



Institutionen för husdjursgenetik

Prospects of performing multiple-country comparison of dairy sires for countries not participating in Interbull international genetic evaluations

by

Anne Torsell

Handledare:

Freddy Fikse

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Examensarbete 293

2007

Examensarbete ingår som en obligatorisk del i utbildningen och syftar till att under handledning ge de studerande träning i att självständigt och på ett vetenskapligt sätt lösa en uppgift. Föreliggande uppsats är således ett elevarbete och dess innehåll, resultat och slutsatser bör bedömas mot denna bakgrund. Examensarbete på D-nivå i ämnet husdjursgenetik, 20 p (30 ECTS).



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Agrovoc: Interbull, Dairy cattle, International genetic evaluation

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Preface

First of all I would like to thank Daniel Casanova, Asociacion Criadores de Holando Argentino (ACHA) in Argentina for submitting the data that made this study possible. Then I would like to thank all the people at the Interbull centre for creating a nice working environment for me while doing this study. I especially would like to thank my supervisors Freddy Fikse and Hossein Jorjani for helping me and answering my questions when ever needed. I'm also very grateful for all the good help I have received from Eva Hjerpe, also at the Interbull centre.

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Abbreviations

DYD	Daughter Yield Deviations
EBV	Estimated breeding values
EDC	Effective Daughter Contribution
G x E	Genotype by environment interactions
MACE	Multiple (-trait) Across Country Evaluation
MGS	Maternal Grandsire
MME	Mixed Model Equations
PGM	Predicted Genetic Merit

Abstract

With the international trade of genetic material of dairy bulls there is a need for genetic evaluations performed internationally. For this reason Interbull and the Interbull centre was established, today 42 countries are members of the organization and 26 countries participating in one or several genetic evaluations.

At this moment there are no alternative to fully participate in the evaluations or not. The aim of this study was to investigate if there is a possibility to include a country in the regular evaluations without including any data from the country in question and in that way provide countries not yet participating in the evaluations with an alternative to fully participate.

In this study Argentina was representing the member countries not yet participating in the international evaluation. Data from Argentina was included in a regular genetic evaluation performed by Interbull, also including data from 25 other countries. From the results the bulls were ranked according to their predicted genetic merit. Predicted genetic merits were also estimated by using a model described by Mark *et al*, 2006b. This model was used with different correlation matrices, giving in total seven different alternatives. The bulls in the different alternatives were ranked according to the same criteria as after the Interbull genetic evaluation.

The results from the Interbull evaluation and the different alternatives was statistically analyzed and compared.

The results showed that it is possible to perform an international genetic evaluation for a country without submitted data. For the top 100 bulls the alternative methods found 37 to 67 co-selected bulls. The best result was found when using the same correlation matrix as in the Interbull evaluation. When looking at the country of origin for the top 100 ranked bulls, the different alternatives did with some exception include the same countries as the Interbull evaluation.

This study has showed that it is possible for the Interbull centre to perform alternative genetic evaluations for countries that do not submit any data. If there are a demand for this kind of service.

Introduction

In the 1970s the international trade with frozen semen increased and the need for improved comparison of bulls between countries became more and more important. After years of discussions between the industry and scientists Interbull was founded in 1983, at that time as a joint committee between the European Association for Animal Production (EAAP), International Dairy Federation (IDF) and ICRPMA later called International Committee for Animal Recording (ICAR) (Philipsson, 2005). Since then Interbull has grown and in 1991 the Interbull Centre was established. The Interbull Centre is responsible for promotion, development and standardisation of international genetic evaluation of dairy cattle. At present 42 countries are members and 26 countries participate in international genetic evaluations.

Countries not participating in Interbull international evaluations today have a disadvantage if they import semen and bulls because they do not have access to predicted genetic merits of foreign bulls adjusted for their country and production environment. This however does not mean that there is no trade. Many non-member countries import semen from big international companies with the aim of improving the national milk production. A study done in Zimbabwe comparing different methods showed that imported semen could be a method that gives high economical returns, when looking at net present value of different strategies after 25 years (Mpofu *et al*, 1993). But this does not prove that imported semen is the economically most favourable choice for the countries not participating in the international genetic evaluations. Several factors contribute to the final output, such as the economic environment of the country, the price of semen, milk prices and daughters performance (Holman *et al*, 1990).

The problem that arises when choosing bulls from another country is that different bulls perform differently in different production environments. This means that the ranking among bulls can differ between countries. Reasons for re-ranking are genotype by environment interaction, differences in trait definitions and differences in the national analyses (Powell & VanRaden, 2002).

The aim of this study is to examine if it is possible to obtain international predicted genetic merits for a country without using the national genetic merit. Argentina will be the country representing countries that do not participate in Interbull international genetic evaluations.

In this study we used the method described by Mark *et al* (2006b) that allows prediction of genetic merit for a non-recorded trait using information about correlated, recorded traits. This method requires genetic correlations between the recorded and non-recorded traits and several different correlation matrices will be used and compared. Correlations will be obtained using the prior correlation method (Mark *et al*, 2006a) that utilizes descriptors of production environment and national genetic evaluation. A simpler alternative will be to use the same correlation between Argentina and all the other countries. National genetic evaluation results from Argentina were available for this study and an international genetic evaluation including Argentinean data will serve as basis for comparison.

Genotype by environment interactions

Specific environments affect different genotypes in different ways; it is called genotype and environmental interactions (G x E). This can be explained by the fact that different genes make an animal more or less superior in different environments. To illustrate this here is an example for growth rate; if animals are fed on high quality feed then the animals appetite could be the factor that make some animals superior over the others, whereas if the animals are fed on poor feed it is likely that it is the animals with the best feed utilization that are superior (Falconer & Mackay, 1996).

In the international trade with semen G x E needs to be accounted for so that the best bulls are used for each environment. As illustrated above, G x E affects the performance of the daughters and daughters of a bull may perform well in one environment but not in another. This is seen in scientific studies and each evaluation done by Interbull. Cienfuegos-Rivas *et al* (1999) observed reranking among bulls when looking at the estimated breeding values (EBV) for bulls in the US compared with bulls in Mexico. Costa *et al* (2000) also observed differences in daughters performance caused by G x E between US and Brazil.

The way G x E is considered today in the predicting of international genetic merits is that the trait of interest is treated as different traits in each country and genetic correlations among them are estimated. In general it can be said that the genetic correlations for milk production are high, ranging between 0.85 and 0.90 among the countries in the Northern hemisphere, around 0.90 in Oceania and between 0.75 and 0.84 between Northern and Southern hemisphere (Fikse, 2004). Many studies have been done to estimate genetic correlations between populations; some examples are given in Table 1.

