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# Binational evaluation of type traits from Germany and France with a single-trait MACE animal model

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*Binational genetic evaluation between Germany and France were performed for each type trait using a single-trait MACE (multiple across-country evaluation) model. Daughter yield deviations (DYD) of bulls having 30 equivalent daughter contributions or more were the data for parameter estimation. Full pedigree information of bulls was used via sire and dam relationships. In general, across-country genetic correlation estimates were in agreement with what is observed by Interbull. The estimated correlations were over 0.93 for stature, rump angle, udder depth, front teat placement, teat length and rear teat placement. These traits have been classified in both countries for a long period of time. However, some other type traits were included later in the French type classification system (most of them since 2000): chest width, body depth, angularity, rump width, rear leg rear view, fore udder and rear udder height. The estimated correlations for these traits were relatively low. In order to check changes in genetic correlations over time, data from bulls born until the end of 1995 were discarded. Higher genetic correlation estimates between both countries were obtained by using more recent data especially for traits having lower genetic correlation, e.g. body depth correlation increased from 0.55 to 0.83. Once genetic correlations were estimated, binational genetic evaluation between Germany and France were performed for each type trait using DYD of bulls. The rankings of bulls obtained from this evaluation had some differences with Interbull rankings but a similar proportion of bulls from each country was found. Finally, more computationally demanding binational evaluations were performed using yield deviations of cows for binational cow comparison. The rankings obtained were influenced by the number of daughters per bull and heritabilities used in each country.*

**Keywords:** multiple across-country evaluation, type traits, daughter yield deviation, dairy cattle

## Implications

Binational genetic evaluations between Germany and France for type traits were performed with a single-trait MACE (multiple across-country evaluation) model. The use of pre-corrected records has some advantages, in particular with the possibility to apply more robust models or to extend to animal models based on cow performances. The paper shows that the implementation of such evaluation is feasible at an international level (even though only two countries are considered here), and gives interesting results, most of the time (but not always) quite consistent with Interbull results.

## Introduction

International genetic evaluations of dairy sires are currently conducted by Interbull using multiple across-country evalua-

tions (MACE) as proposed by Schaeffer (1994). Estimated breeding values (EBVs) from each country are used to obtain deregressed national genetic evaluations for bulls that have daughters with records. Similar traits measured in different countries are considered as distinct, but correlated traits. The required across-country genetic correlations are often difficult to estimate due to weak genetic ties between dairy populations in different countries, as the majority of bulls have daughters in one country only. These genetic correlations are important parameters in the Interbull evaluation to compare bulls across countries. However, these correlations are sometimes surprisingly low for some type traits, e.g. 0.70 for body depth between Germany and France.

Type traits in dairy cattle are scored in a subjective way. A classifier scores an animal following a certain definition for a trait. These definitions are set by each national herdbook organization or for the Holstein breed, by the World Holstein-Friesian Federation (WHFF). So far, WHFF has defined 16 standard traits, which should be scored by all members of

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WHFF identically (Hamoen, 2005). At WHFF level, a lot of effort has been devoted to make the definitions for type traits more uniform across countries. In many countries the definition of several traits was adjusted once or several times during a period of 20 years. However, in national genetic evaluations, the scores for a trait were usually considered to follow the same definition over time. When countries keep on using data based on former trait definitions in national evaluations, breeding values reflect the new trait definition very slowly. Furthermore, the corresponding EBVs are used as input in the international genetic evaluations of Interbull, which pulls down the genetic correlation between countries. In order to avoid this, countries should consider changes in trait definitions in their genetic evaluations. This can be done by omitting data scored with an earlier definition or by treating these different scores as different traits in a multiple-trait national evaluation. De Jong and Harbers (2002) showed that the average correlation with other countries increases in such a case. Tsuruta *et al.* (2004) presented changes over time in genetic parameters of type traits even though there was no official change in the definition. These changes over time can also decrease the genetic correlation between countries.

