



# Interbull Business Meeting

Item 8: Interbull Technical Updates  
Valentina Palucci



THE GLOBAL STANDARD  
FOR LIVESTOCK DATA



# ITC meeting 24-25 August 2023

- Update on work from Working Groups:
  - GREL WG
  - Validation tests WG
  - Genomic pre-selection & future MACE WG (*Pete Sullivan, item 8a*)
  - New trait pipeline WG (*Ezequiel Nicolazzi, item 8b*)
- Update from Interbull Centre
  - Harmonisation of traits



# GREL WG update

- Interbull Methodology:
  - ✓ Harmonize calculation of genomic reliabilities
  - ✓ Make values comparable across countries
- Difficult to reduce computational time required for largest populations:
  - Small variation within birth year in candidate bulls
  - Possible approach: use Interbull methodology at fixed interval of time or when major changes in the model, keep GEDC constant in between for routine evaluations

## WG Members

Zengting Liu (Chair)

Katrine Haugaard

Ismo Strandén

Paul VanRaden

Martin Lidauer

Jérémie Vandenplas

Herwin Eding



# Validation WG update (1/3)

- Focus on improving genomic validations in order to better account for GPS
- Interbull Technical Workshop, Rome February 2023:
  - Presented an enhanced version of the GEBV-test
  - Overall positive feedback from testing countries

## WG Members

Paul VanRaden  
(Chair)

Zengting Liu

Valentina Palucci

Pete Sullivan

Raphael Mrode

Andres Legarra



# Validation WG update (2/3)

- After the Workshop:
  - GEBV-test Software further enhanced to better handle small populations (*countries feedback from technical workshop*)
  - Included information on power of the test to better understand inconclusive results
  - Additional information to allow further analysis at national level (i.e  $R^2$  of base adjustment regression, validation test regression, mean difference ...)
- Aim:
  - New GEBV-test software available January 2024
  - Roll out plan will be communicated before end of 2023



## Validation WG update (3/3)

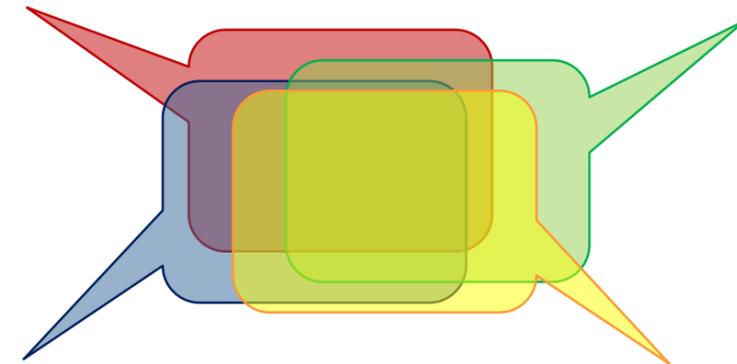
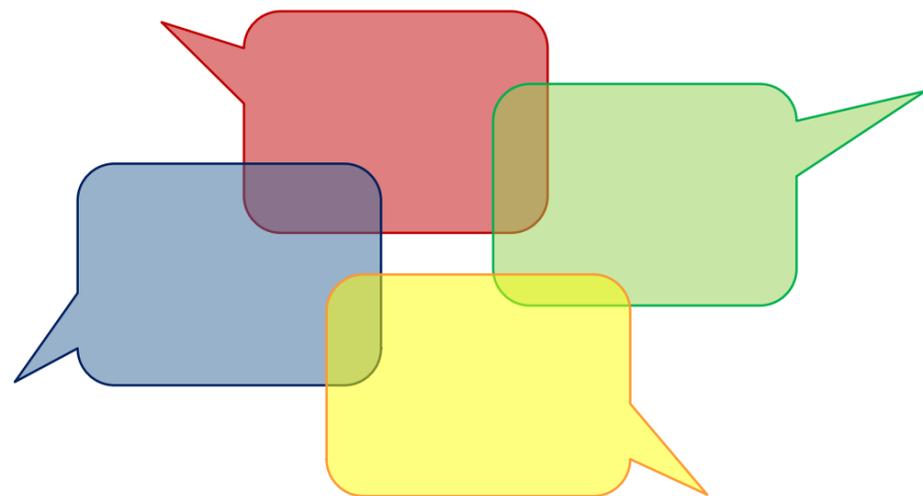
- Interbull test I, II, III and IV give usable results
  - Test III loses power due to fewer bulls available
    - > needs refinements
- WG will continue looking at possibilities to improve Test III
  - Possibly expanding GEBVtest software to account for it