Factors associated with G x E for the Holstein population were temperature, herd size, percentage of North American Holstein genes and peak milk yield (Zwald *et al*, 2003). These factors were found looking at correlations between herds that varied in these and other criteria. Another finding was that herd size might be used as an indicator for management. The result that herd size might indicate management type was supported by a study from Germany (König *et al*, 2005). They also saw indications that herd size is associated with G x E. Herds of Holsteins in West and East Germany were compared and analysed according to heritability, correlations and variance components. The conclusion was that herd size was the factor, which accounted for the difference in correlation between herds, more than any geographic regional difference (König *et al*, 2005).

Table 1. Genetic correlations for production traits

Breed ^a	Trait	Region		No. of animals		R _G	Reference
		A	B	A	B		
<i>Data were performance records</i>							
HOL	305-d milk	US ¹	Brazil ¹	726,932	29,413	0.85	Costa <i>et al.</i> , 2000
		US ¹	Brazil ²	726,932	10,072	0.79	
		US ¹	Brazil ³	726,932	13,789	0.87	
		US ²	Brazil ²	336,678	10,072	0.72	
		US ²	Brazil ³	336,678	13,789	0.86	
		US ³	Brazil ³	336,678	13,789	0.88	
		US ¹	Mexico ¹	499,401	56,162	0.63	
HOL	305-d milk	US ¹	Mexico ²	499,401	21,622	0.60	Cienfuegos-Rivas <i>et al.</i> , 1999
		US ¹	Mexico ³	499,401	18,084	0.71	
		US ³	Mexico ¹	124,351	56,162	0.69	
		US ³	Mexico ²	124,351	21,622	0.72	
		US ³	Mexico ³	124,351	18,084	0.93	
GUE	305-d milk	Canada ¹	US ¹	3,975	32,068	0.87	Fikse <i>et al.</i> , 2003
		Canada ¹	South Africa ¹	3,975	705	0.78	
		US ¹	South Africa ¹	32,068	705	0.86	
		Australia ¹	Canada ¹	4,803	3,975	0.90	
		Australia ¹	US ¹	4,803	32,068	0.87	
		Australia ¹	South Africa ¹	4,803	705	0.87	
<i>Data were bull PGM</i>							
HOL	305-d milk	US ¹	The Netherlands	22,791	9,450	0.91	www.Interbull.org
		US ¹	New Zealand ¹	22,791	4,241	0.75	
JER	305-d milk	US ¹	The Netherlands	2,416	56	0.90	
		US ¹	New Zealand ¹	2,416	2,752	0.75	

^a HOL= Holsteins GUE= Guernsey JER= Jersey

¹Total data set

²Data set include herds with low herd-year standard deviation.

³Data set include herds with high herd-year standard deviation.

International genetic evaluations

The first international genetic evaluations were performed by comparing countries in pairs (conversion equations). These methods had several disadvantages such as being very time-consuming and the results could be biased to suit the importing country (Powell & VanRaden, 2002). They were also outdated as soon as any of the participating countries changed something in their evaluation method (Philipsson, 2005). Schaeffer (1985) presented a linear statistical model that could compare

genetic levels of sires in one or more countries. In this model relationships among bulls were also included to improve the comparison between countries. This model was a big improvement because of the ability to compare more than two countries at a time. Still the results obtained using this method lead to criticism because the bulls were ranked equally in each country. The reason for this is that genetic correlations among countries were assumed to be unity. A breakthrough in international evaluation came in the middle of the 1990s. Schaeffer (1994) modified his original model so that it could handle genetic correlations between countries less than unity and Sigurdsson *et al* (1996) published a method to estimate genetic parameters in a multi-country scenario. These are the methods used today by Interbull.

The international genetic evaluations today performed by Interbull consist of two types of evaluations; routine evaluations performed four times a year and test evaluations performed two times a year, a schematic illustration is shown in Figure 1. The reason for having regular test evaluations is to give participating countries an opportunity to include new traits or countries and to check national evaluations. It is also during test evaluation that the genetic correlations are estimated (Fikse, 2004).

The process of a routine evaluation includes several steps (Figure 1). Firstly, all data that are submitted from participating countries are scanned for errors and then a global pedigree is built and cross-reference list is created, that gives each bull a unique international ID number. Secondly, the national predicted merits are de-regressed and the genetic variance is estimated. The breeding values are de-regressed to remove effects that are included when predicting international breeding values. In the last step the international breeding values are predicted by using Schaeffer's (1994) Multiple (-trait) Across Country Evaluation (MACE). This gives each bull a breeding value for each country expressed in the country's own scale. The participating countries then receive the evaluation and approximated reliabilities and it is their responsibility to rank the bulls and publish the results (Fikse, 2004).

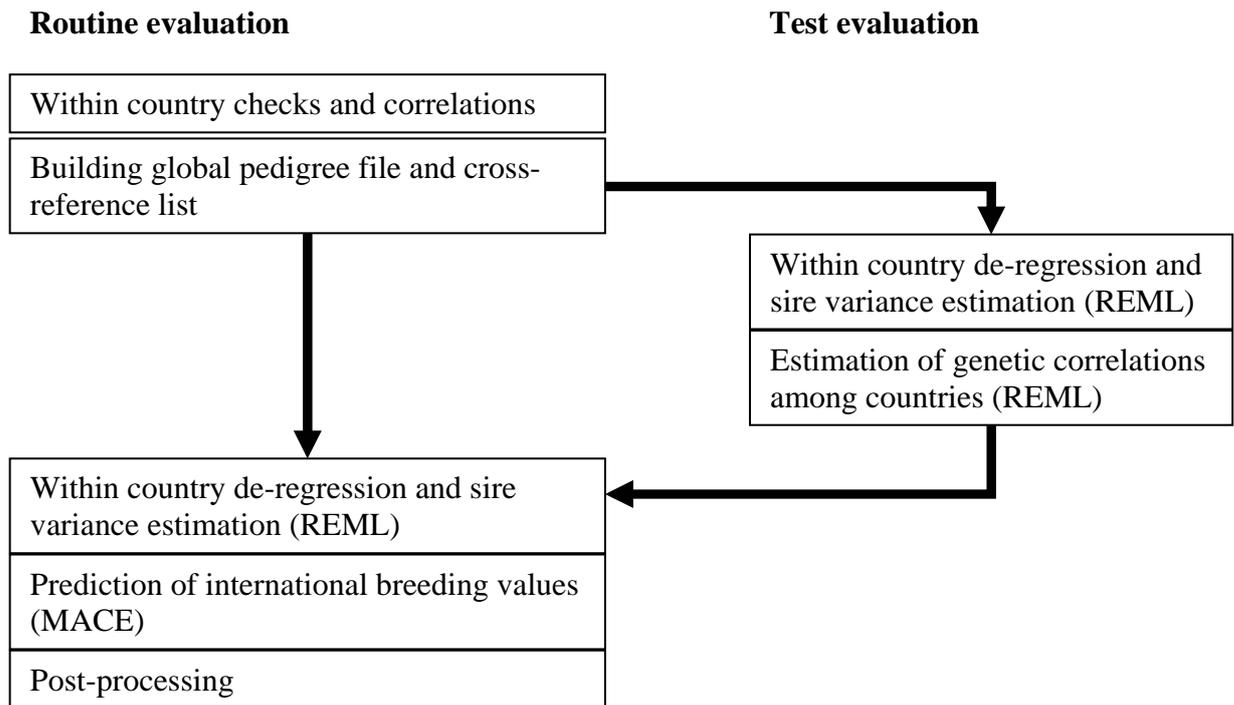


Figure 1. The process of international evaluation performed by Interbull (modified from Fikse, 2004).