In parallel to international bull comparison, Germany and France decided, in 2005, to perform joint German–French bull and cow test evaluations for all traits included in the national total merit indices. These could be performed using a two-country animal model with original performance data (full multi-trait model) but it was not computationally feasible on all traits due to the number of animals and the number of traits involved. Alternatively, an approximate multi-trait model with a time (year) effect using pre-corrected data from a two-step procedure has been shown to be a feasible and robust approach for prediction of breeding values (Ducrocq *et al.*, 2001). Lassen *et al.* (2007) showed, via simulation, that a full multi-trait model was not significantly better than such an approach. Lassen *et al.* (2007) also showed that including a time (year) effect in the approximate multi-trait model led to evaluations more robust to over- or underestimation of genetic trends and improved genetic progress significantly. The two-step approach was similar to current Interbull international evaluations but using pre-corrected records instead of deregressed EBVs. Another potential improvement was the inclusion of full pedigree information of animals with sire and dam relationship in the evaluations as recommended by Van der Linde *et al.* (2005), whereas in the current Interbull evaluations, pedigree information of animals is traced back by sire, maternal grandsire (MGS) and phantom group of maternal granddam (MGD).

The objective of this study was to implement a German–French MACE evaluation for each type trait using pre-corrected records in an approximate multi-trait approach. For each trait: (1) genetic correlation across countries was estimated looking at its stability over time, (2) binational genetic evaluation using daughter yield deviations (DYD) of bulls (DYD-MACE) was performed for bull comparison and (3) binational genetic evaluation using yield deviations (YD) of cows (YD-MACE) was performed for bull and cow comparison.

## Material and methods

### Data

*DYD of bulls for DYD-MACE.* Data from German (August 2006) and French (October 2006) national genetic evaluations were chosen for implementing the DYD-MACE model. Only Black and White Holstein bulls included in the Interbull evaluation for type traits were selected. There were 15 611 and 15 148 bulls with DYD data from Germany and France, respectively. After combining the German and French files for each trait, there were 27 367 bulls, 574 of which had data in both countries (common bulls). For pedigree information, the current Interbull pedigree file for Holsteins was reformatted from the sire, MGS and MGD format to a sire and dam format. The total number of animals in the pedigree file was 57 137. 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.

For parameter estimation, only bulls having 30 equivalent daughter contributions (EDC) or more were included. In order to assess changes in genetic correlation over time, parameter estimation was done using three different datasets. The first one included all bulls that were born since 1985 (18 860 bulls with 413 common bulls). The second one included bulls from the first dataset that were born since 1990 (15 504 bulls with 257 common bulls). The third one included bulls from the second dataset that were born since 1995 (9329 bulls with 45 common bulls). Although the number of common bulls in this last dataset was reduced, the two countries were well connected through the sires of bulls: 7110 bulls had paternal half-sibs in the other country.

*YD of cows for YD-MACE.* Data from the French (November 2006) and the German (February 2007) national genetic evaluations were chosen for implementing the YD-MACE model. There were 1 550 642 and 3 680 288 Black and White Holstein cows with YD available from Germany and France, respectively. After combining both datasets, there were 5 230 930 cows and only one of them had data in both countries. The total number of animals in the joint cow pedigree file related with animals having data was 9 745 489 with 48 unknown parents genetic groups.

*The general outline of the multiple-trait MACE model.* The following statistical model was applied

$$\mathbf{q}_{ij} = \mathbf{X}_{ij}\mathbf{b}_j + \mathbf{u}_{ij} + \mathbf{e}_{ij}, \quad (1)$$

where  $\mathbf{q}_{ij}$  is the vector of pre-corrected records of the  $i$ th animal in country  $j$ ,  $\mathbf{b}_j$  is the vector of birth year effects in the  $j$ th country,  $\mathbf{X}_{ij}$  is known design matrices relating the observations animal  $i$  in country  $j$  to birth year effects of  $j$ th country,  $\mathbf{u}_{ij}$  is a vector of additive genetic effects of animal  $i$  in country  $j$  and  $\mathbf{e}_{ij}$  is a vector of residual effects. Adding a birth year effect in the model provided more robust genetic trends (Ducrocq *et al.*, 2003; Lassen *et al.*, 2007). The pre-corrected records were DYD of bulls in the DYD-MACE evaluation and YD of cows in the YD-MACE evaluation.

