Trend of Within Country Sire Variance and Potential Impact on International Evaluations for Production Traits

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Introduction

Over the last years, the international trade of animal genetic material (semen, embryos) was considerably increased. This situation has accelerated the improvement of statistical methods for genetic evaluation across country.

Several methods are available to compare bulls in different countries (1, 2, 3, 4, 5). An easy procedure is the conversion method based on least square (LS) analyses using the regression of proof of bulls from the importing country on those from the exporting country (1, 2). An alternative method, based on mixed model (MM) procedures, was proposed by Schaeffer (3), and applied by Rozzi (4), Jacques and Klemetsdal (5), Banos et al. (6), and Banos et al. (7). The most recent method used for international comparison of dairy bulls was proposed by Schaeffer and Zhang (8). This method is a MM procedure called Multi-trait Across Country Evaluations (MACE) and actually is the official method used by INTERBULL. Factors influencing international evaluation of dairy bulls, using MACE, were evaluated by Schaeffer et al. (9) which suggested to improve the international evaluations, to exclude proofs of imported bulls, to estimate genetic correlations between countries and to use proofs of bulls born in the last 15 years.

Over the last two years, the continue research of INTERBULL and others research centers around the world, estimated genetic correlations (10, 11, 12) and evaluated the potential bias on MACE evaluations including imported bulls (13). These researches have produced important improvements on international evaluations but notwithstanding this INTERBULL evaluations are still not totally accepted from all countries.

Continue researches to further improve the current method for international evaluation are countinuing. The possibility to increase the present standard level of INTERBULL evaluations is a first-class service to the INTERBULL centre (14).

Our contribute on this issue is due to the scarce study on the effect of time-edit of data on MACE evaluations and on the lack of researches for estimation of trend for genetic variability within country.

The purpose of this study was to estimate for Canada, Germany, Italy and the Netherlands the trend of genetic variability within country for production traits including or excluding imported semen and to suggest potential effetcs on international evaluations.

Materials and Methods

Data

National evaluations and daughters yield deviations (DYDs) for milk, fat and protein yields were used on bulls from Canada (CAN, January '96), Germany (DEU, September '95), Italy (ITA, December '95) and the Netherlands (NLD, August '95). A total numbers of 35,583 bulls was available from the four contries (CAN: 5,453, DEU: 12,655, ITA: 5,415 and NLD: 12,059). Only Holstein bulls with a minimum number of 20 daughters in at least 20 herds were analised. Statistical descriptions of data sets for each country are presented in Table 1.

To estimate the trend of the within country sire variance for milk, fat and protein yield were made four data sets, using: 1) all bulls (ALL), 2) bulls born since 1980 (L10) and 3) bulls born since 1985 (L05). The impact of the imported bulls on the trend of within country sire variance was evaluated using an additional 3 data sets, for each country, excluding bulls with first evaluation in another country. The additional data sets are denoted as ALLNOI, L10NOI, L05NOI, respectivelly. The trend of sire variance, express as sire standard deviation (SD), is presented computing the change of sire SD from the results of L10 and L05 over the ALL data and from the results of L10NOI and L05NOI over ALLNOI data. The potential effect of the trend of sire SD was evaluated computing the theoretical regression coefficient (b) using the genetic correlations estimated by INTERBULL (10).

Statistical model

Within each country and for each trait all the data sets were analysed using a procedure based on Expectation Maximization algorithm to produce Restricted Maximum Likelihood estimates as described by Misztal et al. (15) and Misztal et al. (16). The equation of the model is:

$$y_{ijk} = GG_i + a_j + e_{ijk}$$

where

y_{ijk} = is an average of DYDs (ITA and NLD) and single EBV (CAN and DEU) for bull j of the genetic group i

GG_i = fixed effect of genetic group based on country of origin and birth year of bull. Birth year grouping was by 5 year periods and smaller groups then 5 were combined within country

a_j = random bull effect

e_{ijk} = random residual effect $N(0, A\sigma^2)$

A single-trait animal model procedure was used for each data set. The relationship matrix for all bulls based on sire, dam, maternal-grand sire and maternal-grand dam relationships.

