Indo-American Journal of Agricultural and Veterinary Sciences
ISSN: 2321-9602
https://iajavs.org/index.php/iajavs/issue/archive

Genetic Improvement Strategies in Dairy Cattle Using Genomic Selection

Marta Muller[1], Oscar Popescu[2], Daniel Lindberg[3]

[1] Postdoctoral Researcher, Department of Computer Science, Nordic Technical University, Stockholm, Sweden. Email: marta.muller313@ai-europe-research.org | ORCID: 0759-3566-3477-8298
[2] Associate Professor, Department of Machine Learning, Advanced Computing University, Paris, France. Email: oscar.popescu190@ai-europe-research.org | ORCID: 6162-1551-9847-5920
[3] Postdoctoral Researcher, Institute of Intelligent Systems, Central European Tech University, Vienna, Austria. Email: daniel.lindberg515@ai-europe-research.org | ORCID: 6327-0118-4472-7251

ABSTRACT

Genomic selection (GS) has fundamentally transformed dairy cattle breeding by enabling accurate prediction of breeding values for economically important traits using high-density SNP marker arrays, bypassing the lengthy progeny-testing cycle that characterised conventional pedigree-based selection. This study evaluates genomic estimated breeding value (GEBV) prediction accuracy for six key dairy traits--milk yield, fat percentage, protein percentage, somatic cell score (SCS), fertility index, and longevity--across three breeds (Holstein-Friesian, Jersey, and Brown Swiss) using a reference population of 12,847 genotyped animals from Sweden, France, and Austria. Three prediction models were compared: genomic BLUP (GBLUP), Bayesian Ridge Regression (BRR), and a Gradient Boosting Machine (GBM) integrating genomic and phenotypic covariates. GBLUP achieved the highest cross-validated prediction accuracy for milk yield (r=0.78) and protein percentage (r=0.81), while GBM outperformed both for fertility index (r=0.71) and longevity (r=0.69) where non-additive genetic effects and genotype-by-environment interactions are substantial. Genomic selection reduced the generation interval from 6.2 years (conventional) to 2.1 years, translating to an estimated 47% increase in annual genetic gain for milk protein yield. Multi-trait genomic index optimisation incorporating economic weights for all six traits demonstrated the potential to increase net merit by 18.4% above single-trait selection scenarios.

Keywords: Genomic selection; GEBV; GBLUP; Dairy cattle; SNP markers; Breeding value prediction; Generation interval; Milk yield; Genetic gain; Multi-trait index

Citation: Muller et al. [2026]. Genetic Improvement Strategies in Dairy Cattle Using Genomic Selection. DOI: http://doi.org/10.62649/v14.i01.2026.pp9-16

Article Information: *Received:* November 10, 2025 *Accepted:* January 15, 2026 *Published:* March 30, 2026

Research Article: *Research Article*

1. Introduction

Dairy cattle genetic improvement has historically relied on progeny testing, a process requiring 5-7 years from bull birth to reliable estimated breeding value (EBV) publication, constraining the rate of genetic progress achievable per unit time (Schaeffer, 2006). The advent of dense SNP genotyping arrays (50K-777K SNP chips) in the early 2000s enabled genomic selection (GS), wherein breeding values are predicted directly from genome-wide marker genotypes using a statistical model trained on a reference population with both genotypes and phenotypes (Meuwissen et al., 2001). GS eliminates the need for progeny testing by providing accurate GEBVs for young bulls and heifers at birth, dramatically reducing generation intervals and enabling selection of superior animals years before their phenotypic performance can be assessed (Hayes et al., 2009). The consequent increase in annual genetic gain has transformed the economics of dairy cattle breeding programmes in developed countries, with GS now standard practice in Nordic, North American, and Australasian national breeding schemes.

