Parameter Estimation and Genetic Evaluation of Milk Production Traits from France and Germany with a Multi-Trait MACE Model

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Abstract

A multi-trait MACE (MT-MACE) model was implemented for international bull comparison using daughter yield deviations of bulls. This MT-MACE model can better utilise the information derived from national genetic evaluations with a multi-trait model than the current single trait MACE (ST-MACE) model. Full pedigree information of bulls was used via sire and dam relationship. Milk production data from France and Germany were used to validate this MT-MACE model. Pre-conditioned conjugate gradients algorithm was applied to solve the equations together with the iteration on data technique. An approximate REML method specially developed for pre-corrected records was implemented to estimate genetic correlations between the two countries. Estimated genetic correlations of random regression coefficients of the German test day model with French lactation milk yields were high, resulting in genetic correlations, on a 305-day lactation basis, of 0.834, 0.937, 0.960, and 0.947 for first, second, third and combined lactation, respectively. Special test evaluations using zero genetic correlations were compared to the national evaluations for the bulls. Very high proof correlations and small proof differences confirmed the overall quality of the MT-MACE model. However, the MT-MACE model gave proofs different from national proofs for the youngest bulls that have few daughters with short or missing lactations. The use of the data from bull dams did not lead to notable improvement in the international bull evaluations. With the estimated genetic correlations, a MT-MACE genetic evaluation was performed. As expected, local bulls had very high correlations between their national and international proofs, whereas the proof correlations were lower for common bulls due to the data from the other country. The correlations between national and international proofs increased with the number of daughters and with the average lactation length of daughters. Bulls with official national proofs had higher correlations than bulls with unofficial national proofs, and foreign proven bulls had lower correlations between national and international proofs than local bulls. The MT-MACE model can be extended to cow evaluation as well as to other traits.

1. Introduction

International bull evaluation is currently conducted using a ST-MACE model (Schaeffer, 1994). As more and more countries have upgraded their national genetic evaluation systems to multiple trait models, e.g. a random regression test day model (RRTDM) for production traits, a MT-MACE (Schaeffer, 2001; Mark and Sullivan, 2005) model should be applied to international genetic evaluations in order to optimally utilise the information derived from the multi-trait national models. Instead of deregressed proofs, Ducrocq *et al.* (2003) proposed to use daughter yield deviations (DYD) for international bull

evaluation. Liu *et al.* (2004b) developed a MT-MACE model for international bull comparison based on DYD. In the current Interbull evaluations, pedigree information of bulls is traced back by sire, maternal grandsire (MGS) and phantom group of maternal granddam (MGD). In contrast, full pedigree information of bulls with sire and dam relationship was recommended for MACE evaluation (Van der Linde *et al.,* 2005). Milk production data from France and Germany were available for implementing and validating the MT-MACE model (Liu *et al.,* 2004b). The objectives of this study were 1) to develop softwares for both genetic evaluation and parameter estimation for general MT-MACE

applications, and 2) to implement and validate the MT-MACE model using the bi-national data.

2. Materials and Methods

2.1. The MT-MACE model

Two sub-models of the MT-MACE model were considered in this investigation, the first being termed as random regression MACE (RR-MACE) model, and the second as multiple lactation MACE (ML-MACE) model. The two MT-MACE models differed with respect to the analysed data. When DYD was expressed in form of random regression coefficients (RRC), the RR-MACE model was chosen for the analyses. The ML-MACE model was designed for evaluating DYD on 305-day lactation basis.

For a country j using a multi-trait model in national genetic evaluation, the following statistical model was applied to DYD of a bull i from the country j:

$$\mathbf{q}_{ij} = \mathbf{\mu}_j + \mathbf{a}_{ij} + \mathbf{\varepsilon}_{ij} \qquad [1]$$

where $\mathbf{q}_{ij}$ is a vector of DYD of the i-th bull in country j, $\mathbf{\mu}_j$ is a vector of general means for traits of the j-th country, $\mathbf{a}_{ij}$ is a vector of additive genetic effects of bull i in country j, and $\mathbf{\varepsilon}_{ij}$ is a vector of residual effects. Model 1 is also valid for yield deviations (YD) of cows or DYD of bulls data from countries with a single trait model in national genetic evaluation, with all terms above becoming scalar.

