Joint Nordic Evaluation as a First Step to Joint Breeding Program

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Summary

The four Nordic countries Denmark, Finland, Norway and Sweden have agreed to co-operate in semen production of dairy cattle. This co-operation aims to increased population sizes and more efficient breeding program, but also to better and larger portfolio of proven bulls in commercial breeding. A joint evaluation is needed to improve the accuracy of across country evaluation of bulls and cows. The need for comparison of cows arises from joint nucleus breeding programs and bull dam selection.

The results in several MACE studies have shown that the genetic correlation between Nordic countries is high enough for most of the traits included in the selection. However, there is a need to increase the genetic links between some subpopulations to improve the accuracy of across country evaluation.

In the research in the Nordic project we will concentrate on Nordic linear models fitting the data from all four countries. In the first model for a joint evaluation on production traits we will use very similar modelling within countries under a joint across country model that countries are using today. Combining different data from each country, tracing female pedigrees, forming unified genetic groups, correcting for the within herd and within country heterogeneous variance and including foreign bull information are the major challenges in the joint evaluation.

The aim of this paper is to give a short description of the status and the motivation of the joint Nordic breeding program and to describe the problems and preliminary results in a joint prediction of breeding values.

Keywords: across country evaluation, test day model, functional traits

Introduction

Four Nordic countries, Denmark, Finland, Norway and Sweden, have signed an agreement of joint testing and use of AI-bulls. The motivation for this agreement is to improve the efficiency of current breeding programs in four countries by mowing towards a joint breeding program and to better utilise the existing resources. Joint use of best bulls also guarantees a better assortment of proven bulls for commercial breeding in a single country. Planning an integrated breeding program involves many successive steps, namely comparison of animals across countries, selection of bull dams and bull sires, optimised mating strategies, optimised testing capacity and sustainable use of jointly owned proven bulls. This development has now started in Nordic countries.

Accurate comparison and selection of bulls and cows across Nordic countries is of great importance in the future when running the joint program. To improve the possibilities for such a comparison the breeding organisations have decided to establish a new company *Nordic Cattle Genetic Evaluation (NCGE)*, which has a responsibility to develop and run genetic evaluations from joint Nordic data. The company has started its operation on 2.1.2002 and the joint evaluation of dairy cattle should be running in full scale around 2004 – 2005, when the majority of first crop of jointly owned bulls will have enough daughter information for progeny testing. These Nordic evaluations will then replace the national evaluations. Another advantage in joint evaluation is a possibility for more efficient utilisation of knowledge and resources in the field of genetic evaluation.

The aim of this paper is to describe the plans, problems and preliminary results in a joint prediction of breeding values. The joint evaluation will be an important milestone in Nordic co-operation and its credits will also be elaborated.

The past development in across country comparison

Since establishment of Interbull Centre in 1991 an interest in international evaluation has steadily increased. Currently over 25 countries subscribe to Interbull service of international bull evaluation. International genetic evaluations are across-country measures of genetic merit for three milk production traits (fat, protein and milk yield), 18 conformation traits, and udder health traits. Nordic countries were the first countries to participate in the international genetic evaluation on production traits in 1994. Other countries joined the service in 1995.

Interbull uses a method known as Multiple Across Country Evaluation (MACE) (Schaeffer, 1994; Fikse & Banos, 2001) to calculate International Genetic Evaluations. MACE has two major advantages over other methods. MACE combines information from each country using all known relationships between bulls, both within and across populations. To account for possible G by E interaction MACE accounts for the possibility of animals re-ranking between certain countries.

Current methodology has some practical limitations, e.g. how to deal with multiple trait observations from participating countries. Also quality problems in national evaluations have an effect on the reliability of international comparison. Interbull requires a set of tests to validate the genetic trend in national evaluation (Boichard *et al.*, 1995), before accepting data to international genetic evaluation, but no other quality control measures of the data are required.

Using performance data in across country comparison allow for similar data editing rules, alternative modelling and utilisation of all genetic links i.e. also cow path. It also automatically brings all countries to same quality level, when prediction methodology is considered, but will naturally not help if data from one country is erratic. Recently many results from research on across country evaluation based on performance data have been published (Canavesi *et al.*, 2001; Pedersen *et al.*, 2001; Weigel *et al.*, 2001). The problem in using performance records from many countries is the amount of data, which is easily too large, especially if test day models are considered.

