

‘UNIFIED TRAIT APPROACH’ IN COMBINING INDIVIDUAL TEST DAY AND LACTATION RECORDS OF AYRSHIRE COWS FROM NORDIC COUNTRIES

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INTRODUCTION

Four Nordic countries (Denmark, Finland, Norway and Sweden) have agreed on joint testing and use of AI-bulls. To enable accurate comparison and selection of bulls and cows across countries a joint genetic evaluation based on Nordic data is needed. In order to gain general acceptance the joint Nordic evaluation model has to be at least as good as the current national models and exploit optimally the genetic links between the countries. At the present, genetic evaluation of production traits in Finland is based on test day (TD) observations whereas in Sweden and Norway 305d lactation records are used. In Denmark genetic evaluation will soon move from using only 305d records to include both TD and 305d records. Consequently, the joint Nordic animal model for production traits should be able to deal with both types of records. The objectives of this study were to apply an evaluation model fitting both TD and lactation records using Nordic data and to compare results to those from individual within-country evaluations.

MATERIAL AND METHODS

The data comprised of 28 905 771 TD records (from 1988 onwards) of 1 208 065 Finnish cows (Ayrshire, Holstein, Finncattle) and first lactation 305d records of 975 797 Swedish red-and-white (SRB) cows (from 1984 onwards) used in both countries’ national evaluations in September 2001. National pedigree files from Finland and Sweden were merged together resulting altogether in 3 639 904 animals in the joint evaluation.

The assumed model was based on the current Finnish multiple-trait (milk, protein and fat yield) reduced rank random regression TD model for all lactations (Lidauer *et al.*, 2000). The model was expanded such that observations for 305d yields were added as a set of 6 new traits. Consequently, the model had two parts, the first one describing TD observations (Finland) and the second one describing lactation records (Sweden). Derivation of this ‘unified trait approach’ assuming that 305d records are a special case of TD record, and that both types of records are expressions of the same genetic traits, is given in another paper in this congress (Mäntysaari, 2002). The model equation for full inclusion of 305d records on all lactations was as follows:

$$\begin{bmatrix} milk_1 \\ protein_1 \\ fat_1 \\ milk_{2+} \\ protein_{2+} \\ fat_{2+} \\ milk_{305} \\ protein_{305} \\ fat_{305} \\ milk_{305+} \\ protein_{305+} \\ fat_{305+} \end{bmatrix} = \begin{bmatrix} age_{m1} \\ age_{p1} \\ age_{f1} \\ age_{m2} \\ age_{p2} \\ age_{f2} \\ age * period_{m305} \\ age * period_{p305} \\ age * period_{f305} \\ age * period_{m305+} \\ age * period_{p305+} \\ age * period_{f305+} \end{bmatrix} + \begin{bmatrix} dcc_{m1} \\ dcc_{p1} \\ dcc_{f1} \\ dcc_{m2} \\ dcc_{p2} \\ dcc_{f2} \\ days_dry_{m305} \\ days_dry_{p305} \\ days_dry_{f305} \\ days_dry_{m305+} \\ days_dry_{p305+} \\ days_dry_{f305+} \end{bmatrix} + \begin{bmatrix} yr * mth_{m1} \\ yr * mth_{p1} \\ yr * mth_{f1} \\ yr * mth_{m2} \\ yr * mth_{p2} \\ yr * mth_{f2} \\ season_{m305} \\ season_{p305} \\ season_{f305} \\ season_{m305+} \\ season_{p305+} \\ season_{f305+} \end{bmatrix} + \begin{bmatrix} \sum_{d=1}^5 \phi_t^d b_{m1}^d \\ \sum_{d=1}^5 \phi_t^d b_{p1}^d \\ \sum_{d=1}^5 \phi_t^d b_{f1}^d \\ \sum_{d=1}^5 \phi_t^d b_{m2}^d \\ \sum_{d=1}^5 \phi_t^d b_{p2}^d \\ \sum_{d=1}^5 \phi_t^d b_{f2}^d \\ \sum_{d=1}^5 \phi_t^d b_{m2}^d \\ \sum_{d=1}^5 \phi_t^d b_{p2}^d \\ \sum_{d=1}^5 \phi_t^d b_{f2}^d \end{bmatrix} + \begin{bmatrix} hy_{m1} \\ hy_{p1} \\ hy_{f1} \\ hy_{m2} \\ hy_{p2} \\ hy_{f2} \\ hy_{m305} \\ hy_{p305} \\ hy_{f305} \\ hy_{m305+} \\ hy_{p305+} \\ hy_{f305+} \end{bmatrix}$$

