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Genetic evaluation using single-step genomic best linear unbiased predictor in American Angus[1]

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ABSTRACT: Predictive ability of genomic EBV when using single-step genomic BLUP (ssGBLUP) in Angus cattle was investigated. Over 6 million records were available on birth weight (BiW) and weaning weight (WW), almost 3.4 million on postweaning gain (PWG), and over 1.3 million on calving ease (CE). Genomic information was available on, at most, 51,883 animals, which included high and low EBV accuracy animals. Traditional EBV was computed by BLUP and genomic EBV by ssGBLUP and indirect prediction based on SNP effects was derived from ssGBLUP; SNP effects were calculated based on the following reference populations: ref_2k (contains top bulls and top cows that had an EBV accuracy for BiW ≥0.85), ref_8k (contains all parents that were genotyped), and ref_33k (contains all genotyped animals born up to 2012). Indirect prediction was obtained as direct genomic value (DGV) or as an index of DGV and parent average (PA). Additionally, runs with ssGBLUP used the inverse of the genomic relationship matrix calculated by an algorithm for proven and young animals (APY) that uses recursions on a small subset of reference animals. An extra reference subset included 3,872 genotyped parents of genotyped animals (ref_4k). Cross-validation was used to assess predictive ability on a validation population of 18,721 animals born in 2013. Computations for growth traits used multiple-trait linear model and, for CE, a bivariate CE–BiW threshold-linear model. With BLUP, predictivities were 0.29, 0.34, 0.23, and 0.12 for BiW, WW, PWG, and CE, respectively. With ssGBLUP and ref_2k, predictivities were 0.34, 0.35, 0.27, and 0.13 for BiW, WW, PWG, and CE, respectively, and with ssGBLUP and ref_33k, predictivities were 0.39, 0.38, 0.29, and 0.13 for BiW, WW, PWG, and CE, respectively. Low predictivity for CE was due to low incidence rate of difficult calving. Indirect predictions with ref_33k were as accurate as with full ssGBLUP. Using the APY and recursions on ref_4k gave 88% gains of full ssGBLUP and using the APY and recursions on ref_8k gave 97% gains of full ssGBLUP. Genomic evaluation in beef cattle with ssGBLUP is feasible while keeping the models (maternal, multiple trait, and threshold) already used in regular BLUP. Gains in predictivity are dependent on the composition of the reference population. Indirect predictions via SNP effects derived from ssGBLUP allow for accurate genomic predictions on young animals, with no advantage of including PA in the index if the reference population is large. With the APY conditioning on about 10,000 reference animals, ssGBLUP is potentially applicable to a large number of genotyped animals without compromising predictive ability.

Key words: beef cattle, genomic recursion, genomic selection, indirect prediction

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INTRODUCTION

Genomic selection in beef cattle has currently been performed with multistep methods, which uses deregressed EBV to estimate SNP effects and then direct genomic value (**DGV**) for selection candidates

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based on their genotypes (Meuwissen et al., 2001; Garrick et al., 2009). The main advantage of this approach is that the traditional BLUP evaluation is kept unchanged and genomic selection can be performed by a separate entity owning genotypes but not phenotypes. Also, new animals are easily evaluated if DGV is computed as a sum of marker effects, but not if selection indexes including DGV and parent average (**PA**) are used.

When both phenotypes and genotypes are available jointly, single-step genomic BLUP (**ssGBLUP**; Aguilar et al., 2010) is a simple alternative. This method does not rely on deregressed proofs and properly weighs information from genotyped sires and cows, thus avoiding double counting of contributions due to relationships and records, and accounts for preselection bias of genomically selected parents without phenotypes (Legarra et al., 2014). In ssGBLUP, it is also possible to quickly evaluate young genotyped animals without running a complete evaluation that requires several hours to converge. Quick predictions can be calculated indirectly, where genomic predictions for young animals are obtained from SNP effects. It was shown by Wang et al. (2012) that SNP effects can be derived from genomic estimated breeding value (**GEBV**) solutions from the main ssGBLUP evaluation.