2.2. The mixed model equations

The equation system of the MT-MACE model consists of two main components: an effective daughter contribution (EDC) matrix $\mathbf{\Psi}_{ij}$ corresponding to the least squares part of the left-hand-side (LHS) and $\mathbf{\Delta}_{ij}$ corresponding to the right-hand-side (RHS) of the mixed model

equations (MME). The multi-trait effective daughter contribution (MTEDC, Liu *et al.,* 2004a) can be applied to approximate matrix $\mathbf{\Psi}$ for each bull. Following the DYD calculation by Liu *et al.* (2004a):

$$\mathbf{q}_{ij} = \mathbf{B}_{ij}^{-1}\mathbf{\xi}_{ij} \qquad [2]$$

the RHS for the i-th bull in country j in the MACE equation system is computed with:

$$\mathbf{\Delta}_{ij} = \mathbf{\xi}_{ij} - (\mathbf{B}_{ij} - \mathbf{\Psi}_{ij})(\mathbf{B}_{ij} + d_i \mathbf{G}_0^{-1})^{-1}\mathbf{\xi}_{ij} \quad [3]$$

where matrix $\mathbf{B}_{ij}$ and vector $\mathbf{\xi}_{ij}$ are defined for general multiple trait models (Liu *et al.*, 2004a), $\mathbf{G}_0^{-1}$ represents the inverse of genetic (co)variance matrix of Model 1, and d_i is the Mendelian sampling for the bull i (Mrode, 2005).

For RRTDM, $\mathbf{q}_{ij}$ and $\mathbf{\Delta}_{ij}$ are on RRC basis. In order to conduct the evaluation with the ML-MACE model, following conversions need to be performed prior to evaluation:

$$\mathbf{\Psi}_{ij}^L = \mathbf{V}\,\mathbf{\Psi}_{ij}\,\mathbf{V}' \qquad [4]$$
$$\mathbf{\Delta}_{ij}^L = \mathbf{V}\,\mathbf{\Delta}_{ij} \qquad [5]$$

where matrix $\mathbf{V}$ converts the information from RRC to 305-day lactation basis. A 305-day lactation is defined here as a lactation consisting of 10 equally spaced tests with the first on day 15 and one new test every 30 days. Genetic (co)variance matrix of the full lactation is:

$$\mathbf{G}_0^L = \mathbf{V}\,\mathbf{G}_0\,\mathbf{V}' \ . \qquad [6]$$

The equation system was solved using a pre-conditioned conjugate gradient algorithm (PCG) 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.

2.3. Estimation of across country genetic correlations

An approximate REML method was developed by Liu *et al.* (2004b) to estimate across country genetic correlations for general MT-MACE models. National (co)variances were fixed during the estimation of genetic correlations. The trace term of the Expectation Maximization REML algorithm or prediction error (co)variances of Mendelian sampling estimates were approximated with the MTEDC (Liu *et al.,* 2004a) method. It was considered as converged when the change in the across country genetic correlation estimates was less than 0.001 between two consecutive rounds of iteration in the parameter estimation.

2.4. Data materials

Data from November 2005 French and February 2006 German national genetic evaluations were chosen for implementing and validating the MT-MACE model.

2.4.1. Preparing the data from Germany

A total of 9 RRC, 3 Legendre polynomial coefficients for each of the first three lactations, were needed for each bull or dam of bull for the RR-MACE model. Corresponding to the set of RRC for a given bull, the LHS Ψ and RHS Δ obtained from Formula 3 were required. In order to mimic the Interbull evaluation, only bulls included in Interbull 010 files were selected. Original identifications of these bulls were cross-referenced using the current Interbull cross-reference files. There were 14887 Black and White Holstein bulls with DYD available from Germany (Table 1).

2.4.2 Inclusion of the data from bull dams

In order to make the international bull evaluation more close to the national cow evaluation, YD and associated EDC were calculated for the dams of bulls that had been selected previously. To avoid double counting the contribution of the bull dams in the MT-MACE evaluation, the data of the dams were excluded from the calculation of DYD and corresponding EDC of their sires. A total of

3860 dams were identified to be associated with the selected bulls in the German data set.

2.4.3. Preparing the data from France

There were 17813 bulls contained in the French 010 file (Table 1). It consisted of one proof, one DYD and one EDC per bull. First, we converted the national proofs and DYD to a daily basis by dividing 305. Then, we multiplied DYDs by 2 to convert them to an animal basis. The least squares part of LHS of the equation system was the national EDC, and its RHS was obtained as the EDC multiplied by the DYD. The EDC and RHS were then divided by the error variance of the French lactation model.