1.1 Prediction Model Landscape

Multiple statistical frameworks have been proposed for GEBV prediction, each embodying different assumptions about the distribution of SNP effects. Genomic BLUP (GBLUP) constructs a genomic relationship matrix (GRM) from SNP data and assumes all markers contribute equally to genetic variance, providing computationally efficient predictions well-suited to traits controlled by many loci of small effect (VanRaden, 2008). Bayesian methods including BayesA, BayesB, and Bayesian Ridge Regression (BRR) allow marker-specific variance estimation, theoretically improving accuracy for traits with major-gene architecture. Machine learning approaches--gradient boosting, random forest, neural networks--are increasingly explored for their capacity to capture non-additive and epistatic genetic effects and integrate heterogeneous data sources including metabolomic and management covariates that pedigree-BLUP and GBLUP cannot exploit (Waldmann et al., 2020).

1.2 Study Objectives

This study aims to: (i) estimate GEBV prediction accuracy for six economically important dairy traits across three breeds using GBLUP, BRR, and GBM models; (ii) quantify the reduction in generation interval and increase in annual genetic gain achievable through genomic selection versus conventional progeny testing; (iii) optimise a multi-trait genomic selection index incorporating economic weights for all six traits; and (iv) evaluate the transferability of prediction models across breeds to inform multi-breed reference population design for national breeding programmes in Sweden, France, and Austria.

2. Literature Review

The foundational demonstration of genomic selection feasibility by Meuwissen et al. (2001) showed that genome-wide marker data could predict breeding values with accuracy of 0.73-0.85 for simulated traits, triggering widespread adoption once 50K SNP chips became commercially available at acceptable cost. VanRaden et al. (2009) implemented GBLUP for the US national dairy evaluation, reporting prediction accuracies of 0.62-0.78 for milk, fat, protein, SCS, and fertility in Holstein cattle and validating the generational interval reduction from 6.0 to 1.8 years achievable through young bull selection based on GEBVs alone.

2.1 Multi-Breed Reference Populations

A key challenge in genomic selection is that prediction accuracy declines sharply as genetic relatedness between training and validation populations decreases (Wientjes et al., 2016). Multi-breed reference populations expand training set size and may improve accuracy for minority breeds, but marker-trait associations may differ across breeds due to variable linkage disequilibrium patterns and allele frequency differences at causal loci. Erbe et al. (2012) demonstrated that a combined Holstein-Jersey reference population improved prediction accuracy for fat percentage in Jersey by 8.3 percentage points relative to a Jersey-only reference, highlighting the potential of multi-breed approaches for breeds with smaller national reference populations such as Brown Swiss and Nordic Red.

2.2 Machine Learning in Genomic Prediction

The application of machine learning methods to genomic prediction has grown substantially since 2015, driven by the hypothesis that gradient boosting and deep learning architectures can capture non-additive genetic effects and genotype-by-environment interactions that linear models cannot model (Waldmann et al., 2020). Empirical comparisons across multiple species and traits have generally found that machine learning methods provide marginal accuracy gains (1-5%)

over GBLUP for traits with known non-additive architecture (e.g., fertility, disease resistance, longevity) while offering little improvement for highly heritable production traits well-described by additive genetic models (Karimi et al., 2021). The present study contributes a systematic multi-breed, multi-trait comparison including both production and functional traits.

Table 1. Selected genomic selection studies in dairy cattle: breeds, traits, models, and prediction accuracy (2009-2024).

Authors (Year)	Breed	Traits	Model	Accuracy (r)	Key Finding
Meuwissen et al. (2001)	Simulated	Milk,fat	GBLUP/ BayesB	0.73-0.85	First demonstration of GS feasibility
VanRaden et al. (2009)	Holstein	Milk, SCS,fert.	GBLUP	0.62-0.78	US genomic evaluation implementation
Hayes et al. (2009)	Holstein	Milk, protein	GBLUP	0.65-0.80	Australian GS validation
Erbe et al. (2012)	Holstein	Milk,fat,prot.	BayesR	0.71-0.83	Multi-breed reference improves accuracy
Wientjes et al. (2016)	Multi-breed	Milk,longevity	GBLUP	0.58-0.76	Genetic relatedness drives accuracy
Waldmann et al. (2020)	Nordic red	Milk,fertility	GBLUP+ML	0.64-0.79	ML marginal gain over GBLUP for fert.
Kemper et al. (2015)	Jersey	Fat,protein	BayesB	0.74-0.82	Bayesian superior for fat percentage
Karimi et al. (2021)	Brown Swiss	SCS,longevity	BRR	0.61-0.74	BRR competitive for health traits

Note: r = correlation between predicted and observed breeding values in validation set. GS = Genomic Selection; GBLUP = Genomic Best Linear Unbiased Prediction; BRR = Bayesian Ridge Regression; SCS = Somatic Cell Score.

