Impact of Interbeef on national beef cattle evaluations

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International evaluation models for beef cattle allow to compare animals' estimated breeding values (EBV) across different countries, thanks to sires having offspring in more than one country. In this study we aimed to provide an up-to-date picture of the Interbeef international beef cattle evaluations from a national perspective, considering both large and small populations. Limousin age-adjusted weaning weight (AWW) phenotypes were available for 3,115,598 animals from 10 European countries, born between 1972 and 2017. EBV and reliabilities were obtained using a multi-trait animal model including maternal effects where AWW from different countries are modelled as different traits. We investigated the country of origin of the sires with internationally publishable EBV and, among them, the country of origin of the top 100 sires for each country scale. All countries had 20 to 28,557 domestic sires whose EBV were publishable, according to Interbeef's rules, on the scale of other countries. All countries, except one, had domestic sires that ranked among the top 100 sires on other country scales. Across countries, inclusion of information from relatives recorded in other countries increased the reliability of EBV for domestic animals on average by 9.6 percentage points for direct EBV, and 8.3 percentage points for maternal EBV. In conclusion, international evaluations provide small countries access to a panel of elite foreign sires with EBV on their country scale and a more accurate estimation of EBV of domestic animals, while large countries obtain EBV for their sires on the scale of different countries which helps to better promote them.

Keywords: international breeding values, genotype-by-environment interaction, Interbeef, reliabilities, weaning weight

1 Introduction

The introduction of reproductive technologies such as artificial insemination and embryo transfer had a huge impact on both dairy and beef cattle breeding systems (Moore & Hasler, 2017). The availability of semen from superior proven bulls allowed breeders to increase the number of offspring of elite sires in their herds and to increase the selection intensity of cattle breeding schemes (Vishwanath, 2003). With the availability of such reproductive technologies, bulls started to have recorded offspring in different herds and different environmental conditions. Next to it, with the increased trade of frozen semen across countries, genetic links across populations were established (Fikse & Philipsson, 2007; Philipsson, 2011). With the exchange of genetic material across countries, both the importers, interested in comparing the genetic level of foreign and domestic bulls, and the exporters, interested in accessing foreign markets, sought for methods to express sires' estimated breeding values (EBV) on the scale of other countries (Durr & Philipsson, 2012; Philipsson, 2011). Therefore, following up from the initial conversion equations to translate EBV from one country scale to another (Goddard, 1985; Wilmink et al., 1986), cattle international genetic evaluation models were developed to allow the comparison of animals EBV across different countries (Schaeffer, 1994; Venot et al., 2006; Wickham & Durr, 2011).

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In beef cattle, both farming livestock systems and environmental conditions can be very different between countries, and sometimes even within regions of the same country (Journaux et al., 2006; Renand et al., 2003). In early 2000, the first studies among European countries underlined the need of an international evaluation for beef cattle that would take into account, among others, the presence of genotype-by-environment interaction (Quintanilla et al., 2002a, 2002b). In 2005, the AMACI model (Animal Model accounting for Across-Country Interactions) was developed for comparing beef cattle EBV at the international level (Phocas et al., 2005), and in 2006 the international beef cattle evaluations service (Interbeef) was established as an ICAR working group, with evaluations carried out at the Interbull Centre (Uppsala, Sweden) (Journaux et al., 2006; Interbeef, 2020). Currently, Interbeef collaborates with 13 countries worldwide (Australia, Czech Republic, Denmark, Finland, France, Germany, Ireland, Italy, South Africa, Spain, Sweden, Switzerland, United Kindom) providing international genetic evaluations for 5 breeds (Limousin, Charolais, Beef Simmental, Angus and Hereford) and three traits (weaning weight, birth weight, calving ease).

The main advantage of beef cattle international evaluations is that breeders can access a larger international panel of bulls that better meet their selection objectives and have EBV expressed on their own domestic scale, in addition to the original scale of their country of origin (Renand et al., 2003; Venot et al., 2007). Moreover, for any sires with foreign recorded progeny, the reliabilities of their EBV will increase (Venot et al., 2008, 2009, 2014). In cattle international evaluations, sires with recorded offspring in more than one country are often referred to as common bulls (CB) (Jorjani et al., 2005). These CB provide the genetic connections required to estimate genetic correlations across countries which allow to compare animals' EBV on different country scales during international evaluations (Phocas et al., 2005; Bonifazi et al., 2020). So far, few studies looked into international beef cattle evaluations from a national perspective. We provide here an up-to-date picture of the Interbeef international evaluations from a national point of view, considering both large and small populations. To achieve this, we aimed to show how the Interbeef evaluations: 1) enrich the panel of available sires per country with foreign bulls, and 2) affect animals' EBV reliabilities due to the use of foreign phenotypes.

