

Feasibility of International Genetic Evaluation for Calving Ease and Stillbirth in Holstein

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Introduction

International EBV for milk production and type traits are important criteria for the selection of sires by dairy farmers. However, functional traits become much more important for sire selection. The results of the study leading to international genetic evaluations for udder health showed that MACE is feasible for traits having lower heritabilities. Beside this, there are still important functional traits for which there is no international genetic evaluation yet. Especially the demand for international evaluations for longevity and calving traits is high. VIT and NRS jointly investigated

the feasibility of international evaluations for these traits. The part of calving traits includes a comparison of evaluation systems for calving ease (CE) and stillbirth (SB) and a comparison of EBV for Holstein.

Data and evaluation systems of contributing countries

Nine countries have sent EBV for calving traits (see Table 1 for number of records). Only proofs with evaluation breed HOL and bull breed HOL were included in the evaluation.

Table 1. Number of records delivered and used for parameter estimation per country (DCE=direct calving ease, MCE=maternal calving ease, DSB=direct stillbirth, MSB=maternal stillbirth).

Country	No. Records Delivered	No. Records for DCE-parameter	No. Records for MCE-parameter	No. Records for DSB-parameter	No. Records for MSB-parameter
CAN	7790	4142	3507	-	-
DEU	22233	4704	4931	4704	4931
DNK	6347	3137	3404	3137	3404
FIN	1802	56	51	42	49
FRA	7136	2738	4765	-	-
ISR	708	27	33	27	33
SWE	3829	1293	1207	1293	1207
NLD	8955	2852	2774	1814	2905
NZL	5611	1047	-	-	-

FRA and NZL have few proofs of bulls born before 1989, which might be caused by the recent start of data collection and genetic evaluation. FIN and ISR have only few bull proofs.

The number of common bulls (sire of calf) and the number of common “sire x maternal grand sire (mgs)” families for DCE shown in Table 2 are also representative for MCE, DSB and MSB.

Table 2. Number of common bulls (above diagonal) and number of common “sire x mgs” combinations (below diagonal) in participating countries for DCE.

	CAN	DEU	DNK	FIN	FRA	ISR	SWE	NLD	NZL
CAN	-	477	138	7	80	7	255	23	245
DEU	842	-	182	17	140	13	311	201	237
DNK	450	740	-	9	15	5	175	26	79
FIN	16	21	20	-	8	1	20	7	13
FRA	328	620	275	24	-	1	56	15	45
ISR	11	15	7	1	9	-	8	14	14
SWE	342	433	348	23	232	10	-	27	127
NLD	223	510	233	18	402	12	171	-	194
NZL	272	373	196	18	266	14	205	288	-

Most of the countries are well connected by common bulls and even more by “sire x mgs” combinations. These connections are weak for FIN and ISR, in addition the respective size of

common “sire x mgs” families in these countries is small.

The national evaluation systems are briefly described in Table 3.

Table 3. Most important characteristics of the evaluation systems in the replying countries.

Country	Type of model*	No. CE-classes	Parities in common evaluation	h^2_{DCE}	h^2_{MCE}	h^2_{DSB}	h^2_{MSB}
CAN	Linear ST-AM Rep.	4	All	.11	.12		
DEU	Linear ST -AM Rep.	4/3****	All	.05	.05	.05	.05
DNK	Linear MT-SM**	4	1, 2+	.10 / .05	.07 / .03	.04 / .01	.04 / .01
FIN	Linear ST-SM	3	CE: 1, SB: All	.01	.06	.02	.01
FRA	Threshold ST-SM	5/3****	All	.054	.031		
ISR	Linear ST-SM	2	1	.018	.009	.006	.006
NLD	Linear ST-SM***	4	CE: 2, SB: 1, 2+	.13	.07	.03 / .01	.05 / .01
NZL	Linear ST-SM**	2	1, 2+	.043 / .021			
SWE	Linear ST-SM	2	All	.02	.02	.02	.02

