

INTERBEEF ACROSS-COUNTRY VARIANCE COMPONENTS ESTIMATION FOR CHAROLAIS CALVING EASE

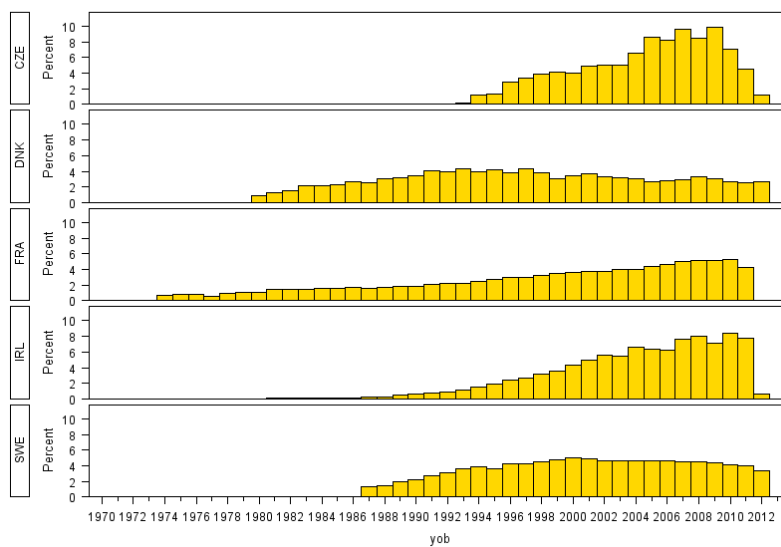
1. Data

We estimated across country correlations across 5 countries for Charolais breed using 5 performance files (CZE, DNK, FRA, IRL, SWE) and 1 pedigree obtained from Interbeef (Table 1).

Table 1. Size of data sets

	Country	N	
Performance	CZE	40,113	0.59%
	DNK	114,093	1.68%
	FRA	6,251,815	92.27%
	IRL	231,866	3.42%
	SWE	137,431	2.03%
	ALL	6,775,318	
Pedigree	ALL	7,772,414	

PROPORTION OF ANIMALS BY BIRTH YEAR



2. Editing data for VCE

First of all the pedigree for calves without official registration numbers (“UUUUUUUUUUUUUUUUUUUU” - dead calves) was added to pedigree file. Phantom registration numbers for dead calves were created and added to pedigree and performance files.

Numbers of calves with calving ease score, but without registration:

CZE – 3,066 (7.64% from all Czech animals with performance)

DNK – 9,313 (8.16%)

FRA – 0 (0%)

IRL – 0 (0%)

SWE – 4,866 (3.54%)

Then edits on performance files included the exclusion of herds without variation of calving ease score, exclusion of embryo transplant calves (ET), exclusion of calves without known sire and maternal grandsire (MGS), a minimum size (3) for contemporary groups (CG) and a minimum number of sires per CG (2) were applied.

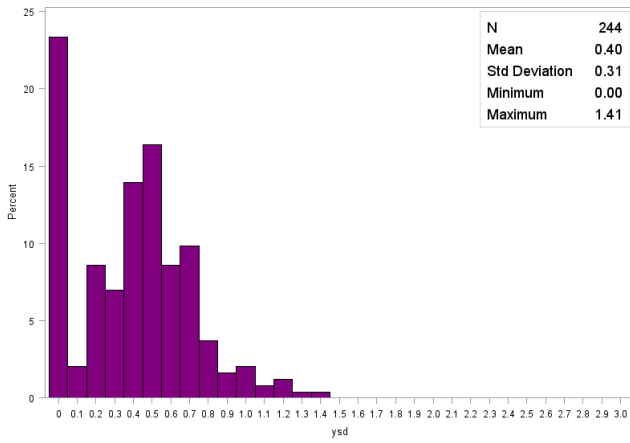
Table 2. Animals successively edited

Country	1. Herds without variation	2. ET	3. No sire or/and MGS	4. CG (min CG size 3)	5. Min sire per CG (2)	Remaining animals
CZE	1,061	1,722	4,114	1,019	3,861	28,336
DNK	6,178	9	43,627	3,729	14,110	46,440
FRA	19,184	0	1,503,113	61,239	635,975	4,032,304
IRL	47,172	2,381	40,408	22,588	14,405	104,912
SWE	4,639	0	7,614	1,789	23,975	99,414