2 Material and methods

Data from the 2018 routine Interbeef evaluations for age-adjusted weaning weight (AWW) of Limousin beef cattle were available, including a total of 3,115,598 phenotypes (one phenotype per animal), recorded on males (49%) and females (51%) between 1972 and 2018, distributed across 19,330 herds (Table 1).

Table 1 Number of age-adjusted weaning weight (AWW), herds and year of birth distribution of recorded animals per country. Table originally reported in Bonifazi et al. (2020)

COU [a]	AWW	%	Herds	Year of Birth
CZE	10,500	0.3	121	1991 – 2017
DFS	90,456	2.9	9,190	1980 – 2017
ESP	33,152	1.1	188	1989 – 2011
GBR	127,840	4.1	745	1972 – 2017
IRL	20,609	0.7	1,304	1975 – 2017
FRA	2,714,368	87.1	6,677	1972 – 2017
DEU	88,628	2.8	881	1981 – 2017
CHE	30,045	1.0	224	1993 – 2017
Total	3,115,598	100	19,330	1972 – 2017

[a] COU = Country: CZE = Czech Republic, DFS = Denmark, Finland and Sweden, ESP = Spain, GBR = Great Britain, IRL = Ireland, FRA = France, DEU = Germany, CHE = Switzerland

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Phenotypes were recorded in the eight populations that participated in the 2018 evaluation: Switzerland (CHE), Czech Republic (CZE), Germany (DEU), Denmark, Finland and Sweden (DFS), Spain (ESP), France (FRA), Great Britain (GBR), and Ireland (IRL). Note that the DFS population was composed of three countries joining together as a single population in the international evaluation. Hereafter we will use the term country to refer to each of the eight populations. Pedigree information were extracted from the Interbeef international pedigree database and, after quality control, the final pedigree included 3,431,742 animals. For a more detailed description of the data and quality control see Bonifazi et al. (2020).

AWW phenotypes were analysed using the AMACI model, which is a multi-trait animal model where the AWW information from each country is modelled as a different trait (Phocas et al., 2005). All country-specific fixed and random effects were fitted in the AMACI model as:

$$
\begin{bmatrix} \mathbf{y}_1 \\ \vdots \\ \mathbf{y}_8 \end{bmatrix} = \begin{bmatrix} \mathbf{X}_1 & \cdots & 0 \\ \vdots & \ddots & \vdots \\ 0 & \cdots & \mathbf{X}_8 \end{bmatrix} \begin{bmatrix} \mathbf{b}_1 \\ \vdots \\ \mathbf{b}_8 \end{bmatrix} + \begin{bmatrix} \mathbf{C}_1 & 0 & 0 & 0 \\ 0 & \mathbf{C}_2 & 0 & 0 \\ 0 & 0 & \mathbf{C}_3 & 0 \\ 0 & 0 & 0 & \mathbf{C}_4 \end{bmatrix} \begin{bmatrix} \mathbf{r}_1 \\ \mathbf{r}_2 \\ \mathbf{r}_3 \\ \mathbf{r}_4 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_1 & \cdots & 0 \\ \vdots & \ddots & \vdots \\ 0 & \cdots & \mathbf{Z}_8 \end{bmatrix} \begin{bmatrix} \mathbf{u}_1 \\ \vdots \\ \mathbf{u}_8 \end{bmatrix} + \begin{bmatrix} \mathbf{W}_1 & \cdots & 0 \\ \vdots & \ddots & \vdots \\ 0 & \cdots & \mathbf{W}_8 \end{bmatrix} \begin{bmatrix} \mathbf{m}_1 \\ \vdots \\ \mathbf{m}_8 \end{bmatrix}
$$

$$
+ \begin{bmatrix} \mathbf{P}_1 & \cdots & 0 \\ \vdots & \ddots & \vdots \\ 0 & \cdots & \mathbf{P}_7 \end{bmatrix} \begin{bmatrix} \mathbf{pe}_1 \\ \vdots \\ \mathbf{pe}_7 \end{bmatrix} + \begin{bmatrix} \mathbf{e}_1 \\ \vdots \\ \mathbf{e}_8 \end{bmatrix}
$$

