Joint Nordic Test Day Model: Experiences with the New Model

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Abstract

This paper is one of the three papers that describe the joint Nordic test day model for yield traits. The paper focuses on the results from the new evaluation models for Red Breeds, Holstein and Jersey, and compares the breeding values from the new model to those from the previous national ones.

1. Introduction

Denmark, Finland and Sweden started their first joint routine evaluation of production traits in April 2006. Routine evaluation is done by Nordic Cattle Genetic Evaluation (Nordisk Avelsværdivurdering, NAV), a company jointly owned by these three countries and which already does the joint genetic evaluation for type traits, milkability, temperament and leakage, as well as for female fertility. The new NAV random regression model (RRM) replaces the national evaluations for yield traits.

The objectives of the joint evaluation were more effective utilization of data and resources available in the three countries, and a desire for a possibility of direct comparison of animals across countries. Even though phenotypic records from different countries are treated as different traits, the genetic correlations between countries are set to 1. Therefore each animal will obtain the same estimated breeding value (EBV) for the same biological trait in each of the three countries thus enabling a direct comparison among Nordic bulls and cows.

Moving to a joint evaluation induces large changes in the assumed statistical model compared to those of previous national ones. Derivation of the NAV evaluation model and variance components, as well as a detailed description of the model are given by Mäntysaari et al. (2006) and Lidauer et al. (2006). Summary of the most important changes in the applied model is given in Table 1.

The objective of this study was to compare EBVs from the new joint genetic evaluation to those from national evaluation systems.

2. Material and methods

2.1. Data

Evaluation is performed separately for the three main breed groups: Red breeds, Holstein and Jersey. Finnish original breed, Finncattle, is evaluated together with the Red breeds whereas Red Holstein evaluation is done with Holstein. When evaluating Red breeds Finnish Holstein-Friesian data is also included to give more information in small herds with both breeds. The same applies also to Holstein evaluation; there Finnish Ayrshire data is included.

The joint evaluation produces EBVs for milk, protein and fat yield separately for first, second and later lactation. From these lactationwise solutions EBVs for protein and fat content, as well as for persistency, are calculated. Lactation yield EBVs of the first, second and later lactations are combined with weights of 0.5, 0.3 and 0.2, subsequently, to produce combined EBVs across lactations. EBVs for different lactations as well as combined across lactations are expressed as relative EBVs where means are set to 100 and standard deviations (SD) are 10 index points. The base group of animals from which the mean is calculated consists of Danish, Finnish and Swedish cows born 4-5 years before evaluation date and having at least one observation. The SDs applied in the standardization are the SDs of A.I. test bulls (born 1997-1998) that have sired the base group cows.

For this study breeding values from the first joint evaluation in April 2006 were taken and merged with EBVs from previous national evaluation systems. Table 2 summarizes the amount of data used.

3. Results and discussion

Joint evaluation provided a large amount of new information for many animals compared to previous national evaluations. In the Holstein (Red breeds) there were 537 (388) sires having daughters at least in two of the three countries.

The group of bulls that benefited most from the joint evaluation was Finnish and Swedish young bulls that were mutually tested in both countries. 153 (21) Red breed (Holstein) bulls have around 150-200 daughters in their country of birth and additional 50-100 daughters in the second country.

Also, for some older proven bulls, changes in their proofs could be seen. As an example of such a bull is Danish elite bull T Funkis (HOLDNKM000000232851). Table 3 describes his proofs in the three countries before the joint evaluation, and finally in the NAV evaluation where daughter information from the three countries have been combined. Although the genetic levels in Denmark and Finland for Holstein are not exactly the same, it can be determined from the table that in Finnish national genetic evaluation the bull was clearly overestimated despite having already over 1000 daughters.

Correlations between EBVs from the joint evaluation and national evaluations ranged in general between 0.95-0.99 for bulls. For cows correlations were lower; between 0.90-0.95 for milk and protein, but lower for fat in Holstein.

As the correlations imply there were some re-ranking among bulls and especially among cows. The biggest reason for re-ranking among bulls was estimation of heterosis effects across countries (Lidauer et al. 2006). The across country estimation gave reasonable estimates for heterosis and recombination loss which earlier were very difficult to estimate from national data only. E.g. Danish national estimates for heterosis were clearly higher than from the joint evaluation (Aamand et al. 1999). For cows, apart from the new procedure for heterosis estimation, accounting simultaneously for heterogeneous variance caused re-ranking. Formerly in Danish and Swedish national evaluation systems correction for heterogeneous variance was done by pre-adjustment of phenotypic data; in the previous Finnish TD model heterogeneous variance was not accounted for at all.

