Interbeef international genetic evaluation for calving traits

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INTERBEEF

ČESKÝ SVAZ CHOVATELŮ MASNÉHO SKOTU

Interbeef

- International genetic evaluation for beef cattle
- Two group of traits and five breeds
  - Weaning weight – CHA, LIM, SIM, AAN, HER
  - Calving traits – CHA, LIM, SIM
- Breeding values estimated by multi-country animal model using raw performance data
- The main task for research partners is to estimate genetic correlations between countries

Interbeef

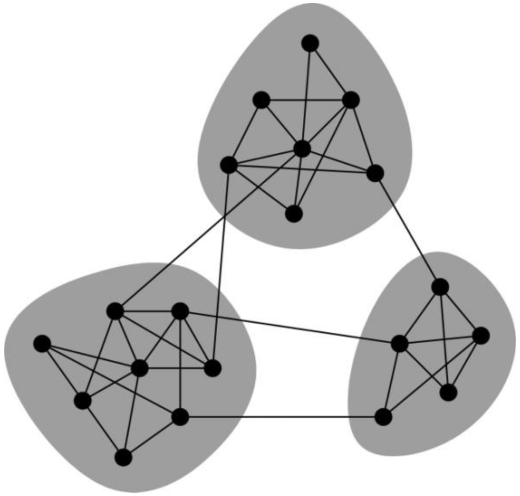
- The main difference between dairy and beef cattle breeding system from a point of view of international genetic evaluation?

Interbeef

- The main difference between dairy and beef cattle breeding system from a point of view of international genetic evaluation?

CONNECTEDNESS

Low usage of AI - low genetic connection



Percentage of population directly connectet throught common sires

CHAROLAIS					
	CZE	**DNK**	**FRA**	**IRL**	**SWE**
CZE		***4.7%***	***16.0%***	***2.2%***	***0.9%***
DNK	***13.6%***		***9.3%***	***10.3%***	***2.6%***
FRA	***30.1%***	***7.0%***		***21.8%***	***1.1%***
IRL	***11.3%***	***5.3%***	***8.6%***		***0.6%***
SWE	***11.6%***	***5.9%***	***7.7%***	***1.3%***	

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	CZE	**DNK**	**FRA**	**IRL**	**SWE**
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IRL	*11.3%*	*5.3%*	*8.6%*		*0.6%*
SWE	*11.6%*	*5.9%*	*7.7%*	*1.3%*	

LIMOUSINE						
	CZE	**DNK**	**FRA**	**GBR**	**IRL**	**SWE**
CZE		*4.1%*	*10.6%*	*3.0%*	*13.1%*	*2.4%*
DNK	*16.4%*		*9.5%*	*4.2%*	*15.9%*	*8.1%*
FRA	*29.4%*	*4.9%*		*7.5%*	*23.7%*	*3.1%*
GBR	*15.4%*	*3.8%*	*11.4%*		*34.8%*	*1.9%*
IRL	*17.4%*	*2.9%*	*10.9%*	*15.4%*		*1.6%*
SWE	*12.6%*	*10.3%*	*9.4%*	*1.3%*	*9.5%*	

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CZE		*4.1%*	*10.6%*	*3.0%*	*13.1%*	*2.4%*
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IRL	*17.4%*	*2.9%*	*10.9%*	*15.4%*		*1.6%*
SWE	*12.6%*	*10.3%*	*9.4%*	*1.3%*	*9.5%*	

