JOINT NORDIC GENETIC EVALUATION OF DAIRY CATTLE

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Abstract. Four Nordic countries: Denmark, Finland, Norway and Sweden have decided to move to a joint genetic evaluation of dairy cattle. A joint evaluation is needed to improve the accuracy of across country evaluation in a joint Nordic breeding program of which the breeding organisations in these countries have agreed.

Multiple Across Country Evaluation (MACE) has been used successfully in international evaluation for production traits, type traits, somatic cell count and mastitis. The results in other MACE studies have shown that the genetic correlation between countries is high enough for many other functional traits, too. In the future research in the Nordic project we will concentrate on Nordic linear models fitting the data from all four countries. MACE will be employed only as a preliminary analysis to investigate the genetic correlation between the countries.

In the first model for a joint evaluation on production traits we will use very similar modelling within the 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 preliminary results of combining a test day model from one country and a 305 day lactation animal model from the other country have shown that a Nordic model on milk traits is technically possible. The results look very promising when comparing the old national model to a new joint model.

The aim of this paper is to describe the rationale behind the joint Nordic breeding program, the problems and preliminary results in a joint prediction of breeding values and discuss the advantages of joint genetic evaluation.

Keywords: across country evaluation, breeding program.

JUNGTINIS ŠIAURĖS ŠALIŲ GENETINIS PIENINIŲ GALVIJŲ ĮVERTINIMAS

Santrauka. Keturios Šiaurės Europos šalys: Danija, Suomija, Norvegija ir Švedija nusprendė vykdyti jungtinį genetinį pieninių galvijų įvertinimą. Jungtinis įvertinimas padėtų patikslinti ir suvienodinti kiekvienos šalies galvijų vertinimą, vykdant jungtinę veislininkystės programą, kuri suderinta ir patvirtinta tų šalių veislininkystės organizacijų.

Sudėtinis tarpvalstybinis vertinimas (MACE) sėkmingai taikomas tarptautiniam galvijų vertinimui pagal produktyvumo požymius, eksterjero konstitucijos požymius, somatinių ląstelių skaičių piene ir segamumą mastitu. Kitų MACE tyrimų rezultatai rodo, kad kitų funkcinių požymių genetinė koreliacija tarp atskirų šalių galvijų taip pat yra gana didelė. Tolimesniuose Šiaurės šalių projekto tyrimuose bus kreipiamas dėmesys į Šiaurės šalių linijinį metodą, apimsiantį visų keturių šalių galvijų vertinimo duomenis. MACE bus tik kaip parengiamųjų tyrimų priemonė genetinėms atskirų šalių galvijų požymių koreliacijoms nustatyti.

Pirmame jungtiniame galvijų produktyvumo požymių vertinimo modelyje bus modeliuojama labai panašiai, kaip dabar modeliuoja atskiros šalys, dalyvaujančios šioje jungtinėje programoje. Pagrindiniai jungtinio galvijų požymių vertinimo tikslai yra sujungti skirtingus kiekvienos šalies galvijų vertinimo duomenis, registruoti patelių kilmę, formuoti jungtines genetines grupes, koreguoti tarpveislines ir tarpvalstybines heterogenines dispersijas bei registruoti informaciją apie importinius bulius. Pirminiai rezultatai rodo, kad Šiaurės šalių pieno produkcijos rodiklių modelis techniškai įmanomas derinant vienos šalies kontrolinių melžimų dienos modelį su kitos šalies 305 dienų laktacijos modeliu. Palyginus seną valstybinį ir naują jungtinį modelius, atrodo, kad bus gauti vertingi rezultatai.

Šio darbo tikslas yra apibūdinti jungtinės Šiaurės šalių programos racionalumą, problemas ir išankstinius rezultatus vykdant jungtinės veislinės vertės įvertinimą bei aptarti jungtinio genetinio galvijų vertinimo privalumus.

Raktažodžiai: tarpvalstybinis vertinimas, veisimo programa.

Introduction. Four Nordic countries, Denmark, Finland, Norway and Sweden, have signed an agreement of joint testing and use of artificially inseminated - bulls. This agreement will result in a joint breeding program in near future. Planning an integrated breeding program involves many successive steps, namely comparison of animals across countries, selection of bulldams and bullsires, optimised mating strategies, optimised testing capacity and sustainable use of jointly owned proven bulls. This development has already started in Nordic countries.

To enable more accurate comparison and selection of bulls and cows across Nordic countries 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 started its operation on 02.01.2002, 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.

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

Across country comparison. There has been an increasing interest in across country evaluation since Interbull Center was established in 1991. Currently, over 25 countries subscribe to Interbull service of international genetic evaluations. 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 scientifically advanced method known as Multiple Across Country Evaluation (MACE) [Schaeffer, 1994; Fikse and Banos, 2001] to calculate International Genetic Evaluations. MACE has two major advantages over other methods, namely the use of all known relationships between bulls and genotype by environment interactions. MACE combines information from each country using all known relationships among animals, both within and across populations. To account for possible G by E interaction MACE accounts for the possibility of animals re-ranking among certain countries. For this reason, a separate set of results is calculated for every participating country.

