
Animal identification, recording and evaluation - Interbull's perspectives

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Genetic improvement of dairy cattle starts with the establishment of selection goals and is realized through the recording of genealogical and performance data, the application of genetic evaluation models and finally the actual selection and mating of the parents of the next generation. Reproductive technologies made it possible the use of animals selected within a single population to contribute genes to the genetic makeup of any population in the world, leading to a globalization of the dairy breeds. International trade of dairy genetics needed reliable tools to compare studs from different origins and this originated Interbull as the international network for dairy cattle improvement. Interbull made it possible to compare Artificial Insemination bulls from all over the world, but also became a cooperative effort to improve the national genetic evaluation programs. Only countries having national animal identification and recording programs are able to develop their own genetic evaluation schemes and, consequently, participate and benefit from Interbull services.

Summary

From the moment mankind managed to domesticate cattle and other species, the most fundamental concept of animal breeding was already established: that is the domesticated animals should provide benefits for the human population. Soon the first animal keepers realized that some individual animals were more beneficial than their counterparts, and the notion of selection started to be developed by segregating these individuals from the rest of the herd. The next step was to observe the resemblance between relatives and to comprehend that the desirable characteristics (as well as the undesirable) were transmitted from parents to offspring, and assortative mating became part of the herd management routine. After generations of empirical selection a clear differentiation between separate populations became evident, opening the way for the future specialized breeds.

Modern animal breeding follows the same basic steps:

1. Establishment of selection goals.
2. Recording of genealogical data.
3. Recording of characteristics of economic importance on each individual.
4. Use of adequate tools to compare animals and to identify the genetically superior ones.
5. Selection and mating of the parents of the next generation.

Genetic improvement essentials

Figure 1 shows in more detail how the genetic improvement process is carried out for dairy cattle. In order to pursue the selection goals elected, information on the respective characteristics need to be available from a representative sample of the population of interest, as well as the corresponding genealogical data. Using both records of performance and pedigrees, mixed models methodologies can be applied to assess the individual animals' genetic merit for the different economically important traits. Genetic merit is commonly expressed as estimated breeding value (EBV), which is used to rank the potential candidates before selection takes place. Finally, the parents of the next generation are chosen to maximize the genetic progress for the established selection goals.

In order to establish a genetic evaluation scheme that allows selection and effective improvement within a population, the absolute premise is the establishment of an animal identification system and a systematic program for performance recording. Even the most advanced technologies for assessing the genetic merit of individuals, such as genomic selection, depend on animal identification and phenotypic expression. The aim of the present paper is to reaffirm the key role of animal identification for genetic improvement programs, particularly considering the internationalization of cattle breeds which is the focus of the Interbull and Interbeef initiatives.

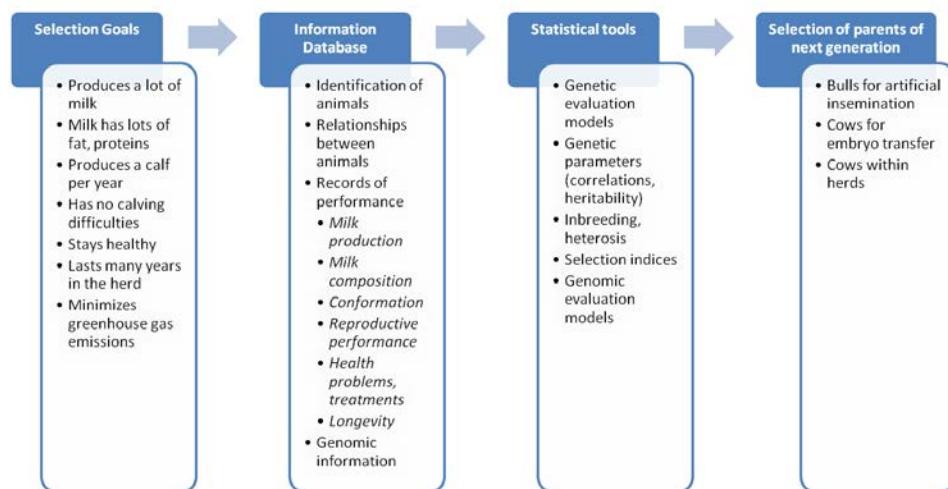


Figure 1. Steps of the dairy cattle improvement process.

Globalization of cattle genetics

Development and widespread use of reproductive technologies such as artificial insemination (AI) and embryo transfer (ET) dramatically increased the impact that a single animal may have in the genetic makeup of the next generation by allowing it to transmit its genes to a significantly larger number of progeny than it would be possible by natural mating. This has fostered the growth of a sizeable breeding industry for bovine genetics, which accelerated the genetic progress in most cattle populations worldwide by making semen and embryos of genetically superior animals available virtually for any dairy herd.

