

Analysis of the Pilot MACE on Longevity: French Report

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Abstract

This paper has two objectives: first, to check the consistency between French domestic and international proofs estimated during the pilot MACE for direct and combined longevity for the bulls having French daughters, secondly, to assess the impact of the low genetic correlations between countries on the proofs of foreign bulls and on their accuracy. The first analyses showed a very good consistency between French domestic and international proofs, even for bulls with a low number of culled daughters. The fact that the domestic proofs of foreign bulls with a small number of French culled daughters are higher on average than the MACE results may be a sign of preferential treatments on the first French daughters born from imported bulls. The second study showed that the low genetic correlations affect the accuracy of proofs of young bulls and that only bulls with French daughters have an acceptable reliability. Moreover, the proofs variability is greatly reduced. Thus, a routine international evaluation is not very helpful from a French point of view, as long as the problem of the low genetic correlations is not solved. More checks should be undertaken in order to verify whether the estimated genetic correlations are biased downwards, particularly by using the most accurate population of bulls and by excluding historical information, by comparing DYDs to deregressed proofs and using more appropriate EDCs in the case of combined longevity. If the genetic correlations are not underestimated, the models and the estimated effects should be investigated more carefully.

Introduction

The aim of this study was to analyse the consistency between the results of the pilot MACE evaluation on longevity in French units and the domestic proofs computed by INRA, and to assess the impact of low genetic correlations on international proofs.

1. Comparison of National and Interbull proofs for bulls with French daughters in the MACE evaluation

MACE proofs for direct and combined longevity were compared to domestic proofs used for the pilot test run, i.e., national proofs released in June 2002. French proofs for direct and combined longevity are expressed in genetic standard deviation, on a male rolling base. One of the "basic checks" was to verify that the MACE proofs of the bulls having French daughters were consistent with domestic proofs.

The results presented in Table 1 are based on proofs of bulls with French daughters and born since 1986. The impact of censored data was checked through the analysis of two sets of bulls without foreign daughters, the first one with a large number of culled daughters (at least 100, 1 French culled daughter=1EDC), the second one with a low number of culled daughters (20 or less).

The last two samples were composed by foreign bulls with French daughters. As French proofs of foreign bulls were included in the pilot test run, the MACE proofs were expected to be very close to the domestic proofs, and a potential bias on French proofs of foreign bulls is difficult to assess with such data. In order to limit the weight of French information, only foreign bulls for which French daughters represent less than 40% of the total EDC were included. Again, two subsets were used, according to the number of French culled daughters (more or less than 20).

Results of Table 1 show the very good consistency of domestic proofs and MACE proofs, when bulls have only French daughters. As expected, when the bulls have foreign daughters, the correlation between domestic and MACE proofs is lower, particularly for the bulls having few French daughters. On average, domestic proofs computed for the foreign bulls with a low amount of French information are higher than MACE proofs. Even if the accuracy of these proofs is low, we cannot exclude preferential treatments on the first French

daughters of foreign bulls, which are often embryo donors and obviously not treated as common cows. As expected, the variability of MACE proofs is very close to French proofs when the MACE proofs are based only on French daughters. The proofs variability is only slightly increased by the use of foreign information for the bulls with only few French daughters, and not at all for the other foreign bulls, probably because of the very low genetic correlations between France and abroad.

Table 1. Consistency between domestic and MACE proofs¹.

	French Bulls without foreign daughters				Foreign bulls(EDC FRA ≤ 40% total EDC)			
	≥100 culled daught.		≤20 culled daught.		>20 culled daught.		≤20 culled daught.	
	Dir	Cmb	Dir	Cmb	Dir.	Cmb	Dir.	Cmb
Nb bulls	730	730	398	398	202	202	131	131
Proofs Correlation	>0.99	>0.99	>0.99	>0.99	0.97	0.96	0.71	0.74
Average difference ²	-0.001	-0.002	-0.014	-0.010	-0.003	0.002	0.028	0.094
Domestic proofs std	0.765	0.783	0.529	0.563	0.772	0.759	0.551	0.550
MACE proofs std	0.764	0.783	0.520	0.556	0.759	0.755	0.573	0.562

¹Dir Direct longevity; cmb=combined longevity; ² Domestic – MACE proof.

