

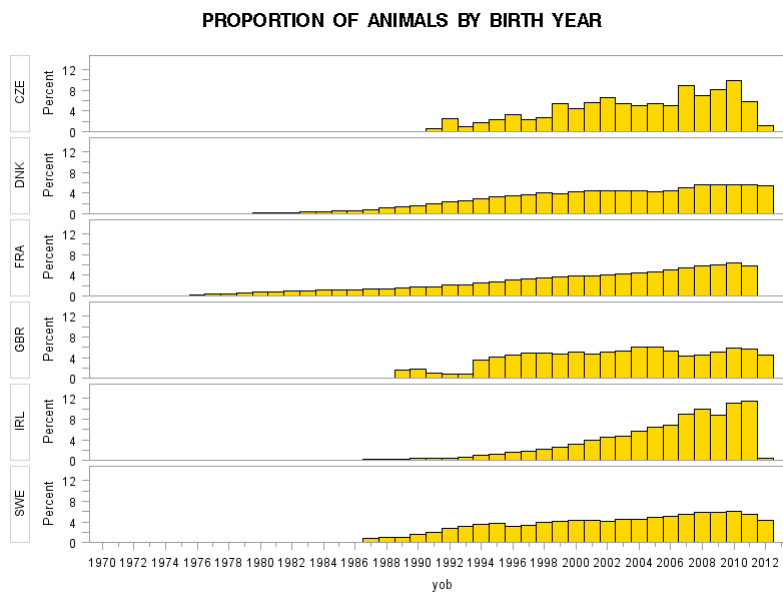
INTERBEEF ACROSS-COUNTRY VARIANCE COMPONENTS ESTIMATION FOR LIMOUSINE CALVING EASE

1. Data

We estimated across country correlations across 6 countries for Limousine breed using 6 performance files (CZE, DNK, FRA, GBR, IRL, SWE) and 1 pedigree obtained from Interbeef (Table 1).

Table 1. Size of data sets

	Country	N	
Perfomance	CZE	9,554	0.2%
	DNK	258,448	6.4%
	FRA	3,468,854	85.5%
	GBR	121,407	3.0%
	IRL	170,856	4.2%
	SWE	26,369	0.6%
	ALL	4,055,485	
Pedigree	ALL	4,523,586	



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.

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

CZE – 4.53%
 DNK – 3.82%
 FRA – 0%
 GBR – 0%
 IRL – 0%
 SWE – 2.98%

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) and a minimum size (3) for contemporary groups (CG) were applied.

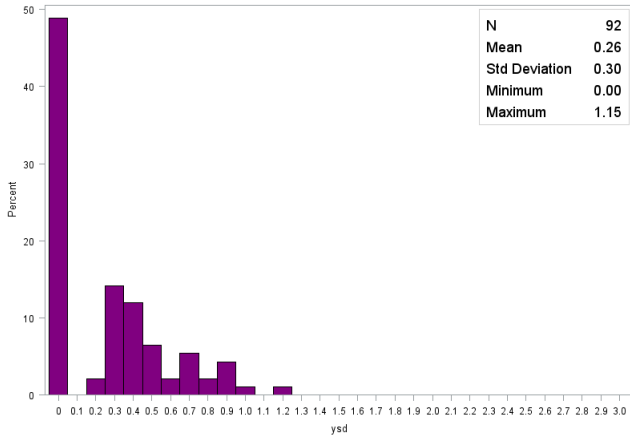
Table 2. Animals successively edited

Country	1. Herds without variation	2. ET	3. No sire or/and MGS	4. CG (min CG size 3)	Remaining animals
CZE	774	552	387	622	7,219
DNK	18,259	22	100,824	17,402	121,938
FRA	68,908	0	947,524	93,754	2,358,665
GBR	15	3,376	2,307	7,891	107,818
IRL	38,272	2,051	27,867	25,292	77,374
SWE	1,230	0	3,467	1,161	20,511

