

Joint Nordic Test Day Model for Milk Production Traits

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Abstract

A joint Nordic evaluation model for milk production traits is under development for Holsteins, Nordic Red Cattle breeds and Jerseys.

Introduction

For many years, Sweden, Finland and Denmark have used the same bull sires in Holsteins and to some degree in the Nordic Red breeds. However, it would be more effective to select animals jointly. To make accurate comparison and selection of bulls and cows across countries possible, a joint genetic evaluation based data from the three countries is needed. In order to gain general acceptance of the joint Nordic evaluation model within the countries the model has to be at least as good as the current national models are. It should also exploit optimally the genetic connections between the countries (Juga, 2002).

As all participating countries will not be able to supply test days records for the time period used in the current national models, the joint evaluation model has to be able to deal with both test day records and 305-day records

Up to now Finland has used test day random regression model including data from all lactations from 1988 onward, whereas Sweden and Denmark have used a 305-day animal model. In Denmark a test day model has been developed for data from 1990 onward, but this evaluation model has not been implemented.

On this background a project on a joint evaluation of dairy cattle in the three participating Nordic countries (Finland, Sweden and Denmark) was initiated in year 2002 in order to build up an evaluation system for milk production traits. It was decided to develop three models:

- “The Ayrshire model” for Finnish Ayrshire, Swedish Red and White and for Red Danish Cattle
- “The Holstein model” for Holstein cattle in the Nordic countries
- “The Jersey model” for Jersey cattle in Nordic countries.

Material and methods

Data

The number of data submitted by Denmark, Finland and Sweden to the joint evaluation is shown in Table 1. Data exchanged were national evaluation data. Data for Holstein and Ayrshire runs from Finland included both Holsteins and Finnish Ayrshires as both breeds are evaluated simultaneously in Finland. The reason is that the many Finnish herds have cows of both breeds and within breed evaluation would split the management groups to very small numbers. In Denmark and Sweden, the number of mixed breed herds is smaller, and the two breeds are evaluated separately. So far the Jersey model has included data from Denmark only, but a very small Jersey population exists in Sweden and will be included in the joint Jersey evaluation.

The data included in the joint Nordic evaluation is the data used in the current National evaluation systems. The data from Sweden include first lactations from 1983 and from 1987 also second and third lactations. Denmark include the first three lactations from 1982 and onwards, whereas the Finnish data

include up to ten lactations per cow from 1988 onward. Sweden supplies only 305-day records whereas Denmark supply both test day record and 305-day records and Finland only test day records. The data has been subjected to the National editing rules, but the differences are small. The 305-day records included incomplete records extended by the national procedures.

The Swedish and Danish Holstein populations are well connected both with respect to number of common sires and

common bull sires. The majority of common bull sires are of North American origin. The links to the Finnish Holstein are mostly due to foreign bull sires. The number of common sires and bull sires has increased during the years

The Finnish and Danish Red populations are relatively well connected to the Swedish Red and White, whereas the direct links between the Finnish and Danish populations are more sparse as sires from Finland usually have very few daughters in Denmark.

Table 1. Number of data in joint Nordic evaluation in November 2003.

Country	Number of cows	Number of records	Number of cows	Number of records	Number of cows	Number of records
	Holstein		Ayrshire		Jersey	
Finland* TD: 1988 -	318,408	7,404,451	1,074,739	26,177,075	0	0
Denmark TD 1990 -	2,172,150	36,967,801	335,754	5,569,901	380,617	6,495,207
Joint Nordic TD-records	2,490,558	44,372,252	1,410,493	31,746,976	380,617	6,495,207
Sweden: 305d 1981 -	929,265	1,608,129	1,167,198	2,010,464	0	0
Denmark: 305d 1981 - 1989	1,322,607	2,445,568	281,824	527,748	291,499	568,885
Joint Nordic 305d records	2,241,872	4,053,697	1,449,022	2,538,212	291,499	568,885

* Finnish Holstein and Finnish Ayrshire data are included in both the Holstein and Ayrshire evaluation

Models

The joint evaluation is based on the concept of the multivariate “meta-model” described by Mäntysaari (2003). The meta-model treats the recordings of the biological traits in different countries as different analytical traits. They are entitled to different environmental effects, different variances and covariances among traits. Since the aim in joint evaluation is not only to rank animals within countries but also across countries, the across country genetic correlation is restricted to unity. In practice this is done by estimating only one set of breeding value coefficients for each animal, but using different covariables for breeding value functions in each country. As only one set of breeding values is calculated per animal, the genetic correlation structures are the same in all countries.