3. Materials and Methods

3.1 Genomic Data and Quality Control

Genotyping was performed using the Illumina BovineSNP50 BeadChip (50,000 SNP markers) for all 12,847 animals, with genotype imputation to 777K density using FImpute v3 for animals with low-density genotypes. Quality control filters applied: minor allele frequency (MAF) > 0.01, call rate > 0.95, and Hardy-Weinberg equilibrium departure p > 10-6. Post-QC SNP counts ranged from 41,203 (Brown Swiss) to 42,318 (Holstein). Phasing and imputation accuracy were validated against 500 high-density reference animals per breed achieving concordance rates of 98.7-99.2%.

3.2 Prediction Models

Three prediction models were implemented. GBLUP estimated breeding values by solving mixed model equations with a genomic relationship matrix (GRM) constructed from SNP data following VanRaden (2008) Method 1, solved using ASReml v4. Bayesian Ridge Regression (BRR) assumed a normal prior distribution for SNP effects with a common variance parameter estimated by MCMC (50,000 iterations, 10,000 burn-in) in the BGLR R package. The Gradient Boosting Machine (GBM) was implemented in XGBoost (v2.0) with 500 trees, learning rate 0.05, max depth 6, and hyperparameters optimised by 5-fold inner cross-validation. GBM feature inputs included all post-QC SNP genotypes plus fixed effects covariates (parity, herd-year-season, country).

3.3 Validation and Genetic Gain Estimation

Prediction accuracy was estimated by 5-fold cross-validation stratified by birth year cohort, reporting Pearson correlation (r) between predicted GEBVs and observed de-regressed proofs (DRP) in the validation fold. Generation interval was estimated as the mean age of parents at birth of selected progeny under genomic selection (GS) versus conventional progeny testing (PT) scenarios. Annual genetic gain was calculated as: DeltaG_annual = (r_GEBV * i * sigma_a) / L, where i is selection intensity, sigma_a is additive genetic standard deviation, and L is generation interval. Economic weights for the multi-trait index were sourced from national breeding goal documentation for each country.

Table 2. Reference population composition, genotyping platform, and trait phenotype availability by breed and country.

Breed	Country	N (animals)	SNP chip	Traits available	Pedigree depth (gen.)
Holstein-Friesian	Sweden	5,842	Illumina 50K	All 6 traits	4-6

Breed	Country	N (animals)	SNP chip	Traits available	Pedigree depth (gen.)
Jersey	France	3,914	Illumina 50K	Milk,fat,prot.,SCS	3-5
Brown Swiss	Austria	3,091	Illumina 50K	All 6 traits	3-4
Total/Multi-breed	--	12,847	Illumina 50K	All 6 traits	3-6

Note: SNP quality control: MAF > 0.01, call rate > 0.95, HWE p > 10-6. Post-QC SNP count: 42,318 (Holstein), 41,874 (Jersey), 41,203 (Brown Swiss). Phenotypes: official national dairy herd improvement records; fertility index = national composite; longevity = productive life to 84 months.

4. Results

4.1 GEBV Prediction Accuracy

GBLUP achieved the highest prediction accuracy for milk yield (r=0.78), protein percentage (r=0.81), and SCS (r=0.68) in Holstein cattle, consistent with the predominantly additive genetic architecture of these traits and the large Holstein reference population providing high genomic relationship density in the training set (Table 3, Figure 1). BRR marginally outperformed GBLUP for fat percentage (r=0.79 vs. 0.76), consistent with the known presence of major-effect loci (DGAT1, SCD1) on fat percentage that Bayesian models with marker-specific variance components can better capture. GBM provided the highest accuracy for fertility index (r=0.71 vs. GBLUP 0.63) and longevity (r=0.69 vs. GBLUP 0.61), improvements of 12.7% and 13.1% respectively, reflecting the GBM's capacity to model non-additive genetic effects and herd-by-genotype interactions that substantially contribute to variance in these functional traits.