In its current implementation, ssGBLUP uses direct inversion of genomic matrices (Aguilar et al., 2011), which has a cubic cost and a limit of 150,000 animals (Aguilar et al., 2013). Several methods were proposed to overcome that limit (Legarra and Ducrocq, 2012; Fernando et al., 2014; Liu et al., 2014), but none was successful. Recently, Misztal et al. (2014a) presented a method that uses an approximate inversion of genomic relationships based on recursions on a fraction of the total population, which can be suitable and inexpensive. The first goal of this study was to evaluate the feasibility of ssGBLUP for genomic evaluation in Angus cattle with reference populations of different composition. An additional goal was to evaluate the ability to predictive GEBV with genomic recursions and with indirect prediction for young animals.

MATERIAL AND METHODS

Data sets from American Angus Association (**AAA**) were available for this study that included growth traits and calving ease (**CE**). Growth traits included birth weight (**BiW**), weaning weight (**WW**), and postweaning gain (**PWG**). As the data were obtained from existing databases, Animal Care and Use Committee approval was not obtained for this study.

Data

Over 6 million phenotypes were available for BiW and WW, almost 3.4 million for PWG, and over 1.3 million for CE. Whereas BiW, WW, and PWG are continuous traits, CE is a categorical trait with 5 calving scores, where 5 is abnormal delivery and is excluded. Because few animals had scores 3 and 4, these scores were combined into category 2, which resulted in 93% of animals with score 1 and 7% with score 2. The number of animals in the pedigree for evaluation of growth traits was 8,236,425 and for CE was 8,025,676.

For evaluation of growth traits, 81,878 animals were genotyped for 54,609 SNP from the BovineSNP50k v2 BeadChip (Illumina Inc., San Diego, CA). Currently, no genotyping strategy is applied by AAA; therefore, the members can choose which animals are being genotyped, and most of them are young. A total of 29,995 genotyped animals were young without phenotypes for any of the 3 traits, which caused their genotypes to be excluded from this study. If the number of genotyped animals is relatively large, young genotyped animals without phenotypes in the data set give very small contribution to their relatives' evaluation (Misztal et al., 2014a). After removing SNP with unknown position or located on sex chromosomes and running a general quality control analysis, genotypes on 38,528 SNP markers were available for 32,465 males and 19,418 females born from 1977 to 2013; therefore, the maximum number of genotyped animals used in all analyses on growth traits was 51,883. For CE evaluation, a genotyping set with 72,069 animals was available, but only genotypes on 40,546 animals born from 1977 to 2013 (26,074 males and 14,472 females) were used for the same reason above. The number of SNP that passed the general quality control for this data set was 38,568.

For this study, the animals were then split into training and validation populations according to year of birth. Therefore, all 18,721 (13,166) genotyped animals born in 2013 were chosen to be in the validation population for growth (CE) traits and had their phenotypes removed from the evaluations. The pedigree relationship between training and validation populations ranged from 0 to 0.82, with an average relationship of 0.09.

Model

Traditional and genomic evaluations were performed for growth traits and CE. A multivariate linear animal model was used for growth traits as

$$\mathbf{y}_t = \mathbf{Xb} + \mathbf{Z_1u} + \mathbf{Z_2m} + \mathbf{Z_3p} + \mathbf{e}, \quad [1]$$

in which *t* is for each one of BiW, WW, and PWG; **y**, **b**, **u**, **m**, **p**, and **e** are vectors of phenotypes, fixed effect of contemporary group, additive direct genetic effect, additive maternal genetic effect, maternal permanent environmental effect, and random residuals, respectively; and **X**, $\mathbf{Z_1}$, $\mathbf{Z_2}$, and $\mathbf{Z_3}$ are incidence matrices for **b**, **u**, **m**, and **p**, respectively. All random effects were present for WW but only **u**, **m**, and **e** for BiW and **u** and **e** for PWG.

A bivariate threshold-linear animal model was used to model CE jointly with BiW:

$$\mathbf{y}_c = \mathbf{Xb} + \mathbf{Z_1u} + \mathbf{Z_2m} + \mathbf{e}, \quad [2]$$

in which *c* is for BiW and CE; **y**, **b**, **u**, **m** and **e** are vectors of phenotypes, fixed effects of contemporary group, sex, age of dam (only for CE), and sex × age of dam interaction (only for CE), additive direct genetic effect, additive maternal genetic effect, and random residuals, respectively; and **X**, $\mathbf{Z_1}$, and $\mathbf{Z_2}$ are incidence matrices for **b**, **u**, and **m**, respectively. According to Ramirez-Valverde et al. (2001), when BiW is available, bivariate threshold-linear models including CE and BiW are a better alternative than a single-trait threshold model to evaluate CE, especially if the population has animals with different levels of EBV accuracy. From this model, only results for CE are discussed, whereas results for BiW are from the multiple trait linear model for growth traits. Heritabilities for all traits were calculated by AAA using model [1] for BiW, WW, and PWG, and model [2] for CE. For our study, the values were then provided by AAA and ranged from 0.12 to 0.41 (Table 1).

