Parameter Estimation of Longevity and Type Traits from France and Germany with a single trait MACE Model

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Abstract

A single-trait MACE model was used to estimate parameters of longevity and type traits using daughter yield deviations of bulls from France and Germany. Data from bulls having fewer than 30 equivalent daughter contribution were excluded from the parameter estimation. Full pedigree information of bulls was used via sire and dam relationship. Genetic correlations between the two countries were estimated with an approximate REML method. In general, genetic correlation estimates are in agreement with Interbull genetic correlations, but higher genetic correlation estimates between France and Germany were obtained by using most recent data.

1. Introduction

International bull evaluation for longevity and type traits is currently conducted using a single trait MACE (ST-MACE) model (Schaeffer, 1994). Estimated breeding values (EBV) from each country are used to obtain deregressed national proofs for bulls that have daughters with records. Instead of deregressed proofs, Ducrocq *et al.* (2003) proposed to use daughter yield deviations (DYD) for international bull evaluation.

In the current Interbull evaluations, pedigree information of bulls is traced back by sire, maternal grandsire and phantom group of maternal granddam. In contrast, full pedigree information of bulls with sire and dam relationship was recommended for MACE evaluation (Van der Linde *et al.*, 2005).

The objectives of this study were to implement the ST-MACE model using DYD of bulls and full pedigree information to estimate across country genetic correlations for type traits and longevity using data from Germany and France.

2. Materials and Methods

2.1. The ST-MACE model

The following statistical model was applied:

$$\mathbf{q}_{ij} = \mathbf{b}_{kj} + \mathbf{a}_{ij} + \mathbf{e}_{ij} \qquad [1]$$

where \mathbf{q}_{ij} is the DYD of the i-th bull in country j, \mathbf{b}_{kj} is the birth year effect k in the jth country, \mathbf{a}_{ij} is a vector of additive genetic effects of bull i in country j, and \mathbf{e}_{ij} is a vector of residual effects. Adding a year effect in the model provided more robust genetic trends and took selection bias into account (Lassen *et al.*, 2007)

2.2. The mixed model equations

The equation system of the ST-MACE model consists of two main components: an effective daughter contribution (EDC) value Ψ_{ij} corresponding to the least squares part of the left-hand-side and $\Delta_{ij} = \Psi_{ij}\mathbf{q}_{ij}$ corresponding to the right-hand-side of the mixed model equations.

The equation system was solved using a pre-conditioned conjugate gradient algorithm and an iteration on data technique (Liu *et al.*, 2004). The convergence criterion, defined as the logarithm of the sum of squares of differences in solutions between two consecutive rounds of iteration divided by the sum of squares of solutions in last round of iteration, was set to -10.

2.3. Estimation of across country genetic correlations

An approximate EM-REML method was used to estimate the across country genetic correlation for type traits and longevity. It was considered as converged when the change in the across country genetic correlation estimates was less than 0.000001 between two consecutive rounds of iteration in the parameter estimation. Current estimated Interbull correlation was used as starting value. The accuracy of the approximate REML method was validated with simulated data for single and multiple trait MACE models by Tarres *et al.* (2007).

2.4. Data materials

Data from October 2006 French and August 2006 German national genetic evaluations were chosen for implementing the MACE model. In order to mimic the Interbull evaluation, only Black and White Holstein bulls included in Interbull 015 files for type traits or the 017 files for longevity were selected. After combining the two 015 files, there were 27367 bulls left for type traits analysis, 574 of them having data in both countries (common bulls) (Table 1). For longevity, the number of bulls with data was 28934, being common bulls 855 of them. Here is important to note that longevity data was not DYD but pseudo-records (Ducrocq *et al.*, 2001).

In order to keep only more recent data for parameter estimation, bulls born before 1995 and having fewer than 30 EDC were discarded. After combining the data sets from both countries, there were 9329 bulls left, 45 of them having data in both countries (common bulls) for type traits. Although the number of common bulls was reduced, the link between the two datasets came through the sires of bulls (7110 bulls had a sire having sons in the both countries). For longevity, the number of bulls with more recent data was 6493, being common bulls 27 of them.

For pedigree information, the current Interbull pedigree file for Holsteins was reformatted from the sire, MGS and MGD format to the sire and dam format. The total number of animals in pedigree file is shown in Table 1. For unknown parents, we defined genetic groups according to the breed, country of origin, selection path (son to sire, son to dam, daughter to sire and daughter to dam) and birth year of the animal.

Table 1. Data and pedigree information for Holstein MACE evaluations and parameter estimation for type traits and longevity.

