Towards standardized LR protocols for international beef cattle genetic evaluations

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THE GLOBAL STANDARD
FOR LIVESTOCK DATA

Network. Guidelines. Certification.

Introduction

Reliable genetic evaluations

- High quality data
- Appropriate models to estimate the EBVs

International evaluations

- Multiple countries contribute data under different models.
- Accuracy and absence of bias become critical requirements when results are combined across national systems.

Country A

Country B
⚠ biased model

Country C

International Evaluation

Entire evaluation compromised

Evolution of Validation Methods

1995

Boichard et al. proposed the first validation framework for international dairy genetic evaluations.

2009

Sullivan et al. extended validation approaches for multi-country dairy evaluations.

2011

Tyrisevä & Mäntysaari refined methods for detecting bias and dispersion in international dairy evaluations.

Interbeef

2026

Interbeef adapted Interbull Method II for Interbeef.

Guidelines published.

2026

Adapt Legarra & Reverter method to the Interbeef

Interbeef

Linear Regression (LR) Method

Whole dataset (dataw)

All available information

→

Partial dataset (datap)

Older or limited information

→

LR Method

Compares EBVs between datasets

✓ **Versatile**

Applicable to any model.

✓ **No pre-adjustment**

Does not require pre-adjustment of phenotypes before validation.

Addresses limitations

Dairy
X
Beef

Objectives

Assess the feasibility of the LR method for validating

international beef cattle genetic evaluations

◎ ***Focusing on the definition of focal individuals using three approaches:***

PA

Parent-Average Bulls

Bulls with progeny records in dataw but not in datap

ΔPROG

Progeny increase

Incrementally increasing progeny information per bull

ΔERC

Effective Record Contribution Difference

Evaluating differences in effective record contribution between datasets (dataw and datap)

Material and Methods

Breeds & Countries

CHA

Charolais

LIM

Limousin

SIM

Simmental

➢ *Up to 5 European countries · Phenotypic & pedigree data from Interbeef evaluations*

Trait Groups

Carcass

- Cwe = carcass weight
- Cco = carcass conformation
- Cfa = carcass fat

carc

Calving

- cae = calving ease
- bwt = birth weight

calv

Material and Methods

Data set design

dataw — Whole dataset

All animals & records up to 2023

datap — Partial dataset

Most recent years removed —
simulates earlier evaluation

Year cutoffs for datap:

Carcass (carc)	≤2018
Calving (calv)	≤ 2019

Software

- **MiX99** EBV calculation from dataw and datap
- **MTEDC** Reliability estimation

Models

- Pedigree based model
- Multi-trait, multi-country model
- Random and fixed effects varied across countries
- Maternal effect only for calving
- Genetic correlations across countries from Interbeef

Focal individual’s selection

- Three approaches were tested to define the focal group of bulls for LR validation:

Parent average bulls (PA)

No progeny in datap AND ≥ 1 progeny in dataw

ΔPROG

Progeny Increase

ΔPROG = NProgw − NProgp

Cumulative threshold:

ΔPROG ≥ 25

ΔERC

ERC Difference

ΔERC = ERCw − ERCp

Cumulative threshold:

ΔERC ≥ 2

LR statistics

- Two statistics calculated following Legarra and Reverter (2018):