The (co)variance matrix of genetic effects of the  $m$  countries and its inverse are denoted as:

$$\mathbf{G}_0 = \begin{bmatrix} \mathbf{G}_{011} & \mathbf{G}_{012} & \cdots & \mathbf{G}_{01m} \\ & \mathbf{G}_{022} & \cdots & \mathbf{G}_{02m} \\ & & \ddots & \vdots \\ \text{symm.} & & & \mathbf{G}_{0mm} \end{bmatrix} \text{ and}$$

$$\mathbf{G}_0^{-1} = \begin{bmatrix} \mathbf{G}_0^{11} & \mathbf{G}_0^{12} & \cdots & \mathbf{G}_0^{1m} \\ & \mathbf{G}_0^{22} & \cdots & \mathbf{G}_0^{2m} \\ & & \ddots & \vdots \\ \text{symm.} & & & \mathbf{G}_0^{mm} \end{bmatrix}, \quad (2)$$

where  $m$  is the number of countries,  $\mathbf{G}_{0jj}$  is the original genetic (co)variance matrix of country  $j$  and  $\mathbf{G}_{0jk}$  is the genetic covariance matrix between countries  $j$  and  $k$ . As usually considered in MACE, an animal has data in only one country so the residual correlation between countries can be assumed to be 0. The inverse of error (co)variance matrix of animal  $i$  in country  $j$  is:

$$[\text{Var}(\mathbf{e}_{ij})]^{-1} = \Psi_{ij}, \quad (3)$$

where  $\Psi_{ij}$  is the EDC matrix for animal  $i$  in country  $j$ . The multiple-trait EDC procedure (Liu *et al.*, 2004a) can be used to approximate matrix  $\Psi$  for each animal.

*The mixed model equations.* The mixed model equations of model (1) consist of equations for additive genetic effects of animals and fixed effects of birth year. Ignoring pedigree contributions, the equations corresponding to animal  $i$  are:

$$\begin{bmatrix} \Psi_{i1}\mathbf{X}_{i1} & & & \mathbf{0} \\ & \Psi_{i2}\mathbf{X}_{i2} & & \\ & & \ddots & \\ \mathbf{0} & & & \Psi_{im}\mathbf{X}_{im} \end{bmatrix} \begin{bmatrix} \hat{\mathbf{b}}_1 \\ \hat{\mathbf{b}}_2 \\ \vdots \\ \hat{\mathbf{b}}_m \end{bmatrix} + \begin{bmatrix} \Psi_{i1} & & & \mathbf{0} \\ & \Psi_{i2} & & \\ & & \ddots & \\ \mathbf{0} & & & \Psi_{im} \end{bmatrix} + \mathbf{a}^{ii} \begin{bmatrix} \mathbf{G}_0^{11} & \mathbf{G}_0^{12} & \cdots & \mathbf{G}_0^{1m} \\ & \mathbf{G}_0^{22} & \cdots & \mathbf{G}_0^{2m} \\ & & \ddots & \vdots \\ \text{symm.} & & & \mathbf{G}_0^{mm} \end{bmatrix} \times \begin{bmatrix} \hat{\mathbf{u}}_{i1} \\ \hat{\mathbf{u}}_{i2} \\ \vdots \\ \hat{\mathbf{u}}_{im} \end{bmatrix} = \begin{bmatrix} \Delta_{i1} \\ \Delta_{i2} \\ \vdots \\ \Delta_{im} \end{bmatrix}, \quad (4)$$

where  $\mathbf{a}^{ii}$  is the diagonal element of animal  $i$  in the inverse of the numerator relationship matrix  $\mathbf{A}$ , and  $\Delta_{ij}$  represents

the right-hand-side (RHS) of animal  $i$  in country  $j$ . Note that  $\Delta_{ij}$  is not dependent from across-country correlations ( $\mathbf{G}_{0jk}$ ) and is a function of country-specific information ( $\mathbf{q}_{ij}$ ,  $\mathbf{G}_{0jj}$ ,  $\mathbf{b}_j$ ) only. Formula 24 in the paper by Liu *et al.* (2004a) can be used to calculate  $\Delta_{ij}$ . Equations for the fixed effects of birth year in model (1) are:

$$\begin{bmatrix} \Psi_{b_1} & & & \mathbf{0} \\ & \Psi_{b_2} & & \\ & & \ddots & \\ \mathbf{0} & & & \Psi_{b_m} \end{bmatrix} \begin{bmatrix} \hat{\mathbf{b}}_1 \\ \hat{\mathbf{b}}_2 \\ \vdots \\ \hat{\mathbf{b}}_m \end{bmatrix} + \begin{bmatrix} \mathbf{X}'_{i1}\Psi_{i1} & & & \mathbf{0} & \mathbf{X}'_{i1}\Psi_{i1} & & & \mathbf{0} \\ & \mathbf{X}'_{i2}\Psi_{i2} & & & & \cdots & & \mathbf{X}'_{i2}\Psi_{i2} \\ & & \ddots & & & & & \\ \mathbf{0} & & & \mathbf{X}'_{im}\Psi_{im} & \mathbf{0} & & & \mathbf{X}'_{im}\Psi_{im} \end{bmatrix} \times \begin{bmatrix} \hat{\mathbf{u}}_1 \\ \hat{\mathbf{u}}_2 \\ \vdots \\ \hat{\mathbf{u}}_n \end{bmatrix} = \begin{bmatrix} \sum_i \mathbf{X}'_{i1}\Delta_{i1} \\ \sum_i \mathbf{X}'_{i2}\Delta_{i2} \\ \vdots \\ \sum_i \mathbf{X}'_{im}\Delta_{im} \end{bmatrix}, \quad (5)$$

where  $n$  is the total number of animals with observation,  $\hat{\mathbf{u}}'_i = [\hat{\mathbf{u}}'_{i1}, \hat{\mathbf{u}}'_{i2}, \dots, \hat{\mathbf{u}}'_{im}]$  represents EBV of animal  $i$  in all  $m$  countries and  $\Psi_{b_j} = \sum_{i=1}^{n_j} \mathbf{X}'_{ij}\Psi_{ij}\mathbf{X}_{ij}$  with  $n_j$  being the number of animals with observation in country  $j$ .

The equation system was simplified in our study because only one trait per country was allowed in order to perform single-trait MACE models (ST-MACE) for each type trait. In this case, all terms in equations (4) and (5) above became scalars except the ones related to birth year effect: the matrix  $\Psi_{b_j}$  and the vectors  $\mathbf{b}_j$  and  $\mathbf{X}_{ij}$ . The equation system was solved using a pre-conditioned conjugate gradient algorithm and an iteration on data technique (Liu *et al.*, 2004b). 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  $-10$ .

*Estimation of across-country genetic correlations.* An approximate expectation maximization restricted maximum likelihood (EM-REML) method (Liu *et al.*, 2004b) was used to estimate the across-country genetic correlation for each type traits. It was considered as converged when the change in the across-country genetic correlation estimates was less than  $10^{-6}$  between two consecutive rounds of iteration. Current estimated Interbull correlations were used as starting values. The unbiasedness of the approximate EM-REML method was validated with simulated data for single and multiple-trait MACE (MT-MACE) models (Tarres *et al.*, 2007a).

## Results

### *Pearson correlation of DYD with national EBV*

The validation of the DYD values was done by calculating their Pearson's correlations with the national EBV derived from national cow evaluations. German DYD had high correlation with national EBV ranging from 0.930 for fore udder to 0.985 for stature (Table 1). The higher the heritability of the trait, the higher the correlations. Only two traits were out of this range: chest width (0.898) and udder support (0.890). When only bulls born since 1995 were included, the correlations were higher, ranging from 0.938 for chest width to 0.991 for stature (Table 1), except for udder support (0.891). This trait was well defined in Germany, but the implementation and interpretation vary among classifiers more than for other type traits. Therefore, this trait was excluded for further analyses.

French DYD had high correlation with national EBV for traits evaluated for a long period of time in France (stature, rump angle, rear leg set, udder support, udder depth, front teat placement, teat length and rear teat placement), ranging from 0.948 for rear leg set to 0.993 for stature (Table 1). The other type traits (chest width, body depth, angularity, rump width, rear leg rear view, fore udder and rear udder height) were included later in the French type classification system (most of them since 2000) (Table 2). For these traits, French DYD had low correlations with national EBV ranging from 0.500 for rear leg rear view to 0.812 for body depth (Table 1). These correlations were especially low for the bulls born until the end of 1995. When these bulls were not included, the correlations reached high values ranging from 0.941 for rear leg rear view to 0.991 for body depth.

