PFHBiPM

Interbull 2025

21st of June, Louisville, KY

with Breeders
into the future

Implementation of single-step genetic evaluation in Poland

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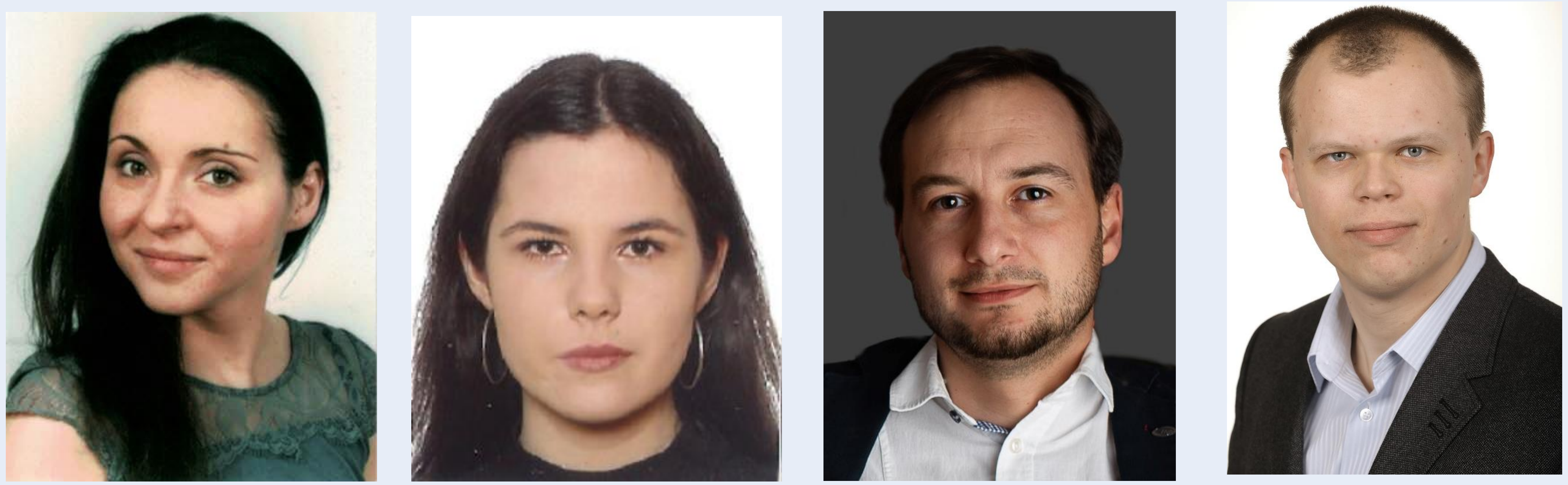
CGen – Centre for Genetics

Polish Federation of Cattle Breeders and Dairy Farmers

- Genetic evaluation centre
- Established: April 2016
- Location: Poznań
- Mission:
  - Estimation of breeding values
  - Genetic analysis
  - Breeding program
  - Selection indexes
  - Implementing innovations