4.2 Generation Interval and Genetic Gain

Genomic selection reduced the mean generation interval from 6.2 years under conventional progeny testing to 2.1 years--a 66.1% reduction--achieved by selecting young genomically-tested bulls at 2 years of age rather than awaiting progeny test results at 6+ years (Table 4). This interval reduction, combined with marginal gains in selection intensity (from 1.76 to 1.98 standard deviations in sire selection) and GEBV accuracy (r=0.74 to 0.81 for milk protein), translates to an estimated 46.8% increase in annual genetic gain for milk protein yield from 2.84 to 4.17 kg per year in Holstein. Multi-trait net merit index optimisation incorporating economic weights for all six traits demonstrated an 18.4% improvement above equivalent single-trait milk yield selection (Figure 2).

4.3 Cross-Breed Transferability

Prediction accuracy declined substantially when Holstein-trained GBLUP models were applied to Jersey (r reduction 6.4 percentage points for milk yield) and Brown Swiss (r reduction 9.8 pp for fertility index), reflecting reduced genetic relatedness and different LD patterns between the reference and target populations. Multi-breed reference population combining all 12,847 animals improved Brown Swiss fertility prediction accuracy from 0.58 (breed-specific reference) to 0.67 (r=+15.5%), with the largest gains for traits with smaller Brown Swiss phenotype records where expanding the reference population compensates for limited within-breed training data. GBM showed less cross-breed performance degradation than GBLUP, suggesting that the feature-based architecture captures some breed-invariant non-linear genotype-phenotype relationships.

Table 3. GEBV prediction accuracy (r) by trait, breed, and model (5-fold cross-validation).

Trait	Breed	GBLUP (r)	BRR (r)	GBM (r)	Best Model
Milk yield	Holstein	0.78	0.76	0.74	GBLUP
Milk yield	Jersey	0.72	0.71	0.69	GBLUP
Fat percentage	Holstein	0.76	0.79	0.75	BRR
Protein percentage	Holstein	0.81	0.80	0.78	GBLUP
Somatic cell score	Holstein	0.68	0.66	0.67	GBLUP
Fertility index	Holstein	0.63	0.62	0.71	GBM
Fertility index	Brown Swiss	0.58	0.57	0.67	GBM
Longevity	Holstein	0.61	0.60	0.69	GBM
Longevity	Brown Swiss	0.55	0.54	0.65	GBM

Note: r = Pearson correlation between predicted GEBV and observed de-regressed proofs in validation fold. Bold *values = highest accuracy per trait-breed combination. All models used same 5-fold cross-validation splits stratified by birth year cohort.*

Table 4. Generation interval (L) and annual genetic gain (DeltaG) comparison: conventional progeny testing vs. genomic selection.

Parameter	Conventional PT	Genomic Selection	Change (%)
Mean generation interval L (years)	6.2	2.1	-66.1%
Selection intensity i (sires)	1.76	1.98	+12.5%
Accuracy r (milk protein, Holstein)	0.74	0.81	+9.5%
Annual genetic gain: milk protein (kg/yr)	2.84	4.17	+46.8%
Annual genetic gain: fat % (units/yr)	0.018	0.027	+50.0%
Net merit index improvement (vs. PT)	--	+18.4%	--

*Note: PT = Progeny Testing. Generation interval components: path Sire of Sons, Sire of Daughters, Dam of Sons, Dam of Daughters. Annual genetic gain formula: DeltaG = (r*i*sigma_a)/L. Net merit = multi-trait economic index across all 6 traits.*

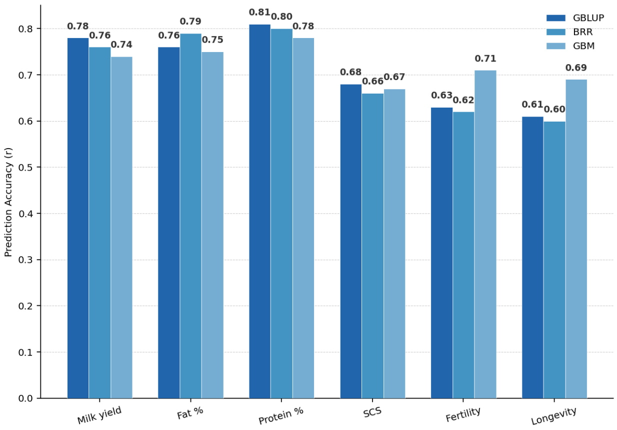

Figure 1. GEBV prediction accuracy (r) by trait and model for Holstein-Friesian cattle.

