Joint Genetic Evaluation of Other Disease Traits in Denmark, Finland and Sweden

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Abstract

Reproductive, metabolic and feet and legs diseases in the three first lactations are included in joint sire evaluations of RDC and Holstein breeds in Denmark Finland and Sweden. The evaluations are multivariate analyses of 13 traits with heritabilities from 0.005 to 0.025. Trait definition differences between countries were made smaller by thorough harmonization. A simple pre-correction for heterogeneous variances across years and countries was made.

Introduction

Animal health constitutes an important part of the Nordic breeding goal.

It is important because diseases reduce animal welfare and will cause economical losses for the farmer. Disease treatments have been reported and used for breeding purposes for long within each of the Nordic countries. Philipsson (1980) proposed that disease information should be used in sire evaluation. Even though other disease treatments include a lot of different diseases, and sometimes ambiguous disease codes, the practical experience is that the evaluations have contributed with important genetic information to the breeding work.

However, the national genetic evaluations have focused on partly different diseases. In addition, while the other disease evaluation in Denmark consists of three traits (reproductive, metabolic and feet and legs diseases), Sweden has two (reproductive and other diseases) and Finland has just one other disease trait containing disease codes from all the three different disease groups. This situation makes it difficult to use the current national breeding values across countries.

Disease treatment policies differ, over time and between countries, which will cause differences in disease frequencies. The differences between countries should lower correlations between countries and lower heritabilities across countries if all diseases were summed together and evaluated as one trait. In this evaluation we divide the other diseases into traits that may differ in means between, but share, as much as possible, the same diseases across the countries. The joint evaluation focuses on utilisation of diseases common to all three countries to give joint Nordic breeding values for common use in the selection for better animal health.

Materials and Methods

Trait definitions and summary statistics

Records from first to third lactation on early reproductive diseases (ERP), late reproductive diseases (LRP), metabolic diseases (MB) and feet and legs (FL) and from first lactation only, on clinical mastitis (CM) were used in the genetic evaluations. Clinical mastitis was included as an information trait. Table 1 gives the disease groups, defined by Østerås et al. (2002), used in each trait. Table 2 gives the abbreviations and the recording periods in all 13 traits together with the calculated indexes.

The majority of infective and other reproductive diseases are within 40 days after calving. Thus for ERP, naturally the cases of retained placenta and infective and other reproductive diseases will dominate. For LRP the incidents of hormonal reproductive diseases will dominate. The detailed disease codes used are given in Johansson (2008).

Table 1. Disease groups (Østerås et al., 2002)) used in the other disease traits.

ERP	LRP	MB	FL
Retained placenta, Hormonal reproductive diseases, Infective reproductive diseases, Other reproductive diseases	Hormonal reproductive diseases, Infective reproductive diseases, Other reproductive diseases	Ketosis, Milk fever, Other metabolic diseases, Other feed related diseases, Other diseases	Feet and leg diseases

Table 2. Abbreviations and definitions of traits included in the evaluation.

Trait abbrev.	Definition
	Trait definitions
ERP1-ERP3	Early repr. disease (1) or not (0), 0 to 40 DIM, lact 1-3
LRP1-LP3	Late repr. disease (1) or not (0), 41 to 305 DIM, lact 1-3
MB1-MB3	Metabolic diseases (1) or not (0), -15 to 305 DIM, lact 1-3
FL1-FL3	Feet & leg diseases (1) or not (0), -15 to 305 DIM, lact 1-3
CM1	Clinical mastitis (1) or not (0), -15 to 305 DIM, lact 1
	Index definitions
ERP	Early reproduction: 0.5*ERP1+0.3*ERP2+0.3*ERP3
LRP	Late reproduction: 0.5*LRP1+0.3*LRP2+0.3*LRP3
MB	Metabolic diseases: 0.5*MB1+0.3*MB2+0.3*MB3
FL	Feet & leg diseases: 0.5*FL1+0.3*FL2+0.3*FL3
OD (RDC)	Other diseases tot.:1.93*ERP+1.04*LRP+1.87*MB+1.7*FL
OD (HOL)	Other diseases tot.:2.0 *ERP+1.05*LRP+1.88*MB+1.75*FL

Phenotypic records for all three countries from 1990 are included. Table 3 gives country means and number of first and third calving. Denmark has highest mean for ERP1 and lowest mean for LPR1, while Finland has most recorded LRP1. See Johansson *et al.* (2008) for further details.