CGen Team

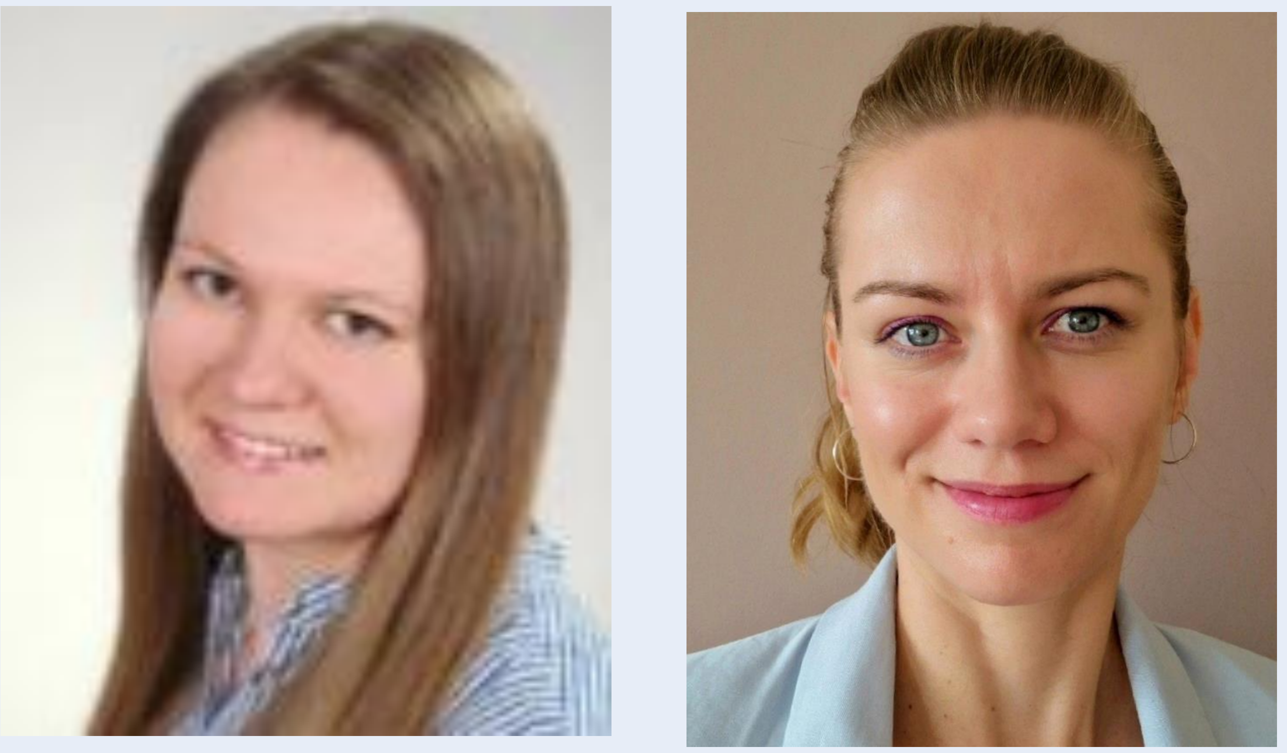
Geneticists



Analytics and knowledge transfer

Data analysis and processing

Administrative support



Cooperation

POZNAŃ UNIVERSITY OF LIFE SCIENCES

WROCŁAW UNIVERSITY OF ENVIRONMENTAL AND LIFE SCIENCES

UNIVERSITY OF AGRICULTURE IN KRAKOW

NATIONAL RESEARCH INSTITUTE OF ANIMAL PRODUCTION

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UNIVERSITY OF GEORGIA

EURO Genomics for reliable cattle breeding

CRV Coöperatie BETTER COWS > BETTER LIFE

Timeline

- June 2022 – project started
- January 2025 – all traits passed ITB EBV and GEBV tests
- April 2025 – first official publication of proofs based entirely on single-step methodology
- April 2025 – CGen became genetic evaluation provider for Holstein cattle in Poland

Changes

- Multi-step -> single-step
- Inclusion of novel traits
- New trait definitions
- Re-modelling existing traits
- New VCs for all traits
- Inclusion of external (MACE) information
- Genetic base cows YOB -10y, to be changed every year in April
- Updated publication criteria

Single-step

- Blupf90 family of programs
- Blup90iod3 – main solver
- Accf90GS3 – reliability approximation incl. genomic
- APY with 18K core animals
- >240K genotypes (including EG reference population)
- Pedigree integrated with Interbull and EG partners
- >4M phenotyped cows, >6M in pedigree, 76M milk production records
- Less data for new traits

