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Across-country test-day model evaluations for Holstein, Nordic Red Cattle, and Jersey

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ABSTRACT

Three random regression models were developed for routine genetic evaluation of Danish, Finnish, and Swedish dairy cattle. Data included over 169 million test-day records with milk, protein, and fat yield observations from over 8.7 million dairy cows of all breeds. Variance component analyses showed significant differences in estimates between Holstein, Nordic Red Cattle, and Jersey, but only small to moderate differences within a breed across countries. The obtained variance component estimates were used to build, for each breed, their own set of covariance functions. The covariance functions describe the animal effects on milk, protein, and fat yields of the first 3 lactations as 9 different traits, assuming the same heritabilities and a genetic correlation of unity across countries. Only 15, 27, and 7 eigenfunctions with the largest eigenvalues were used to describe additive genetic animal effects and nonhereditary animal effects across lactations and within later lactations, respectively. These reduced-rank covariance functions explained 99.0 to 99.9% of the original variances but reduced the number of animal equations to be solved by 44%. Moderate rank reduction for nonhereditary animal effects and use of one-third-smaller measurement error correlations than obtained from variance component estimation made the models more robust against extreme observations. Estimation of the genetic levels of the countries' subpopulations within a breed was found sensitive to the way the breed effects were modeled, especially for the genetically heterogeneous Nordic Red Cattle. Means to ensure that only additive genetic effects entered the estimated breeding values were to describe the crossbreeding effects by fixed and random cofactors and the calving age effect by an age × breed proportion interaction, and to model phantom parent groups as random effects. To ensure that genetic variances were the same across the 3 countries in breeding value estimation, as suggested by the variance component estimates, the applied multiplicative heterogeneous variance adjustment method had to be tailored using country-specific reference measurement error variances. Results showed the feasibility of across-country genetic evaluation of cows and sires based on original test-day phenotypes. Nevertheless, applying a thorough model validation procedure is essential throughout the model building process to obtain reliable breeding values.

Key words: across-country genetic evaluation, covariance function, crossbreeding effect, heterogeneous variance

INTRODUCTION

The first random regression test-day model (**RRM**) for national genetic evaluation of dairy cattle was adopted at the onset of the millennium (Schaeffer et al., 2000). Since then, RRM have become the models of choice for genetic evaluation of production traits in dairy cattle. The main arguments for RRM implementation are that it gives more statistical power for modeling the data and generates information on the change over time for the trajectories of the traits (Jamrozik et al., 1997; Swalve, 2000; Lidauer et al., 2003). As RRM is increasingly being adopted for genetic evaluation of dairy breeds, interest is growing in joint evaluations across countries (Canavesi et al., 2001; Emmerling et al., 2002; de Roos et al., 2004), which adds further complexity to the applied RRM. In the Nordic countries, genetic material has been exchanged across borders for many decades, mainly in terms of semen but also embryos, leading to the initiative to develop a common genetic evaluation for Nordic dairy cattle.

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The first official joint Nordic evaluation for production traits was placed into use in 2006. The applied statistical model was based on a meta-model approach (Mäntysaari, 2006a) that incorporated the original national models and variance parameters but imposed a genetic correlation of unity across the countries. Thus, country-specific heritabilities and environmental effects were included for building the Nordic model (Mäntysaari et al., 2006b; Lidauer et al., 2006b). In principle, each country had its own national model for production traits: Danish test-day (**TD**) observations were modeled based on Danish RRM variance component estimates (Jakobsen et al., 2002), and Finnish TD observations were modeled as in previous Finnish RRM routine evaluation (Lidauer et al., 2000). Swedish 305-d lactation yield observations were modeled using own environmental effects but with the additive genetic animal effect blended into the random regression (**RR**) covariance function (**CF**) for the additive genetic animal effect of the meta-model. The motivation for developing a meta-model was to achieve a model as good as or better than the one already implemented in each respective country. Since the first joint model, additional efforts have been made to harmonize the data from the participating countries as well as the models for these data. In 2008, Swedish 305-d yield observations were replaced by TD observations.

Whereas joint Nordic evaluation enhanced across-country dairy cattle breeding activities, the complexity of the models was difficult to explain to breeders. This initiated research to identify heterogeneity in the data, which the meta-model needs to account for, and to harmonize modeling across countries wherever possible. A first research step was to conduct comprehensive variance component analyses for the different breeds in each country. New CF were built for the RRM based on the results from these analyses, and as an outcome, 3 revised evaluation models for the main breeds Holstein (**HOL**), Nordic Red Cattle (**RDC**), and Jersey (**JER**) were officially adopted in February 2012.

The aim of this paper is to describe the Nordic across-country genetic evaluation model for yield traits. We give special attention to modeling aspects that were found crucial in across-country genetic evaluation based on original observations. Particular focus is on building of the CF, modeling of breed effects, and adjustment for heterogeneous variance.

MATERIALS AND METHODS

Data

Breeds. The Nordic dairy cattle population comprises 4 dairy breeds: HOL, RDC, JER, and Finncattle (**FIC**); HOL and RDC are the main dairy breeds, of which HOL cows are predominant in Denmark and Sweden, and RDC cows in Finland (Table 1). Herds with JER cows are only found in Denmark and in the south of Sweden, and indigenous FIC cows only in Finland. Crossbreeding is used in all the main breeds, both between different breed strains and between breeds. The latter is especially the case for the Danish RDC population, which is a synthetic breed of old Red Danish Cattle, Swedish Red Breed, Brown Swiss, and Red Holstein. The Finnish and Swedish Red Cattle populations also have their own separate histories, making RDC a genetically very heterogeneous breed. Connectedness of the populations across the 3 countries was originally established mainly by the use of common Nordic or international sires.

Test-Day Records. The TD data were collected from farms located between 55°N in southern Denmark to almost 67°N in Finnish Lapland, from an area with wide environmental and seasonal variation. The num-

Table 1. Average breed proportions (%) in dairy cows born in 2010 by main breed and by country of birth (D = Denmark, F = Finland, and S = Sweden)

	Holstein			Nordic Red Cattle			Jersey		Finncattle
Breed	D	F	S	D	F	S	D	S	F
Holstein Friesian	96.2	84.2	91.7	20.6	0.5	1.3	0.1	1.0	3.5
European Black and White	3.7	10.8	6.6	0.4	0.3	0.8		0.4	1.7
Finnish Ayrshire		3.5	0.4	11.0	59.3	28.5		0.3	8.1
Swedish Red Breed		0.5	0.9	22.3	22.2	43.2		0.9	1.7
Red Danish Cattle	0.1			22.5	1.5	6.6			0.1
Norwegian Red Cattle		0.7	0.2	2.1	5.7	7.4		0.1	0.6
Canadian Ayrshire		0.2	0.1	5.6	9.7	8.0		0.1	0.4
American Brown Swiss				13.6	0.7	4.1			
Danish Jersey				0.1			57.9	58.5	
American Jersey							40.2	36.7	
New Zealand Jersey							1.7	1.5	
Finncattle		0.1							83.9
Other breeds			0.1	1.8	0.1	0.1	0.1	0.5	