

Implementation of an Animal Model for Production Traits of Dairy Cattle in Estonia

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Abstract

A multiple lactation animal model (AM) was applied to predict genetic merit for dairy cattle in Estonia. Records from the first three lactations were used and treated as different traits. Evaluations from animal model were found to be less affected from changes in average production across years as was observed for sire model evaluations. Correlations between EBV from animal model and sire model were in a range of .80 for bulls with progeny test. Animal model evaluations will replace current sire model evaluations for bulls. AM does also provide evaluations for cows, which will be released to the industry as well for enhancement of the breeding program.

Introduction

Restructuring of the agricultural system in Estonia had an impact on dairy production systems in Estonia in several aspects. First number of cows under milk recording reduced from about 260,000 cows in 1985 to about 170,000 in 1994. From 1989 to 1994 average milk production per cow declined by nearly 25%, as shown in Figure 1. In 1993 a common project of the ADT-Projekt GmbH, Bonn, Germany and organisations of the cattle industry in Estonia (financed by a grant of the German Ministry of Agriculture) was initiated with the aim of an increase in production of milk and an improvement in the profitability of dairy farming. In the context of this comprehensive project the *Vereinigte Informationssysteme Tierhaltung w.V. (VIT)*, Verden, Germany, was deeply involved in setting up the *Animal Recording Centre (ARC)* in Tartu, Estonia. One duty of ARC is to carry out genetic evaluations for dairy cattle. This report describes the implementation of an animal model for milk production traits, which has been done in

form of a consultancy work of VIT for ARC.

Genetic evaluations have been carried out with a single trait (1st lactation) BLUP sire model since 1992. With help of the improved database, which allows easy access to pedigree and performance records, it was attempted to run an animal model (AM) for genetic evaluation. Increased computing demand for the AM was not a problem, because PC based hardware (75MHz Pentium with 16MB of RAM) under a UNIX operating system (LINUX) was available and commercial software for genetic evaluation (PEST, Groeneveld) could easily be implemented.

A further reason for the change from a sire model to an animal model was the fact, that a negative phenotypic trend, which was mainly caused by bad environment, resulted in a negative trend in estimated breeding values of bulls for several years (Figure 2). Therefore comparison of sire evaluations across birth years was difficult, because only old sires, which had their first crop of daughters end of the eighties, had a chance to rank on top of the sire list.

The objectives of this study were

- a) to describe the implementation of an animal model for genetic evaluation in Estonia
- b) analyse results of the animal model in comparison with the sire model

Materials and Methods

Data

Data consisted of lactation records and 100 day production in first lactation from the database maintained at ARC in Tartu, Estonia. Main breeds are first Black and White, which have a high proportion of Holstein genes, and second Estonian Red, which was gradually upgraded with Red breeds from many countries. Both breeds have only little genetic ties between each other, therefore evaluations were carried out separately. To avoid problems with missing protein information lactation records were used from 1990 to present. Edits were on: age of calving in months (20 to 40, 30 to 56, and 44 to 75, for lactations 1 to 3, respectively), calving interval between 280 and 650 days, and edits on reasonable production in the specific lactation to eliminate errors from data acquisition. Records were precorrected with multiplicative factors for age at calving and calving interval, derived using recent data from Estonia. Table 1 gives some data statistics about the records used.

Pedigree was completed for cows with identification of dam and maternal grandsire from the national pedigree file. Pedigrees for bulls with daughter records or granddaughter records were completed for several generations resulting in about 165,000 animals in the pedigree file for Black and White and 129,000 animals for Estonian Red.

Model

For genetic evaluation a Multiple Trait Animal model was used:

$$y_{ijm} = HYS_{im} + a_{jm} + e_{ijm}$$

where

y_{ijm} is the yield of cow j in part-lactation m (1st trait: day 1 to 100 of 1st lactation, 2nd trait: day 101-305 of 1st lactation, 3rd trait: day 1-305 of 2nd lactation, and 4th trait: day 1-305 of 3rd lactation),

HYS_{im} is a fixed herd-year-season effect (two groups for season of calving, Jan-May and Jun-Dec),

a_{jm} is a random additive genetic effect of animal j , and

e_{ijm} is a random residual effect.