Joint Nordic genetic evaluation

Research and development projects in joint evaluation have already been running in Nordic countries for a couple of years. In first studies MACE methodology was used to evaluate the feasibility of joint Nordic genetic evaluation. Although the functional traits in the Nordic countries vary in trait expression, parities utilised and statistical modelling many of the correlation estimates in Ayrshire breed were found to be from moderate to high, especially among non-return rate, calving ease and calf viability (Svendsen *et al.*, 2001). In the same study the heritabilities were found to be low and the connections between countries weak, however. In another study on Holstein breed genetic correlations were found to be moderate to high between traits that are expected to be similar like non-return rate, disease resistance for other diseases and calving ease (Mark *et al.*, 2001). Both studies concluded that harmonisation in trait definition, data included and evaluation models would most likely increase correlations and enable more accurate across country evaluation.

Genetic correlations between Nordic countries were high for somatic cell count and reasonable for mastitis in Holstein breed and reasonable for both traits in Ayrshire (Mark *et al.*, 2000). The problem with Ayrshire breed was weaker genetic links between countries. Similar results have been found for type traits, but the genetic correlations were even weaker in Ayrshire breed due to shorter data period (Klei Lawlor, 2001). The study on udder health included also other Interbull member countries and has been followed by Interbull routine service on international genetic evaluation of somatic cell count and mastitis for both breeds.

The studies have shown that Ayrshire populations in Finland and Sweden have good genetic links. Norwegian red is quite well linked to Swedish red and moderately well linked to Finland. Danish red is more isolated due to its past breeding policy. In Holstein the populations in all three Nordic countries Denmark, Finland and Sweden have good genetic links. Nordic countries have realised the need for increment in exchange of semen between populations to enable more accurate comparison.

The accuracy of across country comparison can also be improved by utilising joint genetic evaluation from performance records. Three Nordic countries, Denmark, Finland and Sweden, have already tested a joint animal model on full lactation data for both Ayrshire and Holstein breeds (Pedersen *et al.,* 2001). Both multi country ($r_G < 1$) and single country ($r_G = 1$) models were analysed and found suitable for across country evaluation. Genetic trends from joint Nordic models were compared to national models. For Holstein cows the genetic trends obtained by the national and single country model were nearly identical in Denmark and Finland likewise the trend in national and single country model for Finnish Ayrshire. For other breeds and populations small differences, about 1-2 kg protein, in genetic trends from 1980 to 1998 were found (Pedersen *et al.,* 2001). For both Holstein and Ayrshire breeds the correlations between national and single trait model EBVs were high, generally above 0.99. The authors concluded that the single country model should be preferred due to further developments towards an evaluation model that will include 305-days records and test day records. A single country model will in fact be the only working model in practice if also non-Nordic information from international genetic evaluation will be included. Also the size of the exercise will put limits to model choice.

Future plans in joint Nordic evaluation

The future work this year in the Nordic Cattle Genetic Evaluation will concentrate on three projects, which are carried out simultaneously, one in milk traits, one in fertility traits and one in clinical mastitis.

The development of joint Nordic model for milk traits has been carried out as a joint project with Danish and Finnish teams. This work has involved people in Dansk Kvaeg, Danish Institute of Agricultural Sciences, Finnish Animal Breeding Association and MTT Agrifood Research. The testing of models for Holstein breed has been carried out in Denmark and for red breeds in Finland, although e.g. the Finnish data has included both breeds in both places to better account for fixed effects. Actually the biggest task in joining the data has been combining the identity information from each country to build up a proper pedigree data file as well as defining well behaving genetic groups.

The aim is to include test day records from Denmark and Finland, 305 records of three lactations from Sweden and possibly 305 records of first lactation from Norway. The model will be a single country model with $r_G = 1$ between countries, but a multiple trait model for milk, protein and fat as well as 1st and later lactations. The model for environmental effects will follow the current statistical models in respective countries. Additional problems to be solved are correction for heterogeneous variance, accounting for heterosis in breed crosses, blending of foreign information, accuracy of the predicted breeding values and running the Interbull tests for genetic trend.

