

# Joint Nordic Genetic Evaluation for Mastitis

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## 1. Introduction

Development of joint Nordic genetic evaluation for mastitis is part of a project initiated by the dairy cattle breeding organisations in Denmark, Finland, Norway, and Sweden, aiming at joint evaluation of all traits in the breeding programs (Juga, 2002). Joint genetic evaluation will increase accuracy in across country evaluations of sires, and may increase use of AI-sires across countries.

All four Nordic countries have health recording systems for dairy cattle, and use records of veterinary treatments of mastitis in genetic evaluation (Heringstad *et al.*, 2000). The first step in developing a joint Nordic genetic evaluation for mastitis was analyses of first lactation mastitis in linear sire models. Results of these first test-runs are presented here.

## 2. Material and Methods

### 2.1. Data

First lactation mastitis data for Ayrshire (AYS) and Holstein (HOL), respectively, were analysed in single trait sire models. Mastitis was defined as 0 or 1 based on whether or not the cow had at least one veterinary treatment of mastitis (all health recording codes used in national evaluation included) in the period from 15 days before calving to 120 days after first calving. The Nordic AYS dataset had mastitis records of 3.8 million first lactation daughters of 13,497 sires, and the Nordic HOL dataset had mastitis records of 2.1 million first lactation daughters of 20,602 sires. Summary statistics for the two datasets, joint Nordic and by country are given in tables 1 and 2, respectively.

**Table 1.** Summary statistics of the joint Nordic AYS data set.

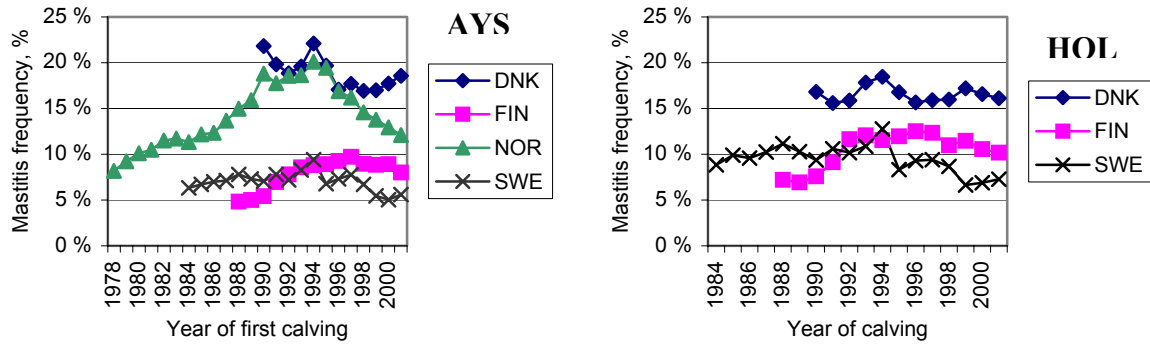
|                                         | Denmark   | Finland   | Norway    | Sweden    | Nordic    |
|-----------------------------------------|-----------|-----------|-----------|-----------|-----------|
| No of first lactation cows              | 187,832   | 818,024   | 1,952,867 | 854,884   | 3,813,607 |
| No of sires with data                   | 2065      | 4040      | 3594      | 3968      | 13,497    |
| No of sires in pedigree                 |           |           |           |           | 15,356    |
| Mean no of daughters per sire           | 91        | 202       | 543       | 215       | 283       |
| Mastitis data available                 | From 1990 | From 1988 | From 1978 | From 1984 |           |
| Overall mastitis freq <sup>a)</sup> , % | 18.5      | 8.0       | 14.9      | 7.1       | 11.8      |
| No of herd-year classes                 | 20,095    | 199,474   | 455,487   | 160,400   | 835,456   |
| Mean no of cows per HY                  | 9.3       | 4.1       | 4.3       | 5.3       | 4.6       |

<sup>a)</sup> mastitis freq = % cows with at least one case of veterinary treated mastitis in the period from 15 days before to 120 days after first calving.

**Table 2.** Summary statistics of the joint Nordic HOL data set.

|                                         | Denmark   | Finland   | Sweden    | Nordic    |
|-----------------------------------------|-----------|-----------|-----------|-----------|
| No of first lactation cows              | 1,086,121 | 241,727   | 789,180   | 2,117,028 |
| No of sires with data                   | 14,199    | 1,234     | 5,460     | 20,602    |
| No of sires in pedigree                 |           |           |           | 22,122    |
| Mean no of daughters per sire           | 76        | 196       | 144       | 103       |
| Mastitis data available                 | From 1990 | From 1988 | From 1984 |           |
| Overall mastitis freq <sup>a)</sup> , % | 16.6      | 10.7      | 9.5       | 13.3      |
| No of herd-year classes                 | 67,198    | 96,226    | 142,534   | 305,958   |
| Mean no of cows per HY                  | 16.2      | 2.5       | 5.5       | 6.9       |

<sup>a)</sup> mastitis freq = % cows with at least one case of veterinary treated mastitis in the period from 15 days before to 120 days after first calving.