Phantom parent grouping was used following the idea of Westell et al. (17), where unknown parents are assigned to a genetic group. These genetic groups are based on birth year of bull. Birth year grouping was by 5 years for data set ALL, L10, ALLNOI, and L10NOI and by 2 year for data set L05 and L05NOI.

The REML procedure after 200 iterations was stopped for each run and in every case the convergence criteria resulted less then E-08 for G and R variance, respectively.

Only results on protein yield are presented. However, results on milk and fat yield are available.

Results and Discussion

Table 1 shows the statistical descriptions of data used for each country. These data were the official national evaluations used by INTERBULL centre for international evaluation estimated on February 1996. The DYDs are express as twice original DYDs. So, means and SD of DYDs presented on this staudyr are re-scaled on individual base. Pearson's correlation between EBV and DYD resulted 0.997 and 0.998 for ITA and NLD, respectively. Size of data sets, number of animals with records, number of genetic group (GG) and minimum size of GG are presented on Table 2. Comparison the size of data sets within country the numbers of import bulls evidenced higher values for european countries, in particular for ITA. The estimates of sire SD for protein yield are present in Table 3. The trend of within country sire SD for CAN and NLD was positive when imported bulls are included in the data set used in the analyses (+4% and +7%, respectively, for L05 data respect to the base level assumed as ALL data). The DEU showed largest increment of sire SD (+19%) on the last 5 years. Italy showed a negative trend on the last 5 years (-12 %) although no change was observed using the last 10 years. Large differences reported among countries on the last 5 yeas are probably due to the number of daughters/bull available at the first evaluation in each country. Size group of progeny were 31, 51, 97 and 101 for ITA, CAN, DEU and NLD, respectively. Similar results were obtained by Banos (18). Effect of genetic selection and different intensity of selection for protein yield in each country, over the last years, might also justify the different trends.

Excluding imported bulls from the analyses, within country sire SD is lower respect to data with imported bulls. The trends of sire SD over the time in data without imported semen showed similar trends of analyses performed including imported semen. In every country the sire SD of L05 and L05NOI data sets reported absolute values fairly close because of few imported bulls (< 60 bulls) are evaluated in each country.

The impact of trend of the within country sire variance on international evalutions are presented in Table 4. Negative or positive trends of the regression coefficient (b) over the time, suggest a change of the converted EBVs for foreign bulls due to the time. The change of b over time of 20-30% can dramatically change the rank of bulls wthin each country, reducing the potential genetic gain that could be obtained by national breeding programs. Similar results were found for milk and fat yield.

Conclusions

Within country sire variance for production traits is affected by time-edit. Change over time of b can produce a significant impact on international evaluations. Results of this study suggest to take into account on the MACE procedure of the trends of within country sire variance. An easy way to reduce this problem could be to use the more recent data which are also reflecting of the current populations.

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Table 1. Statistical descriptions of data for each country (mean ± S.D.)

	CAN	DEU	ITA	NLD
Date of evaluation	January '96	September '95	December '95	August '95
Bulls (N.):	4,913	7,400	3,431	6,465
- Birth year (years)	82±6	81±6	80±8	81±6
Minimum	60	57	52	56
Maximum	91	91	91	91
- Daughters (N.)	395±1561	509±1841	470±1303	589±3503
- Herds (N.)	191±489	276±702	189±389	245±860
EBV:				
- Milk (kg)	-156±910	228±534	-24±853	-503±858
- Fat (kg)	-7.1±35.0	2.3±19.5	-0.5±29.7	-23.0±32.3
- Protein (kg)	-6.3±28.3	3.5±14.6	-0.8±27.4	-17.9±25.5
DYD:[1]				
- Milk (kg)	not available	not used	-21±871	-507±873
- Fat (kg)	"	"	0.1±30.5	-23.1±32.9
- Protein (kg)	"	"	-0.2±27.9	-17.9±25.9