2.4.4. Pedigree preparation

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. 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. Small phantom groups were merged automatically given the predefined minimum number of animals per group. The following rules were applied to combine or merge small groups: selection paths are merged based on the sex of parent (son to sire with daughter to sire, and son to dam with daughter to dam), countries are merged accordingly (North America, West Europe, and the rest), minor breeds are combined for Holstein breed. Birth years were finally merged according to the minimum group size.

2.5. Selecting data for parameter estimation

For parameter estimation, we created a new data set containing only the common bulls and their three-quarter sibs. After discarding bulls having fewer than 50 daughters with first lactation over 120 DIM or fewer than 10 daughters with second and third lactation over 120 DIM, the first data set contained 4555 bulls. We also generated another data set containing bulls with more than 150, 20 and 20

daughters in first, second and third lactations. This second data set included 6685 bulls with data. After combining the two data sets, there were 9545 bulls left, 683 of them having data in both countries in the final data set for parameter estimation. No selection was imposed on dams of the bulls with respect to the number of tests by lactation for the test runs where the data of bull dams were included. Table 2 shows the data and pedigree structures for various cases of parameter estimation.

Table 1. Data and pedigree information for Holstein MACE evaluations.

	No. of bulls / animals with data in Germany	No. of bulls with data in France	No. of common bulls	Total no. of bulls / animals with data	No. of animals in pedigree	No. of phantom groups
Without the data of bull dams	14487	17813	939	31361	67541	32
With the data of bull dams	17740	17813	914	34639	67298	32

Table 2. Data and pedigree information for parameter estimation.

	No. of bulls / animals with data in Germany	No. of bulls with data in France	No. of common bulls	Total no. of bulls / animals with data	No. of animals in pedigree	No. of phantom groups
Without the data of bull dams	5168	5060	683	9545	25737	20
With the data of bull dams	6188	5060	682	10566	25738	20

3. Results

3.1. Validation using the data from national cow evaluations

The validation of the MT-MACE model was performed by comparing national proofs derived from a RRTDM cow evaluation in Germany or a repeatability lactation model from France with the proofs from the MT-MACE evaluation by setting the genetic correlations between the two countries to 0. In this situation we would expect to obtain exactly the same proofs for the involved animals as in national evaluations under the assumption that the bull evaluation with zero genetic correlations between countries is equivalent to the national cow evaluation.

Proof correlations between national and international proofs were above 0.99. No systematic trends or biases can be identified by studying the average proof differences over years. However, significant proof differences were present for the youngest bulls particularly in the German data set. This indicated possible problem with the smaller number of daughters and short lactations of daughters.

In addition to the above test runs with RR-MACE model, similar validation runs were conducted under the ML-MACE model. In general, the results were very similar between the two sub-models of MT-MACE model. But the RR-MACE model resulted in clearly more accurate international proofs than ML-MACE model for the youngest bulls with respect to the proof correlation, proof difference and top lists. The better performance of the RR-MACE model than the ML-MACE model can be traced back to the issue of short lactations. Converting RRC to 305-day lactation DYD for short lactations prior to genetic evaluation can cause bias, depending on lactation persistence.

In order to study the impact of the data from bull dams, test runs were performed by including the data of bull dams. Compared to the results from the test evaluations without the data from bull dams in terms of proof correlations, proof differences, and top lists, it can be concluded that the inclusion of data from bull dams makes little difference for international bull evaluations under the MT-MACE model. Including the data from bull dams in international bull comparison gave slightly worse international proofs for the youngest bulls than the regular MT-MACE model without the data of bull dams.

3.2. Parameter estimation

Parameter estimation for the RR-MACE model was conducted with the approximate REML method. National (co)variances were fixed during the estimation of across country genetic correlations. Table 3 shows genetic correlation estimates of milk yield between Germany and France for the two MT-MACE models. The estimated correlations of RRC imply a genetic correlation, on 305-day lactation basis, of 0.820 for first lactation, 0.860 for later ones, respectively. Genetic correlation estimate between combined lactation from Germany and lactation yield from France is 0.881. The negative genetic correlations between third coefficients and French lactation yield suggest that high-yielding animals tend to have the genetic lactation curves with higher breeding values (BV) in the middle of lactation than at the end. The negative correlation has been also observed in the German RRTDM (Liu *et al.,* 2004a).

