Implementation of single-step genetic evaluation in Poland

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Abstract

In April 2025, Centre for Genetics of Polish Federation of Cattle Breeders and Dairy Farmers (CGen) implemented single-step genomic evaluation for Polish Holstein-Friesian population. The process of implementing the new evaluation system started in December 2024 when CGen became the official provider of dairy genetic evaluations in Poland calculating selection indexes based on breeding values estimated by the National Institute of Animal Production in Balice using a two-step approach. To increase the accuracy of breeding value estimations, CGen developed single-step pipelines using BLUPF90 family of programs. In January 2025 conventional EBVs for all traits were submitted for Interbull test run and successfully passed the evaluation. Next, the results of genomic evaluations were submitted for GEBV test and also passed for all traits. In April 2025 single-step evaluation results were officially published for the industry. In this paper we share the experience from the work undertaken to implement the single-step approach in Poland. The changes to the genetic evaluation models are highlighted. The methodology implemented for the integration of external information (MACE proofs) in single-step evaluations is discussed and results presented. Technical aspects of implementation are also discussed including model running times for individual traits. Highlights from the validation work undertaken are also included. The most noticeable impact on genetic evaluation results of the transition from the two-step evaluation system to the single-step method was increase in reliabilities. For example, for production traits, reliability increased by 12 percentage points for bulls and 10 percentage points for cows. The most significant improvement was observed for longevity, with a reliability increase of 40 percentage points for bulls and 35 percentage points for cows. The new system also demonstrated substantial improvement in the correlation between Polish and international breeding values, as estimated by the Interbull Centre. The most noticeable improvement was for longevity, where correlation increases with some countries reached 46 percentage points.

Key words: genetic evaluation, genomic parameters, single-step evaluation, dairy

Introduction

The implementation of the single-step genetic evaluation in Poland was a significant project undertaken by several organizations, led by the Centre for Genetics of the Polish Federation of Cattle Breeders and Dairy Farmers (CGen) and supported by the National Research Institute of Animal Production in Balice, Poznan University of Life Sciences, Krakow Agricultural University, Wroclaw University of Life Sciences, and AbacusBio Ltd. This initiative aimed to transition from a two-step to a single-step genomic evaluation system for Holstein-Friesian cattle, using the BLUPF90 family of programs (Aguilar *et al*., 2018). The take-over of the routine genetic evaluation by CGen followed the European trend in which breeders' associations are taking responsibility for the national evaluations. Similar changes were implemented in France, Netherlands, or Germany. The final change of the evaluation unit was accepted by the Ministry of Agriculture in December 2024, and the implementation of the new system took place in April 2025 after a successful validation at the Interbull Centre.

The transition to a single-stage system included: implementing BLUPF90 family of programs, change in definition of fertility traits and longevity, changes in models used to evaluate some traits e.g. production and conformation, but also introducing new traits (digital dermatitis (DD), bone quality, and interval from 1st to last insemination. One of the main issues was integration of external breeding values i.e. MACE proofs as bulls' pseudo-phenotypes. In this paper we show the results of implementing the single-step genomic evaluation based on a few selected from all the 47 traits included in the Polish national genetic evaluation system.

Materials and Methods

The population of Polish Holstein-Frisian cows are under routine recording, performed by Polish Federation of Cattle Breeders and Dairy Farmers (PFHBiPM). The database contained over 4M cows with phenotypes. The number of records varied between traits, for example the data set for production traits had over 76M records and for DD 270K. The 3-5 generations of pedigree, depending on the trait, included in the analyses was created based on own herdbook data and integrated with Interbull and EuroGenomics pedigree data including 6M animals. More than 240K genotypes were used in the analyses which comprised of genotypes of Polish cows and bulls supplemented by EuroGenomics' data and data from other international exchanges.

Models

We employed a range of animal models depending on the analyzed trait. In the case of production traits, we employed multi-lactation random regression test-day models with lactation curve modelled with Legendre Polynomials. Calving traits were multi-lactation models with maternal effect. Type traits were analyzed using multi-trait models with correlated traits connected in blocks. For fertility traits, longevity and digital dermatitis we used single trait multi-lactation models. Workability traits were analyzed with single-trait animal models.