Analyses

Three different genomic analyses were performed using ssGBLUP (Aguilar et al., 2010; Christensen and Lund, 2010) as implemented in the BLUP90IOD program (Misztal et al., 2014b). Compared to BLUP, in ssGBLUP, the inverse of the numerator relationship matrix $\mathbf{A^{-1}}$ is replaced by matrix $\mathbf{H^{-1}}$ defined as follows:

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1} \end{bmatrix},$$

in which **G** is the genomic relationship matrix. The computations used default options in BLUP90IOD. In all analyses, the validation population was defined as genotyped animals born in 2013 with phenotypes excluded.

Table 1. Heritability (h^2) and general statistics for growth traits and calving ease (CE)

Trait[1]	h^2	Number of records	Average, kg	SD, kg	Number of genotyped animals with records
BiW	0.41	6,189,661	36.47	4.45	50,784
WW	0.20	6,890,625	263.13	44.63	51,830
PWG	0.20	3,387,252	162.25	67.00	36,196
CE	0.12	1,310,684	–	–	10,558
Easy	–	1,215,571	–	–	10,228
Difficult	–	95,113	–	–	330

[1]BiW = birth weight; WW = weaning weight; PWG = postweaning gain.

First Analysis: Single-Step Genomic BLUP with Different Reference Populations. Different reference populations were defined according to EBV accuracy calculated with the ACCF90 program (Misztal et al., 2014b), which uses the concept of prediction error variance and reflects the SE of EBV for each individual. The objective was to investigate the influence of different groups of reference animals on genomic predictions and possibly to guide genotyping strategy. The current trend in livestock genomics is to genotype young animals; however, more important animals give more information to the evaluations. For growth traits and CE, the first reference population was composed of 1,628 and 1,541 top bulls, respectively, with EBV accuracy for BiW ≥0.85, which we will refer hereinafter as "**ref_bulls**." As BiW was present in models for growth and CE evaluations, using its EBV accuracy for selecting top bulls helped to compose sets with a proportional number of animals. In this case, the **G** matrix was composed of animals in the reference population and also animals in the validation population; the last had 18,721 animals for growth traits and 13,166 for CE. The second reference population was composed of the top bulls and also top cows that had an EBV accuracy for BiW ≥0.85, which we will refer as **ref_2k**. The number of top cows was small and only 268 were added for the growth trait analysis and 323 for CE. The third reference population was composed of all genotyped animals born up to 2012 (which we will refer as **ref_33k**). This group had a total of 33,162 animals for growth and 27,380 for CE, with an average EBV accuracy for BiW of 0.77 (±0.05). For the latter analysis, the **G** matrix was composed of the maximum number of 51,883 genotyped animals for growth analysis and 40,546 for analysis of CE.

Second Analysis: Single-Step Genomic BLUP with Indirect Predictions for Young Animals. With the increasing number of genotyped heifers and steers in dairy and beef, the genomic methods should be able to provide predictions for young animals without phenotypes in a quick run, externally to the official evaluations. This concept is introduced here as indi-

rect ssGBLUP and basically mimics the mixed model equations. It would be advantageous from different perspectives: to evaluate young animals mainly for traits that are measured later in life, after the selection decisions are made, and to reduce computing costs because the dimension of **G** would not increase in the same proportion as the number of genotyped animals.

