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

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Abstract

In this study, we integrated Multiple Across Country Evaluation (MACE) information for Interbull (ITB) bulls into the Swiss Test-day model (TDM). The 9-trait TDM includes test-day records of milk, protein and fat from the first three lactations, while total yield indices submitted to ITB are averages of 305d yields for lactations. A bull was considered to have relevant MACE information if its reliabilities for all indices in MACE were at least 0.1 units higher than its reliabilities from the Swiss TDM. With this integration, the Swiss TDM gained information for round 5,800 bulls with MACE index reliabilities exceeding 0.5.

The integration process had three steps. 1) For selected bulls, the multitrait reversed reliability approximation was used to estimate effective record contributions (ERC) for Swiss and MACE yield indices, based on their respective reliabilities. 2) Yield indices and ERCs were used to calculate multitrait deregressed proofs (DRP) separately for Swiss and MACE evaluation. Correlations between the evaluated indices and pedigree relationships were accounted during the ERC and DRP calculations. 3) Based on the DRPs and ERCs for domestic and MACE indices, pseudo-observations approximating the additional information in the MACE evaluation were calculated for the selected bulls. As a result, for each selected bull a DRP and ERC for milk, protein, and fat were obtained.

The original Swiss TDM describes breeding values using 45 random regression coefficients. The DRP was included in the model as a separate trait, weighted by its ERC. The genetic correlation between pseudo trait and lactation averages of the original traits was assumed to be 1. MACE inclusion improved correlations between MACE and Swiss indices to 0.99 (from 0.78–0.80 for milk, fat, protein). This demonstrates a good alignment between the two evaluation systems. Integration of MACE is now implemented successfully in the Swiss single-step routine genetic evaluation.

Key words: Test-day model, MACE integration, three-step approach, production

Introduction

Accurate genetic evaluation is essential for accelerating genetic improvement in dairy cattle breeding programs (Schaeffer, 1994). Integrating multiple across-country evaluation (MACE) proofs into single-step genomic analyses enables the inclusion of reliable international information, particularly for foreign progeny-tested sires with no or only few domestic offsprings. This integration improves the accuracy of estimated breeding values (EBV), enhances the genetic connectedness between countries, and supports more robust selection decisions in an increasingly globalized dairy industry (Sullivan, et al. 1999, Boerner et al., 2022).

Recent research has proposed several strategies to incorporate MACE information into single-step evaluations. For instance, Nieuwhof et al. (2023) developed a method using deregressed proofs (DRPs) that account for relationships among MACE bulls, improving reliability and reducing bias compared to approaches that assume unrelatedness of bulls. Similarly, Bayesian methods such as ssGBayes and trait-specific

deregression techniques have shown promising results in Canadian and Walloon Holstein populations (Strandén et al., 2022; Splichal et al., 2023)

While some approaches simplify the relationship between international and domestic genetic effects, e.g., by treating MACE DRPs as auxiliary traits or integrating them into reduced-rank test-day models, these often compromise consistency with the full model structure. In contrast, the approach presented here integrates MACE-derived pseudo-observations directly into the full Swiss multi-trait test-day model (TDM). These pseudo-observations are treated as weighted, trait-specific contributions aligned with the genetic lactation curves, ensuring consistency with the model's structure and preserving trait definitions across data sources.

This study describes a three-step approach to integrating MACE information into the Swiss TDM and demonstrates its validity through comparisons of EBV and reliabilities from pedigree-based BLUP (PBLUP) and single-step GBLUP (ssGBLUP) before and after blending. Furthermore, it evaluates the impact of genomic information on the blending procedure, particularly for genotyped bulls. The implementation is now part of the Swiss routine single-step evaluation pipeline.

Materials and Methods

Data

The raw phenotypic dataset encompassed 49,744,608 test day records for the yield traits: milk, fat and protein each in kg for days in milk (DIM) between 5 and 365. Different milk testing methods (A4, ATM4 and AT4) were used to record the data on 1,753,643 cows born between 1984 and 2023.

The total number of herds was 34,896. The number of herd-test-day-parity (HTD) classes was 4,437,539 and the number of time-region-age-parity-season (TRAPS) classes was 476. Time was divided into half-year groups based on the test day, starting from year 2000. Region was defined via geographic classification. Age was divided into monthly classes (≤19 month, 20-24 month, 25-28 month and ≥ 28 month). Parity was divided into first, second and third and ongoing. Season was divided in January-March, April-June, July-September, October-December.

Genotypes of 153,499 animals were included in the single-step evaluations. As animals were genotyped with different SNP panels, all genotypes were imputed together (one reference panel) to 125K SNP following the routine imputation process at Qualitas with FImpute (v3.0; Sargolzaei et al., 2014).