Table 3. Average for other disease traits in first lactation

	Denmark	Finland	Sweden
First lactation, Holstein			
No first calving daughters	1583476	324127	716950
ERP1	0.088	0.039	0.028
LRP1	0.014	0.111	0.066
MB1	0.032	0.049	0.022
FL1	0.058	0.023	0.030
First lactation, RDC			
No first calving daughters	247855	940279	776224
ERP1	0.096	0.033	0.024
LRP1	0.0119	0.132	0.068
MB1	0.033	0.037	0.026
FL1	0.059	0.019	0.028
Third lactation, Holstein			
ERP3	0.126	0.036	0.037
LRP3	0.013	0.105	0.057
MB3	0.101	0.128	0.096
FL3	0.057	0.019	0.028
Third lactation, RDC			
ERP3	0.126	0.038	0.045
LRP3	0.012	0.129	0.073
MB3	0.125	0.094	0.099
FL3	0.055	0.014	0.022

Genetic evaluation model

All traits are pre-corrected for heterogeneous variance due to year of calving and country. The model for estimation of breeding values is a multi-trait, multi-lactation model with herd*year effects as random. The only genetic random effect is for sires. Included as fixed class effects are herd*period, calving age*country, and year*month of calving*country. The periods are 5 years. For the Red Dairy Cattle, effects of Original Red Danes, Danish Friesian, Finnish Ayrshire, Norwegian Red, American Brown Swiss, American Holstein, Swedish Red Cattle, Canadian Ayrshire and Finncattle are accounted for by regressions on population proportions. For the Nordic Holstein populations, the effect of Holstein versus Friesian is accounted for by regression on the population proportion. Heterosis is accounted for using the regression on expected total heterosis of all included populations.

The heritabilities used are found in tables 4 to 6. They are based on estimates from the current data and from an earlier study (Sander-Nielsen *et al.*, 1997). FL traits have on average the lowest heritabilities. The MB3 trait has high heritability for both breeds which is a result of the increased incidence of paresis in lactation 3. Within lactation correlations were largest in first lactation. The genetic correlations are somewhat higher for Holstein. Typically, the genetic correlations to FL1 are almost zero for RDC. A complete description of the genetic parameters used for the 13 traits in the evaluation is given in Johansson (2008).

Table 4. Genetic correlations (under), residual correlations (above), and heritabilities on diagonals. First lactation.

	Holstein				RDC				
Trait	ERP1	LRP1	MB1	FL1	ERP1	LRP1	MB1	FL1	CM1*
ERP1	**0.02**	0.16	0.03	0.01	**0.01**	0.24	0.03	0.01	0.01
LRP1	0.40	**0.01**	0.01	0.01	0.25	**0.01**	0.02	0.01	0.00
MB1	0.40	0.49	**0.01**	0.03	0.30	0.21	**0.01**	0.03	0.01
FL1	0.35	0.36	0.27	**0.01**	0.00	-0.02	0.00	**0.01**	0.01
CM1	0.18	0.15	0.45	0.31	0.33	0.18	0.39	0.23	**0.02**

* For CM1 the residual correlations and heritability are the same for both breeds

Table 5. Genetic correlations (under), residual correlations (above), and heritabilities on diagonals. Second lactation.

