

# Moving Away from Progeny Test Schemes: Consequences on Conventional (Inter)National Evaluations

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## Abstract

Genomic selection is already impacting performance recording in some countries, because extensive data recording at the national level is no longer a prerequisite for genetic evaluations. Collection of type traits receives decreasing attention as corresponding economic incentives have decreased. In contrast, renewed interest is being paid to health traits and/or to data collected automatically at the farm level. These changes induce a segmentation of dairy herds in at least two groups: herds with high quality, possibly subsidized data recording, and commercial herds. For new phenotypes, international (female) reference populations will be needed. Hence, Interbull has a major role to play to facilitate phenotyping and genomic evaluations on these new traits. Its strategic responsibility to ensure fair comparison and smooth circulation of information at the international level is reinforced.

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## 1. Background

In many countries which are part of Interbull, genomic selection is developing rapidly. Routine genomic evaluations produce genomically enhanced breeding values (GEBV) of male calves which are only slightly less precise than conventional estimated breeding values (EBV) obtained after a formal progeny test. In such a context, several authors demonstrated that larger yearly genetic gains can be obtained by intensively using genomically evaluated young sires, without waiting for progeny tested results (e.g., Schaeffer, 2006; de Roos *et al.*, 2010 among others). In practice, genomic selection is implemented in different ways, worldwide and even within country. Genomic selection generates exciting opportunities, but also new fears as well as crucial interrogations at many different levels, regarding data recording, national and international evaluations and trade. These were the focus of our discussions.

The panel represented a large variety of situations regarding genomic selection, from countries with already strong ongoing mutations of the dairy cattle improvement sector to countries with no existing genomic

evaluations where consolidation of performance recording is still crucial. What follows does not pretend to cover all situations: not all the countries involved in genomic selection were represented in the panel. In particular, there was no participant from Oceania.

Preliminary comments were made on the definition of progeny test and its potential ending in genomic selection schemes. In some countries, young bulls are already heavily used in AI without considering their future use as proven sires as essential. Bull barns are being closed or modified to house more young bulls (Germany, France). Others view the new situation as one where a number of young bulls are progeny tested through commercial sales rather than through an established progeny testing scheme (Canada).

## 2. Consequences of genomic selection on performance recording

The short descriptions by each participant on his or her country's situation led to the following observations:

- Delegates from countries where genomic selection is already implemented share the same concern about the future of national performance recording.
- For production traits, short term worries are limited because the main objective of recording is for management purposes and this will remain probably unchanged.
- The most affected traits are clearly type traits for which some countries have announced the reduction or ending of any incentive for type classification (Canada, Sweden, Germany) or the promotion of alternatives such as the use of opinion surveys to farmers (Ireland).
- In contrast, in all countries, increasing attention is being paid to recording of functional traits, in particular health traits, possibly to create female reference populations for genomic selection on new phenotypes. A particular example is the generalization of recording of claw disorders (Nordic countries, Germany) from specialized technicians. Indeed, genomic selection offers possibilities for genetic improvement of new traits for which national data collection and genetic evaluation were previously difficult to envision.
- A promising way to get new health phenotypes is through a better centralization of health information collected by the farmers themselves, for example uploading the management data they currently store on their computer (Sweden, Ireland, Italy, Canada). Alternatively, health recording can be done involving private partners (“new players”) to collect more sophisticated information, as discussed in Canada.
- In Ireland, because of the pasture-based production system, precocity assessed through weight traits and age at first calving represents another set of new phenotypes for which there is a growing interest.

At the national level, this new context may lead to evolutions at two levels:

- first, a segmentation of the herd population with i) a small fraction of herds with high

quality recording on all important traits. These may receive economic incentives for this purpose; ii) commercial herds, with (simple) recording limited to production traits for management purposes. In Ireland, a third category is planned, representing the “next generation research herds” on which studies could be undertaken on management of genomically improved cows while detecting any potential undesirable drift on any trait.

- second, AI companies are getting closer to dairy herd improvement organizations, breed associations and computing centers to maintain data quality and data recording and or to expand it to new traits (USA, France).