$$+ \begin{bmatrix} htm_{m1} \\ htm_{p1} \\ htm_{f1} \\ htm_{m2} \\ htm_{p2} \\ htm_{f2} \end{bmatrix} + \begin{bmatrix} \sum_{d=1}^6 s(dim)_{m1}^d a^{d+6} \\ \sum_{d=1}^6 s(dim)_{p1}^d a^{d+6} \\ \sum_{d=1}^6 s(dim)_{f1}^d a^{d+6} \\ \sum_{d=1}^6 s(dim)_{m2}^d a^{d+6} \\ \sum_{d=1}^6 s(dim)_{p2}^d a^{d+6} \\ \sum_{d=1}^6 s(dim)_{f2}^d a^{d+6} \\ \sum_{d=1}^6 sum_{m1}^d a^d \\ \sum_{d=1}^6 sum_{p1}^d a^d \\ \sum_{d=1}^6 sum_{f1}^d a^d \\ \sum_{d=1}^6 sum_{m2}^d a^{d+6} \\ \sum_{d=1}^6 sum_{p2}^d a^{d+6} \\ \sum_{d=1}^6 sum_{f2}^d a^{d+6} \end{bmatrix} + \begin{bmatrix} \sum_{d=1}^6 t(dim)_{m1}^d p^d \\ \sum_{d=1}^6 t(dim)_{p1}^d p^d \\ \sum_{d=1}^6 t(dim)_{f1}^d p^d \\ \sum_{d=1}^6 t(dim)_{m2}^d p^{d+6} \\ \sum_{d=1}^6 t(dim)_{p2}^d p^{d+6} \\ \sum_{d=1}^6 t(dim)_{f2}^d p^{d+6} \\ P_{m305} \\ P_{p305} \\ P_{f305} \\ P_{m305+} \\ P_{p305+} \\ P_{f305+} \end{bmatrix} + \begin{bmatrix} \sum_{d=1}^6 t(dim)_{m2}^d w^d \\ \sum_{d=1}^6 t(dim)_{p2}^d w^d \\ \sum_{d=1}^6 t(dim)_{f2}^d w^d \end{bmatrix} + \begin{bmatrix} e_{m1} \\ e_{p1} \\ e_{f1} \\ e_{m2} \\ e_{p2} \\ e_{f2} \\ e_{m305} \\ e_{p305} \\ e_{f305} \\ e_{m305+} \\ e_{p305+} \\ e_{f305+} \end{bmatrix}$$

where $milk_1$, $protein_1$, and fat_1 represent the daily yield observations of corresponding traits in the first lactation, and $milk_{2+}$, $protein_{2+}$, and fat_{2+} represent observations of the traits in any of the later lactations. *Age* describes the respective calving age effects, *dcc* the days carried calf effects, *yr*mth* the year-production month interaction effects, and *hy* the corresponding herd-year effects for the measured daily yield traits. The regression equations $\sum_{d=1}^5 \phi_t^d b_{ij}^d$ represent the average effect of lactation stage (*dim*) on daily yields, and were within calving year*season and parity. The 305d observation part of the model included $milk_{305}$, $protein_{305}$, and fat_{305} , and $milk_{305+}$, $protein_{305+}$, and fat_{305+} describing the corresponding 305d traits in first and later

lactations, respectively; $age*period_{i305}$ represents the effect of calving age defined within time periods, $days_dry_{i305}$ is the effect of days dry, $season_{i305}$ is the average calving month effect and hy_{i305} represents the effect of herd-year of the calving. The Swedish part of the model included also two regression effects describing the heterosis effects due to different breed origin. The random effects of the model are given in the second equation line. The htm_{ij} represents the herd-test-day effect for the i^{th} trait and j^{th} parity class for daily yields. The functions for breeding values, permanent environment across lactations and within lactations for trait i and parity j ($j=1,2$) are described by

$$\sum_{d=1}^6 s(dim)_{ij} a^{d+(j-1)6}, \sum_{d=1}^6 t(dim)_{ij}^d p^{d+(j-1)6}, \text{ and } \sum_{d=1}^6 t(dim)_{i2+}^d w^d, \text{ respectively.}$$

Each 305d observation were described by $\sum_{d=1}^6 sum_{ij}^d a^{d+(j-1)6}$, where a sum^d for trait i and parity j is the sum of corresponding dim specific coefficients of the TD model (Mäntysaari, 2002). Summing is over standard 10 dims (15, 45, ...285). Permanent environmental effects are modelled for each trait ij as p_{i305j} . In our case here only the first lactation records were considered, thus the permanent environmental effect for 305d records was excluded. The model assumes that no cows will have both the TD and 305d yields.