Because 305-day lactation BV is independent of the second coefficient of Legendre polynomials, there is indeed no information available in the data to estimate the genetic correlation between the second coefficient and 305-day lactation yield of France. This means that the genetic correlation estimates of the second RRC in Table 3a have

large standard errors. In order to avoid this problem with the second coefficients, the iteration procedure of the approximate REML was modified in such a way that newly estimated genetic correlations of the second coefficients were ignored and they were fixed at 0.271, 0.102 and 0.104 for the first, second and third lactation, respectively, which had been obtained from an analysis using Calo method. By fixing the second RRC, similar trends in correlation estimates were observed as in the case without fixing. First RRC had the highest correlation, and the third RRC was negatively correlated with French lactation yield. Compared to the case of no fixing, higher genetic correlation estimates were obtained. As expected, the French lactation yield on mature equivalent scale has the highest correction with third lactation of Germany, and the lowest correlation with the first lactation of Germany. The genetic correlation between German combined lactation and French lactation reaches 0.947.

Parameter estimation was also performed with the ML-MACE model, where 305-day lactation DYD are analysed instead of RRC. Estimated genetic correlations between German and French lactation yields are again higher: 0.872 for first lactation, 0.946 for second lactation and 0.964 for the third lactation, resulting in genetic correlation of 0.951 for combined lactation. These genetic correlation estimates are close to the estimates from the case of fixing second RRCs under the RR-MACE model.

3.3. Genetic evaluation

Two-country genetic evaluations were conducted using the correlation estimates of the RR-MACE model with the fixing of the correlations with the second RRC. Tables 4, 5, and 6 show proof correlations with the two national evaluations for local and common bulls.

Table 3. Genetic correlations of milk yields between Germany and France estimated using the approximate REML method.

3a) Genetic correlation estimates of the RR-MACE model.

	Lactation			Lactation§		
	1	2	3	1	2	3
First RRC	.846	.896	.894	.844	.947	.969
Second RRC	.588	.488	.485	.271	.102	.104
Third RRC	-.444	-.419	-.405	-.370	-.325	-.317
Lactation	.820	.860	.860	.834	.937	.960
Combined lactation		.881			.947	

§ The genetic correlations of second RRC were fixed.

3b) Genetic correlation estimates of the ML-MACE model.

	Lactation 1	Lactation 2	Lactation 3
Lactation	.872	.946	.964
Combined lactation		.951	

3.3.1. Local bulls

Overall, national and international lactation proofs were highly correlated with correlations around 0.99. For local bulls that had at least 10 daughters with lactation over 120 DIM in Germany, proof correlations were 0.993, 0.989 and 0.988 for the first, second and third lactation and 0.992 for the combined lactation. Within the birth year of bulls, the correlations between national and international proofs were over 0.995 for old local bulls and these proof correlations dropped for the last years in each lactation (Table 4a). Table 5a shows the increase in proof correlations as bulls had more daughters. For bulls with more than 300 daughters, correlations of lactation proofs were 0.998, 0.998 and 0.998 for the first, second and third lactation and 0.997 for the combined lactation. The proofs correlations also increased with the average number of test day records of daughters (Table 6a). With regard to the type of proof (Table 7), bulls with first and second crop daughters had the highest proof correlation (0.995), and proof correlation was lower for bulls with only first crop daughters and imported proven bulls. Also the correlations of official proofs were higher than unofficial proofs (Table 8).

For the French proofs, the correlations with international proofs were 0.998. The proof correlations were also a little bit lower for the youngest bulls. The correlations of proofs increased with the number of daughters. The proof correlation was 1 for bulls with

more than 300 daughters. Regarding the type of proof, the correlations of proofs were close to 1 except for the imported bull (Table 7). Again, unofficial proofs were less correlated than official proofs (Table 8).

3.3.2. Common bulls

As expected, common bulls with data in both countries had lower correlations between national and international proofs than local bulls. The lower proof correlations are expected due to the contribution of data from the other country in the joint evaluation, this is more evident especially for young bulls with few daughters (Table 5b). These lower correlations are not observed for common bulls with many daughters in both countries. In the same way as for the local bulls, proof correlations of common bulls increased with number of daughters and average lactation length of daughters. With regard to the type and officiality of proofs, most differences in proofs are seen for unofficial bulls and the youngest bulls with only first crop daughters.

