Interbull Portfolio: Expansion of Traits

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Abstract

A total of 10 traits for three trait groups of claw health, metabolic diseases and calving were included in a new research run performed in October 2024 with the aim to expand the multiple across-country evaluation (MACE) portfolio. The traits in each trait group were as follows: digital dermatitis (dde), interdigital dermatitis (idd), interdigital hyperplasia (idh), sole hemorrhage (soh), sole ulcer (sou) and white line disease (wld) for claw health; clinical ketosis (cke), sub-clinical ketosis (sck) and milk fever (mfe) for metabolic diseases and direct gestation length (ges) for calving trait group. Although a total of 13 countries provided data for the six different breeds evaluated internationally, the research run could be performed only for four breeds (Holstein (HOL), Brown Swiss (BSW), Red Dairy Cattle (RDC) and Jersey (JER)) as only one country did provide data for Guernsey (GUE) and Simmental (SIM). The research results for across-country correlations, international EBVs and reliabilities were all promising for all evaluated traits. Gestation length was included in the Interbull May 2025 test run and subsequently in the official August 2025 routine run as the fifth trait in the MACE calving trait group alongside direct and maternal calving ease and still birth traits. The implementation of claw health and metabolic diseases traits in the MACE portfolio is currently pending a slightly higher participation rate from countries and it is therefore aimed to happen in the near future.

Key words: International evaluation, MACE, Dairy, claw health, metabolic diseases, direct gestation length

Introduction

In accordance with the Interbull new traits' pipeline introduced in 2021, countries were requested to fill in the Performance Recording, Evaluation and Publication database (PREPdb) (Interbull Centre, 2025), reporting information on any potential new traits that could be of interest for an international evaluation. The collected information included definitions of the trait, the availability of a standard International Committee of Animal Recording (ICAR) definition, the type of service, recording methods, etc. After reviewing the information, three main trait groups stood out, namely gestation length, metabolic diseases and claw health trait groups.

The results were presented during the 2024 Interbull Business Meeting, Bled, Slovenia, where it was sensed an urgency from the participating countries to have Interbull Centre performing a research run on such traits. Thus, a data call deadline for the above-mentioned trait groups was set to October 31, 2024, via the Interbull Data Exchange Area (IDEA)-new traits. By the end of the deadline, 13 countries submitted data for six breeds (Figure 1).

In total, 10 traits were included in the research run. Three and six traits were included in metabolic disease and claw health trait groups, respectively, while gestation length was assigned as the fifth trait of the calving trait group (Table 1).

Table 1. List of the new trait(s) for each trait group along with the abbreviations included in the MACE research run.

Trait group	Trait
Metabolic disease (META)	Clinical ketosis (cke)
	Sub- clinical ketosis (sck)
	Milk fever (mfe)
Claw health (CLAW)	Digital dermatitis (dde)
	Interdigital dermatitis (idd)
	Interdigital hyperplasia (idh)
	Sole hemorrhage (soh)
	Sole ulcer (sou)
	White line disease (wld)
Calving (CALV)	Gestation length (ges)

Materials and Methods

After the data submission deadline, and a preliminary screening of the data to identify the eligible breed-trait combinations, the MACE pipeline was applied. MACE started at the Interbull Centre to estimate and assess the across-country correlations, breeding values (EBVs) and reliability correlations between the national evaluations and the MACE research run

Across-country correlation estimations

The data from 13 countries and for four breeds of HOL, JER, BSW and RDC for the three new trait groups were used to estimate the across-country correlations, based on the number of common bulls between the pair of countries. The default setting for the bulls' inclusion was to have a minimum of 10 daughters in 10 herds for all the new traits. All bulls born since 1970 were included in the analysis. The Restricted Maximum Likelihood (REML) procedure was used. No subset was applied for HOL-traits, as the computing time was within the expected range due to the fact that the number of countries for the new traits was limited (the highest was eight countries for ges).