The meta-model can accommodate different heritabilities in different countries, as well as different phenotypic correlations within lactations or across traits. As only one set of breeding values is calculated per animal, it requires that genetic correlation structures are the same in all countries.

The trait-country groups in the Nordic model are: Finnish TD records, Danish TD records, and 305d records in Sweden and early data in Denmark. In each country the first three lactations are considered as different traits as well as milk, protein and fat. Thus, the number of traits in the analysis is 27 (18 TD traits and 9 305d traits). An exception is the Jersey model where only data from Denmark is included. In the Finnish trait group the third lactation is modelled with repeatability model, which allows inclusion of all lactations to the data.

For each TD trait the animal effects and permanent environmental effects are modelled by second order Legendre polynomials plus an exponential term, $\exp(-c \cdot \text{dim})$ where $c = 0.05$ for milk and 0.04 for protein and fat. Measurement errors are treated homogenous within lactation, but correlated across traits within same the TD-group.

The 305d records are included using the unified trait approach as described by Mäntysaari (2002), with exception that a permanent environment effect is included for each trait. This facilitated the use of diagonal structure for measurement error variance.

In the unreduced model each animal has 36 breeding value coefficients (4 per trait, 3 traits, 3 lactations) and each animal with TD-records has up to 36 permanent environment coefficients. Because a repeatability model is used for Finnish later lactation data each of the Finnish lactations from the third onwards has extra 12 equations. For animals with 305d records the number of permanent environmental effects is 9.

The variance components for the meta-model were derived using a 2-step approach as described in Emmerling *et al.* (2002). The parameters for the derivation were obtained from Jacobsen *et al.* (2002) and Lidauer *et al.* (2002). Both estimated genetic and residual covariances of milk, protein and fat in three lactation and 5 stages of the lactations. Table 2 lists the heritabilities, genetic and phenotypic correlations for 305d standard records derived from TD. Table 2 show the Holstein results and table 3 the corresponding heritabilities for the other breeds.

The computational model was based on reduced rank equations (Mäntysaari, 1999).

For the breeding values, all traits in the first lactation are modelled with 6 equations, and all traits in later lactations by 8 equations. The TD permanent environment effects of each lactation is reduced to 6 equations. At the end, a cow with any number of TD records in 1st, 2nd and 3rd lactation is assigned 14 breeding values, and 6 permanent environmental effects per lactation that are included. For cows with 305d records only 3 permanent environment equations per lactation are used.

The model will account for heterogeneous variance by a multiplicative mixed model approach (Meuwissen *et al.*, 1996). The variance-model for describing the heterogeneity of variance in the data includes a country $\times$ year $\times$ month $\times$ parity effect and a random herd $\times$ year $\times$ parity group effect having an autoregressive structure between herd years. Variance components for the variance-model were estimated for all 27 traits and all breeds. Solving of the multiplicative mixed model was described by Lidauer *et al.* (2002).

Table 4 lists the environmental effects that are included in the models in each country. Great effort was made to make the models similar across countries. Largest difference remaining was in modelling of herd-test day effect, which in Holstein model in Denmark was considered fixed, whereas in Finland herd-test day was divided into a fixed herd-year and a random herd-test day effect. Sweden and especially Denmark are characterized by large herds (45 and 85 cows pr. herd), whereas herd sizes in Finland are still small (20 cows pr herd). The herd sizes are very small for Finnish Holstein, because a large part of these animals are in mixed breed herds.

Table 2. Heritabilities (diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) of 305d yields derived using reduced rank random regression model for Danish Holstein.