Operations

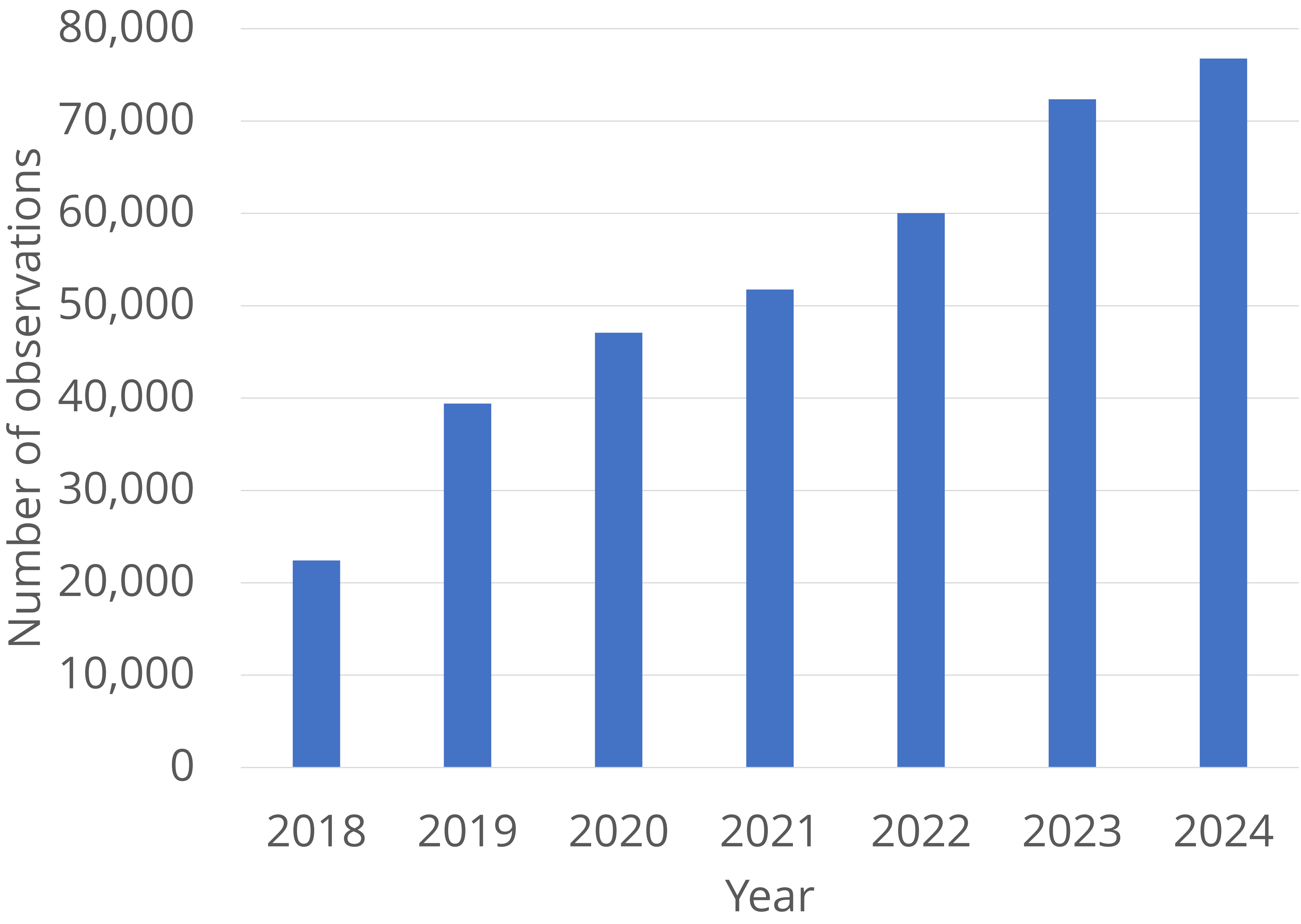
- 47 traits under evaluation
- 3 full runs (new phenotypes) and 3 additional runs (new genotypes and pedigree only) per year
- Working towards monthly
- Solver run times: 1.5h for longevity, 10h for fertility, 5-10h for type, 5h for DDE, 6-18h calving traits, 13-33h production traits (RRM)
- Aim to minimalize time from DNA collection to GEBV publication

What's new?

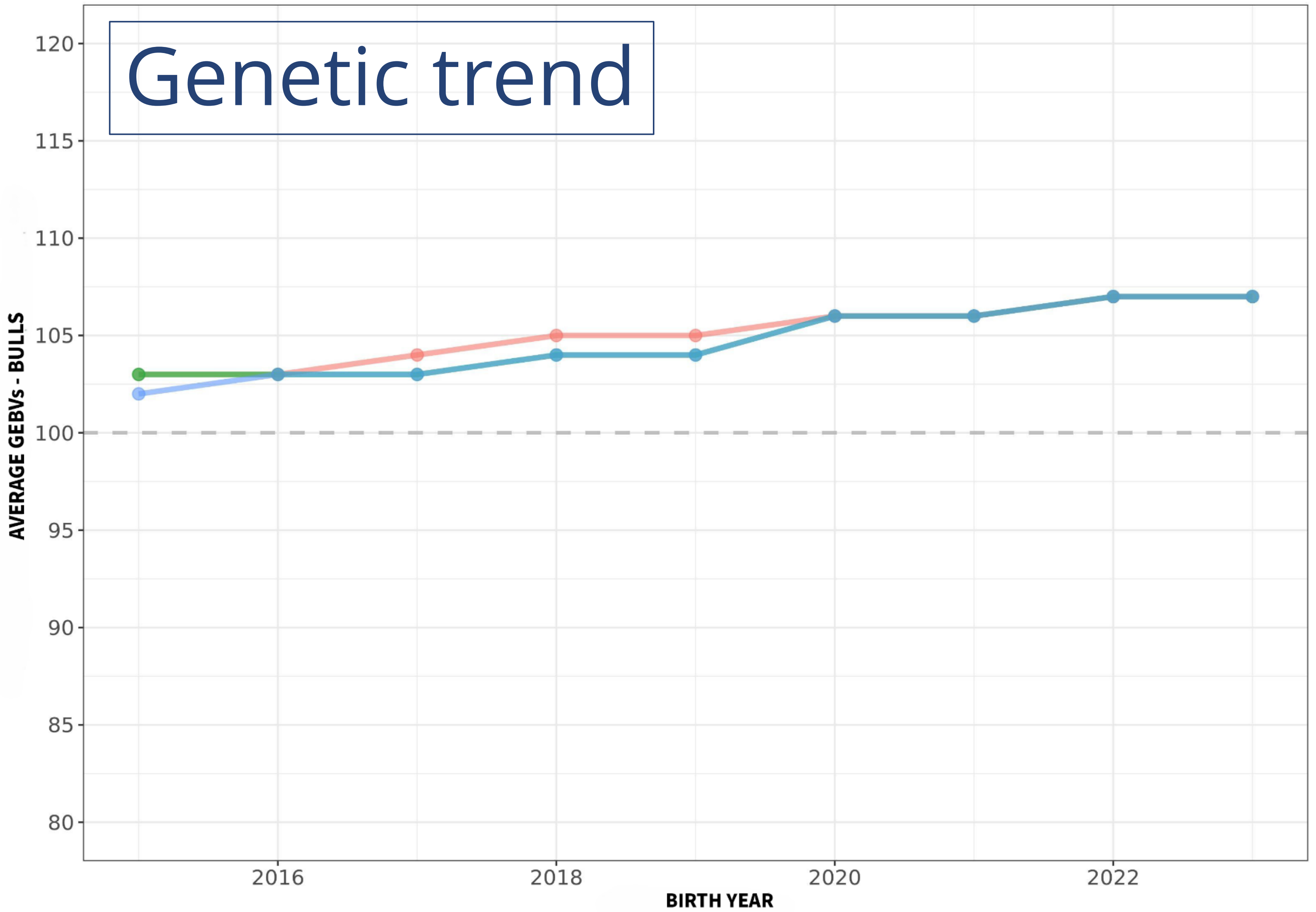
- Claw health - DDE
- Type – Bone quality
- Fertility
    - Interval from 1st to last insemination
    - More parities included
- Longevity
    - New trait definition – probability of survival from one calving to the next one in first 4 lactations (binary)
    - 4 trait AM
    - $h^2 = 0.16$