Δp **Level Bias in genetic standard deviations**

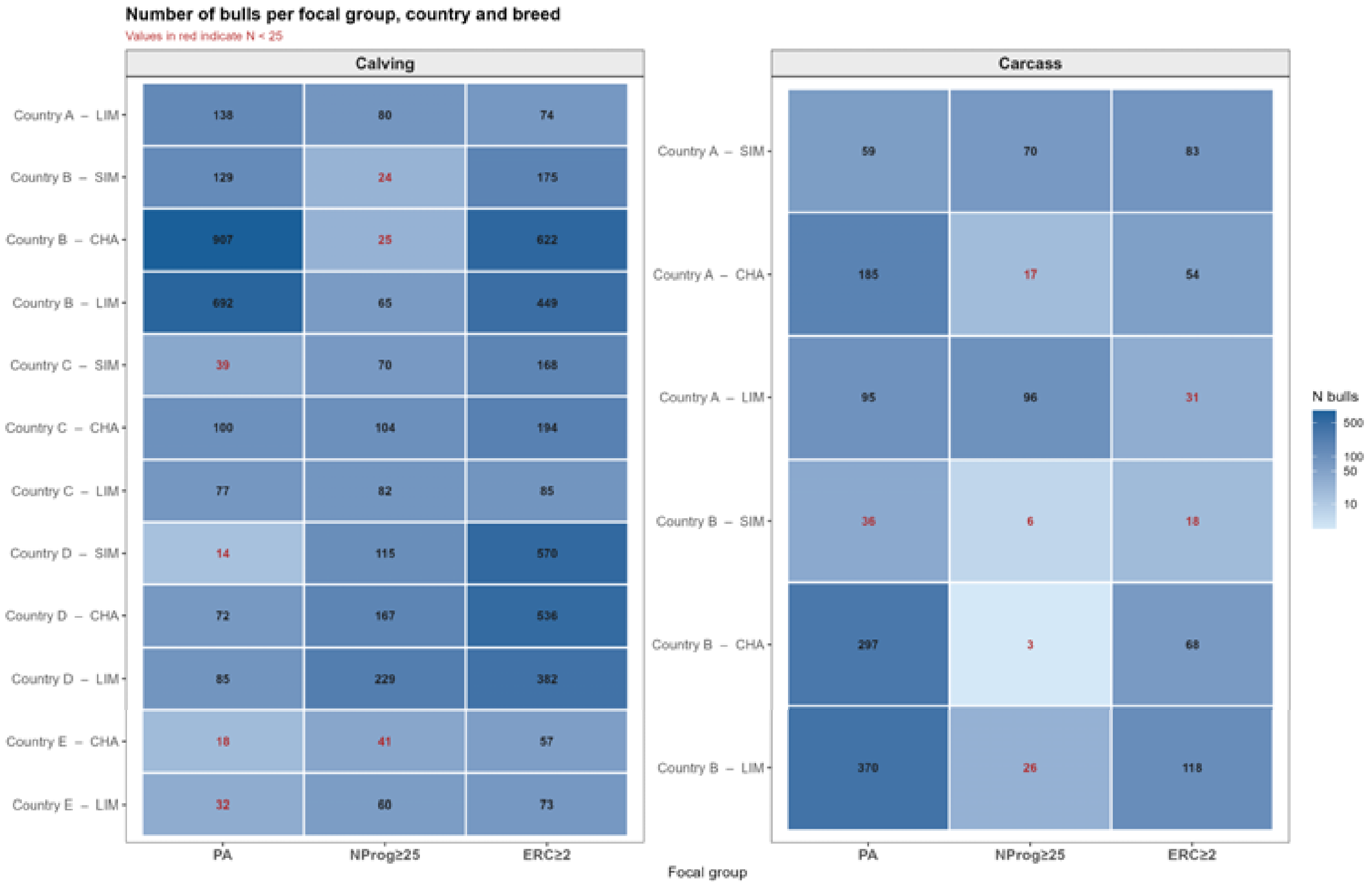
- Δp = (mean EBVp − mean EBVw) / σg

bw,p **Dispersion bias**

slope of regression EBVw on EBVp

- bw,p = Cov(EBVp, EBVw) / Var(EBVp)

