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Year: 2025

Version: Published version

Please cite the original version:

Arash Chegini, Ismo Strandén, Emre Karaman, Terhi Iso-Touru, Jukka Pösö, Gert P. Aamand, Martin H. Lidauer, Marker weighting improves single-step genomic prediction reliabilities of udder health traits in Nordic Red and Jersey dairy cattle populations, Journal of Dairy Science, Volume 108, Issue 1, 2025, Pages 651-663, ISSN 0022-0302, https://doi.org/10.3168/jds.2024-25374. .

J. Dairy Sci. 108:651–663
https://doi.org/10.3168/jds.2024-25374

Marker weighting improves single-step genomic prediction reliabilities of udder health traits in Nordic Red and Jersey dairy cattle populations

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ABSTRACT

The standard single-step genomic prediction model assumes that all SNP markers explain an equal amount of genetic variance, which, however, may not be true. This is because SNPs are located in or near different genes with different functions. Therefore, it seems logical to consider SNP marker-specific weights when predicting genomic breeding values. We hypothesized that allowing differences in the amount of genetic variance explained by each SNP marker will improve prediction reliability and response to selection. To investigate this hypothesis, we first developed multitrait standard single-step genomic models based on the current multitrait random regression evaluation models for udder health traits of the Nordic Red (RDC) and Jersey (JER) dairy cattle populations. The models included 4 clinical mastitis (CM) traits, 3 test-day SCS traits, and the conformation traits fore udder attachment and udder depth. In the second step, we investigated the effect of applying different SNP marker weighting scenarios in the single-step genomic prediction models, for which a single-step SNP best linear unbiased prediction model was applied. We investigated the prediction reliability of the different models by forward prediction, where the last 4 years of the data were removed to estimate breeding values for validation candidates. In addition, genetic trends of the pedigree-based estimated breeding values (PEBV) and GEBV were examined. The datasets for RDC and JER included 6.9 million and 1.2 million animals, of which 5.6 million and 0.9 million cows had records, respectively. The number of genotyped animals was 125,789 and 64,777 for RDC and JER, respectively. Cows had repeated SCS observations but only single observations for all other traits and breeding values for all traits were modeled by one covariance function. This required modeling 12 eigenvalue breeding value coefficients for each cow and developing SNP marker weights for the principal components rather than for the biological traits. We investigated 3 SNP marker weighting scenarios: (1) a nonlinear method similar to BayesA, (2) using the classical formula $2pq\hat{u}^2$ that accounts for allele heterozygosity, and (3) applying a mean SNP weight calculated by $2pq\hat{u}^2$ for every 20 adjacent SNP markers. Bias, dispersion, and prediction reliability were calculated using PEBV or GEBV from the evaluation based on the full dataset on those using the reduced dataset. We found that the recent favorable genetic trend in CM and SCS has been accelerated since the introduction of genomic selection. The study also shows that a significant increase in prediction reliability, i.e., 0.74 versus 0.48 for RDC and 0.72 versus 0.41 for JER cows for CM, can be achieved with a standard single-step genomic prediction model compared with a pedigree-based prediction model. Almost all scenarios with SNP marker weighting further improved the prediction reliability between 0.5% and 12.7%. The highest improvement was achieved by weighing the SNP markers based on the $2pq\hat{u}^2$ formula.

Key words: genomic selection, clinical mastitis, single-step SNPBLUP model, SNP weight, BayesA

INTRODUCTION

Modern dairy cattle breeding programs include udder health traits into total merit index selection to reduce the incidence of mastitis, thereby improving cow welfare and the sustainability of dairy farming. The most important udder health trait is clinical mastitis (**CM**), which is the most costly disease in dairy cows, causing the second largest monetary loss in dairy farming after fertility failure (Egyedy and Ametaj, 2022). The CM traits have relatively low heritability; therefore, test-day SCS traits are often included as correlated traits to improve reliability of prediction (Pösö and Mäntysaari, 1996). Neverthe-

Received July 1, 2024.
Accepted September 4, 2024.
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The list of standard abbreviations for JDS is available at adsa.org/jds-abbreviations-24. Nonstandard abbreviations are available in the Notes.

less, genetic progress is slow when selection is based on predicted breeding values from pedigree-based models (Pösö and Mäntysaari, 1996; Rupp and Boichard, 1999; Negussie et al., 2010). By using a single-step genomic prediction model (Aguilar et al., 2010; Christensen and Lund, 2010), which combines pedigree and genomic information, higher prediction reliability can be expected (Aguilar et al., 2010).

A standard single-step GBLUP (**ssGBLUP**) model assigns equal weights to all SNP markers (i.e., ssGBLUP assumes that each SNP marker contributes equally to the genetic variation; VanRaden, 2008). This assumption may not be true, because some SNP markers are in the proximity of influential genes. Recent studies have highlighted the potential benefits of incorporating alternative SNP marker weighting strategies to improve prediction accuracy (Zhang et al., 2010; Wang et al., 2012; Fragomeni et al., 2019). Several approaches have been proposed to weigh SNPs, including the classical weighting method by $2pq\hat{u}^2$, i.e., based on allele frequencies and marker effect (Falconer and Mackay, 1996; Wang et al., 2012), a BayesA-like procedure, namely Nonlinear A (VanRaden, 2008; Cole et al., 2009), and Bayesian methods (Habier et al., 2010, 2011).

In a simulation study, Zhang et al. (2010) reported an improvement in prediction ability by using a trait-specific genomic relationship matrix calculated based on squared SNP effects. Wang et al. (2012) pointed out that although Bayesian methods are able to account for the variation in the amount of genetic variance explained by each SNP marker, they impose higher computational costs and do not include phenotypic information from nongenotyped animals. Therefore, they proposed an ssGBLUP model that considers SNP marker-specific weights. Another previously used weighting method is Nonlinear A, which is similar to BayesA and where all SNP markers have nonzero weights. Fragomeni et al. (2019) tested the Nonlinear A method on stature in US Holstein cows and attained slightly higher prediction reliabilities (about 3%) when SNP marker weights were implemented in a GBLUP model, but no improvement was achieved when implemented in an ssGBLUP model. Similarly, Zhang et al. (2016) acknowledged the superiority of marker-weighted single-step for both genome-wide association studies and GEBV prediction based on the comparison of different weighting scenarios in the ssGBLUP framework with different Bayesian methods using simulated data. They concluded that SNP marker weighting is useful when a trait is influenced by a large number of QTL. Alternative marker weighting methods, such as the classical SNP weighting, have rarely been implemented in genetic evaluations, and have been reported to diverge in many cases (Fragomeni et al., 2019).

The aim of this study is to investigate whether marker weighting in a single-step genomic prediction framework can improve prediction reliability when the heritabilities of the traits are low. Multiple trait genetic evaluations for udder health traits in the Nordic Red (**RDC**) and Jersey (**JER**) dairy cattle populations are used in the analyses of alternative SNP marker weighting approaches. We investigate the application of marker weighting in a multitrait single-step genomic prediction framework on large datasets, and we hypothesize that incorporating alternative weighting strategies will improve the prediction reliability of single-step genomic prediction for udder health traits. To achieve our objectives, (1) standard multitrait ssGBLUP models are developed and the obtained genetic trends in GEBV are compared with those from the pedigree-based estimated breeding values (**PEBV**), (2) single-step genomic prediction models with SNP marker-specific weights that are based on different weighting approaches are developed, and (3) prediction reliability and bias of breeding values are investigated by forward prediction validation.