where, i = country; $\mathbf{y}_i$ = vector of AWW; $\mathbf{b}_i$ = vector of fixed effects; $\mathbf{r}_i$ = vector of random environmental effects; $\mathbf{u}_i$ = vector of random additive genetic (direct) effects; $\mathbf{m}_i$ = vector of random maternal (indirect) additive genetic effects; $\mathbf{pe}_i$ = vector of random maternal permanent environmental effects; $\mathbf{e}_i$ = vector of random residual effects. $\mathbf{X}_i$ and $\mathbf{C}_i$ are incidence matrices linking records to fixed, and random environmental effects, respectively. $\mathbf{Z}_i$, $\mathbf{W}_i$, and $\mathbf{P}_i$ are incidence matrices linking records to the animal, maternal genetic and maternal permanent environmental effects, respectively.

For each country, genetic and environmental variances in the international model were fixed at the national estimates (Bonifazi et al., 2020). Across the countries, the heritability for AWW ranged from 0.11 to 0.36 for the direct, and 0.05 to 0.15 for the maternal effect. Covariances among countries are assumed to be null for all random effects, i.e. independent from each other, except for the direct genetic and the maternal genetic covariances between countries, which were estimated in a previous study (Bonifazi et al., 2020). A permanent environmental effect (**pe**) was fitted for all countries except DEU, assuming null covariances between countries. One or more random environmental effects (**r**) were fitted in four countries: herd-year-season for CZE, herd-year for DEU and CHE, and sire-herd for CHE. All other countries had a fixed contemporary effect in their model. A more detailed description of the model and of all the fixed and random effects can be found in Bonifazi et al. (2020).

Two scenarios were implemented for comparing national and international evaluations:

1) Scenario INT represents the current Interbeef genetic evaluation for AWW using the AMACI model. Table 2 reports the genetic correlations used between countries.

2) Scenario NAT represents a pseudo-national single trait evaluation for AWW. In this scenario, genetic covariances between countries were set to zero in the AMACI model. Thus, information of one country did not contribute to the EBVs of animals in another country, as it would be in a national evaluation. After the evaluation, for each country, EBVs of all animals with phenotypes of their own, or any of their ancestors, or both, were retained. Hereafter, we will refer to these animals as the domestic set of animals for each country.

The MiX99 software package (MiX99 Development Team, 2017) was used to compute the EBV for both scenarios. Convergence criteria for the preconditioned conjugate gradient (PCG) algorithm, defined as the square root of the relative difference between solutions of the last two PCG iterations rounds, was set to 10^{-7}. From the MiX99 software package, apax99 was used to compute individual approximated reliabilities for both Scenario NAT (REL_{NAT}) and INT (REL_{INT}) using the Tier and Meyer methodology (Tier & Meyer, 2004).

Table 2 Direct (Dir) and maternal (Mat) genetic correlations [a] within and across countries [b]

		Dir								Mat							
		CZE	DFS	ESP	GBR	IRL	FRA	DEU	CHE	CZE	DFS	ESP	GBR	IRL	FRA	DEU	CHE
Dir	CZE																
	DFS	0.87															
	ESP	0.74	0.77														
	GBR	0.71	0.82	0.94													
	IRL	0.83	0.76	0.87	0.91												
	FRA	0.76	0.89	0.77	0.82	0.76											
	DEU	0.76	0.94	0.76	0.77	0.62	0.81										
	CHE	0.85	0.81	0.76	0.71	0.70	0.70	0.70									
Mat	CZE	-0.12	0.04	0.07	0.12	-0.01	-0.10	0.08	0.01								
	DFS	-0.05	-0.14	0.02	-0.01	-0.02	-0.11	-0.07	-0.01	0.68							
	ESP	0.03	0.09	-0.22	-0.08	-0.09	-0.05	0.05	0.02	0.67	0.68						
	GBR	0.14	0.06	-0.03	-0.10	-0.03	-0.14	0.07	0.08	0.79	0.69	0.70					
	IRL	-0.03	0.07	-0.06	-0.05	-0.19	-0.12	0.12	0.11	0.69	0.68	0.81	0.72				
	FRA	-0.02	-0.05	-0.03	-0.06	-0.09	-0.33	-0.01	0.08	0.85	0.69	0.71	0.87	0.82			
	DEU	-0.02	-0.09	-0.03	-0.01	0.06	-0.10	-0.24	0.09	0.68	0.68	0.67	0.69	0.68	0.69		
	CHE	0.12	0.11	0.07	0.08	0.03	-0.05	0.06	0.40	0.73	0.68	0.67	0.66	0.65	0.77	0.66	

