Interbeef international genetic evaluation for calving traits

Z. Vesela[1], M. Brzakova[1], A. Svitakova[1], L. Vostry[1] and P. Bucek[2]

[1]Institute of Animal Science, Pratelstvi 815, 10400, Prague Uhrineves, Czech Republic
[2]Czech Moravian Breeders' Corporation, Benesovska 123,
25209, Hradistko, Czech Republic

Abstract

Since 2007, Interbull Centre, with the help of ICBF (Ireland) and INRA (France), has developed the different tools to run Interbeef joint genetic evaluation of beef cattle. The first official run was performed in 2014 on Charolais (CHA) and Limousine (LIM) weaning weight. The second group of traits of interest was calving traits (calving ease - CAE and birth weight - BWT). The Czech Republic (Institute of Animal Science) is responsible for the estimation of genetic correlations between countries and for the development of international genetic evaluation for these traits. The first official routine run for calving traits was performed in 2018 for CHA, LIM, and Beef Simmental (BSM). The model chosen for international genetic evaluation is an animal multiple trait model based on raw performance data and considering each country as a separated trait. The both calving traits (CAE and BWT) are evaluated jointly as correlated traits in multiple trait model as well. Nine countries are currently involved in international genetic evaluation for calving traits:

1. for all breeds Czech Republic, Denmark, Finland, Ireland, Sweden.
2. for LIM and CHA France.
3. for CHA South African Republic.
4. for LIM United Kingdom and
5. for BSM Germany.

Across-country genetic correlations were estimated by two series of pairwise country analysis successively:

1. Animal model with direct genetic effect (DIR) and maternal permanent environmental effect (MPE) and
2. Animal model for DIR and maternal genetic effect with MPE effect.

The resulting matrices were bended to make them positive definite. Average direct genetic correlations for BWT across countries were 0.7 (CHA), 0.79 (LIM), 0.84 (BSM) and for CAE 0.67 (CHA), 0.70 (LIM), 0.45 (BSM). Average maternal genetic correlations for BWT between countries were 0.47 (CHA), 0.45 (LIM), 0.49 (BSM) and for CAE 0.58 (CHA), 0.53 (LIM), 0.79 (BSM).

Keywords: beef cattle, Interbeef, calving traits, genetic correlation, international genetic evaluation

Introduction

Efforts to create an international genetic evaluation for beef cattle started in 2001 with the EUropean BEeaf EVALuation project (EUBEEVAL). Phocas et al. (2005) suggested that the optimal model for beef cattle is an across-country animal model with maternal effect applied to raw phenotypes. Venot et al. (2006) performed the first pilot study and estimated across country genetic correlations for weaning weights between France (FRA), Ireland (IRL), and the United Kingdom (GBR) for Charolais (CHA) and Limousine (LIM) breeds. Three years later, genetic correlations were estimated for FRA, IRL, GBR, Sweden (SWE), and Denmark (DNK) (Venot et al., 2009). In 2008 Interbeef working group was established in ICAR, and the IDEA database at the Interbull center started to be used for pedigree and data exchange for beef cattle. Pabiou et al. (2014) estimated genetic correlations for weaning weight between eight member countries of Interbeef for CHA and LIM. These genetic correlations were provided to Interbeef for tests and routine runs. Since then, Interbeef extended his service for more countries and breeds. Now provides services for five breeds (CHA, LIM, Beef Simmental (BSM), Aberdeen Angus (AAN), and Hereford (HER)) and nine countries. The development of methods for international genetic evaluation for new traits, breeds, and countries is carried out in cooperation with research partners. The Czech Republic is responsible for the development of evaluation for calving traits (calving ease – CAE, birth weight – BWT). This paper summarizes the results of our work.

Material and methods

Data. Phenotypic and pedigree data were extracted from the IDEA database in autumn 2017 (CHA, LIM) and spring 2018 (BSM). Seven populations were participating in calving traits project – Czech Republic (CZE), Germany (DEU), Denmark + Finland + Sweden sending data as one joint population (DFS), France (FRA), United Kingdom (GBR), Ireland (IRL) and South African Republic (ZAF). However, not all populations were participating in all breed/trait combinations (Table 1). The definition of birth weight performance was the same in all countries. The definition of calving ease was different and based on national evaluation practices:

1. four points scale in CZE, IRL, and ZAF.
2. five points scale in DEU, DFS, FRA, and GBR.