Results



Number of bulls per focal group, country and breed

Values in red indicate N < 25

Calving

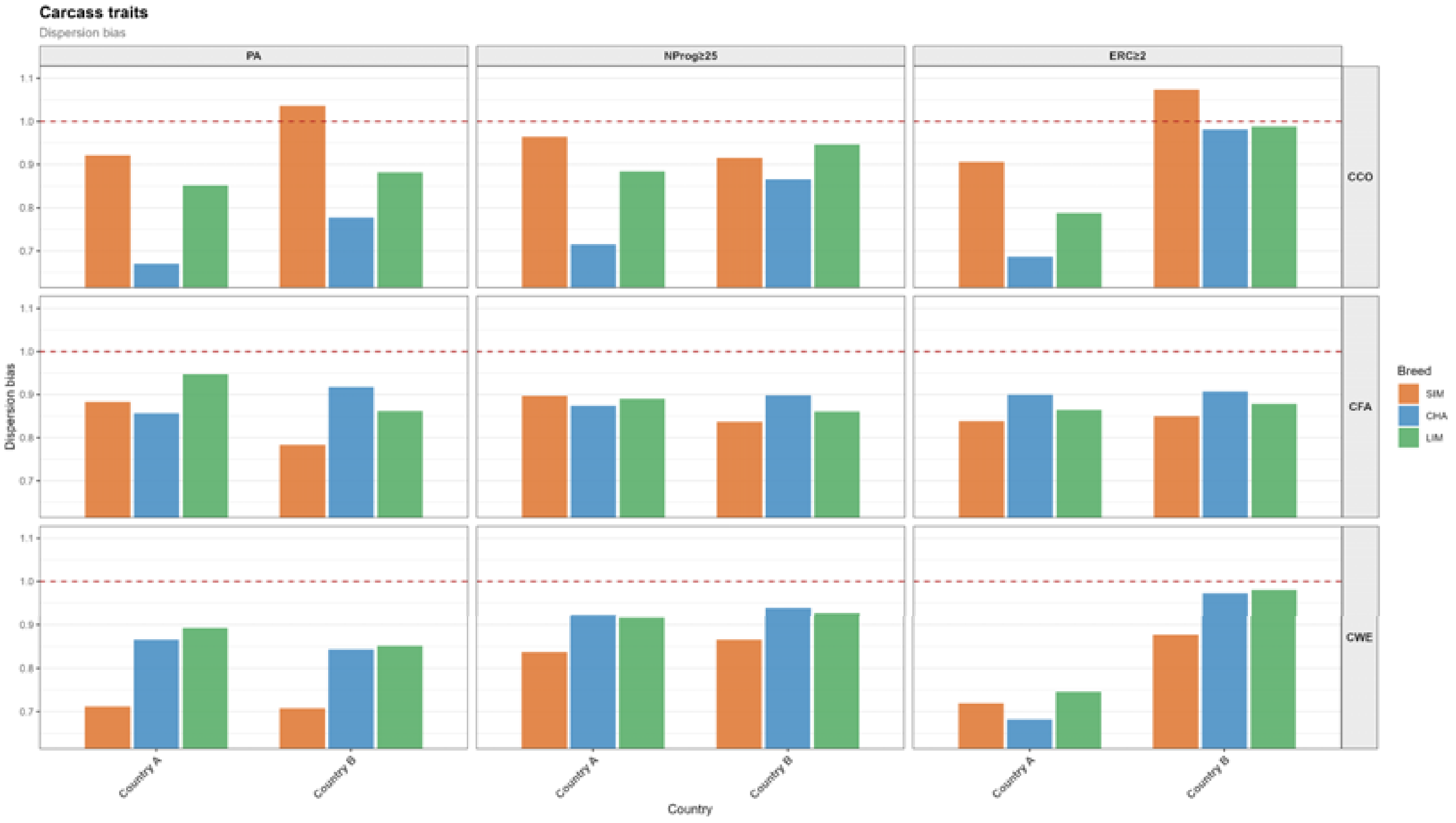
	PA	NProg≥25	ERC≥2
Country A – LIM	138	80	74
Country B – SIM	129	24	175
Country B – CHA	907	25	622
Country B – LIM	692	65	449
Country C – SIM	39	70	168
Country C – CHA	100	104	194
Country C – LIM	77	82	85
Country D – SIM	14	115	570
Country D – CHA	72	167	536
Country D – LIM	85	229	382
Country E – CHA	18	41	57
Country E – LIM	32	60	73

Carcass

	PA	NProg≥25	ERC≥2
Country A – SIM	59	70	83
Country A – CHA	185	17	54
Country A – LIM	95	96	31
Country B – SIM	36	6	18
Country B – CHA	297	3	68
Country B – LIM	370	26	118

- **NProg≥25** smallest for carcass — critically low in Country B for SIM (N=6) and CHA (N=3)
- **ERC≥2** highly variable for calving — large in some countries (>500)