MATERIALS AND METHODS

Data and Trait Definition

The datasets used in this study were the same as those used by the Nordic Cattle Genetic Evaluation (**NAV**; Aarhus, Denmark) for the official evaluation in February 2023. The datasets included all available records for 9 udder health traits collected in Denmark, Finland, and Sweden since 1990. The datasets comprised in total 74.5 million and 17.1 million records for RDC and JER, respectively. The number of cows with records was 5.6 million and 0.9 million for RDC and JER, and the pedigree included in total 6.9 million and 1.2 million animals for RDC and JER, respectively (Table 1). Unknown parents were grouped by selection path, breed, and birth years into 391 and 319 unknown parent groups for RDC and JER, respectively.

The total number of genotyped RDC and JER animals was 249,223 and 136,562, respectively. However, only genotypes of individuals registered in the pedigree and born after 2008 were used for the analyses, leaving 125,789 and 64,777 genotyped RDC and JER animals, respectively. This was done to use the same genomic information as in the genomic evaluation by NAV. Individuals were genotyped with Illumina Bovine SNP50 Bead Chip (Illumina, San Diego, CA). Using the same editing criteria as NAV, 46,914 and 41,897 SNP markers remained for genotyped RDC and JER animals, respectively.

The multitrait model currently used for the NAV udder health evaluation, which describes the observations of 9

Table 1. Summary of pedigree structure for Nordic Red (RDC) and Jersey (JER) dairy cattle

Item	RDC	JER
No. of animals in total	6,885,001	1,166,650
No. of sires (Average no. of daughters per sire)	91,956 (71.7)	26,657 (41.2)
No. of dams (Average no. of daughters per dam)	4,212,920 (1.5)	719,384 (1.5)
No. of unknown parent groups	391	319
Average inbreeding coefficient	0.022	0.037
No. of herds	59,514	12,639

traits, was the starting point for this study. The observations for all 9 traits were adjusted by NAV for heterogeneous variance across countries (Denmark, Finland, Sweden) and time. A description of the trait definitions and the variance components applied by NAV is given in Negussie et al. (2010). Summary statistics for the observations of all 9 traits used in this study are shown in Table 2 for both breeds.

The multivariate data includes 4 CM traits as the traits of interest and 5 correlated traits to increase the reliability of CM breeding values. The CM traits were coded as binary traits, where a 1 was coded for at least one occurrence of CM during a defined period, and a 0 was coded for healthy. In the first lactation, 2 CM traits were defined: one trait (**CM11**) for the period from 15 d before calving until 50 DIM, and another trait (**CM12**) for the period from 51 to 305 DIM. The other 2 CM traits were defined for the second (**CM2**) and third (**CM3**) lactation for the lactation periods from 15 d before calving to 150 DIM.

The 5 correlated traits describe the information from test-day SCS observations from the first 3 lactations, and the observations of fore udder attachment (**UA**) and udder depth (**UD**) for the first lactation. Original test-day somatic cell counts were transformed to SCS observations by a logarithmic transformation, i.e., $\log_e$(1,000cells/mL). A cow's SCS observations were assigned to 3 different traits **SCS1**, **SCS2**, and **SCS3**, categorized by lactation 1, 2, and 3, respectively, where observations within a lactation were modeled by regression functions, as explained in the next section. The included type traits UA and UD were type scores given by classifiers using a scale from 1 to 9.

Multitrait Udder Health Model with Covariance Functions for Animal Effects

The applied multitrait model simultaneously includes the binary observations for the CM traits, the repeated observations for the SCS traits, and the observations for the udder conformation traits. The model is described in detail in Negussie et al. (2010), and here we present only the most important model features relevant for this study. The same model is used for both the RDC and JER breeds, with only minor breed-specific differences, because the JER population is mainly kept in Denmark. To model the animal effects, multivariate variance component analyses were carried out in the first step during model development, with all 9 traits included in the analyses. In these analyses, both the animal nonadditive and additive genetic effects for SCS were described by a second-order Legendre polynomial function plus the exponential term $\exp(-0.05 \times \text{DIM})$. Furthermore, the residual effects for the CM traits and the udder conformation traits were omitted, and an animal non-additive genetic effect was modeled instead. This allowed residual correlations between the repeated SCS observations and the observations of the other 6 traits to be accounted in the model.

Table 2. Summary statistics of the modeled observations given by trait and breed

	Nordic Red					Jersey				
Trait[1]	n	Mean	SD	Minimum	Maximum	n	Mean	SD	Minimum	Maximum
CM11	4,791,842	0.06	0.245	0.00	1.00	601,988	0.14	0.347	0.00	1.00
CM12	4,641,064	0.06	0.237	0.00	1.00	590,198	0.11	0.307	0.00	1.00
CM2	3,452,089	0.11	0.311	0.00	1.00	427,327	0.14	0.344	0.00	1.00
CM3	2,246,733	0.14	0.345	0.00	1.00	287,409	0.16	0.366	0.00	1.00
SCS1	29,944,467	4.05	1.191	0.69	9.90	7,317,581	4.44	1.093	0.69	9.47
SCS2	20,997,798	4.41	1.276	0.69	9.90	5,100,038	4.67	1.190	0.69	9.59
SCS3	12,978,293	4.63	1.302	0.69	9.90	3,301,183	4.84	1.232	0.69	9.62
UA	1,161,944	5.58	1.364	1.00	9.00	307,635	5.47	1.171	1.00	9.00
UD	1,160,324	5.62	1.661	1.00	9.00	307,634	5.39	1.117	1.00	9.00

[1] CM11 and CM12 = incidence of mastitis in the first lactation in 15 d before calving until 50 DIM, and from 51 to 305 DIM; CM2 and CM3 = incidence of mastitis in the second and the third lactations in the range of 15 d before calving up to DIM 150; SCS1, SCS2, and SCS3 = records of SCS in lactations 1, 2, and 3, respectively; UA = fore udder attachment; UD = udder depth.

The (co)variance components for the animal nonadditive and additive genetic effects were used to build covariance functions (**CF**) following Lidauer et al. (2015). The correlation matrices of the original (co)variance matrices were decomposed by an eigenvalue decomposition and the largest eigenvalues and eigenfunctions that explained at least 99.0% of the variances of the original matrices were used to build the CF. The obtained CF for the animal nonadditive genetic effects describes an animal's nonadditive genetic effects of all 9 traits by 15 animal-specific regression coefficients and 15 trait-specific covariables. In analogy, a CF with 12 animal-specific regression coefficients was developed for the animal additive genetic effects. Hence, the animal effects of the multitrait models correspond to the 15 and 12 largest eigenvalues of the original (co)variance matrices for the animal nonadditive and additive genetic effects, respectively.