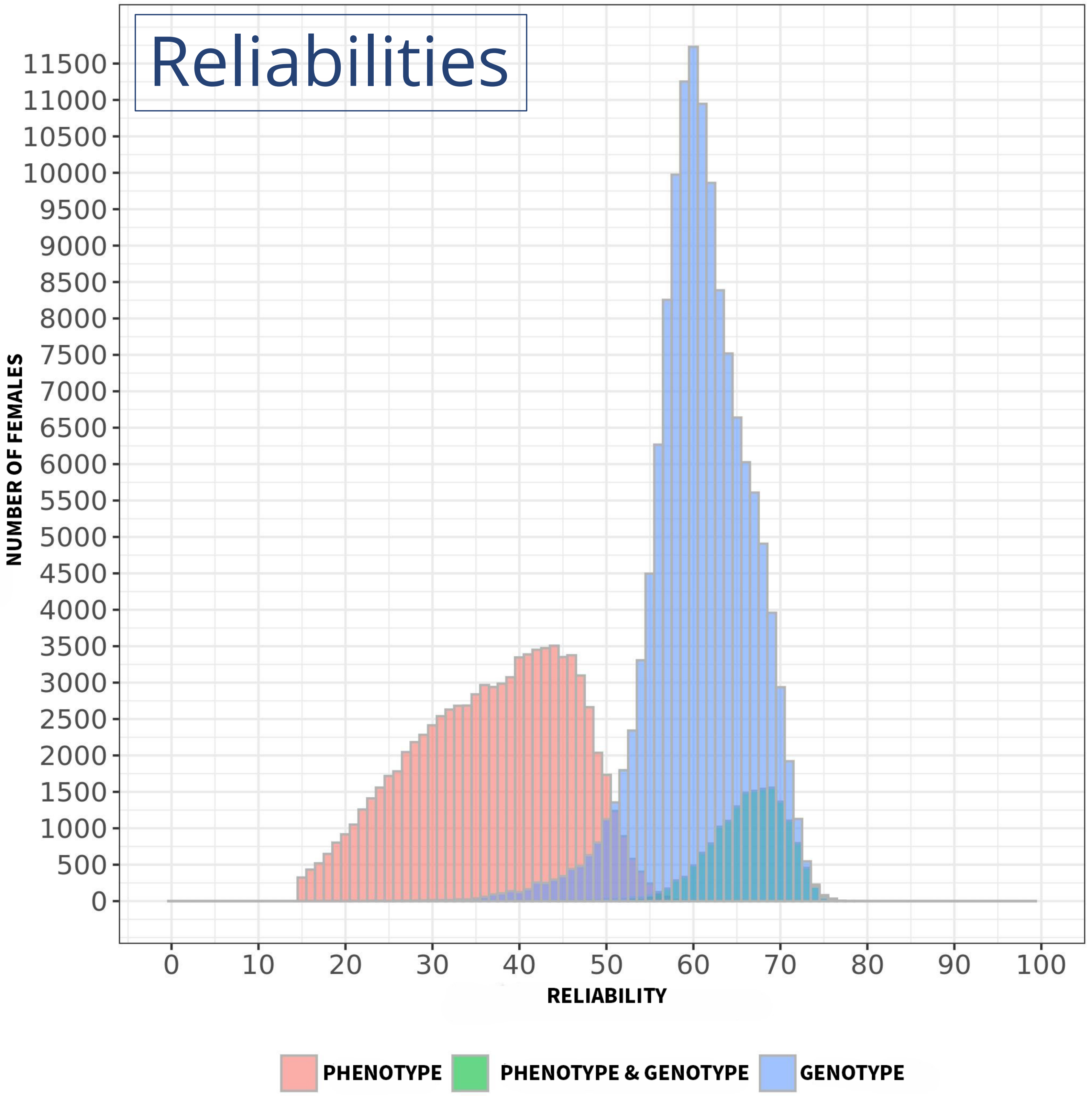
Dermatitis digitalis (DDE)