# Harmonisation of traits



- In the context of across country evaluations, trait correlations play an important role in the quality of the estimations.
- Harmonising traits helps to **improve correlations** and thus to achieve **better international evaluations**.
- ITC has approved recommendations to improve the across country compatibility of **Female Fertility**





# Interbull Business Meeting

Item 8a: International evaluations in genomics era  
(Future MACE working group)

Pete Sullivan (Lactanet, Canada)

Esa Mäntysaari (Luke, Finland)

Gerben de Jong (CRV u.a., Netherlands)



THE GLOBAL STANDARD  
FOR LIVESTOCK DATA





# Future MACE contributions

- Interbull Staff Acknowledgements:
  - Haifa Benhajali (2017-2018)
    - Initial R&D and programming for GPS simulation and modeling
  - Simone Savoia and Marcus Pederson (2019-2021)
    - Transfer and access to Haifa's data and programs, ITBC computing resources, etc.
  - Valentina Palucci (2021-ongoing)
    - Collaboration on routine implementation of GPS-MACE at Interbull Centre
- New working group member in 2023
  - Ismo Strandén, Luke (replaces Esa)



# Role of the Working Group

## Objectives:

1. Develop a **GPS-MACE** international model that accounts for **G**enomic **P**re-**S**election effects without requiring genotypes
2. Reduce bias in future MACE proofs that can still be used as phenotypic input data for national genomic evaluation systems

Background: “Genomic-free EBV webinar” (2021):

<https://Interbull.org> (Publications & Events)



# Key Reports and Activities

- JDS: National EBV are biased w/o genotypes used for GPS (Patry and Ducrocq, 2011)
- JDS: MACE proofs include the national EBV bias (Patry et al, 2013)
- Interbull workshop: **Adapting MACE for GPS** (Slovenia, 2017 Feb)

Interbull Technical Committee and Working Groups: tasked to **quantify** GPS effects **and simulate GPS** data to **test future MACE approaches** (Estonia, 2017 Aug)

- Interbull meeting: **Modifying MACE for GPS** (USA, 2019 Jun) ← Literature Review: IB 55

- Interbull webinar: **Genomic-free input for MACE** (2021 Feb) ← <https://Interbull.org>

- Interbull meeting: **Genetic regressions for GPS in MACE** (Canada, 2022 May)

- Interbull workshop: **Implementing GPS-MACE** (Italy, 2023 Feb) ← Model Application: IB 58



# Summary from the 2023 Workshop

- GPS effects alter the distributions of GEBV, with effects on both the PA (between-family) and MS (within-family) portions of an AI sire's GEBV
  - BLUP handles the PA selection effects, but not the MS pre-selection effects
  - GPS effects on MS distributions can be added to the MACE model:
    - Read how this is done with GPS-MACE in Interbull bulletin 58
- GPS-MACE programs have been developed for use by Interbull
  - Programs were tested on Interbull data and computing systems
  - Solve-time is longer than with MACE, but still feasible



# Current Status of Future MACE

- Accounting for GPS effects on MS means:
  - Encouraging results from sensitivity studies with alternative shrinkage parameters
  - Parameters should be estimated for optimal MS mean adjustments
- Accounting for GPS effects on MS variances:
  - Methods are available but testing is in early stages
- Using GPS-MACE results within the GMACE evaluation:
  - Impacts on GMACE results should be checked with the final GPS-MACE model
  - GMACE results should be more accurate with improved PA from GPS-MACE
  - Biggest impacts are expected for the scales of non-genomic countries



# GPS-MACE model

- Current MACE:  $y = \mu + Q_1g + \mathbf{a} + e$
- Current MACE:  $y = \mu + (Q_1g + \mathbf{PA}) + (\mathbf{MS}) + e$
- **GPS-MACE:**  $y = \mu + (Q_1g + \mathbf{PA}) + (Q_2\mathbf{s} + \mathbf{m}) + e$