The multitrait udder health model can be described in matrix notation as

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Tk} + \mathbf{F}_a\mathbf{a} + \mathbf{F}_p\mathbf{p} + \mathbf{e},$$

where vector $\mathbf{y}$ contains the observations of all traits; vector $\mathbf{b}$ contains all fixed effects; vector $\mathbf{k}$ contains random herd × year effects for CM and udder conformation traits, and random herd × test-day effects for the SCS traits; vector $\mathbf{a}$ contains the random animal additive genetic effects modeled by CF; vector $\mathbf{p}$ contains the random animal nonadditive genetic effects modeled by a CF; and vector $\mathbf{e}$ contains the random residual. The matrices $\mathbf{X}$, $\mathbf{T}$, $\mathbf{F}_a$, and $\mathbf{F}_p$ are design matrices relating the records to the fixed, the random herd, the animal additive and nonadditive genetic effects, respectively, and where $\mathbf{F}_a$ and $\mathbf{F}_p$ contain the trait-specific covariables of the CF. The fixed effects for CM and udder conformation traits included a herd × 5-year time period effect; for SCS traits, a herd × production year effect; for all traits, a calving year × month × country effect, a linear and quadratic regression on calving age × country effect, and a linear regression on the cow's total heterozygosity; and additionally for the SCS traits, a lactation stage effect nested within 4-year time period × season × country, which was modeled by a third order Legendre polynomial plus the exponential term $\exp(-0.05 \times \text{DIM})$; and for the udder conformation traits the effect of the classifier.

The assumptions for the random effects were as follows: $\mathbf{k} \sim MVN\ (\mathbf{0}, \mathbf{I}\otimes\mathbf{K})$, with $\mathbf{K}$ being a (co)variance matrix for the random herd effects; $\mathbf{a} \sim MVN\ (\mathbf{0}, \mathbf{A}\otimes\mathbf{E}_a)$, with $\mathbf{E}_a$ being a diagonal matrix containing the 12 largest eigenvalues of the original (co)variance matrix for the animal additive genetic effects and $\mathbf{A}$ being the numerator relationship matrix; $\mathbf{p} \sim MVN\ (\mathbf{0}, \mathbf{I}\otimes\mathbf{E}_p)$, with $\mathbf{E}_p$ being a diagonal matrix containing the 15 largest eigenvalues of the original (co)variance matrix for the animal nonadditive effects; $\mathbf{e} \sim MVN\ (\mathbf{0}, \mathbf{I}\otimes\mathbf{R})$, with $\mathbf{R}$ being a (co)variance matrix for the random residual effects of all 9 traits, and $\mathbf{R}$ being derived in the same analyses that was applied for deriving the CF for the animal nonadditive genetic effects; and $\mathbf{I}$ is an identity matrix of size specific to the random effect. As can be seen, a linear model was used for the CM traits, which is computationally feasible compared with a logistic model given the volume of data in the present study. However, to make the linear model applicable for binary traits (Cook et al., 2017), the observations have been adjusted for heterogeneity of variance to account for differences in CM incidence rate between participating countries.

We applied the same variance components as in Negussie et al. (2010). For RDC, heritability was 0.038, 0.019, 0.051, and 0.046 for CM11, CM12, CM2, and CM3, and 0.30, and 0.39 for UA and UD, respectively. The lactational heritability for SCS was 0.135, 0.178, and 0.175 for SCS1, SCS2, and SCS3, respectively. For JER, the corresponding heritabilities were 0.037, 0.016, 0.040, and 0.065 for CM11, CM12, CM2, and CM3, and 0.24, and 0.32 for UA, and UD, respectively. The lactational heritabilities for SCS were 0.154, 0.191, and 0.205 for SCS1, SCS2, and SCS3, respectively.

Models

For both breeds, we investigated the reliability of prediction for 5 different model alternatives. The effects of the above-described multitrait CF model can be predicted by pedigree-based BLUP, which yields PEBV. Hereafter, pedigree-based BLUP (**PBLUP**) refers to this model. For the other 4 model alternatives, we investigated different alternatives for including genomic information into the models to monitor the prediction reliability of GEBV.

Single-Step Genomic Prediction with Equal SNP Marker Weights. As a first genomic prediction model, we applied a standard ssGBLUP model, which was identical with the PBLUP model, except that the numerator relationship matrix $\mathbf{A}$ in the PBLUP model was substituted with an $\mathbf{H}$ matrix calculated using both the pedigree and genotype information (Aguilar et al., 2010; Christensen and Lund, 2010), i.e., $\mathbf{a} \sim MVN\ (\mathbf{0}, \mathbf{H}\otimes\mathbf{E}_a)$, where $\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1} \end{bmatrix}$, with $\mathbf{G}$ equal to the genomic relationship matrix (**GRM**) and $\mathbf{A}_{22}$ being the pedigree-based relationship matrix of the genotyped individuals. The standard ssGBLUP predictions were computed using a method called single-step GBLUP with a T factoring (**ssGTABLUP**) proposed in Mäntysaari et al. (2017). This method allows efficient solving of GEBV. In ssGTABLUP, GRM has the form $\mathbf{G} = \mathbf{ZZ}' + \mathbf{C}$, where $\mathbf{Z}$ is a centered and scaled marker matrix, $\mathbf{C} = w\mathbf{A}_{22}$, with

w equal to the residual polygenic proportion, which was 0.10. For scaling the $\mathbf{Z}$ matrix, we required the average diagonal of $\mathbf{ZZ}'$ to be equal to the average diagonal of $\mathbf{A}_{22}$.

Single-Step Genomic Prediction with SNP Marker-Specific Weights. We studied 4 single-step genomic prediction models, of which 3 had marker-specific weights. Thus, the trait-specific (j), i.e., for the models studied here the eigenvalue-specific trait, GRM_j was $\mathbf{G}_j = \mathbf{Z}_j\mathbf{W}_j\mathbf{Z}_j' + \mathbf{C}$, where the SNP markers received different weights in the diagonal matrix $\mathbf{W}_j$. For the models with SNP marker-specific weights, the predictions were computed by applying the single-step single-step single nucleotide polymorphism BLUP (**ssSNPBLUP**; Liu et al., 2014) approach, which is equivalent to ssGTABLUP when the $\mathbf{W}_j$ matrix is an identity matrix. The ssSNPBLUP approach allows to apply trait-specific SNP marker weights (Strandén and Jenko, 2024). Solving an ssSNPBLUP model needs less memory than that of an ssGTABLUP model, although ssSNPBLUP needs a higher number of iterations to reach the same convergence (Vandenplas et al., 2023; Strandén and Jenko, 2024).

In the computation of SNP marker weights, we used SNP marker estimates obtained from the standard ssGBLUP model using the reduced dataset, which will be explained i the Prediction of Breeding Values section. The mean marker weight was standardized to be one within every trait. The SNP marker weights were computed for each of the 12 eigenvalue-based traits separately by 3 different approaches:

1. A nonlinear formula (hereafter "Nonlinear") introduced by VanRaden (2008) and Cole et al. (2009) for the weight of marker i of eigenvalue trait j is $1.25^{\frac{\left|\hat{u}_{ji}\right|}{\mathrm{sd}\left(\hat{u}_j\right)}-2}$, where $\left|\hat{u}_{ji}\right|$ is the absolute value of the estimated SNP effect for marker i and $\mathrm{sd}\left(\hat{u}_j\right)$ is the SD of all estimated SNP effects for eigenvalue j. No restriction was applied for the upper bound of $\frac{\left|\hat{u}_{ji}\right|}{\mathrm{sd}\left(\hat{u}_j\right)}$ because there were only a few SNPs with values higher than 10 (between 10 and 11).
2. In the second approach, which we will refer to as "$2pq\hat{u}^2$," the SNP marker weights were calculated using the classical method described by Falconer and Mackay (1996) and Zhang et al. (2010), where there are no dominance and epistatic effects assumed among SNPs. The weight formula is $2p_iq_i\hat{u}_{ji}^2$, where p_i and $q_i = 1 - p_i$ are allele frequencies and $\hat{u}_{ji}$ is the estimated SNP effect for marker i for eigenvalue trait j.
3. The third approach was similar to the method used by Zhang et al. (2016), in which average weights are calculated from the weights obtained by the $2pq\hat{u}^2$ approach. The average weights of every 20 adjacent SNPs (**20SNP_window**) were calculated.