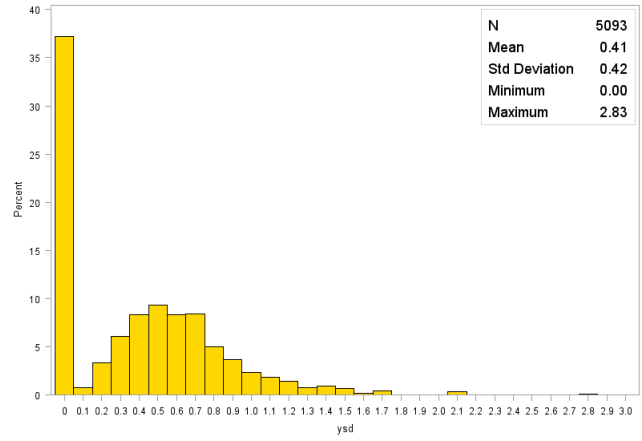
Table 3. Frequencies of herds without variations before editing

Country	N herds	N herds without var	% herds without var
CZE	99	45	45.4%
DNK	5,896	1,892	32.1%
FRA	11,538	2,401	20.8%
GBR	2,127	5	0.2%
IRL	6,798	3,324	48.9%
SWE	322	89	27.6%

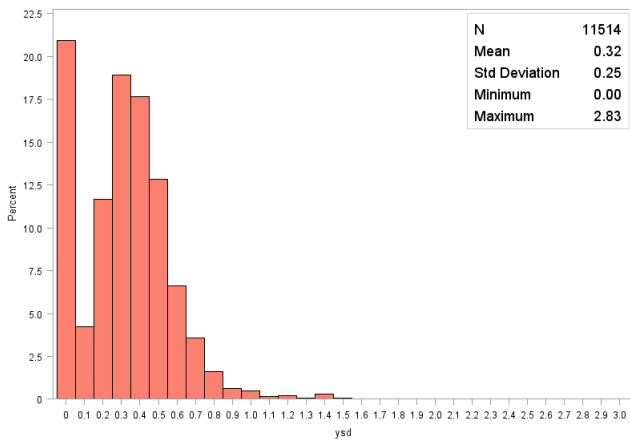
DISTRIBUTION OF SD OF CALVING EASE SCORE IN HERDS — CZE



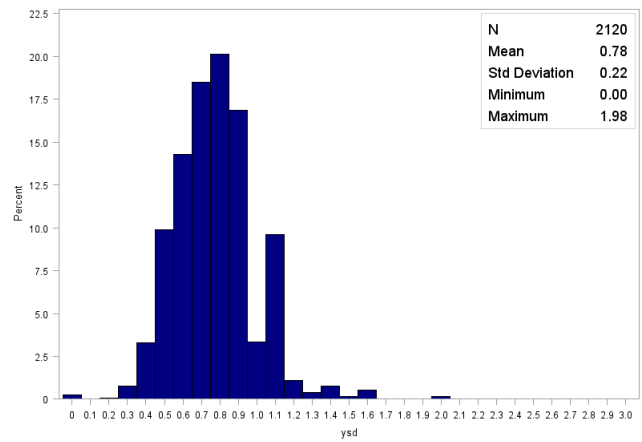
DISTRIBUTION OF SD OF CALVING EASE SCORE IN HERDS — DNK



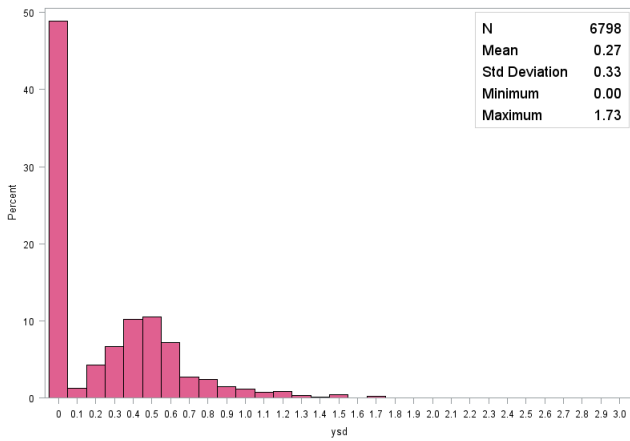
DISTRIBUTION OF SD OF CALVING EASE SCORE IN HERDS — FRA



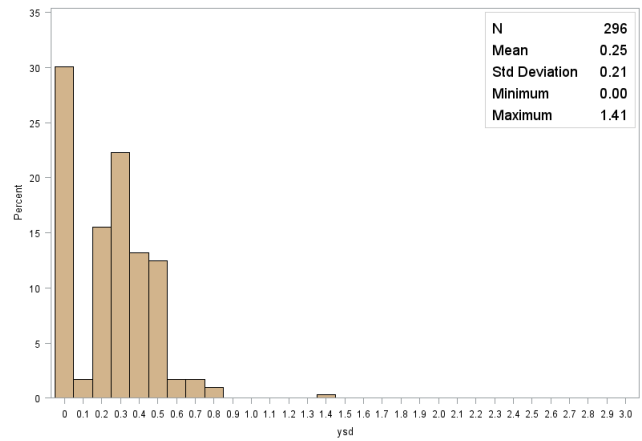
DISTRIBUTION OF SD OF CALVING EASE SCORE IN HERDS — GBR