2. Impact of low genetic correlations on longevity proofs

2.1 Accuracy of the top bulls' proofs

One of the most important purposes of the Interbull evaluations is to have accurate evaluations on the young foreign bulls, that are potentially useful for the national breeding programs. Therefore, it was interesting to look at the MACE proofs for longevity of the present top population of bulls.

The selection of the "best bulls" was based on a very simplistic criterion: the bulls should have obtained an Interbull proof of at least 20 kg Protein in February 2003 (proofs expressed in French units). Only bulls having most daughters in the most important countries (NLD, FRA, DEU, DNK and USA) were considered. Over the 3180 bulls meeting these requirements, 1761 received a MACE proof for combined longevity. Table 2 shows that a majority of these bulls are young. The accuracy of the domestic proofs used in the pilot MACE evaluation could be low for some of these bulls. Therefore, table 2 presents the percentage of bulls having at least 40 EDCs, which should lead to an acceptable proofs accuracy in the country of

origin.

The proportion of bulls having MACE proofs for longevity is quite high (55%), however, the reliability of these results is very low. This is only partially explained by a low amount of information in the country of origin, since the proportion of bulls having at least 40 EDC reaches 60% in Germany, the Netherlands and in USA. If French rules of publication were applied, only 18% of the proofs of foreign bulls would be published. Moreover, most of the bulls with a sufficient reliability are in fact old foreign bulls with French second crop daughters, which helped them to have a reliable proof. This is confirmed by the results of Danish bulls (the genetic correlation between France and Denmark is the highest above all genetic correlations with France), since over the 36 Danish bulls born since 1993 and with at least 40 EDCs, only 2 had a MACE proof with a reliability of less than 50%.

In conclusion and as expected, as the genetic correlations between France and other countries are low, a foreign bull has little chance of having a publishable proof, as long as he has no French information.

Table 2. Number of bulls per country according to the reliability of the proofs expressed in French units (combined longevity, “best bulls”)¹.

Country	Available proof on longevity				REL≥50% on cmb lonvevity			
	All		Birth Y.≥1993		All		BirthY.≥1993	
	NB bulls	% with ≥40 EDC	NB bulls	% with ≥40 EDC	NB bulls ²	(%)	NB bulls ²	(%)
DEU	152	68%	139	65%	9	(6%)	2	(1%)
DNK	118	30%	114	28%	34	(29%)	30	(25%)
FRA	291	42%	235	28%	278	(95%)	222	(94%)
NLD	379	67%	332	62%	130	(34%)	85	(26%)
USA	821	63%	706	58%	92	(11%)	18	(3%)
NB of bulls	1761		1526		543	(31%)	357	(23%)
NB of foreign bulls	1470		1291		265	(18%)	135	(10%)

¹ “best bulls” = bulls with at least 20 kg protein (Interbull evaluation of February 2003, proofs expressed in French units);

² : in parenthesis : percentage of bulls within country reaching a REL of 50%.

This situation is more difficult in France as in other countries because the genetic correlations with France are often lower than between the other countries. However, when MACE proofs are expressed in other units (Table 3), the reliabilities are also highly affected by the genetic correlations. The use of MACE proofs expressed in German units is very limited when the goal is to select bulls from Danish, French or US origins.

The same observation was made with other units, such as in Italy. In the USA, given the level of the genetic correlations (0.72 between Germany and USA for instance), the higher proportion of bulls with an acceptable reliability is probably due to the fact that most of the bulls have US origins and that pedigree information has an important weight.

Table 3. Number (and percentage) of bulls per country with a reliability of 50%; proofs expressed in German and US units (combined longevity, “best bulls”)¹.