The pedigree was built up using cows with phenotypes as well as young, genotyped animals and pruned to three generations and finally included 2,367,788 animals. Genetic groups were divided by breed but also separated over different periods of time and sex.

Swiss test-day model

A multi-trait (yield traits), multi-parity (5 lactations) random regression model, defined as

$$\boldsymbol{y} = \boldsymbol{X\beta} + \boldsymbol{Z_p p} + \boldsymbol{Z_a a} + \boldsymbol{\epsilon}, \quad (1)$$

was used, where $\boldsymbol{y}$ is the vector of observations, $\boldsymbol{\beta}$ represents the fixed effects of HTD and the fixed lactation curve for TRAPS, $\boldsymbol{p}$ is the vector of random permanent environmental effects, $\boldsymbol{a}$ is the vector of random genetic effects, and $\boldsymbol{\epsilon}$ represents the random residuals. $\boldsymbol{X}$ and $\boldsymbol{Z_p}, \boldsymbol{Z_a}$ are respective incidence matrices.

To account for the accuracy of the phenotype, different weights were used for different milk testing method (1=A4, 0.94=ATM4, 0.88=AT4).

The TRAPS effect was modeled using a six-order Legendre polynomial. Both the genetic and permanent environmental lactation curves were modeled using fourth-order Legendre polynomials. Lactations 4 and 5 were treated as repeated measures of the third lactation for the fixed effects and the genetic effect, while lactation-specific effects were included for permanent environmental effects. Assumptions were that

$$var\begin{bmatrix}\boldsymbol{a}\\ \boldsymbol{p}\\ \boldsymbol{\epsilon}\end{bmatrix} = \begin{pmatrix}\boldsymbol{G}_o \otimes \boldsymbol{A} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \boldsymbol{I} \otimes \boldsymbol{P} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \boldsymbol{R}\end{pmatrix}, \quad (2)$$

where $\boldsymbol{G}_o$ is the covariance (45×45) matrix for the random genetic effects, assumed to be the same for each cow. $\boldsymbol{A}$ is the pedigree relationship matrix between the animals used for pedigree BLUP (PBLUP). To include genomic information, the **A** matrix was replaced by an augmented matrix (**H**) that includes both pedigree and genomic information, and was incorporated by applying ssGTABLUP (Mäntysaari et al., 2017), where the genomic relationship matrix (**G**) was constructed using VanRaden method I (VanRaden, 2008) and blending the **G** matrix with a 5% residual polygenic component. Pedigree inbreeding coefficients were incorporated into both $\mathbf{A}^{-1}$ and $\mathbf{A}_{22}^{-1}$. Genetic groups were accounted for in the single-step models through a partial QP transformation that excluded $\mathbf{G}^{-1}$ from the QP matrix (Koivula et al., 2021).

$\boldsymbol{P}$ is the covariance (75×75) matrix for the permanent environmental effects.

$\boldsymbol{R}$ is the covariance matrix of the residuals, composed of 3×3 covariance matrices corresponding to four lactation periods based on DIM: 5–45, 46–115, 116–265, and 266–365. Each period was associated with its own 3×3 residual covariance matrix.

Lactation specific breeding values were calculated by summing up the breeding values for DIM 5 to 305. Combined breeding values were calculated as a weighted sum of lactation specific breeding values by using weight of 1/3 for each lactation. The combined breeding value was standardized by subtracting the mean EBV of cows aged between 6 and 8 years. Standardized breeding values for milk, protein and fat and their reliabilities were submitted to Interbull for all bulls.

Bulls Chosen to be Blended

After performing MACE, ITB returned MACE breeding values and reliabilities. Bulls were selected for blending if their MACE reliability exceeded 0.5 and exceeded their domestic reliability by more than 0.1 units, irrespective of whether the bull was genotyped or not.

In total 5,864 bulls were selected per yield trait, whereof 5,466 were genotyped and 247 had information in domestic evaluation.

Calculation of pseudo-observations

Integration of additional information in MACE breeding values for milk, protein and fat to domestic evaluation was done using deregressed proofs (DRP) as pseudo-observations and effective record contribution (ERC) as weights. The integration process includes calculating ERCs from reliabilities and DRPs from EBV based on domestic and MACE proofs (Pitkänen et. all 2020, Pabiou et. all 2018, Vandenplas et. all 2014).

DRPs and ERCs were calculated assuming that EBV and reliabilities are from linear multitrait animal model:

$$\begin{bmatrix}y_m\\ y_p\\ y_f\end{bmatrix} = \mu + a + e, \quad (3)$$

where y_m, y_p and y_f are combined 305d observations for milk, protein and fat, μ is intercept, a is random genetic effect, containing breeding values for combined milk, protein, and fat for each animal, and e is the residual effect. The variance components for a and e were derived for 305d yields based on test-day model variance components. Residual variance covariance matrix included variation due to residual and permanent environment effects in the test-day model.

