Multi-Country Evaluation to Study the Impact of Genotype by Model Interaction

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Introduction

The aim of the PROTEJE project is to develop an international genetic evaluation system for bulls and cows (Canavesi *et al.,* 2001). The participating countries with data are France (FRA), Germany (DEU), Italy (ITA) and the Netherlands (NLD). Data available are projected or realised 305-day yields for milk production traits, precorrected for national precorrections (raw data), yield deviations precorrected for national precorrections, national fixed effects and heterogeneity of variance (precorrected data) and pedigree data.

Aim of the NRS participation in the project is to determine to what extent genotype by environment interaction is caused by genotype by model interaction. Considerations for the aim of the project are:

1. Current genetic correlations estimated by Interbull may include genotype by model interaction besides genotype by environment interaction, due to different modelling of fixed and random effects.

2. Genotype by model interaction is unwanted because it causes unnecessary reranking of animals across countries.

3. Differences in genetic correlations across countries using raw or precorrected data quantify the effect of national fixed effects on genetic correlations. National fixed effects may better remove non-genetic effects, however, it may also cause genotype by model interaction.

Material and Methods

National genetic evaluation models and data

The French data included first three parity records of all Holstein cows having calved between 1988 and 1998. Raw data were precorrected for heterosis and recombination and for parity to mature equivalent, but not precorrected for age at calving. Precorrected data included the precorrections of the raw data and adjustment for fixed effects herd-year, parity-region-year, calving month-parity-region-year, age at calving-parity-region-year, length of proceeding dry period-parity-region-year and for heterogeneity of variance due to herd and year of calving. The heritability is 0.30 and repeatability is 0.50. The Italian data included first three parity records of all Holstein cows having calved between 1988 and 1998. Raw data were precorrected for age at calving to mature equivalent and month of calving-parity, days open and heterogeneity of variance (genetic adjustment). Precorrected data included the precorrections of the raw data and adjustment for herd-year-season-parity. The heritability is 0.30 and repeatability is 0.50. The Dutch data included first three parity records of all Black and White cows having at least 75% Holstein genes with calving year between 1990 and 1998. Raw data were precorrected for age at calving, days open, heterosis and recombination. Precorrected data included the precorrections of the raw data and adjustment for heterogeneity of variance due to herd-year of calving and for herd-year-season-parity and month-year of calving. The heritability is 0.35 and repeatability is 0.55. The German data could not be used in this study because 305-day yields (raw data) were not available.

Data edits

Minimum requirements for inclusion of the data were a lactation length of 60 days, age at first calving of 640 days, known sire and a calving interval of 215 days. For cows with less than 5 herdmates with the same parity, consecutive herd-year-season-parity classes were combined within calving year. Second and third parity herdmates were combined in herd-year-season classes. Data characteristics are shown in Table 1.

Genetic evaluation models

Genetic evaluations were carried out using either national fixed and random effects or general fixed and random effects. With general is meant a model that included the most commonly used fixed and random effects of the national genetic evaluation models of the participating countries. The general model was an animal model including fixed effects for age at calving, month and year of calving and herd-year-season-parity (first vs. higher), random effects for permanent environment and the additive genetic effect and correction for heterogeneity of variance due to herd and year of calving and age at calving. The heritability in the general model was 0.30 and the repeatability is 0.50. Evaluations with national fixed effects used data precorrected for the national fixed effects and only the mean plus the random effects in the model. Four analyses per country were carried out (Table 2), one evaluation with national fixed and random effects (analysis 1), one evaluation with national fixed and general random effects (analysis 2), one evaluation with general fixed effects and national random effects (analysis 3) and one evaluation with general fixed and random effects (analysis 4). The evaluation model of analysis 1 and 2 only included random effects for permanent environment and additive genetic effect. For analysis 3 and 4 the general model for fixed effects was applied. The model for correction for heterogeneity of variance included herd-year of calving and age at calving with an autocorrelation of 0.95 between different herd-years of calving and a herd-year variance of 10% of the error variance. The heritability and repeatability were 0.30 and 0.50 respectively for France and Italy in all analyses and for the Netherlands in analyses 2 and 4 and 0.35 and 0.55 respectively for the Netherlands in analysis 1 and 3.