Country	DEU= Units of expression of Longevity				USA = Units of expression of Longevity			
	All		Birth Y.≥1993		All		Birth Y.≥1993	
	NB bulls	(%)	NB bulls	(%)	NB bulls	(%)	NB bulls	(%)
DEU	152	(100%)	139	(100%)	95	(63%)	82	(59%)
DNK	5	(4%)	1	(1%)	33	(28%)	29	(25%)
FRA	27	(9%)	6	(3%)	38	(13%)	6	(3%)
NLD	244	(64%)	198	(60%)	213	(56%)	167	(50%)
USA	131	(16%)	45	(6%)	646	(79%)	531	(75%)
NB of bulls	559	(31%)	389	(26%)	1025	(58%)	815	(53%)
NB of foreign bulls	407	(28%)	250	(19%)	379	(26%)	284	(22%)

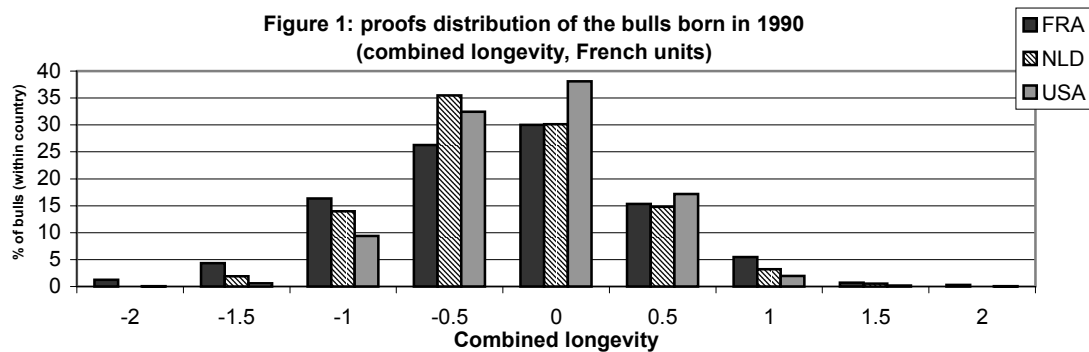
¹ “best bulls” = bulls with at least 20 kg protein (Interbull evaluation of February 2003, proofs expressed in French units).

2.2 Distribution of the proofs

In order to have a complete generation of bulls with accurate domestic proofs, only bulls born in 1990 were selected for this part of the study.

Figure 1 presents the proofs distribution of the French, US and Dutch bulls. Most of the bulls without French daughters have MACE proofs that do not vary a lot around the average. Over the 12 bulls with at least an EBV of 1.3 (classes of

proofs: 1.5 and more), 7 were French and all the others had French second crop daughters. Over the 77 bulls having a proof between 0.8 and 1.2 (class of proof:1), there were 39 French, 12 Dutch and 26 US bulls, but 30% of the US bulls had French daughters. We should not conclude that this is a sign of preferential treatments on French daughters. This may be due to the fact that the proofs variability of foreign bulls without French daughters is highly affected by the low genetic correlations.



3. Why are the genetic correlations so low?

Several reasons may explain the low genetic correlations estimated during the pilot project. The comparison of the descriptions of the evaluation method used by the 14 countries participating to the pilot project (Van der Linde and de Jong, 2002) can reveal the main differences.

- Differences between trait definitions and units of measurement: use of a number of lactations, of a productive life span limited or not to a maximum age; countries correcting for production or not... However the genetic correlation between countries having very close definitions, such as France, Germany, the Netherlands, Italy, Switzerland and Denmark are not much higher than between the others. Even if the trait definition is the same, the culling policy may be different. But here again, how to explain that the genetic correlation between France and Germany is lower than between France and Australia?
- Differences between models of evaluation: here again, how can we explain that the genetic correlations between countries using the same method (survival analysis), with exactly the same model, are very often lower than the genetic correlations between these countries and USA, Canada and Great Britain (Table 4)?

These points must be investigated more carefully. We could for instance look at the effects estimated by countries using survival analysis in order to see whether the tendencies are the same, which could help to know whether the culling policies are consistent between these countries.