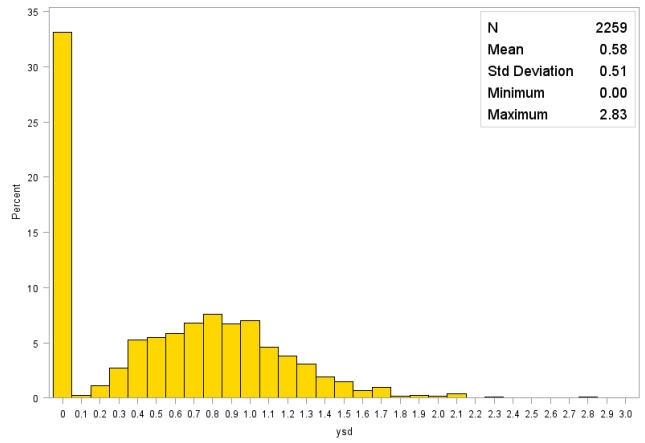
Table 3. Frequencies of herds without variations before editing

Country	N herds	N herds without var	% herds without var
CZE	265	57	21.51%
DNK	2,674	748	27.97%
FRA	22,413	2,239	9.99%
IRL	9,613	4,034	41.96%
SWE	1,542	385	3.38%

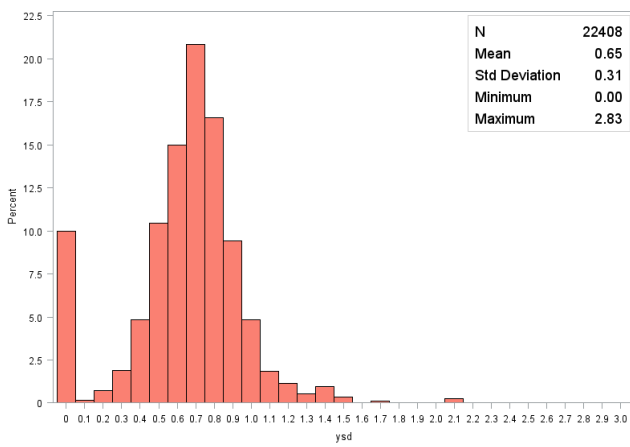
DISTRIBUTION OF SD OF CALVING EASE SCORE IN HERDS — CZE



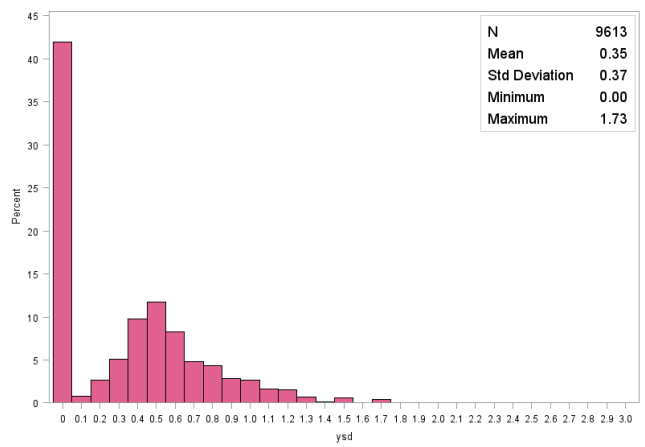
DISTRIBUTION OF SD OF CALVING EASE SCORE IN HERDS — DNK



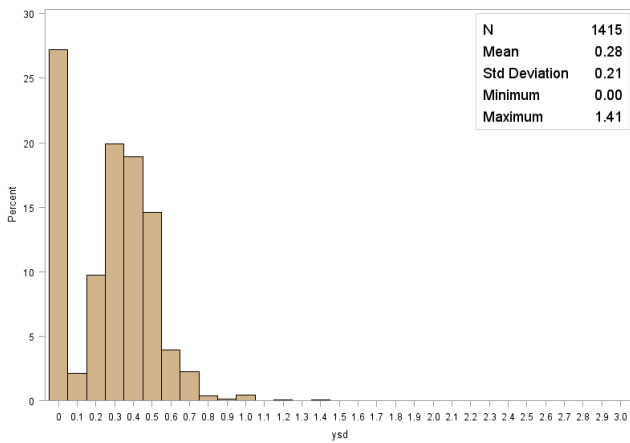
DISTRIBUTION OF SD OF CALVING EASE SCORE IN HERDS — FRA



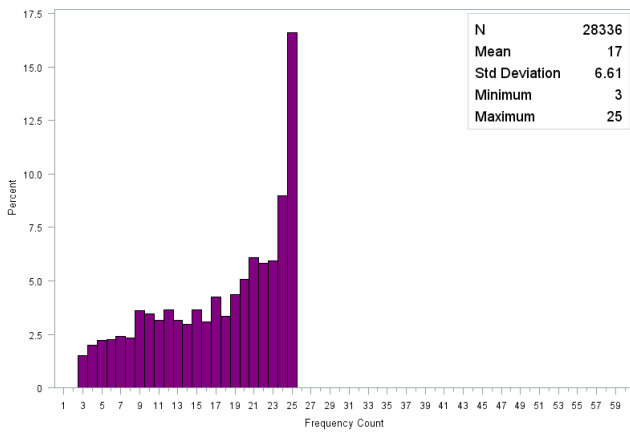
DISTRIBUTION OF SD OF CALVING EASE SCORE IN HERDS — IRL



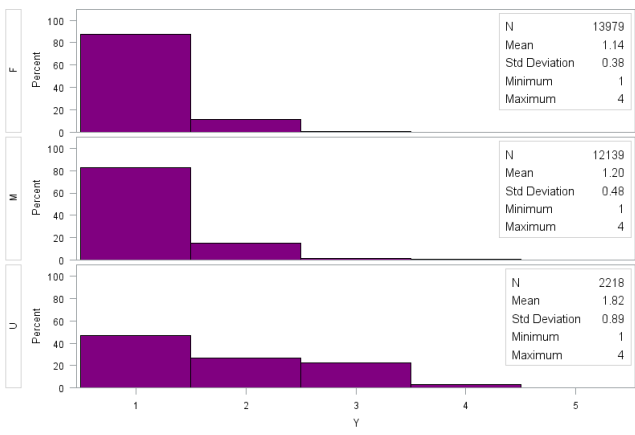
DISTRIBUTION OF SD OF CALVING EASE SCORE IN HERDS — SWE



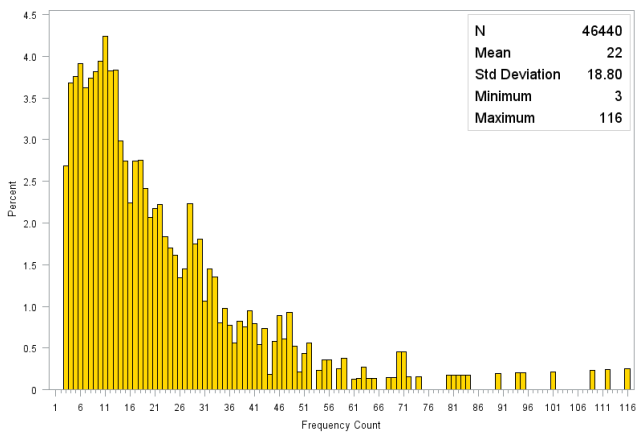
DISTRIBUTION OF SIZE OF C. GROUPS – CZE



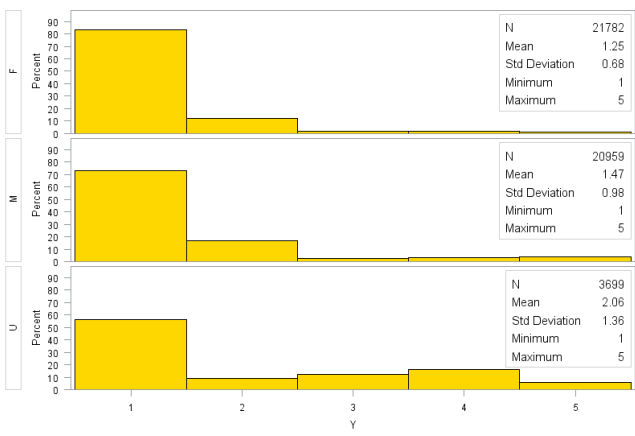
DISTRIBUTION OF CALVING EASE – CZE



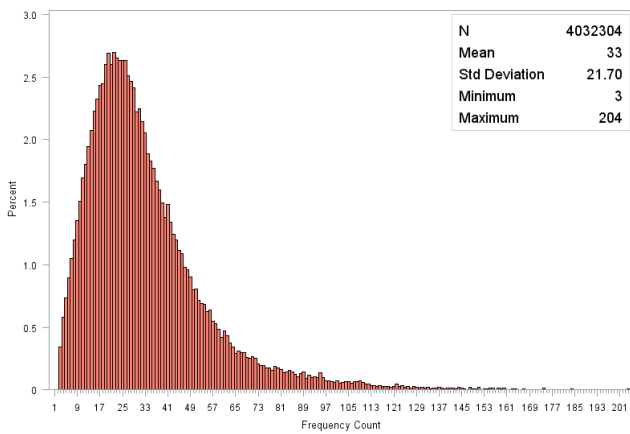
