

GMACE Reliability Approximation

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Abstract

Reliabilities of genomic GEBV are approximated nationally by country, and via GMACE at the international level. In previous studies, GMACE reliabilities were sometimes lower than expected, relative to corresponding national values. Reasons for misalignment were investigated in the present study, which revealed that two important data contributions were being ignored for the GMACE reliabilities; the effective daughter contributions (EDC) of a bull's maternal grand-sire, and the contribution of cow records for the dam. The GMACE system was updated to properly incorporate maternal grand-sire EDC for both reliability approximation and for genomic variance estimation. The information from cow records for the dam was added only for reliability approximation, and only if it was helpful to align approximate reliabilities, since records of the dam are otherwise excluded from the GMACE model. These updates improved alignment of GMACE reliabilities with national values. With only a few exceptions, GMACE reliabilities became consistently equal or higher than national values, which is the generally expected pattern of alignment.

Key words: genomics, international evaluation, GMACE, reliability

Introduction

Results distributed from GMACE pilot 3 (Jakobsen and Sullivan, 2012) included international genomic evaluations and reliabilities. In some cases, the international reliabilities were lower than the corresponding national reliabilities, which is not expected. The purpose of this study was to review the reliability approximation used for GMACE and consider methods to align GMACE with national reliabilities.

Data

The data and edits for the present study are described in detail by Jakobsen and Sullivan (2012). In summary, there were five traits included: protein (pro), stature (sta), somatic cells (scs), direct longevity (dlo) and female fertility (cow conception trait #1; cc1). August 2011 national GEBV data from eleven populations (CAN, DEU, DFS, FRA, NLD, POL, USA, CHE, CHR, ITA and JPN), and EBV data from all countries participating in the August 2011 MACE service of Interbull were used for the present study. The total numbers of national GEBV on young genotyped bulls without daughter data, across all populations, were: 57902 for pro, 47285 for sta, 53820 for scs, 54663 for dlo, and 44395 for cc1.

Methods

Reliabilities for GMACE are approximated from an animal's information matrix (\mathbf{X}) that

includes effective records from progeny, ancestors and genomic predictions, as follows:

1. Progeny EDC are absorbed chronologically into parents, using multivariate absorptions (Mark and Sullivan, 2006).
2. Reliabilities for all animals are approximated based on the animal's own EDC plus all progeny accumulations from step 1, using multivariate methods (Mark and Sullivan, 2006; Harris and Johnson, 1998).
3. Parent contributions to progeny are determined with univariate methods of Harris and Johnson (1998).
4. *Effective records needed to increase reliabilities from step 2 to the equivalent reliabilities after step 3 are derived by iteration (effective independent EDC from all ancestors).*
5. Additional effective records from national genomic evaluations (E^* from Sullivan and VanRaden, 2010) are added to the animal's information matrix after step 4 (\mathbf{X}) and reliabilities derived from $[\mathbf{X}+\mathbf{G}^{-1}]^{-1}$.
6. *If GMACE reliability from step 5 was lower than the national reliability, an adjustment was made to add dam's own records (included in national reliability) to dam contributions in matrix \mathbf{X} (based on Harris and Johnson methods for MACE). Dam reliability was increased as needed, but to a maximum 0.95.*

In the pilot 3 analyses, steps 4 and 6 were not included. The most critical implication without step 4 was that maternal grandsire EDC were not included in the young bull's GMACE reliability. Step 4 has now been added for both the reliability approximation and for genomic variance estimation, but not for the international prediction of bull GEBV. The method for GEBV prediction includes a subtraction of parent solutions and thus parent equations are not absorbed, so step 4 does not apply. Step 6 has been added only for the purpose of approximating reliability.

Impacts of adding step 4 on genomic variances were reviewed in a separate report. The present report focuses on the impacts of adding step 4 and subsequently step 6 on the difference between GMACE and national genomic reliabilities.

Results and Discussion

Tables 1 through 5 show results for each of the five traits studied. For all traits, there were countries with GMACE reliabilities lower on average than the national reliabilities in pilot 3. Adding step 4 (e.g. Add MGS) to the GMACE approximation increased both the average and minimum GMACE reliability for almost every country and trait. Adding step 6 (e.g. Add Dam) only increased reliabilities where there was still a negative minimum or average difference between GMACE and national genomic reliability.

After adding both new steps, 4 and 6, very few cases remained where GMACE reliability was lower than the national. Several cases existed where GMACE reliability was slightly higher than national, presumably where parent average from

MACE included more complete international data that were used in the national genomic systems.