In the first step, two sets of reliabilities—one from the domestic evaluation and one from MACE—were used to calculate effective record contributions (ERC_D and ERC_M) for combined milk, protein, and fat.

In the second step, DRPs for combined milk, protein and fat for domestic (DRP_D) and MACE (DRP_M) were calculated based on combined EBV from evaluations and using ERCs from the first step as weights. The standardized EBV

were back transformed to original scale before calculations.

Since DRP_M, contains information also from domestic animals, it can't be directly included in the model due to double counting of information. In the third step, the double counting was removed by calculating DRP^B, ERC^B, within trait as:

$$ERC^B = ERC_M - ERC_D \quad (4)$$

$$DRP^B = \frac{DRP_M \cdot ERC_M - DRP_D \cdot ERC_D}{ERC^B}. \quad (5)$$

Blending Model

Pseudo-observations for milk, protein and fat yield were included as separate traits for the test-day model assuming the pseudo-observation is a weighted sum of 305d breeding values of lactations 1 to 3. The model for pseudo-observations for animal *i* is:

$$\begin{bmatrix} DRP^B_{im} \\ DRP^B_{ip} \\ DRP^B_{if} \end{bmatrix} = \mu + \boldsymbol{C}a_{i1} + \boldsymbol{C}a_{i2} + \boldsymbol{C}a_{i3} + \boldsymbol{e}_i,$$

where

$$\boldsymbol{C} = \boldsymbol{I}_3 \otimes \boldsymbol{C}_{305},$$

and

$$\boldsymbol{a}_{il} = \begin{bmatrix} a_{i,ml} \\ a_{i,pl} \\ a_{i,fl} \end{bmatrix}.$$

The vector $\boldsymbol{C}_{305}$ is sum of covariable values for genetic lactation curve between DIM 5 to 305. Residual covariance matrix for pseudo-observations was the same as used in model (3). The genetic regression coefficients, $a_{i,tl}$, for trait *t*, and lactation *l*, are the same as for the test-day observations. Hence, the genetic correlation between MACE and domestic evaluation was assumed to be 1. All calculations were done using MiX99 software suite, Release X/2023.

Results & Discussion

In the following only the results for milk are shown (Figure 1, 2 and 3) and discussed, because they are similar for the other traits.

PBLUP reliabilities

Integrating MACE proofs improved correlations between MACE and domestic reliabilities (R2) towards the expected value of 1 (Figure 1). The intercept of the reliabilities decreased, and the slope increased indicating that the reliabilities after blending are not biased.

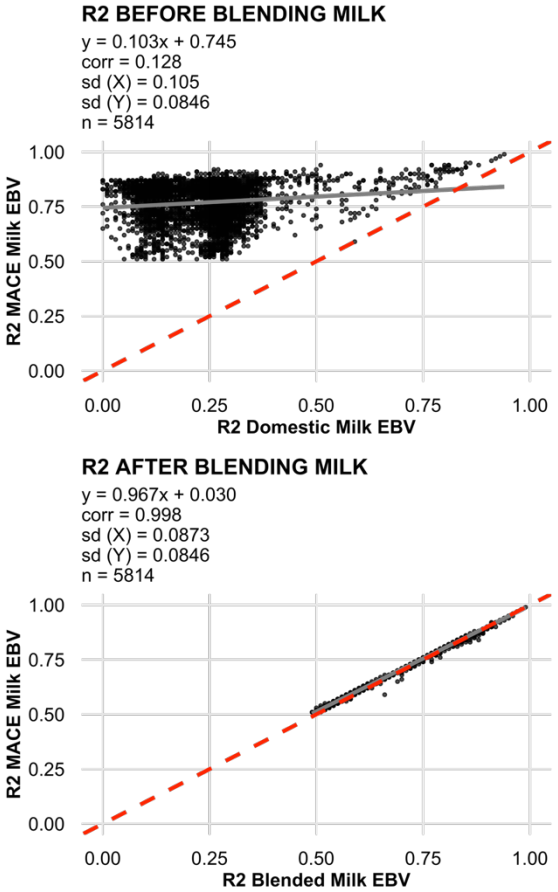

Figure 1. Comparison plots between PBLUP reliabilities (R2) before (top) and after blending (bottom) with MACE reliabilities. The red, dotted line represents the expectation if blending works.

PBLUP breeding values

Integrating MACE proofs improved correlations between MACE and domestic EBV (Figure 2). The intercept of the EBV increased, while the slope of the EBV decreased.

The intercept deviates from 0. However, compared to the scale of the EBV ranging from -2000 to +2000 this deviation is small. More important is the slope which is quite close to the expectation. Traits are modelled independently

in MACE but dependently in the domestic ERC and DRP calculation, which might explain the deviation from the expectation.