*Estimated genetic correlations across Germany and France*  
Parameter estimation for traits evaluated for a long period of time in France was done using the first dataset. Estimated across-country genetic correlations were high, ranging from 0.923 for front teat placement to 0.981 for stature (Table 3), except for rear leg set (0.806). These correlations were similar to the Interbull ones. For traits

**Table 2** Year when definition<sup>†</sup> of each trait was updated in German and French dairy cattle

Group of traits	Trait	Germany	France
Body traits	Stature	1984	1986
	Chest width	1984	2000
	Body depth	1984	2000
	Angularity	1984	2000
	Rump angle	1984	1986
	Rump width	1984	2000
Feet and legs	Rear leg set	1984	1986
	Rear leg rear view	1998	2003
Udder traits	Fore udder	1984	1996
	Rear udder height	1984	1994
	Udder support	1984	1986
	Udder depth	1984	1986
	Front teat placement	1984	1986
	Teat length	1984	1986
	Rear teat placement	2000	1986

<sup>†</sup>These definitions are set by each national herdbook organization or for the Holstein breed, by the World Holstein-Friesian Federation (WHFF). For information about WHFF definitions see Hamoen (2005). For information about German type classification system go to Deutscher Holstein Verband (2007). For information about French type classification system go to Prim'holstein France (2007).

**Table 1** Pearson correlation (*r*) of daughter yield deviations (DYD) with national estimated breeding values (EBVs) of Holstein bulls for type traits

Group of traits	Trait	$h^2$ <sup>†</sup>	Bulls with data in Germany				Bulls with data in France				
			All bulls		Bulls born since 1995		All bulls		Bulls born since 1995		
			$n$ <sup>‡</sup>	<i>r</i>	<i>n</i>	<i>r</i>	$h^2$	<i>n</i>	<i>r</i>	<i>n</i>	<i>r</i>
Body traits	Stature	0.41	15 611	0.985	5766	0.991	0.51	15 148	0.993	3612	0.995
	Chest width	0.18	15 242	0.898	5778	0.938	0.19	6969	0.705	3581	0.961
	Body depth	0.24	15 611	0.958	5781	0.976	0.36	6969	0.812	3582	0.991
	Angularity	0.24	15 242	0.961	5778	0.969	0.28	6969	0.803	3581	0.986
	Rump angle	0.26	15 611	0.970	5777	0.981	0.33	15 148	0.984	3603	0.989
	Rump width	0.28	15 610	0.969	5776	0.980	0.31	6969	0.806	3597	0.988
Feet and legs	Rear leg set	0.15	15 611	0.941	5781	0.961	0.15	15 148	0.948	3602	0.962
	Rear leg rear view	0.15	11 140	0.933	5781	0.964	0.10	4257	0.500	1903	0.941
Udder traits	Fore udder	0.21	15 441	0.930	5779	0.976	0.25	9312	0.798	3603	0.980
	Rear udder height	0.22	15 611	0.956	5778	0.968	0.21	11 240	0.866	3602	0.972
	Udder support	0.13	15 611	0.890	5782	0.891	0.23	15 148	0.970	3603	0.977
	Udder depth	0.26	15 611	0.973	5777	0.985	0.36	15 148	0.985	3604	0.991
	Front teat placement	0.22	15 611	0.956	5778	0.965	0.35	15 148	0.986	3604	0.990
	Teat length	0.25	15 610	0.968	5777	0.981	0.39	15 148	0.988	3603	0.993
	Rear teat placement	0.28	9456	0.947	5655	0.968	0.29	15 148	0.980	3603	0.986

<sup>†</sup> $h^2$  denotes heritability used in the national evaluations.

<sup>‡</sup> $n$  denotes number of bulls with records.



**Table 3** Estimated genetic correlations between Germany and France for type traits estimated using an approximate restricted maximum likelihood (REML) software

Group of traits	Trait	Interbull	Approximate EM-REML		
			Bulls born since 1985 <sup>1</sup>	Bulls born since 1990 <sup>1</sup>	Bulls born since 1995 <sup>1</sup>
Body traits	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
Feet and legs	Rear leg set	0.85	0.806	0.828	0.848
	Rear leg rear view	0.86	0.808	0.817	0.866
Udder traits	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 placement	0.94	0.923		
	Teat length	0.94	0.942		
	Rear teat placement	0.97	0.971		

EM-REML = expectation maximization restricted maximum likelihood.