	Data set	No of bulls with data in Germany	No of bulls with data in France	No of common bulls	Total no of bulls with data	No of animals in pedigree	No of phantom groups
Type traits	All bulls	12801	15148	574	27367	53987	36
	After 1995	5775	3599	45	9329	24503	15
Longevity	All bulls	13675	16114	855	28934	58243	40
-	After 1995	4020	2500	27	6493	14851	16

3. Results

3.1. Validation using the data from national cow evaluations

The validation of the DYD was done by calculating their Pearson's correlations with the national EBVs derived from national cow evaluations in Germany or in France. The DYD correlation with national EBVs is high in both countries for stature, rump angle, udder depth, front teat placement, teat length and rear teat placement (Table 2). German DYDs had a relatively low correlation for udder support. This trait was well defined in Germany, but the implementation and interpretation vary between classifiers more than for other type traits. French DYDs had a relatively low correlation for traits included later in the type classification system (most of them after 2000): chest width, body depth, angularity, rump width, rear leg rearview, foot angle, fore udder and rear udder height. In this case, the bulls born before 1995 caused the relatively low correlations. After discarding these bulls and the ones having fewer than 30 EDC, the DYD correlation with national EBVs is high in both countries except for foot angle and udder support.

Table 2. Pearson correlation of daughter yield deviations (DYD) with national proofs of Holstein bulls[¶] for type traits.

		Bulls with data in Germany			Bulls with data in France		
		Heritability	Correlations DYD Her		Heritability	Correlations DYD	
			vs national proofs			vs national proofs	
Trait	French trait		All bulls	Bulls		All bulls	Bulls
	clasification			After			after
	started on			1995			1995
Stature		0.41	0.985	0.991	0.51	0.993	0.995
Chest width	01/01/2000	0.18	0.898	0.938	0.19	0.705	0.961
Body depth	01/01/2000	0.24	0.958	0.976	0.36	0.812	0.991
Angularity	01/01/2000	0.24	0.961	0.969	0.28	0.803	0.986
Rump angle		0.26	0.970	0.981	0.33	0.984	0.989
Rump width	01/01/2000	0.28	0.969	0.980	0.31	0.806	0.988
Rear leg set		0.15	0.941	0.961	0.15	0.948	0.962
Rear leg	06/10/2003	0.15	0.933	0.964	0.10	0.500	0.941
rearview							
Fore udder	01/12/1996	0.21	0.930	0.976	0.25	0.798	0.980
Rear udder	01/01/1994	0.22	0.956	0.968	0.21	0.866	0.972
height							
Udder		0.13	0.890	0.891	0.23	0.970	0.977
support							
Udder depth		0.26	0.973	0.985	0.36	0.985	0.991
Front teat pl.		0.22	0.956	0.965	0.35	0.986	0.990
Teat length		0.25	0.968	0.981	0.39	0.988	0.993
Rear teat pl.		0.28	0.947	0.968	0.29	0.980	0.986
Longevity		0.17	0.900	0.959	0.11	0.771	0.943

3.2. Parameter estimation

The parameter estimation was done including all bulls in the 015 file for the type traits with high DYD correlations with national EBVs (stature, rump angle, udder depth, front teat placement, teat length and rear teat placement). In this case, the estimated across country genetic correlations were similar to the Interbull ones which was already high (over 0.93) (Table 3). For the other type traits, the genetic correlations were lower than Interbull values when all bulls in the 010 file were included. After deleting bulls born before 1995 and having fewer than 30 EDC, the estimated across country genetic correlations reached in general values much higher than Interbull ones (Table 3). This can be explained because

newer data are classified in a more unified way, i.e. more homogeneous, than the older data. This applies to almost all type traits. In other words, it makes more sense to use more recent data of all type traits for the parameter estimation than using all available data in 015 file.

For longevity a similar pattern was found. When the parameter estimation is done including all bulls in the 017 file the estimated across country genetic correlations were slightly higher than the 0.66 used in Interbull evaluation. The genetic correlation increased to 0.85 after deleting older bulls born before 1995 and having fewer than 30 EDC (Table 3).

	Interbull	Approximate EM-REML			
Trait		Bulls after 1985	Bulls after 1990	Bulls after 1995	
Stature	0.98	0.981			
Chest width	0.88	0.865	0.872	0.905	
Body depth	0.70	0.550	0.625	0.833	
Angularity	0.73	0.726	0.750	0.781	
Rump angle	0.97	0.962			
Rump width	0.93	0.868	0.933	0.973	
Rear leg set	0.85	0.806	0.828	0.848	
Rear leg rearview	0.86	0.808	0.817	0.866	
Fore udder	0.89	0.847	0.856	0.927	
Rear udder height	0.88	0.830	0.859	0.903	
Udder depth	0.97	0.965			
Front teat pl.	0.94	0.923			
Teat length	0.94	0.942			
Rear teat pl.	0.97	0.971			
Longevity	0.66	0.694	0.731	0.845	

Table 3. Genetic correlations between Germany and France for type traits and longevity estimated using an approximate REML software.

5. Conclusion

This study shows that using newer data (i.e. better data due to more homogenous type classification systems) led to higher genetic correlation estimates between France and Germany for type traits and longevity. Higher genetic correlations will have a clear impact on reranking of sires, top lists, etc.

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