[a] Genetic correlations originally reported in Bonifazi et al. (2020). [b] Country: see Table 1

As agreed within Interbeef, international EBV (EBV_{INT}) for foreign sires are required to fulfil the following set of rules (in place since 2013) to allow them to be distributed and published in another country. For direct EBV_{INT}, a sire must have: a REL_{INT} greater or equal to 0.5 in at least one country scale for the direct EBV, and at least 25 recorded progeny across all countries. For maternal EBV_{INT}, a sire must have: a publishable direct EBV_{INT}, a REL_{INT} greater or equal to 0.3 in at least one country scale for the maternal EBV, at least 15 daughters with recorded progeny, and at least 25 recorded grand-progeny across all countries. In Interbeef, direct and maternal EBV_{INT} are distributed as two separate sets of EBV_{INT}. Thus, in each country scale, sires can be ranked for either their direct or their maternal EBV_{INT}.

After identifying publishable sires' EBV_{INT} for each country, we ranked and selected the top 100 sires for each country scale, for both direct and maternal EBV_{INT}. To identify the origin of the top 100 sires for each country, we then extracted the sire's country of first registration. Furthermore, to show how the composition of top sires changes between national and international evaluations, we applied the same Interbeef publication rules to national EBV computed under Scenario NAT, with the exception that the required number of recorded offspring and grand-offspring per sire was considering only national phenotypes.

To show the gain in reliability for domestic animals when moving from a national evaluation to an international evaluation, i.e. from Scenario NAT to INT, the difference (Δ_{REL}) between REL_{INT} and REL_{NAT}, both expressed on a scale from 0 to 100, was computed, for both direct and maternal EBV.

3 Results and discussion

Domestic sires with at least one recorded offspring were identified from the pseudo-national pedigree (Scenario NAT) and their number ranged from 554 for CZE to 57,784 of FRA (Table 3). Among domestic sires with at least one recorded offspring, on average, across all countries, 464 sires were also CB, ranging from 212 for CZE to 1,171 for FRA (Table 3). The number of domestic sires in the

pedigree for each country under Scenario NAT may be different compared to a real national evaluation for two reasons. First, countries may have a different pedigree depth for national evaluations, for instance when not all national data are also used for international evaluations. Second, the international pedigree of Interbeef may provide connections that allow to track relationships that go further back in the pedigree compared to the national ones.

The total number of sires' EBV_{INT} that were publishable was equal to 32,208 and 13,016 for the direct and the maternal EBV, respectively, and the distribution of their country of first registration is reported in Table 4. The majority of the publishable sires' EBV_{INT} were from France (89% and 90% for direct and maternal genetic effect, respectively), followed by GBR, DFS and DEU (2-4% for both direct and maternal EBV). 1% or less of the total publishable sires' EBV_{INT} were registered in the remaining participating countries (Table 4). The lowest number of publishable sires' EBV_{INT} were for CZE: 66 and 20 for the direct and the maternal EBV, respectively. Less than 1% of the publishable sires' EBV_{INT} were from sires whose country of first registration was not among the eight participating countries in the evaluation: 102 and 47 for the direct and maternal EBV, respectively.

Table 3 Description of the pseudo-national pedigree under Scenario NAT, including numbers of domestic sires with at least one recorded offspring, and domestic sires that are also common bulls (CB)

COU [a]	Number of:		
	Pedigree entries	Domestic sires with > 1 rec. off [b]	Domestic sires that are CB
CZE	30,843	554	212
DFS	117,623	4,375	227
ESP	63,526	1,188	364
GBR	172,229	5,486	524
IRL	56,694	2,073	321
FRA	2,942,297	57,784	1,171
DEU	121,228	4,366	473
CHE	55,104	1,699	421

[a] COU = country: see Table 1
[b] Domestic sires with at least one recorded offspring in the country

Table 4 Country of origin of sires with publishable international EBV. The number of sires for both direct and maternal EBV are reported [a]

