Optimizing Dairy Cattle Breeding Programs using International Genetic Evaluations

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Abstract

The aim of this study was to investigate genetic gain in dairy cattle breeding programs using international genetic evaluations. Selection of bulls and cows across countries on average EBV, combining EBV of different countries into one average EBV (= joint breeding goal), was compared with selection of bulls and cows across countries on national EBV. Two domestic dairy cattle breeding programs in two different countries were simulated using a deterministic model approximating BLUP-selection.

Selection on average EBV yielded a higher genetic gain than selection on national EBV, when the genetic correlation was higher than 0.70. Benefits of selection across countries were at maximum an increase in genetic gain of 15%, when the genetic correlation was 1.00. Selection on national EBV was reduced to within-country selection, when the genetic correlation was 0.90 or lower. Trait and breeding goal definition should be harmonized as much as possible to increase genetic gain by selection of bulls and cows across countries. Development of (sub)global rankings (= joint breeding goal, e.g. average EBV) would increase benefits of selection of bulls and cows across countries.

Introduction

Dairy cattle breeding programs are selecting bulls worldwide using international genetic evaluations provided by Interbull. The procedure MACE is used to convert EBV of bulls from one country to another accounting for genotype by environment interaction (G × E) (Schaeffer, 1994). Worldwide selection of bulls can increase genetic gain in comparison to selection within one country, because the same number of bulls can be selected from a larger number of selection candidates increasing selection intensity (Banos and Smith, 1991; Smith and Banos, 1991; Lohuis and Dekkers, 1998). However, genetic correlations between countries lower than 0.80 – 0.90 can already remove benefits from worldwide selection (Smith and Banos, 1991; Mulder and Bijma, 2005). Genetic correlations for production traits are higher than 0.8 between most countries, but genetic correlations for functional traits, e.g. longevity, are substantially lower (Mark, 2004).

As a consequence of non-unity genetic correlations, especially for functional traits, breeding programs tend to select more domestic bulls (Van der Beek, 2003). Selection of only domestic bulls would make international genetic evaluations redundant. Furthermore, the opportunity to increase selection intensity by selection across countries would not be used.

The aim of this study was to investigate genetic gain in dairy cattle breeding programs using international genetic evaluations. Selection across countries on average EBV (= joint breeding goal) was compared with selection across countries on national EBV for a range of genetic correlations.

Material and Methods

Situation

To simplify, a situation with two dairy cattle breeding programs operating each in one country was simulated. The breeding goal of both breeding programs was to improve milk yield. Due to G × E, milk yield in both countries was considered as two different traits, which were correlated. Bulls in breeding program 1 were progeny tested in country 1; bulls in breeding program 2 were progeny tested in country 2. A joint country genetic evaluation based on an animal model was used to calculate for all bulls and cows an EBV for both countries, which was in contrast with the sire model used in MACE (Schaeffer, 1994). The EBV of bulls were based on performance of progeny and pedigree information; EBV of cows were based on own performance in first lactation and pedigree information. Four selection paths were considered: sires to breed sons (SS), sires to breed daughters (SD), dams to breed sons (DS) and dams to breed daughters (DD). Values of input parameters are summarized in Table 1.

Table 1. Values of genetic correlation, heritability, phenotypic variance, number of bulls per breeding program, number of progeny per bull, number of cows in each country and proportions of selected animals in each selection path.

Parameter	Value
Genetic correlation	0 – 1
Heritability	0.3
Phenotypic variance (kg^2)	$1{,}000^2$
Number of test-bulls per breeding program	200
Number of progeny per bull	100
Population size cows per country	$1*10^6$
Proportion selected SS	0.05
Proportion selected SD	0.10
Proportion selected DS	0.005
Proportion selected DD	0.80

Selection methods

Selection of SS, SD and DS was across countries, while DD were completely selected within their own country. Two types of rankings were used to select SS, SD and DS across countries and DD within countries.

National EBV: truncation selection across countries on national EBV. Each breeding program selected sires and dams on the EBV corresponding to the country of progeny testing. The breeding goal of each breeding program included only the country of progeny testing.

Average EBV: truncation selection on average EBV, weighting the EBV in both countries with 0.5. Both breeding programs selected sires and dams on the same ranking. The breeding goal of both breeding programs contained both countries (= joint breeding goal).

Prediction of genetic gain

Genetic gain in both countries was predicted deterministically approximating BLUP-selection under an animal model using a pseudo-BLUP selection index model (Wray and Hill, 1989; Villanueva *et al.,* 1993). The model accounted for changes in genetic variances and covariances due to linkage disequilibrium caused by selection (Bulmer, 1971), but also due to selection of SS, SD and DS across countries with different genetic means (Mueller and James, 1983). Generations were assumed to be discrete. The model was fully described in Mulder and Bijma (2005).