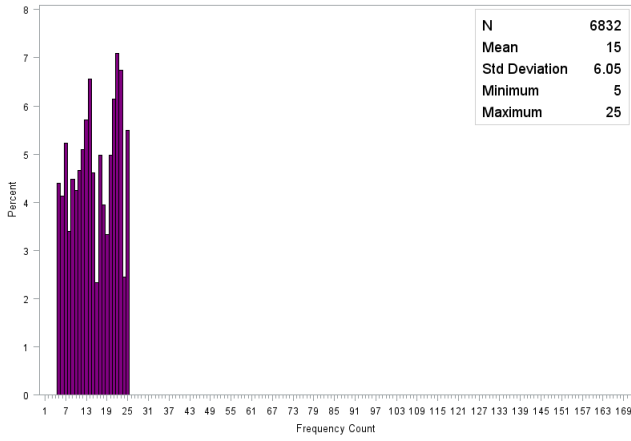
DISTRIBUTION OF SD OF CALVING EASE SCORE IN HERDS — IRL



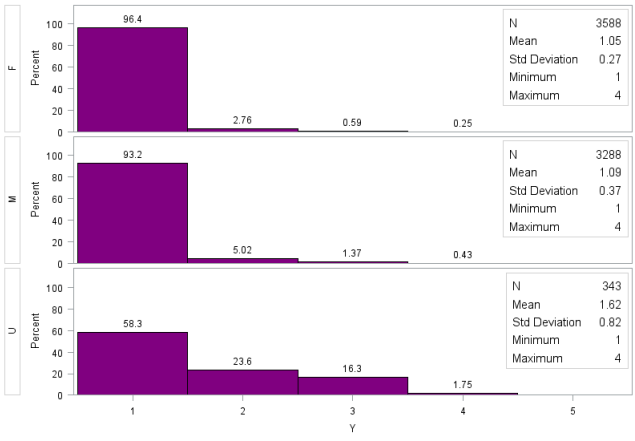
DISTRIBUTION OF SD OF CALVING EASE SCORE IN HERDS — SWE



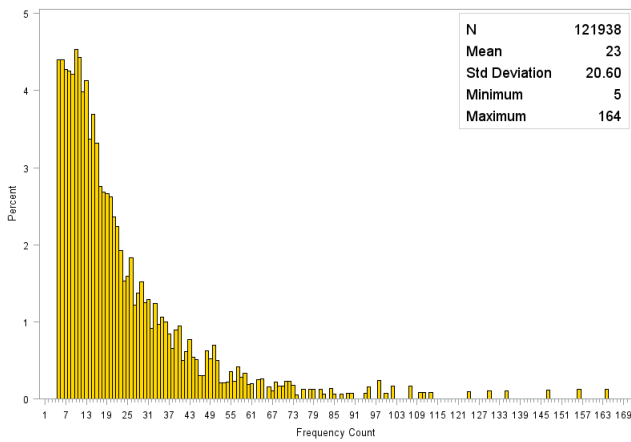
DISTRIBUTION OF SIZE OF C. GROUPS – CZE



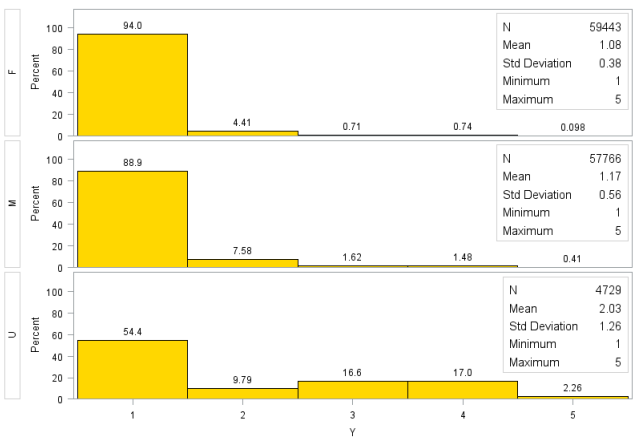
DISTRIBUTION OF CALVING EASE – CZE



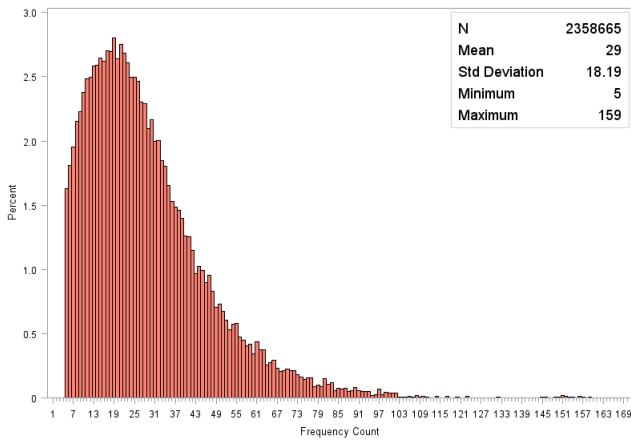
DISTRIBUTION OF SIZE OF C. GROUPS – DNK



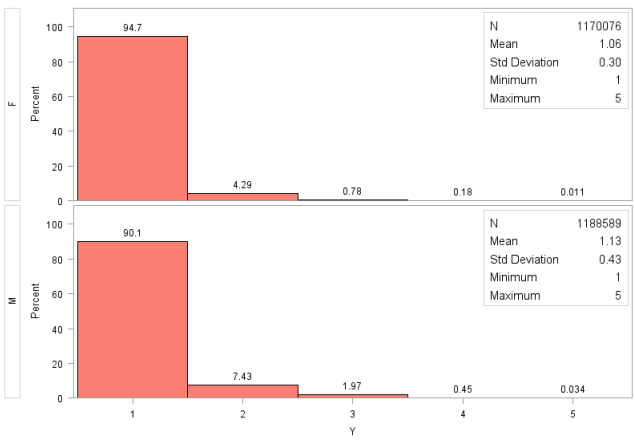
DISTRIBUTION OF CALVING EASE – DNK



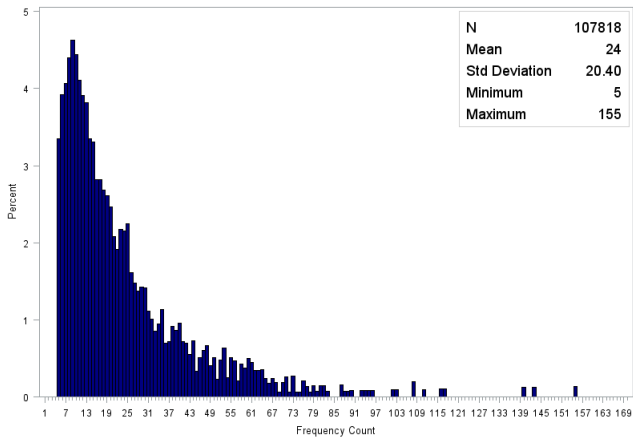
DISTRIBUTION OF SIZE OF C. GROUPS – FRA



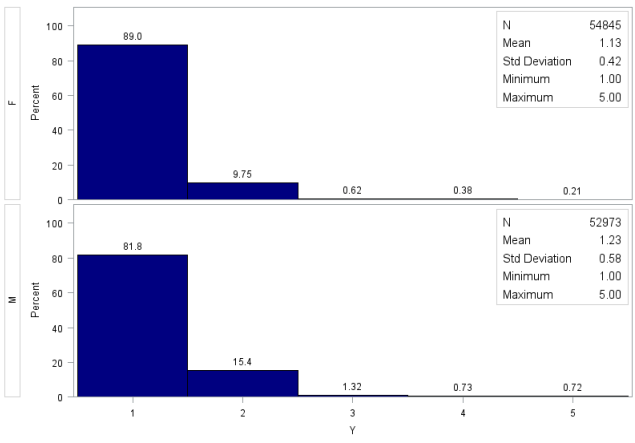
DISTRIBUTION OF CALVING EASE – FRA