The Interbull post- processing procedure (https://interbull.org/ib/rg_procedure) was applied; all countries were assigned in one group/window of correlations defined as follows:

- Final correlations were estimated by applying a 10% percentile used for the minimum correlation
- The maximum was set to 0.99
- The median was calculated as: Median [10%;0.99]

One important step in the post-processing procedure is to assess the magnitude of the Correlation used in previous run (as there was **NO** previous run, it was set to **0.85**)

- Magnitude of changes tested was considered major for all traits meaning that the applied weight on the final correlation **was equal to 0** (equation displayed below).
- HOL correlations and common bulls were used as weighting factors for all other breeds

The windowed correlation was then calculated as follows:

$$corr_{win} = \frac{(min_{cb} * group_{medianvalue} + cb_{cou1,2} * corr_{cou1,2})}{min_{cb+}\, cb_{cou1,2}}$$

where ***cb*** is the number of common bulls between country 1 and 2.

Then, the $Corr_{win}$ were first bended to ensure that the matrix was all positive definite, and weighted against the previous correlations and the magnitude of the changes made by countries. In the next step, the results from the preceding step and the previously used correlations are combined into a weighted average to avoid large changes in correlations between consecutive test runs,

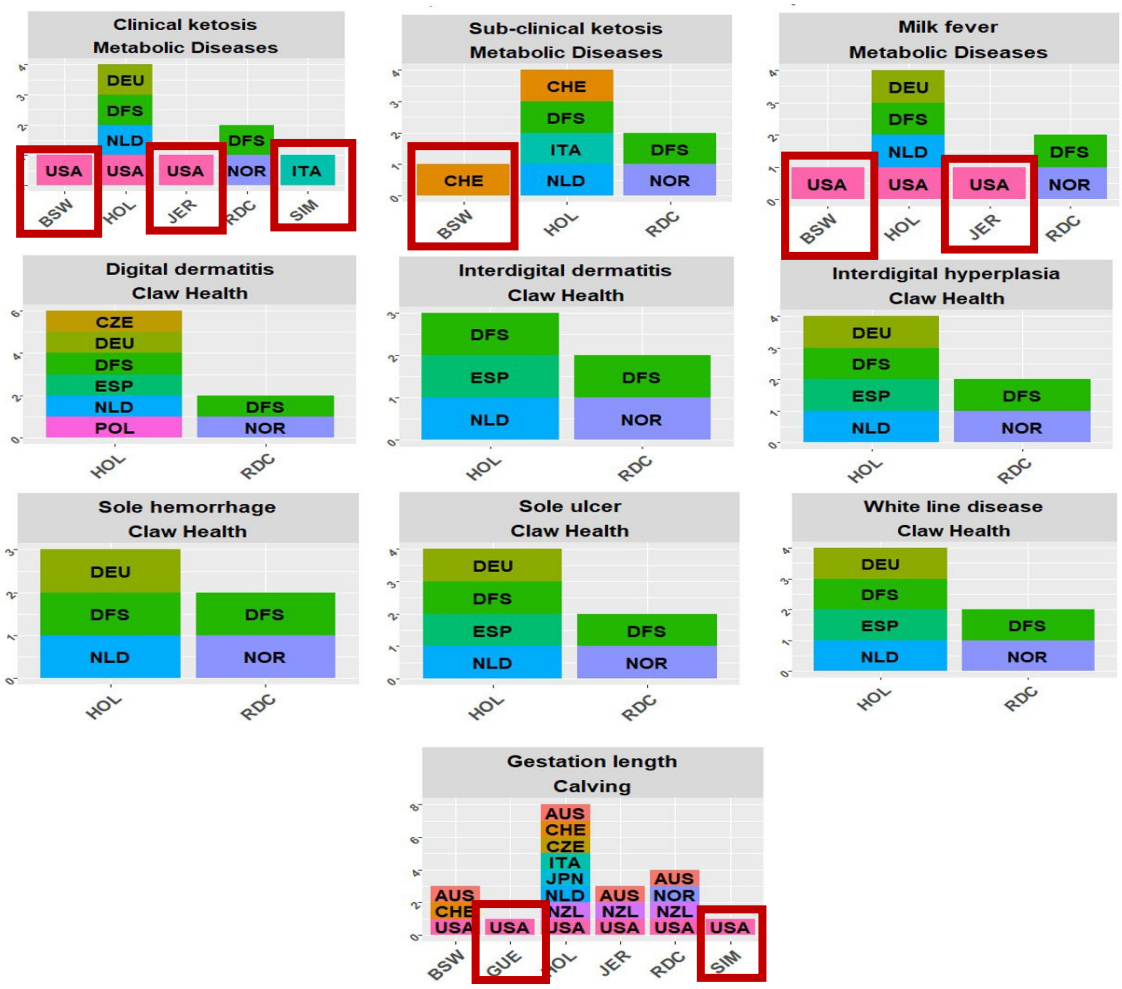

Figure 1. Breeds and countries participated for each trait and trait groups. Red ones show the breed-trait combinations which were submitted by only one country and were not included in the MACE research run.

