



Inclusion of genetic groups in the Interbeef evaluations

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Background

- Interbeef-WG and the Interbeef Service
- Why the genetic groups?

Genetic Groups in Interbeef

- Principles and implementation
- Results
- Validation

Conclusions

- Achievements
- Next steps

Interbeef-WG

- Working Group of **ICAR**
- Developing and promoting national and **international genetic and genomic evaluations of beef cattle**

Interbeef Service

- by **Interbull Centre** (contracted by ICAR) on behalf of Interbeef-WG
- released since 2015
- independent genetic evaluations



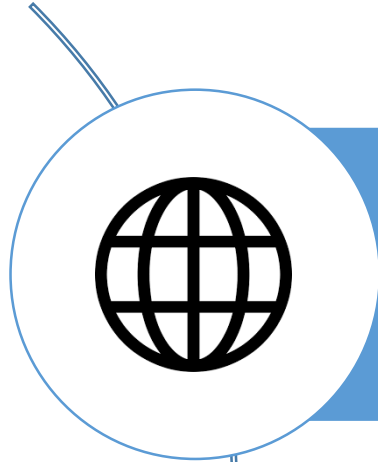
The Interbeef Service



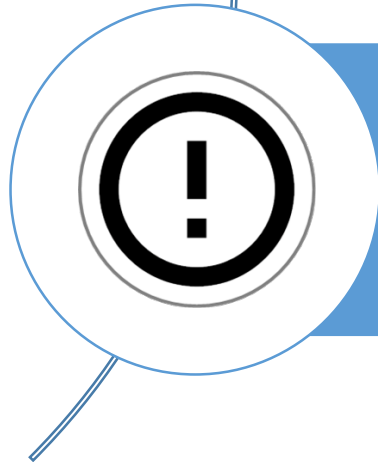
- Released by Interbull Centre 3 times/year (2 routine + 1 test runs)
- The **model** (Phocas, et al., 2005)
 - BLUP animal model
 - multiple trait
 - trait evaluated in each country as a different traits (GxE – **genetic correlations** across countries)
 - direct and maternal genetic effects
 - maternal permanent environmental effect
- Considering:
 - **performance + pedigree data**
 - country-trait specific fixed **effects** chosen by the **submitting organisation**.

- **2 trait-groups**
 - **Adjusted weaning weight** (animal weaning weight)
 - **calving traits** (calving ease and birth weight)
- **5 breeds**
- **15 countries** (13 populations):
AUS, CHE, CZE, DEU, DFS, EST, FRA, GBR, IRL, ITA, LVA, SVN, ZAF
- **86 breed-trait-country combinations**
- **~45mln of performances**





Base population animals (unselected and unrelated, sampled from a population with same genetic level).
If base animals are from populations that differ in genetic value (**imported sires**) this must be considered in the model.