DISTRIBUTION OF SIZE OF C. GROUPS – DNK



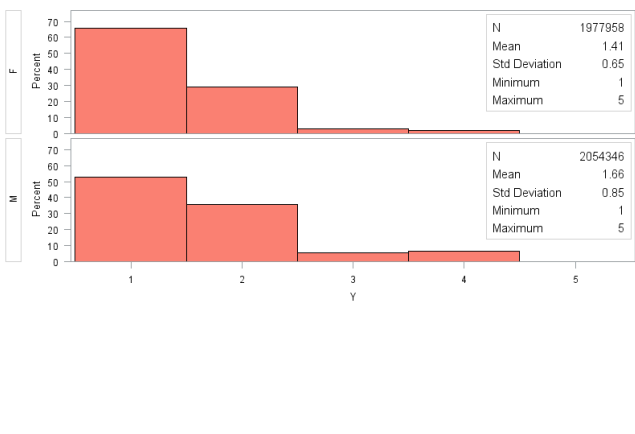
DISTRIBUTION OF CALVING EASE – DNK



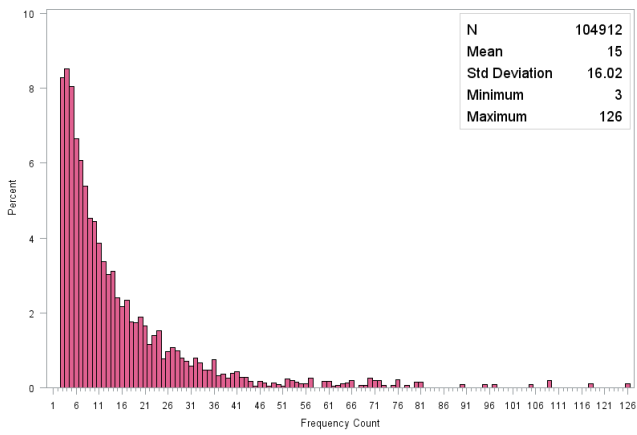
DISTRIBUTION OF SIZE OF C. GROUPS – FRA



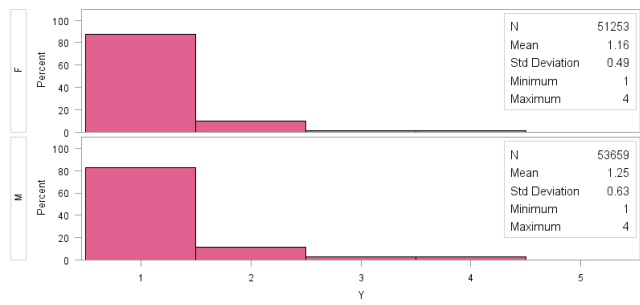
DISTRIBUTION OF CALVING EASE – FRA



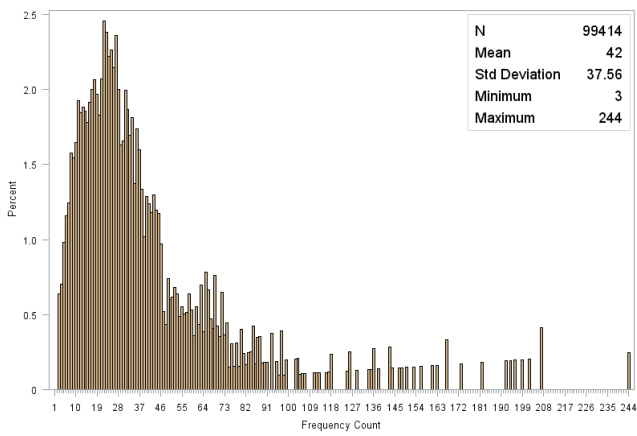
DISTRIBUTION OF SIZE OF C. GROUPS – IRL



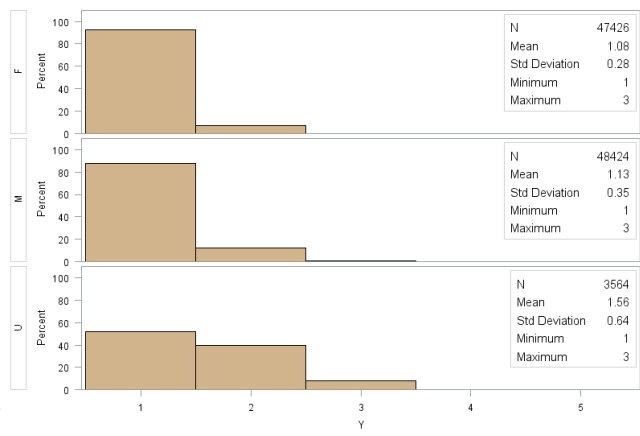
DISTRIBUTION OF CALVING EASE – IRL



DISTRIBUTION OF SIZE OF C. GROUPS – SWE



DISTRIBUTION OF CALVING EASE – SWE



3. Building data sets for VCE

Method and software: SAS code from ICBF was used (See ICBF report: “Interbeef Across-country variance components estimation for Limousine Weaning Weight”).

Pedigree file: 5 generations with phantom parent group (according to country of origin of animal with unknown parent).

4. The VCE files

Numbers of sires are between { } and number of MGS between [].

	Ped: 64,850	
	CZE Perf: 22,933	DNK Perf: 16,248