- First published in April 2024
- First trait implemented with single-step
- Data collected by hoof trimers using a custom build app
- 120K cows with observations
- 370K records in total



Dermatitis digitalis (DDE)

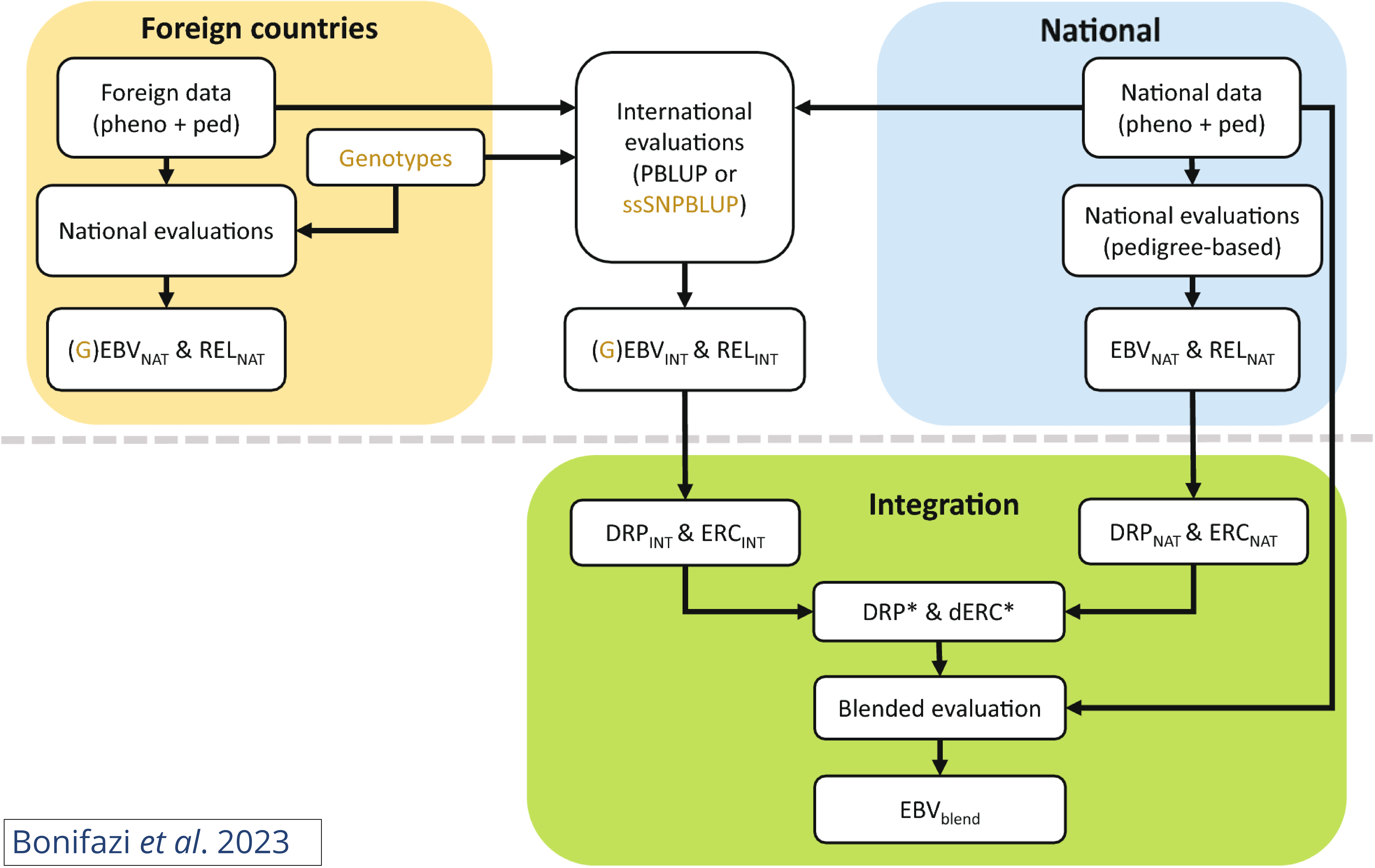




- $h^2 = 0.07$
- Reliability:
  - 60% for genotyped animals
  - 70% reference population

    (17K - genotyped and phenotyped cows)

MACE Integration



Foreign countries

Foreign data (pheno + ped)

