Integration of MACE breeding values into Swiss multi-trait test-day model evaluation

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Objective

The objective of this study was to **integrate information** from Multiple Across Country Evaluation (MACE) to **Swiss PBLUP evaluation model** in Holstein and Brown Swiss (BSW)

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- **Single-step evaluations**

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Swiss PBLUP evaluation model

- Swiss test-day model: multi-trait multi-parity linear mixed effect model
- **3 traits (t): milk (m), protein (p)** and **fat (f)**
- **parity (p):** first **three parities (1,2,3ff)**
- **Genetic lactation curves** for 9 traits are modelled using **45 random regression coefficients** per animal

Swiss PBLUP evaluation model, genetic part

$$\boxed{y_{i,m1,dim} = \cdots + c_{dim} a_{i,m1} + \cdots e}$$

$$\begin{aligned}
y_{i,m2,dim} &= \cdots + c_{dim} a_{i,m2} + \cdots e \\
y_{i,m3,dim} &= \cdots + c_{dim} a_{i,m3} + \cdots e \\
y_{i,p1,dim} &= \cdots + c_{dim} a_{i,p1} + \cdots e \\
y_{i,p2,dim} &= \cdots + c_{dim} a_{i,p2} + \cdots e \\
y_{i,p3,dim} &= \cdots + c_{dim} a_{i,p3} + \cdots e \\
y_{i,f1,dim} &= \cdots + c_{dim} a_{i,f1} + \cdots e \\
y_{i,f2,dim} &= \cdots + c_{dim} a_{i,f2} + \cdots e \\
y_{i,f3,dim} &= \cdots + c_{dim} a_{i,f3} + \cdots e
\end{aligned}$$

- c_{dim} :vector including 5 covariables specific for each day in milk (5 <= dim <=365)
- $a_{i,m1}$: breeding value vector e.g. for milk in parity 1 includes 5 random regression coefficients

Swiss PBLUP evaluation model, postprocessing

- 305d EBVs for each animal i, trait t and parity p are calculated as sum of genetic lactation curve over dim 5-305:

$$EBV_{i,tp} = \sum_{dim=5}^{305} c_{dim} * \widehat{a_{i,tp}}$$

- Domestic (DOM) EBV is weighted sum of 305d EBVs:
- $EBV_{i,t}^{DOM} = \frac{1}{3}\sum_{p=1}^{3} EBV_{i,tp}$
- Reliability for EBV is calculated.
- $EBV_{i,t}^{DOM}$ and $R2_{i,t}^{DOM}$ for bulls are submitted to Interbull

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Interbull MACE

After the MACE Interbull (ITB) returns

$EBV_{i,t}^{MACE}$ and $R2_{i,t}^{MACE}$ back to us

These MACE EBVs contain all available information for bulls:

- DOM
- Other countries participating in ITB evaluation (foreign)

Choosing bulls to be blended

We chose **ITB** bulls with additional (foreign) information to be blended into the Swiss PBLUP evaluation model

- Require: $R2_{i,t}^{MACE}$ - $R2_{i,t}^{DOM}$ > 0.1 & $R2_{i,t}^{MACE}$ >0.5

- Around 5,800 bulls (trait dependent) were selected, some of them had daughters with records in DOM evaluation

Calculation of information to be integrated

- Based on **MACE** and **DOM** EBVs and reliabilities for each bull, multi-trait **ERC** and **DRP** for milk, protein and fat were calculated (Pitkänen et. al, EAAP 2019)
- To avoid double counting, Swiss information has to be removed from MACE EBVs before “blending” it to test-day model (Pitkänen et. al, EAAP 2020)
- As result, pseudo-observations ($DRP_{i,t}^{BLEND}$) and its weights ($ERC_{i,t}^{BLEND}$) are obtained.

Swiss PBLUP evaluation model for blending

Pseudo observations (DRPs) are included in the test-day model as separate traits:

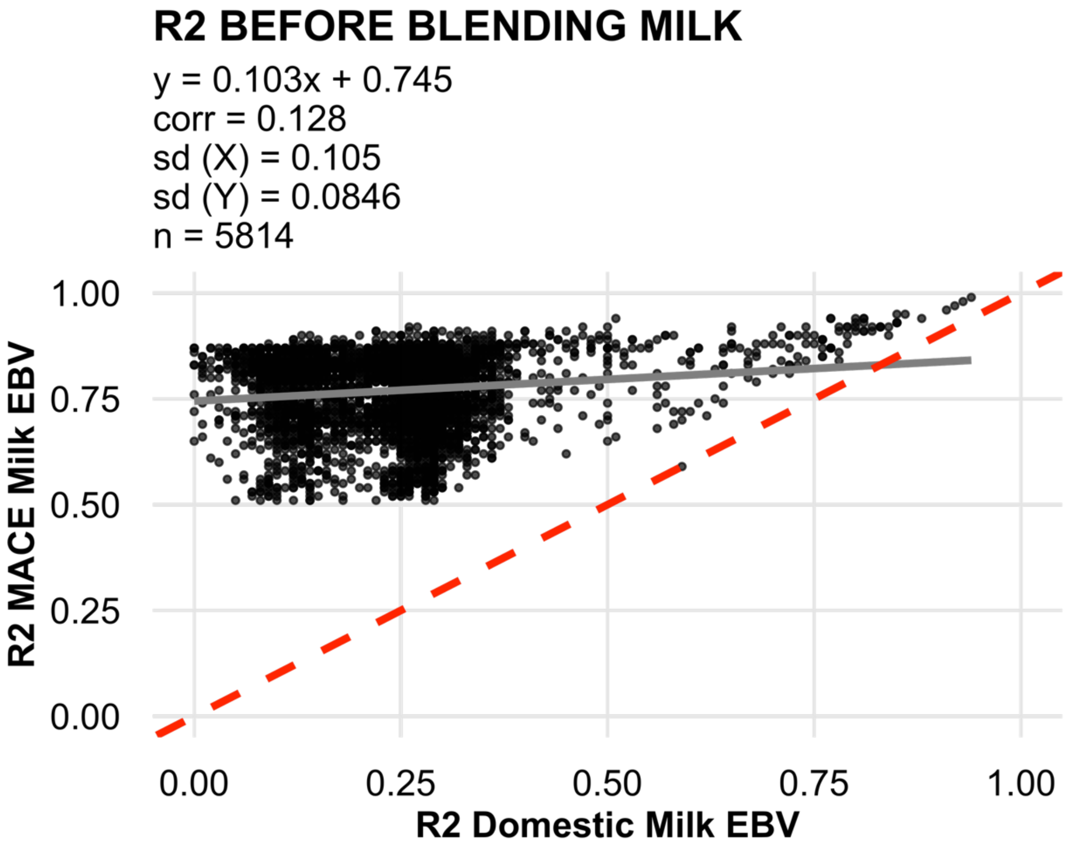
$$\boldsymbol{DRP_{i,t}^{Blend}} = \mu + c_{total} a_{i,t1} + c_{total} a_{i,t2} + c_{total} a_{i,t3} + e,$$

where

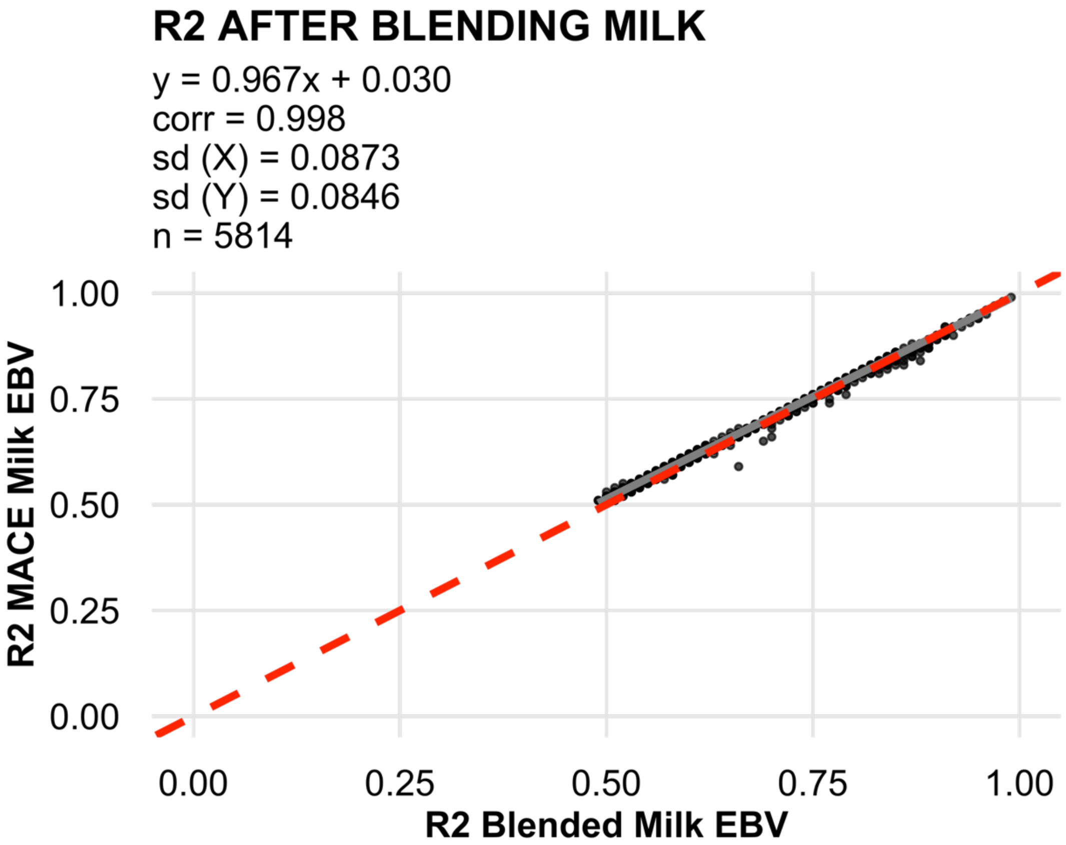
$$c_{total} = \frac{1}{3} \sum_{dim=5}^{305} c_{dim}$$