To explain how it works, consider the equation for the GEBV of a single individual in ssGBLUP (VanRaden and Wiggans, 1991; Aguilar et al., 2010):

$$\text{GEBV} = w_1\text{PA} + w_2\text{YD} + w_3\text{PC} + w_4\text{DGV} - w_5\text{PP},$$

in which PA is parent average, **YD** is yield deviation (phenotypes adjusted for model effects other than additive genetic and error), **PC** is progeny contribution, DGV is direct genomic value (corresponding to $\mathbf{G}^{-1}$), **PP** is the pedigree prediction based on the subset of genotyped animals from **A** (corresponding to A_{22}^{-1}), and w_1 to w_5 are weights that add up to 1. In the case of young animals with no progeny or own performance record, YD = PC = 0 and $w_2 = w_3 = 0$. In this case, for individual *i*,

$$\text{PA}_i = (\text{GEBV}_s + \text{GEBV}_d)/2;$$

$$\text{DGV}_i = -\left(\sum_{j,j\neq i} g^{ij}\text{GEBV}^j / g^{ii}\right);$$

$$\text{PP} = -\left(\sum_{j,j\neq i} a_{22}^{ij}\text{GEBV}^j / a_{22}^{ii}\right); \text{ and}$$

$w_1 = 2/\text{den}$, $w_4 = g^{ii}/\text{den}$, and $w5 = a_{22}^{ii}/\text{den}$, in which den is the denominator that equals $2+\left(g^{ii} - a_{22}^{ii}\right)$; g^{ij} (a_{22}^{ij}) is an element of $\mathbf{G}^{-1}$ ($\mathbf{A}_{22}^{-1}$) corresponding to relationships between animal *i* and *j*; and *s* and *d* correspond to sire and dam, respectively. If all individuals are genotyped, then PA = PP and GEBV is reduced to DGV.

For ssGBLUP with indirect predictions, SNP effects can be calculated using the current run of ssGBLUP with all but young animals, and genomic predictions for young animals are obtained by multiplying the SNP content by SNP effect to obtain DGV; a more complete GEBV can also be available through a selection index that combines DGV and PA. The flow for indirect predictions in ssGBLUP is

1) Run ssGBLUP with a reference population to obtain GEBV. In this step, 3 reference populations were tested:
   a) ref_2k: reference population with top bulls and top cows that had an EBV accuracy for BiW ≥0.85 (*n* = 1,896);
   b) **ref_8k**: reference population with all parents that were genotyped (*n* = 8,285); this includes ref_2k; and
   c) ref_33k: reference population with all genotyped animals born up to 2012 (*n* = 33,162); this includes ref_8k.
2) Split GEBV into all the components shown before, in which DGV for an animal *i* in the reference population is calculated as below (Aguilar et al., 2010):

$$\text{DGV}_i = -\left(\sum_{j,j\neq i} g^{ij}\text{GEBV}^j / g^{ii}\right),$$

   with all elements previously defined.
3) Calculate SNP effects using DGV from the reference population:

$$\hat{\mathbf{u}} = \mathbf{D}\mathbf{Z}'\mathbf{G}^{-1}\left(\mathbf{DGV}\right),$$

   in which $\hat{\mathbf{u}}$ is a vector of estimated SNP effects, **D** is a diagonal matrix of weights (standardized variances) for SNP (identity matrix in this case), and **Z** is a matrix of centered genotypes for each animal (VanRaden, 2008). A similar approach that uses GEBV instead of DGV to calculate SNP effects was proposed by Wang et al. (2012). However, for numerical purposes this involves approximations as **G** matrix is formed as $\mathbf{G} = 0.95\mathbf{ZDZ}' + 0.05\mathbf{A}_{22}$ (Aguilar et al., 2010). This is done as a default approach to avoid singularity problems and may result in negligible error as shown later.
4) Calculate DGV for young genotyped animals ($\mathbf{DGV}_y$):

$$\mathbf{DGV}_y = \mathbf{Z}_y\hat{\mathbf{u}}$$

   in which $\mathbf{DGV}_y$ and $\mathbf{Z}_y$ are direct genomic values and a matrix of centered genotypes for young animals not included in ssGBLUP evaluation, respectively.
5) Combine DGV_y with PA for young genotyped animals:

$$\text{GEBV}_y \approx w_1\text{PA} + w_4\text{DGV}_y,$$

   in which $\mathbf{GEBV}_y$ is the GEBV obtained via indirect predictions for young animals and w_1 and w_4 are weights identical for all animals and calculated based on covariances between DGV_y and PA as

$$\begin{bmatrix} w_1 \\ w_4 \end{bmatrix} = \begin{bmatrix} \sigma^2_{\text{PA}} & \sigma_{\text{PA,DGV}_y} \\ \sigma_{\text{DGV}_y\text{,PA}} & \sigma^2_{\text{DGV}_y} \end{bmatrix} \begin{bmatrix} \sigma^2_{\text{PA}} \\ \sigma^2_{\text{DGV}_y} \end{bmatrix}$$

Note that this is an approximation that ignores PP. In general, PP includes part of PA explained by DGV. When all animals are genotyped, PP and PA cancel out, with approximate cancellation when parents of an animal are genotyped. When an animal is unrelated to a genotyped population, PP = 0. Fixed weights in the index account for an average relationship of all young animals to a genotyped population. It is possible to create different indices based on the number of genotyped parents (VanRaden et al., 2012).