Overall, the results are in accordance Pitkänen et al. (2019 and 2020), where similar blending strategies were applied to Nordic Holstein evaluations, and Vanderick et al. (2025). In contrast to this study, their approach sets the residual correlation for DRP computation to zero.

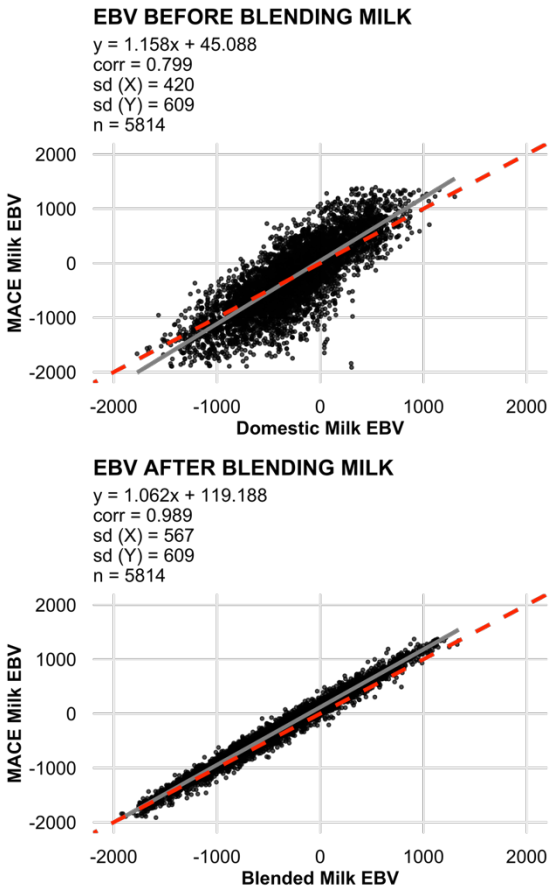

Figure 2. Comparison plots between PBLUP breeding values (EBV) before (top) and after blending (bottom) with MACE EBV. The red, dotted line represents the expectation if blending works.

ssGBLUP reliabilities and breeding values

The integration of genomic information led to a higher standard deviation of the ssGBLUP reliabilities compared to their MACE equivalent (Figure 3). All genotyped bulls gained in reliability. The reliability of non-genotyped bulls has not changed after blending.

The standard deviation of the EBV increased when integrating genomic information.

These findings are consistent with the observations of Rostellato et al. (2024) who demonstrated that genomic-free Single-Step EBVs used for MACE derivation increase reliability, particularly for genotyped animals.

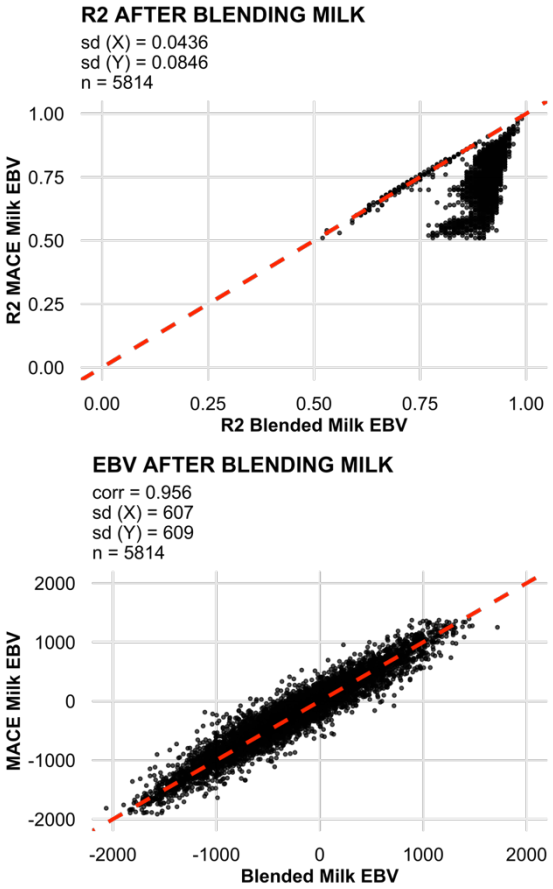

Figure 3. Comparison plots between ssGBLUP – and MACE reliabilities (R2) on top and ssGBLUP – and MACE breeding values (EBV) on bottom. The red, dotted line represents the expectation for PBLUP.

Conclusions

The three-step approach integrates well MACE results into PBLUP and ssGBLUP and allows recovering indirectly a large amount of phenotypic information. All available external sources of information are correctly propagated avoiding double counting of contributions due to relationships and due to own records. Furthermore, the results are in accordance with the findings from the literature. Therefore, the

approach proves to be a good choice for the Swiss genomic evaluation system integrating domestic and MACE EBV and is now implemented successfully in the routine genetic evaluation.

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