GPS effects

GPS effects

$$\overline{\mathbf{MS}} = Q_2\mathbf{s}, \quad \overline{\mathbf{m}} = 0$$



# GPS-MACE equations

$$\begin{bmatrix}
 \mathbf{X}'\mathbf{D}\mathbf{X} & \mathbf{X}'\mathbf{D}\mathbf{Z} & \mathbf{X}'\mathbf{D}\mathbf{Z}\mathbf{Q}_2 \\
 \mathbf{Z}'\mathbf{D}\mathbf{X} & \mathbf{Z}'\mathbf{D}\mathbf{Z} + \mathbf{W} \otimes \mathbf{G}_t^{-1} & \mathbf{Z}'\mathbf{D}\mathbf{Z}\mathbf{Q}_2 \\
 \mathbf{Q}_2'\mathbf{Z}'\mathbf{D}\mathbf{X} & \mathbf{Q}_2'\mathbf{Z}\mathbf{D}\mathbf{Z} & \mathbf{Q}_2'\mathbf{Z}'\mathbf{D}\mathbf{Z}\mathbf{Q}_2 + \mathbf{c}\mathbf{I}
 \end{bmatrix}
 \begin{bmatrix}
 \mu \\
 \mathbf{Q}_1\mathbf{g} + \mathbf{a} \\
 \mathbf{s}
 \end{bmatrix}
 =
 \begin{bmatrix}
 \mathbf{X}'\mathbf{D}\mathbf{y} \\
 \mathbf{Z}'\mathbf{D}\mathbf{y} \\
 \mathbf{Q}_2'\mathbf{Z}'\mathbf{D}\mathbf{y}
 \end{bmatrix}$$

Covariables in  $\mathbf{s}$  have Incidence Matrix:  $\mathbf{Z}\mathbf{Q}_2$

We can add a Ridge-regression factor:  $c$

$$\mathbf{EBV} = \hat{\mu} + \mathbf{Q}_1\hat{\mathbf{g}} + \hat{\mathbf{a}} + \mathbf{Q}_2\hat{\mathbf{s}}$$