As mentioned earlier, in the marker-weighted ssSNPBLUP model, each trait (in our model eigenvalue trait) had its own specific marker weights in the $\mathbf{W}_j$ matrix. Thus, each eigenvalue trait j had a diagonal marker weight matrix $\mathbf{W}_{jj}$. The marker-weighted ssSNPBLUP model requires weights for the eigenvalue-by-eigenvalue trait combinations, i.e., a weight matrix $\mathbf{W}_{jl}$ for every combination of eigenvalues j and l. In our study, these weights were computed from the eigenvalue-specific weights by assuming a correlation of one between the trait-specific marker weights. Thus, the weight for marker i between eigenvalue traits j and l was $w_{jl,i} = \sqrt{w_{jj,i}w_{ll,i}}$ where $w_{jj,i}$ is the weight of eigenvalue trait j for marker i.

Prediction of Breeding Values

For each breed and for each model studied, 2 genetic evaluations were performed to facilitate model validation by forward prediction. One evaluation with full data (denoted with subscript f), and a second evaluation with reduced data (denoted with subscript r) where all observations in the last 4 years were excluded. Inbreeding coefficients were included in the pedigree-based relationship matrix computations. For calculating the inbreeding coefficients, the RelaX2 program was used (Strandén and Vuori, 2006). The preconditioned conjugate gradient method implemented in the MiX99 program suite (Strandén and Lidauer, 1999) was employed to solve the mixed model equations. In all analyses, a square root of relative difference between consecutive solutions equivalent to 10^{-6} was considered as a convergence criterion.

An animal's PEBV and GEBV for CM and SCS were calculated by multiplying the animal's 12 regression coefficient estimates for the animal's additive genetic effects with the trait-specific covariables used in $\mathbf{F}_a$. For studying the reliability of predictions, we formed combined breeding value indices for CM and for SCS. For CM, the trait-specific breeding value index weighted CM11, CM12, CM2, and CM3 by 0.15, 0.15, 0.25, and 0.45, respectively, hereafter denoted combined_CM. For SCS, first an average daily SCS breeding value was estimated for each lactation for the period DIM 8 to DIM 312, followed by combining the lactation averages for SCS1, SCS2, and SCS3 by applying the weights of 0.30, 0.25, and 0.45, respectively, denoted combined_SCS. The applied weights correspond to those currently used by NAV. For both combined_CM and combined_SCS, negative estimated breeding values are favorable.

Summary statistics of the combined GEBV were tabulated for CM and SCS, and the yearly means of the combined PEBV and GEBV from the reduced and full data evaluations were examined for both breeds to assess the genetic trends in CM. In addition, to show the source of the difference between different single-step scenarios, SNP weights calculated by the $2pq\hat{u}^2$ and Nonlinear approaches were plotted.

Model Validation

For the calculation of validation statistics, suitable sets of validation animals were selected that received a breeding value evaluation without their own phenotypic information in the reduced data and a breeding value evaluation using the full data. The following steps were used to select validation candidate bulls and cows for each breed. First, individual animal reliabilities of PEBV were calculated for both the full and reduced datasets (**$PEBV_f$** and **$PEBV_r$**), using the method proposed by Tier and Meyer (2004) for multitrait models. The reliabilities of CM and SCS were computed for the combined_CM and combined_SCS breeding values. Second, the combined reliabilities of genotyped bulls and cows were used to calculate effective record contributions (**ERC**) separately for bulls and cows. This was carried out using the reversed reliability approximation method introduced by Harris and Johnson (1998) as implemented in MiX99 (Ben Zaabza et al., 2022). Then, genotyped bulls with an ERC ≥2 using the full data evaluation and equal to zero using the reduced data evaluation were selected as candidate bulls, yielding for CM 86 and 115 candidates, and for SCS 125 and 119 candidates for RDC and JER, respectively. Correspondingly, genotyped cows with an ERC ≥0.9 using the full data and equal to zero using the reduced data were selected as candidate cows, yielding for CM 8,440 and 8,224 candidates, and for SCS 18,112 and 6,537 candidates for RDC and JER, respectively.

Following Legarra and Reverter (2018), we used linear regression of $PEBV_f$ on $PEBV_r$, and genomic estimated breeding values using full and reduced datasets, respectively (**$GEBV_f$** on **$GEBV_r$**), to measure bias (b_0; intercept), dispersion (b_1; slope of regression), and prediction reliability (R^2; square of correlations between obtained estimates using reduced and full datasets) for the 5 different models. For investigating the consistency of the estimates in different scenarios, the SE of the estimates were estimated by bootstrapping. The number of bootstrap samples was set to 10,000, and the method used was Ordinary Nonparametric Bootstrap (R Core Development Team, 2012). All the analyses were performed on a server with an AMD EPYC 7443P CPU (2.85 GHz).

RESULTS AND DISCUSSION

Summary Statistics and Input Parameters

Two large datasets of RDC and JER cows were used in this study to evaluate the value of applying SNP marker weights in single-step genomic prediction for the Nordic udder health evaluation. The 9 traits included in the Nordic multitrait model for udder health are CM and SCS in the first 3 lactations and UA and UD in the first lactation only, and of these, only a combined GEBV for CM has been incorporated in the Nordic Total Merit Index. Therefore, our main interest was on the effect of the different modeling alternatives on the reliability of the combined breeding values for CM. Furthermore, because breeding values for SCS are used in many countries, we also investigated the effect on the combined breeding values for SCS.

The CM incidences were higher in JER cows than in RDC cows, ranging from 0.11 to 0.16 for JER cows and from 0.06 to 0.14 for RDC cows, with the highest difference in the first lactation (Table 2). In addition, JER cows exhibited a higher susceptibility to new infections at the beginning of lactation as they had a higher incidence rate, which was more than double that of RDC cows during this period. Furthermore, JER cows also had higher SCS averages, ranging from 4.44 in the first lactation to 4.84 in the third lactation, compared with RDC cows with average SCS of 4.05 and 4.63, respectively. The heritability of the combined_CM trait was 0.09 and 0.12 for RDC and JER cows, respectively, and the heritability of the combined_SCS trait was 0.25 and 0.26 for RDC and JER cows, respectively.