Variance components were estimated with a REML Animal model, using the software package VCE (3.1) from Groeneveld. Heritabilities were in a range of .20 to .25 depending on the trait, genetic correlations between lactations were in a range of .74 to .94 indicating that different lactations during the life of an animal should not be considered as repeated observations of the same trait.

For more details about the evaluation method see the Appendix.

Results and Discussion

Computational aspects

Available computing capacity was sufficient to apply the described model to the national dataset of Estonia. Evaluations were done for 3 traits within each breed, i.e. milk yield, fat yield, and protein yield. Percentage proofs were calculated from the respective yield traits. Iteration (200 rounds) for one trait for Black and White (with 688,856 equations) took about 70 minutes on the already described PC.

Analysis of the results

In sire model evaluations genetic trend estimates (Figure 2) followed (with a time lag)

the irregular phenotypic trend (Figure 1), therefore ranking across birth years was difficult. As expected, animal model evaluations better separate phenotypic trend in a genetic and environmental component, resulting in a positive genetic trend (Figure 2) which is not that much affected by the decrease in phenotypic production beginning of the nineties.

Correlations of EBV from the animal model with EBV from the sire model were in a range of .80, thus significant reranking occurred, mainly because now also younger bulls showed up on top of the sire list.

With the old evaluation system no cow EBVs were computed, therefore selection of bull dams was nearly completely based on phenotypic information and to a certain degree on sire of cow EBV. The animal model provides a reliable selection criterion for selection of females for the breeding program.

Through using this additional information higher genetic gain should be achieved compared to the old system.

In Estonia daughters from imported semen or imported bulls provide ties to foreign countries, which can be used for comparing EBVs from Estonian animals to animals in foreign countries. Using animal model evaluations for Black and White from Estonia and evaluations from Germany 14 bulls could be identified that had daughter records in both evaluations. Correlation between EBV from both countries were in a range of .75. Due to high proportion of imported semen in recent years it can be expected, that more data for derivation of conversion factors or inclusion in international evaluations in MACE procedures will be available, resulting in a reliable comparison of Estonian genetic material to breed stock all over the world.

Table 1. Statistics of the datasets used for genetic evaluation

part	Lact- ation	No of cows	Milk yield		Fat yield		Protein yield	
			mean	std	mean	std	mean	std
Black and White								
1-100	1	91614	1582.4	456.1	59.7	19.5	46.1	14.0
101-305	1	86690	2322.2	732.9	91.9	30.4	76.5	24.4
1-305	2	53299	4164.0	1260.9	164.1	53.0	129.8	40.6
1-305	3	31245	4322.5	1285.2	170.7	54.9	133.3	41.2
Estonian Red								
1-100	1	70882	1335.8	363.9	52.8	16.2	40.4	11.6
101-305	1	66039	1919.6	568.8	80.0	24.8	63.4	19.4
1-305	2	39489	3428.5	975.7	140.8	42.4	110.7	32.1
1-305	3	21839	3551.9	1036.1	145.8	45.3	113.1	33.9