- Breeding value vectors, $a_{i,tp}$ are same as for normal traits
- $\boldsymbol{ERC_{i,m}^{Blend}}$ is used as a weight.
- 3x3 covariance matrix for residual of DRPs

Results PBLUP for BSW: R2 for EBVs


R2 BEFORE BLENDING MILK

y = 0.103x + 0.745
corr = 0.128
sd (X) = 0.105
sd (Y) = 0.0846
n = 5814

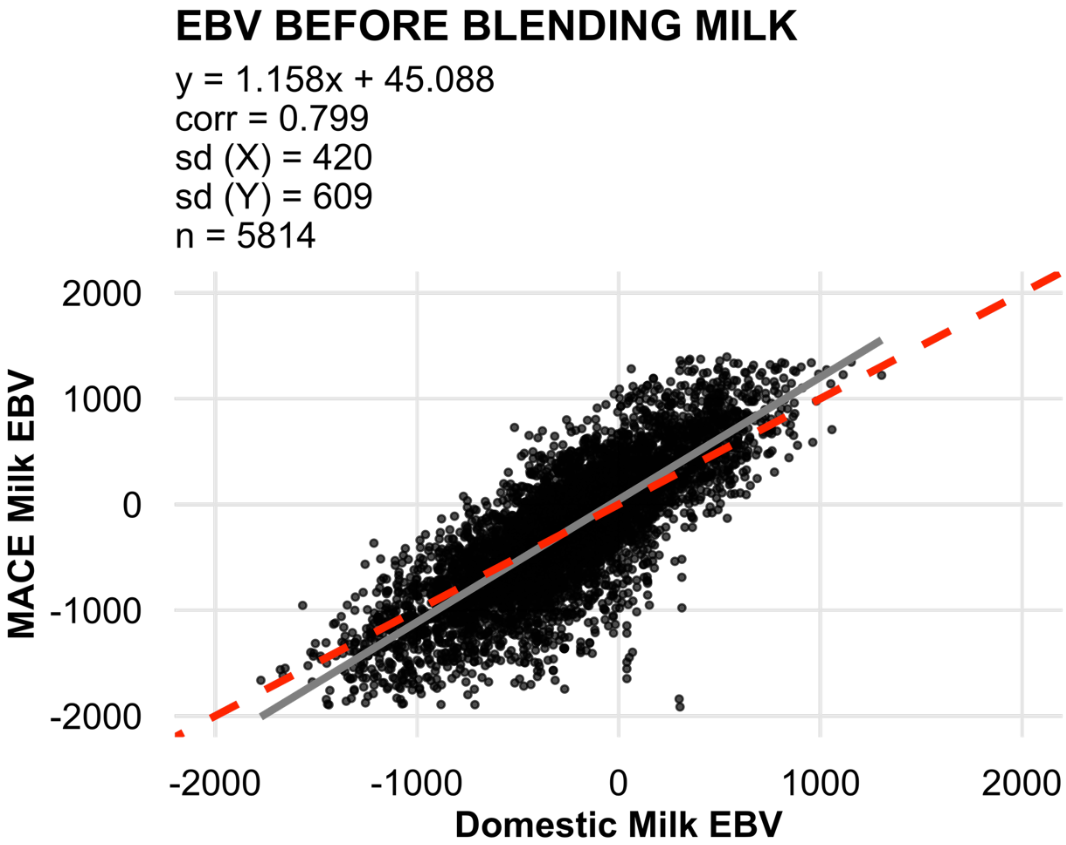

R2 AFTER BLENDING MILK

y = 0.967x + 0.030
corr = 0.998
sd (X) = 0.0873
sd (Y) = 0.0846
n = 5814

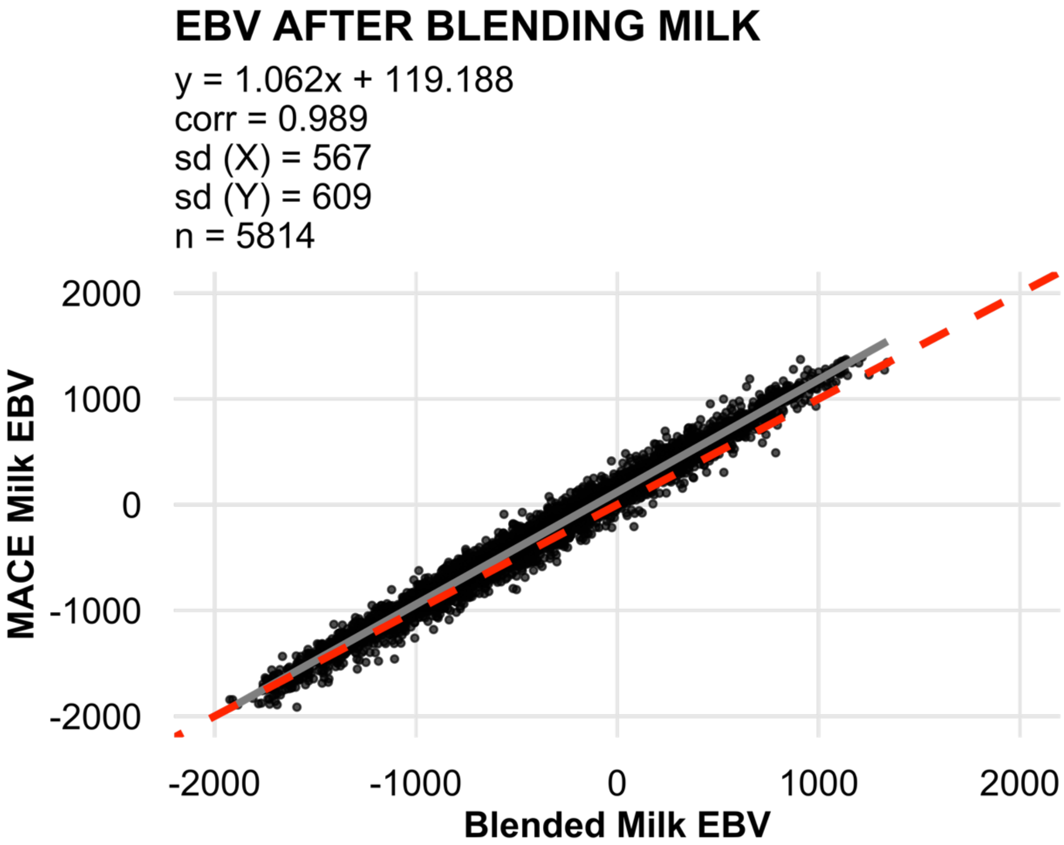
Regression line: grey line

Angle bisector: red, dotted line = Expected for PBLUP R2

Results PBLUP for BSW: milk EBVs


EBV BEFORE BLENDING MILK

$y = 1.158x + 45.088$
corr = 0.799
sd (X) = 420
sd (Y) = 609
n = 5814


EBV AFTER BLENDING MILK

$y = 1.062x + 119.188$
corr = 0.989
sd (X) = 567
sd (Y) = 609
n = 5814

Regression line: grey line

Angle bisector: red, dotted line = Expected for PBLUP

Conclusion

- Blending of MACE information to Swiss PBLUP evaluation model works

- No bias in reliability
- The regression slope and correlation between MACE and Blended EBVs are about 1

→Integration of MACE is now implemented successfully in the Swiss Single-Step routine genetic evaluation for BSW

Thank you for your attention!

Source: Braunvieh Schweiz

Questions?

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