weighted by the number of common bulls. The final correlation was calculated as follows:

$$Final_{corr} = \frac{blend_{corr} + \boldsymbol{w} * prev_{blendcorr}}{1 + \boldsymbol{w}}$$

Where $\boldsymbol{w}$ is the magnitude of changes as **0 = big change (in our case)**, 1=small and 2 = no change. If there are no changes in the national evaluations for the two countries, then the new processed correlation is not expected to deviate much from the previous one. However, if one of the countries has introduced changes in its national evaluations, it is expected that the genetic correlation between them would change as well. It is also expected that an increase in the number of common bulls would yield a more precise estimate of the genetic correlation, and in this case, less weight is given to the previous correlations. This is achieved by decreasing the weight on the previous correlations, proportionally to the increase in number of common bulls (https://interbull.org/ib/rg_procedure).

Finally, the updated (co)variance matrix is bended using the bending procedure described by (Jorjani et al., 2003).

Estimated Breeding Values (EBVs) calculation

Once all the correlation values were checked to be in the expected range the evaluation moved towards the estimation of the international EBVs. In this step, the correlation between national and international (MACE) EBVs, along with the reliability was estimated and compared.

Results and Discussion

Challenges: a) Change in directions of scales

After checking all the initial correlation estimates, some directions of scales for some countries, traits, and breeds changed as presented in Table 2, due to some results being on the negative scale.

Challenges: b) Gestation length

After the initial across-country correlation estimations for ges, two countries, ITA and CHE, had the lowest correlations with the other countries.

Table 2. Changes in direction of scale for the affected country, breed,trait with negative across-countries correlation estimations.

Breed(s)	Trait(s)	Country[1]	Change in Direction of scale
HOL, BSW, JER, RDC	ges	USA	T+ → T-
HOL		NLD	B+ →B-
HOL, BSW		CHE	B+ →B-
HOL		ITA	B+ →B-
RDC	cke, sck and mfe	NOR	B+ →B-

[1] United States of America (USA), the Netherlands (NLD), Switzerland (CHE), Italy (ITA), Norway (NOR)

In order to understand the root cause of the problem, Interbull Centre initiated an extensive exchange of information with the two countries involved until it came out that what those countries had submitted was *maternal* gestation length while all the other participating countries had provided the direct trait. ITA and CHE were then asked to submit direct gestation and after receiving the new data and re-estimating the across-country correlation the values became high and in line with other countries (Table 4).

Correlation estimation

All the minimum and median values applied to post-process the correlations for all breeds-traits are shown in Table 3.

Direct gestation length (ges)

Across-country correlation for direct gestation length for HOL breed is shown in Table 4. An example of number of common bulls and common ¾ sib groups only for HOL breed is presented in Table 5. Correlation estimates for RDC, JER and BSW breeds are reported in Table 6, 7 and 8, respectively. The correlation estimates ranged from 0.90 between ITA and Czech Republic (CZE) to 0.995 between USA and Japan (JPN) for the HOL breed. For the RDC breed there were four countries and the lowest and highest values were as 0.961 between NOR and New Zealand (NZL) and 0.982 between NOR and USA, respectively.

For JER breed that included three countries, correlation ranged from 0.953 to 0.983 between NZL, USA and AUS, USA respectively. The range for across-country correlation estimates for BSW breed including three countries ranged from 0.966 and 0.980 for AUS, CHE and AUS, USA accordingly.

Table 3. Minimum and Median values used for the post-processing correlation estimations for all breeds and new traits.