Nevertheless, the low genetic correlations may also be explained by some difficulties to estimate them, which could lead to underestimated genetic correlations. This may be due to several reasons, such as:

- Difficulties to deregress proofs with a poor accuracy and use of an inadequate dependent variable in case of MACE on traits estimated with non linear models (Ducrocq et al., 2003). It would be interesting to compare DYDs and deregressed proofs, particularly for bulls with low EDCs. This problem has been already partially investigated by computing genetic correlations based on proofs of bulls having at least 50 culled daughters or evaluated in more than 50 herds (Van der Linde and de Jong, 2002). However, these requirements, even if they are more severe than the conditions used in the present pilot test run, are still not very restrictive, given the low heritability of the trait and the requirements of Interbull in routine evaluations (presently: official proofs or more than 150 daughters for proofs of imported bulls). What happens when the genetic correlations are computed using only common bulls having at least 150 EDCs in the considered countries? The use of proofs with a high EDC would also present the advantage of reducing the risks of bias due to preferential treatments on the first 2nd crop daughters.
- Inappropriate EDCs for combined longevity, when a survival analysis is used: the accuracy of the national proofs is underestimated, if it is computed from number of culled daughters.
- Use of a selected population in some countries: no requirement was made on the earliest birth year of the bulls. Some studies showed that sire variances estimated in importing countries could be biased by the use of historical domestic performance data of bulls from breed that have been replaced by imported stock (Weigel and Banos, 1997). Presently, the routine Interbull evaluations are focused on the most recent bulls. Although the conditions used by Interbull to select the bulls would be certainly too severe in the case of Longevity, the eldest bulls (bulls born before 1980 for instance) could be deleted from the MACE for

longevity.

- Use of bulls having a high proportion of censored data. Here also, the problem has already been investigated in the first pilot evaluation, by computing genetic correlations on bulls born before 1992. However, the common bulls are the most important source of information used to compute the genetic correlations, and most of these bulls were progeny tested in one country and had second crop daughters many countries. Therefore, a lot

of service bulls born before 1992 had probably still a large part of daughters still alive in 2001 (year of national releases used for the first pilot evaluation) and the requirement of a maximum birth year of 1992 led only to the suppression of the bulls simultaneously progeny tested in two countries, which are often known with a smaller number of daughters than service bulls and thus, which have a lower weight in the estimation of genetic correlations.

Table 4. Average genetic correlations estimated during the pilot evaluation.

	AUS	CAN	CHE	DEU	DNK	FRA	GBR	IRL	ITA	NLD	NZL	SWE	USA
AV Surv.*	0.54	0.77	0.72	0.71	0.78	0.65	0.73	0.57	0.70	0.78	0.39	0.52	0.74
AV Surv 2	0.49	0.80	0.74	0.76	0.78		0.77	0.60	0.74	0.80	0.39	0.51	0.75
AV USA, GBR, CAN	0.59	0.91	0.80	0.81	0.74	0.61	0.86	0.77	0.82	0.76	0.51	0.66	0.88
AV Non Surv.	0.57	0.72	0.63	0.54	0.63	0.66	0.69	0.63	0.64	0.58	0.47	0.6	0.73

AV Surv. = Average genetic correlation with all countries using a Survival analysis; AV Surv 2= Average genetic correlation with all countries using a Survival analysis, FRA excluded; Av. Non Surv.= Average genetic correlation with all countries that do not use a Survival analysis, ISR excluded; AV USA, GBR, CAN= Average genetic correlation with USA, CAN, GBR;

In bold: countries using a survival analysis; in bold + italic: correlations between countries using a survival analysis and USA, CAN, GBR.

Conclusion

The comparison of French domestic and MACE proofs showed a very good consistency of the international proofs with the national data for bulls having French daughters. A MACE seems to be technically feasible. However, the results will not be very useful if we do not solve the problem of the low genetic correlations. More checks are needed, such as the selection of accurate proofs of the most recent population of bulls with a low percentage of censored data (for instance, discard bulls born before 1980, proofs of imported bulls born after 1990 or based on less than 150 EDCs) or as the comparison of deregressed proofs. Moreover, a number of culled daughters may be inappropriate to compute EDCs for combined longevity in countries using a survival analysis. If the genetic correlations are not underestimated, we should look at the models and the trait definitions in order investigate potential improvements leading to a better harmonisation.

References

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