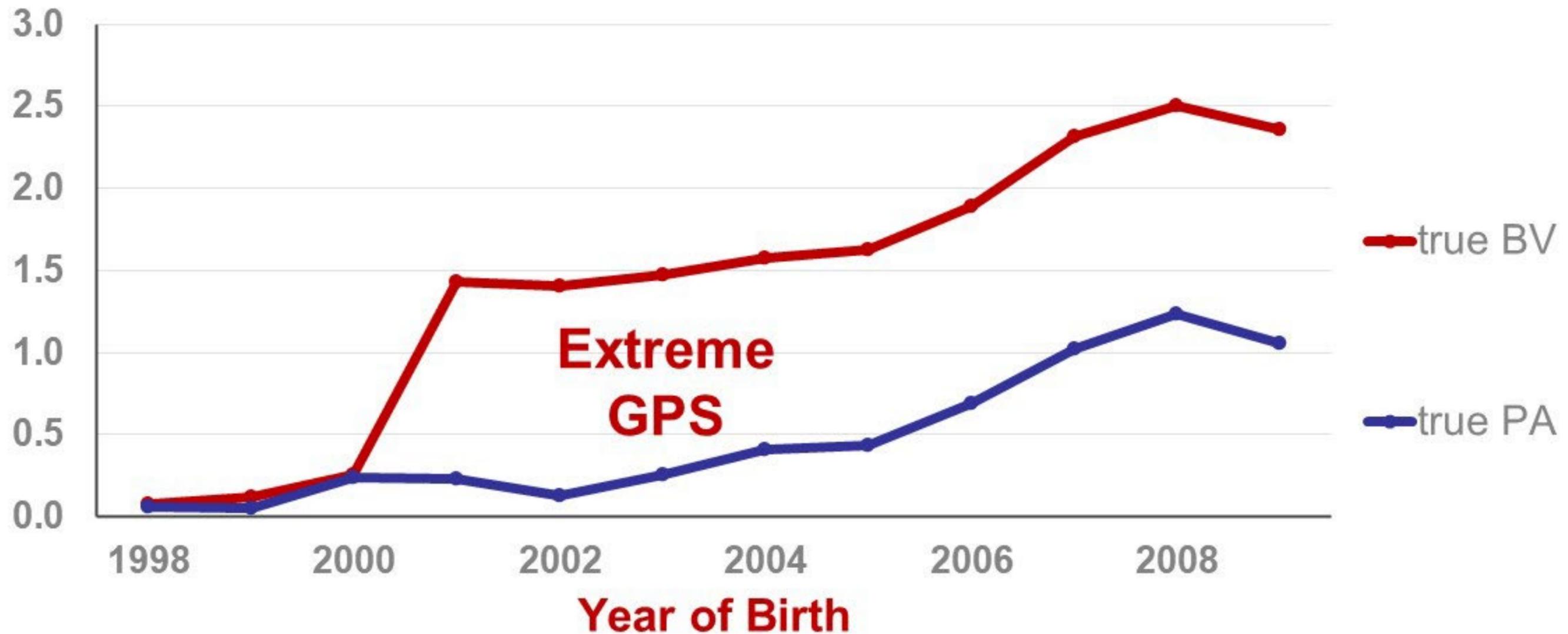
# Testing the GPS-MACE model

1. **Simulation study:** *unbiased national EBV* input for MACE
  1. A simple design with GPS practiced in only one country
  2. Expectation of MACE output that is unbiased, which is easily tested
2. **Official data study:** *biased national EBV* input used in MACE, after years of GPS