Breed-Trait	Min (10% percentile)	Median (10%,0.99)	Breed-Trait	Min (10% percentile)	Median (10%,0.99)
HOL-ges	0.90	0.94	HOL-idd	0.77	0.88
BSW-ges	0.96	0.98	HOL-idh	0.35	0.67
JER-ges	0.95	0.97	HOL-soh	0.59	0.79
RDC-ges	0.96	0.97	HOL-sou	0.73	0.86
HOL-cke	0.56	0.78	HOL-wld	0.63	0.81
HOL-sck	0.56	0.77	RDC-dde	0.79	0.89
HOL-mfe	0.44	0.72	RDC-idd	0.79	0.89
RDC-cke	0.54	0.77	RDC-idh	0.60	0.80
RDC-sck	0.45	0.72	RDC-soh	0.81	0.90
RDC-mfe	0.59	0.79	RDC-sou	0.91	0.95
HOL-dde	0.78	0.89	RDC-wld	0.95	0.97

Table 4. Correlation estimation for the ges in the HOL breed.

Country[1]	AUS	CHE	CZE	ITA	JPN	NLD	NZL	USA
AUS	1							
CHE	0.978	1						
CZE	0.901	0.926	1					
ITA	0.954	0.952	0.900	1				
JPN	0.986	0.982	0.901	0.956	1			
NLD	0.989	0.986	0.915	0.959	0.989	1		
NZL	0.979	0.959	0.901	0.929	0.969	0.975	1	
USA	0.985	0.981	0.902	0.962	0.995	0.993	0.974	1

[1] Australia (AUS), Switzerland (CHE), Czech Republic(CZE), Italy (ITA), Japan (JPN), the Netherlands (NLD), New Zealand (NZL), United States of America (USA)

Table 5. Number of common bulls (below diagonal) and the common 3/4 sib groups (above diagonal) for the ges and HOL breed.

Country	AUS	CHE	CZE	ITA	JPN	NLD	NZL	USA
AUS	0	320	579	854	590	823	778	1083
CHE	271	0	333	536	374	541	270	677
CZE	431	227	0	1568	917	1573	703	1846
ITA	673	444	1186	0	1325	1928	957	3103
JPN	511	284	625	935	0	1020	528	1923
NLD	691	488	1322	1396	765	0	1228	2248
NZL	716	227	520	716	397	1016	0	1206
USA	1092	580	1530	2385	1586	1725	1086	0

Table 6. Correlation estimation for the ges in the RDC breed.

RDC-ges	AUS	NOR	NZL	USA
AUS	1			
NOR	0.971	1		
NZL	0.970	0.961	1	
USA	0.979	0.982	0.966	1

Table 7. Correlation estimation for the ges in the JER breed.

JER-ges	AUS	NZL	USA
AUS	1		
NZL	0.963	1	
USA	0.983	0.953	1

Table 8. Correlation estimation for the ges in the BSW breed.

BSW-ges	AUS	CHE	USA
AUS	1		
CHE	0.966	1	
USA	0.980	0.974	1

Claw health

Across-country correlation estimations range for six claw health traits and for the two breeds of HOL and RDC are shown in Tables 9 and10. The highest value for the HOL breed was 0.928 for dde between NLD and Poland (POL) and the lowest estimate was 0.356 for idh between Spain (ESP)-NLD (Table 9).

For the RDC breed, the highest and the lowest correlations were estimated as 0.953 and 0.619 for wld and idh, respectively, between the two countries of NLD and Denmark-Finland-Sweden (DFS) (Table 10).

Table 9. Summary statistics for correlation estimation for the all six claw health traits in the HOL breed.

Traits	Breed	Min	Mean	Max
dde	HOL	0.79 (CZE,DFS)	0.86	0.928 (NLD,POL)
idd	HOL	0.772 (ESP[1]-NLD)	0.81	0.88 (ESP-DFS)
idh	HOL	0.356 (ESP-NLD)	0.59	0.881 (DEU-DFS)
soh	HOL	0.593 (DEU[1]-NLD)	0.69	0.828 (DFS-NLD)
sou	HOL	0.732 (ESP-NLD)	0.79	0.853 (ESP- DFS)
wld	HOL	0.633 (DEU –ESP)	0.71	0.8 (DEU-DFS)

[1] Spain (ESP), Germany (DEU)

Metabolic Diseases

For HOL and RDC breeds, the summary statistics for across-country correlation estimates are presented in Table 11. For the HOL breed the correlation estimations ranged between 0.444 (for mfe and Germany (DEU)-USA)) and 0.946 (sck and DFS-ITA). The highest and lowest across-country correlation estimates ranged between 0.493 and 0.605 for sck and mfe, respectively, for the RDC breed and the two countries of NLD and DFS (Table 11).