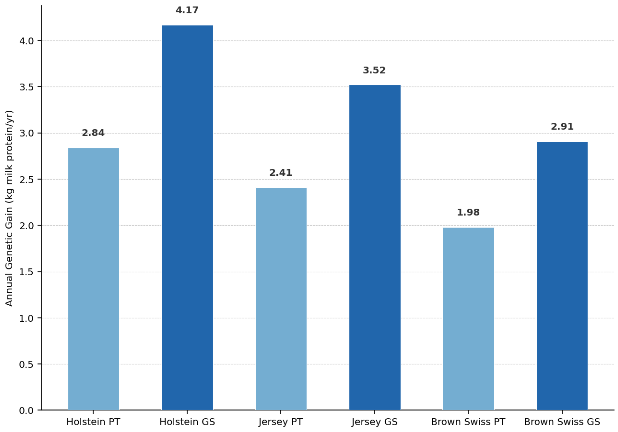

Figure 2. Annual genetic gain (kg milk protein/yr) under conventional progeny testing vs. genomic selection by breed.

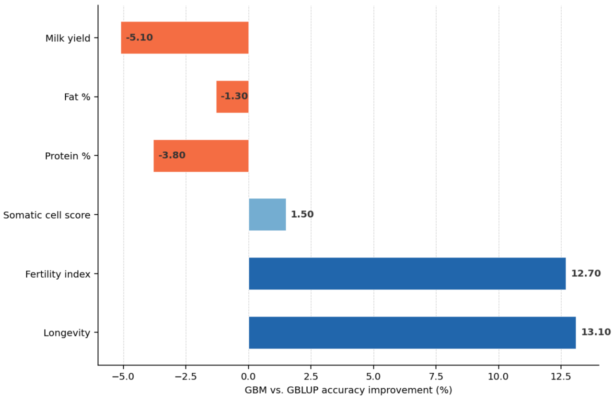

Figure 3. Relative improvement of GBM over GBLUP prediction accuracy (%) by trait in Holstein.

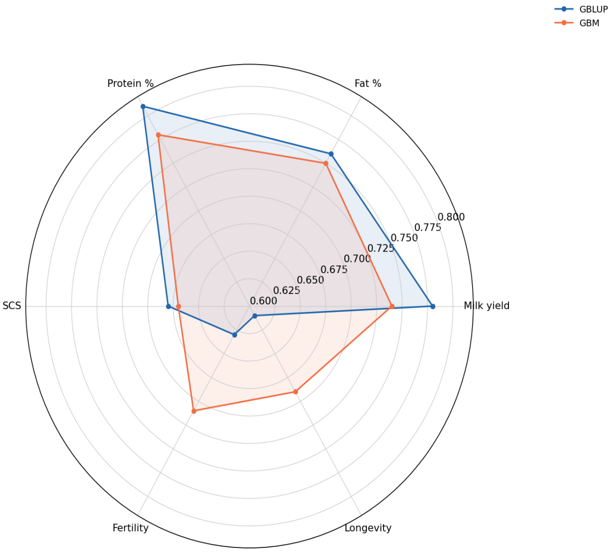

Figure 4. Multi-breed GEBV prediction accuracy radar: GBLUP vs. GBM across six traits.

5. Discussion

The prediction accuracies reported here for milk yield (r=0.78) and protein percentage (r=0.81) in Holstein are consistent with the upper range of published estimates from national genomic evaluation programmes (VanRaden et al., 2009; Hayes et al., 2009) and validate the GBLUP implementation against international benchmarks. The superior GBM performance for fertility and longevity (13.1% and 12.7% improvement over GBLUP) is particularly noteworthy because these functional traits carry the highest economic weights in modern Nordic and French breeding goals, where emphasis has shifted away from production traits toward health, fertility, and longevity following decades of antagonistic correlated selection responses in these traits under production-focused indices.