Countries with currently no available genomic evaluations are often semen importers. Genomic selection may be considered as a threat to the existing (small) progeny test being put into place with big efforts. Top farmers are aware of the growing possibilities to import semen from genomically selected bulls and need advice and fair comparison between the different national or foreign semen suppliers.

This evolution may have various consequences for Interbull. In particular, the growing attention towards health traits could lead to increased international exchanges.. Female reference populations for these traits will be created (e.g., for claw disorders), but to get good genomic predictions, collaborations between countries will certainly be needed. Some standards on recording will have to be defined, possibly with ICAR, but Interbull could be proactive on this to avoid long delays.

More generally, Interbull will need to pay attention to potential changes in data quality and quantity.

### **3. Consequences of genomic selection on national evaluations**

It is now generally acknowledged that genomic pre-selection of young bulls – whether they are heavily used immediately or after a progeny test – leads to biased conventional genetic evaluations if this pre-selection step is not properly accounted for. This requires that

information on which pre-selection is based be included in national evaluations. In other words, this means that the genotypes or the GEBV of young bulls culled after a genomic evaluation be made available to national computing centers. Correction for pre-selection will have to be implemented nationally but Interbull still has a role to play: first, standard methods and guidelines for this correction must be shared and accepted. Second, statistical tests must be developed to verify that genomic evaluations are not biased by pre-selection, before they are included in international evaluations. Third, one must check to what extent international GEBV are biased if GEBV of culled bulls are not sent to Interbull. This should be looked at even in the case where computing centers remove this bias at the national level.

It is important to warn countries that are tempted by bilateral exchanges of genotypes that such biases will exist (i.e., the foreign bulls will be underestimated) if their exchanges are limited to top marketed bulls.

#### **4. Consequences of genomic selection on international evaluations and the role of Interbull**

The Interbull responsibility to perform conventional multiple across country evaluations (MACE) is far from over. Even if all countries decided to share genotypes to create a single multi-country reference population, they would still need on a routine basis good quality, “bias-corrected” phenotypes (e.g., deregressed proofs) as input for their national genomic evaluations. This requirement is a key factor for the quality and accuracy of their genomic evaluation.

In contrast with conventional genetic evaluations, there is no universal approach for genomic evaluation, even though GBLUP, followed by blending of Direct Genomic Values (DGV) and conventional EBV is currently the most popular one. Interbull has the strategic responsibility of ensuring that GEBV comparisons remain fair. Validation of genomic evaluations is only one aspect Interbull members will require. For example,

standard approaches to compute genomic reliabilities are essential, in particular because these reliabilities play a key role in (simple) GMACE.

As has already been discussed, data from some female reference populations will probably need to be merged internationally to get better genomic evaluations on new traits. This may require the extension to females of some of the current Interbull services (maintenance of international pedigree for females in these reference population, estimation of between countries genetic correlations, joint evaluations, etc.).

Another desirable task for Interbull could be to become a provider of basic information for the management of genetic variability, e.g., to scan for original lines, in a context where intense genomic selection in smaller nucleus populations may result in faster inbreeding.

#### **5. Conclusion**

The impact of genomic selection is far from being limited to breeding schemes. The traits recorded, the way they are recorded and the relationship between the different actors of the animal breeding sector are changing. Progressive adaptation of computing centers to this new context is needed to maintain fair and precise conventional and genomic evaluations at national levels. Interbull needs to take this evolution into account, and should remain the key component to ensure fair comparison and smooth circulation of information at the international level.

#### **References**

- Schaeffer, L.R. 2006. Strategy for applying genome-wide selection in dairy cattle. *J. Anim. Breed. Genet.* 123, 218-223.
- de Roos, A.P.W., Schrooten, C., Veerkamp, R.F. & van Arendonk, J.A.M. 2011. Effects of genomic selection on genetic improvement, inbreeding, and merit of young versus proven bulls. *J. Dairy Sci.* 94, 1559-1567.