<sup>1</sup>Bulls with fewer than 30 equivalent daughter contributions were discarded.

introduced more recently in France, the genetic correlations estimated using the first dataset ranged from 0.55 for body depth to 0.868 for rump width and were lower than the Interbull values (Table 3). These correlations increased as older bulls were discarded by using the second and especially the third dataset for parameter estimation. In this case (including only bulls born since 1995), the estimated across-country genetic correlations reached values much higher than the Interbull ones (Table 3). This applies to almost all type traits but specially for the ones with the lowest correlations, i.e. body depth (0.83 v. 0.70) and angularity (0.78 v. 0.73).

#### *Binational DYD-MACE genetic evaluations*

A birth year effect was included in the binational evaluations to check the validity of national genetic trends as recommended by Ducrocq *et al.* (2003) and Lassen *et al.* (2007). For almost all type traits, the year effects were small indicating that in general there was no bias in the genetic trend estimated in national evaluations. Small differences in annual genetic trend between 1% and 2.5% of genetic standard deviation were only detected for chest width, body depth, rear leg set, udder support and rear teat placement on the German scale, and for rear leg set, udder support and rear teat placement on the French scale (results not shown).

The DYD-MACE binational evaluation provided EBVs on the German and French scales for all bulls, which could be compared to EBVs published by Interbull. After discarding unofficial bulls and bulls born until the end of 1985, top 100 rankings on the German and French scale were obtained based on DYD-MACE and Interbull breeding values. For traits evaluated for a long period of time, the DYD-MACE top-100 list had around 80 bulls also present in the Interbull rankings, both on the German (Table 4) and French scales (Table 5).

The proportions of German and French bulls in the DYD-MACE top-100 lists were also similar to the proportions in the Interbull top-100 lists (Tables 4 and 5).

For traits introduced more recently in France, the DYD-MACE top-100 list had around 70 bulls present also in the Interbull rankings, on both the German and French scales (Tables 4 and 5). The proportions of bulls from the two countries were similar for almost all traits. The differences can be partially explained by the higher genetic correlations assumed in the DYD-MACE evaluation that increased the presence of foreign bulls on each country scale.

#### *Binational YD-MACE genetic evaluations*

The binational evaluation using YD of cows was tested for stature and teat length, but it will be generalized in the future to other type traits. A birth year effect was included to correct for potential bias in genetic trend. The slopes of the birth year effect were small and similar to the values obtained in the DYD-MACE evaluation (results not shown).

The YD-MACE binational evaluation provided EBVs for all bulls and cows on the German and French scales. The EBVs of bulls were sorted to obtain top-bull lists on both scales that were comparable to the Interbull and DYD-MACE lists. The YD-MACE top-100 bull list for stature and teat length had around 80 bulls present in the Interbull and also the DYD-MACE lists, on both scales (Table 6). The proportions of German and French bulls in the YD-MACE top-100 bull lists were also similar to the proportions in the Interbull and DYD-MACE lists, both for stature and teat length (Table 6). The EBVs of cows were also sorted to obtain top-cow lists on both scales. However, in this case it was difficult to compare the proportion of cows with data from each country because of the different number of cows with data, and the different heritability of the traits in both countries (results not shown).

**Table 4** Number of bulls in the top 100 rankings for type traits on the German scale

Group of traits	Trait	Interbull <sup>†</sup>			DYD-MACE <sup>‡</sup>			No. of bulls in both DYD-MACE and Interbull
		rG <sup>‡</sup>	Bulls with data in Germany	Bulls with data in France	rG <sup>‡</sup>	Bulls with data in Germany	Bulls with data in France	
Body traits	Stature	0.98	56	43	0.98	52	47	82
	Chest width	0.88	55	44	0.90	58	41	67
	Body depth	0.70	82	17	0.83	72	27	71
	Angularity	0.73	88	11	0.78	86	12	75
	Rump angle	0.97	56	41	0.96	48	49	80
	Rump width	0.93	59	40	0.97	53	46	79
Feet and legs	Rear leg set	0.85	51	46	0.85	56	40	68
	Rear leg rear view	0.86	64	34	0.87	62	36	76
Udder traits	Fore udder	0.89	83	14	0.93	79	18	72
	Rear udder height	0.88	77	20	0.90	68	29	78
	Udder depth	0.97	71	26	0.97	72	25	74
	Front teat placement	0.94	43	55	0.92	47	50	80
	Teat length	0.94	44	52	0.94	44	52	81
	Rear teat placement	0.97	64	34	0.97	59	39	76

DYD-MACE = daughter yield deviations multiple across-country evaluations.