Genotypes

National evaluations

(G)EBV$_{NAT}$ & REL$_{NAT}$

International evaluations (PBLUP or ssSNPBLUP)

(G)EBV$_{INT}$ & REL$_{INT}$

National

National data (pheno + ped)

National evaluations (pedigree-based)

EBV$_{NAT}$ & REL$_{NAT}$

Integration

DRP$_{INT}$ & ERC$_{INT}$

DRP$_{NAT}$ & ERC$_{NAT}$

DRP* & dERC*

Blended evaluation

EBV$_{blend}$

Bonifazi *et al*. 2023

MACE Integration

- Combining MACE and national EBVs

$$DRP_i^* = \frac{(dERC_{MACE_i} * DRP_{MACE_i}) - (dERC_{NAT_i} * DRP_{NAT_i})}{dERC_i^*}$$

where: $dERC_i^* = dERC_{MACE_i} - dERC_{NAT_i}$

  - If $dERC_i^*$ is ≤ 0 or if gain in reliability is smaller than 0.01, both $dERC_i^*$ and DRP_i^* are set to 0.
  - If a bull has no daughters in Poland $DRP_i^* = DRP_{MACE_i}$ and $REL_{DRP_i^*} = REL_{MACE_i}$
  - If bull has daughters only in Poland, then DRP_i^* is not included

- Including in the analysis

DRP^* are used as pseudo-phenotypes for bulls, with $dERC^*$ as their corresponding weights. Bulls are included in the phenotype file with one common level of fixed effect ("bull" CG). No other fixed effects are not fitted for bulls. Weights for cow's phenotypes =1 or 0.8. A RRM is used for production traits and SCS.

Bonifazi *et al*. 2023; Eding, 2024

MACE integration results for – Milk

Group	N	Genotyped	MACE DRP	MACE vs PBLUP	MACE vs SSMACE
				correlation	correlation
Domestic	6,963	4,002	0	0.99	0.99
Domestic + dtrs	289	158	2	0.99	0.98
Foreign	148,330	31,165	148,330	0.79	0.98
Foreign + dtrs	5,867	3,435	2,332	0.97	0.97

MACE integration results for – Milk

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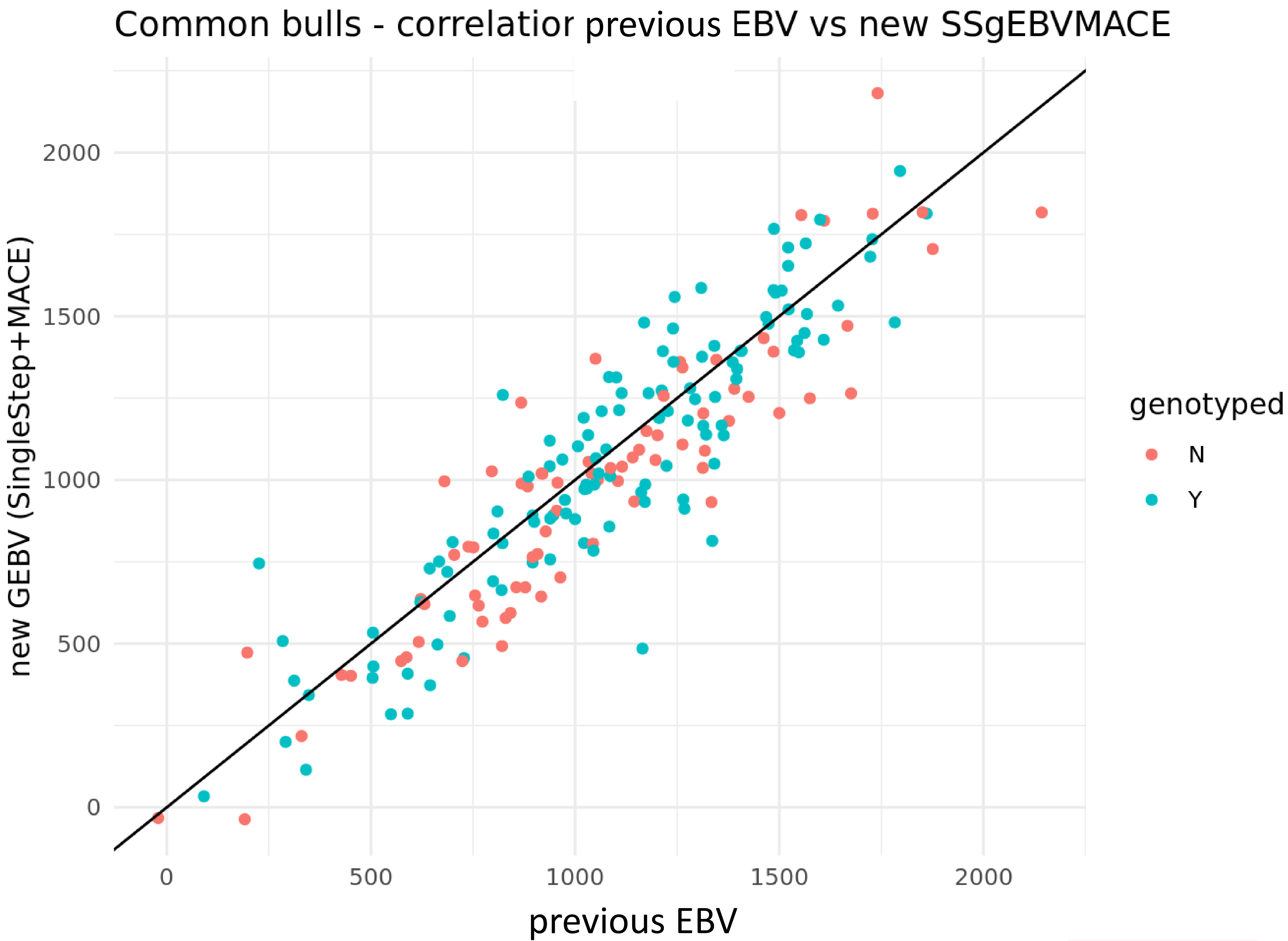
Foreign	148,330	31,165	148,330	**0.79**	**0.98**
Foreign + dtrs	5,867	3,435	2,332	0.97	0.97