Software

The variance components and breeding values were estimated using BLUPF90 family of programs. The variance components were estimated using Gibbs sampling algorithm with GIBBSF90+, BLUP90IOD3 to solve mixed models and ACCF90GS3 to approximate reliability including genomic information. The genomic runs utilized APY (Algorithm for Proven and Young) algorithm for genomic evaluations (Misztal *et. al*., 2014, Misztal, 2016). The core for the APY consisted of 18K animals, which is related to the number of independent chromosome segments (haplotypes) in bovine, this number of core animals allowed to capture 99% of genetic variation (Pocrnic *et al.*, 2016). The list of the core animals was created using a strategy that prioritized animals from the reference population common across seven different trait groups. A "reference list" was first built by randomly sampling animals present in the most trait groups, with special consideration for key traits like digital dermatitis, conformation and fertility. This list was then supplemented with a selection of the most popular insemination bulls to finalize the sample.

MACE Integration

MACE breeding values obtained from the Interbull Centre were used as bulls' pseudo-phenotypes in order to integrate international breeding values in the national genomic evaluation following Bonifazi *et al.* (2023). In short, the international and national breeding values for bulls were de-regressed using their reliability. Then the national de-regressed proofs were used to remove the contribution of Polish cows to the MACE proofs. The MACE proofs were used only if they were more accurate than the national proofs. The converted MACE proofs were weighted using their reliability and included in the data as bulls' phenotypes. All bulls were assigned to one contemporary group to account for differences in the average level between phenotypes and the de-regressed proofs. In the case of random-regression models, we additionally converted the de-regressed proofs such that they were on the level of the test-day records instead of the full lactation EBV using Eding (2024) approach.

EBV Standardization

The final breeding values were standardized using the rolling base population that consists of cows with phenotypes born 10 years before the evaluation and will be updated on a yearly basis. All traits except milk production traits are expressed on a scale with the mean of 100 and SD of 10.

Results and Discussion

Selection of traits for comparison

To show the outcomes of implementing single-step evaluation system in Poland we present results for a few selected traits only. We selected: milk yield, longevity, and digital dermatitis (DD). Milk yield was included due to its extensive history in Polish genetic evaluation, having undergone moderate modifications (comparing to changes in other trait groups) regarding data filtering and model in new system. This provides a stable baseline for comparison. The heritability for milk yield was estimated at the level of 0.37. Longevity was chosen as a trait with a substantial period of being included in the evaluation in Poland and a comprehensive phenotypic data set. Notably, the current evaluation for longevity has undergone a complete revision, including changes in trait definition, data filtering and variance components estimation (Stachowicz *et al.*, 2024). The heritability level for longevity was estimated to be 0.16. The third trait, digital dermatitis, represents a recent addition to the genetic evaluation with breeding value evaluation started in 2024. Phenotypic data for DD have been incorporated into the evaluation system since 2018. It represents low heritable traits with a heritability of 0.07.

EBV correlations with previous system

The introduction of the new single-step system caused significant re-ranking of animals. Correlation between indexes from previous and new system ranged from 0.83 to 0.96 depending on focal group of animals. In the top 200 ranking bulls only 96 were in common between the two systems and only 66 females. Correlations for production traits were the highest, ranging from 0.88 for protein to 0.94 for fat. The larger changes were observed for longevity and fertility with correlations of 0.6 and 0.5, respectively.

MACE Integration results

Correlation between domestic pedigree-based (conventional) evaluations and international proofs for bulls with daughters in Poland for milk production was 0.99. The same correlation for international bulls without daughters in Poland was 0.79. The inclusion of MACE proofs in single-step evaluation resulted in an increase in the correlation with MACE proofs to 0.98. For longevity the corresponding value increased from 0.72 to 0.96, respectively.