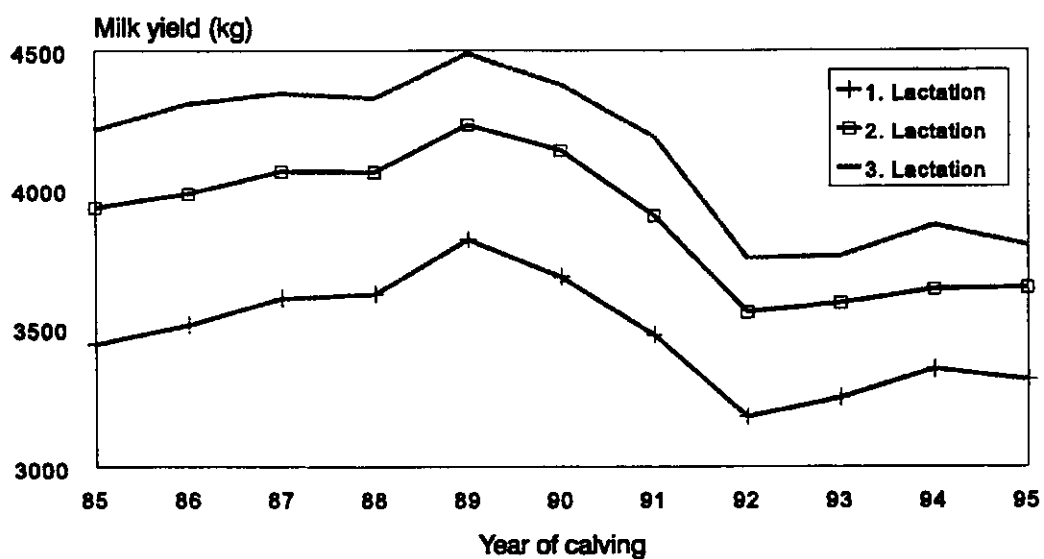


Figure 1. Phenotypic trend for dairy cattle in Estonia

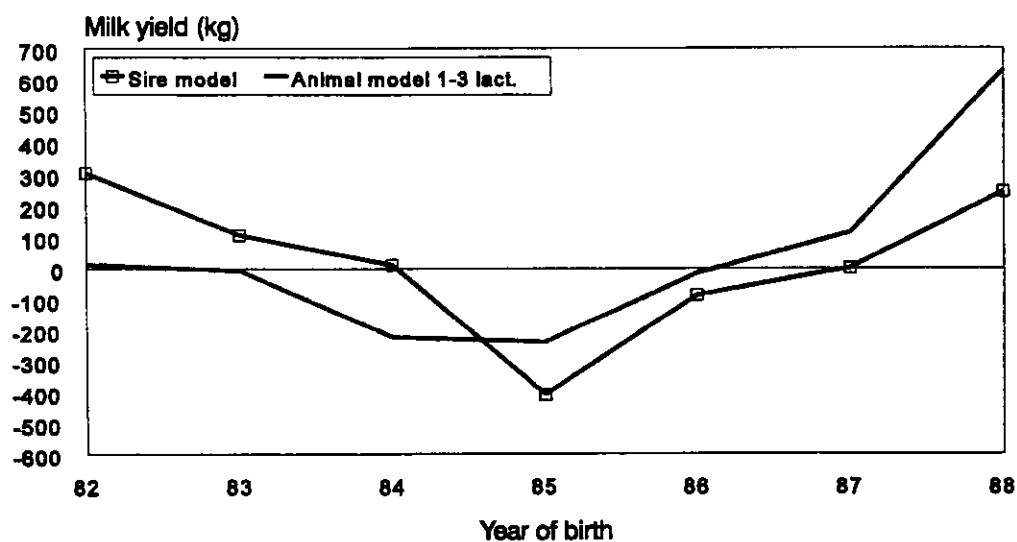


Figure 2. Genetic trend for EBV of bulls (Black and White from animal model and sire model)

Appendix

Facts on Estimation of Breeding Values in Estonia

Breeds	Estonian Red (ER), Estonian Black and White (EBW)
Traits evaluated	Milk, fat, and protein yield (kg); fat and protein concentration (%) proofs are calculated from respective yield trait proofs
Number of lactations	1, 2, and 3
Genetic parameters applied	Heritabilities: milk yield (.21 - .25) fat yield (.21 - .24) protein yield (.21 - .24) genetic correlations depending on trait combination (.74 - .94)
Inclusion and extension of records	Age at calving: 1st lactation: 20 - 40 months 2nd lactation: 30 - 56 months 3rd lactation: 44 - 75 months no extension of records, lactation yield has to be based on a minimum of 250 milking days
Sire categories	All sires
Effects considered by - pre-adjustment - model of evaluation	Age at calving, calving interval Herd - year - season, animal
Base for age adjustment	not necessary
Use of genetic groups	-
Method of evaluation	Multiple - trait BLUP Animal model. Four traits are 1st: Production 100 days of 1st lactation 2nd: Production 101-305 days 2nd lactation 3rd: Production 305 days in 2nd lactation 4th: Production 305 days in 3rd lactation
Expression of genetic merit	Breeding values (BV) for milk, fat and protein (kg), fat and protein (%) as average EBV from lactations 1 to 3 Relative breeding values (RBV) for production index SPAV ($BV_{fat_{kg}} + 6 * BV_{protein_{kg}}$) with mean of 100 and SD of 12 points
Genetic base	BV: Fixed cow base 95 RBV: Defined by actually proven AI bulls (in 1996 by testbulls born in 1986 - 1988)
Minimum requirements for pub. of sire proofs	20 daughters in 3 herds