Combining test day data and full lactation data has been tested both in Finland and Denmark. Two alternative methods for utilising both type of data have been developed and will be presented in 7th WCGALP, Montpellier, France (Mäntysaari, 2002; Villumsen *et al.,* 2002). Preliminary results show that combining lactation records from one country and TD records from another country with a random regression model (Lidauer *et al.,* 2000) is technically feasible even with large nationwide data sets. These results will also be published in 7th WCGALP, Montpellier, France (Pösö & Mäntysaari, 2002).

The development of Nordic model for fertility traits is carried out in Denmark and Sweden and the development of mastitis resistance evaluation in Norway and Denmark. In fertility traits the heifers will be evaluated for non-return rate, interval from first to last insemination, number of inseminations, heat strength and fertility treatments. Cows will additionally be evaluated on interval from calving to first insemination and day's open. The development and testing of models for functional traits will include testing the traits as single traits or multiple traits, heifers and cows with different parities and single versus multiple country models. Like in the milk traits the model for environmental effects will follow the current statistical models in respective countries.

Joint breeding program

The Nordic dairy cattle breeding programs have been successful in improving production traits and simultaneously achieving a favourable, or at least not unfavourable, genetic change in many functional traits, e.g. udder health, milking speed and conformation as was reported by Juga *et al.*, (1999) in Finnish Ayrshire population. Also Heringstad *et al.*, (2001) published favourable selection responses for clinical mastitis and protein production in the Norwegian cattle population. They found that selection for increased production is not necessarily in conflict with mastitis resistance.

Typical for Nordic cattle breeding has been a well organised national breeding plan for testing bulls. This has enabled the wide use of young bulls and hence testing them in large numbers. Decreasing number of herds and cows in all Nordic countries means that resources for testing programs decline also. Simultaneously the Nordic red breeds have lost some of their share to Holstein breed. To be able to conserve the red breed breeding program and the Nordic profile in Holstein breeding the Nordic cattle breeding programs have to be competitive against global Holstein breeding. To better respond to competition the Nordic countries have agreed on joint semen production of both Ayrshire and Holstein bulls starting with bulls born in 1999. This will enable a joint testing program of about 400 bulls in both breeds. Such a large testing scheme is well comparable to biggest testing schemes in other European countries.

Bull testing schemes are also accompanied with integrated nucleus breeding programs. Finland is already running a nucleus breeding program ASMO in Ayrshire breed (Mäntysaari *et al.,* 1996) supported by large research program in embryo technology (Kochhar *et al.,* 2001; Markkula *et al.,* 1999). Sweden will start a similar program with both Swedish Red and Holstein breeds. Also Denmark is running a nucleus breeding program in both breed groups under Future Genetics. The ASMO program in Finland has increased also commercial embryo flushings and transfers and generated farmer networks to increase the efficiency of ET. The challenge in the future is to operate these nucleus programs jointly and fully integrate them into joint AI breeding program.

Closer co-operation and more effective selection among all Nordic populations will also introduce a higher risk of decreasing the effective population size and hence increasing the change in inbreeding (Meuwissen & Woolliams, 1994). This risk can be accounted for by utilising the results of modern selection theory, for example by maximising the response of selection with a predefined rate of inbreeding or constraining the variance of response (Meuwissen, 1997). There will be a linked research project on sustainable breeding program with Nordic Gene Bank to look for alternative selection and mating schemes.

Conclusions

International genetic evaluation has proved to be successful in global trade of cattle genetics. Interbull evaluations have also brought up more interest to Nordic cattle breeding among other Ayrshire breeding countries. Moving from MACE methodology to joint evaluation of breeding values from performance records will increase the accuracy of selection across Nordic countries, enable comparison of cows and bulls between countries, enable harmonisation of data editing and genetic evaluation systems and make the comparison of animals easier for farmers in different Nordic countries.

More accurate comparison of animals over the borders is a necessity for the development of joint breeding program. A testing scheme of 400 bulls per breed with an integrated nucleus breeding program will be competitive on European scale and enable the selection of animals according to Nordic profile. A challenge for the future is to avoid the possible negative side effects of effective breeding program by utilising modern methods to of optimising selection and risk in breeding program.

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