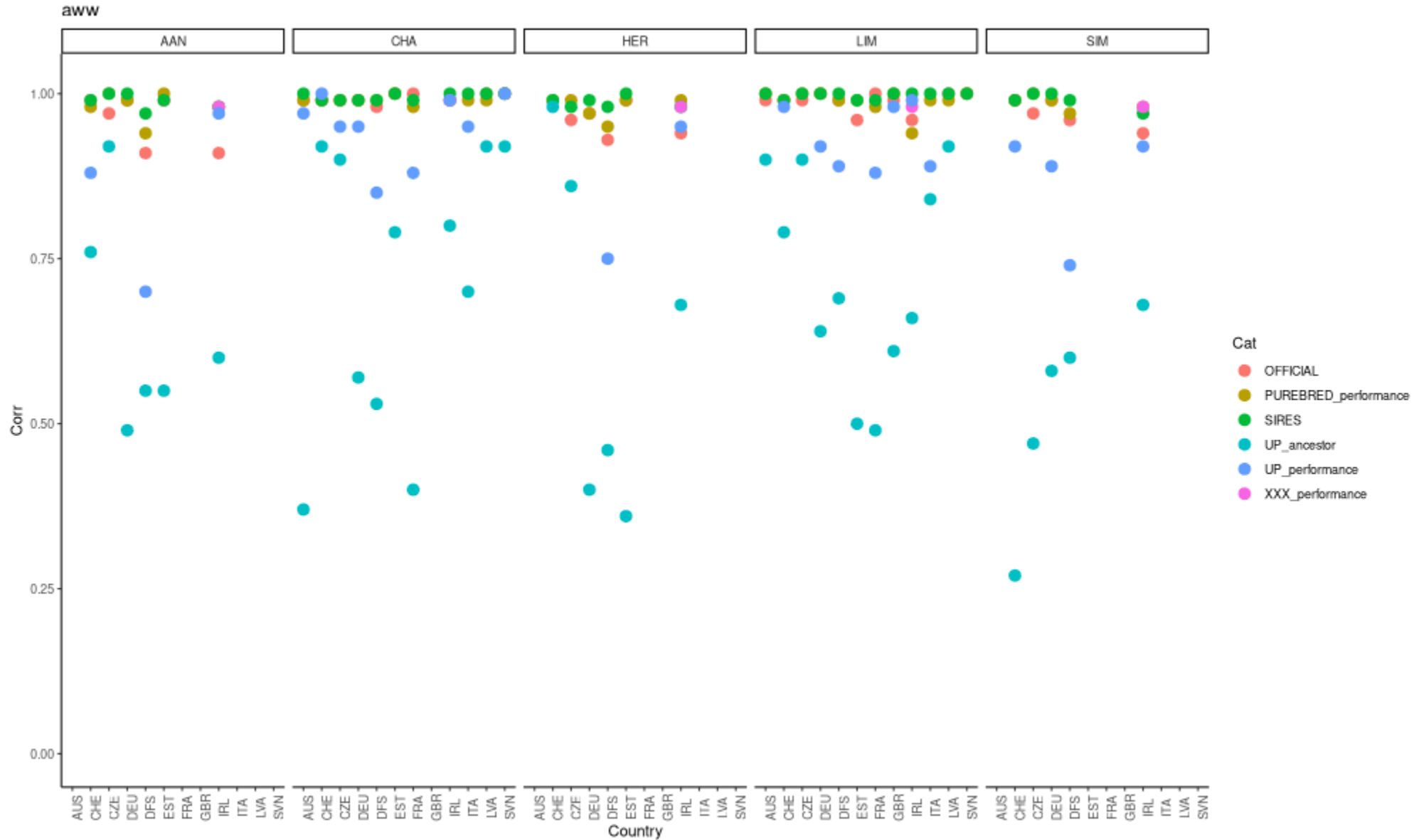


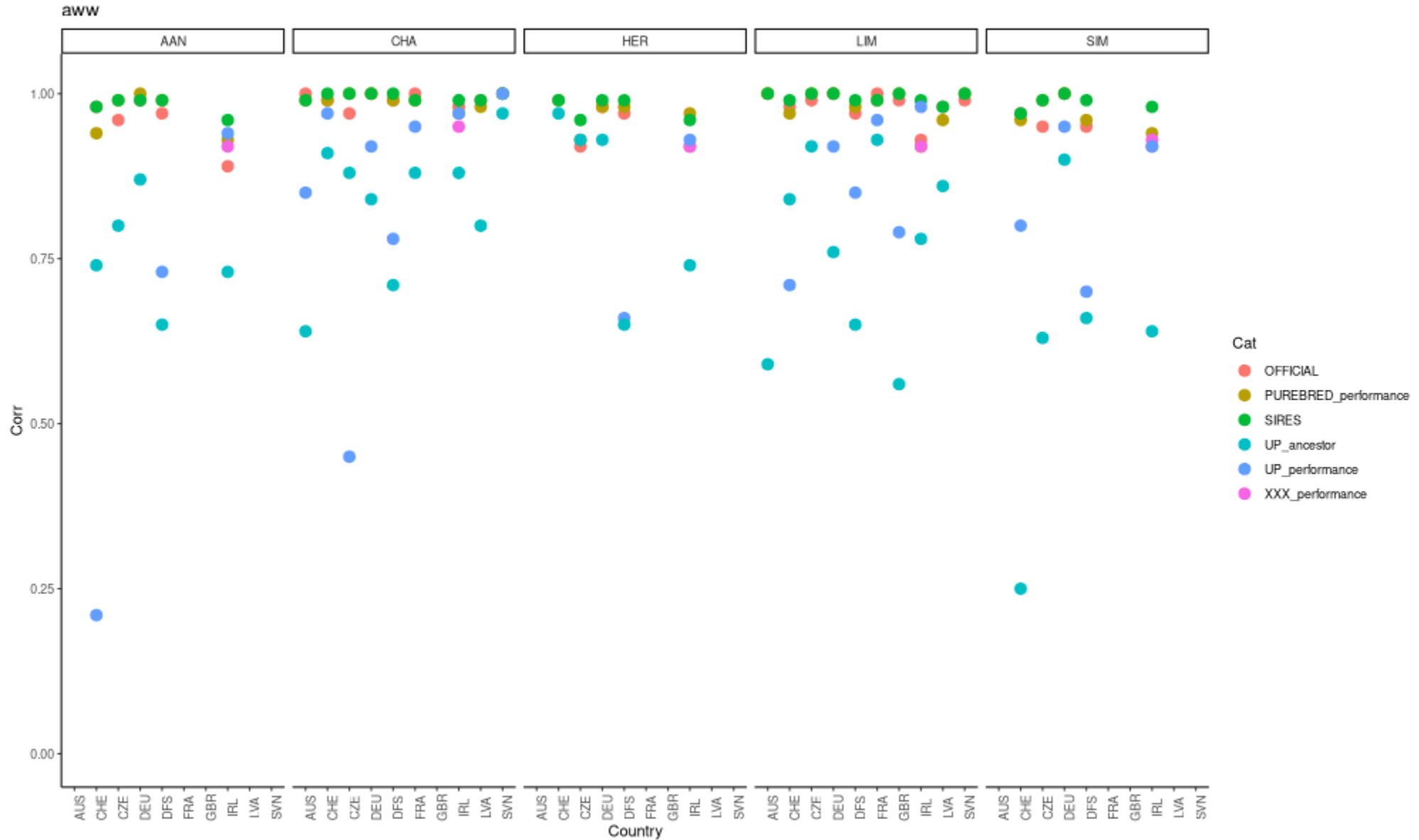
In the recent years several Interbeef members implemented genetic groups in the models used at national level.
Difficulties in comparing **Interbeef vs domestic EBVs** (genetic level and genetic trends)