**Fig. 1.** Phenotypic mastitis frequency in first lactation AYS and HOL cows by country. Mastitis defined as 0 or 1 based on whether or not the cow had at least one veterinary treatment in the period from 15 days before to 120 days after first calving.

The overall mastitis frequencies were 11.8 % for AYS and 13.3 % for HOL. Both the level and the phenotypic trend of mastitis vary between countries as shown in Figure 1.

Sire pedigree-files were build by tracing the pedigrees of the bulls with daughters, via sires and maternal grandsires. The joint Nordic pedigree file for AYS and HOL included 15,356 and 22,122 males, respectively.

## 2.2. Model

The following linear sire models were chosen as a starting point:

$$MA_{ijklm} = A_i + MYC_j + HY_k + s_l + e_{ijklm} \quad (1)$$

$$MA_{ijklm} = A_i + MYC_j + hy_k + s_l + e_{ijklm} \quad (2)$$

where  $MA_{ijklm}$  is the mastitis record (0 or 1) of daughter  $m$  of sire  $l$ ;  $A_i$  is the fixed effect of

age  $i$  at first calving, in months;  $MYC_j$  is the fixed effect of month $\times$ year $\times$  country class  $j$  of calving;  $HY_k$  is the fixed effect (Model 1) and  $hy_k$  is the random effect (Model 2) of herd $\times$ year of calving  $k$ ;  $s_l$  is random effect of transmitting ability for sire  $l$ ; and  $e$  is a residual effect.

Heritability of mastitis was assumed to be 0.03 (Heringstad *et al.*, 1999), and the following variance components were used for model 1;  $\sigma_s^2=0.00114$ ,  $\sigma_e^2=0.12810$ , and model 2;  $\sigma_s^2=0.00119$ ,  $\sigma_{hy}^2=0.01076$ ,  $\sigma_e^2=0.13618$ , respectively. The DMU package (Madsen and Jensen, 2002) was used for prediction of sire transmitting abilities.

Model validation was carried out for AYS using method 3 described by Boichard *et al.* (1995) and predictive ability.

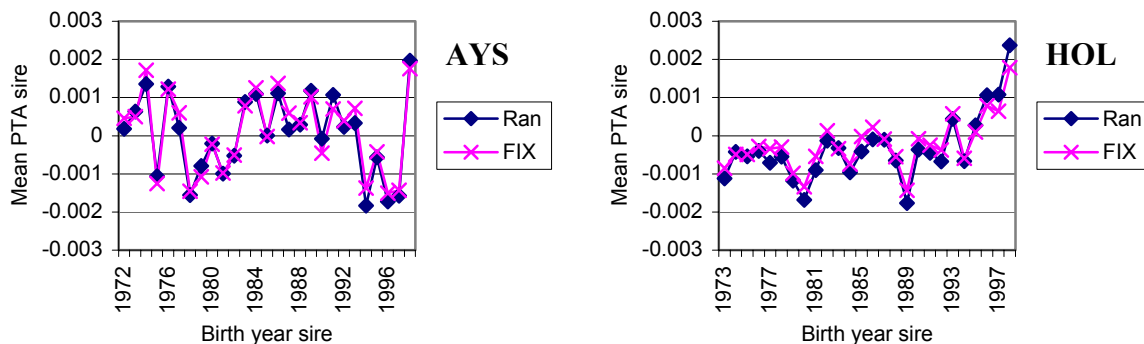
### 3. Results and Discussion

Genetic trends of mastitis given as mean PTA of sire by birth year of sire are presented in Fig. 2. The figure shows a favourable trend for AYS, and an unfavourable genetic trend for HOL. Linear regressions of sire PTA on sire's birth year indicate an annual genetic change of  $-0.002$  %-points mastitis for AYS sires born from 1972 to 1998, and  $+0.009$  %-points mastitis for HOL sires born from 1980 to 1998.