Results



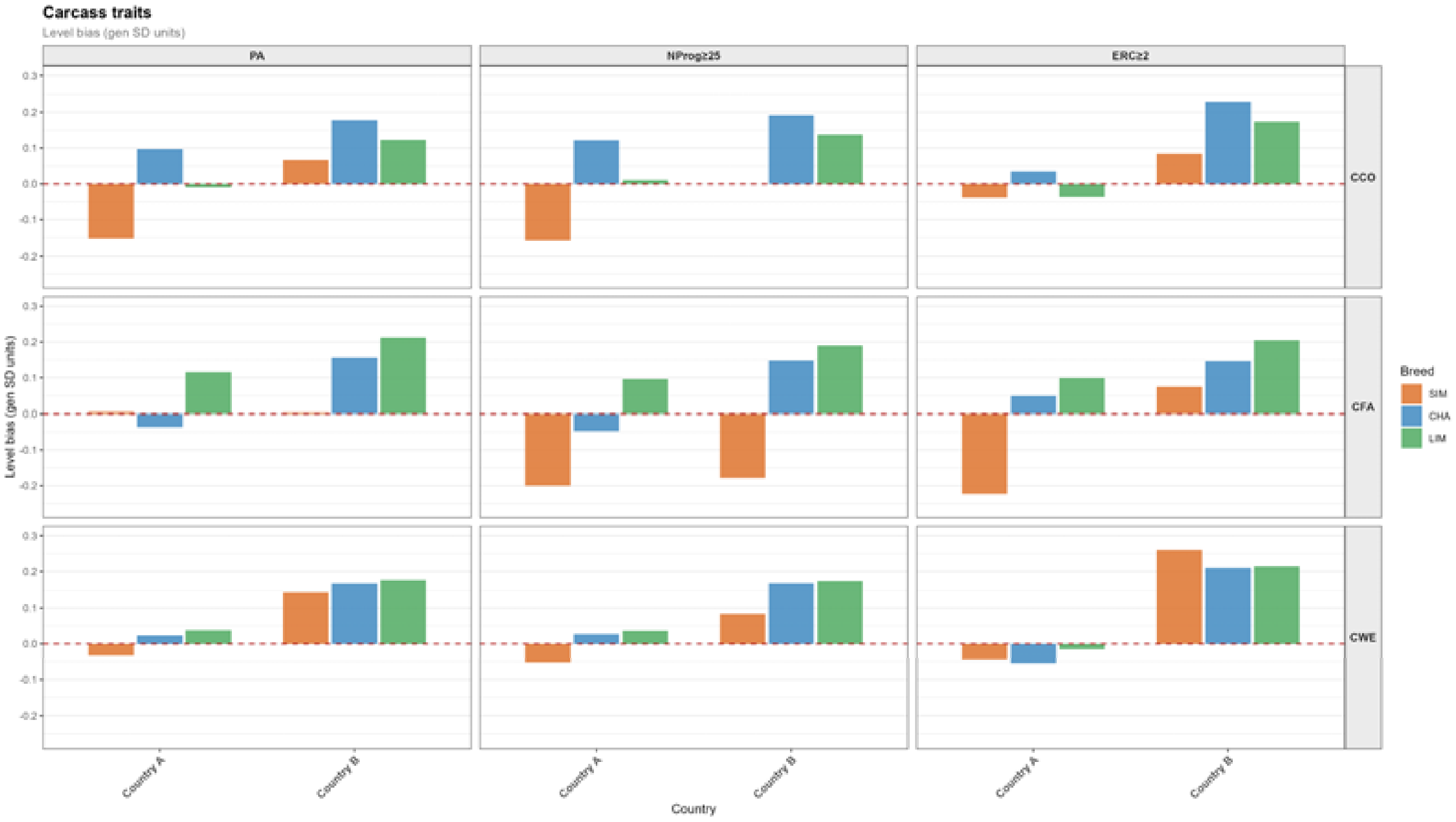
- **Dispersion bias below 1.0** for most combinations — general underdispersion across breeds and countries

- **CHA** shows the strongest underdispersion, especially CCO (≈0.65–0.70 in Country A)