in many countries, but with GPS effects not properly included in the national EBV computed without genotypes



# 1. Simulated Data with strong GPS (Tyrisevä, 2018<sub>JDS</sub>; Benhajali, 2019<sub>IB</sub>)

## TRUE Genetic Values

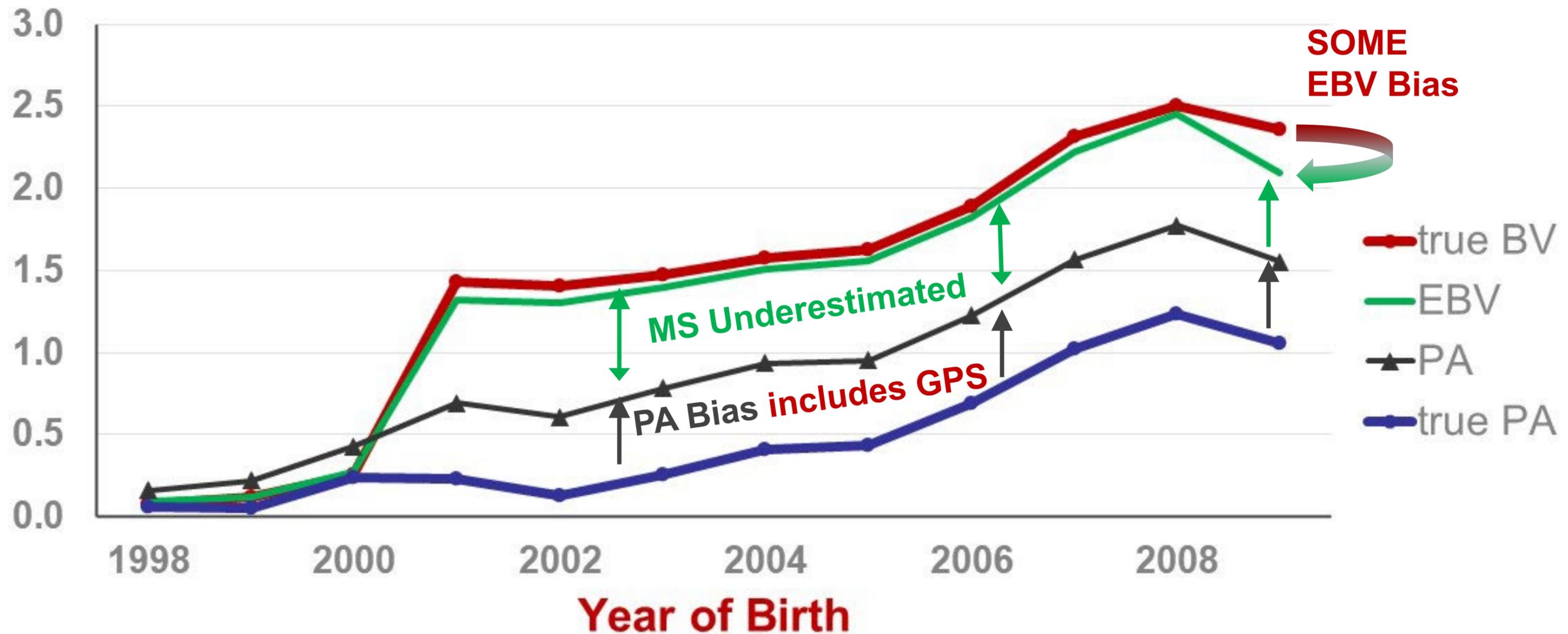




# 1. Simulated Data with strong GPS

( **MACE with unbiased EBV input** )