Genetic correlations with other countries

For production traits the correlations between countries from previous and current system are high and stable, at approximately 0.9 for milk yield (ranged from 0.87-0.9). The lowest correlation was obtained between Poland and New Zealand 0.66 for both current and previous systems. This means that the changes introduced did not significantly impact the results obtained in Poland and are consistent with the evaluation obtained in other countries. For traits where significant changes were made in the definition, model, or data editing, such as longevity, the improvement in correlation is significant, ranging from approximately 0.2 to 0.45. The highest increase was observed between Poland and counties: USA, Germany, DFS and Spain. This means that the changes introduced positively influenced the estimated breeding value results.

Digital dermatitis is a new trait evaluated in Poland since April 2024. Based on results from the Interbull research run for new traits Poland received very high correlations for digital dermatitis with six other countries participating in the study, with the highest correlation being 0.93 with the Netherlands. These results confirm that the breeding value estimated in Poland is consistent with those estimated in other countries.

Reliability

A notable observation in the current genomic evaluation system is an increase in reliability, particularly for genotyped animals and reference population. This improvement is evident in both male and female. For milk yield, the average increase in reliability was 10 and 12 percentage points for bulls and cows, respectively, when comparing the previous two-step evaluation system to the current single-step approach. In the case of longevity, this increase in reliability is substantial, averaging 40 percentage points for bulls and approximately 35 percentage points for females. As mentioned, digital dermatitis has not previously undergone a two-step evaluation, which makes it impossible to directly compare the reliability of both systems. However, Figure 1 illustrates the distribution of genomic breeding value reliability for females derived from the single-step system. As shown, females with only phenotypes showed the lowest reliability, with an average reliability of 0.4 in this group. In contrast, females from the reference population (having both the phenotype and genotype) show the highest reliability, averaging around 0.7. Females with only a genotype achieve an average reliability of approx. 0.6. These reliability levels are notable given that DD is a low-heritability trait with a relatively small number of recorded phenotypes. For all 47 traits currently under evaluation, an observed increase in reliability ranged from 5 to 40 percentage points.

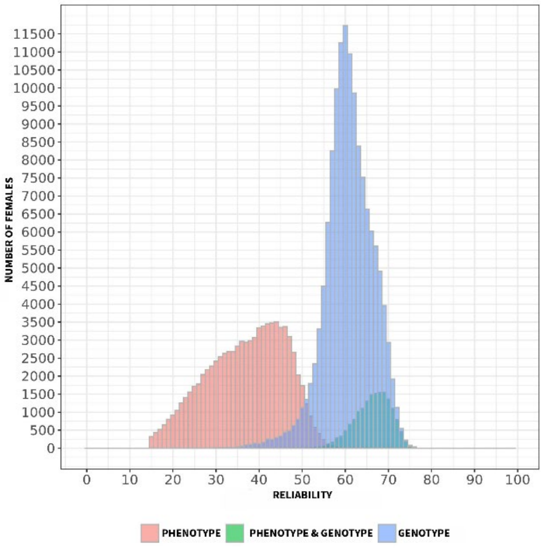

Figure 1. Reliability of the genomic breeding values for digital dermatitis in three groups of Holstein-Friesian females.

Run times

The implementation of the APY (Algorithm for Proven and Young) approach, combined with multi-core processing options within the BLUP90IOD3 software, has resulted in relatively short computational times for full genomic evaluation runs. The processing time varies depending on the trait under consideration, ranging from (in clock hours): 1.5h for longevity, to 5h for digital dermatitis (DD), and between 13h to 33h for production traits.

Conclusions

Implementation of single-step evaluation system utilizing APY algorithm allowed to improve the national genetic evaluation system in Poland. The international correlations estimated by Interbull Centre for conventional proofs, generally, increased. The genomic breeding values reliability increased substantially thanks to including phenotyped and genotyped cows in the reference population while utilizing MACE proofs for bulls evaluated based on foreign daughters. Including cows in the reference population allowed for a successful implementation of hoof health trait which is not a routinely recorded trait in Poland.

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