- Missing parents assigned to genetic groups based on:
 - **SEX** of the missing parent (sire or dam)
 - **BREED** of the animal with missing parental information
 - **COUNTRY** of origin of the animal with missing parental information
 - **YEAR of BIRTH** of the animal with missing parental information
- Reduce the number of small genetic groups, merging genetic groups by:
 - **BREED** (not evaluated in Interbeef): beef_other, dairy
 - **COUNTRY** (not providing participating in Interbeef): e.g. north america="USA CAN", south america="ARG BRA MEX URY", [...]
 - **YEAR of BIRTH**, by defining intervals: <1940, 1960, 1980, 1990, 2000, 2005, 2010, 2015, 2015>
 - Groups smaller than 50 animals merged if belonging to the same SEX, BREED and COUNTRY
- Include genetic groups in the model as random effect ("Quaas-Pollak" transformation, 1988): minimize the impact of small groups, avoid confounding between genetic groups and fixed effects in model.

Implementation of Genetic Groups has an impact on EBVs' mean and sd in most of the breed-trait-country combinations.

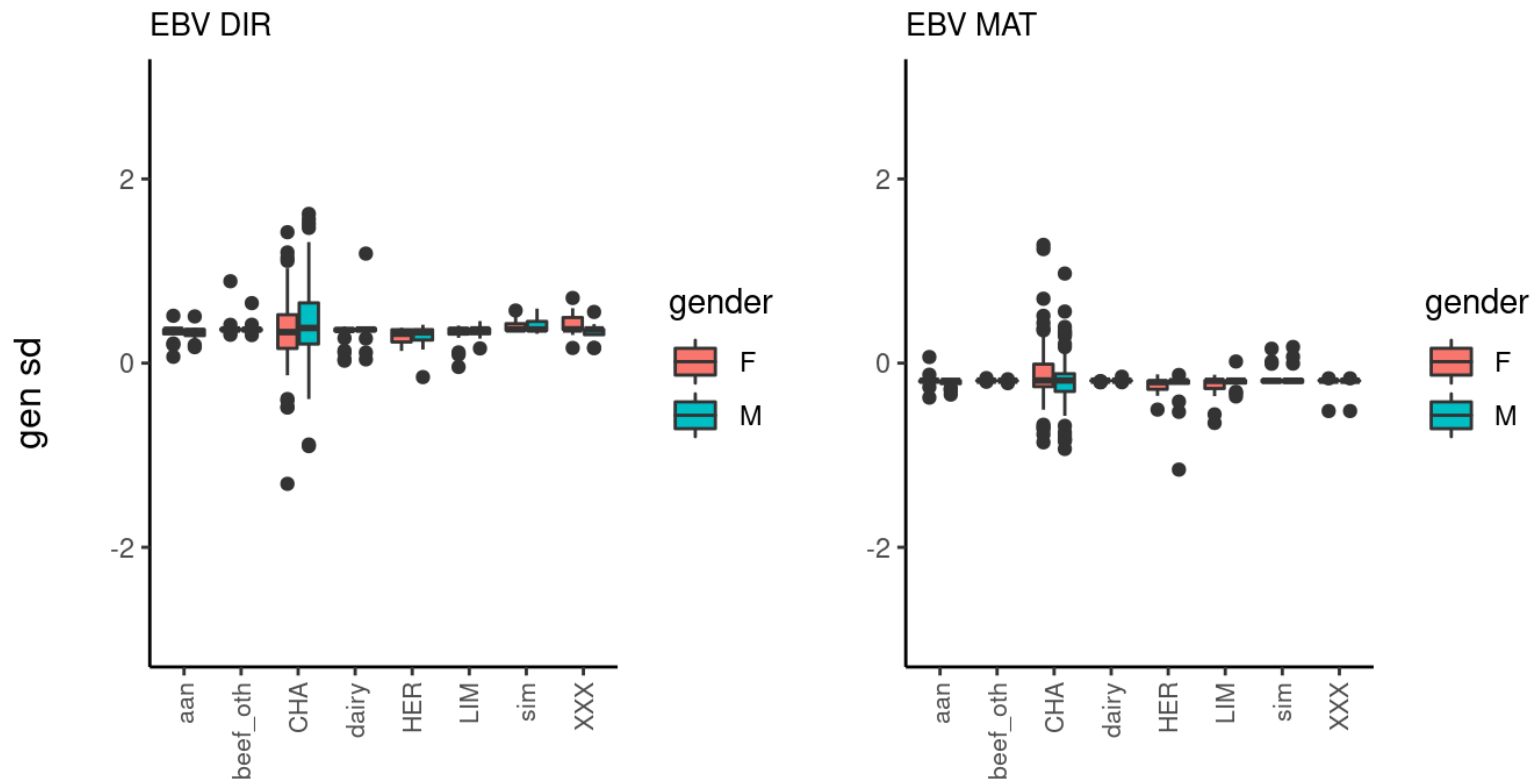
Trait – SD EBV		Change in σ_g		
		Average	Min	Max
aww				
	DIR sd	0.09	-0.02	0.97
bwt	MAT sd	0.04	-0.01	0.41
	DIR sd	0.04	-0.01	0.25
cae				
	MAT sd	0.03	-0.01	0.25
cae	DIR sd	0.04	-0.03	0.27
	MAT sd	0.04	0.00	0.27





Genetic groups' solutions showed distributions $\pm 3 \sigma_g$ (min -2.81 max +3.17) across all 86 breed-trait-country combinations

CHA – cae Group solutions: in 1 country scale:



- Validation performed in all **86 breed-trait groups** combinations using the **Linear Regression (LR) method** (Legarra & Reverter, 2018)
- Comparing results of the January 2022 routine run **without (REF) and with Genetic Groups (GG)**.
- LR based comparison animals EBVs using “whole” and “partial” information: partial evaluations performed by **cut-off performances of animals born >2017**
- 3 estimators of bias:
 - **level bias**, u = difference in mean EBV between partial and whole evaluations; $E(0)$
 - **dispersion bias**, b = regression coefficient of the EBVs whole on EBVs partial; $E(1)$
 - **ratio of accuracies**, r = correlation between EBVs partial and EBVs whole; $E(\text{ratio accp/accw})$
- **Validation animals:**
 - Direct EBV: animals with own performance in whole evaluation
 - Maternal EBV: cows with 1 progeny in whole evaluation



Validation Results



Breed	Trait	Ebv	Lev_REF	Lev_GG	Disp_REF	Disp_GG	Rat_REF	Rat_GG
AAN		DIR	-0.06	-0.11	0.81	0.81	0.51	0.54
	aww	MAT	0.01	-0.02	0.86	0.89	0.59	0.61
		DIR	0	-0.04	0.94	0.92	0.53	0.53
	bwt	MAT	-0.01	0.04	0.84	0.8	0.53	0.52
		DIR	-0.02	0.04	0.8	0.78	0.52	0.54
	cae	MAT	0.03	0.04	0.89	0.98	0.54	0.63
All combinations			-0.02	-0.02	0.90	0.90	0.62	0.63

- The results showed that the implementation of genetic groups in Interbeef evaluation is **feasible**
- The implementation of genetic groups **affected mainly animals with unknown parents**
- Monday, 30 May 2022: Interbeef April 2022 test run **results distributed** to countries
- Monday, 13 Jun 2022: deadline for countries to provide comments and feedback on distributed results
- Tuesday, 12 Jul 2022: **Technical Committee and Interbeef-WG** will make **final decision** about routine implementation of genetic groups in Interbeef evaluations



Please, feel free to contact interbeef@slu.se if you are interested in the Interbeef Service.