Especially in dairy cattle, the selection process has been based on a solid foundation: progeny testing schemes. Given the fact that most traits of economic interest are expressed only in females and have moderate to low heritability, a reasonably large

number of progeny records is necessary to estimate the genetic merit of a bull with an acceptable accuracy. The AI technology made it achievable and profitable. Soon breeders from different parts of the globe realized that it was possible to speed up the genetic merit of their herds by importing semen from bulls that had been proven as improvers in their population of origin.

In order to increase the overall knowledge about the genetic resources available worldwide for the Holstein-Friesian populations, the FAO established a well known comparison between 10 different strains of black and white dairy cattle in Poland during the 1970's (Stolzmann *et al.*, 1981). The results from the experiment showed a consistent superiority of the North-American Holstein-Friesian cows over the European strains of Friesian cattle in milk production, and these results added fuel to a process of massive importation of semen from North-America into all continents, phenomenon known as the "*Holsteinization*" of the breed (Philipsson, 2005; Harris and Kolver, 2001). The Holstein case is the best example of the impact that reproductive technologies associated to animal improvement programs can have on cattle populations: a small number of AI bulls have progeny spread over most existing populations, creating genetic links between them. The same pattern of trading was also established for the other dairy breeds and, to a smaller extent, to some well known beef breeds.

Milk production levels have risen to levels unimaginable before the "*Holsteinization*" took place, but also deterioration of functional traits related to fitness and health was observed in these populations as a consequence of unidirectional selection. Figures 2 to 4 show international genetic trends for the Holstein breed computed from the Interbull international evaluations (Philipsson, 2011). Figure 2 shows clearly a steep improvement in the average genetic merit for protein yield (3 standard deviations in 20 years), which is the trait with heaviest weight on most national

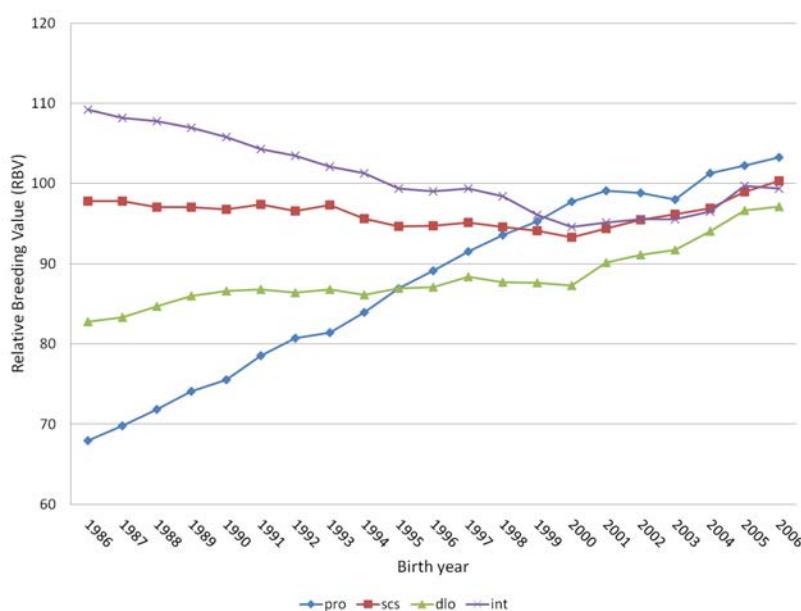


Figure 2. Global genetic trends for the Holstein breed in the Scandinavian scale, expressed as relative breeding values (mean=100, standard deviation = 10). Traits included: protein yield (pro), somatic cell score (scs), direct longevity (dlo) and fertility interval traits (int). Source: Philipsson, 2011.