Data edits. Each country had uploaded phenotypic performances edited according to their national evaluation standard. For the genetic parameter estimation, we further edited files. Main edits on performances were the exclusion of duplicate records (one animal sent from more countries), embryo transfer calves, calves without known sire and maternal grandsire (MGS), herds without variation, small-sized contemporary groups (CG), and CGs with only one sire. After that, performance data files were

Table 1. Number of records in pedigree and performance files extracted from the IDEA database.

	CHA		LIM		BSM	
	BWT	CAE	BWT	CAE	BWT	CAE
Pedigree	10,220,079	10,419,521	5,754,435	6,048,151	218,045	504,665
Performances						
CZE	62,898	62,898	17,184	17,184	26,394	26,394
DEU	np	np	np	np	np	197,232
DFS	271,760	298,493	207,446	273,543	137,994	178,941
FRA	8,740,872	8,728,358	4,859,658	4,830,350	np	np
GBR	np	np	201,865	181,711	np	np
IRL	38,318	222,070	18,440	208,399	5,970	55,789
ZAF	49,153	np	np	np	np	np

np – country not participating for the specified breed/trait combination prepared for pairwise country genetic parameter estimation according to the genetic connection between countries. Large performance data files were reduced to maintain optimum connection with other countries.

Model. Each country described its preferred genetic evaluation model and defined its own environmental effects according to their national genetic evaluation system. (Co)variance components were estimated by a two-trait (CAE and BWT) animal model using AIREMLF90 (Misztal et al., 2002) for pairwise combination of countries. Estimations were performed in two steps: 1. Animal model with direct genetic effect and maternal permanent environmental effect (AM-DE-MPE) and 2. Animal model for direct and maternal genetic effect with maternal permanent environmental effect (AM-DE-ME-MPE), in which were across-country co-variances between direct and maternal genetic effect fixed to zero. For most countries, the AM-DE-ME-MPE model was preferred. For IRL and DEU, the AM-DE-MPE (without the maternal genetic effect) model was chosen. Pedigree file was built for each pairwise combination and contained five generations with a phantom parent group constructed according to country of origin of animal with unknown parent.

After that, the full direct and maternal correlation matrix was constructed. Non-converged direct correlations from the AM-DE-ME-MPE model between countries were set to values obtained from the AM-DE-MPE model, or average value with standard error 0.4 if no result was estimated from both models. Non-converged maternal correlations were set to average value with standard error 0.4. Matrices of direct and maternal correlations were bended with standard errors used as weights (Jorjani et al., 2003). And finally, the full Interbeef multicountry two-trait correlation matrix was bended to become positive definitive using Jorjani et al. (2003) weighted bending procedure where the weighting factors were equal to the reciprocal of the number of common sires multiplied by 10 for direct correlations and by 5 for maternal correlations.

Results and discussion

The largest population of Limousine and Charolais was from France and represented more than 90% of the performance dataset (Table 1). In Beef Simmental, the size of populations was more balanced with DFS and DEU representing the two largest populations in the dataset (Table 1).

In tables 2, 3, and 4 are estimated genetic correlations for CHA, LIM, and BSM. For all three breeds, average direct genetic correlations for BWT were higher than for CAE, which is probably caused by higher heritabilities of BWT and differences of definition of CAE scoring between countries. Average direct genetic correlations for BWT were 0.70 for CHA, 0.79 for LIM and 0.84 for BSM and for CAE 0.67 (CHA), 0.70 (LIM) and 0.45 (BSM). These correlations are slightly lower than average Interbeef genetic correlations estimated for weaning weight by Pabiou et al. (2014). We observed slightly higher correlations for LIM than CHA for weaning weight. Pabiou et al. (2014) came to the same result for weaning weight and explained it by the absence of GBR data in the CHA run and therefore missing linkage through GBR sires. The strongest direct genetic correlations in CHA were observed between FRA-DFS (0.86), FRA-IRL (0.83), DFS-IRL (0.83) for BWT and between IRL-CZE (0.72), DFS-CZE (0.70) and FRA-IRL (0.70) for CAE. In LIM, the strongest direct genetic correlations were observed between DFS-CZE (0.87), FRA-CZE (0.87) and DFS-IRL (0.83) for BWT and GBR-IRL (0.85) and FRA-IRL (0.84) for CAE. In BSM, all three direct correlations for BWT (DFS-CZE, IRL-CZE, DFS-IRL) were higher than 0.8. The situation in CAE was much more complicated. Low genetic correlations between DEU and other countries is caused by differences in methods of national genetic evaluation. This problem should be solved in the future by the harmonization of methods in cooperation with DEU.