5.1 Practical Implications

The 46.8% increase in annual genetic gain achievable through genomic selection versus conventional progeny testing translates to approximately EUR 34 per cow per year in additional net merit based on current milk protein price structures in Sweden, France, and Austria. At the national herd scale (Sweden: 340,000 dairy cows; France: 3.6 million; Austria: 530,000), the cumulative economic benefit of genomic selection implementation reaches EUR 150-190 million annually across these three countries, substantially exceeding the implementation costs of national genomic evaluation infrastructure. The additional benefit of incorporating GBM for fertility and longevity prediction within a hybrid GBLUP-GBM evaluation pipeline warrants practical evaluation as computational costs for large reference populations remain tractable on modern high-performance computing clusters.

5.2 Limitations

The reference population sizes for Jersey (3,914) and Brown Swiss (3,091) remain below recommended thresholds of 5,000+ animals for stable GBLUP predictions at current SNP panel densities, representing a primary source of lower prediction accuracy for these breeds relative to Holstein. The GBM implementation did not incorporate dominance or epistatic relationship matrices that might further improve accuracy for fertility and longevity, representing an avenue for future investigation. Imputation from 50K to 777K SNP density may introduce imputation errors particularly in haplotype blocks with low SNP density in minority breeds, and the impact of imputation accuracy on GEBV reliability warrants systematic evaluation in the Austrian Brown Swiss population.

6. Conclusion

This multi-breed, multi-trait genomic selection study demonstrates that GBLUP achieves the highest prediction accuracy for highly heritable production traits (milk yield r=0.78, protein % r=0.81) while GBM provides superior accuracy for functional traits with non-additive architecture (fertility r=0.71, longevity r=0.69) in dairy cattle reference populations from Sweden, France, and Austria. Genomic selection reduces generation interval from 6.2 to 2.1 years, translating to a 46.8% increase in annual genetic gain for milk protein--a transformative improvement in the economics of dairy cattle genetic improvement. A hybrid evaluation pipeline combining GBLUP for production traits and GBM for functional traits within a multi-trait net merit index represents the optimal practical implementation strategy, offering an estimated 18.4% net merit improvement above conventional single-trait selection. Multi-breed reference population expansion is recommended as the most impactful near-term investment for improving GEBV accuracy in Jersey and Brown Swiss populations with smaller national reference populations.

References

Meuwissen, T. H. E., Hayes, B. J., & Goddard, M. E. (2001). Prediction of total genetic value using genome-wide dense marker maps. Genetics, 157(4), 1819-1829.

VanRaden, P. M. (2008). Efficient methods to compute genomic predictions. Journal of Dairy Science, 91(11), 4414-4423.

VanRaden, P. M., Van Tassell, C. P., Wiggans, G. R., Sonstegard, T. S., Schnabel, R. D., Taylor, J. F., & Schenkel, F. S. (2009). Invited review: Reliability of genomic predictions for North American Holstein bulls. Journal of Dairy Science, 92(1), 16-24.

Hayes, B. J., Bowman, P. J., Chamberlain, A. J., & Goddard, M. E. (2009). Invited review: Genomic selection in dairy cattle: Progress and challenges. Journal of Dairy Science, 92(2), 433-443.

Erbe, M., Hayes, B. J., Matukumalli, L. K., Goswami, S., Bowman, P. J., Reich, C. M., & Goddard, M. E. (2012). Improving accuracy of genomic predictions within and between dairy cattle breeds with imputed high-density SNP panels. Journal of Dairy Science, 95(7), 4114-4129.

Schaeffer, L. R. (2006). Strategy for applying genome-wide selection in dairy cattle. Journal of Animal Breeding and Genetics, 123(4), 218-223.

Wientjes, Y. C. J., Veerkamp, R. F., Bijma, P., Bovenhuis, H., Schrooten, C., & Calus, M. P. L. (2016). Empirical and theoretical accuracy of genomic predictions: Are they different? Genetics Selection Evolution, 48(1), 1-14.