- **SIM Country B (CCO/PA/ERC)** only case exceeding 1.0 — slight overdispersion

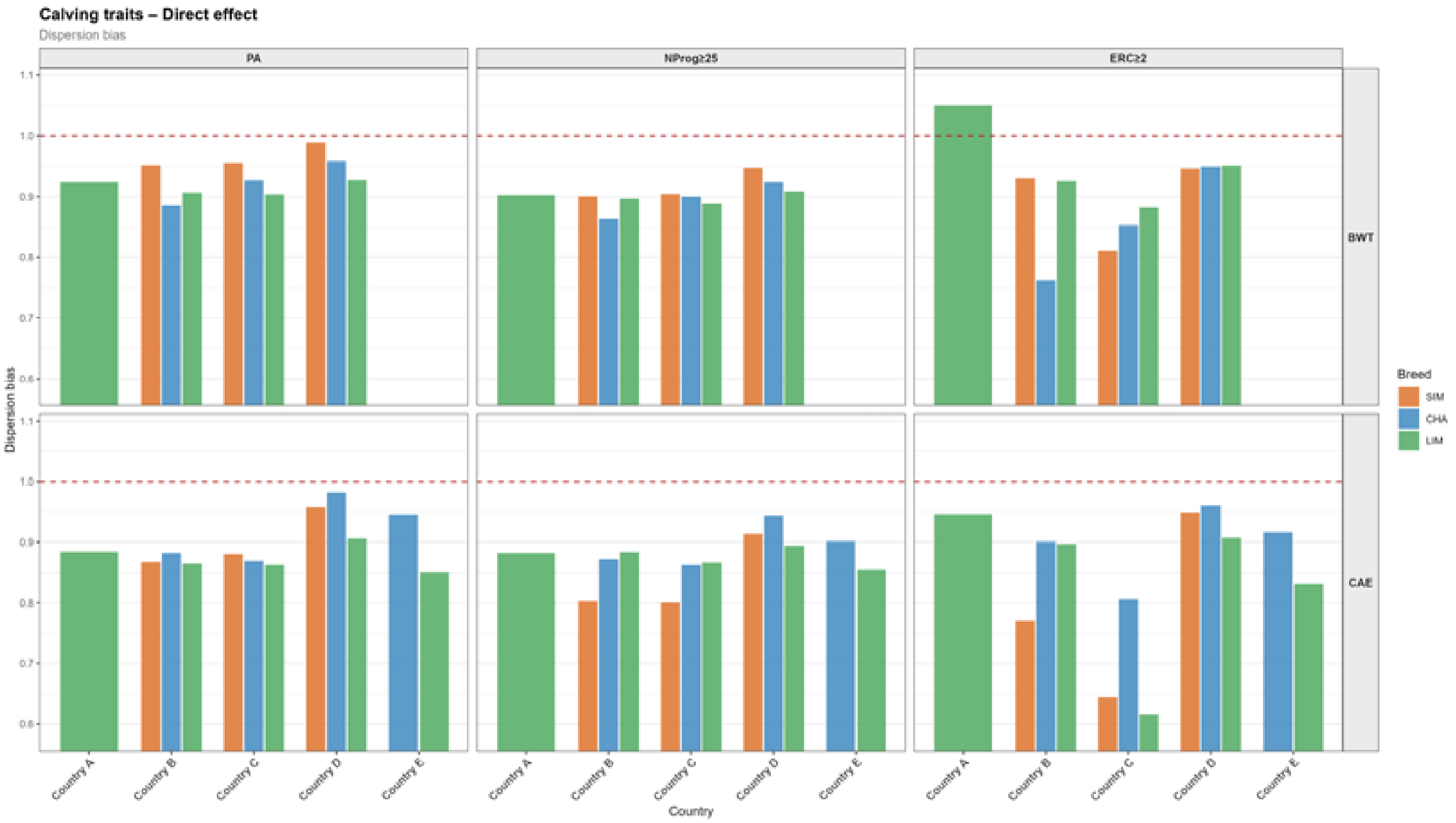
- **Results consistent** across the 3 focal groups