Predicting genetic merit

For recorded traits

Interbull Centre uses MACE for prediction of international genetic merits. The advantages of this model are that it allows different genetic parameters for each country and as a consequence different heritability for different traits. It also allows for different units of measurements for the traits in different countries, making it possible to compare bulls in USA where yield for example are expressed in pounds (lbs) with bulls in Germany where kilograms (kg) are used. The genetic correlations between countries are also accounted for in this model. It can therefore reveal G x E interactions and rank animals different in different countries (Schaeffer, 1994). The model also allows the use of data on all bulls in all participating countries, which minimize the risk of data being biased due to selection (Fikse, 2004).

For the prediction of international genetic merit Schaeffer (1994) proposed to use average daughter yield deviations (DYD), which is the phenotypic value of a daughter, adjusted for all fixed effects within a country and for bulls' mate and animal permanent environmental effects. In Interbull evaluations DYD is not used but de-regressed national predicted genetic merits (Fikse, 2004).

The model in MACE is as follows:

$$Y_i = X_i\mu_i + Z_iQg_i + Z_i s_i + e_i \quad (1.1)$$

Where

Y_i = the vector of DYD or de-regressed predicted genetic merit (PGM) from country i for a particular trait such as milk yield,

μ_i = a scalar for country i , which reflects the definition of the genetic base for that country,

g_i = a vector of genetic group effects of phantom parents,

s_i = a vector of random sire effects for country i ,

e_i = a vector of effects of random mean residuals,

Z_i = the matrix that relates DYD or de-regressed PGM to sires, and

Q = the matrix that relates sires to phantom parent groups.

For t countries, the variance-covariance matrices of the random vectors are:

$$V \begin{pmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \\ \vdots \\ \mathbf{e}_t \end{pmatrix} = \begin{pmatrix} \mathbf{D}_1\sigma_{e1}^2 & \mathbf{0} & \cdots & \mathbf{0} \\ \mathbf{0} & \mathbf{D}_2\sigma_{e2}^2 & \cdots & \mathbf{0} \\ \vdots & \vdots & \ddots & \vdots \\ \mathbf{0} & \mathbf{0} & \cdots & \mathbf{D}_t\sigma_{et}^2 \end{pmatrix} = \mathbf{R} = \mathbf{R}_o \otimes \mathbf{D} \quad (1.2)$$

and

$$V \begin{pmatrix} \mathbf{s}_1 \\ \mathbf{s}_2 \\ \vdots \\ \mathbf{s}_t \end{pmatrix} = \begin{pmatrix} \mathbf{A}g_{11} & \mathbf{A}g_{12} & \cdots & \mathbf{A}g_{1t} \\ \mathbf{A}g_{12} & \mathbf{A}g_{22} & \cdots & \mathbf{A}g_{2t} \\ \vdots & \vdots & \ddots & \vdots \\ \mathbf{A}g_{1t} & \mathbf{A}g_{2t} & \cdots & \mathbf{A}g_{tt} \end{pmatrix} = \mathbf{G} \otimes \mathbf{A} \quad (1.3)$$

Where g_{ij} is the sire (co)variance between countries i and j , \mathbf{A} is the additive genetic relationship matrix for all bulls based on sire and maternal grandsire (MGS) relationships, σ_{ei}^2 is the residual variance for country i , and \mathbf{D}_i is a diagonal matrix with elements equal to 1 over the number of daughters in a bulls DYD (Schaeffer, 1994). Today Interbull uses effective daughter contribution (EDC) instead of number of daughters because it improves the international genetic comparison (Fikse & Banos, 2001).

The predicted international genetic merit (\hat{u}) is:

$$\hat{u} = Q\hat{g} + \hat{s} \quad (1.4)$$

For MACE to work properly each bull needs a unique identification number, the national evaluations need to be unbiased, the (co)variances need to be known and there has to be genetic links between countries (Schaeffer, 1994).

Non-recorded traits

To be able to do genetic evaluations with MACE there need to be sufficient records for the trait in question. This can be a problem due to numerous reasons. For example, there is no registration of health traits in many countries; those countries then lack the possibility to include the health traits in their national genetic evaluations.

Mark *et al* (2006b) proposed a method to predict international PGM for a non-measured trait, using records for correlated traits. Mark *et al* (2006b) illustrated his method with clinical mastitis in the US as the unrecorded trait and somatic cell count as the correlated recorded trait. However, the method was developed to be able to handle any unrecorded trait with a known correlated recorded trait. In this study milk yield in Argentina will be the unrecorded trait and recorded milk yield in other countries will be the recorded traits.

According to this method PGM for the recorded traits are first calculated with MACE. These values are then combined into PGM for the non-measured trait by using the following model:

$$U_{i+} = g'V^{-1}\hat{u}_i \quad (1.5)$$

Where

\hat{u}_i = the vector of MACE solutions for recorded traits

i = recorded traits

$i+$ = a non-measured trait

g = a vector containing correlations between the recorded and non-recorded traits

V = the (co)variance matrix among the predicted international breeding values (u_i) from MACE (Mark *et al*, 2006b)

Estimating correlations

For recorded traits

Interbull uses the EM-REML method for estimation of correlation. In the estimations de-regressed national PGM for AI bulls are used. The estimation is performed simultaneously for all countries, except Holstein where the dataset is too large. For Holstein the countries are divided in subsets consisting of three countries, with USA as the link provider. All possible combinations of the subsets are considered to estimate correlations between all countries (Interbull).