Creating datasets for genetic parameters estimation

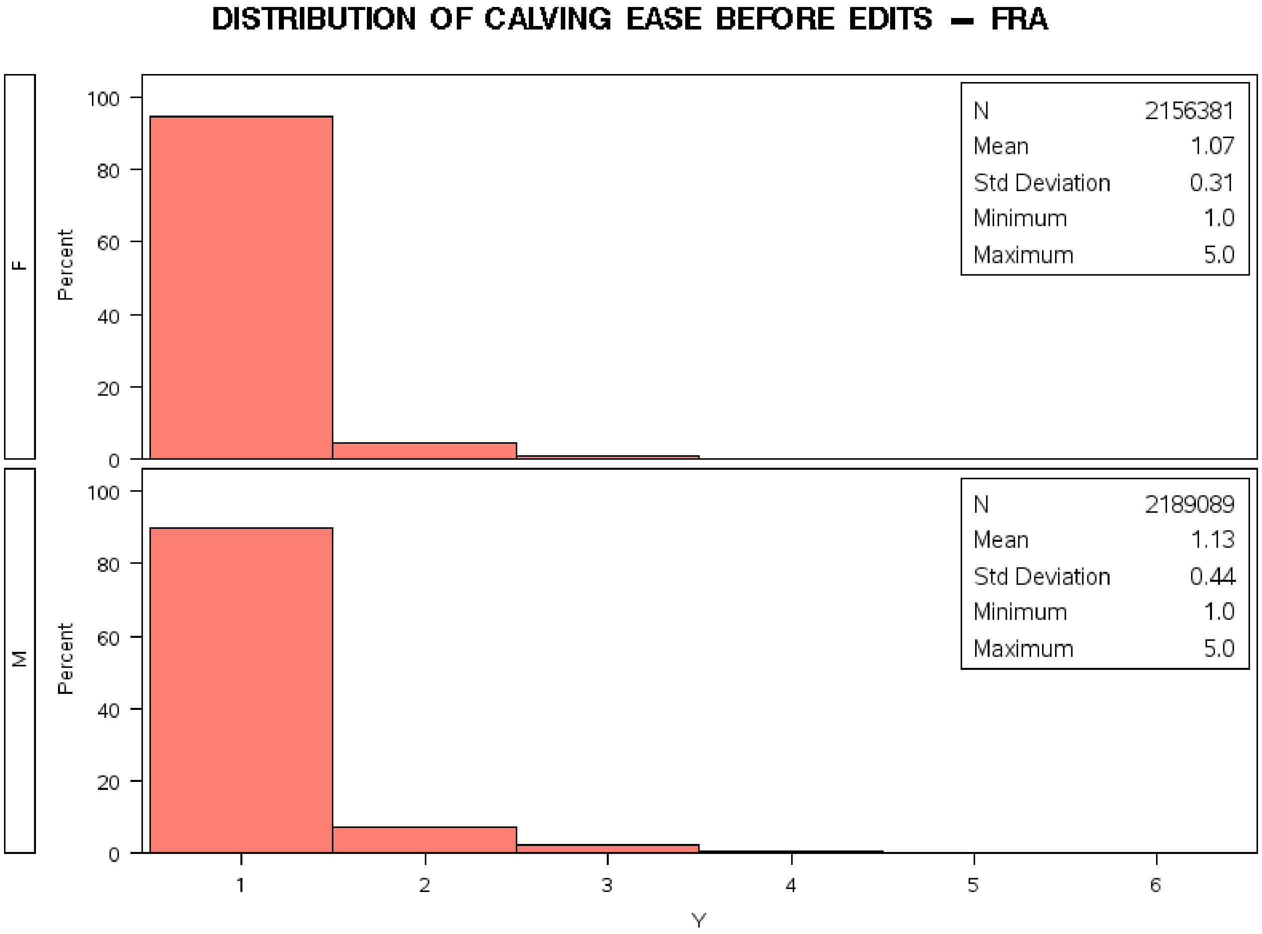
1. Assigning alternative IDs to calves without registration IDs
   - „UUUUUUUUUUUUUUUUUUU“
   - Merging with pedigree
2. Exclusion of ETs
3. Exclusion of calves with unknown sire and MGS

Creating datasets for genetic parameters estimation

4. Exclusion of herds without variation (CAE)

Creating datasets for genetic parameters estimation

4. Exclusion of herds without variation (CAE)



Creating datasets for genetic parameters estimation

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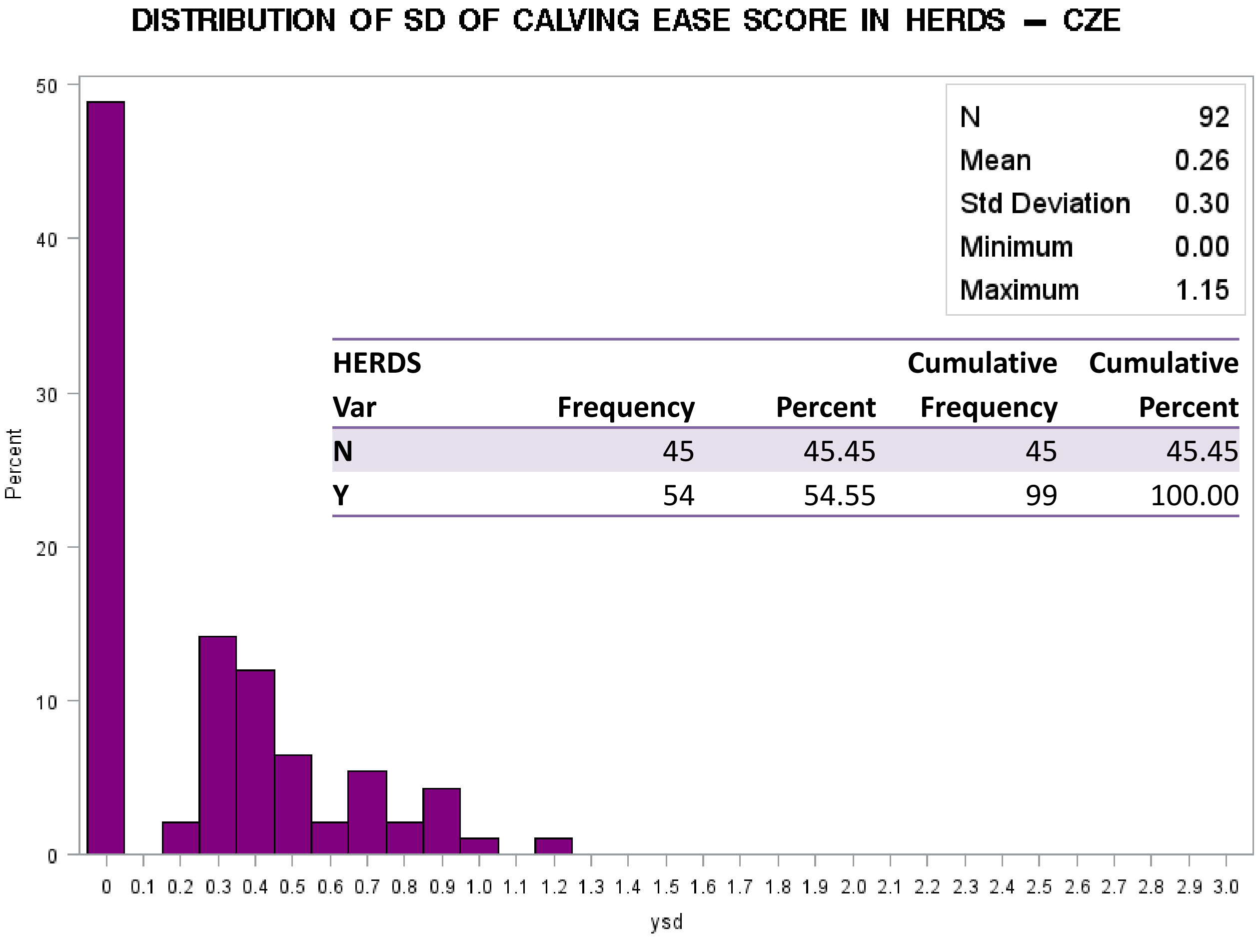