CZE	{671} [1,163]	[49]
DNK	{43}	{719} [929]

	Ped: 137,589	
	CZE Perf: 22,797	IRL Perf: 65,869
CZE	{682} [1,158]	[53]
IRL	{38}	{3,316} [2,575]

	Ped: 172,322	
	CZE Perf: 17,660	FRA Perf: 36,716
CZE	{497} [735]	[240]
FRA	{95}	{2,836} [5,224]

	Ped: 81,525	
	CZE Perf: 23,124	SWE Perf: 28,837
CZE	{689} [1,179]	[34]
SWE	{33}	{1,022} [1,274]

	Ped: 182,025	
	DNK Perf: 16,087	FRA Perf: 43,001
DNK	{708} [894]	[86]
FRA	{62}	{2,851} [5,243]

	Ped: 83,542	
	DNK Perf: 13,100	SWE Perf: 44,813
DNK	{625} [811]	[55]
SWE	{36}	{1,458} [1,777]

	Ped: 124,005	
	DNK Perf: 15,826	IRL Perf: 65,510
DNK	{710} [914]	[58]
IRL	{52}	{3,259} [2,539]

	Ped: 223,999	
	FRA Perf: 42,620	IRL Perf: 36,711
FRA	{3,097} [5,538]	[118]
IRL	{88}	{2,001} [1,856]

	Ped: 111,971	
	FRA Perf: 18,932	SWE Perf: 25,276
FRA	{1,177} [2,098]	[34]
SWE	{37}	{865} [1,141]

	Ped: 119,316	
	IRL Perf: 57,301	SWE Perf: 20,957
IRL	{2,767} [2,232]	[23]
SWE	{26}	{825} [1,045]

5. Variance components estimation

Two series of 2-country analysis were done successively:

1. Animal model with direct genetic effect and maternal permanent environmental effect (AM-DE-MPE).
2. Animal model with direct and maternal genetic effect with maternal permanent environmental effect (AM-DE-MPE-ME).

Software: AM-DE-MPE models were ran in AIREML1F90 (Misztal et al., 2002). AM-DE-MPE-ME models were ran in GIBBS1F90 using Bayesian approach with 500,000 chains and 300,000 burn-in (Misztal et al., 2002). Some tests were conducted with DMU (Madsen et al., 2012).

Table 4. Environmental effects used in models

CZE	DNK	FRA	IRL	SWE
CG*	CG	CG	CG	CG
	Season	Season		
Birth year				
Sex × Twin	Sex		Sex	Sex
	Twin			
Dam age	Dam age		Dam age**	Dam age
		Dam age × parity	Parity	Parity

* treated as random

** fixed regression

5.1. Animal model with direct genetic effect and maternal permanent environmental effect (AM-DE-MPE)

In these models, all residual correlations were set to zero.