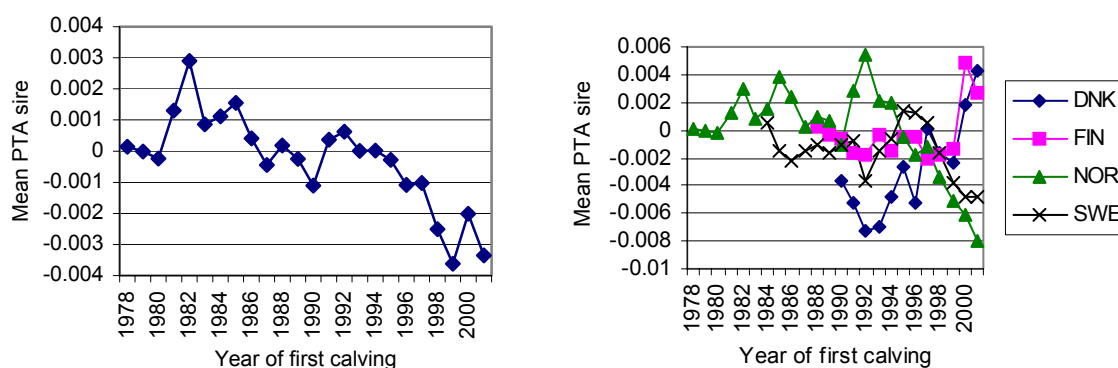
The two models (herd $\times$ year effect defined as random or fixed) gave similar genetic trends for both AYS and HOL (Fig. 2). Model validation was carried out for AYS. Both models met Interbuls trend validation criterion (estimated bias less than  $0.02 \times$  genetic SD). No significant bias was detected in estimation of genetic trend, indicating that any of these models can be used for genetic evaluation. However, based on predictive ability, the model defining herd-year as random is a better model. The correlations between observed (mastitis) and predicted values were 0.16 and 0.20 for models with herd $\times$ year effect defined as fixed and random, respectively.

Genetic trends of mastitis from model 2, joint Nordic and by country, given as mean PTA of sire by year of first calving of daughters are given for AYS and HOL in figures 3 and 4, respectively. Here sires are weighted according to the number of daughters, and this measure reflects sire usage as well as possible genetic change in the population. Figure 3 shows genetic improvement for mastitis in Nordic AYS, corresponding to an annual genetic change of  $-0.02$  %-points mastitis from 1978 to 2001. Genetic trend for mastitis varies between countries as shown in Figure 3; there has been a genetic improvement in the populations in Norway and Sweden and a genetic deterioration in Denmark and Finland.

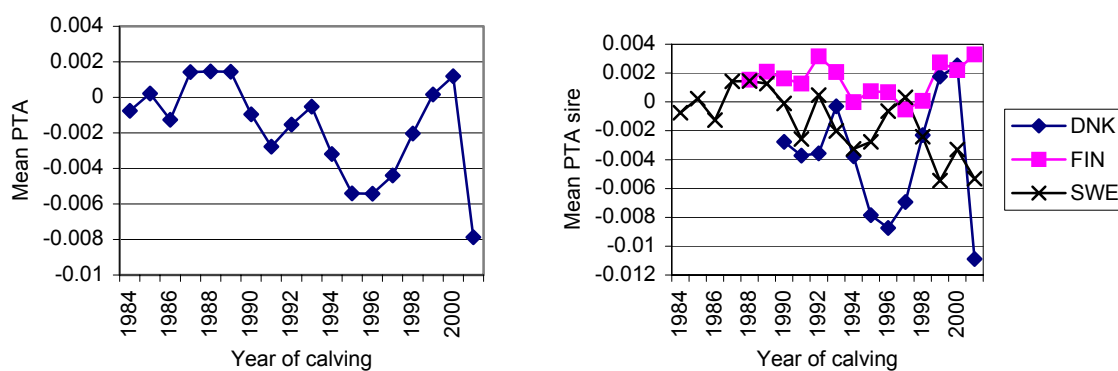
For HOL there has been approximately no genetic change in Finland, genetic improvement in Sweden, and in Denmark mean PTA of sires has varied between years (Fig. 4). The influence of one Danish sire is the main reason for the drop in 2001, joint Nordic and for Denmark (Fig. 4). This sire had 14,477 daughters with first calving in 2001 and he was ranked as the top HOL sire in this genetic evaluation.



**Fig. 2.** Genetic trends for mastitis for AYS and HOL, respectively, given as mean PTA by birth year of sire, from models with effect of herd $\times$ year defined as random (Ran) or fixed (FIX). Includes all sires in the joint Nordic pedigree files born from 1973 to 1998.



**Fig. 3.** Genetic trends for mastitis in AYS, joint Nordic and by country, given as mean PTA of sire by year of first calving of daughters. Includes all cows in the joint Nordic AYS datafile.



**Fig. 4.** Genetic trends for mastitis in HOL, joint Nordic and by country, given as mean PTA of sire by year of first calving of daughters. Includes all cows in the joint Nordic HOL datafile

This represents the first test-run of a joint Nordic genetic evaluation for mastitis. Further work remains before this can be implemented, e.g. extension to multi-lactation analysis, allow for heterogenous variance, include heterosis in

the model, as well as further work on trait definition and model validation. Later, also somatic cell count and some udder traits will be included in the joint Nordic genetic evaluation.

## References

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