Figures 1-4 describe genetic trends for Nordic bulls and cows in yield index, which is a combination of milk, protein and fat indices with weights of -1, 4 and 1, respectively. The graphs include information from animals fulfilling joint publishing criteria. Sires need to have a minimum reliability of 60% in protein yield and have at least 10 daughters milking 100 days after calving. Cows must have at least one observation (either a TD or a 305d record) in evaluation to get their indices published.

From the top 100 Nordic Holstein bulls (according to yield index) 80 came from Denmark, 16 from Sweden and 4 from Finland. In the Red breeds the top 100 bull list consisted of 45 Finnish Ayrshire bulls, 32 Swedish Red bulls, and 23 Danish Red bulls.

4. Conclusions

The new joint Nordic evaluation of yield traits has been well received by farmers and A.I. sector in Denmark, Finland and Sweden. Combining information from the three countries has increased reliability of the EBVs for bulls having daughters spread over these three countries. Especially the young bulls in the joint testing program have benefited from the increased information. More reliable proofs for bulls means also more reliable EBVs for their daughters which enables more accurate selection of best cows in the farms. Direct comparison of animals across borders will make it easier for farmers to buy and market genetic material outside their own country.

Developing Nordic yield evaluation continues; the next big step will be including also Swedish TD records.

References

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Table 1. The most important changes in the joint NAV model compared to previous national models

change	DNK	FIN	SWE
data	change from 305d to TD model, exclusion of older data (1981-1989)	-	exclusion of older data (1982-1989)
model type	multi-lactation, multi-trait model	-	multi-lactation model
calving age	modified	modified	modified
heterosis	modified	new	modified
recombination loss	new	new	new
HV correction	modified	new	modified

Table 2. Size of the evaluation data (in million)

	Red Breeds	Holstein	Jersey
Animals	4.05	6.64	0.59
TD yields	45.66	81.61	7.21
305d-yields	1.93	1.60	-

Table 3. Indices for yield traits of bull T Funkis in national evaluation of Denmark, Finland and Sweden, and in the joint NAV evaluation

	DNK	FIN	SWE	NAV
milk kg	108	116	110	107
fat kg	107	121	112	108
protein kg	109	118	112	109
daughters	45411	1039	8134	54584

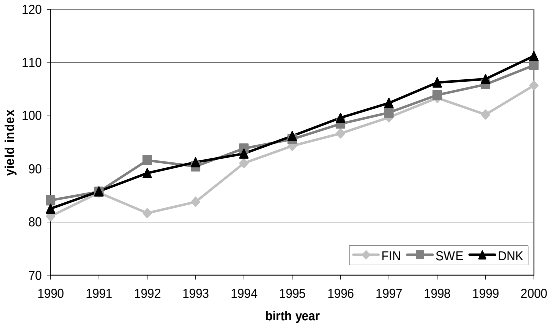

Figure 1. Genetic trend in yield index of Nordic Holstein sires

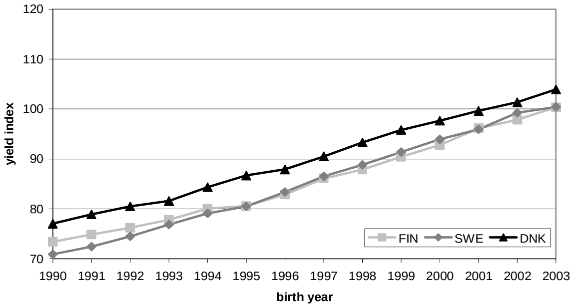

Figure 2. Genetic trend in yield index of Nordic Holstein cows

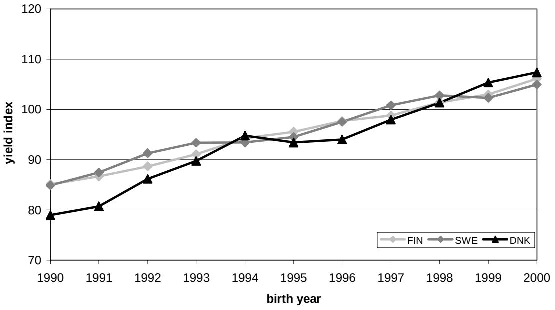

Figure 3. Genetic trend in yield index of Nordic Red breed sires

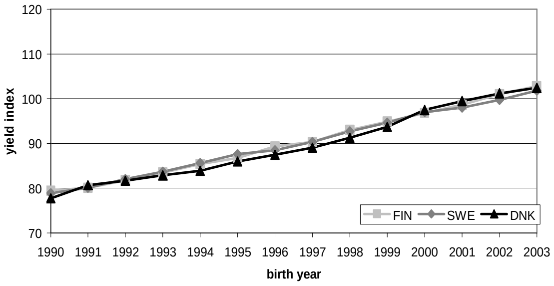

Figure 4. Genetic trend in yield index of Nordic Red breed cows