Program used for genetics parameters estimation: aireml1f90

Table 5. Across-country genetic correlations (standard errors) for direct effect from AM-DE-MPE

Average direct genetic correlation = 0.62

	CZE	DNK	FRA	IRL	SWE
CZE					
DNK	0.32 (0.06)				
FRA	0.44 (0.04)	0.78 (0.02)			
IRL	nc	0.77 (0.03)	0.88 (0.02)		
SWE	nc	nc	nc	0.52 (0.06)	

5.2. Animal model with direct and maternal genetic effect with maternal permanent environmental effect (AM-DE-MPE-ME)

In these models, all residual correlations and all direct – maternal correlation were set to zero.

Program used for genetics parameters estimation: gibbs1f90 (500,000 chains, 300,000 burn-in)

Table 6. Across-country genetic correlations (standard errors) for direct (bellow diagonal) and maternal (above diagonal) effect from AM-DE-MPE-ME

Average direct genetic correlation = 0.68, average maternal genetic correlation = 0.51

	CZE	DNK	FRA	IRL	SWE
CZE		0.47 (0.10)	0.69 (0.06)	0.56 (0.3)	nc
DNK	0.40 (0.07)		0.39 (0.09)	0.60 (0.09)	nc
FRA	0.45 (0.07)	0.90 (0.02)		0.36 (0.12)	nc
IRL	0.90 (0.02)	0.49 (0.06)	0.95 (0.02)		nc
SWE	nc	nc	nc	nc	

6. Getting the InterBeef calving ease correlation matrix

Jorjani et al. (2003) weighted bending was used to compute the InterBeef genetic correlation matrix in 3 steps:

1. Direct correlations non-converged (or statistically not significant) from AM-DE-MPE-ME were set to their value from AM-DE-MPE. Direct correlation non-converged from both models were set to 0.8 with standard error 0.3. Matrix of direct correlation was then bended with standard errors used as weights.
2. Maternal correlation non-converged were set to 0.6 with standard error 0.3. Matrix of maternal correlations was than bended with standard errors used as weights.
3. The full matrix of direct and maternal genetic correlations were created with direct-maternal correlations within country from national genetic evaluation (CZE = -0.18, DNK = -0.20, FRA = -0.40, IRL = -0.16, SWE = -0.13). Full correlation matrix was than bended with weighting factor equal to the reciprocal of number of common sires multiplied by 4 for direct correlations and common MGS multiplied by 2 for maternal correlations, number 40 for non-converged direct correlation, number 20 for non-converged maternal correlation, number 9999 on the diagonal and for direct-maternal correlation within countries, and number 1 for direct-maternal correlation between countries (table 7).

Table 7. Reciprocal weighting factors

		DIRECT					MATERNAL				
		CZE	DNK	FRA	IRL	SWE	CZE	DNK	FRA	IRL	SWE
DIRECT	CZE	9999									
	DNK	172	9999								
	FRA	380	248	9999							
	IRL	152	208	352	9999						
	SWE	40	40	40	104	9999					
MAT.	CZE	9999	1	1	1	1	9999				
	DNK	1	9999	1	1	1	98	9999			
	FRA	1	1	9999	1	1	480	172	9999		
	IRL	1	1	1	9999	1	106	110	236	9999	
	SWE	1	1	1	1	9999	20	20	20	20	9999

Table 8. Banded full Interbeef correlation matrix

Average direct genetic correlation = 0.65, average maternal genetic correlation = 0.54

		DIRECT					MATERNAL				
		CZE	DNK	FRA	IRL	SWE	CZE	DNK	FRA	IRL	SWE
DIRECT	CZE										
	DNK	0.42									
	FRA	0.42	0.86								
	IRL	0.80	0.49	0.74							
	SWE	0.71	0.86	0.63	0.52						
MAT.	CZE	-0.18	0.03	0.01	-0.04	-0.05					
	DNK	0.01	-0.20	-0.10	0.04	-0.07	0.47				
	FRA	0.08	-0.18	-0.40	-0.16	0.02	0.69	0.39			
	IRL	-0.06	0.02	-0.07	-0.16	0.03	0.56	0.60	0.36		
	SWE	-0.05	-0.03	-0.01	0.03	-0.13	0.59	0.59	0.59	0.59	

7. Getting the InterBeef calving ease correlation matrix

(Co)variances matrices were computed using national estimates of genetic variance, residual variances, variances of permanent maternal environment and other variance (CG for CZE).