Set of variance components for the unified trait model were derived from the variance components for the Finnish TD model. This implied that the genetic parameters, i.e., heritabilities and genetic correlations for 305d traits would equal to corresponding parameters derived from TD model (table 1). Such an assumption can be relaxed by modifying the sum coefficients in $\sum_{d=1}^6 sum_{ij}^d a^{d+(j-1)6}$, and the variance parameters for permanent environment and residual effects.

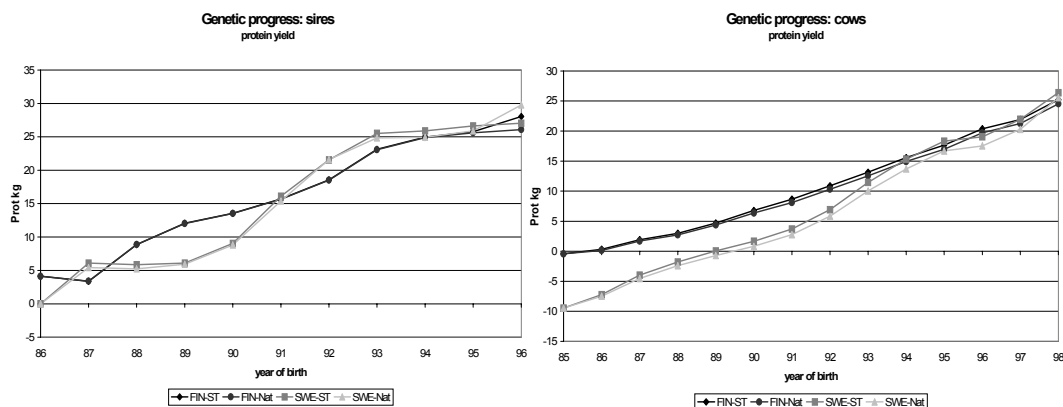
Convergence was monitored by the relative squared difference between the left-hand and right-hand side; when smaller than 4.0×10^{-7} the system was considered to be converged. This required 607 rounds of iteration.

Table 1. Characterisation of genetic parameters for 305d records. Heritabilities on the diagonal, genetic correlations above and phenotypic correlations below diagonal. Derived from the corresponding parameters of TD model

	Milk 1	Protein 1	Fat 1	Milk 2+	Protein 2+	Fat 2+
Milk 1	0.42	0.80	0.60	0.80	0.59	0.46
Protein 1	0.80	0.28	0.70	0.51	0.70	0.56
Fat 1	0.67	0.71	0.29	0.40	0.47	0.76
Milk 2+	0.54	0.39	0.29	0.34	0.72	0.50
Protein 2+	0.42	0.44	0.34	0.65	0.27	0.71
Fat 2+	0.32	0.37	0.46	0.65	0.66	0.30

RESULTS AND DISCUSSION

Results from the across-country analysis were compared to those from within-country evaluations with national models (Sweden: single-trait analysis of protein with heritability of 0.30). Estimated breeding values (EBV) for sires and cows with records were in general very similar from both national and combined models. Correlations between EBVs from the two models within birth years were virtually 1 for Finnish Ayrshire sires and cows born 1990 onwards. For Swedish SRB sires and cows correlations were somewhat lower, ranging from 0.95 to 0.98. EBVs for the Swedish animals were expected to change more than the Finnish ones due to the extra information from milk and fat records in the combined multi-trait evaluation. Genetic trends for sires (figure 1) and cows (figure 2) changed only slightly; for Finnish cows and for Swedish sires and cows the combined model increased the genetic trend somewhat. Some individual animal EBVs changed considerably due to additional information.



Figures 1 and 2. Genetic trend in protein yield of Finnish (FIN) and Swedish (SWE) animals with combined across-country model (ST) or within-country model (NAT)

CONCLUSION

The results show that combining lactation records from one country and TD records from another country with a random regression model is feasible even with large nationwide data sets. This enables a joint evaluation of animals from different countries and with different types of production records allowing thus true joint selection of best animals across country borders.

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REFERENCES

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