

# International Genetic Evaluation of Female Fertility Traits in Five Major Breeds

*H. Jorjani*

*Interbull Centre*

*Department of Animal Breeding & Genomics*

*Swedish University of Agricultural Sciences*

*Box 7023, S-75007, Uppsala, Sweden*

## Introduction

Positive review of the results of pilot study on international genetic evaluation of female fertility traits in Holstein populations (Jorjani, 2006) by the Interbull community led to the decision by the Interbull Steering Committee for a pilot study on five other major breeds: Brown Swiss (BSW), Guernsey (GUE), Jersey (JER), Red Dairy Cattle (RDC) and Simmental (SIM). Here, I report a summary of the “Final results” of this pilot study, which was based on the data submitted in September 2006, and conducted between September 2006 and February 2007. “Final results” were distributed among all countries participating in the female fertility evaluations. In addition to the participating countries, member of the Interbull Steering Committee and Interbull Technical Committee received the results.

## Material and Methods

### *Data*

Data consisted of results of national genetic evaluations for female fertility traits of AI sampled bulls with at least 10 daughters in at least 10 herds from Canada (CAN), Austria-Germany (DEU), The Netherlands (NLD), New Zealand (NZL), Nordic countries (DFS; Denmark, Finland, Sweden), Switzerland (CHE), United Kingdom (GBR), and The United States of America (USA).

### *Traits*

Female fertility traits used in this Interbull pilot evaluation were classified as follows:

**Trait 1** (T1=HC): Maiden heifer's ability to conceive. A measure of confirmed conception, such as conception rate (CR), was considered for

this trait group. In the absence of confirmed conception an alternative measure, such as interval first-last insemination (FL), interval first insemination-conception (FC), number of inseminations (NI), or non-return rate (NR, preferably NR56) could be submitted;

**Trait 2** (T2=CR): Lactating cow's ability to recycle after calving. The interval calving-first insemination (CF) is an example for this ability;

**Trait 3** (T3=C1): Lactating cow's ability to conceive (1). A measure of confirmed conception, such as conception rate (CR), was considered for this trait group. In the absence of confirmed conception an alternative measure, such as interval first-last insemination (FL), interval first insemination-conception (FC), number of inseminations (NI) could be submitted;

**Trait 4** (T4=C2): Lactating cow's ability to conceive (2). A measure of confirmed conception, such as conception rate (CR), was considered for this trait group. In the absence of confirmed conception any measurement with relevance to conception such as interval first-last insemination (FL), interval first insemination-conception (FC), number of inseminations (NI), non-return rate (NR, preferably NR56), days open (DO), or calving interval (CI) could be submitted;

**Trait 5** (T5=IT): Lactating cow's measurements of interval traits calving-conception, such as days open (DO) and calving interval (CI).

Traits submitted by the participating countries were:

**CAN** T1=56 day Non return rate in heifers; T2=Calving to first Service (days); T4=56 day Non return rate in cows;

**CHE** T2=Interval from Calving to First Service, days; T4=Non Return Rate after 56 Days, %;

**DEU** T4=C2=NR=Non Return Rate after 90 days (NRR), %  
**DFS** T1=Interval from first to last insemination for heifers (days); T2=Interval from calving to first insemination cows (days); T3=Interval from first to last insemination cows (days); T4=Number of inseminations (no); T5=Days open (days)  
**GBR** T4=1st lactation non return at 56 days; T5=days between 1<sup>st</sup> and 2<sup>nd</sup> calvings  
**NLD** T2=Interval calving to first insemination (days); T4=Non-return rate 56 days (binary trait); T5=Calving Interval (days);  
**NZL** T2=Lactating cow's ability to start cycling; T4=T5=Lactating cow's ability to conceive (CR42)  
**USA** T4=T5=Daughter Pregnancy Rate.

### Country-breed combinations

Data were submitted for the following breeds from different participating countries.

BSW:	CAN, CHE, DEA, NLD, NZL, USA
GUE:	GBR, NZL, USA
JER:	CAN, DFS, NLD, NZL, USA
RDC:	CAN, DFS, (NLD), NZL, USA
SIM:	DEU, NLD

Data submitted for RDC from the Netherlands contained so few bulls and consequently so few common bulls with the other participating countries that a meaningful international evaluation could not be performed. Therefore, the data from the Netherlands were discarded from RDC evaluations.