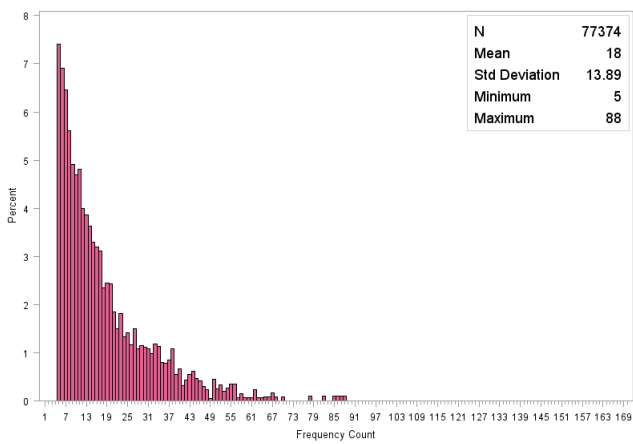
DISTRIBUTION OF SIZE OF C. GROUPS – GBR



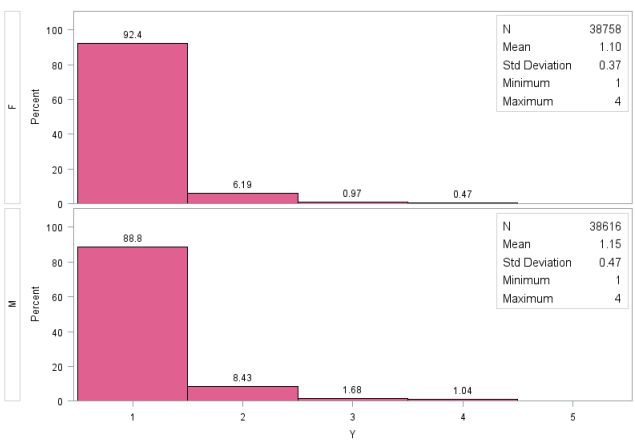
DISTRIBUTION OF CALVING EASE – GBR



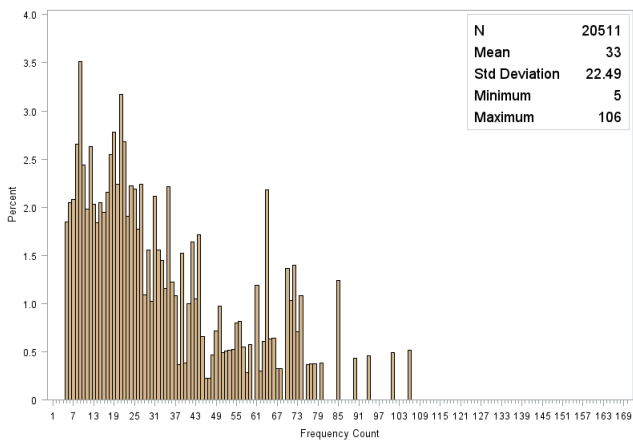
DISTRIBUTION OF SIZE OF C. GROUPS – IRL



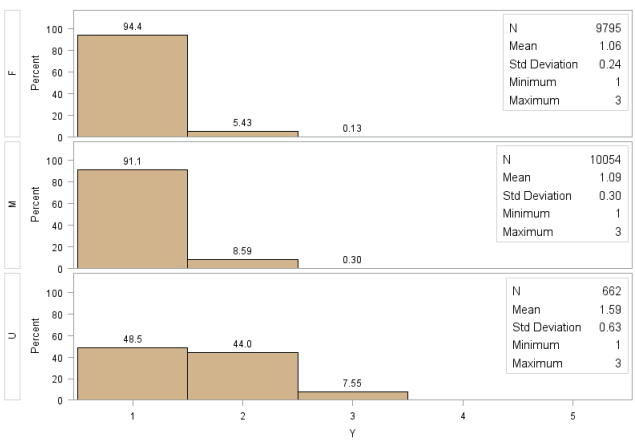
DISTRIBUTION OF CALVING EASE – IRL



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”).

Models: creating 7 subsets for FRA according to random selection of herds; using series of 2-country analysis; starting with animal model with direct genetic effect and MPE (Venot et al., 2007); moving to animal model with direct and maternal genetic effect and MPE, where all direct-maternal correlations were set to zero.

