

Research on development of international beef genetic evaluations for calving traits

Research report prepared by Czech Research Team

*ICAR/Interbeef Genomics Workshop
24 – 27 November 2014*



VÚŽV, v.v.i.



INSTITUTE OF ANIMAL SCIENCE
PRAHA UHŘÍNĚVES

InterBeef – Calving traits research

- Birth weight - BWT
- Calving ease - CAE
- Stillbirth - STB

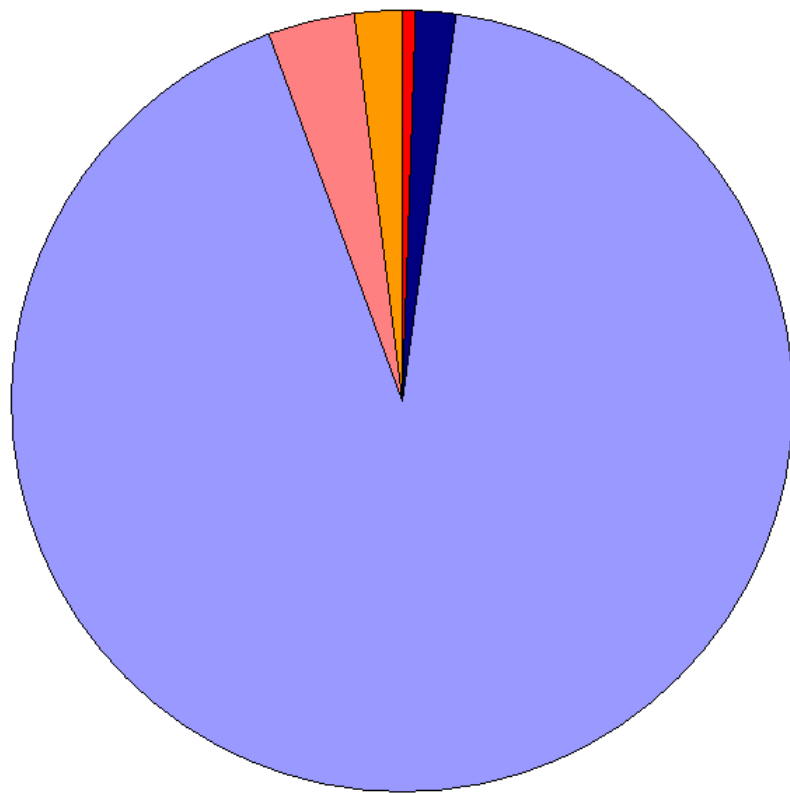
InterBeef – Calving traits research

	CHAROLAIS			LIMOUSINE		
	BWT	CAE	STB	BWT	CAE	STB
CZE	Y	Y	-	Y	Y	-
DNK	Y	Y	Y	Y	Y	Y
ESP	-	-	-	Y	-	-
FRA	Y	Y	-	Y	Y	-
GRB	-	-	-	Y	Y	-
IRL	-	Y	Y	-	Y	Y
SWE	Y	Y	-	Y	Y	-

InterBeef – Calving traits research

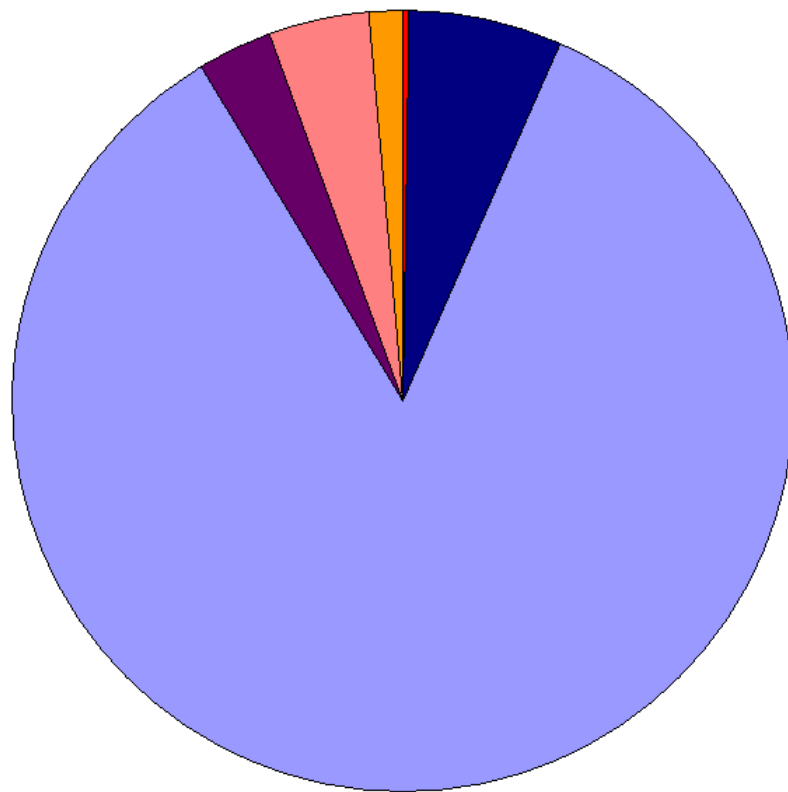
CALVING EASE

Charolais

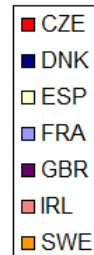


N = 6,775,318

Limousine



N = 4,055,484



Current situation in research

- What has been done
 - Loading and checking of datasets
 - Basic statistical characteristics
 - Connectedness between countries
 - Genetic parameters estimation