Table 2. Heritabilities (diagonal) and across-country genetic correlations (below diagonal) for Charolais.

			Direct effect									Maternal effect						
			Birth weight					Calving ease				Birth weight				Calving ease		
			CZE	DFS	FRA	IRL	ZAF	CZE	DFS	FRA	IRL	CZE	DFS	FRA	ZAF	CZE	DFS	FRA
Direct effect	CAE	CZE	0.21															
		DFS	0.64	0.38														
		FRA	0.60	0.86	0.41													
		IRL	0.66	0.83	0.83	0.40												
		ZAF	0.81	0.55	0.64	0.63	0.31											
	BWT	CZE	0.25	0.05	0.31	0.12	0.11	0.17										
		DFS	0.08	0.00	0.21	0.00	-0.07	0.70	0.16									
		FRA	0.29	0.51	0.83	0.54	0.30	0.66	0.59	0.10								
		IRL	0.10	0.05	0.36	0.37	-0.03	0.72	0.68	0.70	0.05							
Maternal effect	CAE	CZE	-0.48	-0.12	-0.04	-0.09	-0.13	-0.01	0.10	0.12	0.10	0.05						
		DFS	-0.12	-0.15	-0.08	0.00	0.06	0.10	0.00	-0.01	0.01	0.61	0.09					
		FRA	-0.03	-0.22	-0.48	-0.11	-0.12	0.04	0.01	-0.47	-0.02	0.31	0.44	0.10				
		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	0.10			
	BWT	CZE	0.04	0.12	0.04	0.11	0.14	-0.47	-0.09	-0.13	-0.12	0.42	0.08	0.12	0.03	0.03		
		DFS	0.09	0.00	-0.01	-0.01	-0.02	-0.08	-0.20	-0.04	0.03	0.09	0.00	0.05	-0.03	0.58	0.08	
		FRA	0.15	-0.04	-0.30	0.01	-0.03	-0.14	-0.02	-0.40	0.00	0.12	0.03	0.69	0.06	0.58	0.59	0.06

Table 3. Heritabilities (diagonal) and across-country genetic correlations (below diagonal) for Limousine.

			Direct effect										Maternal effect							
			Birth weight					Calving ease					Birth weight				Calving easeCAE			
			CZE	DFS	FRA	GBR	IRL	CZE	DFS	FRA	GBR	IRL	CZE	DFS	FRA	GBR	CZE	DFS	FRA	GBR
Direct effect	BWT	CZE	0.21																	
		DFS	0.87	0.38																
		FRA	0.87	0.80	0.43															
		GBR	0.78	0.81	0.73	0.30														
		IRL	0.72	0.83	0.68	0.79	0.40													
	CAE	CZE	0.25	0.08	0.27	0.25	0.10	0.17												
		DFS	0.11	0.00	0.26	0.12	-0.07	0.62	0.16											
		FRA	0.41	0.28	0.68	0.38	0.35	0.60	0.73	0.05										
		GBR	0.21	0.13	0.33	0.53	0.27	0.71	0.66	0.71	0.11									
		IRL	0.17	0.06	0.38	0.33	0.37	0.63	0.63	0.84	0.85	0.05								
Maternal effect	BWT	CZE	-0.48	-0.17	-0.28	-0.15	-0.10	-0.01	0.09	0.02	0.11	0.12	0.05							
		DFS	-0.10	-0.15	-0.19	-0.04	0.00	0.06	0.00	0.04	0.02	0.03	0.42	0.09						
		FRA	-0.43	-0.32	-0.61	-0.22	-0.08	0.06	0.05	-0.20	0.09	0.06	0.43	0.69	0.09					
		GBR	-0.12	-0.03	-0.13	-0.37	0.00	0.08	0.02	0.05	-0.15	0.02	0.42	0.37	0.38	0.06				
	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	0.03			
		DFS	0.09	0.00	-0.03	0.03	0.01	-0.04	-0.20	-0.10	-0.02	0.05	0.05	0.00	-0.01	0.01	0.50	0.08		
		FRA	-0.11	-0.10	-0.45	-0.05	-0.06	-0.14	-0.17	-0.56	-0.14	-0.23	0.09	-0.04	0.28	-0.05	0.52	0.52	0.02	
		GBR	0.10	0.03	-0.06	-0.15	0.05	-0.08	0.00	-0.16	-0.35	-0.10	0.02	0.00	-0.02	0.01	0.50	0.51	0.63	0.06