To update the genetic (co)variances (G) equation (1.6) is used. When using this equation the iteration scheme converges slowly. To increase the speed, the traces can

be moved to the denominator. To increase the speed further the genetic correlations could be extrapolated periodically (Sigurdsson, 1996).

$$G_{ij}^{(k+1)} = \frac{[\hat{u}_i^{(k)} T_{uu} \hat{u}_j^{(k)} - \hat{g}_i^{(k)} T_{gg} \hat{g}_j^{(k)} + tr(T_{uu} W_{ij}^{uu(k)}) + 2tr(T_{gu} W_{ij}^{ug(k)}) + tr(T_{gg} W_{ij}^{gg(k)})]}{q} \quad (1.6)$$

to approximate the error variance:

$$R_{0ii}^{(k+1)} = G_{ii}^{(k+1)} \lambda_i \quad (1.7)$$

where:

$i = 1, \dots, c$ and $j = i, \dots, c$

c = number of countries

q = total number of bulls

k = iteration round

$tr(\cdot)$ = trace operator

λ = the assumed environmental to sire variance ratio G_{ii} / R_{0ii} according to the heritability estimated in each country (Sigurdsson *et al*, 1996)

Mixed model equations (MME) (1.8) and (1.9) are used to get estimates needed in the G matrix (1.6).

$$T = \begin{pmatrix} Q' A^{-1} Q & -Q' A^{-1} \\ -A^{-1} Q & A^{-1} \end{pmatrix} = \begin{pmatrix} T_{gg} & T_{gu} \\ T_{ug} & T_{uu} \end{pmatrix} \quad (1.8)$$

and

$$W = \begin{pmatrix} X' R^{-1} X & 0 & X' R^{-1} Z \\ 0 & T_{gg} \otimes G^{-1} & T_{gu} \otimes G^{-1} \\ Z' R^{-1} X & T_{ug} \otimes G^{-1} & Z' R^{-1} Z + T_{uu} \otimes G^{-1} \end{pmatrix}^{-1} = \begin{pmatrix} W^{cc} & W^{cg} & W^{cu} \\ W^{gc} & W^{gg} & W^{gu} \\ W^{uc} & W^{ug} & W^{uu} \end{pmatrix} \quad (1.9)$$

where:

G^{-1} = the inverse of the sire genetic (co)variance matrix of order equal to number of countries

X = incidence matrix

Estimates for $\hat{\mu}$, \hat{g} , \hat{s} are obtained by solving:

$$\begin{pmatrix} \hat{\mu} \\ \hat{g} \\ \hat{u} \end{pmatrix} = W \begin{pmatrix} X'R^{-1}y \\ 0 \\ Z'R^{-1}y \end{pmatrix} \quad (1.10)$$

For non-recorded traits

The method developed by Mark *et al* (2006a) is a way to work around the problem of estimation of genetic correlations for non-recorded traits. With this method genetic correlations are predicted using a multiple regression method. Values that potentially explain variations between countries are variables in model (1.11) and (1.12). The variables are from different sources: climate variables, production system indicators and national evaluation descriptors. Model (1.12) is a modification of model (1.11) where variables not directly associated with G x E are excluded. These variables are included in μ' and are fixed at their maximum values.

Prior:

$$r^5 = \mu + b_1\text{milk} + b_2\text{grass} + b_3\text{wind} + b_4\text{temp} + b_5h^2 + b_6\text{par} + b_7\text{CB} \quad (1.11)$$

Prior +:

$$r^5 = \mu' + b_1\text{milk} + b_2\text{grass} + b_3\text{wind} + b_4\text{temp} \quad (1.12)$$

where

milk = ratio for milk yield

grass = grazing

wind = ratio for average wind speed

temp = ratio for average temperature

h^2 = ratio for heritability

par = ratio for number of parities

CB = ratio for number of common bulls

$\mu = -0.586$

$\mu' = \mu + b_5(1) + b_6(1) + b_7(990)$

Variables are either expressed as ratios or binary variables. For continuous values such as milk, temperature or wind a ratio was calculated, putting the highest value in the denominator. This gives a value between 1 and 0; the more similar two countries are the higher the value. For class variables the variable was set as 1 or 0, 1 if both countries belonged to the same group, for example grazing countries. Number of common bulls where used as is.

Dairy in Argentina

The second largest country in Latin America is Argentina with an area of 2,800,000 km² in the southeast of the continent. The climate conditions vary greatly throughout the country. About 52 % of the land is used for pasturing cattle and sheep, most of it in the central area called the Pampas. 90% of the milk production in Argentina is located in the provinces of Santa Fe, Cordoba and Buenos Aires. During the last decade of the 20th century the Argentinean milk production increased rapidly (Haumann & Wattiaux, 1999). Between 2001 and 2006 the fluid milk production increased from 9.5 to 10.3 million tons, while the number of cows decreased from 2.45 to 2.15 million heads and consequently the efficiency for each cow increased from 3.88 to 4.79 tons per head (Foreign Agriculture Service).

Argentina uses a single trait best linear unbiased prediction, animal model (ST-BLUP-AM) for their genetic evaluation. They include herd-year-season, month of calving, cow age at calving and lactation number as environmental effects. Genetic groups and relationships are based on country of origin, sex and birth year. The data are measured and collected through an official milk recording system, following ICAR rules and guidelines. The data includes lactation records from 1988 (www.Interbull.org).

Material

In this study three different datasets were used (Table 2), all containing data submitted to Interbull. The datasets EBVtot and EBVpub contains the results from the international genetic evaluation of performance for Holstein performed by Interbull Centre in August 2006. The dataset EBVpub is smaller than EBVtot, the reason being that phantom groups, ancestors and bulls which participating countries do not want to have published is excluded.

Table 2. Data sets used

Dataset	No of bulls	Includes
EBVtot	100 642	All bulls included in MACE. 24 countries.
EBVpub	92 503	Bulls with publishable estimated breeding values (EBV), information about year of birth and country of origin of bull. 24 countries.
Argentina	909	Bulls with daughters in Argentina

The codes used in this study for the different countries are in Table 3. Some codes include joint national evaluation or multiple populations. They will all though be referred to as countries in this report. The number of bulls in Table 3 is not equal to the number of bulls in Table 2, the reason being that one bull can be registered in one or more countries.

Table 3. Codes of the countries used in the study

Code	Country	N _{pub} ^a	N _{incl} ^b
ARG	Argentina		744
AUS	Australia	4,203	4,666
BEL	Belgium (Walloon only)	320	589
BRA	Brazil		
CAN	Canada	4,110	6,594
CHE	Switzerland	390	652
CHR	Swiss Red Holstein	894	1,012
CZE	Czech Republic	1,315	1,776
DEU	Germany & Austria	12,904	15,590
DFS	Denmark, Finland & Sweden	7,620	8,405
EST	Estonia	345	399
ESP	Spain	929	1,355
FRA	France	8,950	10,479
FRR	French Pie Rough	129	133
GBR	United Kingdom	3,254	4,152
HUN	Hungary	1,494	1,754
IRL	Ireland	909	1,182
ISR	Israel	668	711
ITA	Italy	4,944	5,905
JPN	Japan	2,819	2,947
NLD	Netherlands & Flanders	7,486	9,185
NZL	New Zealand	3,191	3,915
POL	Poland	4,671	4,754
SVN	Slovenia	107	161
USA	United States of America	20,207	22,119
ZAF	South Africa	644	772

^a number of publishable bulls

^b number of records included in MACE

Argentina data

The data from Argentina contained information on milk yield for about 909 Holstein bulls. The distribution over birth years is in Figure 2.