COU [a]	Direct	Maternal
CZE	66	20
DFS	931	333
ESP	166	36
GBR	1,099	480
IRL	93	23
FRA	28,557	11,721
DEU	959	306
CHE	235	50
Others	102	47
Total	32,208	13,016

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[a] COU = country: see Table 1; Others: country of first registration different from participating countries

The country of origin of the top 100 publishable sires' EBV_{INT} ranked on each country scale is reported in Table 5. For each country scale, the majority of the top 100 sires originated from France. In the top 100 sires of each country, at least one foreign sire appeared, except for FRA for direct EBV (Table 5). CZE was the only country with all top 100 sires being foreign, both for direct and maternal EBV. The distribution of the country of origin for the top 100 publishable sires for each country scale based on Scenario NAT is shown in Table 6. Comparison of Table 6 and 5 shows the change in the composition of the top 100 publishable sires after the inclusion of international information. As expected, a higher proportion of nationally registered sires was present when sires were ranked based on their national EBV instead of EBV_{INT}. Interbeef publication rules may be more restrictive compared to real national ones; for instance, publishable sires for maternal EBV in CZE and IRL were less than 100, but in practice this number may be higher. Nevertheless, the presence of publishable sires registered in other countries based on Scenario NAT (Table 6) underlines the importance of international evaluations for large populations, which allows a more accurate estimation of their sires' EBV on the scale of other countries.

We have used the current set of rules for publication of sires' EBV_{INT} to give a close representation of Interbeef evaluations. Other rules may apply to the international evaluation and they were not considered in this study, for instance, the distinction between AI bulls and natural service bulls, and country-specific restrictions for publishing sires' EBV_{INT} on the scale of other countries. Nevertheless, Table 4 shows how each country has sires that fulfil the requirements and that could be publishable on other country scales. FRA was the country with the highest proportion of domestic sires with recorded offspring that were also publishable in other countries: 49% and 20% for direct and maternal EBV, respectively. Moreover, FRA sires were prominent in top 100 publishable sires' EBV_{INT} for each country scale (Table 5). Nonetheless, each country besides CZE had one or more sires ranking within the top 100 publishable sires' EBV_{INT} of another country scale (Table 5), showing the potential exchange of their superior genetics across participating countries. Exchanging AI bulls across countries allow to create new genetic connections. In a previous study conducted on five Limousin beef cattle populations, Bouquet et al. (2009) concluded that despite Limousin European populations were connected to the French one via AI bulls, genetic diversity was still maintained between populations.

The impact of additional information from relatives as provided with the international evaluations can be reflected in the gain in individuals' reliabilities when moving from Scenario NAT to Scenario INT (Venot et al., 2014). Hereafter, all mentioned reliabilities are expressed on a 0-100 scale, and any gains in reliability are expressed in percentage points. The distribution of REL_{NAT} is reported in Table 7. Average REL_{NAT} ranged from 23.2 of CZE to 52.1 of FRA, and from 15.5 for CZE and CHE to 33.8 for DEU, for the direct and the maternal EBV, respectively. As expected, the average REL_{NAT} for maternal EBV was lower than the average REL_{NAT} for direct EBV for all countries. The distribution of REL_{INT} is reported in Table 8. Average REL_{INT} ranged from 38.3 of CHE to 52.1 of FRA, and from 28.0 for GBR to 39.0 for CZE, for the direct and the maternal EBV, respectively. Also, for Scenario INT, as expected, for all countries the average REL_{INT} for maternal EBV was lower than the average REL_{INT} for direct EBV. The gain in reliability when moving from Scenario NAT to Scenario INT (Δ_{REL}) for both direct and maternal EBV is shown in Figure 1, with the smallest countries having the highest Δ_{REL}. In each country, the highest frequency of Δ_{REL} was observed for the 0 to 5 bin, for both direct and maternal EBV, comprising more than 20% of the domestic animals. The average Δ_{REL} across countries was 9.6 and 8.3 for the direct and the maternal EBV, respectively. FRA was the only country with no increase in average Δ_{REL} for both direct and maternal EBV: this was expected since FRA had relatively the largest amount of data at the national level. Larger countries, like GBR and DFS, had smaller Δ_{REL} (average direct EBV Δ_{REL} of 3.9 and 4.4, respectively) compared to those of smaller countries like CZE, CHE and IRL (average direct EBV Δ_{REL} of 24.3, 14.5 and 10.7, respectively). The same pattern was observed for the maternal EBV Δ_{REL} being the smallest for DFS (average Δ_{REL} of 2.2) and the largest for CZE (average Δ_{REL} of 23.6). Δ_{REL} for maternal EBV was smaller in all countries compared to the Δ_{REL} for direct EBV (Figure 1). There were no large differences between males and females for Δ_{REL} (results not shown). The observation that almost all Δ_{REL} values are greater than 0 shows that the information from foreign phenotypes is propagated to almost all animals in the national pedigree, with the individual Δ_{REL} depending on the relationship with CB and the genetic correlations between countries.