	Holstein				RDC			
Trait	ERP2	LRP2	MB2	FL2	ERP2	LRP2	MB2	FL2
ERP2	**0.02**	0.16	0.03	0.01	**0.01**	0.23	0.03	0.01
LRP2	0.33	**0.02**	0.01	0.01	0.25	**0.02**	0.02	0.01
MB2	0.17	0.28	**0.01**	0.03	0.11	0.20	**0.01**	0.03
FL2	0.10	0.20	0.39	**0.01**	0.00	0.02	0.03	**0.01**

Table 6. Genetic correlations (under), residual correlations (above), and heritabilities on diagonals. Third lactation.

	Holstein				RDC			
Trait	ERP3	LRP3	MB3	FL3	ERP3	LRP3	MB3	FL3
ERP3	**0.02**	0.16	0.03	0.01	**0.01**	0.20	0.01	0.01
LRP3	0.36	**0.02**	0.01	0.01	0,28	**0.02**	0.03	0.01
MB3	0.17	0.31	**0.03**	0.03	0,16	0,18	**0.03**	0.03
FL3	0.10	0.24	0.20	**0.01**	0,00	0.00	0.03	**0.01**

Results and Discussion

The joint evaluation of harmonized data from the three NAV countries should make it possible to make better decisions regarding other diseases compared to earlier when selection decisions were taken on national data alone. By design traits in the current national evaluations are more or less different from the NAV traits. EBVs from the joint evaluation have thus rather varying correlations with those from national evaluations. Highest correlations, are 0.8 to 0.9, occur naturally when traits are more or less similar, lowest, around 0.3, points at the large differences that exist between the current national evaluations and the new NAV evaluation.

The new NAV evaluation has been validated by Interbull method 3 and 7 out of the 10 combined traits are passing the test. For both breeds the OD-index, which will be included in the total merit index, passes the validation.

The rather large differences found in country means for ERP and LRP in table 3 causes differences between countries in standard deviations of EBVs even though variation has been precorrected phenotypicly between countries and years. Figures 1 and 2 show the differences. The reason for different frequencies is probably due to environmental differences and differences in treatment policies. A good harmonisation should also include the recording scheme. Such a joint project is started in the Scandinavian countries.

