

How to select the best bulls worldwide for a particular national market?

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ABSTRACT: Genomic selection has increased the range of tools available for bull selection. It has also increased the genetic gap between countries having access or not to genomics. Our study aims at measuring the consequences on genetic progress regarding contrasted levels of information access: only foreign, or domestic but restricted to domestic progeny tested bulls, then extended to foreign ones, and finally to young bulls. All data available in France were considered and then discarded to mimic the identified scenarios. The average genetic level of the 30 best bulls on the national scale was computed for 3 traits. Genetic progress was favored information on young bulls was available. This is no longer true when selection was based on foreign information while low genetic correlations between countries. Selection on foreign information can only be considered as a short-term solution while developing domestic genomic evaluations.

Keywords: International evaluation; Genomic evaluation; Breeding scheme

Introduction

Farmers or breeding organizations have a large panel of genetic indices to choose from when they take selection decision. The available information is very heterogeneous (with or without inclusion of genomic information or of foreign data; expression on national or foreign scales). To handle this complexity, it is essential to measure the consequences on genetic progress of disregarding some sources of information voluntarily or because they are not available locally (e.g., in emerging countries). This study addresses this challenge using the French situation as an illustration.

Materials and Methods

In the present study, we considered the situation of a country where there is a need to compare the genetic merit of domestic and foreign bulls in order to select the best ones to be used domestically according to a specific market with its own environment and production objectives.

Bulls can be compared based on estimated breeding values, which can be categorized according to:

- the type of information considered: (1) pedigree and progeny performance usually analyzed using a BLUP animal model. These estimated breeding values will be referred to as EBV; or (2) genomic information using genome-wide approaches. In this case, estimated breeding values will be called GEBV.

- the scale of expression of the breeding values: either (1) the domestic scale for national or international evaluations when national EBV or GEBV are processed at the Interbull level using the MACE methodology

(Schaeffer, 1994) to get EBV on up to 30 country scales or using the robust GMACE methodology (Sullivan, 2013) to get GEBV on each of these scales; or (2) foreign scales from national or international evaluations.

We can therefore distinguish 4 situations where breeders have access to different amounts of information for domestic and foreign bulls:

- Case 1 considers countries without an own national evaluation system. Breeders can only rely on EBV or GEBV expressed on foreign scales. In this case, the quality of the breeding values is altered by genetic correlations between country of origin and country of use. Moreover, breeders only have information on foreign sires. No information on local genetic resources is available.

- Case 2 considers countries with a performance recording system from which national breeding values are computed based on phenotypic information only. They do not have national genomic evaluations. For domestic sires, breeders do have access to EBV on the domestic scale, but for foreign sires, they only have information on foreign scales. A fair comparison between domestic and foreign sires is not possible.

- Case 3 considers countries which in addition are Interbull members and therefore benefit from information about foreign sires on their domestic scale. Until now, they can get MACE breeding values from Interbull for bulls with daughter performances on their domestic scale. GMACE breeding values are not yet official and therefore are not available for countries that do not provide GEBV to Interbull.

- Case 4 represents the situation with the most complete information about domestic and foreign sires on the domestic scale. National EBV and GEBV are available for domestic sires and sent to Interbull. Consequently, such countries have access to EBV and GEBV results from MACE and GMACE for foreign sires on their domestic scale.

Data. To mimic the bull selection process as operated by a breeding organization or a breeder to choose a bull sire or a bull to extensively mate with the local population of dairy cows, we considered as an example all the breeding values available in France for the Holstein breed at the national data base level. In this case, official and non official, national and international EBV and GEBV were available on the French scale according to the most recent official genetic evaluations (national: October 2013, international: December 2013). From this complete situation, cases 2, 3 and 4 were mimicked by simply removing the relevant information. To mimic case 1, we also considered the possibility to have access to official breeding values from 3 particular foreign countries on their own scale. Note that GEBV were supposed to be available

Table 1. Type and number of estimated breeding values available on the domestic and foreign (FS) scales for bull selection on Production, Udder health or Fertility for four different cases

Cases	Domestic bulls (domestic scale)	Foreign bulls (domestic scale)	Foreign bulls (foreign scales)	Total number of breeding values in the analyses		
				For Production	For udder health	For fertility
4	EBV + GEBV	MACE + GMACE	None	151,022	32,238	31,077
3	EBV	MACE	None	139,829	23,466	21,899
2	EBV	None	None	25,939	3,727	4,099
1	None	None	EBV + GEBV	274,212 (FS1*)	39,584 (FS1*)	39,693 (FS1*)
				22,461 (FS2*)	-	-
				9,785 (FS3*)	-	-

*FS1, FS2, FS3 correspond to 3 foreign scales with 3 different national evaluation systems.

on these 3 foreign scales but the numbers of animals with breeding value estimates were extremely variable.