* ST-AM Rep– single trait repeatability animal model, MT-SM – multi trait animal model, ST-SM – single trait sire model

** Separate proofs for 1st and later parities. DNK sent 1st parity proofs for direct traits and combined proofs for maternal traits

*** Separate proofs for 1st and later parities for stillbirth only

**** In DEU classes “no assistance” and “1 assistant”, in FRA classes “difficult calving”, “caesarean” and “embryotomy” are combined for analysis

Methods

Genetic correlations

Parameter estimation was carried out using the EM-REML programs of the US Holstein Association (Klei & Weigel, 1998). Convergence criteria were ten times as strict, except for the maximum change in absolute correlation (which remained 10^{-4}). National EBV were weighted according to number of born calves or number of calving daughters of a bull.

Genetic evaluation

The purpose of the evaluation is to check for systematic problems that do not appear in parameter estimation. EBV of sires born from 1984 onwards from all nine countries, included in the parameter estimation, were used for evaluation. Information of foreign sires was only

used when they had at least 75 daughters in at least 50 herds. Genetic correlations out of the first parameter estimation were used as input parameters.

Results and Discussion

Estimation of genetic parameters

The absolute genetic correlations of FIN and ISR are generally low due to low heritable traits and weak genetic links with the other countries. Inclusion of extremely low heritable traits in populations without very strong genetic links with other populations, where the situation is different, may not be useful. Therefore $|r_g|$ is averaged over all countries except FIN and ISR and discussion about $|r_g|$ of FIN and ISR is limited. Average, minimum and maximum $|r_g|$ for the calving traits in the participating countries except FIN and ISR are put in Table 4.

Table 4. Average, minimum and maximum $|r_g|$ for CE and SB across countries with exception of FIN and ISR (min. 10 herds).

	CAN	DEU	DNK	FIN	FRA	ISR	SWE	NLD	NZL
CE-direct									
Av. $ r_g $.79	.78	.88	.43	.66	.83	.88	.80	.70
Min. $ r_g $.53	.66	.71	.14	.46	.54	.73	.69	.46
Max. $ r_g $.94	.91	.99	.73	.76	.92	.99	.91	.83
CE-mat.									
Av. $ r_g $.90	.80	.83	.43	.91	.44	.87	.86	
Min. $ r_g $.81	.73	.78	.22	.83	.33	.73	.76	
Max. $ r_g $.99	.86	.88	.78	.99	.60	.94	.95	
SB-direct									
Av. $ r_g $.84	.89	.22		.48	.87	.80	
Min. $ r_g $.75	.81	.09		.32	.85	.75	
Max. $ r_g $.93	.93	.41		.64	.92	.85	
SB-mat.									
Av. $ r_g $.75	.83	.22		.22	.73	.60	
Min. $ r_g $.58	.70	.02		.01	.53	.53	
Max. $ r_g $.90	.90	.43		.62	.90	.70	

Average absolute correlations of direct CE and SB are similar except for DEU, where the average absolute correlation is higher for direct SB than for direct CE. Absolute correlations with other countries of maternal CE are higher than those of maternal SB for NLD and SWE, to a lesser extent for DEU too.

The estimated correlation of the EBV used for conversion of EBV for direct CE from USA to NLD (.72) is comparable to the average $|r_g|$'s among countries for this trait found in this study. The estimates of r_g between SWE and DNK in this study for direct CE and maternal SB were comparable to those estimated by Mark *et al.*

(2001). Those for maternal CE and direct SB were higher in this study. Absolute genetic correlations of SWE or DNK with FIN are much lower in this study. Especially correlations for the maternal traits are almost zero.

Adaptation of maternal EBV

Average absolute genetic correlations among the „pure maternal“ effects, i.e. $\text{mat. EBV} - 0.5 * \text{dir EBV}$ in case of sire models, were lower or equal to those among the delivered maternal EBV with exception of the absolute genetic correlations of stillbirth in NLD. The average of these increased by .05, but is still relatively low.