DISTRIBUTION OF SD OF CALVING EASE SCORE IN HERDS – CZE

N	92
Mean	0.26
Std Deviation	0.30
Minimum	0.00
Maximum	1.15

HERDS Var	Frequency	Percent	Cumulative Frequency	Cumulative Percent
N	45	45.45	45	45.45
Y	54	54.55	99	100.00

Creating datasets for genetic parameters estimation

4. Exclusion of herds without variation (CAE)

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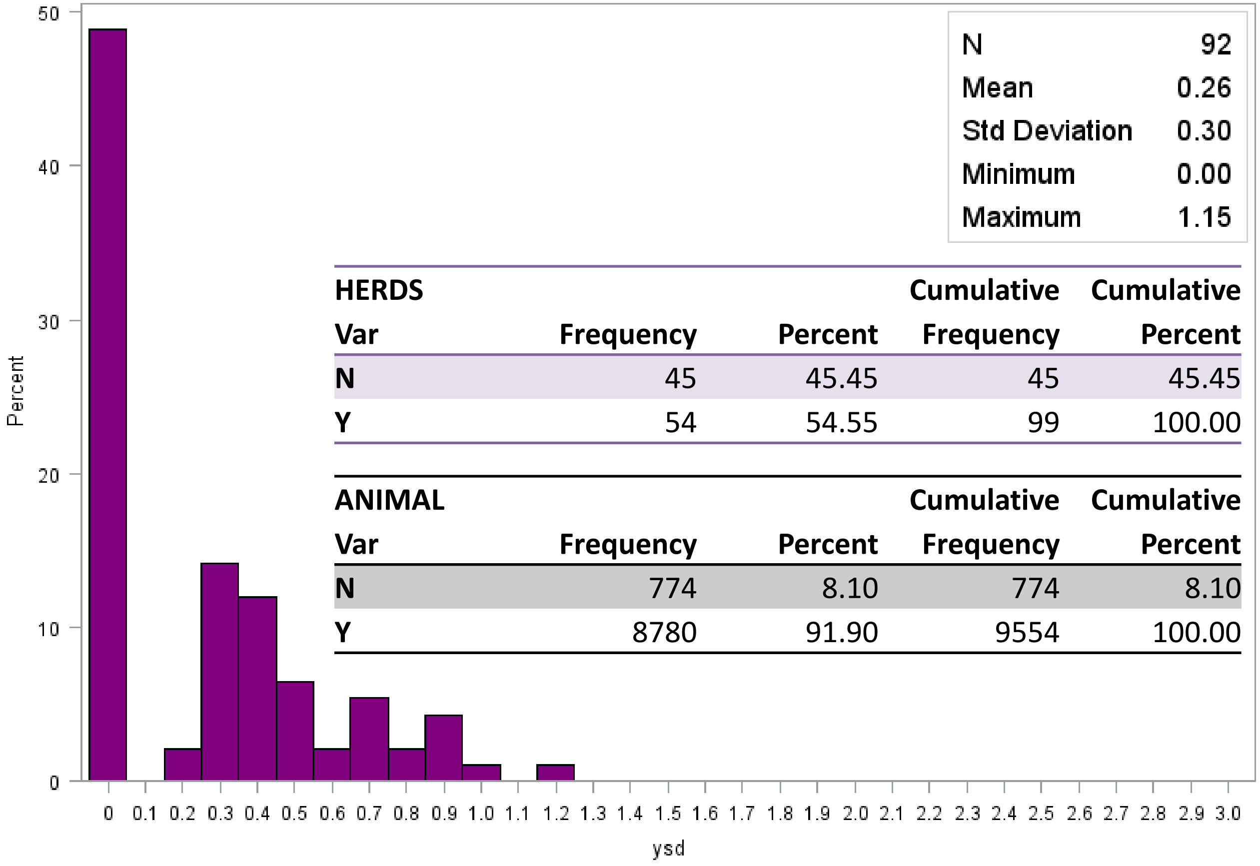