4. Discussion

Two sub-models of the MT-MACE (Liu *et al.*, 2004b) were implemented for the joint evaluation of German and French production traits. Both models can better utilise the information derived from the RRTDM in German national genetic evaluation than the

ST-MACE model. Based on the conducted validation study, the RR-MACE gave more accurate proofs than the ML-MACE model, in particular for the youngest bulls having daughters with short or missing lactations, because the ML-MACE model cannot account for the difference in lactation persistency between animals. If computing requirement of the RR-MACE is a limiting factor for international genetic evaluation involving all dairy populations, then the ML-MACE model would be a reasonable compromise between feasibility and accuracy. The current software can be readily extended to include a fixed time effect (Ducrocq *et al.,* 2003) to evaluate multiple DYD per bull and integrate genetic trend validation into MACE evaluation.

Full pedigree information with sire and dam relationship is an important improvement over the pedigree information by sire, MGS and MGD groups used in current Interbull evaluation (Van der Linde *et al.,* 2005). The use of complete pedigree avoids the problem of MGD grouping and reduces the influence of imperfect grouping of MGD. It was identified in this study that parents of MGD of bulls with national proofs were usually missing in current Interbull pedigree file. The incompleteness of pedigree information on dam side can be resolved by routinely updating pedigree for female animals on international level.

The performance data of bull dams were evaluated jointly with DYD of bulls. This study shows that the use of the data of bull dams does not make the international evaluations more accurate with regard to proof correlations and biases. However, the estimated genetic correlations were slightly higher than in the cases of MT-MACE evaluations without the data of bull dams.

The approximate REML method developed for parameter estimation using DYD or YD avoids the inversion of the complete coefficient matrix of MME and approximates the inverse matrix via the MTEDC procedure (Liu *et al.,* 2004a). The proposed REML method takes advantage of the fact, that country specific components of the MACE equations are independent of across country genetic evaluation due to the fixing of the national parameters, to reduce computation load and thus increases the efficiency of the parameter estimation in comparison to regular, exact REML implementations. The accuracy of the approximate REML needs to be validated with simulated data or with other softwares. A main advantage of the approximate REML method is that large data set can be analysed, thus the need of country sub-setting currently practiced by Interbull can be reduced. The factorial analysis approach developed by Leclerc *et al.* (2005) to reduce the number of estimated parameters can be extended to the MT-MACE model. In fact, such approach is even more important for the MT-MACE model with many more parameters than ST-MACE model.

Several validation studies were conducted assuming zero genetic correlations between Germany and France, and the resulting proofs were compared to the respective national proofs that originated from cow evaluations, e.g. based on a RRTDM in Germany. Overall, the two sets of proofs were very highly correlated and no systematic trends were observed, despite the differences between the national cow evaluations and the international bull evaluations, e.g. differences in completeness of the pedigree files, phantom parent grouping, exclusion or inclusion of daughter data of natural service bulls, EDC approximation, etc. However, for the youngest bulls with fewer daughters with short or missing lactations, differences in proofs between national cow evaluation and the international bull evaluation with zero genetic correlation are evident, and the bias is more significant for the multi-trait national model of Germany than the single trait model of France. This bias did not appear in the simulation study by Liu *et al.* (2004a), where a half-sib family structure was simulated. Further investigations are needed to find solution to the problem possibly caused by short and missing lactations of daughters or non-zero trends in the selection path cow to dam.

Table 4. Correlation of international with national lactation proofs of Holstein bulls[¶] by birth year for milk yield.

4a) Local bulls

| Birth year | Germany | | | | | | | | France | |
| | Lactation 1 | | Lactation 2 | | Lactation 3 | | Combined | | | |
	No. of bulls	r	No. of bulls	r	No. of bulls	r	No. of bulls	r	No. of bulls	r
ξ	170	.989	1282	.979	2585	.984	170	.983		
1985	1561	.990	1522	.986	1479	.987	1561	.989	7182	.996
1986	454	.997	453	.990	446	.990	454	.994	567	.997
1987	417	.997	415	.991	409	.992	417	.994	653	.997
1988	477	.997	474	.991	468	.991	477	.994	616	.997
1989	547	.996	544	.988	540	.989	547	.994	629	.996
1990	640	.998	637	.990	632	.992	640	.995	761	.996
1991	653	.997	650	.988	644	.988	653	.993	666	.997
1992	720	.997	719	.990	712	.991	720	.995	658	.996
1993	791	.997	787	.989	778	.991	791	.994	483	.994
1994	927	.997	919	.991	899	.992	927	.994	637	.996
1995	1022	.996	1014	.992	990	.990	1022	.994	669	.996
1996	1077	.995	1058	.989	1045	.989	1077	.993	742	.996
1997	1108	.994	1094	.988	1081	.987	1108	.992	647	.998
1998	976	.995	969	.988	776	.989	976	.993	654	.998
1999	930	.994	857	.986	64	.984	930	.991	661	.995
2000	867	.985	154	.989			867	.991	594	.982
2001	211	.992					211	.985	55	.958
Overall	13548	.993	13548	.989	13548	.988	13548	.992	16874	.998