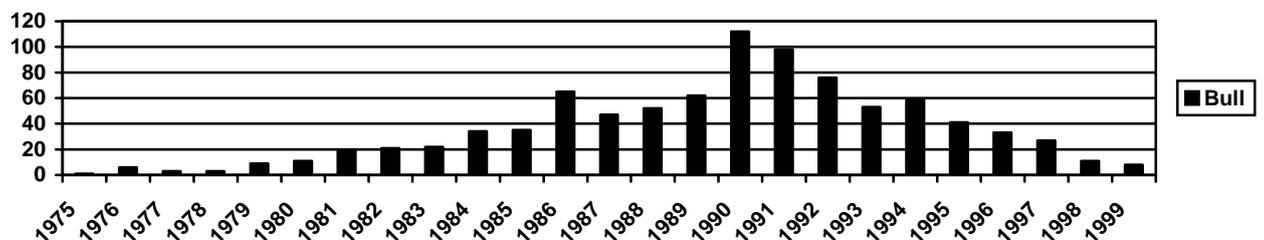


Figure 2. Birth year of bulls with daughters in Argentina

The data from Argentina included many imported bulls, mostly from North America. The country of test for bulls, sires and dams are in Table 4.

Table 4. Country of test for animals in the data from Argentina

Country ^a	Bull	Sire	Dam
ARG	137	5	91
USA	609	722	678
CAN	136	177	134
ESP	15		2
NLD	10	4	2
NZL	1	1	1
BRA	1		
BEL			1

^a See Table 3

Several of the bulls in the data from Argentina also have daughters in other countries; the number of bulls that each country has in common with Argentina is shown in Table 5.

Table 5. Common bulls (CB) between Argentina and other countries.

Country ^a	CB
AUS	174
BEL	114
CAN	321
CHE	82
CHR	42
CZE	94
DEU	185
DFS	157
EST	10
ESP	306
FRA	198
FRR	1
GBR	269
HUN	178
ISR	9
ITA	181
IRL	139
JPN	222
NLD	197
NZL	150
POL	78
SVN	17
USA	569
ZAF	204

^a See Table 3

Methods

Analysis with Argentina data

Estimation of correlations and prediction of international genetic merits for Argentina was performed in the same way as in common Interbull evaluations, with the methods EM-REML and MACE. The PGM obtained this way will be used as reference.

Prior to running EM-REML and MACE with Argentina some preparations needed to be made. The Argentinean breeding values were de-regressed and the sire variance was estimated. A new pedigree file and cross-reference list was created that included the information about the bulls registered in Argentina.

The genetic (co)variance matrix that was obtained after running EM-REML went through a statistical method called bending, the reason for this is to make the result positive definite. The method used is described by Jorjani *et al* (2003).

The order of the analysis is seen in Figure 1.

Analysis without Argentina data

When predicting genetic merit without data from Argentina model (1.5) (Mark *et al* 2006b) was used. As the recorded trait predicted genetic merits for 24 countries participating in Interbull international evaluations were used, calculated with MACE for the August 2006 Interbull evaluations.

The correlation matrix in model (1.5) was different for different alternatives. First, predictions of genetic merit were done with the assumed correlations of 0.5; 0.6; 0.7 and 0.8 between Argentina and all the different countries. Next varying correlations were used between Argentina and the other countries. These correlations were estimated with two different methods. First with the prior genetic correlations method (Mark *et al*, 2006a), equation (1.11) and (1.12), giving two correlations matrices called prior and prior+. Second with EM-REML, equation (1.6). The EM_REML correlations used were the same matrix that was estimated for the alternative including data from Argentina.

Prior genetic correlations

The values used for temperature and wind came from the Danish Meteorological Institute (www.DMI.dk). The value for average milk yield came from ICAR's yearly inquiries for 2002 (www.ICAR.org). The national genetic evaluation descriptors are taken from the information provided by each country's genetic evaluation centre to the Interbull Centre, available on the Interbull homepage (www.interbull.org). Argentina, New Zealand, Ireland and Australia are considered to be countries with mostly grazing.

The b-values used for predicting prior correlations were from Mark *et al* (2006a).

Table 6. b-values for prior genetic correlations

Variable	b
b ₁	0.491
b ₂	0.103
b ₃	0.235
b ₄	0.187
b ₅	0.144
b ₆	0.042
b ₇	0.225

Alternatives

The alternatives using model (1.5) for prediction of genetic merit are named according to the method used when estimating the correlations and the alternative including Argentina data are called r_{ref} for reference. In Table 7 the different alternatives are described.

Table 7. Different alternatives used to predict international genetic merits

Alternative	r_G^a	σ_s^b	PGM ^c	Data ^d	N ^e
r_{ref}	EM-REML	EM-REML	MACE	25 countries	100,895
r_{REML}	EM-REML	EM-REML	model (1.5)	24 countries	100,642
$r_{0.5}$	0.5	1.0	model (1.5)	24 countries	100,642
$r_{0.6}$	0.6	1.0	model (1.5)	24 countries	100,642
$r_{0.7}$	0.7	1.0	model (1.5)	24 countries	100,642
$r_{0.8}$	0.8	1.0	model (1.5)	24 countries	100,642
r_{prior}	Prior ^f	1.0	model (1.5)	24 countries	100,642
r_{prior+}	Prior + ^g	1.0	model (1.5)	24 countries	100,642

^a Method of estimating correlation or the value of the correlation

^b Sire standard deviation

^c The method used for predicting international genetic merit

^d Number of countries included for prediction of international genetic merit

^e Number of bulls included in each alternative

^f Equation (1.11) was used when estimating correlations

^g Equation (1.12) was used when estimating correlations

For prediction of international genetic merit and estimation of genetic parameters Interbull software was used and when performing the statistical analysis and comparisons the software package SAS, was used.

Results

Correlation

In Table 8 the different correlations between Argentina and the other countries are seen for the alternatives where correlations have been estimated.