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Mean	0.26
Std Deviation	0.30
Minimum	0.00
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HERDS Var	Frequency	Percent	Cumulative Frequency	Cumulative Percent
N	45	45.45	45	45.45
Y	54	54.55	99	100.00

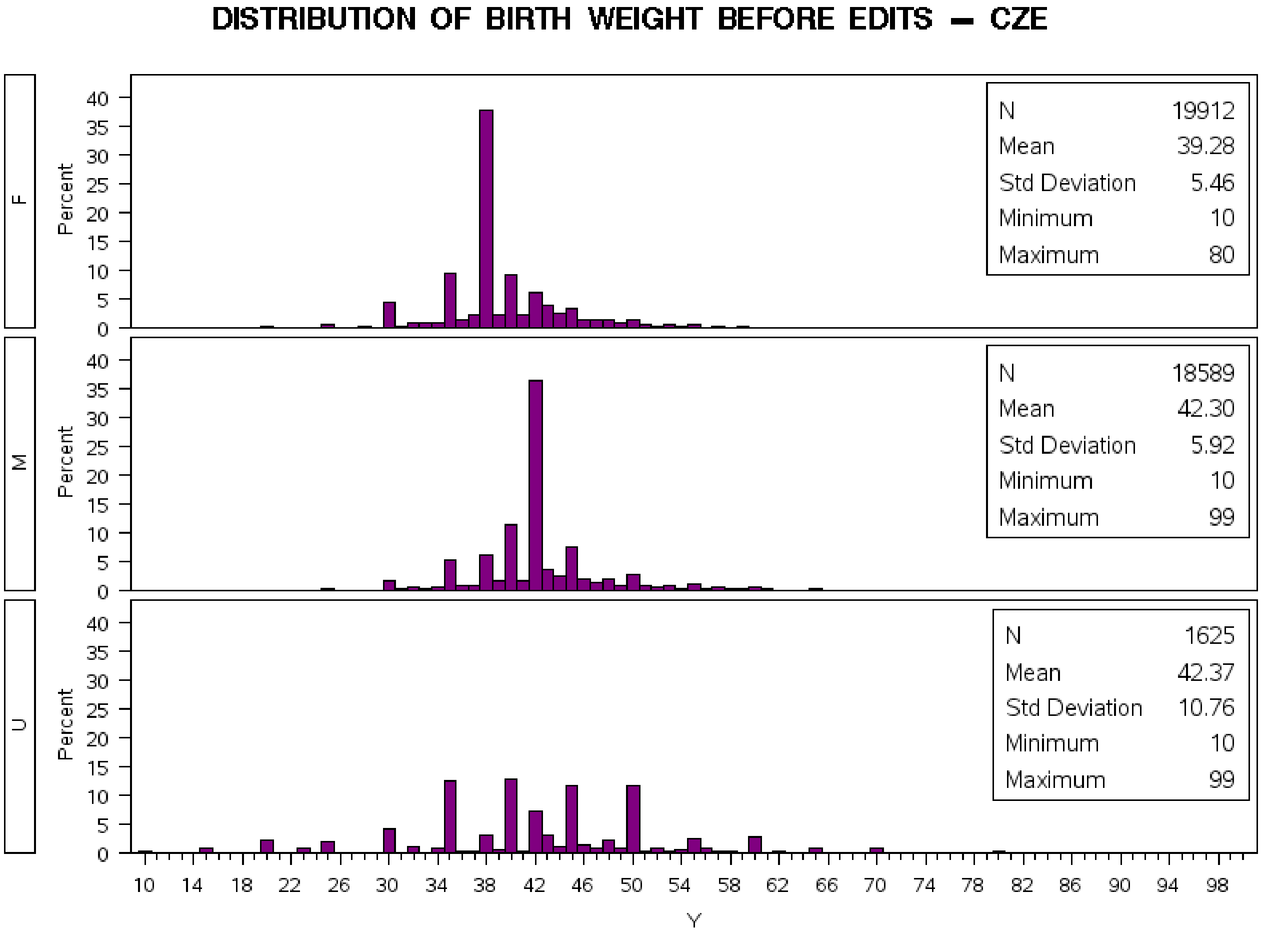
ANIMAL Var	Frequency	Percent	Cumulative Frequency	Cumulative Percent
N	774	8.10	774	8.10
Y	8780	91.90	9554	100.00

Creating datasets for genetic parameters estimation

4. Exclusion of herds + sex without variation (BWT)

Creating datasets for genetic parameters estimation

4. Exclusion of herds + sex without variation


DISTRIBUTION OF BIRTH WEIGHT BEFORE EDITS – CZE

Creating datasets for genetic parameters estimation

5. Exclusion of CG smaller than 5
6. Exclusion of performances < 1980
7. Running ICBF SAS code (Thierry Pabiou)
    - Basic principle:
        - Creating datasets based on connectedness across sires in 3 generations
    1. Retrieve animals with performance linked to common ancestors
    2. Retrieve additional animals with performance present in the selected CGs
5. Build pedigree file

Estimation of genetic correlations

- We estimated genetic correlations for 2 x 2 country combinations
- Software used BLUPF90 family from Ignacy Misztal et al.
  - AIREML1F90
  - GIBBS1F90