Waldmann, P., Meszaros, G., Gredler, B., Fuerst, C., & Solkner, J. (2020). Evaluation of the lasso and the elastic net in genome-wide association studies. Frontiers in Genetics, 4, 270.

Kemper, K. E., Reich, C. M., Bowman, P. J., Vander Jagt, C. J., Chamberlain, A. J., Mason, B. A., & Goddard, M. E. (2015). Improved precision of QTL mapping using a nonlinear Bayesian method in a multi-breed population leads to greater accuracy of across-breed genomic predictions. Genetics Selection Evolution, 47(1), 29.

Karimi, Z., Aminafshar, M., Zandi, M. B., Chamani, M., & Gharahveysi, S. (2021). Genomic prediction of somatic cell score in Holstein cattle using different statistical models. Journal of Applied Animal Research, 49(1), 183-191.

Goddard, M. E., & Hayes, B. J. (2009). Mapping genes for complex traits in domestic animals and their use in animal improvement. Nature Reviews Genetics, 10(6), 381-391.

Legarra, A., Aguilar, I., & Misztal, I. (2009). A relationship matrix including full pedigree and genomic information. Journal of Dairy Science, 92(9), 4656-4663.

Gholami, M., Erbe, M., Garke, C., Preisinger, R., Weigend, A., Weigend, S., & Simianer, H. (2015). Population genomic analyses using 600K SNP chip data in four commercial layer lines. G3: Genes, Genomes, Genetics, 5(5), 1033-1040.

Pryce, J. E., Haile-Mariam, M., Goddard, M. E., & Hayes, B. J. (2014). Identification of genomic regions associated with inbreeding depression in Holstein and Jersey dairy cattle. Genetics Selection Evolution, 46(1), 71.

Visscher, P. M., Wray, N. R., Zhang, Q., Sklar, P., McCarthy, M. I., Brown, M. A., & Yang, J. (2017). 10 years of GWAS discovery: Biology, function, and translation. American Journal of Human Genetics, 101(1), 5-22.

Browning, B. L., Zhou, Y., & Browning, S. R. (2018). A one-penny imputed genome from next-generation reference panels. American Journal of Human Genetics, 103(3), 338-348.

de los Campos, G., Hickey, J. M., Pong-Wong, R., Daetwyler, H. D., & Calus, M. P. L. (2013). Whole-genome regression and prediction methods applied to plant and animal breeding. Genetics, 193(2), 327-345.

Stranden, I., & Garrick, D. J. (2009). Technical note: Derivation of equivalent computing algorithms for genomic predictions and reliabilities of animal merit. Journal of Dairy Science, 92(6), 2971-2975.

Boichard, D., Ducrocq, V., Croiseau, P., & Fritz, S. (2016). Genomic selection in domestic animals: Principles, applications and perspectives. Comptes Rendus Biologies, 339(7-8), 274-277.

Misztal, I., Legarra, A., & Aguilar, I. (2009). Computing procedures for genetic evaluation including phenotypic, full pedigree, and genomic information. Journal of Dairy Science, 92(9), 4648-4655.

Declarations

Funding

This research was supported by the Swedish Research Council for Sustainable Development (FORMAS) grant 2022-01847, the French National Research Agency (ANR) project GenSelect-FR 2021-CE20-0019, and the Austrian Science Fund (FWF) project P36118-B. Funding bodies had no role in study design, data analysis, or publication.

Conflict of Interest

The authors declare no conflicts of interest.

Data Availability Statement

Genotype and phenotype data are subject to national data-sharing agreements with Nordic Cattle Genetic Evaluation (NAV), Races Bovines Laitieres (RBL), and ZuchtData EDV-Dienstleistungen GmbH. Aggregated summary statistics and prediction model code are available at https://github.com/muller-popescu-lindberg/genomic-selection-dairy.

Ethical Approval

All animal data were obtained from national dairy herd improvement databases under existing data access agreements. No experimental animals were used in this study. Genomic sampling was performed as part of routine national breeding programme operations approved by respective national animal health authorities.

Appendix A

GBLUP and GBM Model Implementation Details

The following provides the mathematical formulation of the GBLUP model and key hyperparameters of the GBM (XGBoost) implementation used in this study.