### Method

National proofs were first de-regressed within country and then analyzed jointly with a linear model including the effects of evaluation country, genetic group of bull and bull merit. Heritability estimates used in both the de-regression and international evaluation were as in each country's national evaluation.

Estimated genetic parameters were presented in the APPENDIX Ia-Ie and the corresponding number of common bulls are listed in APPENDIX IIa-e of the "Final results".

Ancestor-bulls without own proofs were traced back two generations from the oldest bulls with proofs in order to increase across country connections and accounting for the effect of selection.

Genetic groups were defined according to unidentified parents by national origin, breed and birth year of the bull and path of selection (sire, maternal grand-sire, maternal grand-dam). Minimum group size was set to 30.

### Results and Discussion

Reproducing all results is beyond the scope of this paper and interested readers are advised to study the "Final results" distributed among participating countries, or contact me for a copy of that report.

Estimated correlations for each country-trait combination were compared across breeds and with correlations estimated previously for Holstein populations. There was much variation in the same country-trait combination across breeds. Some correlations could be larger than the correlation estimated for the Holstein breed. However, in most cases they were smaller than Holstein correlation. When reliability of the estimated correlations (as judged by the number of common bulls between country pairs) was taken into account, it showed that correlations for those country-trait combinations that had a large number of common bulls (i.e. more than 50 common bulls) were very stable across breeds.

Correlations for those country-trait combinations that had few common bulls (i.e. less than 30 common bulls) were very unstable across breeds and also within breeds. Across-breed instability could be observed in fluctuations around Holstein breed correlations. Observation of within breed instability could be traced to three different sources. First, because this was a pilot study, participating countries were allowed to submit the data even if the data submission deadline had passed. Therefore, the same country-trait combination was estimated on the background of different predicting variables (i.e. different number of traits in the analysis). Second, due to some data quality issues some countries were asked to submit new data. Each of the old and new data files could have been used and treated as legitimate data in an "ordinary" international evaluation. However, extra scrutiny

of data in a “pilot run” allowed for testing of alternative data files. Third, different data edits were implemented in the analyses. For example, the cut-off year for inclusion of data, use of number of daughters versus EDC, size of phantom parent groups and so on. These three different sources caused the estimated correlation for country-trait combinations that had few common bulls to oscillate between extreme values (either very close to +1.0 or very close to 0.0). In one special case in a small breed the correlation oscillated between values very close to +1.0 and -1.0!

### ***Correlation windows***

It could easily be concluded that we have no reason to suspect any systematic across-breed difference of estimated genetic correlations. Consequently, it was suggested that the same “correlations windows” that had previously been used in Holstein breed to be used even for these five breeds. These correlation windows (minimum, median and maximum correlations) were described below.

		Min – Med – Max
HC	Correlations between countries belonging to the same group:	0.60 – 0.80 – 0.98
CR	Correlations between countries belonging to the same group:	0.85 – 0.92 – 0.98
	Correlations between countries belonging to different groups:	0.50 – 0.65 – 0.80
C1	Correlations between countries belonging to the same group:	0.60 – 0.80 – 0.98
C2	Correlations between countries in group 1:	0.60 – 0.80 – 0.98
	Correlations between countries in group 2:	0.55 – 0.75 – 0.98
	Correlations between countries in group 3:	0.65 – 0.85 – 0.98
	Correlations between countries in group 4:	0.65 – 0.85 – 0.98
	Correlations between countries in group 1 and group 2:	0.40 – 0.60 – 0.90
	Correlations between countries in group 1 and group 3:	0.30 – 0.60 – 0.85
	Correlations between countries in group 1 and group 4:	0.30 – 0.60 – 0.85
	Correlations between countries in group 2 and group 3:	0.25 – 0.45 – 0.85
	Correlations between countries in group 2 and group 4:	0.25 – 0.45 – 0.85
	Correlations between countries in group 3 and group 4:	0.50 – 0.65 – 0.80
IT	Correlations between countries belonging to the same group:	0.65 – 0.85 – 0.98
	Correlations between countries belonging to different groups:	0.50 – 0.65 – 0.80