Connectedness

- Across-country connection
- Important for estimation of genetic correlations

RELATIVE NUMBER OF OFFSPRING OF COMMON SIRE

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%	

LIMOUSINE						
	CZE	DNK	FRA	GBR	IRL	SWE
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Creating datasets for genetic parameters estimation

- 2 x 2 country
- Basic principle:
 - Creating datasets based on connectedness across sires in 3 generations (ICBF software)
 1. Retrieve animals with performance linked to common ancestors
 2. Retrieve additional animals with performance present in the selected CGs
 - Performance file can't exceed 100,000 lines

Genetic parameters estimation

- Estimation of genetic parameters for 2 x 2 country
- Software BLUPF90 Family (Ignacy Misztal)
 - AIREML1F90
 - GIBBSF90

Models

- 2 x 2 analysis

- Linear model

1. AM with direct genetic effect and MPE

- residual correlation = 0
- MPE correlation = 0
- Software: airemlf90

2. AM with direct and maternal genetic effect and MPE

- direct – maternal correlations = 0
- residual correlation = 0
- MPE correlation = 0
- Software: gibbs1f90

		COUNTRY 1		COUNTRY 2	
		dir1	mat1	dir2	mat2
COUNTRY 1	dir1	var_{dir1}			
	mat1	0^*	var_{mat1}		
COUNTRY 2	dir2	$\text{cov}_{\text{dir1,dir2}}$	0^*	var_{dir2}	
	mat2	0^*	$\text{cov}_{\text{mat1,mat2}}$	0^*	var_{mat2}

Full correlation matrix

1. CORRELATION MATRIX FOR DIRECT EFFECT

- All correlations non-converged and correlations < 0.2 from 2. AM-DE-ME-MPE were set to their value from AM-DE-MPE.
- All correlations non-converged from both models and correlation < 0.2 were set to 0.71 for LIM and 0.68 for CHA with SD 0.25
- Bending (Jorjani et al., 2003) - SD of estimated correlations were used for weighting.

2. CORRELATION MATRIX FOR MATERNAL EFFECT

- All correlations non-converged and correlations < 0.25 were set to 0.53 for LIM and 0.51 for CHA with SD 0.13.
- Bending - SD of estimated correlations were used for weighting.

3. FULL CORRELATION MATRIX

- Correlations between direct and maternal genetic effect from national genetic evaluation in participant countries
- Bending - Numbers of bulls and common bulls were used for weighting.

LIM – Bended full matrix

		DIRECT						MATERNAL					
		CZE	DNK	FRA	GBR	IRL	SWE	CZE	DNK	FRA	GBR	IRL	SWE
DIRECT	CZE												
	DNK	0.76											
	FRA	0.52	0.78										
	GBR	0.84	0.67	0.71									
	IRL	0.62	0.64	0.90	0.80								
	SWE	0.58	0.45	0.62	0.55	0.83							
MATERNAL	CZE	-0.18	0.00	-0.03	-0.01	0.01	0.00						
	DNK	-0.04	-0.20	-0.16	0.05	0.02	0.05	0.53					
	FRA	0.08	-0.26	-0.56	-0.10	-0.30	-0.06	0.53	0.63				
	GBR	-0.02	0.04	-0.10	-0.05	0.01	0.03	0.53	0.53	0.63			
	IRL	0.01	0.05	-0.19	-0.04	-0.22	-0.06	0.53	0.53	0.55	0.46		
	SWE	-0.02	0.04	-0.08	0.04	-0.03	-0.11	0.52	0.39	0.55	0.52	0.52	

Average direct genetic correlation = 0.68; Average maternal genetic correlation = 0.53

CHA – Bended full matrix

		DIRECT					MATERNAL				
		CZE	DNK	FRA	IRL	SWE	CZE	DNK	FRA	IRL	SWE
DIRECT	CZE										
	DNK	0.41									
	FRA	0.41	0.76								
	IRL	0.80	0.47	0.63							
	SWE	0.68	0.82	0.60	0.52						
MATERNAL	CZE	-0.17	0.02	-0.02	0.00	-0.01					
	DNK	0.00	-0.18	-0.02	0.00	-0.01	0.48				
	FRA	0.01	-0.04	-0.46	-0.03	0.01	0.66	0.37			
	IRL	-0.01	0.00	0.00	-0.21	0.01	0.55	0.59	0.35		
	SWE	0.00	0.00	-0.01	0.01	-0.11	0.51	0.51	0.49	0.51	

Average direct genetic correlation = 0.61; Average maternal genetic correlation = 0.50

Thank you for your attention