Table 9. National variances used for computing of full Interbeef (Co)variances

	var _{GD}	var _{GM}	var _{MPE}	var _{HYS}	var _e
CZE	0.0122	0.0054	0.004375	0.03855	0.0775
DNK	0.052	0.052	0.084		0.4004
FRA	0.0298	0.0182	0.0099		0.2356
IRL	0.02498	0.01	0.00585	0.21017298	0.22709
SWE	0.0533	0.04	0.003		0.2177

8. References

ICBF (2013): Interbeef across-country variance components estimation for Limousine weaning weight. Report for Interbeef.

Jorjani H., Klei L., Emanuelson U. (2003): A Simple Method for Weighted Bending of Genetic (Co)variance Matrices. J. Dairy Sci., 86, 677-679.

Madsen P., Jensen J. (2012): A user's guide to DMU – A Package for Analysis Multivariate Mixed Models. Version 6, release 5.2, University of Aarhus.

Misztal I., Tsuruta S., Strabel T., Auvray B., Druet T., Lee D.H. (2002) BLUPF90 and related programs (BGF90). In: 7th World Congress on Genetics Applied to Livestock Production, Montpellier, 19–23 August 2002.

Table 10. Full Interbeef genetic covariance matrix

		DIRECT					MATERNAL				
		CZE	DNK	FRA	IRL	SWE	CZE	DNK	FRA	IRL	SWE
DIRECT	CZE	0.0122	0.0106721	0.0080318	0.0140561	0.0182261	-0.001461	0.0003486	0.0011501	-0.000647	-0.001018
	DNK	0.0106721	0.052	0.0340468	0.0177009	0.0452467	0.0005334	-0.010399	-0.005541	0.0004539	-0.001602
	FRA	0.0080318	0.0340468	0.0298	0.0201439	0.025291	0.0001048	-0.004078	-0.009314	-0.001215	-0.000356
	IRL	0.0140561	0.0177009	0.0201439	0.02498	0.01909	-0.00042	0.0012878	-0.003365	-0.002529	0.001109
	SWE	0.0182261	0.0452467	0.025291	0.01909	0.0533	-0.000796	-0.003509	0.0007388	0.0007647	-0.006002
MAT.	CZE	-0.001461	0.0005334	0.0001048	-0.00042	-0.000796	0.0054	0.0078982	0.0068904	0.0041038	0.0086734
	DNK	0.0003486	-0.010399	-0.004078	0.0012878	-0.003509	0.0078982	0.052	0.0120703	0.0135919	0.0269093
	FRA	0.0011501	-0.005541	-0.009314	-0.003365	0.0007388	0.0068904	0.0120703	0.0182	0.0048733	0.0159307
	IRL	-0.000647	0.0004539	-0.001215	-0.002529	0.0007647	0.0041038	0.0135919	0.0048733	0.01	0.0118272
	SWE	-0.001018	-0.001602	-0.000356	0.001109	-0.006002	0.0086734	0.0269093	0.0159307	0.0118272	0.04

Table 11. Variances for permanent maternal environment

	CZE	DNK	FRA	IRL	SWE
CZE	0.004375	0	0	0	0
DNK	0	0.084	0	0	0
FRA	0	0	0.0099	0	0
IRL	0	0	0	0.00585	0
SWE	0	0	0	0	0.003

Table 13. Variance for HYS for IRL

	CZE	DNK	FRA	IRL	SWE
CZE	0	0	0	0	0
DNK	0	0	0	0	0
FRA	0	0	0	0	0
IRL	0	0	0	0.21017298	0
SWE	0	0	0	0	0

Table 12. Variance for HYS for CZE

	CZE	DNK	FRA	IRL	SWE
CZE	0.03855	0	0	0	0
DNK	0	0	0	0	0
FRA	0	0	0	0	0
IRL	0	0	0	0	0
SWE	0	0	0	0	0

Table 14. Residual variances

	CZE	DNK	FRA	IRL	SWE
CZE	0.0775	0	0	0	0
DNK	0	0.4004	0	0	0
FRA	0	0	0.2356	0	0
IRL	0	0	0	0.22709	0
SWE	0	0	0	0	0.2177