Some national genomic reliabilities were extremely high (e.g. for country POL). Also, some countries had exactly the same genomic reliability for all young bulls, while other countries had different reliabilities for different bulls. Additional programs have also been developed to check incoming data for consistency between genomic reliability and genomic GEDC. It seems a lot of data checking will be required by Interbull to ensure a high quality GMACE service.

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Table 1. Difference between GMACE and national reliability for bulls with a national genomic evaluation from only one country, for trait protein.

	ave(Nat)		ave(GM-Nat)			min(GM-Nat)		
	n	grel	pilot 3	Add MGS	Add Dam	pilot 3	Add MGS	Add Dam
CAN	1949	68	-1	1	1	-8	-4	-1
DEU	12778	73	-1	1	1	-4	-2	-1
DFS	4148	65	3	5	5	-1	1	1
FRA	6470	71	-4	-2	0	-9	-5	-2
ITA	670	69	2	3	3	0	2	2
NLD	4342	62	4	6	6	-1	3	3
USA	64	72	2	3	3	1	1	1
CHE	103	77	-2	-1	0	-4	-2	-1
CHR	530	62	-5	-2	-1	-12	-8	-3
POL	122	54	6	8	8	2	5	5
JPN	653	64	3	5	5	1	2	2

Table 2. Difference between GMACE and national reliability for bulls with a national genomic evaluation from only one country, for trait somatic cell score.

	ave(Nat)		ave(GM-Nat)			min(GM-Nat)		
	n	grel	pilot 3	Add MGS	Add Dam	pilot 3	Add MGS	Add Dam
CAN	5627	68	-1	1	1	-10	-6	-1
CHE	159	43	-7	-1	1	-19	-8	-1
DEU	12499	77	-1	0	0	-3	-2	-1
DFS	4155	71	2	3	3	-1	0	0
FRA	6466	68	-5	-3	0	-11	-7	-3
NLD	4214	62	4	6	6	0	3	3
USA	24	69	3	4	4	2	2	2
ITA	926	66	3	4	4	0	2	2
CHR	328	54	-8	-4	-1	-18	-11	-3
JPN	668	55	4	7	7	2	4	4
POL	122	57	6	7	7	2	5	5

Table 3. Difference between GMACE and national reliability for bulls with a national genomic evaluation from only one country, for trait stature.

	ave(Nat)		ave(GM-Nat)			min(GM-Nat)		
	n	grel	pilot 3	Add MGS	Add Dam	pilot 3	Add MGS	Add Dam
CAN	11647	71	-1	1	1	-12	-7	-1
CHE	178	62	-3	-1	0	-7	-4	-1
DEU	12894	71	-1	0	0	-5	-3	-1
DFS	4125	64	3	5	5	-2	2	2
FRA	6362	69	-7	-4	0	-13	-9	-5
ITA	962	67	3	4	4	0	2	2
NLD	4259	70	3	4	4	-1	1	1
POL	118	73	-13	-12	-6	-16	-15	-8
JPN	667	63	4	6	6	1	2	2

Table 4. Difference between GMACE and national reliability for bulls with a national genomic evaluation from only one country, for trait direct longevity.

	n	ave(Nat)	ave(GM-Nat)			min(GM-Nat)		
		grel	pilot 3	Add MGS	Add Dam	pilot 3	Add MGS	Add Dam
CAN	5656	61	-1	2	2	-7	-4	0
DEU	13524	52	1	4	4	-5	-1	0
DFS	4434	54	3	6	6	-1	1	1
FRA	6700	54	-10	-5	-1	-15	-9	-1
ITA	1659	39	4	8	8	-3	1	1
NLD	4260	44	5	9	9	-1	4	4
USA	24	63	3	4	4	1	2	2

Table 5. Difference between GMACE and national reliability for bulls with a national genomic evaluation from only one country, for trait cow conception (cc1).

	n	ave(Nat)	ave(GM-Nat)			min(GM-Nat)		
		grel	pilot 3	Add MGS	Add Dam	pilot 3	Add MGS	Add Dam
CAN	11620	57	-1	1	1	-9	-4	-1
CHE	150	27	-1	8	8	-23	-7	0
DEU	12467	43	-7	-1	0	-18	-8	-1
DFS	3797	60	2	4	4	-1	1	1
FRA	6654	61	-7	-4	-1	-13	-8	-4
NLD	4337	40	7	11	11	0	5	5
POL	130	87	-51	-48	-36	-57	-52	-42