Table 10. Summary statistics for correlation estimation for the all six claw health traits in the RDC breed.

Traits	Breed	Min	Mean	Max
dde	RDC	(DFS[1]-NOR)	_	0.799
idd	RDC	(DFS-NOR)	_	0.799
idh	RDC	(DFS-NOR)	_	0.619
soh	RDC	(DFS-NOR)	_	0.821
sou	RDC	(DFS-NOR)	_	0.917
wld	RDC	(DFS-NOR)	_	0.953

[1] Denmark- Finland- Sweden (DFS)

Table 11. Summary statistics for correlation estimation for the all three metabolic diseases traits in HOL and RDC breeds.

Traits	Breed	Min	Mean	Max
cke	HOL	0.563 (DEU-USA)	0.63	0.709 (DEU-NLD)
sck	HOL	0.565 (CHE-ITA)	0.73	0.946 (DFS-ITA)
mfe	HOL	0.444 (DEU-USA)	0.55	0.695 (DEU-NLD)
Cke	RDC	NOR-DFS	-	0.558
Sck	RDC	NOR-DFS	-	0.493
mfe	RDC	NOR-DFS	-	0.605

EBVs and reliability correlation estimations; National vs International (MACE) evaluations

Direct gestation length

All the EBVs and reliability correlation estimations between the national and International (MACE) evaluations for ges and all breeds are presented in Figure 2-3. For the HOL breed, the highest EBV correlation was 1 for JPN and for the rest of the countries, the EBVs correlation were above 0.983 (Figure 2). For the RDC breed, the highest correlation is for NOR (1) and NZL (0.999) (Figure 3). For BSW and JER breeds the highest values are 0.999 for CHE and 1 for NZL, respectively (Figure 3).

Claw Health

For claw health traits, the EBV correlations between national and MACE evaluation, were quite high with the lowest being estimated for dde in the HOL breed with value of 0.9 for CZE. The highest value was 0.997 for idh and wld in NLD (Figure 4). For the RDC breed and having only two countries of NOR and DFS, the minimum value was estimated as 0.991 for wld in NOR and the highest value was estimated as 0.999 for NZL.

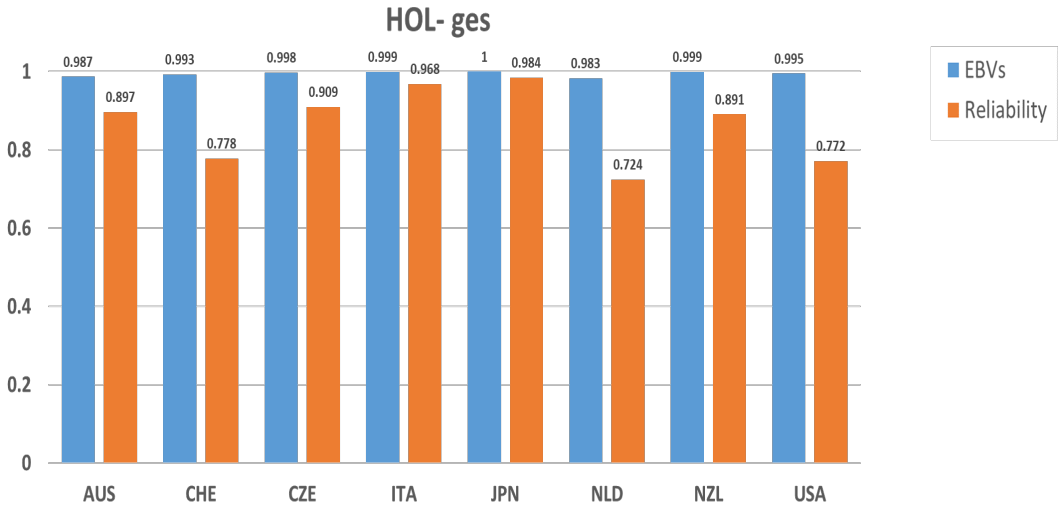

Figure 2. Correlations of EBVs and reliability estimates between national and International (MACE) evaluations for ges in the HOL breed.