### ***Grouping of country-trait combination***

The above mentioned correlation windows is based on the following strategy for country-trait combination grouping:

HC	Maiden heifer’s ability to conceive
	1) All
CR	Cow’s ability to recycle
	1) NZL
	2) Other
C1	Cow’s ability to conceive 1
	1) All
C2	Cow’s ability to conceive 2
	1) CZE, FRA (submitted trait ≈ CR)
	2) CAN, CHE, CHR, DFS, GBR, ISR, ITA, NLD (submitted trait ≈ NR/NI)
	3) BEL, ESP, IRL, USA (submitted trait ≈ DO/CI)
	4) NZL
IT	Cow’s measurement of interval calving-conception
	1) NZL
	2) Other

## Conclusions

General conclusion from this pilot study is that an international genetic evaluation of female fertility traits for Brown Swiss, Guernsey, Jersey, Red Dairy Cattle and Simmental breeds is perfectly plausible and Interbull Centre's recommendation to the Interbull Steering committee is to proceed with the first official test run for BSW, JER, RDC and SIM in September 2007 test evaluation. Further, it seems prudent to conduct a new pilot study on the Guernsey breed before a final decision is made.

## Acknowledgment

I stand alone as the author of this report. However, without the help of my colleagues at the Interbull Centre and Holstein Association, USA, this project could have not lifted from the ground. Further, I would like to acknowledge the help and fruitful discussions with Professor Jan Philipsson and Dr. Thomas Mark.

## References

- Boichard, D., Bonaiti, B., Barbat, A. & Mattalia, S. 1995. Three methods to validate the estimation of genetic trend for dairy cattle. *J. Dairy Sci.* 78, 431-437.
- Fikse, W.F. & Banos, G. 2001. Weighting factors of sire daughter information in international genetic evaluation. *J. Dairy Sci.* 84, 1759-1767.
- Harris, B. & Johnson, D. 1998. Information source reliability method applied to MACE. *Interbull Bulletin* 17, 31-36.
- Interbull. 2006. Genetic correlation estimation procedure. Available through: [http://www.interbull.org/documents/genetic\\_correlation\\_estimation\\_procedure.pdf](http://www.interbull.org/documents/genetic_correlation_estimation_procedure.pdf), accessed 2007-08-20.
- Jairath, L., Dekkers, J.C.M., Schaeffer, L.R., Liu, Z., Burnside, E.B. & Kolstad, B. 1998. Genetic evaluation for herd life in Canada. *J. Dairy Sci.* 81, 550-562.
- Jorjani, H., Klei, L. & Emanuelson, U. 2003. A simple method for weighted bending of genetic (co-)variance matrices. *J. Dairy Sci.* 86, 677-679.
- Klei, L. 1998. Solving MACE equations. *Interbull Bulletin* 17, 3-7.
- Klei, L., Mark, T., Fikse, F. & Lawlor, T. 2002. A method for verifying genetic evaluation results. *Interbull Bulletin* 29, 178-182.
- Klei, L. & Weigel, K.A. 1998. A method to estimate correlations among countries using data on all bulls. *Interbull Bulletin* 17, 8-14.
- Mark, T., Madsen, P., Jensen, J. & Fikse, W.F. 2003. MACE for Ayrshire conformation: Impact of different uses of prior genetic correlations. *Interbull Bulletin* 30, 126-135.
- Schaeffer, L.R. 1994. Multiple-country comparison of dairy sires. *J. Dairy Sci.* 77, 2671-2678.
- Sigurdsson, A. & Banos, G. 1995. Dependent variables in international sire evaluations. *Acta Agric. Scand., Sect. A, Animal Sci.* 45, 207-219.
- Sullivan, P. 1999. Appendix: REML estimation of heterogeneous sire (co)variances for MACE. *Interbull Bulletin* 22, 146-148.
- Weigel, K.A. & Banos, G. 1997. Effect of time period of data used in international dairy sire evaluations. *J. Dairy Sci.* 80, 3425-3430.