There were two different rankings based on DYD-MACE and Interbull EBV (estimated breeding values).

<sup>†</sup>In the rankings there were also bulls with data in both countries (not shown).

<sup>‡</sup>Estimated across-country genetic correlation among Germany and France.

**Table 5** Number of bulls in the top 100 rankings for type traits on the French scale

Group of traits	Trait	Interbull <sup>†</sup>			DYD-MACE <sup>‡</sup>			No. of bulls in both DYD-MACE and Interbull
		rG <sup>‡</sup>	Bulls with data in Germany	Bulls with data in France	rG <sup>‡</sup>	Bulls with data in Germany	Bulls with data in France	
Body traits	Stature	0.98	52	47	0.98	48	51	85
	Chest width	0.88	49	50	0.90	56	43	58
	Body depth	0.70	30	69	0.83	39	60	74
	Angularity	0.73	40	59	0.78	58	40	67
	Rump angle	0.97	49	49	0.96	43	55	79
	Rump width	0.93	54	45	0.97	53	46	82
Feet and legs	Rear leg set	0.85	13	84	0.85	15	82	82
	Rear leg rear view	0.86	45	53	0.87	45	52	76
Udder traits	Fore udder	0.89	58	39	0.93	60	37	73
	Rear udder height	0.88	57	40	0.90	46	52	74
	Udder depth	0.97	62	35	0.97	65	32	73
	Front teat placement	0.94	30	68	0.92	32	65	83
	Teat length	0.94	32	64	0.94	31	65	85
	Rear teat placement	0.97	54	44	0.97	45	52	76

DYD-MACE = daughter yield deviations multiple across-country evaluations.

There were two different rankings based on DYD-MACE and Interbull EBV (estimated breeding values).

<sup>†</sup>In the rankings there were also bulls with data in both countries (not shown).

<sup>‡</sup>Estimated across-country genetic correlation among Germany and France.

## Discussion

Binational evaluations from Germany and France were done separately for each type trait with ST-MACE model. Although evaluations were performed using pre-corrected records instead of deregressed proofs, it is not our intention

to try to rigorously compare both methods because often they give the same (or very similar) results, especially on large datasets. Some people have done that in the past, with debatable conclusions (Madsen *et al.*, 2001; Madsen and Mark, 2002; Ducrocq *et al.*, 2003). However, pre-corrected records have some advantages, in particular with

**Table 6** Number of bulls in the top 100 bull rankings for stature and teat length on the German and French scale

Trait	Genetic evaluation	German scale <sup>†</sup>			French scale <sup>†</sup>		
		Bulls with data in Germany	Bulls with data in France	No. of bulls in common with YD-MACE	Bulls with data in Germany	Bulls with data in France	No. of bulls in common with YD-MACE
Stature	Interbull	56	43	80	52	47	76
	DYD-MACE	52	47	80	48	51	77
	YD-MACE	50	49		46	53	
Teat length	Interbull	44	52	83	32	64	82
	DYD-MACE	44	52	80	31	65	85
	YD-MACE	49	46		35	61	

DYD-MACE = daughter yield deviations multiple across-country evaluations; YD-MACE = yield deviations multiple across-country evaluations. There were three different rankings based on Interbull, DYD-MACE and YD-MACE breeding values.

<sup>†</sup>In the rankings there were also bulls with data in both countries (not shown).

the possibility to apply more robust models (see Lassen *et al.* (2007) for convincing arguments about the superiority of such models, not applicable to deregressed proofs) or to extend to animal models based on cow performances. So pre-corrected records here are an improvement and our intention has been to show that implementation is feasible at international level (even though only two countries are considered here), and gives interesting results, most of the time (but not always) quite consistent with Interbull results. The identification of the instances where these results are different from Interbull ones' is the major contribution of this paper, rather than the actual values of the correlations. Some of these results were already presented in the Interbull congress (Tarres *et al.*, 2007b).