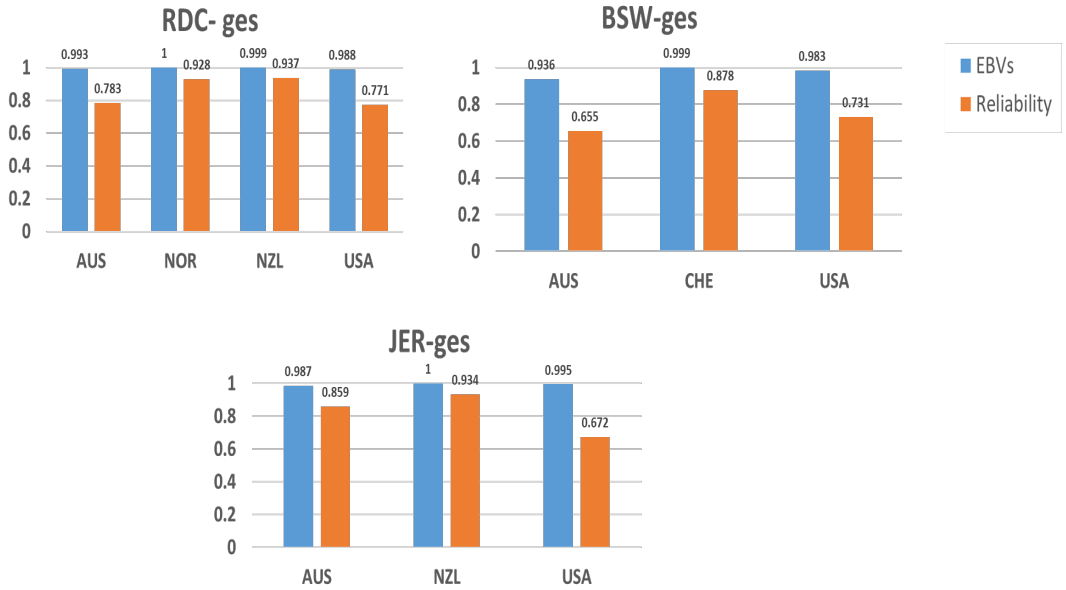

Figure 3. Correlations of EBVs and reliability estimates between national and International (MACE) evaluations for ges in RDC, BSW and JER breeds.

Metabolic disease

Table 12 presents the EBVs and Reliability correlation estimates for all three metabolic diseases traits in the HOL breed. For the HOL breed the EBVs correlations ranged from 0.924 (NLD-mfe) to 0.998 (NLD-sck; DFS-mfe). For the RDC breed and having only two countries of NOR and DFS the EBVs correlation estimations were 1 between these two countries.

May MACE test run(2505t) results- Direct gestation length (ges)

According to the new MACE service schedule, introduced in 2025, an extra MACE test run was conducted in May 2025.

Six countries participated for direct gestation length. The list of countries and breeds is presented in Figure 5. In general, the correlation estimations were similar to the research run estimates. The correlation of EBVs and reliability estimates between National and MACE May test run 2025 (2505t) evaluations was promising; Moreover, EBVs and reliability correlation estimations between May test run (2505t) and research run were also similar and promising.