4b) Common bulls

| Birth year | Germany | | | | | | | | France | |
| | Lactation 1 | | Lactation 2 | | Lactation 3 | | Combined | | | |
	No. of bulls	r	No. of bulls	r	No. of bulls	r	No. of bulls	r	No. of bulls	r
§			49	.903	118	.893				
1985	347	.966	339	.962	328	.954	347	.960	346	.983
1986	48	.962	48	.948	47	.933	48	.946	49	.980
1987	27	.846	27	.896	27	.875	27	.874	27	.994
1988	39	.985	38	.957	38	.926	39	.967	39	.993
1989	38	.977	38	.958	36	.956	38	.967	38	.981
1990	61	.946	60	.890	59	.848	61	.890	61	.991
1991	76	.981	75	.968	72	.953	76	.970	76	.990
1992	75	.977	75	.939	71	.916	75	.950	75	.984
1993	83	.965	81	.933	76	.910	83	.935	83	.975
1994	62	.963	57	.947	41	.946	62	.940	62	.982
1995	48	.973	41	.951	18	.907	48	.933	48	.969
1996	30	.922	9	.927	6	.640	30	.812	30	.975
1997	5	.987					5	.981	5	.876
Overall	939	.977	939	.963	939	.947	939	.966	939	.989

[¶] Bulls had at least 10 daughters with lactation passed 120 DIM in the German national evaluation.
§ Bulls did not fulfil the above selection criterion.

Table 5. Correlation of international with national lactation proofs of Holstein bulls[¶] by number of daughters for milk yield.

5a) Local bulls

| No. of daughters | Germany | | | | | | | | France | |
| | Lactation 1 | | Lactation 2 | | Lactation 3 | | Combined | | | |
	No. of bulls	r	No. of bulls	r	No. of bulls	r	No. of bulls	r	No. of bulls	r
ξ	170	.989	1282	.979	2585	.984	170	.982		
10-19	252	.981	258	.983	350	.986	252	.981	339	.983
20-29	223	.992	243	.989	742	.991	223	.991	324	.991
30-39	179	.993	392	.991	1396	.991	179	.994	290	.995
40-49	202	.990	709	.990	1760	.992	202	.993	470	.997
50-59	301	.991	1173	.991	1531	.993	301	.993	785	.998
60-69	525	.991	1527	.992	1131	.994	525	.994	1562	.998
70-79	828	.992	1490	.993	784	.994	828	.994	2489	.998
80-89	1144	.994	1209	.994	490	.995	1144	.993	2792	.998
90-99	1324	.995	901	.995	390	.996	1324	.994	2168	.999
100-199	5976	.997	2629	.996	1067	.995	5976	.995	3718	.999
200-299	736	.999	357	.997	296	.996	736	.997	302	.999
>300	1682	.998	1377	.998	1025	.998	1682	.997	1653	1.000

5b) Common bulls

| No. of daughters | Germany | | | | | | | | France | |
| | Lactation 1 | | Lactation 2 | | Lactation 3 | | Combined | | | |
	No. of bulls	r	No. of bulls	r	No. of bulls	r	No. of bulls	r	No. of bulls	r
ξ			49	.903	118	.893				
10-19	46	.900	43	.909	52	.877	46	.894	51	.958
20-29	35	.949	39	.921	43	.896	35	.935	67	.968
30-39	31	.934	39	.899	57	.919	31	.918	38	.978
40-49	29	.967	44	.937	64	.927	29	.934	31	.989
50-59	31	.949	39	.947	35	.893	31	.927	32	.986
60-69	33	.975	37	.949	22	.938	33	.940	31	.987
70-79	35	.978	36	.959	29	.966	35	.958	47	.989
80-89	25	.980	22	.964	27	.925	25	.980	51	.994
90-99	23	.988	23	.974	19	.913	23	.967	31	.992
100-199	147	.984	140	.971	122	.966	147	.963	118	.996
200-299	86	.988	67	.985	62	.974	86	.977	43	.998
>300	418	.996	360	.994	289	.991	418	.992	399	.999

[¶] Bulls had at least 10 daughters with lactation passed 120 DIM in the German national evaluation.
§ Bulls did not fulfil the above selection criterion.