The structure of the full and reduced datasets created by truncating the last 4 years of the data is shown in Table 3. Truncation reduced the number of cows with phenotypic records by 6% and 13% for RDC and JER, respectively. On average, there were more test-day records per JER cow than per RDC cow, because in Finnish RDC herds, test-day recording is done in bi-monthly intervals. As genotyping gradually became cheaper, there was an increasing trend in the number of genotyped cows such that more than half of the genotyped cows had observations in the last 4 years of the data. However, not all of these genotyped cows could be used as candidates because many of them only had observations in the reduced dataset.

Validation of Clinical Mastitis

Before performing the forward validation, the PEBV and GEBV of animals were standardized based on the averages of PEBV and GEBV of animals, respectively, born between 2000 and 2002. The results of the forward

Table 3. Structure of the full and reduced validation datasets and number of records of any trait

	Nordic Red		Jersey	
Item	Full	Reduced	Full	Reduced
No. of cows	5,550,887	5,223,866	916,258	801,873
No. of records per cow	13.42	13.12	18.64	18.80
Genotyped cows with records	123,436	59,881	63,531	28,865
No. of records per genotyped cows	15.74	14.11	17.56	19.07
No. of sires	91,956	47,197	26,657	7,875
Genotyped sires with daughter records	1,818	1,640	895	569
No. of daughter records per genotyped sire	3,692	1,939	3,467	2,277

validation for bull and cow candidates of RDC and JER breeds for combined_CM are shown in Table 4. Regression of breeding values using the full dataset on those of using the reduced dataset showed slightly lower bias and dispersion for PBLUP compared with the single-step genomic prediction models. The estimated bias using regression of PEBV_f on PEBV_r for RDC cows was −0.001, compared with 0.003 to 0.005 for the single-step model scenarios. The SD of PEBV_f and GEBV_f for RDC breed were 0.032 and 0.032, respectively. Among the genomic models, the standard ssGBLUP model generally resulted in b_1 estimates closer to 1.0 than the marker-weighted scenarios. Similarly, Liu et al. (2020) reported higher dispersion when whole genome sequence was added to the conventional 50K SNP chip in genomic evaluation compared with using the conventional 50K SNP chip alone. This is difficult to interpret, but it seems that achieving an increase in prediction accuracy comes along with slightly lower precision (i.e., higher dispersion).

Results showed that GEBV are significantly more accurate than PEBV. In the standard ssGBLUP model, the reliability of predictions for RDC and JER bull candidates were 0.50 and 0.65, respectively, which corresponds to 82% and 132% higher reliability than when using PBLUP. Corresponding values for RDC and JER cow candidates were 0.74 and 0.72, respectively, representing 54% and 77% improvements over PBLUP. We observed a higher relative improvement in reliability for JER compared with RDC when moving from PBLUP to single-step genomic prediction. This is probably due to

Table 4. Results of forward validation (SE in parentheses) of bull and cow candidate groups for combined clinical mastitis breeding values based on pedigree-based or single-step genomic prediction with different SNP weights for Nordic Red (RDC) and Jersey (JER) dairy cattle

					Forward validation[1]			
Breed	Group	n	ERC[2]	Model[3]	b_0	b_1	R^2	% Gain[4]
RDC	Bull	86	8.37	PBLUP	0.000 (0.006)	0.79 (0.175)	0.28 (0.078)	
				Standard ssGBLUP	0.002 (0.005)	0.75 (0.084)	0.50 (0.077)	
				Nonlinear	0.001 (0.005)	0.73 (0.078)	0.51 (0.079)	1.8
				$2pq\hat{u}^2$	0.001 (0.004)	0.68 (0.063)	0.57 (0.082)	12.7
				20SNP_window	0.000 (0.004)	0.70 (0.073)	0.50 (0.082)	−1.4
	Cow	8,440	1.63	PBLUP	−0.001 (0.000)	0.83 (0.010)	0.48 (0.009)	
				Standard ssGBLUP	0.005 (0.000)	0.87 (0.006)	0.74 (0.005)	
				Nonlinear	0.005 (0.000)	0.85 (0.005)	0.74 (0.005)	1.1
				$2pq\hat{u}^2$	0.003 (0.000)	0.79 (0.005)	0.78 (0.004)	5.3
				20SNP_window	0.005 (0.000)	0.85 (0.005)	0.75 (0.005)	1.8
JER	Bull	115	45.20	PBLUP	0.006 (0.007)	0.85 (0.128)	0.28 (0.066)	
				Standard ssGBLUP	0.013 (0.004)	0.78 (0.052)	0.65 (0.049)	
				Nonlinear	0.015 (0.005)	0.77 (0.051)	0.66 (0.049)	0.5
				$2pq\hat{u}^2$	0.010 (0.004)	0.70 (0.043)	0.66 (0.047)	1.1
				20SNP_window	0.012 (0.005)	0.74 (0.050)	0.64 (0.050)	−2.5
	Cow	8,224	1.30	PBLUP	0.004 (0.001)	0.90 (0.011)	0.41 (0.008)	
				Standard ssGBLUP	0.010 (0.000)	0.89 (0.006)	0.72 (0.005)	
				Nonlinear	0.012 (0.000)	0.88 (0.006)	0.73 (0.005)	1.9
				$2pq\hat{u}^2$	0.008 (0.000)	0.79 (0.005)	0.76 (0.005)	5.3
				20SNP_window	0.011 (0.000)	0.87 (0.006)	0.74 (0.005)	3.1

[1] Forward validation: b_0 = intercept (bias), b_1 = regression coefficient (dispersion), R^2 = validation reliability.

[2] Average of effective record contribution (ERC) using full dataset for each candidate groups.

[3] Prediction of breeding values without genomic information (PBLUP) and with genomic information where equal SNP marker weights (standard ssGBLUP) or SNP marker-specific weights (Nonlinear, $2pq\hat{u}^2$, 20SNP_window) have been applied.

[4] Percent of gain in R^2 relative to standard ssGBLUP.

the differences in the population structure between these 2 breeds, resulting in differences in linkage disequilibrium. The JER breed is genetically more homogeneous and more inbred than the RDC breed. Higher heritability of CM in JER breed and additionally higher ERC for JER bull than RDC bull candidates could be the reasons for obtaining higher reliability in JER bulls. Previous studies (Meuwissen et al., 2001; Calus et al., 2008; Liu et al., 2015) showed that linkage disequilibrium has a direct significant effect on prediction reliability. Liu et al. (2015) found that when there is a high linkage disequilibrium between QTL and marker, there is higher stability in prediction accuracy over generations. Therefore, according to the results, it could be concluded that linkage disequilibrium is higher in JER cows than in RDC cows. On the other hand, Wientjes et al. (2013) expressed that the level of relationship with individuals in the reference population has a much higher impact on the prediction reliability than linkage disequilibrium per se. Accordingly, JER bull candidates might have on average higher relationship with their reference population, as they have on average a higher ERC in the full dataset.

All marker weighting scenarios, except for 20SNP_window in bulls, resulted an increase in reliabilities compared with the standard ssGBLUP ranging from 0.5% (for the Nonlinear weighting approach for JER bull candidates) to 12.7% (for the $2pq\hat{u}^2$ weighting approach for RDC bull candidates). Nonetheless, it should be noted that the validation reliability estimates had large standard errors, especially for the bulls. The amount of improvement in reliability by marker weighting differed by breed. Considering the reliability of ssGBLUP as the basis, the RDC breed gained relatively higher improvements than the JER breed.

