to be read, we build and invert directly the submatrix corresponding to the fixed effects other than herd-year (i.e  $W'W$ ), as detailed by Schaeffer and Kennedy (1986). The convergence criteria is :

$$\left( \|u^{(n)} - u^{(n-1)}\| / \|u^{(n)}\| \right)^{0.5}$$

where  $u^{(n)}$  is the solution vector at  $n$ th round of iteration, and  $\|u^{(n)}\|$  is the norm of the vector.

The performance data used in the analysis were the same as used in the reference sire testing program of natural service bulls. The Limousine file included 5313 animals with performance, which were born between 1980 and 1988, and 10292 ancestors without performance. The numbers of sires and dams of animals with performance were respectively 224 and 3393. The numbers of levels of the fixed factors were 222 for herd-year, 6 for parity of dam, 6 for sex-managements and 7 for season of birth.

## RESULTS

After 100 successive overrelaxation-type iterations, with a relaxation factor of 1.5, the convergence criteria were  $3 \cdot 10^{-3}$ .

The correlation between direct genetic values estimated in this analysis and the estimations from reference sire program was 0.95.

Some basic parameters about the estimated values are resumed in the table 1.

Table 1. Estimates (kg) of the random effects in the model :

Effects	Mean	Standard Deviation	Maximum	Minimum
Direct genetic effects	-0.02	2.67	18.71	-20.72
Maternal genetic effects	-0.16	2.70	12.69	-15.52
Permanent environment effects	0	1.56	5.51	-07.15

#### DISCUSSION AND CONCLUSION

This procedure is at beginning. The main aspects to be improved are :

a) To speed the convergence, with strategies like adaptive overrelaxation (Berger et al., 1989) or non linear accelerations (Misztal et al., 1987).

b) The presented model didn't take into account the unknown ancestors groups. If a model including such groups is theoretically easy to solve (Westell et al., 1988), the way to build them is not obvious in beef cattle populations, where selection paths are less differentiated than in dairy cattle.

c) The measure of (dis)connexion of the entire design remains to be solved, for the procedure used in natural service bulls evaluation is not adapted to large size systems (Foulley et al., 1983).

d) Other traits will be included in the evaluation, specially reproductive traits like calving intervals or easy calving scores.

e) Optimal combinations of these estimations must be found to be used in the best way by breeders for their selection decisions.

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