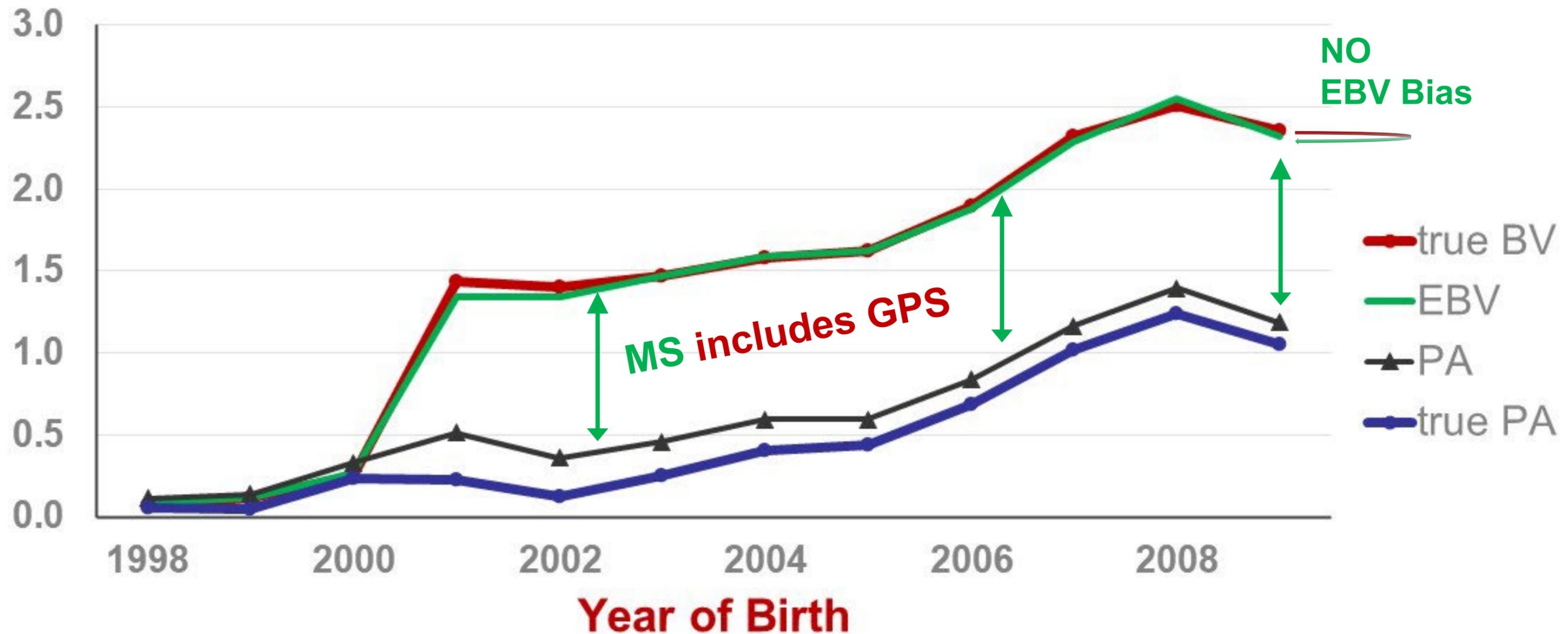
## PREDICTED Genetic Values





# 1. Simulated Data with strong GPS (GPS-MACE with unbiased EBV input)

## PREDICTED Genetic Values





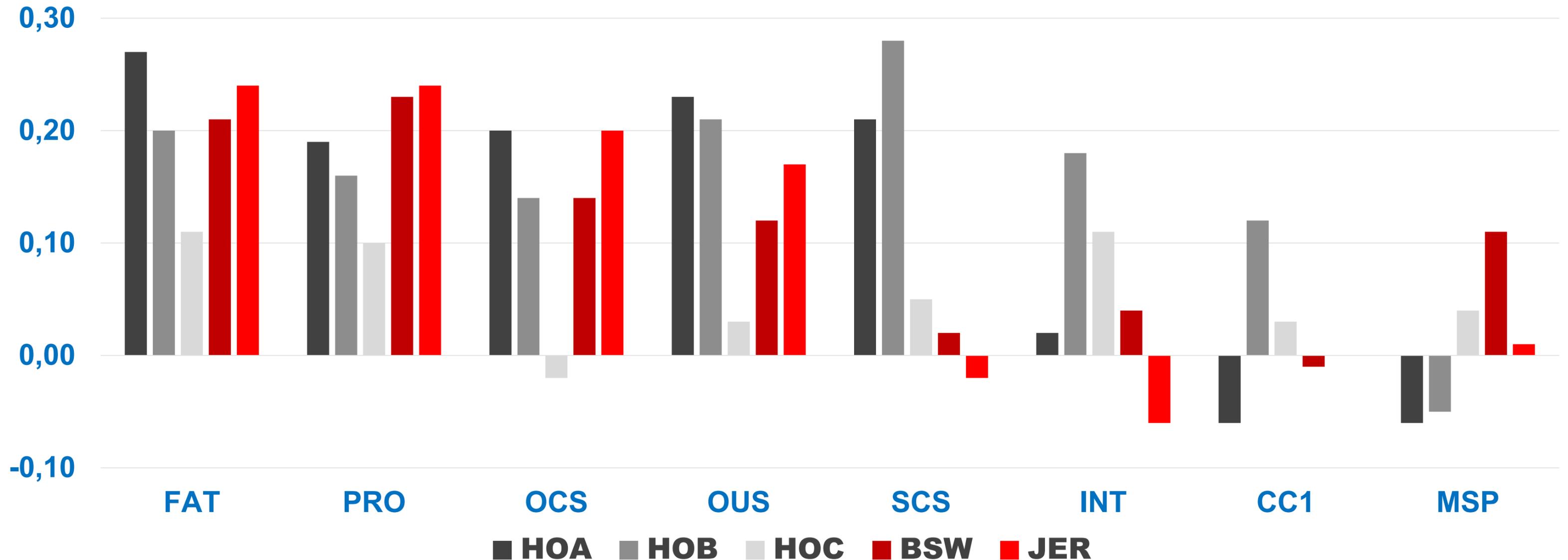
## 2. Official MACE Data

- Official input data used for MACE in **April 2022** for:
  - **Eight traits:** pro, fat, ocs, ous, scs, cc1, int, msp
  - **Three “genomic” breeds:** Holstein, Jersey, Brown Swiss
- Proven bulls were born as recently as 2017, with approximately 8 completed years of progeny-proven **GPS bulls (2009-2016)**
- National EBV are biased (i.e. with estimated MS effects that are too small) due to the requirement of ignoring genotypes
  - **Expecting** GPS effects to be **“underestimated”** from these data