Results



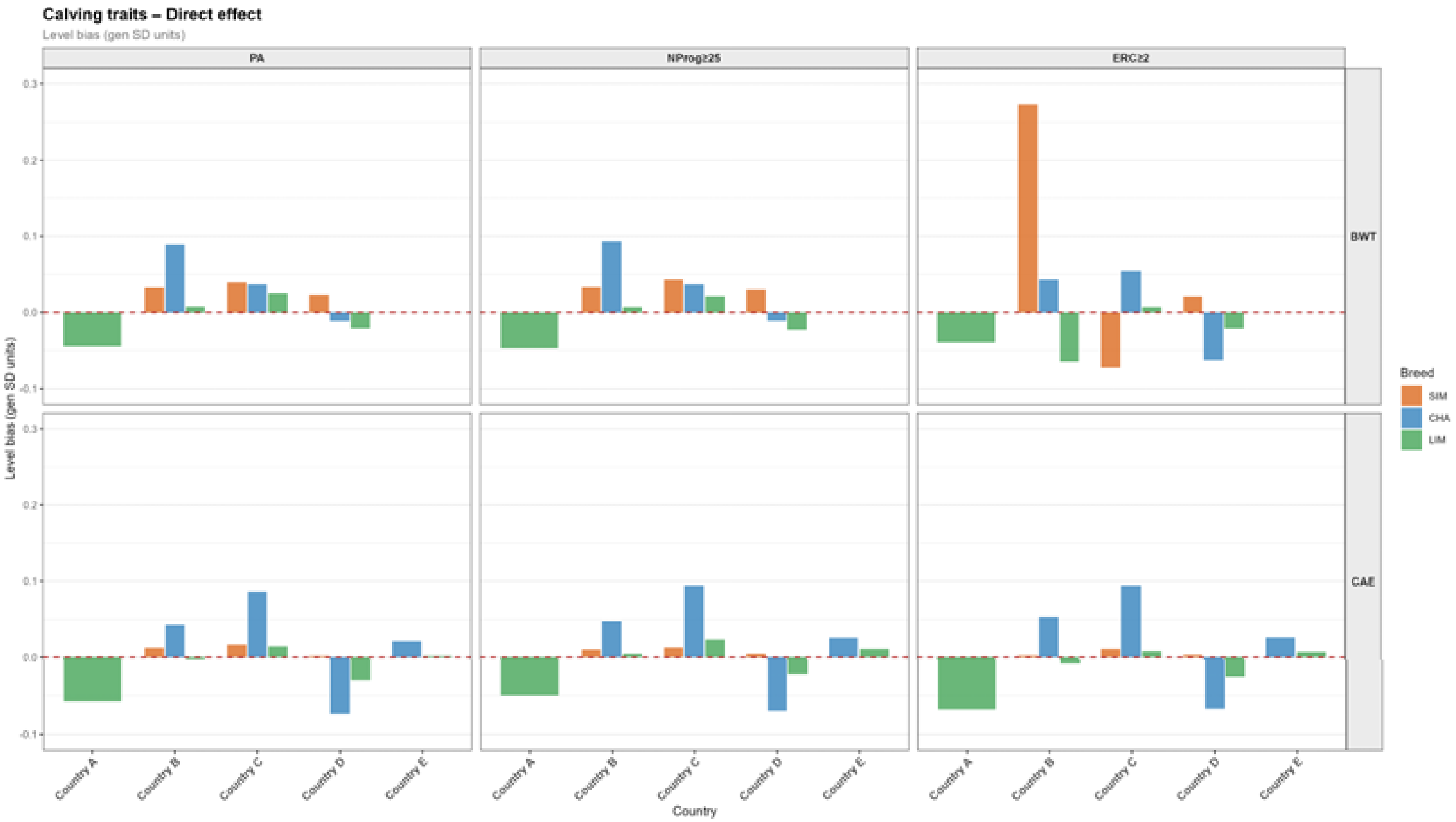
- **Level bias close to zero** for most combinations, especially CWE across all groups
- **SIM:** consistent negative bias for CFA in Country A (≈−0.15 gen SD)
- **CHA and LIM:** positive bias for CCO and CFA in Country B

Results



- **BWT direct:** stable dispersion ≈0.85–0.90 with PA and NProg≥25 across all 5 countries
- **ERC≥2** introduces high variability for BWT — LIM Country A exceeds 1.0, large drops in Countries B and C
- **CAE direct:** similar but slightly lower (≈0.83–0.88); more variable with ERC≥2 in Countries B and C

Results



- **CAE direct:** level bias essentially zero across all countries, breeds and groups
- **BWT direct:** close to zero with PA and NProg≥25; small negative bias for LIM in Country A
- **ERC≥2 clearly unstable for BWT**
  - SIM Country B reaches ≈+0.27 gen SD

CONCLUSIONS

- **LR method is feasible** for validating international beef cattle genetic evaluations — applicable across breeds, countries, trait groups and effects

- **Underdispersion is a general pattern** across all groups and traits — more pronounced for carcass than calving

- **NProg≥25 produced the most stable results** — lower bias and dispersion closer to unity, consistent across carcass and calving traits

- **ERC≥2 showed higher instability,** particularly for calving traits

- **Next steps:** Testing other focal group bulls
- How to communicate the results to the countries

Thank you