MACE integration results for – Longevity

Group	N	Genotyped	MACE DRP	MACE vs PBLUP	MACE vs SSMACE
				correlation	correlation
Domestic	6,963	4,002	0		
Domestic + dtrs	289	158	2		
Foreign	148,330	31,165	148,330	0.72	0.96
Foreign + dtrs	5,867	3,435	2,332		

Correlations with previous system

- Milk 0.90
- Fat 0.94
- Protein 0.88
- Longevity 0.60
- Fertility 0.50
- Index correlation 0.83-0.96 depending on group of animals



Changes in rankings

- **200 top bulls** - 96 bulls in common
- **200 top cows** - 66 females in common

Reliability gains for all genotyped bulls

	Milk
Two-step	0.72
Single-step	0.84
Gain	+0.12

Reliability gains for all genotyped bulls

	Milk	BCS
Two-step	0.72	0.58
Single-step	0.84	0.79
Gain	+0.12	+0.21

Reliability gains for all genotyped bulls

	Milk	BCS	Udder Width
Two-step	0.72	0.58	0.34
Single-step	0.84	0.79	0.75
Gain	+0.12	+0.21	+0.41

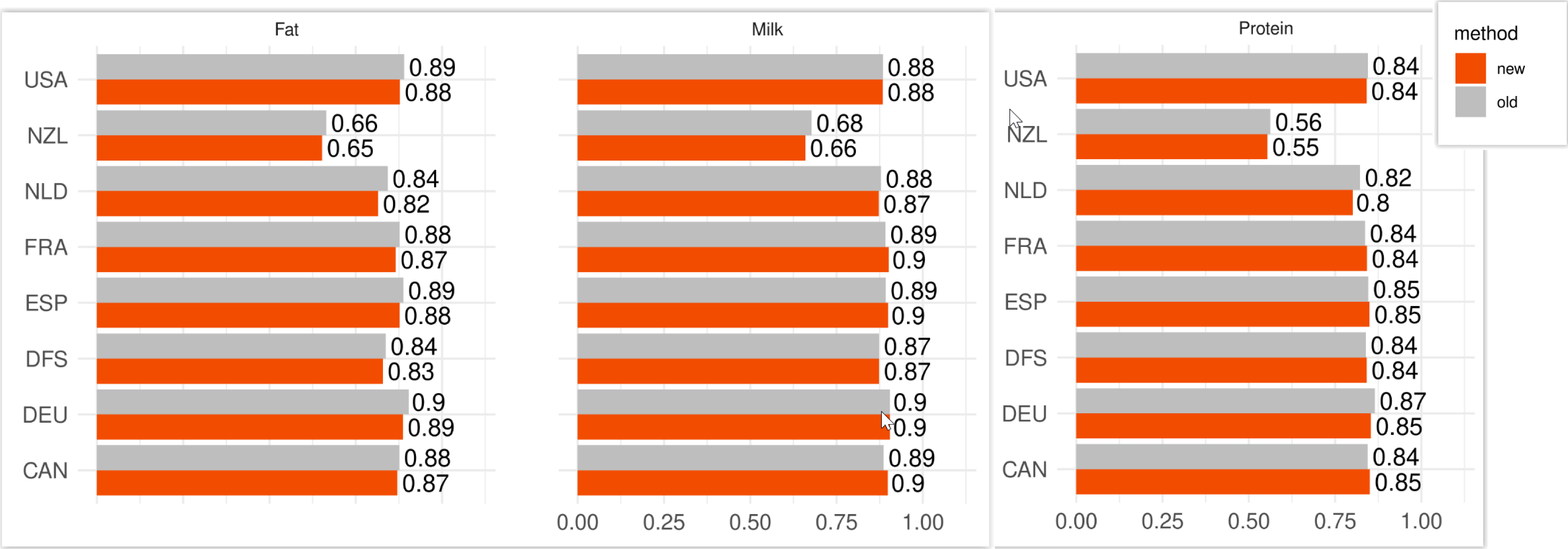
Reliability gains for all genotyped bulls