Table 8. Genetic correlations between Argentina and other countries

Country ^a	r^b	r_{bend}^c	r_{Prior}	$r_{\text{Prior+}}$
CAN	0.668	0.656	0.612	0.828
DEU	0.567	0.578	0.621	0.843
DFS	0.612	0.648	0.702	0.811
FRA	0.721	0.713	0.678	0.856
ITA	0.665	0.652	0.627	0.849
NLD	0.655	0.683	0.661	0.847
USA	0.661	0.649	0.635	0.833
CHE	0.727	0.701	0.681	0.840
GBR	0.648	0.643	0.809	0.854
NZL	0.667	0.643	0.766	0.916
AUS	0.733	0.704	0.649	0.875
BEL	0.707	0.687	0.752	0.839
IRL	0.713	0.706	0.701	0.883
ESP	0.693	0.698	0.593	0.854
CZE	0.644	0.650	0.725	0.822
SVN	0.865	0.748	0.725	0.861
EST	0.206	0.470	0.698	0.832
ISR	0.607	0.609	0.658	0.832
CHR	0.797	0.720	0.654	0.844
FRR	0.692	0.680	0.706	0.859
HUN	0.657	0.646	0.684	0.840
POL	0.745	0.662	0.716	0.865
ZAF	0.745	0.684	0.702	0.865
JPN	0.651	0.663	0.665	0.850

^a See Table 3

^b The correlations obtained after EM-REML

^c Correlations after bending r (Jorjani *et al*, 2003), the correlation matrix used in alternatives r_{ref} and r_{REML}

When looking at the correlations between the genetic correlations after bending and the two prior alternatives we see that it is medium correlation between r_{bend} and $r_{\text{prior+}}$, 0.307 and an almost nonexistent correlation between r_{bend} and r_{prior} , 0.004.

Predicted genetic merit

The mean of PGM obtained with alternative r_{ref} and r_{REML} were higher than the others (Table 9), the reason being that the sire variance used for Argentina was calculated with EM-REML. Between the four alternatives with a set correlation the mean EBV increase with higher correlations. For the two alternatives with prior correlations $r_{\text{prior+}}$ has a higher EBV than r_{prior} .

Table 9. Statistics for estimated Argentina breeding values for milk

Alternative ^a	N	PGM (Mean)	Std Dev	Min	Max
r_{ref}	100,895	30.36	145.08	-607.04	561.86
r_{REML}	100,642	212.13	144.88	-432.84	761.61
r_{prior}	100,642	1.31	0.98	-2.32	5.26
r_{prior+}	100,642	1.56	1.18	-3.34	5.93
$r_{0.5}$	100,642	0.89	0.69	-2.08	3.44
$r_{0.6}$	100,642	1.07	0.83	-2.50	4.13
$r_{0.7}$	100,642	1.24	0.97	-2.91	4.82
$r_{0.8}$	100,642	1.42	1.11	-3.33	5.51

^a See Table 7

When looking at the genetic trend over year, an increase in PBV is seen for all alternatives (Figure 3, Figure 4 and Figure 5). For the alternatives with assumed correlation only the genetic trend for alternative $r_{0.5}$ and $r_{0.8}$ are shown. The two other alternatives follow the same trend and are located in-between the two presented lines.

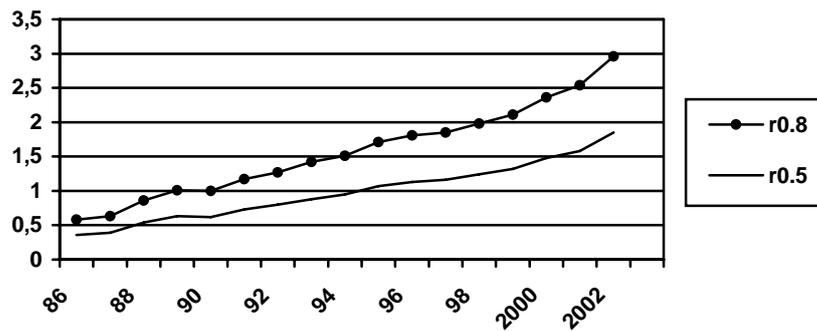


Figure 3. Genetic trend for alternatives $r_{0.5}$ and $r_{0.8}$.

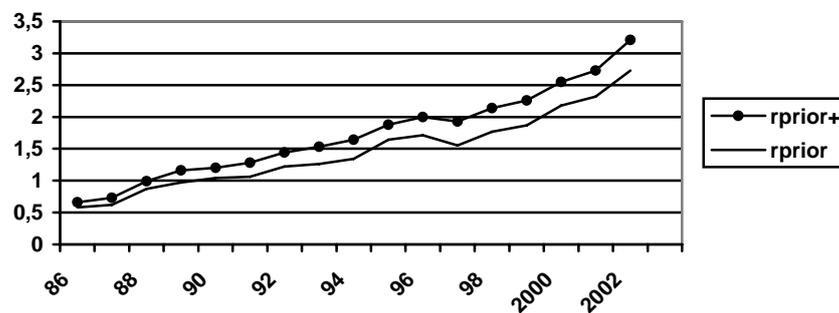


Figure 4. Genetic trend for alternatives r_{prior} and r_{prior+} .

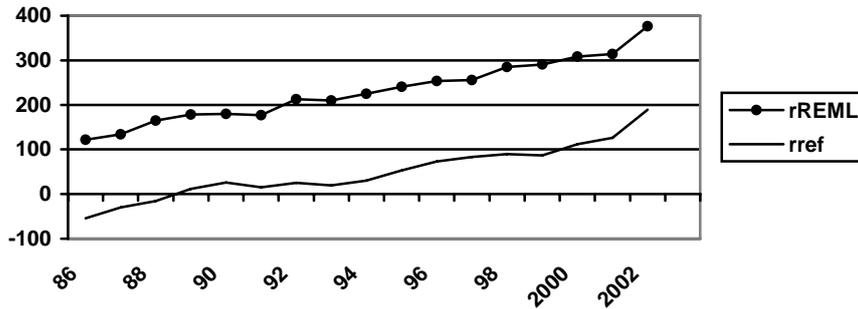


Figure 5. Genetic trend for alternatives r_{ref} and r_{REML} .

The highest correlation between PGM from alternative r_{ref} and the other alternatives is there with alternatives r_{REML} and r_{prior+} (Table 10 and Table 11). The correlation between PGM from the alternatives with assumed correlations, 0.5; 0.6; 0.7 and 0.8 is close to one (Table 10 and Table 11).

Table 10. Pearson correlations of Argentina PGM between different methods

Alternative ^a	r_{ref}	r_{REML}	r_{prior}	r_{prior+}	$r_{0.5}$	$r_{0.6}$	$r_{0.7}$	$r_{0.8}$
r_{ref}	1	0.973	0.925	0.944	0.926	0.926	0.926	0.926
r_{REML}		1	0.946	0.962	0.952	0.952	0.952	0.952
r_{prior}			1	0.987	0.969	0.969	0.969	0.969
r_{prior+}				1	0.992	0.992	0.992	0.992
$r_{0.5}$					1	1*	1*	1*
$r_{0.6}$						1	1*	1*
$r_{0.7}$							1	1*
$r_{0.8}$								1