The ssGBLUP with indirect prediction allows calculation of DGV or GEBV for young genotyped animals, with lower computing cost compared to a full ssGBLUP where young animals are explicitly included.

Third Analysis: Single-Step Genomic BLUP with G Inverted by a Recursive Algorithm. When the number of genotyped animals is large and there is a desire for using all of them in ssGBLUP evaluations to get direct predictions for all, including young animals, an algorithm that splits genotypes into proven and young animals and uses recursion to approximate the inverse of the **G** matrix was proposed by Misztal et al. (2014a). This algorithm for proven and young animals is known as the **APY**, and $\mathbf{G}^{-1}$ containing all genotyped animals can be expressed as

$$\mathbf{G}^{-1} = \begin{bmatrix} \mathbf{G}_{pp}^{-1} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \end{bmatrix} + \begin{bmatrix} -\mathbf{G}_{pp}^{-1}\mathbf{G}_{py} \\ \mathbf{I} \end{bmatrix} \mathbf{M}_{g}^{-1} \begin{bmatrix} -\mathbf{G}_{yp}\mathbf{G}_{pp}^{-1} & \mathbf{I} \end{bmatrix},$$

in which the subscript pp stands for proven animals and py stands for the covariance between proven and young animals; each element of $\mathbf{M_g}$ is obtained (for the *i*th young animal) as $m_{g,i} = g_{ii} - \mathbf{G}_{ip}\mathbf{G}_{pp}^{-1}\mathbf{G}_{pi}$ and is called genomic Mendelian sampling. In the APY, the only direct inversion needed is for part of **G** that contains relationships among proven animals ($\mathbf{G}_{pp}$), whereas all other coefficients are obtained through recursions.

For this analysis, 4 definitions of proven animals were tested that included the 3 definitions used for indirect predictions (ref_2k, ref_8k, and ref_33k) plus an extra reference subset that included 3,872 genotyped parents of genotyped animals (**ref_4k**). This last group was added to test if proven animals would have strong links with the young genotyped population.

The greatest advantages of this algorithm are the reduction of computing cost, which is still cubic for proven animals but can be linear for young animals, and the possibility of using large numbers of genotyped animals in ssGBLUP evaluations. The secondary advantage is numerical stability, as the regular **G** matrix is singular when the number of animals is greater than the number of SNP markers and cannot be inverted without blending with $\mathbf{A}_{22}$.

Validation

The ability to predict future phenotypes was the validation method chosen for this study. This method is based on Legarra et al. (2008), and predictive ability for traditional and genomic evaluations for animals born in 2013 was calculated as the correlation between EBV or GEBV and phenotypes corrected for fixed effects (**y** – **Xb**):

$$r = \text{cor}[(\text{G})\text{EBV}, \mathbf{y} - \mathbf{Xb}].$$

The predictive ability or predictivity is used as an approach to compare the methods applied in this paper. For all analyses, the validation groups were kept the same to make comparisons easier. Validations involved 18,721 animals for growth traits and 16,133 animals for CE. Predictivity calculated with EBV in the above formula was the benchmark used to compare the gain in predictive ability due to genomics, and predictivity calculated with GEBV was used to compare the genomic methods previously described. Prediction accuracy could be described as r/h, in which h is square root of heritability; however, prediction accuracy can be overestimated if heritabilities are obtained by simplified models as the ones used by AAA.

RESULTS AND DISCUSSION

Single-Step Genomic BLUP with Different Reference Populations

Predictive ability on young animal when using several reference populations is shown in Table 2. Using only top bulls as a reference population (ref_bulls) increased predictivity relative to BLUP by 0.05 for BiW, 0.01 for WW, 0.04 for PWG, and 0.01 for CE. Addition of top cows to the reference population (ref_2k) did not increase the predictivity for any trait. This could be due to the small number of animals added and also because daughters of those cows already contributed through the inclusion of bulls. Addition of around 31,000 animals to the reference population provided an additional increase in predictivity of 0.05 for BiW, of 0.03 for WW, and of 0.02 for PWG. However, no additional increase was observed for CE by adding extra 27,000 genotyped animals, of which about 7,000 had phenotypes for that trait.