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Table 5 Country of first registration of the top 100 publishable sires for direct and maternal international EBV for each country scale

EBV	COU [a]	CZE	DFS	ESP	GBR	IRL	FRA	DEU	CHE
						Country of first registration			
Direct	CZE		2				98		
	DFS		2				98		
	ESP		1		4		95		
	GBR		1		6		93		
	IRL				4		96		
	FRA						100		
	DEU		2				98		
	CHE		2				97		1
Maternal	CZE		1	1	2		95		1
	DFS		12	1	3		84		
	ESP			2	1		97		
	GBR		1		5		94		
	IRL		1				99		
	FRA		1	1	1		97		
	DEU		1	1	2		94	2	
	CHE		1				95	1	3

[a] Country scale of the top 100 publishable sires; COU = country: see Table

Table 6 Country of first registration of the top 100 [a] publishable sires for direct and maternal national EBV for each country scale

EBV	COU [b]	CZE	DFS	ESP	GBR	IRL	FRA	DEU	CHE	Others
						Country of first registration				
Direct	CZE	44	4				48	4		
	DFS		77				22			1
	ESP			35			65			
	GBR				82	3	15			
	IRL				12	37	51			
	FRA						100			
	DEU		2		1		29	67		1
	CHE						38	8	53	1
Maternal	CZE	19	1				33	3		
	DFS		80		1		17			2
	ESP			23			77			
	GBR				80	1	19			
	IRL				9	14	67			
	FRA						100			
	DEU		2				33	63		2
	CHE						53	4	42	1

[a] Total number of publishable sires for CZE and IRL maternal EBV are 56 and 90
[b] Country scale of the top 100 publishable sires; COU = country: see Table 1; Others = Country not among those participating in the evaluation

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Table 7 Distribution of national individuals' reliabilities (REL_{NAT}) for domestic animals direct and maternal EBV per country [a]

Effect	COU [b]	First Quartile	Median	Mean	Third Quartile	Maximum
Direct	CZE	0.8	6.3	23.2	52.8	96.3
	DFS	43.0	47.2	42.1	49.1	98.6
	ESP	8.7	40.6	30.5	45.5	98.3
	GBR	45.6	50.1	45.2	51.9	99.3
	IRL	10.5	32.8	30.3	48.6	98.1
	FRA	50.7	52.4	52.1	53.9	100.0
	DEU	43.9	48.5	42.4	50.1	97.2
	CHE	3.3	31.7	23.8	37.1	96.4
Maternal	CZE	1.0	7.0	15.5	25.4	91.8
	DFS	18.1	24.7	25.8	31.4	96.5
	ESP	9.3	19.7	20.4	28.0	93.7
	GBR	16.3	23.0	23.6	29.1	97.8
	IRL	11.2	22.1	22.3	31.4	96.5
	FRA	23.2	28.3	30.0	34.0	99.9
	DEU	24.0	30.8	33.8	36.8	97.1
	CHE	3.1	16.0	15.3	22.6	92.1

[a] Minimum not shown (all countries had a minimum REL_{NAT} equal to 0)
[b] COU = Country: see Table 1

Table 8 Distribution of international individuals' reliabilities (REL_{INT}) for domestic animals direct and maternal EBV per country [a]