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: 58,098	
	CZE Perf: 4,595	DNK Perf: 29,559
CZE	{232} [411]	[40]
DNK	{36}	{1,217} [1,860]

	Ped: 52,331	
	CZE Perf: 4,887	IRL Perf: 23,912
CZE	{232} [416]	[36]
IRL	{32}	{1,146} [1,155]

	Ped: 133,493 – 158,357	
	CZE Perf: 5,609 – 5,734	FRA Perf: 62,810 – 66,846
CZE	{214 - 225} [299 - 325]	[150 - 176]
FRA	{63 - 73}	{2,522 - 3,000} [4,077 - 4,765]

	Ped: 20419	
	CZE Perf: 3,702	SWE Perf: 7,179
CZE	{215} [389]	[22]
SWE	{21}	{360} [405]

	Ped: 63,617	
	CZE Perf: 4,916	GBR Perf: 20,819
CZE	{240} [409]	[54]
GBR	{34}	{1,568} [2,510]

	Ped: 158,734 – 184,384	
	DNK Perf: 26,393 – 29,328	FRA Perf: 55,564 – 64,595
DNK	{1,102 – 1,165} [1,564 – 1,673]	[91 - 115]
FRA	{61 - 70}	{2,414 – 2,909} [3,872 – 4,574]

	Ped: 87,381	
	DNK Perf: 24,123	IRL Perf: 29,424
DNK	{1,021} [1,507]	[62]
IRL	{61}	{1,338} [1,328]

	Ped: 116,900	
	DNK Perf: 28,117	GBR Perf: 33,794
DNK	{1,142} [1,620]	[95]
GBR	{60}	{2,302} [3,390]

	Ped: 75,907	
	DNK Perf: 39,576	SWE Perf: 15,481
DNK	{1,539} [1,988]	[82]
SWE	{59}	{530} [526]

	Ped: 184,785 – 213,549	
	FRA Perf: 59,165 – 74,665	GBR Perf: 27,143 – 28,088
FRA	{2,336 – 2,856} [3,704 – 4,537]	[255 - 319]
GBR	{96 - 120}	{1,798 – 1,856} [2,702 – 2,768]

	Ped: 101,351 – 115,571	
	FRA Perf: 38,920 – 45,455	SWE Perf: 7,545 – 7,785
FRA	{1,945 – 2,268} [3,186 – 3,693]	[33 - 35]
SWE	{39 - 40}	{336 - 368} [397 - 423]