Among the weighting scenarios, $2pq\hat{u}^2$ was the best and 20SNP_window was less prominent. However, the Nonlinear weights were only run for one round of analysis. In a simulation study for a relatively highly heritable trait, Zhang et al. (2016) showed that the Nonlinear weighting method is superior and yields higher prediction accuracy compared with the 20SNP_window method when the number of QTL affecting the trait is high (~500) and, by decreasing the number of influential QTL, the 20SNP_window method became more advantageous. Fragomeni et al. (2019) obtained about 3% lower reliability by applying quadratic SNP weights, which is inconsistent with our results. They did not include allele frequencies when calculating quadratic weights (i.e., $\hat{u}^2$). Moreover, they studied a different trait and, probably, with a different architecture. However, Lourenco et al. (2014) reported improvements in prediction reliability for fat and protein percentages in a small Israeli Holstein population by using quadratic weights. It can be expected that for CM, similar to milk yield traits, there are few QTL with large effects and many QTL with small effects (Cai et al., 2024). As inbreeding and consequently linkage disequilibrium are higher in JER than in RDC, SNP weights will undergo smaller changes over time in this breed and could therefore be used for a longer period before being updated.

In several studies, biological information has been used as priors to improve the prediction reliability of genomic prediction for different traits and species (Brøndum et al., 2015; Abdollahi-Arpanahi, 2017; Fang et al., 2017; Liu et al., 2020; Rezende et al., 2020; Farooq et al., 2021). However, there was no general consensus on the usefulness of employing biological information. Brøndum et al. (2015) obtained some improvement in prediction reliability, ranging from 0.5 percentage points for fertility to up to 5 percentage points for production traits in French Holsteins. Fang et al. (2017) reported that by using the best gene ontology, an average of 0.16 higher prediction accuracy was attained for production traits and CM. In another study, by including whole genome sequence information, Liu et al. (2020) reported significant improvement in prediction reliability for milk and protein production. However, negligible improvement was obtained for mastitis in their study. No improvement in the predictive ability of the models enriched with biological information was obtained by Abdollahi-Arpanahi et al. (2017) for sire conception rate in US Holstein cows. In contrast, using the same methodology, Rezende et al. (2020) obtained a 7% higher prediction accuracy for sire conception rate in US JER cows. Abdollahi-Arpanahi et al. (2017) stated that the predictive ability of functional classes of SNPs is not primarily influenced by their biological roles, but rather by considering the genomic relationship. By this definition, assigning weights to SNPs, such as constructing a trait-specific GRM, is better able to include the actual relationship between individuals for the trait of interest. In fact, this definition implies that the size of the relationship between 2 individuals is different for 2 different traits. For instance, considering that CM has different forms in terms of duration of disease as well as types of symptoms and can be caused by different species of bacteria, it can be expected that by allocating specific marker weights for a specific form, higher genetic improvement for that form of CM could be obtained.

The ranking of candidate bulls for combined_CM between different scenarios was compared. Spearman correlations between GEBV of candidate bulls estimated using $2pq\hat{u}^2$ and those of estimated using Nonlinear, 20SNP_window, and standard ssGBLUP were 0.94, 0.94, and 0.92, respectively. In addition, Spearman correlations between GEBV of the 20 best candidate bulls selected based on $2pq\hat{u}^2$ and their corresponding GEBV estimated using Nonlinear, 20SNP_window, and standard ssGBLUP were 0.83, 0.83, and 0.77, respectively.

Table 5. Results of forward validation (SE in parentheses) of bull and cow candidate groups for combined SCS breeding values based on pedigree-based or single-step genomic prediction with different SNP weights for Nordic Red (RDC) and Jersey (JER) dairy cattle

					Forward validation[1]			
Breed	Group	n	ERC[2]	Model[3]	b_0	b_1	R^2	% Gain[4]
RDC	Bull	125	15.28	PBLUP	0.45 (3.210)	0.89 (0.124)	0.28 (0.064)	
				Standard ssGBLUP	6.83 (2.622)	0.86 (0.062)	0.58 (0.069)	
				Nonlinear	7.34 (2.587)	0.83 (0.058)	0.59 (0.068)	2.6
				$2pq\hat{u}^2$	7.21 (2.433)	0.77 (0.049)	0.64 (0.060)	11.1
				20SNP_window	6.66 (2.555)	0.82 (0.062)	0.59 (0.068)	2.6
	Cow	18,112	1.10	PBLUP	1.94 (0.185)	1.01 (0.007)	0.50 (0.005)	
				Standard ssGBLUP	6.11 (0.155)	0.97 (0.004)	0.77 (0.003)	
				Nonlinear	6.84 (0.155)	0.94 (0.004)	0.78 (0.003)	0.5
				$2pq\hat{u}^2$	5.82 (0.156)	0.87 (0.003)	0.79 (0.003)	2.2
				20SNP_window	6.63 (0.154)	0.94 (0.004)	0.78 (0.003)	0.9
JER	Bull	119	65.94	PBLUP	−5.13 (5.164)	0.63 (0.143)	0.15 (0.061)	
				Standard ssGBLUP	8.17 (3.354)	0.81 (0.055)	0.61 (0.055)	
				Nonlinear	7.80 (3.284)	0.80 (0.052)	0.63 (0.052)	2.6
				$2pq\hat{u}^2$	4.06 (3.116)	0.70 (0.045)	0.65 (0.051)	5.5
				20SNP_window	7.55 (3.378)	0.80 (0.053)	0.64 (0.052)	4.1
	Cow	6,537	1.07	PBLUP	4.06 (0.500)	1.00 (0.014)	0.41 (0.009)	
				Standard ssGBLUP	8.43 (0.313)	0.97 (0.006)	0.79 (0.005)	
				Nonlinear	8.43 (0.314)	0.96 (0.006)	0.80 (0.004)	0.9
				$2pq\hat{u}^2$	5.71 (0.292)	0.87 (0.005)	0.81 (0.004)	2.8
				20SNP_window	7.66 (0.306)	0.95 (0.006)	0.80 (0.004)	1.3

[1] Forward validation: b_0 = intercept (bias), b_1 = regression coefficient (dispersion), R^2 = validation reliability.

[2] Average of effective record contribution (ERC) using full dataset for each candidate groups.

[3] Prediction of breeding values without genomic information (PBLUP) and with genomic information where equal SNP marker weights (standard ssGBLUP) or SNP marker-specific weights (Nonlinear, $2pq\hat{u}^2$, 20SNP_window) have been applied.

[4] Percent of gain in R^2 relative to standard ssGBLUP.

The corresponding correlations for the 100 best cows selected from the candidate cows were 0.59, 0.56, and 0.47, respectively.

Validation of SCS

Results of forward validation for bull and cow candidates of RDC and JER for combined_SCS are shown in Table 5. For combined_SCS, prediction biases were lowest for PBLUP, and among genomic scenarios, the $2pq\hat{u}^2$ weighting approach generally yielded lower biases. Biases for combined_SCS were higher than those for combined_CM, ranging from 0.45 for PBLUP in RDC bull candidates to 8.43 for the standard ssGBLUP approach in JER cow candidates. The SD of PEBV_f and GEBV_f for the RDC breed were 27.59 and 27.80, respectively. The corresponding values for the JER breed were 23.14 and 24.01, respectively. Dispersions followed the same pattern as for CM. Among the different scenarios, the standard ssGBLUP and the $2pq\hat{u}^2$ weighting approaches showed the lowest and highest dispersion, respectively.

