Effect of Heterosis and Imported Germ Plasm on Production Traits Estimated in the Danish Multi-Breed Animal Model

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Introduction

The Danish dairy industry consists of cattle from four native breeds: Danish Red (RDM), Danish Friesian (SDM), Danish Jersey (DJ) and Danish Red & White (DRK), and crossbreed between these breeds. During the last decades, germ plasm has been imported to all four breeds, so in addition to the native breeds, the following breeds: American Brown Swiss (ABS), Holstein Friesian (HF), New Zealand Jersey (NZJ) and American Jersey (USJ), have made major contributions to the genetic make up of the dairy cattle population, imports from other breeds such as Swedish Red & White (SRB), Ayrshire (AYR) and Norwegian Red (NRF) have only made minor contributions.

At present, breeding values of bulls for milk production are estimated by a modified BLUP-Sire model on 1'st lactation 305 days yield (Nielsen et al., 1994). Cows breeding values are estimated by means of Direct Updating (Christensen, 1980). Change to a Multi-Breed Animal Models is planned to take place by November 1997.

The objectives of this paper are to present the Danish Multi-Breed Animal Model, and to present some preliminary results from the first test run of the model.

Statistical model

$$
\begin{aligned}
y = \ & \text{Management group} \\
& + \text{Lact(1-4+)} * \text{TP} \\
& + \text{Year-month of calving} * \text{Lact(1-4+)} \\
& + \text{Age at calving} * \text{Lact(1-4+)} * \text{TP} \\
& + \text{Previous Calving Interval} * \text{Lact(1-4+)} * \text{TP} \\
& + \text{Current Calving Interval} * \text{Lact(1-4+)} * \text{TP} \\
& + \Sigma \text{ additive effects of gene import / crossbreeding (Phantom parent groups)}
\end{aligned}
$$

+ Σ heterosis due to dominance effects of gene import /crossbreeding * lact(1-4+)
+ Permanent environment
+ Animal
+ Residual

where management groups are defined as clusters of calvings close in time within herd and 1'st vs. later lactations. The clustering is performed by an algorithm developed by Schmitz et al. (1991). Lact(1-4+) is grouping in 1'st, 2'nd 3'rd and 4'rd and later lactations. TP is time periods defined in 5 years intervals going back from the latest calving date in the data.

The environmental effects in the model correspond to the effects in the present model for sire evaluation (Nielsen et al., 1994) augmented with effects of age at calving in later lactations, calving interval (both previous and current), and permanent environment effect of each animal with record.

The additive effects of gene import/crossbreeding are included in the model as phantom parent groups. Each animal's pedigree is traced back to pure breed unknown parents. Animals with unknown parents are assigned breed composition based on average for the population and birth year it belongs to. Dummy individuals are then inserted until the parent of the dummy individual are pure breed. To take into account genetic trend in the imported germ plasm, the unknown parents are grouped by breed and year of birth of the progeny. Breed*year of birth subclasses with a small number of progenies are merged into groups covering several years.

The heterosis due to dominance effects are defined as the regression on additional heterozygosity above the proportion that is present on average in the contributing breeds.

Heterogeneous variance among breeds, calving year and lactations within breeds is taken into account by standardisation of data with

breed*calving year*lactation specific standard deviations.

Heterogeneous variance due to management group and lactation length is taken into account as follows:

1. Estimate the variance in each management group (MG).
2. Combine the estimated variance in each MG with the base variance and the variances in the two previous MG's with weights equal to degree of freedom (DF) on the variance from the MG itself, & *DF on the variances from the two previous MG's and 20 on the base variance.
3. Adjust the heritability in each MG based on the square root of the ratio between the MG variance and the base variance.
4. Adjust the phenotypic and genetic variances for lactation length.
5. Standardise data to constant genetic variance.
6. Weight each observation with the ratio between the base residual variance and the residual variance for the observation.

This method to account for heterogeneous variance is an extension of a method developed by Madsen et al. (1995).

Model validation

The following methods are used for model validation:

1. Comparison of evaluations based on all lactation data or on first lactation data only.
2. Within-bull variation of daughter yield deviation.
3. Analysis of proof variation over time.
4. Regression of proof on parents proofs.

Method 1 to 3 are the methods proposed by INTERBULL. In method 4, the regressions are calculated in different categories of animals, and the estimated regression coefficients are tested against their expectation. Expectations are calculated assuming an average amount of information on the individual itself and its sire and dam for that category.