	Ped: 165,546 – 188,586	
	FRA Perf: 53,796 – 67,479	IRL Perf: 30,512 – 31,064
FRA	{2,314 – 2,681} [3,760 – 4,394]	[109 - 134]
IRL	{72 - 93}	{1,342 – 1,390} [1,310 – 1,348]

	Ped: 142,278	
	GBR Perf: 37,439	IRL Perf: 41,038
GBR	{2,253} [3,243]	[233]
IRL	{181}	{1,678} [1,427]

	Ped: 37,199	
	GBR Perf: 8,590	SWE Perf: 6,499
GBR	{749} [1,305]	[22]
SWE	{27}	{352} [409]

	Ped: 41,050	
	IRL Perf: 16,469	SWE Perf: 6,459
IRL	{865} [878]	[21]
SWE	{21}	{349} [407]

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).

The correlations for FRA from 7 subsets were calculated by means of following formula:

$$\mu^* = \frac{1}{SW} \sum_{i=1}^7 \frac{\mu_i}{SE_i^2}$$

where μ_i was the parameter estimate from subset i. The sum of weights (SW) was calculated using the following formula:

$$SW = \sum_{i=1}^7 \frac{1}{SE_i^2}$$

where SE_i is the standard error of the estimate from subset i.

Table 4. Environmental effects used in models

CZE	DNK	FRA	GBR	IRL	SWE
CG*	CG	CG	CG	CG	CG
	Season	Season			
Birth year					
			Birth month		
Sex x twi	Sex			Sex	Sex
	Twi				
		Parity x age dam	Parity x sex	Parity	Parity
Age dam	Age dam			Age dam**	Age dam
			Birth type		
			Purebred status		

* 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 = 0.71

	CZE	DNK	FRA	GBR	IRL	SWE
CZE						
DNK	0.95 (0.03)					
FRA	0.53 (0.13)	0.89 (0.02)				
GBR	0.95 (0.02)	0.68 (0.04)	0.59 (0.04)			
IRL	nc	0.60 (0.09)	0.98 (0.01)	0.79 (0.03)		
SWE	nc	0.47 (0.10)	0.66 (0.08)	0.48 (0.01)	nc	

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 = 0.70, average maternal genetic correlation = 0.54

	CZE	DNK	FRA	GBR	IRL	SWE
CZE		nc	nc	nc	nc	nc
DNK	nc		0.63 (0.07)	nc	nc	0.39 (0.11)
FRA	0.62 (0.08)	0.92 (0.01)		0.63 (0.08)	0.55 (0.09)	0.56 (0.10)
GBR	nc	nc	0.77 (0.03)		0.47 (0.11)	nc
IRL	nc	nc	0.88 (0.02)	0.68 (0.05)		nc
SWE	nc	0.42 (0.11)	0.64 (0.08)	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 = -0.56, 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	GBR	IRL	SWE	CZE	DNK	FRA	GBR	IRL	SWE	
DIRECT	CZE	9999												
	DNK	144	9999											
	FRA	272	260	9999										
	GBR	136	240	432	9999									
	IRL	40	244	328	724	9999								
	SWE	40	236	156	104	40	9999							
MAT.	CZE	9999	1	1	1	1	1	9999						
	DNK	1	9999	1	1	1	1	20	9999					
	FRA	1	1	9999	1	1	1	20	206	9999				
	GBR	1	1	1	9999	1	1	20	20	574	9999			
	IRL	1	1	1	1	9999	1	20	20	242	466	9999		
	SWE	1	1	1	1	1	9999	20	164	68	20	20	9999	

Table 8. Banded full Interbeef correlation matrix

Average direct genetic correlation = 0.69, average maternal genetic correlation = 0.57