#### Changes in genetic correlation over time

Estimated genetic correlations across Germany and France were very consistent with those of Interbull, although none of the datasets are of exactly the same time period as used for Interbull evaluations. For traits introduced more recently in France, increasing genetic correlations over time were observed. Using newer data led to higher genetic correlation estimates between Germany and France. This can be explained because more recent cows are classified in a more unified way, i.e. more homogeneous, than the older ones. De Jong and Harbers (2002) also showed that when there was a redefinition of the scoring system for a type trait, the average correlation with other countries increased by omitting data scored with an earlier definition. Consistency of trait definition across time can be assessed using DYD (Van Pelt *et al.*, 2006). The national genetic evaluations of both countries (especially France) can be improved by removing records of cows scored with an earlier definition rather than by removing bulls born before 1995. It seems to be reasonable to exclude records of cows scored with an earlier definition from the national genetic evaluations and use the resulting DYD of bulls or YD of cows for a ST-MACE model. It would be easily applicable and useful to remove potential bias in DYD of bulls and YD

of cows attributable to simultaneously evaluating records scored with different definition. However, Tsuruta *et al.* (2004) argued that genetic parameters could change over time not only by redefinition of the recording system but also by other factors such as selection, migration, segregation, mutation and inbreeding.

Omitting older data is a way to deal with changes in genetic parameters over time for type traits in international bull comparisons without changing national evaluations. Currently, most national genetic evaluations for type traits in Holsteins are conducted with a multiple-trait model that assumes that additive genetic and environmental variances, and genetic and environmental correlations among traits are constant over time. In the future, countries should consider changes over time in their genetic evaluations. De Jong and Harbers (2002) proposed to treat older and newer scores as different traits in a multiple-trait national evaluation. Tsuruta *et al.* (2004) estimated changes in genetic parameters for productive life, production and selected type traits over time using random regression (RR) models. They compared estimates of variance components and genetic correlations among traits with those estimated with a multiple-trait interval model, which assumed a distinct trait for every 3-year interval. As verified by simulation (Tsuruta *et al.*, 2003), such estimation using RR can be successful but changes in genetic parameters should be gradual over time and residual variances need to be modelled as heterogeneous. Uribe *et al.* (2000) and Tsuruta *et al.* (2002) also performed genetic evaluations of dairy cattle for type traits using RR models, but in this case to take into account age-specific changes (i.e. the trajectory was over the age of cow when classified, rather than over the period of classification).

#### Binational genetic evaluations

Once the genetic correlations were estimated, binational evaluations using DYD of bulls were performed for each type trait. Bulls' rankings differed somewhat from Interbull rankings but a similar proportion of bulls was found from each country in the top lists. Binational evaluations were



extended to animal models based on cow performances (YD) for stature and teat length in order to show that they are feasible. This was very appealing because the more computationally demanding full multi-trait model, i.e. two-country animal model with original performance data, may not be feasible using these large datasets, especially if in the future more countries are added to such evaluation. The cow rankings obtained are influenced by the differences in heritability and the number of cows from each country. In most cases, this favours French cows because type traits had higher heritabilities and bulls' EBVs were often more reliable in France because of a higher number of scored daughters per bull.

Finally, type traits are currently evaluated in both countries in three blocks of traits (udder/feet and legs/other traits). Within each block, a multiple-trait model is used and genetic correlations among traits are considered. The information of other correlated type traits is included using the genetic correlations to the other traits in the same block. In contrast, in the ST-MACE only one trait is evaluated each time. In order to avoid these differences between models for national and international evaluations, an MT-MACE model allowing a variable number of correlated traits per country should be used in the future. In such case, multiple-trait DYD and multiple-trait EDC should be obtained from national genetic evaluations (Liu *et al.*, 2004a).

## Conclusions

The estimated genetic correlations for type traits between Germany and France appear to be reasonably consistent with what is observed by Interbull. This study shows that using data from more homogeneous type classification systems led to higher genetic correlation estimates between Germany and France for type traits. Higher genetic correlations will have a clear impact on re-ranking of sires and top lists for international bull comparison. International cow comparisons are possible if YD of cows are used as input data in MACE models.

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