Effect	COU [a]	Min	First Quartile	Median	Mean	Third Quartile	Maximum
Direct	CZE	0.4	41.0	50.3	47.5	55.3	97.4
	DFS	0.0	45.0	47.9	46.1	49.6	99.0
	ESP	0.3	40.5	44.9	43.5	47.3	98.5
	GBR	0.0	48.0	50.6	49.6	52.4	99.3
	IRL	0.0	32.0	44.5	41.0	50.7	98.6
	FRA	0.2	50.7	52.4	52.1	53.9	100.0
	DEU	0.2	47.0	49.2	48.7	50.8	98.0
	CHE	0.6	34.3	37.6	38.3	41.4	97.4
Maternal	CZE	0.1	28.7	39.0	39.0	47.6	97.4
	DFS	0.0	20.2	26.3	28.1	33.3	96.5
	ESP	0.4	22.0	28.3	29.8	35.2	96.2
	GBR	0.0	19.6	26.0	28.0	33.9	97.8
	IRL	0.0	22.1	30.7	31.7	40.2	97.4
	FRA	0.2	23.2	28.4	30.1	34.1	99.9
	DEU	0.3	27.0	32.3	37.4	42.1	97.2
	CHE	0.4	20.5	27.7	29.0	36.5	95.3

[a] COU = Country: see Table 1
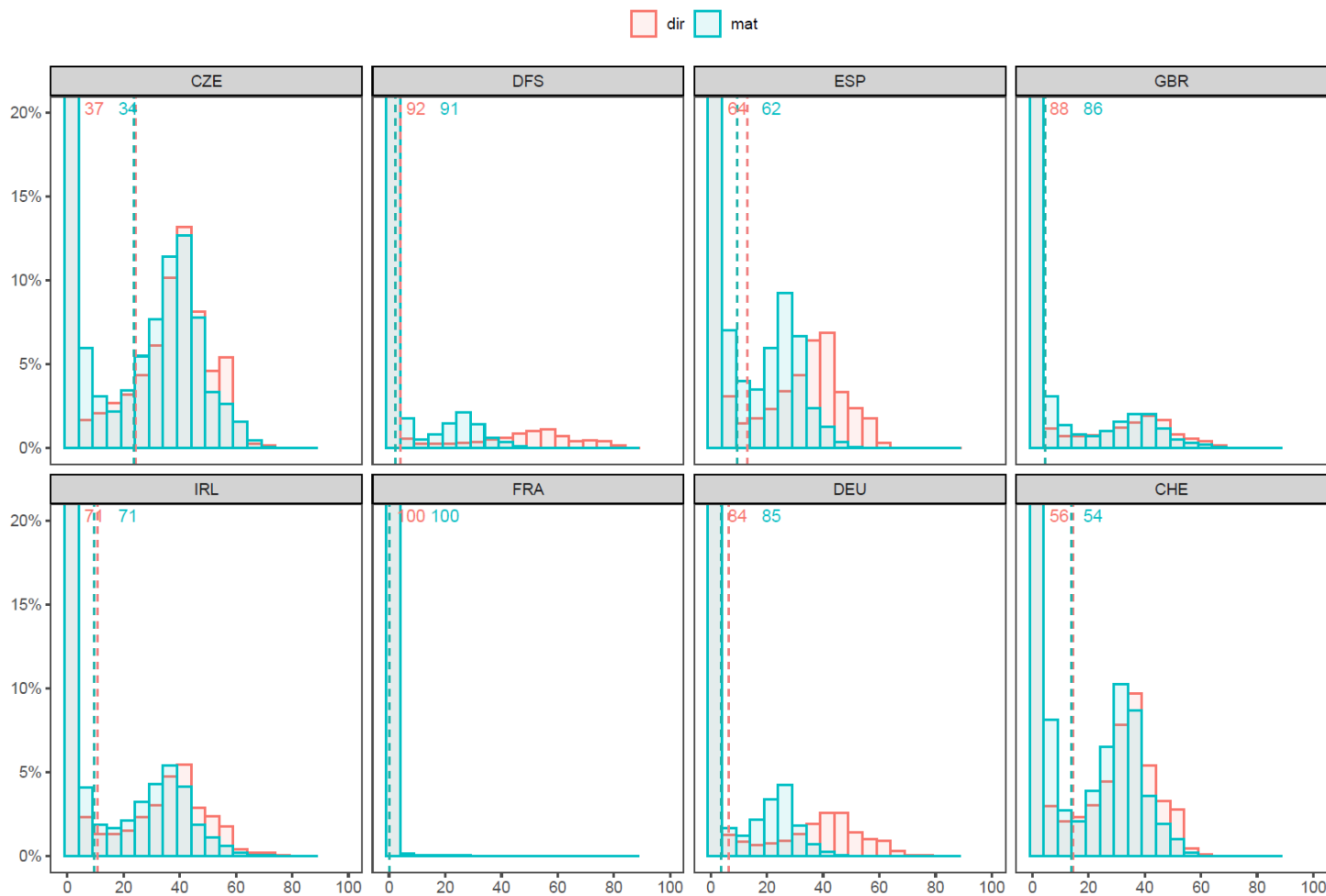
a The y-axis is the percentage of domestic animals in each bin (bin size of 5); b Dotted lines indicate the average Δ_{REL}; c The frequency of Δ_{REL} between 0 and 5 was always greater than 20%; the actual percentage in these bins are reported as text in each plot