Average absolute genetic correlations for „pure MGS“ effects, i.e. $\text{maternal EBV} + 0.5 * \text{direct EBV}$ in case of animal models, were also not higher than those among the delivered maternal

EBV with exception for calving ease in DEU and SWE (increases by .07 and .04 respectively) and for stillbirth in SWE (increase by .03).

The changes in correlations of the maternal EBV in FIN and ISR after adaptations were inconsistent with those in the other countries.

Use of calving ease as information source for stillbirth

Genetic correlations among the countries with stillbirth evaluations were changed at the most by .01, except of the absolute genetic correlation between SWE and NLD for maternal stillbirth (.57 instead of .53). Average, maximum and minimum of absolute genetic correlations of calving ease in CAN, FRA and NZL with stillbirth in other countries are presented in Table 5.

Table 5. Average, minimum and maximum of absolute genetic correlations ($|r_g|$) of CE in CAN, FRA and NZL with stillbirth in other countries except FIN and ISR (at least 10 herds).

Direct CE	CAN	FRA	NZL
Average $ r_g $.68	.49	.54
Minimum $ r_g $.55	.47	.43
Maximum $ r_g $.78	.51	.66
Maternal CE*	CAN	FRA	NZL
Average $ r_g $.64	.54	
Minimum $ r_g $.42	.42	
Maximum $ r_g $.77	.66	

* as sent in by the participating countries

Increase of minimum number of herds

There is a small but consistent increase in absolute genetic correlations among countries for maternal effects on stillbirth. Surprising is the considerable increase of absolute genetic correlations of FRA with other countries for direct calving ease. This increase may be due to smaller differences between EBV of linear and threshold models when they are based on more data. Beside this large increases of $|r_g|$ with other countries of maternal calving ease in ISR and both stillbirth traits in FIN were observed. For the other traits in these countries $|r_g|$ did not increase. Therefore

results for FIN and ISR should be interpreted carefully. The results for FIN may be explained by the fact that stillbirth in Finland is recorded at first milk recording and calving ease at first AI-service.

Genetic evaluation

International genetic evaluation for calving traits was carried out applying Interbull conditions regarding birth years and number of observations. Table 6 contains results of a comparison of national and international proofs.

Table 6. Comparison of international (I.pr_f) and national proofs (N.pr_f) for bulls with at least 50 herds in national proofs.