^a For explanation see Table 7

1* > 0.99998

Table 11. Spearman correlation of Argentina PGM between different methods

Alternative ^a	r_{ref}	r_{REML}	r_{prior}	r_{prior+}	$r_{0.5}$	$r_{0.6}$	$r_{0.7}$	$r_{0.8}$
r_{ref}	1	0.961	0.905	0.927	0.905	0.905	0.905	0.905
r_{REML}		1	0.934	0.953	0.942	0.942	0.942	0.942
r_{prior}			1	0.984	0.960	0.960	0.960	0.960
r_{prior+}				1	0.989	0.989	0.989	0.989
$r_{0.5}$					1	1*	1*	1*
$r_{0.6}$						1	1*	1*
$r_{0.7}$							1	1*
$r_{0.8}$								1

^aFor explanations see Table 7

1* > 0.99998

The results from the reference evaluation (r_{ref}) were divided into subgroups according to country of test (Table 12). Correlations for PGM were estimated between the subgroups and the other alternatives. The correlation for PGM between the bulls tested in Argentina evaluated with reference evaluation and the PGM from the other alternatives ranges between 0.393 and 0.550, the highest correlation is seen with

alternative $r_{\text{prior+}}$. For the other countries of test, the correlation between PGM is around 0.8 and 0.9. The difference is explained by the fact that data from all countries except Argentina was included when predicting genetic merits.

Table 12. Pearson correlation for PGM between subgroups from alternative r_{ref} with the other alternatives

Country ^a	r_{REML}	r_{prior}	$r_{\text{prior+}}$	r_{assumed}^b	N ^c
ARG	0.442	0.507	0.550	0.393	264
AUS	0.966	0.928	0.936	0.890	3690
BEL	0.971	0.958	0.976	0.964	84
CAN	0.933	0.864	0.911	0.900	5753
CHE	0.966	0.932	0.960	0.950	415
CHR	0.987	0.971	0.983	0.980	745
CZE	0.965	0.858	0.904	0.875	928
DEU	0.973	0.933	0.952	0.935	14148
DFS	0.976	0.925	0.950	0.921	7692
EST	0.971	0.900	0.931	0.918	290
ESP	0.941	0.856	0.900	0.880	811
FRA	0.963	0.885	0.910	0.880	9834
FRR	0.997	0.960	0.985	0.983	75
GBR	0.951	0.952	0.962	0.943	2866
HUN	0.967	0.931	0.946	0.932	1163
IRL	0.991	0.965	0.970	0.950	777
ISR	0.989	0.948	0.950	0.916	636
ITA	0.957	0.880	0.904	0.876	5109
JPN	0.936	0.839	0.878	0.854	2746
NLD	0.986	0.937	0.950	0.924	9162
NZL	0.986	0.957	0.968	0.956	2995
POL	0.991	0.980	0.980	0.971	4345
SVN	0.984	0.923	0.932	0.887	100
USA	0.903	0.758	0.817	0.800	20555
ZAF	0.962	0.933	0.943	0.910	438

^a See Table 3

^b Compose of the alternatives with assumed correlation of 0.5; 0.6; 0.7 and 0.8. They have the same correlation at three decimals

^c Numbers of bulls tested in each country

When looking at correlations between the national PGM for Argentina and international PGM obtained from the different alternatives (Table 13) it is seen that the highest correlation is with the reference alternative r_{ref} . This is as expected considering that the national PGM for Argentina only are included in that alternative. For the other alternatives the highest correlation is seen with alternative r_{REML} .

Table 13. Correlation between the national PGM for Argentina bulls with international PGM obtained from the different methods

	r_{ref}	r_{REML}	r_{prior}	$r_{\text{prior+}}$	r_{assumed}^a
NatPGM ^b	0.992	0.521	0.455	0.500	0.472

^a Compose of the alternatives with assumed correlation of 0.5; 0.6; 0.7 and 0.8. They have the same correlation with NatPGM at three decimals

^b Argentina national PGM

To compare PGM in the different alternatives (Table 14), the mean PGM for the different alternatives was calculated. The top 100 bulls in each alternative were identified with the PGM that was estimated within that alternative. Within these 100 bulls the mean PGM value for the bulls estimated in the reference alternative was calculated. The smallest deviation from the reference alternative was obtained when ranking the bulls with the PGM values from r_{REML} and the largest deviation was obtained with bulls ranked from the r_{prior} . The mean PGM calculated when the data was ranked according to the correlations (0,5; 0,6; 0,7 and 0,8) all shows very similar values. The reason for that can be seen in Table 15, correlation 0.6 and 0.7 have all top 100 co-selected and between the others there are 98 or 99 co-selected bulls.

Table 14. Mean Argentina estimated breeding values for milk

Alternative ^a	PGM _{rG} ^b	Deviation (%)
r_{ref}	451.54	-
r_{REML}	438.79	2.82
r_{prior}	397.99	11.9
r_{prior+}	417.10	7.6
$r_{0.5}$	402.13	10.9
$r_{0.6}$	402.69	10.8
$r_{0.7}$	402.69	10.8
$r_{0.8}$	403.06	10.7

^a For explanations see Table 7

^b Mean value of PGM for Argentina when the top 100 bulls are selected according to the different alternatives.

The alternative that had most bulls co-selected with the reference in the top 100 was r_{REML} with 67 co-selected bulls (Table 15). The least co-selected bulls with the reference had r_{prior} . Some connections among alternatives within a method are seen. The four alternatives with assumed correlations (0.5; 0.6; 0.7 and 0.8) have 98 to 100 bulls co-selected. The two alternatives with prior correlations (r_{prior} and r_{prior+}) have 68 bulls co-selected and the two alternatives with EM-REML correlations (r_{ref} and r_{REML}) have 67 bulls co-selected.

Table 15. Number of co-selected top 100 bulls between different methods

	r_{ref}	r_{REML}	r_{prior}	r_{prior+}	$r_{0.5}$	$r_{0.6}$	$r_{0.7}$	$r_{0.8}$
r_{ref}	100	67	37	56	46	46	46	47
r_{REML}		100	42	53	45	45	45	46
r_{prior}			100	68	52	53	53	53
r_{prior+}				100	78	79	79	79
$r_{0.5}$					100	99	99	98
$r_{0.6}$						100	100	99
$r_{0.7}$							100	99
$r_{0.8}$								100

All alternatives have identified most of the countries that are in the top 100 of the reference except Belgium which only r_{REML} identified (Table 16). The alternatives in prior correlation did not include South Africa and the alternatives with assumed correlation did not include Spain. For Spain and South Africa only one respectively two bulls were among the top 100 for the reference situation. For three countries the deviation in number of bulls identified per country was substantial. The reference

evaluation had five bulls from Germany in the top100; all alternatives except r_{REML} have highly overestimated the bulls from Germany. The reference evaluation had 24 bulls from France among top100, the alternative r_{REML} , r_{prior} and r_{prior+} overestimated the number of bulls and the alternatives with assumed correlations ($r_{0.5}$, $r_{0.6}$, $r_{0.7}$ and $r_{0.8}$) underestimated the number of bulls. For USA there is also both over- and underestimations, but alternative r_{prior+} has the same number of bulls, 22.