LIMOUSINE

- Two traits:
  - Calving ease - CAE
  - Birth weight - BWT
- Five populations:
  - Czech Republic - CZE
  - Denmark, Finland, Sweden - DFS
  - France - FRA
  - Great Britain - GBR
  - Ireland - IRL

Full CAE + BWT model

LIMOUSINE

1. Correlations estimate by 2 x 2 country analysis

			DIR										MAT							
			BWT					CAE					BWT				CAE			
			CZE	DFS	FRA	GBR	IRL	CZE	DFS	FRA	GBR	IRL	CZE	DFS	FRA	GBR	CZE	DFS	FRA	GBR
DIR	BWT	CZE	ITB correlations																	
		DFS																		
		FRA																		
		GBR																		
		IRL																		
	CAE	CZE						ITB correlations												
		DFS																		
		FRA																		
		GBR																		
		IRL																		
MAT	BWT	CZE											ITB correlations							
		DFS																		
		FRA																		
		GBR																		
	CAE	CZE															ITB correlations			
		DFS																		
		FRA																		
		GBR																		

Full CAE + BWT model

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1. Correlations estimate by 2 x 2 country analysis

			DIR										MAT							
			BWT					CAE					BWT				CAE			
			CZE	DFS	FRA	GBR	IRL	CZE	DFS	FRA	GBR	IRL	CZE	DFS	FRA	GBR	CZE	DFS	FRA	GBR
DIR	BWT	CZE																		
		DFS	0.9																	
		FRA	0.95	0.83																
		GBR	0.82	0.85	0.8															
		IRL	Nc	0.87	Nc	0.84														
	CAE	CZE																		
		DFS						Nc												
		FRA						0.62	0.76											
		GBR						0.75	0.68	0.73										
		IRL						0.65	0.64	0.88	0.86									
MAT	BWT	CZE																		
		DFS											Nc							
		FRA											Nc	0.72						
		GBR											Nc	0.39	0.41					
	CAE	CZE																		
		DFS															Nc			
		FRA															0.56	0.54		
		GBR															Nc	Nc	0.67	

Full CAE + BWT model

LIMOUSINE

2. Non-converged correlations were set to average values

			DIR										MAT							
			BWT					CAE					BWT				CAE			
			CZE	DFS	FRA	GBR	IRL	CZE	DFS	FRA	GBR	IRL	CZE	DFS	FRA	GBR	CZE	DFS	FRA	GBR
DIR	BWT	CZE																		
		DFS	0.9																	
		FRA	0.95	0.83																
		GBR	0.82	0.85	0.8															
		IRL	0.86	0.87	0.86	0.84														
	CAE	CZE																		
		DFS						0.73												
		FRA						0.62	0.76											
		GBR						0.75	0.68	0.73										
		IRL						0.65	0.64	0.88	0.86									
MAT	BWT	CZE																		
		DFS											0.51							
		FRA											0.51	0.72						
		GBR											0.51	0.39	0.41					
	CAE	CZE																		
		DFS															0.59			
		FRA															0.56	0.54		
		GBR															0.59	0.59	0.67	

Full CAE + BWT model

LIMOUSINE

3. Matrices were then bended with standard errors used as weights

			DIR										MAT							
			BWT					CAE					BWT				CAE			
			CZE	DFS	FRA	GBR	IRL	CZE	DFS	FRA	GBR	IRL	CZE	DFS	FRA	GBR	CZE	DFS	FRA	GBR
DIR	BWT	CZE																		
		DFS	0.9																	
		FRA	0.95	0.83																
		GBR	0.82	0.85	0.8															
		IRL	0.86	0.87	0.86	0.84														
	CAE	CZE																		
		DFS						0.73												
		FRA						0.62	0.76											
		GBR						0.75	0.68	0.73										
		IRL						0.65	0.64	0.88	0.86									
MAT	BWT	CZE																		
		DFS											0.51							
		FRA											0.51	0.72						
		GBR											0.51	0.39	0.41					
	CAE	CZE																		
		DFS															0.59			
		FRA															0.56	0.54		
		GBR															0.59	0.59	0.67	

Full CAE + BWT model

LIMOUSINE

4. The full matrix was created with:

   BWT-CAE and direct-maternal correlations within countries from national evaluation

			DIR										MAT							
			BWT					CAE					BWT				CAE			
			CZE	DFS	FRA	GBR	IRL	CZE	DFS	FRA	GBR	IRL	CZE	DFS	FRA	GBR	CZE	DFS	FRA	GBR
DIR	BWT	CZE																		
		DFS	0.9																	
		FRA	0.95	0.83																
		GBR	0.82	0.85	0.8															
		IRL	0.86	0.87	0.86	0.84														
	CAE	CZE	**0.25**																	
		DFS		**0**				0.73												
		FRA			**0.69**			0.62	0.76											
		GBR				**0.53**		0.75	0.68	0.73										
		IRL					**0.37**	0.65	0.64	0.88	0.86									
MAT	BWT	CZE	**-0.48**					**-0.01**												
		DFS		**-0.15**					**0**				0.51							
		FRA			**-0.61**					**-0.2**			0.51	0.72						
		GBR				**-0.37**					**-0.15**		0.51	0.39	0.41					
	CAE	CZE	**0.04**					**-0.47**					**0.42**							
		DFS		**0**					**-0.2**					**0**			0.59			
		FRA			**-0.45**					**-0.56**					**0.28**		0.56	0.54		
		GBR				**0**					**-0.35**					**0**	0.59	0.59	0.67	