Test-Run

The Multi-Breed Animal Model has been tested on 305 days protein yield of 4464113 cows with a total of 9013814 completed and extended lactations. The lactations were initiated in the years 1978 to 1996 both inclusive. After tracing pedigree information back to pure breed phantom parent, the relationship matrix included 6335203 individuals and 323 phantom parent groups.

During the model validation some problems showed up:

1. There are problems with the correction for current calving interval. This is due to the fact that culled cows and cows with records in progress do not have a current calving interval and were treated as a separate group.
2. There are problems with the way dummy individuals are inserted into the pedigree for animals with unknown parents. The way it is done tends to overestimate the amount of heterozygosity in animals with unknown parents, and to reach pure breed phantom parents of imported breeds to early.

The results presented in the following are therefore very preliminary.

Heterosis estimates for the 32 breed combination times four lactation groups considered are give in Table 1.

Table 1. Preliminary estimates of F_1 heterosis for 305 days protein yield (kg).

Breed combination	Lactation			
	1st	2nd	3rd	4th + later
RDM < SDM	5	4.5	3.4	2.6
RDM < DJ	7.6	6.9	5.9	5.4
RDM < DRK	3.8	2.0	3.7	3.5
RDM < ABS	8.8	10.5	9.1	7.7
RDM < HF	4.7	4.2	4.0	3.8
RDM < NZJ	13.6	10.3	6.5	9.4
RDM < USJ	7.9	6.8	1.7	3.7
RDM < SRB	4.6	5.1	2.9	-1.6
RDM < other	3.8	3.0	1.9	-0.2
SDM < DJ	5.4	6.5	4.9	4.6
SDM < DRK	1.2	1.5	3.0	2.3
SDM < ABS	8.8	9.5	4.6	6.5
SDM < HF	2.8	2.7	2.8	2.7
SDM < NZJ	-0.1	-2.1	12.1	11.5
SDM < USJ	6.7	7.2	-1.5	2.3
SDM < other	1.2	2.1	1.4	1.4
DJ < DRK	7.2	7.6	6.0	6.0
DJ < ABS	9.0	13.1	8.7	9.2
DJ < HF	7.3	7.0	6.4	5.6
DJ < NZJ	5.2	3.4	2.3	2.2
DJ < USJ	5.9	2.3	1.4	0.7
DJ < other	-1.6	0.4	-1.3	-2.8
DRK < ABS	7.9	8.7	11.3	10.0
DRK < HF	4.3	2.7	2.9	2.1
DRK < other	1.6	0.6	0.9	1.9
ABS < HF	5.6	9.3	6.8	5.9
ABS < NZJ	12.4	5.5	-7.5	-0.7
ABS < USJ	5.8	14.3	15.7	0.0
HF < NZJ	9.0	7.5	2.4	-6.6
HF < USJ	8.9	7.4	9.9	5.0
NZJ < USJ	8.9	7.5	4.2	5.5
Other < other	3.6	3.6	2.7	1.6

Genetic merit of phantom parent groups are in Table 2. For breeds were phantom parent groups are defined for each year, the figures given are averages for five years periods.

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Table 2. Preliminary estimates of genetic merit for 305 days protein yield (kg) of phantom parent groups.

Years	RDM %	RDM &	SDM %	SDM &	DJ %	DJ &	DRK %	DRK &	ABS % + &	HF % + &	NZJ % + &	USJ % + &
-1965	-17.1	-4.8	-13.7	-2.3	-13.5	-23.1	-19.4	-5.1		-8.6		-6.4
1966-70	-15.9	-5.0	-3.5	-6.3	-20.3	-20.1	-16.7	-4.7	-4.4	-3.2	-23.3	-24.7
1971-75	-5.9	-7.5	-5.6	-7.4	-17.7	-19.5	-6.8	-3.2		-1.3		
1976-80	-4.8	-7.2	-4.6	-6.0	-18.4	-18.7	-6.4	-5.8		0.0	-19.4	-9.9
1981-85	-3.4	-6.9	-3.1	-3.0	-17.3	-16.1	-4.2	-8.3	1.5	14.5	-	-
1986-90	0.1	-2.0	3.9	5.6	-11.8	-15.3	-2.8	-2.1	-	5.0	-	-
1991-	0.4	-	7.6	-	-7.9	-15.5	-3.8	-	-	10.4	-	-