Reliabilities of the standard ssGBLUP model for combined_SCS ranged from 0.58 to 0.79 depending on the breed and sex. The improvement in reliability by employing the standard ssGBLUP model was more pronounced for combined_SCS than for combined_CM, and the amount of gain was higher for bull than for cow candidates. On average, the reliability of genomic prediction was 5.6% higher for combined_SCS than for combined_CM, which indicates that reliability for combined_CM was close to that of combined_SCS, although the heritability of combined_CM was clearly lower. The decreased discrepancies between the reliabilities of these 2 composite traits could be attributed to the type of model, which was a multitrait model. Schaeffer (1984) and Thompson and Meyer (1986) showed that low heritable traits benefit more when analyzed with high heritable traits, and the amount of gain in reliability depends on the absolute value of the difference between the genetic and environmental correlations among the traits included in the model. Moreover, additional improvement in reliability would be obtained by establishing better connections in the data by using a multitrait model (Thompson and Meyer, 1986). In estimating genetic and environmental correlations between udder health traits in Finnish dairy cows, Pösö and Mäntysaari (1996) reported a large difference in the absolute value of genetic and environmental correlations between CM and SCS. Considerable differences between genetic and environmental correlations of udder type traits and CM have been observed in other studies (Rupp and Boichard, 1999; Amin et al., 2002).

Similarly, marker weighting was also beneficial and improved reliabilities of GEBV for combined_SCS, and the amount of gain (compared with the standard ssGB-

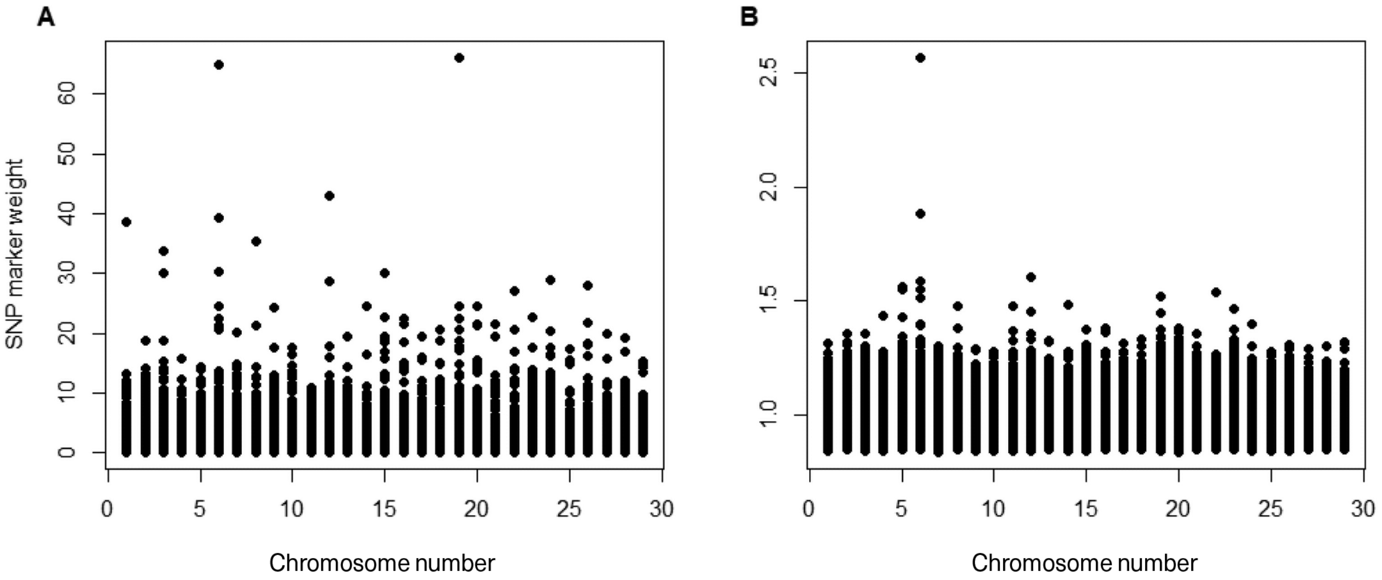

Figure 1. Distribution of SNP marker weights calculated by average of 12 eigenvalue traits for $2pq\hat{u}^2$ (A) and nonlinear (B) models in the Nordic Red dairy cattle breed.

LUP) was higher for bulls (ranging from 2.6% to 11.1%) than for cows (ranging from 0.5% to 2.8%). Obtained reliabilities of genomic predictions were higher for cows than bulls. This could be because the candidate bulls had much more information in the full dataset compared with the candidate cows, and therefore more deviation from GEBV using the reduced dataset and subsequently lower reliability can be expected. Also, dispersions were lower for cows. Similar results were found in previous studies (Kudinov et al., 2022; Zavadilova et al., 2022).

For combined_SCS, the $2pq\hat{u}^2$ weighting scenario also outperformed the other marker weighting methods, and there was a trivial difference between the reliabilities obtained by the Nonlinear and 20SNP_window methods. An average improvement obtained by all marker weighting scenarios over the standard ssGBLUP was about 2.8% for both traits, and an average increase in reliability obtained by all ssGBLUP scenarios over the PBLUP scenarios was 84% for combined_CM and 110% for combined_SCS.

SNP Marker Weights

In general, weighting markers by $2pq\hat{u}^2$ resulted largest increase in reliability and the estimates for $2pq\hat{u}^2$ had also a lower standard error compared with the other weighting scenarios. Figure 1 illustrates the distribution of the average of SNP weights for 12 eigenvalues calculated by 2 approaches ($2pq\hat{u}^2$ and Nonlinear) in the RDC breed. The differences in SNP weights using $2pq\hat{u}^2$ were significantly higher than those of Nonlinear. This indicates that the proportion of genetic variance that would be explained by different SNPs are different in these scenarios. The $2pq\hat{u}^2$ formulation accounts for the allele frequencies and by doing so gives more weight to markers with a high rate of heterozygosity and no weight to noninformative markers. Therefore, more weight is allocated to gene regions which potentially can be under selection. Solving the models with marker weighting increased the computational costs. However, the additional computing costs do not preclude the use of such models. The computing time required to solve the full models for the RDC was 31.7 h for standard ssGBLUP, 34.6 h for Nonlinear, 45.7 h for $2pq\hat{u}^2$, and 45.9 h for 20SNP_window.

Trends of CM and SCS

Summary statistics of the GEBV for genotyped RDC and JER individuals for combined_CM and combined_SCS, predicted by the standard ssGBLUP model, are shown in Table 6. It should be noted that a lower (or negative) GEBV is favorable for these traits. Compared with the average of their populations, genotyped RDC individuals had better ranking in their population relative to genotyped JER individuals. Genotyped JER bulls were even slightly inferior compared with the mean of their population. A similar pattern was observed for combined_SCS. One reason is most likely that genotyping was started earlier for JER than for RDC cows; another is that more JER individuals were genotyped in the early years.