Estimation of genetic correlations

The possible existence of genotype by model interaction was analysed by comparing genetic correlations between countries for milk, fat and protein within analysis. Genetic correlations of analysis 1 were compared to genetic correlations used for the Interbull evaluation of August 1998, because only lactations before 1998 were available. Genetic correlations were estimated for milk, fat and protein using an EM algorithm for Restricted Maximum Likelihood (Klei and Weigel, 1998), including all bulls having 10 daughters in 10 herds and 10 effective daughter contributions (EDC).

Validation methods

To test whether the fit of the general model was as good as the national model, Interbull test 2 was applied to validate the non-genetic time trend over the entire period considered in the national evaluation (Boichard *et al.*, 1995). Results were also validated by estimating correlations between DYD per year of calving, to investigate the goodness of fit of the data to the evaluation models of the different analyses.

Table 1. Number of cows with lactations, herds, bulls with daughters with lactations, lactations per HYS-class.

Country	France	Italy	The Netherlands
Number of lactations	10,869,832	3,530,755	3,222,377
Number of cows with lactations	5,347,985	1,836,228	1,616,359
Number of pedigrees	7,304,452	2,341,613	3,036,160
Number of herds	71,183	16,234	24,851
Number of bulls with daughters with lactations	46,870	33,093	21,473
Number of lactations per HYS-class	6.76	9.20	6.77

Table 2. Analyses carried out with data from the Netherlands (NLD), France (FRA) and Italy (ITA). Every analysis will be carried out per country separately. GEN means general fixed or random effects.

Country	fixed effects			random effects		
	NLD	ITA	FRA	NLD	ITA	FRA
Analysis 1	NLD	ITA	FRA	NLD	ITA[1]	FRA[1]
Analysis 2	NLD	ITA	FRA	GEN	GEN[1]	GEN[1]
Analysis 3	GEN	GEN	GEN	NLD	ITA[1]	FRA[1]
Analysis 4	GEN	GEN	GEN	GEN	GEN[1]	GEN[1]

[1] Analysis 1 and 2 and analysis 3 and 4 are the same for France and Italy

These correlations were calculated between two years with at least 50 bulls with at least 50 DYD in both years and were weighted for the number of bulls. Rank correlations between breeding values of bulls within country between analyses were calculated to investigate reranking of bulls.

Results and Discussion

Estimated genetic correlations between France, Italy and the Netherlands for all four analyses and genetic correlations estimated by Interbull are in Table 3. Differences in genetic correlations between the four analyses are very small (absolute maximum 0.01). Differences between the genetic correlations estimated by Interbull minus analysis 1 are –0.02 to 0.03. Although the differences are small, an explanation might be the influence of other countries (e.g. USA and Canada) on mutual genetic correlations of countries in this study.

Results from Interbull test 2 are in Table 4. The regression factor of DYD on year of calving of daughters has to be less than 1% of the genetic standard deviation. The genetic standard deviation was calculated as two times

the sire standard deviation estimated by MACE. Regression factors for the Netherlands for all traits of analysis 1 and 2 (national fixed effects) and for Italy for fat and protein (analysis 1 and 2) were below 1%, all other traits of all analyses were above 1%. All countries in this study provided data from less calving years as included in their national genetic evaluation. These data differences might cause a different genetic trend estimation and a worse fit of the model to data in this project and therefore regression factors deviating more from zero. According to the genetic correlations of the different analyses, no genotype by model interaction was found. But a worse fit of the model might have a negative influence on the genetic correlations and therefore undo possible genotype by model interaction. The average correlations between DYD in different years of calving are in Table 5. The average correlations between DYD for Italy and the Netherlands were comparable for all analyses. Although the models with general fixed effects (analyses 3 and 4) did estimate the genetic trend less well, the correlations between DYD were not lower compared to the models with national fixed effects.

Table 3. Estimated genetic correlations between countries for milk, fat and protein by Interbull (ITB) and for analysis 1 to 4 (A1 to A4), difference between A1 and A3 (A 1-3) and A2 and A4 (A 2-4), and ITB and A1 (ITB-A1).