For illustration, production, udder health and fertility were used as selection criteria. Production was defined as a linear combination of 4 breeding values (fat yield (kg), protein yield (kg), fat content (FP in g/kg), and protein content (PP in g/kg)), identical to the economic index for production in France:

$$\text{INEL} = 0,98 * (0,2 * \text{Fat} + \text{Protein} + 0,5 * \text{FP} + \text{PP})$$

In the French evaluations, the fertility trait was cow conception rate and the udder health trait was somatic cell score. Traits with the closest definition in the foreign evaluation systems were targeted. All estimated breeding values were expressed in genetic standard deviation units of the trait.

Data editing. The set of candidate bulls was restricted to animals born between 2003 and June 2012. Semen from each candidate was assumed to be always available. Table 1 summarizes the scenarios considered and the size of the corresponding populations of candidates.

Analyses. Two types of top lists were defined for production, fertility and udder health, selecting either the best 30 bulls (TOP30 ranking) or the best 30 bulls coming from 30 different sires (VAR30 ranking). The latter strategy prevents from having many full or half sibs among the top list, i.e., it helps to maintain a good level of genetic variability. To avoid selection of inappropriate bulls, the production index was required to be positive for the top lists for fertility and udder health.

For each top list (TOP30 on INEL, VAR30 on INEL, TOP30 on udder health, TOP30 on fertility) and country case, the (G)EBV average and range of the selected bulls were computed. The composition of the top rankings was also analyzed with regard to the proportion of young bulls (without daughter performance) and of domestic bulls. For country case 1, the TOP30 or VAR30 lists were also established according to the bull's breeding values on three particular foreign scales (FS1 to FS3). Their average genetic level was then computed using their corresponding (G)EBV on the French scale.

Results and Discussion

The average (G)EBV of the top 30 bulls for production for the 4 types of countries are presented in table 2. The highest average genetic level was observed for case 4 when the largest collection of estimated breeding values on the domestic scale was available. In this case, breeders can choose among young bulls and progeny tested bulls, as well as between domestic and foreign sires to select the best ones and maximize genetic progress without loss of information due to genetic correlations between countries lower than 1. Even without information on young bulls (case 3), countries can select bulls with a high genetic level by increasing the proportion of foreign bulls based on the EBV provided by Interbull on their domestic scale. There was an important loss of genetic merit when comparing case 2 to cases 3 and 4. The pool of bulls to select from is much smaller and older in case 2. In such a situation, it can be more beneficial to consider foreign scales. The lower (implicit) local reliability of foreign breeding values can be compensated by selecting from a larger set of younger bulls. This was observed when selecting on the FS1 foreign scale. However, the results for foreign scales were very heterogeneous. It was not only a question of genetic level but also of size of the evaluated population. The larger the population, the higher the selection intensity will be.

Table 2. Characteristics of the TOP30 ranking bulls (the 30 best bulls on production) for four cases: genetic level (average and range in genetic standard deviation units) and composition (proportion of young bulls and of domestic bulls)

Cases	Average and range	Young Bulls (%)	Domestic sires (%)
4	3.62 (3.45-4.25)	54%	40%
3	3.50 (3.20-4.25)	0%	29%
2	3.08 (2.80-4.25)	0%	100%
1 (FS1*)	3.27 (2.35-4.00)	87%	87%
1 (FS2*)	2.93 (2.30-3.40)	83%	33%
1 (FS3*)	2.73 (0.75-3.55)	83%	83%

*FS1, FS2, FS3 correspond to 3 foreign scales with 3 different national evaluation systems.