	I.pr _f – N.pr _f [*]		Std. Dev. [*]						
Country	Mean	Max.	N.pr _f	I.pr _f	r	#Bulls	Rel. _{dom}	Rel. _{for}	std _{for} /std _{dom}
Direct calving ease									
CAN	0.000	0.623	0.786	0.785	0.999	3056	83.6	52.6	0.799
DEU	-0.001	1.375	0.757	0.757	0.998	6691	82.6	48.5	0.739
DNK	-0.001	1.146	0.682	0.684	0.995	1084	72.2	62.0	1.084
FIN	0.005	0.717	0.543	0.530	0.960	370	34.0	31.9	0.763
FRA	-0.046	1.467	0.691	0.724	0.948	876	73.1	43.5	0.856
ISR	-0.013	0.647	0.886	0.876	0.988	82	75.8	54.0	0.785
SWE	0.008	1.212	0.648	0.646	0.978	1333	56.6	62.7	1.079
NLD	0.000	0.506	0.867	0.866	0.999	3795	87.7	48.0	0.723
NZL	0.002	0.899	0.906	0.897	0.992	1458	66.3	44.3	0.708
Maternal calving ease									
CAN	0.001	0.740	0.674	0.673	0.996	1692	73.6	48.8	0.848
DEU	0.001	1.514	0.639	0.640	0.995	6050	67.3	44.8	0.814
DNK	-0.002	0.569	0.722	0.718	0.998	4227	65.5	44.9	0.797
FIN	0.000	0.628	0.756	0.751	0.998	363	65.4	32.6	0.526
FRA	-0.005	1.017	0.646	0.645	0.989	2172	54.9	50.2	0.908
ISR	-0.001	0.275	0.483	0.485	0.992	494	40.6	24.4	0.741
SWE	0.001	1.058	0.686	0.688	0.979	1147	56.7	47.0	0.849
NLD	-0.006	0.866	0.675	0.674	0.994	971	62.9	46.1	0.847
Direct stillbirth									
DEU	0.000	0.667	0.750	0.750	0.999	6637	82.5	41.6	0.642
DNK	-0.006	0.576	0.601	0.606	0.991	1077	63.7	56.0	1.075
FIN	0.001	1.221	0.789	0.776	0.996	534	72.0	21.2	0.505
ISR	-0.017	0.301	0.857	0.847	0.997	82	67.6	24.5	0.523
SWE	-0.001	1.218	0.607	0.621	0.976	1303	54.8	51.2	1.029
NLD	0.003	0.601	0.894	0.883	0.998	1928	64.9	43.9	0.719
Maternal stillbirth									
DEU	0.002	1.523	0.657	0.666	0.997	5997	66.9	36.9	0.752
DNK	-0.001	1.111	0.667	0.667	0.993	4218	53.6	44.5	0.934
FIN	-0.002	0.753	0.663	0.637	0.986	559	45.0	14.1	0.621
ISR	-0.004	1.336	0.477	0.514	0.916	494	41.0	19.6	0.907
SWE	0.002	1.006	0.693	0.711	0.986	1119	55.2	38.1	0.826
NLD	0.004	0.562	0.969	0.958	0.999	2873	57.5	32.3	0.621

^{*} in units sire standard deviation estimated by REML in MACE

Agreement between national and international proofs for FIN, ISR, SWE and FRA was less than the respective correlations reported for somatic cell count by Mark *et al.* (2001). For FIN and ISR MACE genetic evaluation may be unstable due to insufficient genetic links, extremely low heritabilities in some cases, and therefore inaccurately estimated genetic correlations with other countries. The national and international proofs of bulls having offspring in SWE correspond well for all traits. This may be due to a strong genetic relationship of calving traits in SWE with those in other countries whilst

reliabilities of national EBV are relatively low. A similar situation exists for maternal calving ease in FRA. For SWE, another cause may be the underestimated heritabilities. Recent estimates of h^2 for calving traits in SWE were higher than those submitted. The large disagreement between national and international proofs of bulls with offspring in FRA for direct calving ease may be caused by proofs from FRA being the only ones estimated with a threshold model. Differences among national and international proofs for direct calving ease in FRA become smaller with increasing minimum number of calvings. It seems

that the different way of handling data by linear and threshold models only have an effect on the EBV when numbers of calvings are small.

Conclusions

Estimates of genetic correlations of calving traits among countries show the possibility of international genetic evaluation for all participating countries except FIN and ISR. Introducing MACE evaluation for calving traits would support national breeding schemes in identifying foreign bull increasing calving difficulties and stillbirth.

Substantial differences between national and international proofs for direct calving ease were found only for FRA, which might be caused by the different models used in national and international evaluation. FRA is the only country in this study estimating EBV for calving traits with a threshold model.

Pre-correction of maternal EBV did not lead to stronger genetic relationships among countries and is theoretically problematic.

Some additional information for a stillbirth EBV may be obtained from calving ease when there is no stillbirth EBV available, without affecting estimates of genetic correlations among countries estimating BV for stillbirth. However, it is questionable whether calving ease of these countries should be included in MACE for stillbirth.

The effects of further restrictions on number of calvings and calving daughters are mostly negligible. For MSB there are small but consistent increases. For DCE consistent increases in absolute genetic correlations were found only for FRA.

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