Full CAE + BWT model

LIMOUSINE

4. The full matrix was created with:

   BWT-CAE and direct-maternal correlations between countries set to 0

			DIR										MAT							
			BWT					CAE					BWT				CAE			
			CZE	DFS	FRA	GBR	IRL	CZE	DFS	FRA	GBR	IRL	CZE	DFS	FRA	GBR	CZE	DFS	FRA	GBR
DIR	BWT	CZE																		
		DFS	0.9																	
		FRA	0.95	0.83																
		GBR	0.82	0.85	0.8															
		IRL	0.86	0.87	0.86	0.84														
	CAE	CZE	**0.25**	0	0	0	0													
		DFS	0	**0**	0	0	0	0.73												
		FRA	0	0	**0.69**	0	0	0.62	0.76											
		GBR	0	0	0	**0.53**	0	0.75	0.68	0.73										
		IRL	0	0	0	0	**0.37**	0.65	0.64	0.88	0.86									
MAT	BWT	CZE	**-0.48**	0	0	0	0	**-0.01**	0	0	0	0								
		DFS	0	**-0.15**	0	0	0	0	**0**	0	0	0	0.51							
		FRA	0	0	**-0.61**	0	0	0	0	**-0.2**	0	0	0.51	0.72						
		GBR	0	0	0	**-0.37**	0	0	0	0	**-0.15**	0	0.51	0.39	0.41					
	CAE	CZE	**0.04**	0	0	0	0	**-0.47**	0	0	0	0	**0.42**	0	0	0				
		DFS	0	**0**	0	0	0	0	**-0.2**	0	0	0	0	**0**	0	0	0.59			
		FRA	0	0	**-0.45**	0	0	0	0	**-0.56**	0	0	0	0	**0.28**	0	0.56	0.54		
		GBR	0	0	0	**0**	0	0	0	0	**-0.35**	0	0	0	0	**0**	0.59	0.59	0.67	

Full CAE + BWT model

LIMOUSINE

5. Full correlation matrix was bended (Jorjani et al.) with weighting factor equal to the reciprocal number of common sires

			DIR										MAT							
			BWT					CAE					BWT				CAE			
			CZE	DFS	FRA	GBR	IRL	CZE	DFS	FRA	GBR	IRL	CZE	DFS	FRA	GBR	CZE	DFS	FRA	GBR
DIR	BWT	CZE																		
		DFS	0.87																	
		FRA	0.87	0.80																
		GBR	0.78	0.81	0.73															
		IRL	0.72	0.83	0.68	0.79														
	CAE	CZE	**0.25**	0.08	0.27	0.25	0.1													
		DFS	0.11	**0**	0.26	0.12	-0.1	0.62												
		FRA	0.41	0.28	**0.68**	0.38	0.35	0.60	0.73											
		GBR	0.21	0.13	0.33	**0.53**	0.27	0.71	0.66	0.71										
		IRL	0.17	0.06	0.38	0.33	**0.37**	0.63	0.63	0.84	0.85									
MAT	BWT	CZE	**-0.48**	-0.17	-0.28	-0.15	-0.1	**-0.01**	0.09	0.02	0.11	0.12								
		DFS	-0.1	**-0.15**	-0.19	-0.04	0	0.06	**0**	0.04	0.02	0.03	0.42							
		FRA	-0.43	-0.32	**-0.61**	-0.22	-0.1	0.06	0.05	**-0.2**	0.09	0.06	0.43	0.69						
		GBR	-0.12	-0.03	-0.13	**-0.37**	0	0.08	0.02	0.05	**-0.15**	0.02	0.42	0.37	0.38					
	CAE	CZE	**0.04**	0.16	0.04	0.13	0.13	**-0.47**	-0.04	-0.11	-0.12	-0.06	**0.42**	0.08	-0.01	0.06				
		DFS	0.09	**0**	-0.03	0.01	0.01	-0.04	**-0.2**	-0.1	-0.02	0.05	0.05	**0**	-0.01	0.01	0.50			
		FRA	-0.11	-0.1	**-0.45**	-0.06	-0.1	-0.14	-0.17	**-0.56**	-0.14	-0.23	0.09	-0.04	**0.28**	-0.05	0.52	0.52		
		GBR	0.1	0.03	-0.06	**0.05**	0.05	-0.08	0	-0.16	**-0.35**	-0.1	0.02	0	-0.02	**0.01**	0.50	0.51	0.63	

Full CAE + BWT model

LIMOUSINE

5. Full correlation matrix was bended (Jorjani et al.) with weighting factor equal to the reciprocal number of common sires