		DIRECT						MATERNAL					
		CZE	DNK	FRA	GBR	IRL	SWE	CZE	DNK	FRA	GBR	IRL	SWE
DIRECT	CZE	1											
	DNK	0.76	1										
	FRA	0.51	0.80	1									
	GBR	0.85	0.70	0.72	1								
	IRL	0.63	0.64	0.87	0.79	1							
	SWE	0.60	0.46	0.62	0.57	0.87	1						
MAT.	CZE	-0.18	-0.02	-0.03	-0.06	0.02	-0.01	1					
	DNK	-0.03	-0.20	-0.16	0.00	0.03	0.04	0.59	1				
	FRA	0.08	-0.25	-0.56	-0.16	-0.27	-0.05	0.58	0.63	1			
	GBR	-0.11	0.02	-0.15	-0.35	-0.06	0.06	0.59	0.58	0.63	1		
	IRL	0.01	0.03	-0.14	-0.03	-0.16	-0.08	0.59	0.59	0.55	0.47	1	
	SWE	-0.01	0.05	-0.07	0.00	-0.03	-0.13	0.59	0.39	0.55	0.59	0.58	1

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	0.0041	0.0013	0.003		0.0733
GBR	0.04	0.02	0.01		0.28
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	GBR	SWE	CZE	DNK	FRA	IRL	GBR	SWE
DIRECT	CZE	0.0122	0.0191252	0.0036055	0.0187324	0.0110825	0.0154361	-0.001461	-0.000759	0.0003077	-0.001749	0.000095	-0.000179
	DNK	0.0191252	0.052	0.0116269	0.0321013	0.0229293	0.0243655	-0.000399	-0.010399	-0.002086	0.0006152	0.0008099	0.0021846
	FRA	0.0036055	0.0116269	0.0041	0.0092623	0.008848	0.0091686	-0.000157	-0.002329	-0.001292	-0.001391	-0.000933	-0.000888
	GBR	0.0187324	0.0321013	0.0092623	0.04	0.0249628	0.0264747	-0.00085	-4.171E-6	-0.001195	-0.009898	-0.000667	0.0001952
	IRL	0.0110825	0.0229293	0.008848	0.0249628	0.02498	0.0319016	0.0003002	0.0011916	-0.001518	-0.001459	-0.002528	-0.000897
	SWE	0.0154361	0.0243655	0.0091686	0.0264747	0.0319016	0.0533	-0.000194	0.0022889	-0.000454	0.0020385	-0.001831	-0.006002
MATERNAL	CZE	-0.001461	-0.000399	-0.000157	-0.00085	0.0003002	-0.000194	0.0054	0.0098402	0.0015434	0.006086	0.0043131	0.0086312
	DNK	-0.000759	-0.010399	-0.002329	-4.171E-6	0.0011916	0.0022889	0.0098402	0.052	0.0051628	0.0188821	0.0133698	0.0177522
	FRA	0.0003077	-0.002086	-0.001292	-0.001195	-0.001518	-0.000454	0.0015434	0.0051628	0.0013	0.0032084	0.0019781	0.0040028
	GBR	-0.001749	0.0006152	-0.001391	-0.009898	-0.001459	0.0020385	0.006086	0.0188821	0.0032084	0.02	0.0066408	0.0165709
	IRL	0.000095	0.0008099	-0.000933	-0.000667	-0.002528	-0.001831	0.0043131	0.0133698	0.0019781	0.0066408	0.01	0.0117103
	SWE	-0.000179	0.0021846	-0.000888	0.0001952	-0.000897	-0.006002	0.0086312	0.0177522	0.0040028	0.0165709	0.0117103	0.04

Table 11. Variances for permanent maternal environment

	CZE	DNK	FRA	GBR	IRL	SWE
CZE	0.004375	0	0	0	0	0
DNK	0	0.084	0	0	0	0
FRA	0	0	0.003	0	0	0
GBR	0	0	0	0.01	0	0
IRL	0	0	0	0	0.00585	0
SWE	0	0	0	0	0	0.003

Table 13. Variance for HYS for IRL

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

Table 12. Variance for HYS for CZE

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

Table 14. Residual variances

	CZE	DNK	FRA	GBR	IRL	SWE
CZE	0.0775	0	0	0	0	0
DNK	0	0.4004	0	0	0	0
FRA	0	0	0.0733	0	0	0
GBR	0	0	0	0.28	0	0
IRL	0	0	0	0	0.22709	0
SWE	0	0	0	0	0	0.2177