Table 6. Mean, SD, minimum, and maximum of combined genomic estimated breeding values for clinical mastitis and log-transformed SCS for all genotyped Nordic Red dairy cattle (RDC) and Jersey (JER) bulls and cows

Trait[1]	Breed	Sex	n	Mean	SD	Minimum	Maximum
CM	RDC	Bull	1,830	0.000	0.037	−0.131	0.129
		Cow	123,959	−0.006	0.036	−0.167	0.196
	JER	Bull	900	0.004	0.045	−0.115	0.147
		Cow	63,877	0.000	0.044	−0.184	0.214
SCS	RDC	Bull	1,830	−7.735	38.430	−113.601	155.751
		Cow	123,959	−9.531	36.604	−164.312	159.639
	JER	Bull	900	3.707	32.126	−84.610	112.958
		Cow	63,877	−1.433	31.107	−139.761	143.647

[1] CM = clinical mastitis.

The trajectories of PEBV and GEBV for the combined_CM using both the full and reduced datasets for RDC and JER cows, respectively, are plotted to monitor the genetic and genomic trends, as well as their consistency with each other (Figures 2 and 3). The average PEBV and GEBV of cows born in 1990 were considered as the baselines, and all PEBV and GEBV were adjusted according to their baselines. The PEBV_f and GEBV_f of CM overlapped until 2010 and, henceforward, as expected due to genomic preselection, the trend in PEBV_f was less favorable than that of GEBV_f. The PEBV_r and GEBV_r in the most recent years were slightly overestimated (were inflated), as also indicated by the forward validation b_1 estimates. Both breeds have a relatively similar trend, starting with unfavorable increasing trends until 2002 (for RDC) and 2005 (for JER), when a favorable declining trend began. This is because of the inclusion of udder health traits into the breeding goals due to increased attention to health traits and societal demand to improve animal welfare.

CONCLUSIONS

We conducted this study to investigate the effect of different SNP marker weighting scenarios in a single-step SNPBLUP framework on the prediction reliability of CM and somatic cell score in the Nordic Red and Jersey dairy cattle. According to the obtained results, the implementation of single-step genomic evaluation immensely impacts the rate of genetic gain for udder health traits compared with genetic evaluations based on pedigree relationship information. All the applied marker weighting scenarios in this study outperformed the standard single-step genomic prediction approach. In particular, the classical method of marker weighting by $2pq\hat{u}^2$ was superior to the other studied approaches. In general, lower dispersion along with higher prediction reliability were obtained for cow candidates than for bull candidates, although the proportion of increase in reliability by applying marker weights was higher for bulls. The application of this method of marker weighting to

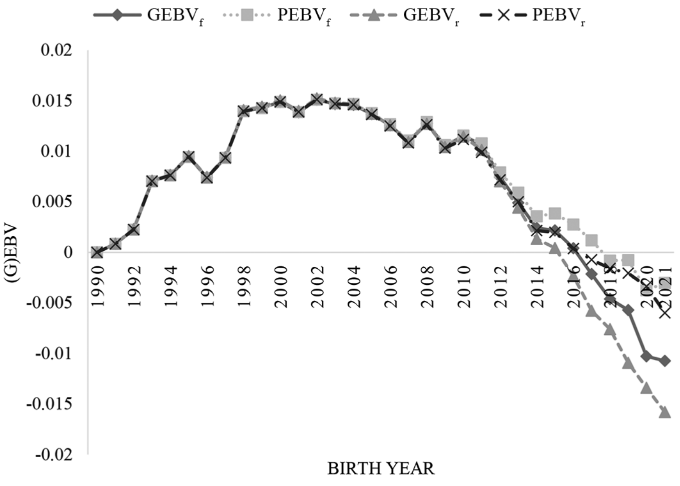

Figure 2. Trends of genomic (GEBV) and pedigree-based (PEBV) estimated breeding values for clinical mastitis using the full (f) and the reduced (r) datasets for Nordic Red dairy cattle (SD of averages of GEBV_f and PEBV_f across the years were 0.008 and 0.006, respectively).

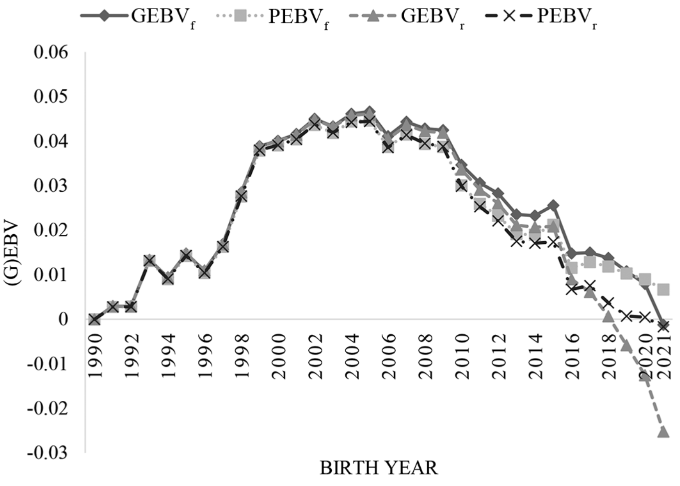

Figure 3. Trends of genomic (GEBV) and pedigree-based (PEBV) estimated breeding values for clinical mastitis using the full (f) and the reduced (r) datasets for Jersey cows (SD of averages of GEBV_f and PEBV_f across the years were 0.016 and 0.015, respectively).

other evaluated traits and populations deserves further research.

NOTES

This study has received funding from the European Union's Horizon 2020 research and innovation program under grant agreement no. 815668. The authors acknowledge Faba Co-op (Vantaa, Finland), Nordic Cattle Genetic Evaluation (NAV; Aarhus, Denmark), and VikingGenetics Ltd. (Randers, Denmark) for providing all data necessary for the analyses. No human or animal subjects were used, so this analysis did not require approval by an Institutional Animal Care and Use Committee or Institutional Review Board. The authors have not stated any conflicts of interest.

Nonstandard abbreviations used: 20SNP_window = 20 adjacent SNPs; CF = covariance function; CM = clinical mastitis; CM2 = CM trait for the second lactation from 15 d before calving to 150 DIM; CM3 = CM trait for the third lactation from 15 d before calving to 150 DIM; CM11 = CM trait for 15 d before calving until 50 DIM in the first lactation; CM12 = CM trait for 51 to 305 DIM in the first lactation; ERC = effective record contribution; $\mathrm{GEBV_f}$ = genomic estimated breeding values using the full dataset; $\mathrm{GEBV_r}$ = genomic estimated breeding values using the reduced dataset; GRM = genomic relationship matrix; JER = Jersey; NAV = Nordic Cattle Genetic Evaluation; PBLUP = pedigree-based BLUP; PEBV = pedigree-based estimated breeding value; $\mathrm{PEBV_f}$ = PEBV calculated based on full dataset; $\mathrm{PEBV_r}$ = PEBV calculated based on reduced dataset; RDC = Nordic Red; SCS 1, SCS2, and SCS3 = SCS observations in lactations 1, 2, and 3; ssGBLUP = single-step GBLUP; ssGTABLUP = single-step GBLUP with a T factoring; ssSNPBLUP = single-step single nucleotide polymorphism BLUP; UA = fore udder attachment; UD = udder depth.

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