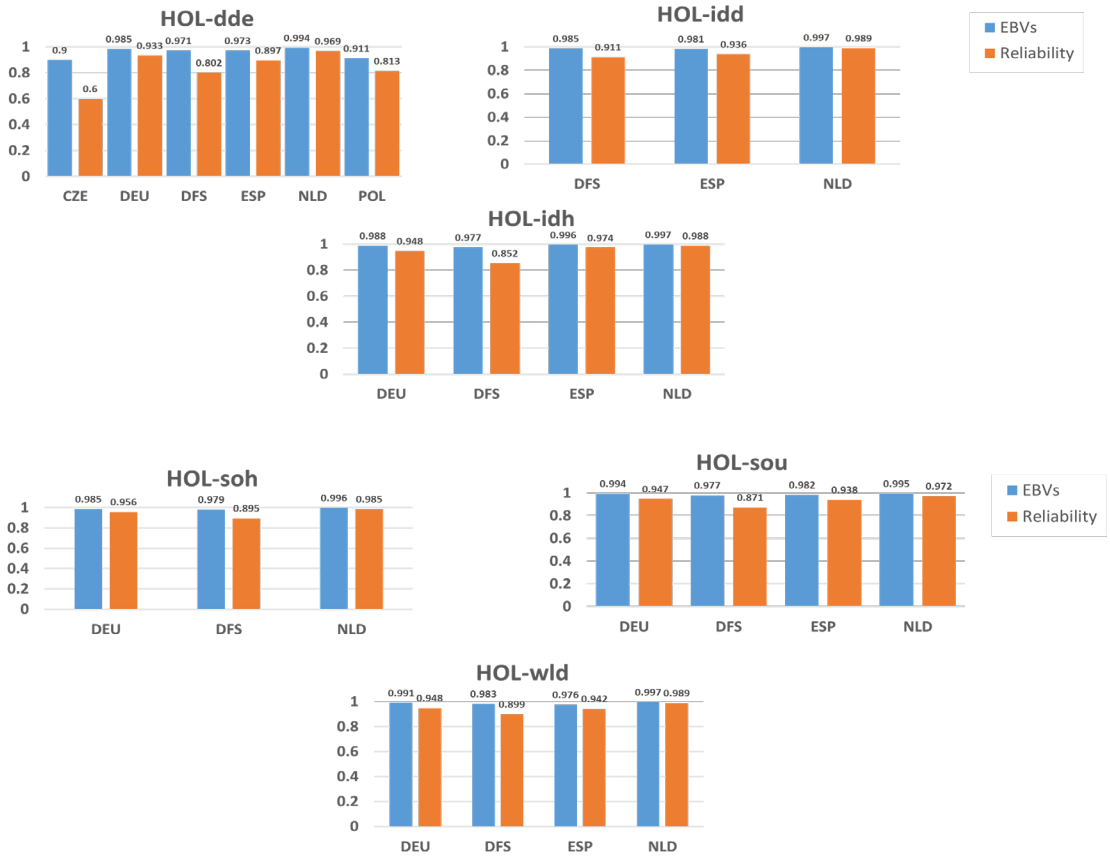

Figure 4. Correlations of EBVs and reliability estimations between national and International (MACE) evaluations for all claw health traits in the HOL breed.

Table 12. EBVs' and reliability correlation estimates between National and International (MACE) evaluations for metabolic diseases traits in the HOL breed.

		Correlation		Reliability	
Trait	**Breed**	**Min**	**Max**	**Min**	**Max**
cke	**HOL**	0.925 (NLD)	0.997 (USA)	0.868 (NLD)	0.994 (USA)
sck		0.965 (ITA)	0.998 (NLD)	0.732 (ITA)	0.986 (CHE, NLD)
mfe		0.924 (NLD)	0.998 (DFS)	0.843 (NLD)	0.996 (DFS)

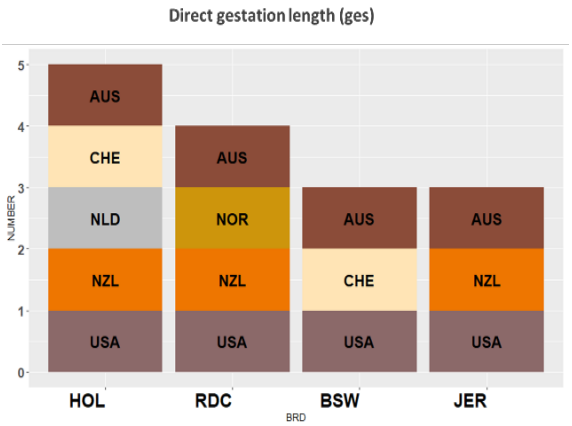

Figure 5. List of the countries and breeds, participated for "ges" in MACE May test run 2025.

Conclusion

To conclude, the new traits' MACE research run showed promising results which led to the official May test run 2025 for "ges" trait and its subsequent inclusion in the official 2025, August MACE evaluation.

Moreover, the research run results for metabolic and claw health traits have also shown the feasibility to include such trait groups in the current MACE portfolio. The offering of an official test run for those two trait groups would require a bit higher participation rate from the MACE countries/organizations and it is therefore aimed to happen in the near future. Interbull Centre will continue reviewing the new information provided by the participating countries in the PREPdb so as to timely identify any new other traits/trait groups that could be suitable for an international evaluation. In order to do that, Interbull Centre would gladly renew the invitation to all countries/organizations to continue to fill in the PREPdb "other traits" electronic form. More also can be an inclusion of more new traits and Interbull services for the new traits, such as GMACE and Intergenomics.

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