Countries	Trait	A1	A2	A3	A4	A 1-3	A 2-4	ITB	ITB-A1
FRA – ITA	Milk	0.96	0.96	0.97	0.97	0.00	0.00	0.96	0.00
FRA - ITA	Fat	0.96	0.96	0.96	0.96	0.00	0.01	0.93	0.03
FRA - ITA	Protein	0.96	0.96	0.96	0.96	0.00	0.00	0.93	0.03
FRA - NLD	Milk	0.93	0.93	0.94	0.94	-0.01	-0.01	0.95	-0.02
FRA – NLD	Fat	0.93	0.94	0.93	0.94	0.00	0.00	0.92	0.01
FRA – NLD	Protein	0.91	0.91	0.91	0.92	0.00	-0.01	0.91	0.00
ITA - NLD	Milk	0.95	0.95	0.95	0.95	0.00	0.00	0.95	0.00
ITA – NLD	Fat	0.93	0.93	0.92	0.92	0.01	0.01	0.93	-0.01
ITA – NLD	Protein	0.94	0.94	0.94	0.94	0.00	0.00	0.91	0.03

Table 4. Results of Interbull test 2 for milk, fat and protein for France, Italy and the Netherlands for analysis 1 to 4.

Country	Trait	Regression factor			
		Analysis 1	Analysis 2	Analysis 3	Analysis 4
France	Milk	3.1%	3.1%	2.4%	2.4%
France	Fat	2.9%	2.9%	2.4%	2.4%
France	Protein	3.9%	3.9%	2.7%	2.7%
Italy	Milk	1.1%	1.1%	1.2%	1.2%
Italy	Fat	0.8%	0.8%	1.0%	1.0%
Italy	Protein	0.9%	0.9%	1.3%	1.3%
The Netherlands	Milk	0.7%	0.7%	1.8%	1.5%
The Netherlands	Fat	0.8%	0.9%	2.0%	1.6%
The Netherlands	Protein	0.3%	0.3%	1.9%	1.5%

Table 5. Average correlation between DYD in different years of calving for analyses 1 to 4 for France, Italy and the Netherlands.

Country	Analysis	Number of DYD	Milk	Fat	Protein
FRA	1 and 2	20500	0.85	0.82	0.81
	3 and 4	20500	0.91	0.90	0.90
ITA	1 and 2	14914	0.92	0.92	0.92
	3 and 4	14914	0.92	0.92	0.92
NLD	1	8020	0.93	0.91	0.91
	2	8020	0.93	0.91	0.91
	3	8020	0.93	0.92	0.92
	4	8020	0.93	0.91	0.92

Table 6. Rank correlations between breeding values of bulls between the four analyses for France, Italy and the Netherlands.

Country	Analysis	Number of bulls	Milk	Fat	Protein
FRA	1 and 2 - 3 and 4	9417	0.985	0.976	0.983
ITA	1 and 2 - 3 and 4	3959	0.997	0.995	0.997
NLD	1 - 2	3541	0.999	0.999	0.999
NLD	1 - 3	3541	0.995	0.992	0.992
NLD	1 - 4	3541	0.996	0.992	0.993
NLD	2 - 3	3541	0.995	0.991	0.992
NLD	2 - 4	3541	0.996	0.992	0.993
NLD	3 - 4	3541	0.999	0.999	0.999

This indicates that for Italy and the Netherlands differences between the models with either general or national fixed effects are mainly due to different estimation of the genetic trend. Main difference between both models was the correction for heterogeneity of variance due to age at calving in the model with general fixed effects. But more research is needed to investigate if this correction caused a different estimation of the genetic trend. Average genetic correlations between DYD for milk, fat and protein for France for analyses 1 and 2 were 0.06 (milk) to 0.09 (protein) lower compared to analyses 3 and 4. It would have been expected that correlations between DYD were higher for analyses 1 and 2 compared to

analyses 3 and 4, because the precorrected data of analyses 1 and 2 should better describe the French conditions.

Rank correlations between breeding values of bulls between analyses are in Table 6. For Italy and the Netherlands, rank correlations between all analyses were above 0.99. This means that there was hardly any reranking of bulls between analyses. The rank correlations for France were between 0.976 and 0.985, giving some reranking of bulls when using different genetic evaluation models.

Conclusions

There is no evidence found for the existence of genotype by model interaction but it can not be excluded that a worse fit of the general model might have influenced the genetic correlations between countries negatively.

Application of another general model might improve the estimation of the genetic trend and therefore make clear possible genotype by model interaction.

References

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