Table 3. Characteristics of the VAR30 ranking (the 30 best bulls on production coming from 30 different sires) for four cases: genetic level (average and range in genetic standard deviation units) and composition (proportion of young bulls and of domestic sires)

Cases	Average and range	Young Bulls (%)	Domestic sires (%)
4	3.54 (3.25-4.25)	53%	50%
3	3.27 (2.80-4.25)	0%	40%
2	3.01 (2.65-4.25)	0%	100%
1 (FS1*)	3.26 (2.25-4.00)	67%	67%
1 (FS2*)	2.87 (2.20-3.65)	67%	50%
1 (FS3*)	2.44 (0.75-3.55)	73%	77%

*FS1, FS2, FS3 correspond to 3 foreign scales with 3 different national evaluation systems

With the more reasonable VAR30 ranking, an additional selection criterion forcing a diversification of pedigree origins was introduced. This constraint had a limited effect: the results observed in table 3 are quite similar to the ones observed in table 2. Using VAR30 slightly increased the gap between cases 3 and 4, highlighting the impact of the quality of younger bulls selected from genomic information on domestic or foreign scales (cases 4 and 1).

Compared with case 4, the average genetic level observed in case 1, i.e., when information is only available on foreign scales, was hampered by genetic correlations lower than 1. For illustration, two types of traits with contrasted genetic correlations between France and the first foreign country (FS1) were scrutinized. Genetic correlations used by Interbull are higher for udder health (-0.90) than for fertility (<0.80). Average genetic levels of the TOP30 list are compared in Table 4. For case 1, despite the availability of young bulls GEBV on a foreign scale, the average genetic level on the national scale significantly dropped relative to case 4. The drop was much larger for fertility traits.

A similar (but smaller) drop was also observed between cases 4 and 2. In case 2, breeders could only rely on national resources. This underlines the benefit of having access (through Interbull) to information on foreign sires on the relevant domestic scale. It also illustrates once more the importance of trait harmonization at an international level.

Table 4. Characteristics of the TOP30 ranking bulls (the 30 best bulls on udder health and fertility traits) for four cases: average genetic level (in genetic standard deviation units) and composition (proportion of young bulls and of domestic sires)

Cases	Average	Udder health		Fertility		
		Young Bulls (%)	Domestic sires (%)	Average	Young Bulls (%)	Domestic sires (%)
4	3.20	80%	7%	2.38	93%	3%
3	2.96	0%	17%	2.03	0%	27%
2	2.44	0%	100%	1.71	0%	100%
1 (FS1*)	2.97	84%	79%	1.12	72%	72%

*FS1: foreign scale, country of type 1.

Conclusions

This study showed that the highest genetic gain can be expected when the broadest and most accurate information is available; extending the pool of candidates to foreign sires based on information on the domestic scale is always relevant. Genetic gain is even larger with the availability of a larger number of younger bulls. However, many countries do not benefit yet from either international evaluations on their own scale or genomic evaluation tools. Thus, the genetic gap between members of Interbull with developed genetic and genomic evaluations and countries with limited or missing genetic evaluation systems is becoming larger and larger. In fact, the development of a national genetic and genomic evaluation system is a very long process. Becoming an Interbull member is also quite a tedious procedure. This membership is not only essential to be able to compare domestic with foreign sires in the selection process but also to be able to access a large reference population for reliable genomic predictions. To immediately benefit from the current genetic advances, it is indeed very tempting to directly look at foreign scales. However, our results showed that this can be hazardous for traits with low genetic correlations at the international level. So far, we have not assessed the consequences of this on selection on a total merit index

For countries without organized breeding programs, importing semen from foreign countries to increase genetic diversity and selection intensity is natural but gathering, interpreting and comparing (G)EBV from different foreign scales requires expertise and does not provide any information on the local genetic level, nor on the best foreign sources to improve it. For such countries, selection choices based on foreign information is a short term solution to avoid broadening the gap. But efforts should simultaneously be invested locally in genomic evaluations on the most relevant scale, i.e., the domestic scale.

Acknowledgments

This study was part of the GENOSOUTH project funded by the INRA SELGEN Metaprogramme.

Literature Cited

Schaeffer L..R. (1994) J. Dairy Sci. 77: 2671-2678

Sullivan P.G., Jakobsen J.H. (2012). 45th Proc. of the 2012 Interbull technical workshop.