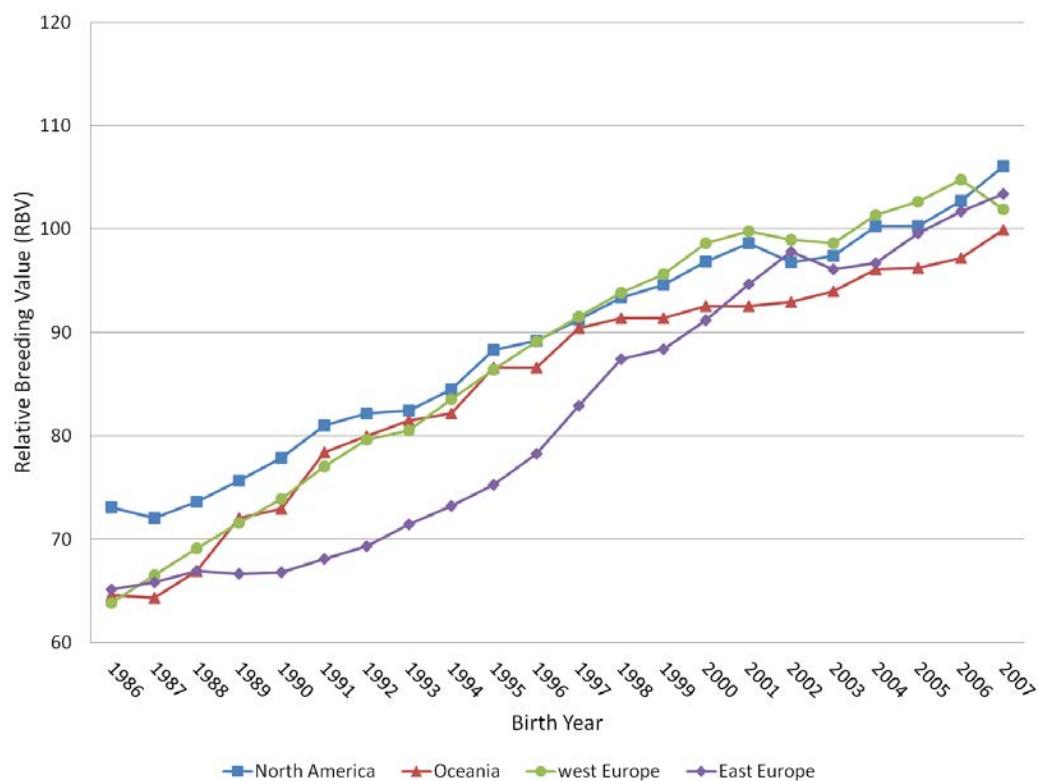


Figure 3. Regional genetic trends for protein yield within the Holstein breed in the Scandinavian scale, expressed as relative breeding values (mean=100, standard deviation = 10).
Source: Philipsson, 2011.

selection indices; a good improvement in direct longevity; no significant change for udder health; and a rapid deterioration of the genetic merit for fertility (interval traits). The most probable causes for this are the negative genetic correlations between production and fertility, increase in inbreeding rates and, mainly, lack of direct selection to improve fertility in many countries. It is possible to see that by the year 2000 the genetic trends change direction, indicating that the decline in fertility ended and a slow improvement seem to be taking place, while protein yield continues progressing at a slower pace. This is a consequence of the discussions promoted by Interbull to increase the awareness about the dangers of unidirectional selection and about the importance of functional traits in dairy cattle breeding schemes. Figures 3 and 4 show that trends are similar in different regions of the world for protein yield but for fertility the negative trends happened only in the regions where the "Holsteinization" took place, since the average genetic merit for fertility was already low in North America.

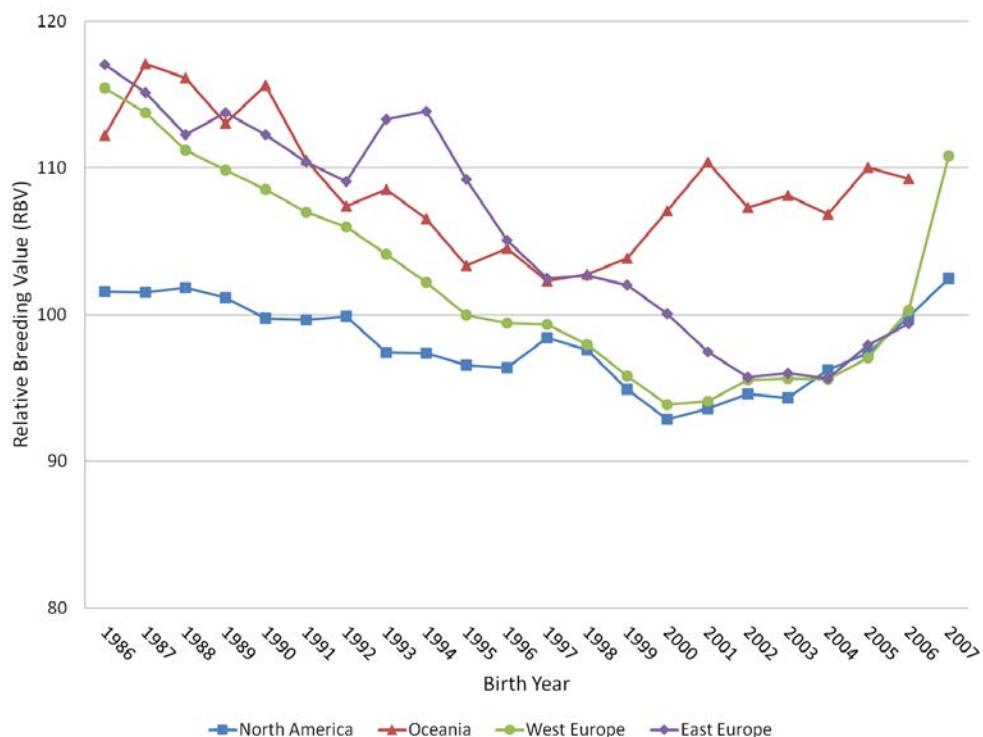


Figure 4. Regional genetic trends for fertility interval traits within the Holstein breed in the Scandinavian scale, expressed as relative breeding values (mean=100, standard deviation = 10). Source: Philipsson, 2011.