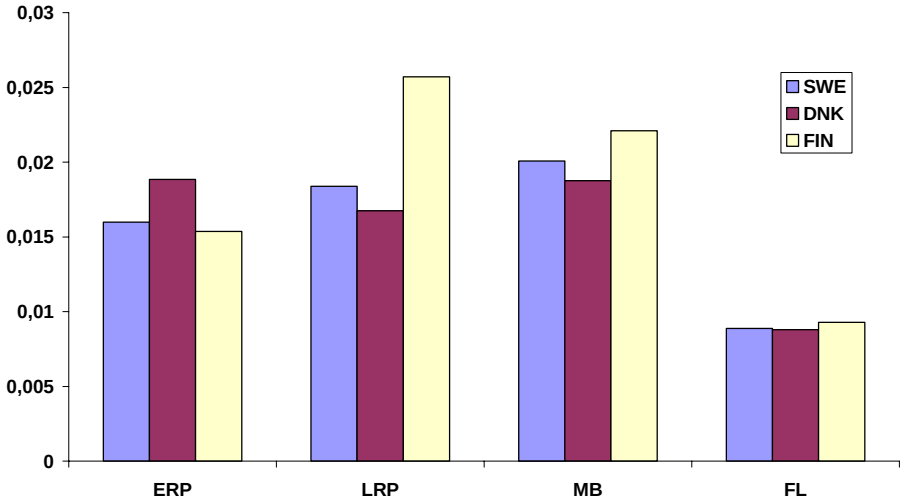

Figure 1. Mean standard deviation of estimated sire breeding values. Holstein

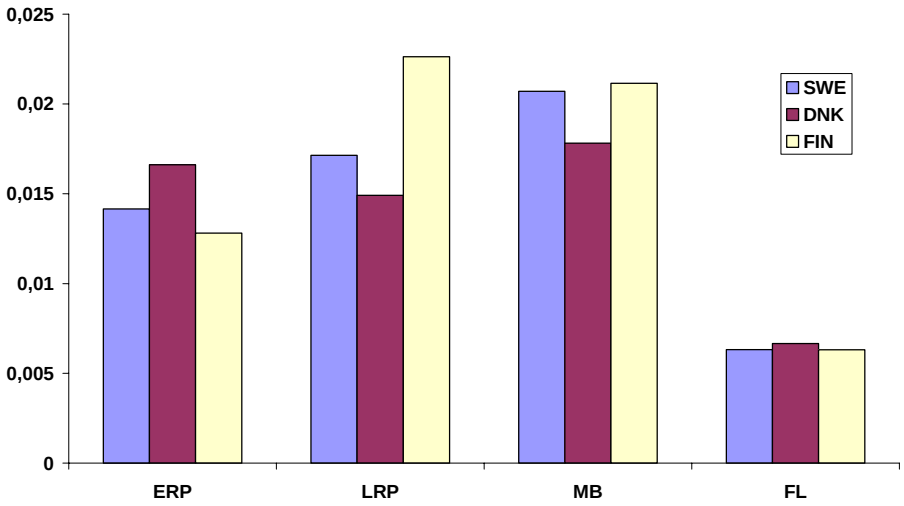

Figure 2. Mean standard deviation of estimated sire breeding values. RDC.

Most genetic trends for Red and Holstein cattle were unfavourable. The trends for RDC are given in figure 3. The early reproductive trait has a trend near zero . The scale to the left is an index scale for which high values are favourable. More work will be done to penetrate the reasons behind those trends.

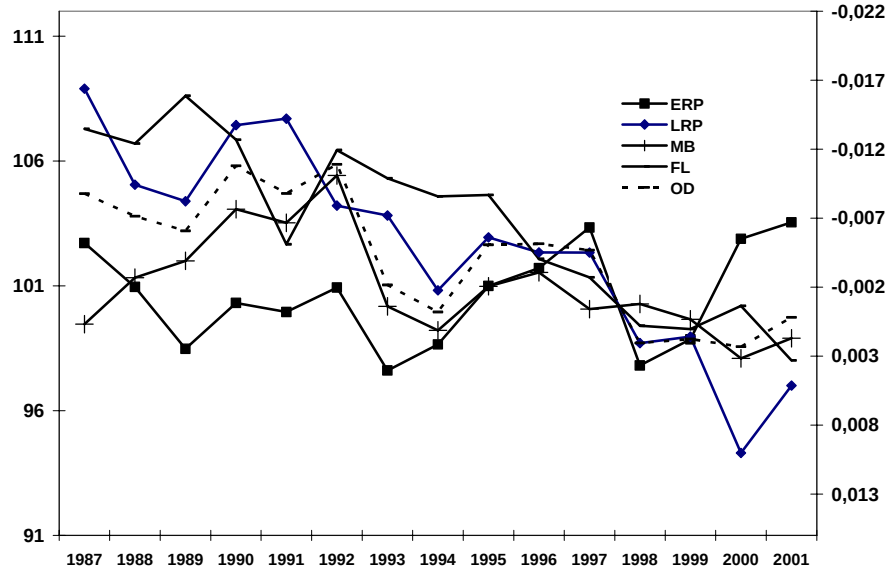

Figure 3. Genetic trends for RDC. Average of relative sire EBVs.

Despite the many problems that are connected with other diseases i. e. the heterogeneous nature and the varying recording policies, we feel that the evaluation of other diseases is a valuable and necessary tool to keep track of diseases that may be connected to the expected increases in production. Traits involving animal welfare should always receive a special attention on top of what is approved by the revenues found from economical considerations.

Conclusions

A joint evaluation between Denmark, Finland and Sweden makes it possible to utilize sire information on other diseases across countries.

Some of the trends are unfavourable and will need thorough studies.

The OD index will be included in Total Merit Index.

A genetic control of other disease traits is valuable both from economical considerations and from the importance of animal welfare.

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