Figure 1 Distribution of the gain in individual reliability ($\Delta_{REL} = REL_{INT} - REL_{NAT}$, on a scale from 0 to 100) for domestic animals for the direct (dir) and maternal (mat) EBV in each country [a, b, c]

To further illustrate how international data from foreign relatives allows for a more accurate estimation of EBV, we also compared the variance of EBV between Scenario NAT and Scenario INT, for all countries. When more information is used for the estimation of the genetic merit of an animal, EBV are less regressed to the mean, and thus show larger variance (Mrode & Thompson, 2005; Robinson, 1986). The variance of EBV of domestic animals increased on average by 91% and 55% for direct and maternal EBV, respectively, under Scenario INT compared to Scenario NAT (Figure 2). These increases in EBV variance ranged from 24% (GBR) to 307% (CZE) for direct EBV, and from 10% (DEU) to 238% (CZE) for maternal EBV (Table 6). FRA was the only country without an increase in EBV variance (Figure 2). The increase in EBV variance was particularly evident in smaller countries (Figure 2), confirming that in those countries more accurate estimates of EBV of domestic animals were obtained under Scenario INT by considering the information of recorded relatives in other countries.
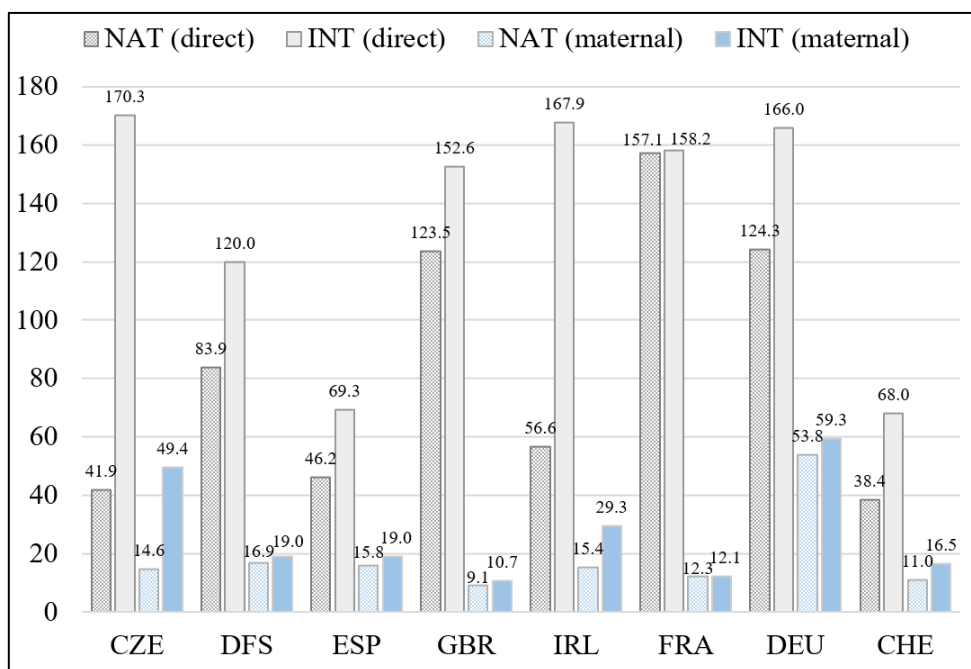
Figure 2 Direct and maternal EBV variances across all domestic animals under Scenario NAT and Scenario INT per country [a]

[a] Country = see Table 1

4   Conclusions

Our study gives an up-to-date picture of the Interbeef international evaluations from the national perspective, for both large and small countries. On one hand, small countries get access to a panel of elite foreign sires with EBV on their own country scale, as well as more reliable EBV for domestic animals via the international model, which is reflected in the increase of EBV variance and reliabilities. On the other hand, especially elite sires from large countries obtain EBV on different country scales, which facilitates the comparison of sires' EBV, and, in turn, the export of their genetic material across countries.

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