The International Bull Evaluation Service (Interbull) is a permanent subcommittee of the International Committee for Animal Recording (ICAR) with the vision of being the worldwide network providing genetic information services for improvement of livestock. Interbull was created as a consequence of the globalization of dairy genetics described above. Importing countries did not have an objective assessment of the foreign bulls' genetic merit in their own national scale, considering differences in scale of expression, cow genetic base, genetic evaluation model and genotype-environment interactions. Using a methodology proposed by Schaeffer (1994), the Multiple-trait Across Country Evaluation (MACE), it is possible to use the genetic links between populations (progeny of the same bulls performing in different countries) to estimate genetic correlations between countries and subsequently estimate the genetic merit of all bulls with a reliable proof in at least one of the participating populations in all national scales. At the end of the process, all countries submitting national evaluation data receive back a list with the genetic merit of all available bulls in the world expressed in their own scale. This is an invaluable tool for exporting countries to advertise their studs and for importing countries to sort out what kind of genetics they are really interested for their dairy herds.

The Interbull international genetic evaluation of dairy breeds involves 81 populations from 30 countries and 6 breeds at the end of 2011. Evaluations for 38 traits are carried out 5 times a year and represent a continuous information flow from national evaluation centers to the Interbull Centre and vice-versa. Before even considering what methodologies should be used for genetic comparisons, pedigrees have to be harmonized through verification of every single animal reported by

International cooperation for dairy cattle improvement: Interbull

different participating countries. Besides the animal identification, date of birth, sire and dam identifications also need to be verified. Any inconsistency on relationships or bull identification represents a threat for the accuracy of the genetic evaluations. Currently the Interbull Centre data base contains more than 4 million beef and dairy animals, and there is a permanent effort to assure the correctness of the information provided by the national centers. This points out to a close interdependence between the main areas covered by ICAR: identification, animal recording and genetic evaluations. International standards for identification are the most fundamental pre-requisite for any form of cooperation which involves exchange of genetic material. Some may think that the question of identification and genealogy will be simplified or even solved by the use of genomic tools, but this is a fallacy. Knowledge of genotypes only becomes useful when it can be associated to phenotypic data bases in which the absolute key will always be animal identification.

The Interbull customers are mainly distributed between North America, Oceania and Europe, with one representative from Africa and three from Asia. No country from Latin America participates, and the same happens to some of the largest milk producers in the world: China, India and Russia. Why this is the case? It is certainly not because of lack of opportunity or even lack of interest. It is mainly due to the fragility of the national identification and recording programs, which does not allow the development of national genetic evaluation systems for dairy cattle. The absence of well developed structures for animal improvement in many of these countries might explain why they do not participate in an important international forum such as ICAR. There are evidently exceptions to the rule, and efforts to include Argentina and Uruguay in Interbull evaluations are quite advanced.

As Dürr *et al.* (2011) point out, the main consequences for a country not having well developed animal identification and recording programs are:

- Suboptimal herd management practices.
- Erratic technical support to dairy farms.
- Ineffective programs for improving milk quality.
- Lack of strategic planning for the sector as a whole.
- Lack of effective traceability of animals and products.
- Impossibility of genetic evaluation of livestock.

An additional consequence for countries that rely on the breeds evaluated by Interbull for their milk production but do not have a consistent national genetic evaluation in place is that genetic progress depends solely on the importation of semen, embryos and livestock. Not having breeding values for the foreign animals expressed in their own scale, however, expose the dairymen to a situation in which it is impossible to make sense of all bull catalogs available, each one in a different country scale.

Conclusions

Animal improvement involves integrating animal identification, animal recording and genetic evaluation programs, which are the essence of the ICAR mandate. Countries lacking a solid infrastructure for animal identification and recording cannot establish their own genetic evaluation services and, consequently, depend permanently on imported genetics without having an actual control of the selection process. The globalization of the dairy breeds created the need for international comparisons of livestock and Interbull provides the network for harmonization of methods and procedures, as well as regular international genetic evaluations for the most important traits.

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