# Estimated GPS effects (std. proof scales)

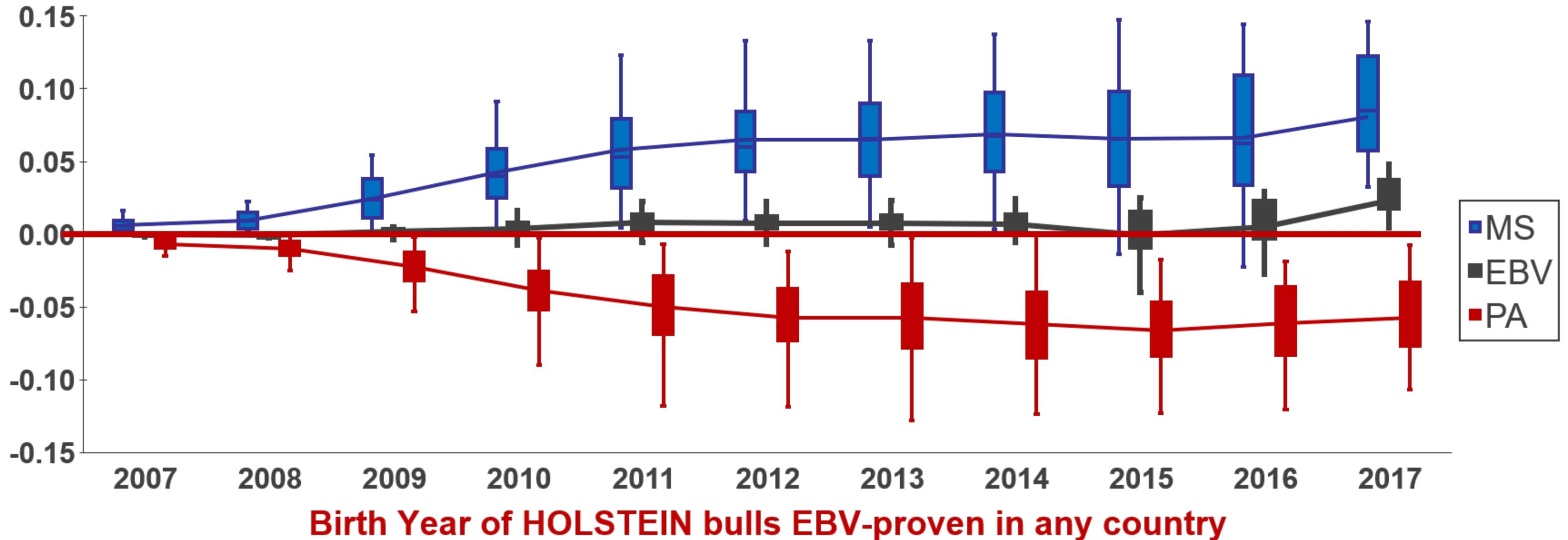
GPS effects on MS means since 2014 by breed group, averaged across countries of selection





# Impact of GPS on MACE proofs (std. scale)

Distributions of Averages by Country of Registration,  
for the **Holstein** trait **Protein in Canada**





# Improving GPS-MACE input data

- GPS-MACE works now, but it will be even better with new national EBV
  - National EBV without genotypes do not include GPS effects
    - True GPS effects are underestimated (but not zero) from the current national EBV
    - The underestimates are better than assuming no GPS effects at all
- Better inclusion of GPS effects in national EBV will increase the magnitudes of GPS effects estimated in GPS-MACE, but how do we do it?
  - Can a GPS-EBV model that is like GPS-MACE be used at the national level?
  - Can ssGEBV be partitioned to remove individual genotype effects but keep GPS?
  - Can a de-regressed ssGEBV be used instead of a de-regressed EBV?