	Milk	BCS	Udder Width	Days open
Two-step	0.72	0.58	0.34	0.53
Single-step	0.84	0.79	0.75	0.74
Gain	+0.12	+0.21	+0.41	+0.21

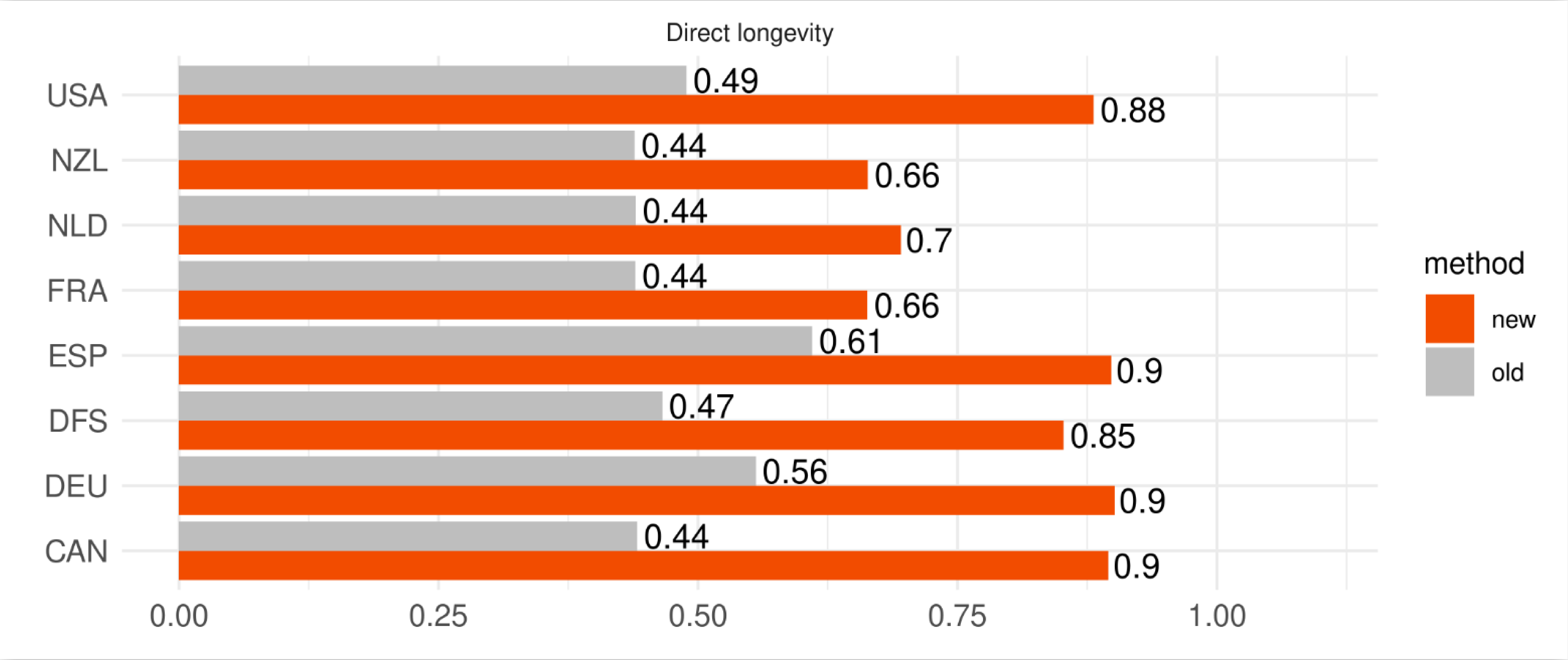
Reliability gains for all genotyped bulls

	Milk	BCS	Udder Width	Days open	Longevity
Two-step	0.72	0.58	0.34	0.53	0.38
Single-step	0.84	0.79	0.75	0.74	0.78
Gain	+0.12	+0.21	+0.41	+0.21	+0.40

Production – stable MACE correlations



Longevity – large improvement



Work in progress

- Work on optimisation of the pipeline
- New traits in development (lactation persistency, subclinical ketosis, subclinical mastitis, clinical mastitis, 3 claw health traits)
- Other traits, no phenotypes yet (other health traits, feed efficiency, methane emission)
- Work towards single step evaluations for minor breeds: Polish Red, Simmental, Polish Whitebacked

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Thank you!

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