

## **Interbull Scientific Advisory Committee (SAC)**

### **Annual report (2006-2007) to the Interbull Steering Committee (SC)**

*Interbull SAC: Vincent Ducrocq, Mike Goddard, Larry Schaeffer, Georgios Banos (convener)*

#### **INTRODUCTION**

This has been the fourth year since the formation of the Interbull SAC. At the end of each previous year a report on our activities was prepared for the SC. In the last three reports we addressed the following issues:

- |      |   |
|------|---|
| 2004 | Review of and feedback on the Interbull research portfolio and priorities<br>Estimation of genetic correlation among countries  |
| 2005 | Data/product quality and validation<br>- Trend validation methods<br>- Mendelian sampling validation method<br>- Data subset validation<br>- Robust models<br>- Data mining |
| 2006 | Genetic evaluations for functional traits (emphasis on fertility)<br>Estimation of genetic correlation among countries  |

Since the 2006 Interbull meeting in Kuopio, Finland, members of the SAC:

- attended a meeting with members of the ITC, SC and the Interbull Center during the 8<sup>th</sup> WCGALP in Belo Horizonte, Brazil;
- engaged in e-mail discussion on issues of deemed importance.

There have been no specific requests from Interbull for feedback on particular issues this year.

#### **1. MEETING AT BELO HORIZONTE, BRAZIL (August 15, 2006)**

During this meeting, issues discussed were: a) Interbull evaluations for fertility and b) Data quality and validation

Notes from the meeting are attached in Appendix I.

#### **2. A LOOK INTO THE (NOT SO DISTANT) FUTURE: advent of large-scale genomic information**

The arrival of DNA chip technology enables quick genotyping of thousands of animals, currently for as many as 50,000 (soon to be even more) SNP genome-wide. This is a major step forward in the assessment of an animal's genetic merit that is bound to change the scene in the genetic evaluation sector. The effect on genetic evaluation units worldwide, including the Interbull Center, can be substantial. New methods will need to be developed to:

- Optimally combine the ever increasing amounts of genomic (e.g. SNP) data with phenotypic records and pedigrees for the calculation of genetic evaluations.
- Validate genomic data with the use of phenotypic records of traits with economic importance (i.e., that are routinely evaluated and selected for).

Several approaches to utilizing this information can be visualized, the merits of each one of which need to be thoroughly investigated. Figure 1 illustrates three possible ways of combining phenotypic records, pedigrees and genomic data. Under the first scenario (a), genomic data are combined with conventionally computed genetic evaluations in a meta-analysis that produces “enhanced” evaluations (where all possible information has been incorporated). In such case, MACE can continue to cater for the need for conventional international evaluations. Under scenario (b), all data (phenotypic, pedigree, genomic) are simultaneously used for the calculation of a single genetic evaluation. Here, the properties of MACE must be revisited in order to ascertain its suitability for this kind of input. At best, individual animal records would be combined with genomic data from various countries in order to compute international genetic evaluations. The third scenario (c) assumes that only genomic data are used for the assessment of an animal’s genetic merit. This implies that breeding values can be predicted from DNA alone before any phenotypic records are available from the animal or its relatives. Under scenario (c) pedigree and phenotypic records are periodically used to derive appropriate prediction equations and validate the association of genomic data with individual traits. Here, not only new optimal methodology must be developed, but the role of traditional genetic evaluation units will have to be redefined.

In addition to technical and scientific issues, data ownership is expected to play a crucial role in any of the above scenarios. Depending on the country, genomic data will most likely be property of the corporate sector. New means of cooperation between breed associations, milk recording agencies, breeding companies and genetic evaluation units at national, regional and international levels will have to be sought.

In view of these very likely developments, Interbull should start preparing for a new era in the genetic evaluation and selection business. The following activities are recommended as they may safeguard its position as an independent service provider and an international focal point for animal genetic evaluations:

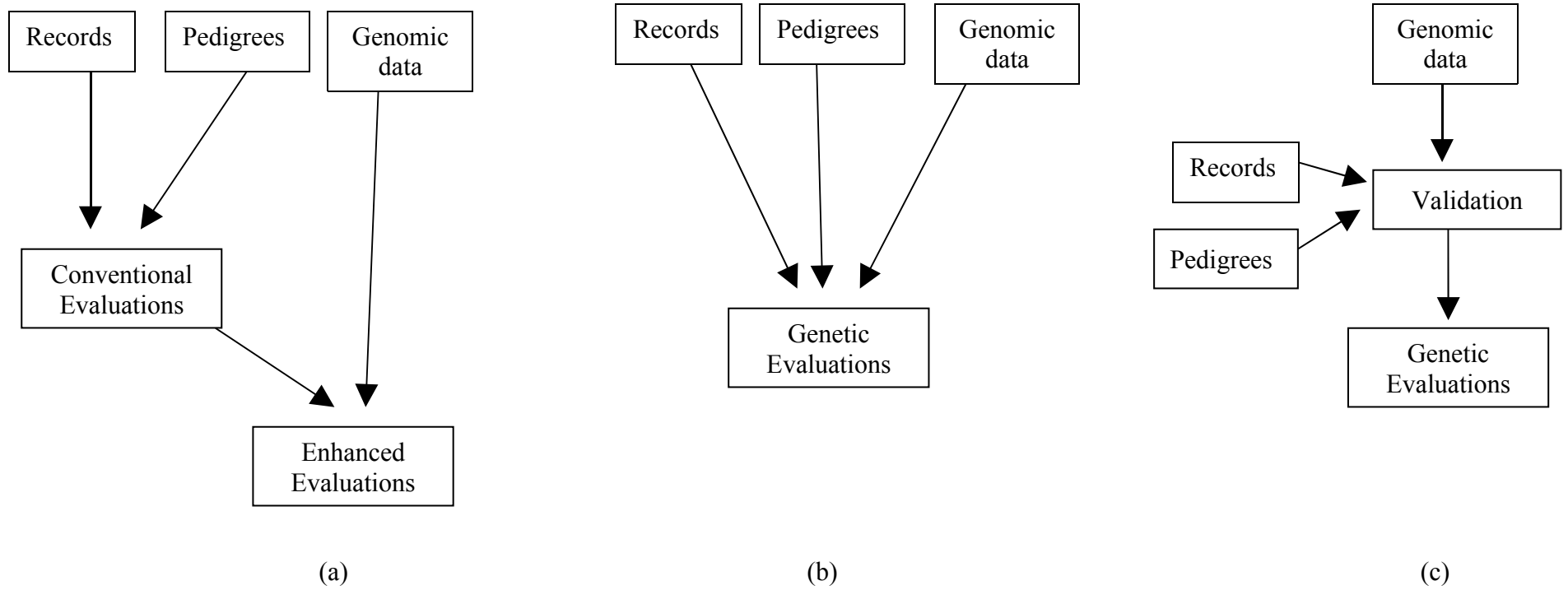
- Provide a forum for information exchange about methodology on the calculation of breeding values using genomic data. This is a continuation of one of Interbull’s traditional roles in the area of information exchange about genetic evaluation methodology leading to international agreement and standardization of the best methods.
- Perform/coordinate collaborative studies on optimal combination of genomic, phenotypic and pedigree data for the genetic evaluation (including simulation studies and field data analyses). This can lead to a new set of standards and recommendations. The benefit from combining data across countries/breeding programs will have to be revisited. The future of the genetic evaluation services may largely hinge on the outcome of these studies.
- Perform/coordinate studies on the association between genomic data and traits in different countries, leading to the prediction of an animal genetic merit from genomic data. Such studies can be initiated with a trait of lesser importance (i.e. that receives a very small or no weight in the selection indices in various countries) and, possibly, a numerically small breed. Animal genotypes and records can be collected at the Interbull Center from different countries and the degree to which SNP-trait associations are found to differ in these countries will determine their true biological

genetic correlation. Comparisons can then be made with the current MACE-correlations.

- Use these data to perform/coordinate studies on the genetic affiliation between various populations in terms of common SNP genotypes and on levels of inbreeding and genetic diversity in the different countries,
- Produce and provide mechanisms for routine validation of genomic data in the various countries.
- Prepare for the possibility that genomic selection results in private companies promoting their brand name (and breeding program) instead of individual bulls. In the long run, this may reduce the perceived value of genetic evaluations. The need for independent monitoring and objective input will have to be reestablished and confirmed. Interbull may want to forge closer links with world industry associations to collaborate in such matters.

August 16, 2007

The Interbull SAC



**Figure 1.** Three possible scenarios of utilization of genomic data in animal genetic evaluations.

## **Interbull Scientific Advisory Committee**

### **Notes from Interbull Committees meeting**

**August 15, 2006, Belo Horizonte, Brazil**

#### **Attendance**

Scientific Advisory Committee: V. Ducrocq, M. Goddard, G. Banos  
Technical Committee: G. Kistemaker, T. Lawlor, Z. Liu, E. Mäntysaari, R. Mrode  
Steering Committee: G. Aamand Pedersen  
Interbull Center: F. Fikse, J. Jakobsen

The following topics were discussed:

#### **1. Fertility evaluations in relation to the 2006 SAC report**

The objective was to exchange views; no decisions were to be taken.

Major points of the report were re-visited:

- Investigate impact of potential milk selection bias on fertility.
- Ensure appropriate de-regression procedures are used when national evaluations are based on multi-trait models including milk production (e.g. Netherlands, UK, Italy etc).
- Depending on the above, trend validation methods II and III may lead to erroneous results.
- Emphasize that national priority is to produce appropriate genetic evaluations rather than pass validation tests.

Trend differences have been observed between analyses that included or excluded milk from a fertility evaluation.

If the genetic correlation between milk and fertility is 0.50, then the maximum impact of milk on fertility proofs is about 0.25, which is substantial.

The possibility to increase minimum accuracy of bull fertility proofs (number of daughters or herds) in order to be included in MACE was discussed. This may alleviate the problem but will probably result in considerable data reduction.

The best course of action is multi-trait de-regression yielding purely fertility DYDs. This, however, requires multivariate EDCs.

#### **2. Data quality and validation**

The objective was to exchange views and identify priority areas where the new hire at the Interbull Center (1-year post) will work.

One area is the development of robust MACE with the inclusion of a country-by-year effect to investigate the extent to which trend bias may be recovered. Simulation work will be needed.

Another area is related to cross-validation work with data subsets, as it has been described in SAC reports for 2005 and 2006. This will be a diagnostic tool implemented at national level.

The new hire should review the proceedings of the last few Interbull meetings where entire sessions were dedicated to data quality and various other techniques were presented.

At the end, a complete platform should consist of both diagnostic and fixing procedures, and should be straightforward to implement.

September 10, 2006

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