	1st Lactation			2nd Lactation			3rd Lactation		
	Milk	Protein	Fat	Milk	Protein	Fat	Milk	Protein	Fat
M1	0.43	0.86	0.46	0.85	0.71	0.23	0.81	0.63	0.09
P1	0.92	0.35	0.67	0.75	0.85	0.46	0.71	0.81	0.33
F1	0.75	0.85	0.36	0.42	0.68	0.85	0.43	0.70	0.78
M2	0.52	0.48	0.37	0.29	0.84	0.42	0.99	0.78	0.32
P2	0.46	0.50	0.45	0.94	0.25	0.72	0.84	0.99	0.62
F2	0.31	0.39	0.51	0.79	0.88	0.29	0.47	0.76	0.98
M3	0.47	0.43	0.34	0.49	0.44	0.34	0.27	0.79	0.37
P3	0.41	0.46	0.42	0.42	0.47	0.41	0.92	0.25	0.69
F3	0.22	0.31	0.45	0.30	0.39	0.49	0.79	0.86	0.29

Table 3. Heritabilities of 305d yields derived using reduced rank random regression model for Finnish Ayrshire (FAY), Danish Red Cattle (RDM), Swedish Red and White (SRB) and Danish Jersey (DJ).

	1st Lactation			2nd Lactation			3rd Lactation		
	Milk	Protein	Fat	Milk	Protein	Fat	Milk	Protein	Fat
FAY	0.38	0.26	0.27	0.30	0.23	0.27	0.30	0.23	0.24
RDM	0.42	0.35	0.41	0.21	0.28	0.20	0.20	0.19	0.25
SRB	0.35	0.30	0.35	0.20	0.20	0.25	0.20	0.20	0.20
DJ	0.44	0.38	0.35	0.27	0.23	0.22	0.27	0.23	0.23

Table 4. Environmental effects included in the joint Nordic evaluation model.

	Denmark 305 d Sweden 305d	Denmark TD	Finland TD
Herd	Herd x Year x Season	Herd test day	Herd x Production year Herd test day (Random)
Calving age	Country x Month x time period	Calving month	Calving month or >5 th lact.: Parity
Year x Season	Country x Calving year x Month	Test year x month	Test year x month
Fertility	Country x Days open dev	Days carried calf	Days carried calf
Previous CI/Days dry	Country x Previous CI	Days dry	Days dry
Lactation curve	-	Second order polynomial + 2 exp. terms nested in calving year x season	Second order polynomial + 2 exp. terms nested in calving year x season
Herd lactation curve	-	First order polynomial Nested in herd x time period	First order polynomial Nested in herd x time period
Heterozygoty	3 effects for HOL 4-6 effects for AYS 2 effects for Jersey	3 effects for HOL 4-6 effects for AYS 2 effects for Jersey	

Computations

All computations have been made with the Mix99-program (Lidauer *et al.*, 2003). The test runs have been carried out on 4 separate Linux clusters with different configuration, number of nodes, speed and size. Solving of the current Nordic model with 133 million equations in the mean-model, 10 million equations in the variance-model, and 41 million TD and lactation records takes about 44 hours. Solving the Nordic Holstein model is nearly twice as big task.

Results

Up to now, the results of test runs have shown correlations between national evaluation and the joint Nordic evaluation between 0.93-0.99 for sires and 0.88-0.97 for cows. The correlations was highest for Finnish animals where the change in model has been very moderate, and lowest for Danish animals. In Denmark the correlations are partly due to the shift from 305d to TD-model and partly due to the joint Nordic evaluation.

Conclusion

At this point a Nordic Animal Model for milk production traits has been developed. Some additional “fine tuning” is still needed before implementation.

The development of the Nordic model for milk production traits was made in a joint project of MTT Agrifood Research, Jokioinen, Finland and Danish Institute of Agricultural Sciences at Foulum, Denmark. The practical application and test of the models are made by The Finnish Animal Breeding Association, Vantaa, The Danish Agricultural Advisory Service, Aarhus and The Swedish Dairy Association, Eskilstuna

In another joint Nordic project, models for sire evaluation of some functional traits are currently under development. The traits included in these projects are: Fertility, conformation, udder health and calving performance. The objective of these projects is to develop a comprehensive joint Nordic evaluation covering all traits of economic importance.

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