Genomic Conversion Equations

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Abstract

The new opportunity to use genomic information in selection of animals has created a new group of animals; young animals with no progeny information. In dairy cattle breeding these animals are mostly young bulls. The system in use today to evaluate bulls internationally is built up to handle bulls with breeding values based on traditional breeding values. In this the feasibility of using the conversion equations used today for these animals was investigated. This was done in two steps. The change in correlations between countries when including genomic data was compared with correlations estimated with traditional data. And the reliabilities for young bulls in importing countries were calculated. The results when looking at the change in correlation are very varying between traits and no real trends can be seen. The young bulls reliabilities varied between the traits and countries. One conclusion is that this methods feasibility is depended on the traits heritability.

Keywords: conversion equation, Genomic selection, International evaluation

Introduction

Today there are more traits than ever being included in the international evaluations. Still there are traits only evaluated in national evaluations, and this will most likely always be the case due to the countries' different objectives and prerequisites. For the Import purposes countries can select bulls without international breeding values for a specific trait using conversion equations to convert the exporting countries' breeding value to their own scale.

The results from a survey about use of genomic evaluations in Interbull member countries showed that eleven countries plan to start genomic evaluation during the years 2009 and 2010, in addition fourteen countries answered not decided yet which could in practice mean that even more countries will begin genomic evaluations in the near future. (Loberg and Dürr, 2009).

The implementation of genomic evaluations on the national scale will introduce a new group of animals without international breeding values. The young bulls with genomic estimated breeding values (GEBV), whose GEBV does not rely on their daughters' information.

The aim of this study is divided into two parts. First: to see if correlations between countries change when GEBV values are used. Second: to see if it is feasible to use conventional equations for young bulls with GEBV values and no daughter information.

Material

Three sets of Holstein data was used; (1) data set containing GEBV values for old bulls (G – files), (2) data set containing GEBV values for young bulls with no daughter information (C – files) and (3) data used in May test run. For number of bulls included in G – files and C – files see Table 1 and Table 2.

Table 1. G - files. Number of bulls with GEBVs submitted to the different traits.

	Production			Confor-mation	Udder health	Longevity	Fertility		
	mi[1]	fa[1]	pr[1]		sc[1]	dl[1]	c1[1]	c2[1]	it[1]
France	2267	2267	2267	2228	2266		2198	2198	
New Zealand	4944	4944	4944	4944	4944	4944		4944	4944
Poland	1086	1086	1086	1077					

[1] mi=milk, fa = fat, pr = protein, sc = somatic cell score, dl = direct longevity, c1 = cows ability to conceive (1), c2 = cows ability to conceive (2) and it = interval trait

Table 2. C – files. Number of bulls with GEBVs submitted to the different traits.

	Production			Confor-mation	Udder health	Longevity	Fertility				Work-ability
	mi[1]	fa[1]	pr[1]		sc[1]	dl[1]	cr[1]	c1[1]	c2[1]	it[1]	
France	2267	2267	2267	1218	929			998			
The Netherlands	905	905	905	905	905	905	905	905	905	905	905
New Zealand	1318	1318	1318	1487	1631	1415			1415	1415	

[1] mi=milk, fa = fat, pr = protein, sc = somatic cell score, dl = direct longevity, cr = cows ability to recycle, c1 = cows ability to conceive (1), c2 = cows ability to conceive (2) and it = interval trait

Methods

Comparison of correlations

The EDC value in submitted G – files is the extra EDC value gained from including genomic information, the rest of the EDC value was extracted from files used in May test run. Estimation of correlations was performed in the same way as in Interbull test runs. There was one run for each trait and each country with GEBV data, making in total 16 correlation matrices from the G – files. In addition one run for each trait was performed with data from May test run, these matrices was used for comparison.

Reason for including only one country with GEBV values at a time is that one of the requirements in MACE is that the residual covariance is zero. With traditional EBVs calculated on daughter performance, with all daughters in different countries, the covariance is assumed to be zero. The GEBVs are estimated on both daughter performance and genomic information. In this case there will be a covariance for a bull with estimates in more than one country due to the fact that he has the same genomic information regardless of where he is evaluated.

For the production traits only ten countries was included in the runs, in way of saving computational time.

Reliability values for young bulls

Reliability values for young bulls in importing countries were calculated using the following formula:

$$REL_{IMP} = REL_{EXP} * r^2_{G_{IMP,EXP}}$$

where: REL_{IMP} = reliability in importing country, REL_{EXP} = reliability in exporting country and $r^2_{G_{IMP,EXP}}$ = the squared correlation between importing and exporting country.

The correlations used are the ones calculated during May test run.

To identify bulls qualified for importation a threshold of reliability over 50% was created.

Results and Discussion

Comparison of correlations

The change in correlation when including GEBV for one country is not consistent across traits. For most of the production traits there are only the correlations with the country with GEBV that are changing. For fertility traits change are seen for more countries than the country with GEBV. For longevity and udder health there was no change in correlation.

Reliability values for young bulls

Number of qualifying young bulls can be seen in Table 3. The results show a big difference between the low heritable fertility traits and production and udder health. In most cases there is only one country with any bulls with reliability over 50 % and this country is then the country of origin. For production traits and udder health a large number of countries have many bulls with reliability over 50%.

The correlations used when calculating the reliability in importing counties were high or medium high. The only other factor is the reliability of the bull in the exporting country. Indicating that when using this method, the traits need to have sufficiently high heritability.

Acknowledgments

References

Loberg, A. & Dürr, J.W. 2009. Interbull survey on the use of genomic information. *Interbull Bulletin 39,* 3-14.

Table 3. Number of young bulls with reliability higher than 50%.

| | Trait | No. of countries | No. of Bulls | Countries with qualifying bulls | | | |
				0% of the bulls	> 50% of bulls	100% of bulls	Any fraction
FRA	mi	26	929	3	6	7	23
NLD	mi	26	905	13	10	0	13
NZL	mi	26	1318	24	1	0	2
FRA	fa	26	929	5	10	3	21
NLD	fa	26	905	15	7	0	11
NZL	fa	26	1318	25	1	0	1
FRA	pr	26	929	6	0	1	20
NLD	pr	26	905	16	5	1	10
NZL	pr	26	1318	25	1	0	1
FRA	sc	24	929	0	8	12	24
NLD	sc	24	905	8	9	0	16
NZL	sc	24	1631	3	4	0	21
NLD	cy	13	905	12	0	0	1
FRA	c1	12	998	9	1	0	3
NLD	c1	12	905	11	0	0	1
NLD	c2	16	905	15	1	0	1
NZL	c2	16	1415	15	1	0	1
NLD	dl	21	905	21	0	0	0
NZL	dl	21	1415	20	1	0	1