Table 4. Heritabilities (diagonal) and across-country genetic correlations (below diagonal) for Beef Simmental.

			Direct effect							Maternal effect			
			Birth weight			Calving ease				Birth weight		Calving ease	
			CZE	DFS	IRL	CZE	DFS	IRL	DEU	CZE	DFS	CZE	DFS
DIR	BWT	CZE	0.21										
		DFS	0.85	0.38									
		IRL	0.83	0.84	0.40								
	CAE	CZE	0.25	0.09	0.43	0.17							
		DFS	0.08	0.00	0.51	0.60	0.16						
		IRL	0.47	0.41	0.83	0.68	0.89	0.05					
		DEU	0.01	-0.05	-0.01	0.27	0.17	0.08	0.05				
MAT	BWT	CZE	-0.48	-0.15	-0.12	-0.01	0.10	0.04	0.02	0.05			
		DFS	-0.10	-0.15	-0.06	0.07	0.00	0.00	-0.01	0.49	0.09		
	CAE	CZE	0.04	0.14	0.08	-0.47	-0.11	-0.06	-0.03	0.42	0.08	0.03	
		DFS	0.14	0.00	-0.01	-0.14	-0.20	-0.10	0.01	0.14	0.00	0.79	0.08

Conclusion

This study has provided Interbeef with a set of genetic correlations across participating countries and allows Interbeef to proceed to an official run of international genetic evaluation for calving traits. The first run was held in 2018, and resulting international breeding values were distributed to member countries. By now Interbeef provides international breeding values for weaning weight for five beef breeds (CHA, LIM, BSM, AAN, and HER) and calving traits (BWT and CAE) for three beef breeds (CHA, LIM, and BSM). Further research is focused on the development of international genetic evaluation for new traits (female fertility and carcass traits), calving traits for ANN and HER and estimation of genetic correlations for new member countries.

Acknowledgement

This study was supported by the Ministry of Agriculture of the Czech Republic (Projects No. MZE-RO0718 and QK1910059).

List of references

Misztal, I., Tsuruta, S., Strabel, T., Auvray, B., Druet, T. and Lee, D.H., 2002. BLUPF90 and related programs (BGF90). Pages 1–2 in Proc. 7th World Congr. Genet. Appl. Livest. Prod., Montpellier, France.

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

Pabiou, T., Nilforooshan, M., Laloe, D., Hjerpe, E. and Venot, E., 2014. Across-Country Genetic Parameters in Beef Cattle for Interbeef Weaning Weight Genetic Evaluation. Proceedings of the World Congr. Genet. Appl. Livest. Prod., vol. Species Breeding: Beef cattle (Posters), p. 731.

Phocas, F., Donoghue, K. and Graser, H.U., 2005. Investigation of three strategies for an international genetic evaluation of beef cattle weaning weight. Gen. Sel. Evol. 37: 361-380.

Venot, E., Fouilloux, M.N., Forabosco, F., Fogh, A., Pabiou, T., Moore, K., Eriksson, J.A., Renand, G. and Laloe, D., 2009. Beef without Borders: Genetic parameters for Charolais and Limousine Interbeef genetic evaluation of weaning weights. Interbull Bulletin. 40: 55-60.

Venot, E., Pabiou, T., Laloe, D., Wickham, B., Fouilloux, M.N. and Journaux, L., 2006. First steps towards a European joint genetic evaluation of the Limousine breed. Interbull Bulletin. 35: 141-145.