[1]DYD = 2*DYD

Table 2. Number of records, animals and genetic groups (GG) used for the analyses[1]

	Data set					
	All	L10	L05	ALLNOI	L10NOI	L05NOI
Birth year of bull	all	>80	>85	all	>80	>85
Import bulls	YES	YES	YES	NO	NO	NO
CAN:						
Records #	4,912	3,482	2,089	4,468	3,322	2,048
Animals #	8,794	6,227	3,786	8,028	5,959	3,710
GG #	8	6	4	8	6	4
Minimum#animal/GG	230	126	136	106	281	110
DEU:						
Records #	7,391	4,430	2,392	6,316	4,192	2,348
Animals #	14,039	8,450	4,687	12,145	8,012	4,605
GG #	17	11	8	9	7	4
Minimum#animal/GG	12	6	8	9	5	7
ITA:						
Records #	3,425	1,921	1,391	2,446	1,546	1,335
Animals #	6,720	3,789	2,790	4,909	3,062	2,662
GG #	18	13	9	11	7	6
Miminum#animal/GG	10	8	7	10	6	5
NLD:						
Records #	6,461	3,797	1,972	5,522	3,540	1,911
Animals #	11,430	7,023	3,542	10,038	6,554	3,428
GG #	18	14	10	18	14	9
Minimum#animal/GG	9	9	7	8	8	7

[1]Animals = number of pedigree known + phantom group.

Table 3. Trend of within country sire SD for country for protein yield[1]

	Data set					
	All	L10	L05	ALLNOI	L10NOI	L05NOI
Birth year of bull	all	>80	>85	all	>80	>85
Import bulls	YES	YES	YES	NO	NO	NO
CAN:						
- Protein Kg	10.75	11.22	11.14	10.18	10.95	11.12
- Δ %	-	+4.4	+3.6	-	+7.6	+9.2
DEU:						
- Protein Kg	5.70	6.00	6.77	5.63	6.13	6.75
- Δ %	-	+5.3	+18.8	-	+8.9	+19.9
ITA:						
- Protein Kg	7.89	7.73	6.95	6.78	7.67	6.86
- Δ %	-	-0.2	-11.9	-	+13.1	+1.2
NLD:						
- Protein Kg	7.00	7.52	7.52	6.90	7.37	7.44
- Δ %	-	+7.4	+7.4	-	+6.8	+7.8

[1]For all data set animals = number of pedigree known + phantom group.

Table 4. Trend of theoretical regression coefficient (b) between countries for protein yield[1]

		Data set					
		All	L10	L05	ALLNOI	L10NOI	L05NOI
Birth year of bull		all	>80	>85	all	>80	>85
Import bulls	rg[2]	YES	YES	YES	NO	NO	NO
CAN:							
- DEU	0.90	1.697	1.683	1.481	1.627	1.608	1.483
- ITA	0.92	1.253	1.335	1.475	1.381	1.313	1.491
- NLD	0.91	1.397	1.358	1.348	1.343	1.352	1.360
DEU:							
- CAN	0.90	0.477	0.481	0.547	0.498	0.504	0.546
- ITA	0.88	0.636	0.471	0.535	0.487	0.493	0.534
- NLD	0.92	0.749	0.734	0.828	0.751	0.765	0.835
ITA:							
- CAN	0.92	0.675	0.634	0.574	0.613	0.644	0.567
- DEU	0.88	1.218	1.134	0.903	1.060	1.101	0.894
- NLD	0.90	1.014	0.925	0.832	0.983	1.041	0.830
NLD:							
- CAN	0.91	0.593	0.610	0.614	0.617	0.612	0.609
- DEU	0.92	1.130	1.153	1.022	1.127	1.106	1.014
- ITA	0.90	0.798	0.875	0.974	0.916	0.865	0.830

[1]Animals = number of pedigree known + phantom group.
[2]rg = genetic correlation estimated by Interbull centre (10).