			DIR										MAT							
			BWT					CAE					BWT				CAE			
			CZE	DFS	FRA	GBR	IRL	CZE	DFS	FRA	GBR	IRL	CZE	DFS	FRA	GBR	CZE	DFS	FRA	GBR
DIR	BWT	CZE																		
		DFS	0.87																	
		FRA	0.87	0.80																
		GBR	0.78	0.81	0.73															
		IRL	0.72	0.83	0.68	0.79														
	CAE	CZE	**0.25**	0.08	0.27	0.25	0.1													
		DFS	0.11	**0**	0.26	0.12	-0.1	0.62												
		FRA	0.41	0.28	**0.68**	0.38	0.35	0.60	0.73											
		GBR	0.21	0.13	0.33	**0.53**	0.27	0.71	0.66	0.71										
		IRL	0.17	0.06	0.38	0.33	**0.37**	0.63	0.63	0.84	0.85									
MAT	BWT	CZE	**-0.48**	-0.17	-0.28	-0.15	-0.1	**-0.01**	0.09	0.02	0.11	0.12								
		DFS	-0.1	**-0.15**	-0.19	-0.04	0	0.06	**0**	0.04	0.02	0.03	0.42							
		FRA	-0.43	-0.32	**-0.61**	-0.22	-0.1	0.06	0.05	**-0.2**	0.09	0.06	0.43	0.69						
		GBR	-0.12	-0.03	-0.13	**-0.37**	0	0.08	0.02	0.05	**-0.15**	0.02	0.42	0.37	0.38					
	CAE	CZE	**0.04**	0.16	0.04	0.13	0.13	**-0.47**	-0.04	-0.11	-0.12	-0.06	**0.42**	0.08	-0.01	0.06				
		DFS	0.09	**0**	-0.03	0.01	0.01	-0.04	**-0.2**	-0.1	-0.02	0.05	0.05	**0**	-0.01	0.01	0.50			
		FRA	-0.11	-0.1	**-0.45**	-0.06	-0.1	-0.14	-0.17	**-0.56**	-0.14	-0.23	0.09	-0.04	**0.28**	-0.05	0.52	0.52		
		GBR	0.1	0.03	-0.06	**0.05**	0.05	-0.08	0	-0.16	**-0.35**	-0.1	0.02	0	-0.02	**0.01**	0.50	0.51	0.63	

Average direct genetic correlations:	0.79 (BWT), 0.70 (CAE)
Average maternal genetic correlations:	0.45 (BWT), 0.53 (CAE)

CHAROLAIS

- Two traits:
  - Calving ease - CAE
  - Birth weight - BWT
- Five populations:
  - Czech Republic - CZE
  - Denmark, Finland, Sweden - DFS
  - France – FRA
  - Ireland - IRL
  - Republic of South Africa – ZAF (only BWT)

Full CAE + BWT model

CHAROLAIS

FULL BENDED ITB GENETIC CORRELATION MATRIX:

			DIR									MAT						
			BWT					CAE				BWT				CAE		
			CZE	DFS	FRA	IRL	ZAF	CZE	DFS	FRA	IRL	CZE	DFS	FRA	ZAF	CZE	DFS	FRA
DIR	BWT	CZE																
		DFS	0.64															
		FRA	0.60	0.86														
		IRL	0.66	0.83	0.83													
		ZAF	0.81	0.55	0.64	0.63												
	CAE	CZE	**0.25**	-0.05	0.31	0.12	0.11											
		DFS	0.08	**0.00**	0.21	0.00	-0.07	0.70										
		FRA	0.29	0.51	**0.83**	0.54	0.30	0.66	0.59									
		IRL	0.01	0.05	0.36	**0.37**	-0.03	0.72	0.68	0.70								
MAT	BWT	CZE	**-0.48**	-0.12	-0.04	-0.09	-0.13	**-0.01**	0.10	0.12	0.10							
		DFS	-0.12	**-0.15**	-0.08	0.00	0.06	0.01	**0.00**	-0.01	0.01	0.61						
		FRA	-0.03	-0.22	**-0.48**	-0.11	-0.12	0.04	0.01	-**0.47**	-0.02	0.31	0.44					
		ZAF	-0.07	0.04	-0.05	0.03	**-0.03**	0.07	-0.01	-0.02	-0.01	0.47	0.47	0.52				
	CAE	CZE	**-0.04**	0.12	0.04	0.11	0.11	**-0.47**	-0.09	-0.13	-0.12	**0.42**	0.08	0.12	0.03			
		DFS	0.09	**0.00**	-0.01	-0.01	-0.01	-0.08	**-0.02**	-0.04	0.03	0.09	**0.00**	0.05	-0.03	0.58		
		FRA	0.15	-0.02	**-0.30**	0.01	0.01	-0.14	-0.02	**-0.4**	0.00	0.12	0.02	**0.69**	0.06	0.58	0.59	

Average direct genetic correlations: 0.70 (BWT), 0.67 (CAE)

Average maternal genetic correlations: 0.47 (BWT), 0.58 (CAE)

Full CAE + BWT model

CHAROLAIS

FULL BENDED ITB GENETIC CORRELATION MATRIX:

			DIR									MAT						
			BWT					CAE				BWT				CAE		
			CZE	DFS	FRA	IRL	ZAF	CZE	DFS	FRA	IRL	CZE	DFS	FRA	ZAF	CZE	DFS	FRA
DIR	BWT	CZE																
		DFS	0.64															
		FRA	0.60	0.86														
		IRL	0.66	0.83	0.83													
		ZAF	0.81	0.55	0.64	0.63												
	CAE	CZE	**0.25**	-0.05	0.31	0.12	0.11											
		DFS	0.08	**0.00**	0.21	0.00	-0.07	0.70										
		FRA	0.29	0.51	**0.83**	0.54	0.30	0.66	0.59									
		IRL	0.01	0.05	0.36	**0.37**	-0.03	0.72	0.68	0.70								
MAT	BWT	CZE	**-0.48**	-0.12	-0.04	-0.09	-0.13	**-0.01**	0.10	0.12	0.10							
		DFS	-0.12	**-0.15**	-0.08	0.00	0.06	0.01	**0.00**	-0.01	0.01	0.61						
		FRA	-0.03	-0.22	**-0.48**	-0.11	-0.12	0.04	0.01	**-0.47**	-0.02	0.31	0.44					
		ZAF	-0.07	0.04	-0.05	0.03	**-0.03**	0.07	-0.01	-0.02	-0.01	0.47	0.47	0.52				
	CAE	CZE	**-0.04**	0.12	0.04	0.11	0.11	**-0.47**	-0.09	-0.13	-0.12	**0.42**	0.08	0.12	0.03			
		DFS	0.09	**0.00**	-0.01	-0.01	-0.01	-0.08	**-0.02**	-0.04	0.03	0.09	**0.00**	0.05	-0.03	0.58		
		FRA	0.15	-0.02	**-0.30**	0.01	0.01	-0.14	-0.02	**-0.4**	0.00	0.12	0.02	**0.69**	0.06	0.58	0.59	

Average direct genetic correlations:	0.70 (BWT), 0.67 (CAE)
Average maternal genetic correlations:	0.47 (BWT), 0.58 (CAE)

BEEF SIMMENTAL

- Two traits:
  - Calving ease - CAE
  - Birth weight - BWT
- Four populations:
  - Czech Republic - CZE
  - Denmark, Finland, Sweden – DFS
  - Ireland - IRL
  - Germany – DEU (only CAE)

Full CAE + BWT model

BEEF SIMMENTAL

FULL BENDED ITB GENETIC CORRELATION MATRIX:

			DIR							MAT			
			BWT			CAE				BWT		CAE	
			CZE	DFS	IRL	CZE	DFS	IRL	DEU	CZE	DFS	CZE	DFS
DIR	BWT	CZE											
		DFS	0.85										
		IRL	0.83	0.84									
	CAE	CZE	**0.25**	0.01	0.43								
		DFS	0.08	**0.00**	0.51	0.60							
		IRL	0.47	0.41	**0.83**	0.68	0.89						
		DEU	0.01	-0.05	-0.01	0.27	0.17	0.08					
MAT	BW	CZE	**-0.48**	-0.15	-0.12	**-0.01**	0.10	0.04	0.02				
		DFS	-0.10	**-0.15**	-0.06	0.07	**0.00**	0.00	-0.01	0.49			
	CAE	CZE	**0.04**	0.14	0.08	**-0.47**	-0.11	-0.06	-0.03	**0.42**	0.08		
		DFS	0.14	**0.00**	-0.01	-0.14	**-0.20**	-0.10	0.01	0.14	**0.00**	0.79	

Full CAE + BWT model

BEEF SIMMENTAL

FULL BENDED ITB GENETIC CORRELATION MATRIX:

			DIR							MAT			
			BWT			CAE				BWT		CAE	
			CZE	DFS	IRL	CZE	DFS	IRL	DEU	CZE	DFS	CZE	DFS
DIR	BWT	CZE											
		DFS	0.85										
		IRL	0.83	0.84									
	CAE	CZE	**0.25**	0.01	0.43								
		DFS	0.08	**0.00**	0.51	0.60							
		IRL	0.47	0.41	**0.83**	0.68	0.89						
		DEU	0.01	-0.05	-0.01	0.27	0.17	0.08					
MAT	BW	CZE	**-0.48**	-0.15	-0.12	**-0.01**	0.10	0.04	0.02				
		DFS	-0.10	**-0.15**	-0.06	0.07	**0.00**	0.00	-0.01	0.49			
	CAE	CZE	**0.04**	0.14	0.08	**-0.47**	-0.11	-0.06	-0.03	**0.42**	0.08		
		DFS	0.14	**0.00**	-0.01	-0.14	**-0.20**	-0.10	0.01	0.14	**0.00**	0.79	

Average direct genetic correlations:	0.84 (BWT), 0.44 (CAE)
Average maternal genetic correlations:	0.49 (BWT), 0.79 (CAE)

ITB breeding values for BWT + CAE

- Animal model
  - Direct genetic effect (all countries)
  - Maternal permanent environmental effect (all countries)
  - Maternal genetic effect (except DEU, IRL)
- MIX99
- Variance and covariance components
  - Variances from national evaluations
  - Covariances calculated from ITB correlation matrix
- Environmental effects
  - Defined from national evalutions

Next steps

- New countries
- Crossbred animals
- New breeds:
  - – Aberdeen Angus
  - – Hereford

Thank you for your attention

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