# Interbull Business Meeting

Item 8b: New Traits Pipeline

E Nicolazzi, G. de Jong, V. Palucci, T. Roozen

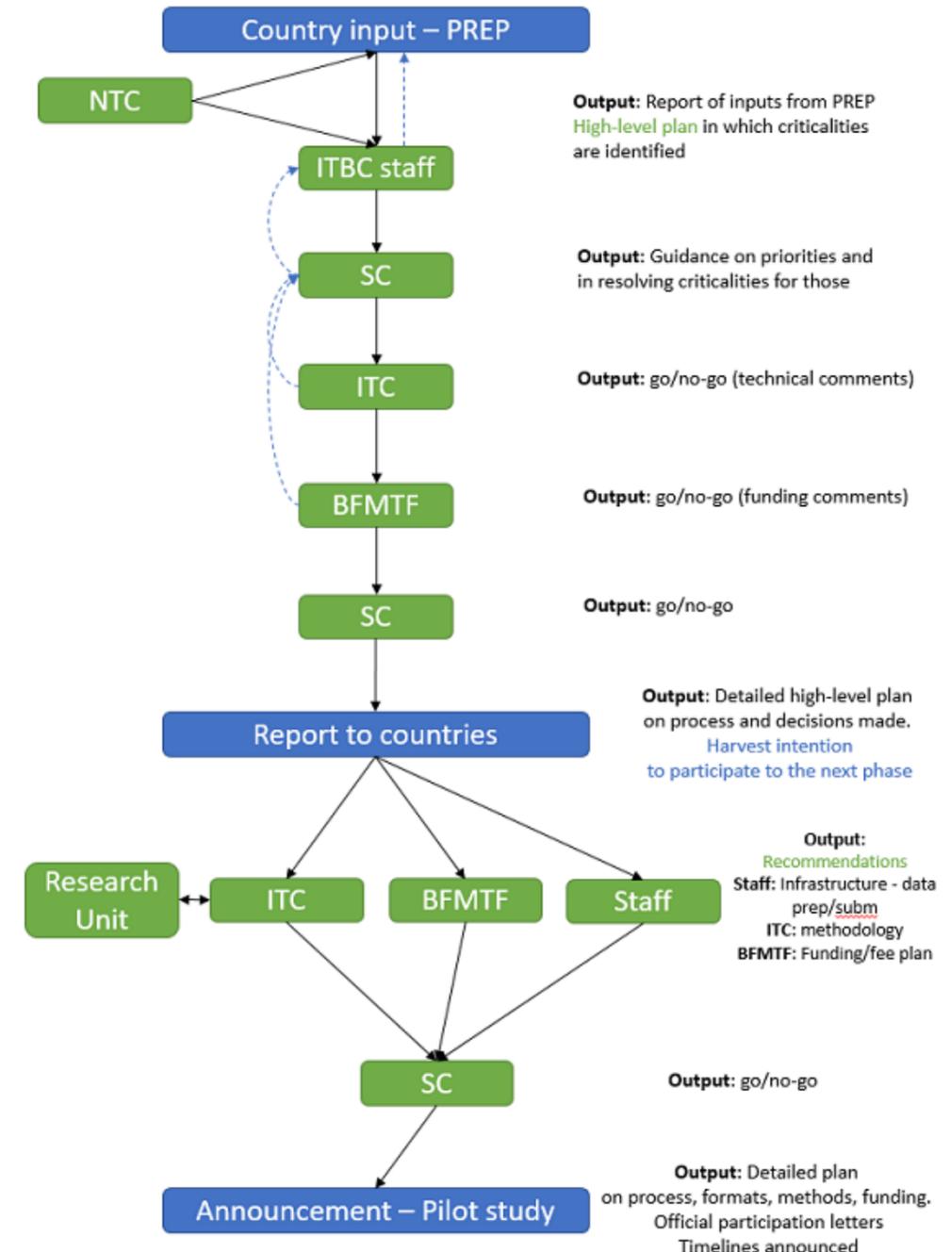


THE GLOBAL STANDARD  
FOR LIVESTOCK DATA



# New Traits Pipeline WG

- 2021: WG defined to establish a clear pipeline to:
  - ✓ Identify key decision factors for implementing any traits
  - ✓ Define infrastructure needed and programs/methodology
  - ✓ Develop business model, business plan and appropriate fee structure





# New Traits Pipeline WG

- PREP-DB chosen as platform
  - Continuous flow of information
  - Transparent
  - Accessible worldwide
- Active inputs from member countries on their needs for new int'l evaluations
  - Which traits have enough data available?
  - Which traits have a national evaluation (conventional/genomic) in place?
  - Is there a need to combine information (data/EBV) across countries?
  - What service is requested?
    - One of the current available
    - New service



# Most Promising Next Traits

Feed efficiency

Claw-health related traits

	Retained placenta	Hypocalcaemia/Milk fever	Gestation length	Feed efficiency	Residual feed intake	Methane emission	Sub-clinical ketosis	Clinical Ketosis	Calf Survival	Lactation Persistency	Anestrus	Metritis	Endo-metritis	Cystic ovaries	Digital dermatitis	Interdigital dermatitis	Interdigital hyperplasia	Sole hemorrhage	Sole ulcer	White line disease	Body weight	
ANABLE																						
ANAFI			/																			
ANAPRI																						
CDCB	/	/	/		/			/				/										
CONAFE	D											D										
CRV	/	/	/				/	/			/	D	/	/		/	/	/	/	/	/	/
DATAGENE																						
GENO	/	/	/					/			/	/	/	/	/					/	/	/
ICBF			/																			
LACTANET																						
NAV																						
NIAP																						
NLBC																						
PLEMDAT																						
QUALITAS			/						/	/												
VIT	/	/						/	/	/			/		/		/			/	/	/

- Legend:
- = High interest
  - = Medium Interest
  - = No information provided
  - = Low Interest
  - / = Evaluation implemented
  - D = Evaluation under development
  - { = New potential traits identified

## Next steps:

- Fill in PREP in relation to new traits identified by 15 Sep
- Review of information
- Decision on how to proceed