Table 16. Country of test for the top 100 bulls, in the different alternatives

Country ^a	R_{ref}	r_{REML}	r_{prior}	r_{prior+}	$r_{0.5}$	$R_{0.6}$	$r_{0.7}$	$r_{0.8}$
BEL	1	1						
CAN	1	3		2	5	4	4	4
CZE	3	2	4	4	5	5	5	5
DEU	5	4	13	15	13	13	13	11
DFS	7	11	5	7	7	7	7	7
ESP	1	3	1					
EST	2	1	1	1	1	1	1	1
FRA	24	34	30	18	13	13	13	13
GBR	7	5	8	9	9	9	9	9
HUN	4	2	1	1	2	2	2	2
IRL			1					
ITA	3	3	6	8	6	7	7	7
JPN	8	4	5	5	5	5	5	6
NLD	8	11	6	7	5	5	5	5
POL	2	2	1	1	1	1	1	1
USA	22	12	18	22	27	27	27	28
ZAF	2	2			1	1	1	1

^a For explanation see Table 3.

Discussion

The results showed that all the alternatives tried in this study work to predict genetic merit. But the similarities between the reference evaluation (r_{ref}) results and the results from the other alternatives differed.

Most similarities between breeding values (Table 9) as well as number of co-selected bulls (Table 15) are seen between the reference evaluation and the alternative r_{REML} . This is not surprising considering the two alternatives used the same genetic parameters, obtained with the EM-REML. Of the alternatives that did not use EM-REML it seems like the alternative r_{prior+} correlations gave the best estimates.

One possible explanation for the alternative r_{prior+} to have more similar results to the Interbull evaluation than the alternative r_{prior} can be seen in the correlations between genetic correlations. The genetic correlations used in alternative r_{prior+} had a medium correlation with the genetic correlations used in the reference evaluation, whereas the correlations between the Interbull genetic correlations and the ones used in alternative r_{prior} was close to zero.

In this study PGM for milk yield was used, this could influence the results for country of origin among the top100 bulls. If instead PGM for protein or fat percentage was compared, it is likely that the distribution of bulls in country of test would be different. Between countries the design of their breeding goal differs, putting

emphasis on different traits. When looking at the PGM for milk yield it is possible that it favors countries that weight milk yield high in their breeding goal. When looking at e.g. fat percentage it is likely that the list of countries with the top100 bulls will change. In this case countries are favored that give high weight on fat percentage in their breeding goal. This should be considered if using a method that predicts genetic merits for only one trait. The bulls should be ranked according to the trait that is of most interest for the importing country or to an index of traits weighted according to local circumstances.

The estimated correlations in alternative r_{prior} and $r_{\text{prior+}}$ are apparently very different compared to the banded correlations obtained from the reference evaluation. To see such big difference was surprising considering that the two alternatives are two version of the same method. The only difference between alternative r_{prior} and $r_{\text{prior+}}$ is that three variables in $r_{\text{prior+}}$ have been fixed at there maximum values; heritability, parity and common bulls. Consequently it is likely that the reason for their difference in similarities with the reference evaluation lies with at least one of them. For example, for Argentina parity is set at 10 whereas it for the other countries is around 1-5. This may perhaps contribute to the big differences that were observed, but to be able to conclude anything further research need to be done.

The magnitude of the genetic correlations does not seem to have an affect on the final result. For the four different alternatives with correlation matrixes 0.5; 0.6; 0.7 and 0.8 the number of co-selected bulls with the reference evaluation is almost the same, three alternatives have 46 co-selected bulls and one alternative have 47 co-selected bulls. Among the four alternatives co-selected bulls range between 98 and 100 bulls (Table 15).

The mean of the PGM for the four alternatives with correlations 0.5; 0.6; 0.7 and 0.8 increased with increasing correlations (Table 9). The mean PGM for alternative $r_{0.5}$ was 0.89 and for alternative $r_{0.8}$ it was 1.42. The correlations between these four alternatives were close to one showing that the PGM for all bulls in all alternatives increase equally. The increase in PGM is explained by drawing an analogy with the phenomenon of correlated response. Graphically this can be presented with the genetic trend curves (Figure 3). The correlated genetic trend curves for correlated traits will follow an imaginary original curve, which relates to a trait with correlation equal to 1.0. In our example there will be four curves between the original curve and the x-axis. The curve with correlation 0.8 will be closest to the original curve and the curve with correlation 0.5 will be closest to the x-axis. This explains why, when reading the PGM values at the y-axis the 0.8 curve will always have a higher value then the 0.5 curve at a given x-value.

Choosing the same genetic correlation between Argentina and all the other countries for prediction of genetic merit did not seem to be very effective. The alternatives with assumed correlations only have 46 or 47 co-selected bulls with the reference evaluation. However, to have one genetic correlation between the country with unknown genetic merits and the others is easier than the other alternatives. The method does not need e.g. environmental data to get the estimates. The method is much less time consuming compared to the other methods. So if resources are limited and 50 percent certainty is good enough, it is an alternative to relatively easy get an idea of the highest ranked bulls.

Looking at the power of identifying co-selected bulls among the top 100, the results vary between 37 to 67 bulls compared with the reference evaluation. Although when looking at country of origin the different alternatives have targeted the same countries as the Interbull evaluation and with some exceptions the proportions are the same. This illustrates that the methods used for estimating international genetic merits without data from the country of interest can predict which countries that have bulls that may possibly be of interest.

Mark *et al.* (2006b) concluded that the method to predict genetic merits for unrecorded traits with data for a correlated recorded trait worked when selecting for resistance to clinical mastitis. They also concluded that the method could be used to predict genetic merits for countries not participating in international genetic evaluations. The results obtained in this study support that conclusion.

For the Interbull Centre, evaluations with these alternative methods studied would be possible to perform. The necessary factors such as data, software and knowledge are present. The time needed to perform the evaluations would not be more than the Interbull Centre staff could do it without disrupting their other obligations. The result is not comparable with a normal Interbull evaluation but for a country not yet participating in the evaluations but considering it, this could be one way to try international evaluations to a smaller cost and without any further obligations.

Possible future improvements could be to modify the prior correlation model. It would for example be interesting to see the outcome if a variable herd size was added to the model. Since herd size have been identified as a potential factor to influence G x E (König *et al.*, 2005, Zwald *et al.*, 2003). Mark *et al.* (2006a) also discussed possible improvements of the prior correlation models.

Conclusion

The method described by Mark *et al.* (2006b) can be used to predict international genetic merits for countries not participating in Interbull international genetic evaluations. Using this method is considerably less time consuming than Interbull' standard evaluations and PGM from the latest routine evaluation can be used. The disadvantage of the method is the certainty. Nevertheless if there is a request for this service this study has shown that it is possible to perform.

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