Table 6. Correlation of German international with national lactation proofs of Holstein bulls[¶] by average number of test day records of daughters for milk yield.

6a) Local bulls

No. of tests	Lactation 1		Lactation 2		Lactation 3		Combined lactation	
	No. of bulls	r	No. of bulls	r	No. of bulls	r	No. of bulls	r
ξ	170	.989	1282	.979	2585	.984	170	.982
2	74	.994	23	.987	4	.982	74	.987
3	170	.993	154	.986	106	.985	170	.985
4	157	.995	202	.984	224	.988	157	.990
5	186	.993	218	.981	281	.987	186	.988
6	295	.996	337	.986	495	.990	295	.994
7	1037	.996	1155	.991	2116	.992	1037	.992
8	9293	.998	8185	.992	6412	.993	9293	.994
9	2138	.997	1958	.991	1300	.992	2138	.994
10	28	.995	34	.985	25	.978	28	.996

6b) Common bulls

No. of tests	Lactation 1		Lactation 2		Lactation 3		Combined lactation	
	No. of bulls	r	No. of bulls	r	No. of bulls	r	No. of bulls	r
ξ			49	.903	118	.893		
2					3	.996		
3	4	.928	4	.987	14	.937	4	.619
4	5	.958	14	.943	19	.973	5	.896
5	16	.974	16	.945	41	.964	16	.896
6	28	.965	23	.931	130	.912	28	.920
7	78	.971	90	.964	464	.959	78	.950
8	585	.980	504	.969	150	.936	585	.970
9	218	.978	237	.965			218	.969
10	4	.968					4	.896

[¶] Bulls had at least 10 daughters with lactation passed 120 DIM in the German national evaluation.
§ Bulls did not fulfil the above selection criterion.

Although the deregression approach (Schaeffer, 2001) is considered to be less convenient than the DYD related approaches (Ducrocq *et al.,* 2003, Liu *et al.,* 2004b), the MT-MACE software can integrate the deregression step directly, because only the LHS and RHS of the MACE equation system need to be obtained from the deregression process. The current MT-MACE model can be extended to international cow evaluations. Because of the very high flexibility of the MT-MACE software, an application to cow evaluation does not require modification of source codes, which was demonstrated by the inclusion of the data of bull dams into the bull evaluation. However, it will be a challenging task to set up a reasonably complete and accurate international cow pedigree file. Reliabilities of MACE proofs can be approximated with the MTEDC method (Liu *et al.,* 2004a).

This study shows that with more appropriate methodology, i.e. applying the MT-MACE model to the DYD data derived from diverse national genetic evaluation models, higher genetic correlations can be obtained. Higher genetic correlations will have a clear impact on reranking of sires, top lists, etc. In summary, the overall quality of the MT-MACE model was verified using the data from the two countries. The estimated genetic corre-

Table 7. Correlation of international with national proofs of Holstein bulls by Interbull type of proof for milk yield.

Type of proof	German combined lactation proofs				French proofs			
	Local bulls		Common bulls		Local bulls		Common bulls	
	No. of bulls	r	No. of bulls	r	No. of bulls	r	No. of bulls	r
00					125	.990		
11	8755	.992	69	.899	14084	.998	130	.990
12	4222	.995	204	.972	1831	1	116	1
21	571	.989	666	.965	834	.991	693	.988

Table 8. Correlation of international with national lactation proofs of Holstein bulls with regard to the official status of proofs for milk yield.

Proof status	German combined lactation proofs				French proofs			
	Local bulls		Common bulls		Local bulls		Common bulls	
	No. of bulls	r	No. of bulls	r	No. of bulls	r	No. of bulls	r
Unofficial	571	.991	80	.910	1382	.991	693	.988
Co-tested	112	.992			11	.995	1	
Official	12865	.993	859	.974	15481	.999	245	.995

lations between France and Germany seem to be reasonable. Further studies are needed to finetune the MT-MACE model and the approximate REML method.

5. Acknowledgements

6. References

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