International genetic evaluation has seen many improvements during its ten-year old history, which have increased the confidence in across country comparison. Current methodology has some limitations; e.g. the impact of heterogeneity of sire variances over time [Canavesi, 2000] and how to deal with multiple trait observations from participating countries. Quality problems in national evaluations have also an effect on the reliability of international comparison. The set of tests [Boichard *et al.,* 1995], which Interbull requires before accepting data to international genetic evaluation, measures if the genetic trend in national evaluation is unbiased, but there are no other quality control measures of the data.

Recent methods, utilise performance data in across country evaluation [Canavesi *et al.*, 2001; Pedersen et. al., 2001; Weigel *et al.*, 2001]. Using performance data in across country comparison allow to apply similar data editing rules, alternative modelling and utilisation of all genetic links i.e. also cow path. It also brings automatically all countries to the same quality level, when prediction methodology is considered, but will naturally not help if data from one country is erratic. The problem in using performance records from many countries is that amount of data increases easily to impracticability, especially if test day models are considered.

Nordic cattle genetic evaluation. Nordic countries have co-operated in joint genetic evaluation for a couple of years. In the first studies MACE methodology was used to estimate genetic correlations among countries in different traits and 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 between country correlation estimates in Ayrshire were found to be from moderate to high, especially among non-return rate, calving ease and calf viability [Svendsen *et al.*, 2001]. However, in the same study the heritabilities were found to be low and the connections between countries weak. In another study Holstein breed genetic correlations were found to be moderate to high among traits that are expected to be similar like non-return rate, disease resistance to 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.

For udder health traits the 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 caused by weaker genetic links among 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 and Lawlor, 2001]. These studies included even other Interbull member countries and have been followed by Interbull routine service on international genetic evaluation of somatic cell count and mastitis for both breeds and of type traits for Holstein.

The problem of weak genetic links is common to all small breeds among Interbull member countries. The studies have shown that in Ayrshire populations Finland and Sweden have good genetic links; Norway has quite good genetic links to Sweden and reasonable genetic links to Finland. Denmark is more isolated due to its past breeding policy. All three Nordic countries: Denmark, Finland and Sweden have good genetic links in Holstein populations. The estimation of genetic correlations between countries is very sensitive to weak genetic links. Nordic countries have agreed to increase genetic links by exchange of semen among populations. This will increase the accuracy of across country selection of animals.

Another alternative to increase the accuracy is to move to 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 a multi country ($r_G < 1$) and a 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 Holsteins and Ayrshires 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-day records and test day records. In fact, a single country model will be the only working model in practice if non-Nordic information from international genetic evaluation will be also included. The size of the exercise will put limits to the model choice as well.

Future development in joint Nordic evaluation. Encouraged by the positive results in preliminary studies four Nordic countries have agreed to continue the development of joint evaluation of breeding values for bulls and cows. Three projects 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 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.

The model has been tested using data of 28 905 771 TD records of 1 208 065 Finnish cows of three breeds: Ayrshire, Holstein and Finncattle and first lactation 305d records of 975 797 Swedish red-and-white cows. 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. Results will be published in 7th WCGALP, Montpellier, France [Pösö and Mäntysaari, 2002].

The development of Nordic model for fertility traits will be carried out jointly in Denmark and Sweden and the development of mastitis evaluation - in Norway and Denmark. In fertility traits the heifers will be evaluated for non-return rate of 56 day, interval from first to last insemination, number of inseminations, heat strength and fertility treatments. For cows non-return rate of 56 days, interval from calving to first insemination, interval from first to last insemination, day's open, number of insemination, heat strength and fertility treatments will be used. 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 Nordic versus multiple country model. Like in the milk traits the model for environmental effects will follow the current statistical models in respective countries.

Nordic breeding program. A well organised national breeding plan for testing bulls has been typical for Nordic cattle breeding. This has enabled the wide use of young bulls and hence testing them in large numbers. 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. Heringstad *et al.* (2001) also 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.

The number of herds is declining in all Nordic countries as well as the number of cows, which means that resources that are available for testing programs decrease 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 respond better 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 to use a joint testing program of about 400 bulls in both breeds (Table 1). Such a large testing scheme is well comparable to biggest testing schemes in other European countries.

Table 1. **The number of progeny tested bulls in Nordic countries**

	Holstein	Ayrshire	Jersey
Finland	45-50	120-130	-
Sweden	70	100	-
Denmark	300	60-70	85
Norway	1	140	-
Total	415-420	420-440	85

Bull testing schemes are also accompanied with integrated nucleus breeding programs. Finland is already running a nucleus breeding program ASMO in Ayrshire breed supported by a large research program in embryo technology. Sweden will start a similar program with both Swedish Red and Holstein breeds. Denmark is also running a nucleus breeding program in both breed groups under Future Genetics. The ASMO program in Finland has also increased 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 and 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].

Conclusions. International genetic evaluation has proved to be successful in global trade of cattle genetics. Interbull evaluations have also brought up more interest in 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 among 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 possible negative side effects of effective breeding program by utilising modern methods to optimise selection and avoid risk in breeding program.

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