Results

Figure 1 shows genetic gain in milk yield in country 1 and 2 as a function of the genetic correlation for selection on national EBV or average EBV. Genetic gain in both countries was equal due to equal input parameter values. When the genetic correlation was higher than 0.70, selection on average EBV resulted in higher genetic gain than selection on national EBV. Selection across countries on national EBV was reduced to selection within countries (genetic gain = 512 kg/generation), when the genetic correlation was lower than 0.91 (see also Mulder and Bijma, 2005). When the genetic correlation was 0.91 or higher, the differences in increase in genetic gain were small between both selection methods, but selection on average EBV had still the highest genetic gain. When the genetic correlation was 1.00, both selection methods had the same genetic gain of 587 kg/generation (increase of 15% in comparison to within-country selection), because breeding goals were essentially the same. Selection on average EBV would not be recommended, when the genetic correlation was 0.70 or lower, because genetic gain was lower than with within-country selection.

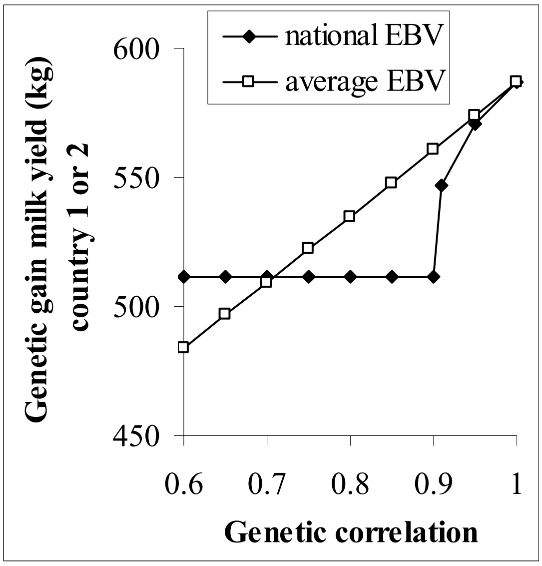

Figure 1. Genetic gain in milk yield (kg/generation) for country 1 and 2 as a function of the genetic correlation for selection across countries on national EBV and selection on average EBV. (input: see Table 1).

Table 2 shows the number of selected SS for breeding program 1 within country 1 and 2 for both selection methods. With selection on national EBV, it was obvious that more sires were selected within country 1, when the genetic correlation decreased. When the genetic correlation was 0.90 or lower, all sires were selected within country 1. With selection on average EBV, half of sires were selected in each country, irrespective of the value of the genetic correlation. Both breeding programs were selecting the same sires, because of using the same ranking. Note that with selection on national EBV, both breeding programs could select different sires even in the same country, because the correlation between the EBV for both countries was not 1.00, when the genetic correlation was smaller than 1.00. Similar trends were observed for both selection methods in the selection paths SD and DS.

Table 2. Number of selected SS (total = 0.05 * 400 = 20) for breeding program 1 in country 1 and 2 for different values of the genetic correlation, when selecting on national or average EBV.

Selection method	r_g	Number of bulls country 1	2
National EBV	1.00	10	10
	0.95	12	8
	0.91	15	5
	≤0.90	20	0
Average EBV	all	10	10

Discussion

In this study the effect of international genetic evaluation on genetic gain was quantified for selection on average EBV and selection on national EBV. Benefits of international genetic evaluations might be larger than predicted in this study, because with more than two countries benefits of across-country selection increase approximately linear with the logarithm of the number of selection candidates (Smith and Banos, 1991). Furthermore, the minimal value of the genetic correlation to benefit from international genetic evaluations might decrease as well with more than two countries (Mulder and Bijma, 2005).

To increase genetic gain in breeding programs by using international genetic evaluation, selection on average EBV was a successful method. Conceptually, the method is similar to the development of subglobal and global rankings as investigated in Powell and VanRaden (2002). In the present study, the weights given to both EBV was 0.5, but other weightings, e.g. reflecting population size, might be used as well when applying in practice. Development of (sub)global rankings or establishment of a joint breeding goal increases genetic gain leading to a higher profit for farmers. A negative side-effect is that individual farmers might not be interested in using (sub)global rankings for selection of bulls. As a by-product, use of (sub)global rankings would increase connectedness between participating countries.

Based on the results, it is obvious that benefits of international genetic evaluations depend largely on the value of the genetic correlation between countries. Genetic correlations are generally higher than 0.80 for production traits, but lower for functional traits (Mark, 2004). Furthermore, breeding goal differences exist between countries due to differences in economic circumstances leading to even lower genetic correlations between breeding goals. To increase potentials for across-country selection, trait and breeding goal definition should be harmonized as much as possible to increase genetic correlations between countries on a trait-by-trait level or on breeding goal level.

Conclusions

- Benefits of international genetic evaluation depend largely on the value of the genetic correlations between countries. Trait and breeding goal definition should be harmonized as much as possible.
- Development of (sub)global rankings based on combining EBV of different countries in one index (= joint breeding goal) would increase benefits of selection of bulls and cows across countries.

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