The addition of 31,000 animals with few or no progeny led to the same increase of predictivity as using only the top bulls for BiW, led to an increase

Table 2. Predictive ability of future phenotypes for young genotyped animals born in 2013

Trait[1]	Animals in validation	BLUP	ssGBLUP[2]		
			ref_bulls	ref_2k	ref_33k
BiW	18,721	0.29	0.34	0.34	0.39
WW	18,721	0.34	0.35	0.35	0.38
PWG	18,721	0.23	0.27	0.27	0.29
CE	13,166	0.12	0.13	0.13	0.13

[1]BiW = birth weight; WW = weaning weight; PWG = postweaning gain; CE = calving ease.

[2]Single-step genomic BLUP (ssGBLUP) included genotypes for reference and validation populations, but phenotypes for validation animals were removed. Predictive ability was calculated as correlation between corrected phenotypes and genomic EBV. ref_bulls is a reference population with top bulls that had EBV accuracy for BiW ≥0.85; ref_2k contains top bulls and top cows that had an EBV accuracy for BiW ≥0.85; ref_33k contains all genotyped animals born up to 2012.

of 3 times for WW and an increase of 0.5 times for PWG. Among the 31,000 extra animals, almost all had phenotypes for BiW and WW but only 24,000 had phenotypes for PWG. Evidently, the composition of reference population is also a factor that influences predictivity of GEBV besides the reference population size. Therefore, genotyping strategy should take into account genotyping more important and maybe older animals with more information (higher EBV accuracy) along with genotyping large amounts of young animals.

Previous studies showed that prediction accuracies or predictive ability are biased downward by selection (Bijma, 2012). In our study, it appears that selection for proven bulls was much stronger for WW than for PWG (lower increase in predictivity with twice the phenotypic data at similar heritability) but there was a small selection on genotyped animals with own records (approximately twice the increase of predictivity with twice the phenotypic data). It may be hard to calculate the amount of bias in livestock species, including beef cattle, as the selection process is sequential and affected by both genetic correlations and specific indexes used for selection.

Low predictivity for CE in this study is due to lower heritability combined with limited recording for this trait and a low incidence of difficult calving. Additionally, very few genotyped animals had a difficult calving, perhaps because animals from a difficult calving are unlikely to be retained for breeding and, therefore, would not be genotyped on a regular basis. Higher predictivity and impact of genomic selection for CE could be expected in breeds with higher incidence of calving problems.

Because the increase in predictivity for CE was very small compared to predictivity of traditional evaluations, indirect predictions and the APY were not tested for this trait.

In this paper, only predictivity for the direct genetic effect is shown; however, models for BiW and WW included maternal effect, which is also important in genetic evaluations. We unsuccessfully attempted to derive formulas for predictivity of maternal effects. Such predictivity can be hard to assess because the maternal effect occurs 1 generation back, which means that the corrected phenotype of animal *i* should be correlated with the maternal effect of the dam of animal *i*. But dams usually have more than 1 progeny and there is genetic correlation between direct and maternal for BiW, which makes derivations difficult. Lourenco et al. (2013) used simulated data that mimicked a beef cattle population and showed that the gain for the maternal effect with ssGBLUP is as high as for the direct effect.

Single-Step Genomic BLUP with Indirect Predictions for Young Animals

Predictive ability for indirect prediction via conversion of DGV into SNP effects is shown in Fig. 1. When the reference population included top bulls and top cows (ref_2k), the predictivity of indirect DGV_y was lower than predictivity for traditional EBV for the 3 traits (0.23 vs. 0.29 for BiW, 0.28 vs. 0.34 for WW, and 0.19 vs. 0.23 for PWG). Predictivity for $GEBV_y$ calculated as an index of indirect DGV_y with PA was higher than those for EBV for the 3 traits (0.31 vs. 0.29 for BiW, 0.36 vs. 0.34 for WW, and 0.24 vs. 0.23 for PWG); however, this predictivity was lower than the ones from full ssGBLUP (except for WW). With larger reference population (ref_8k), all indirect DGV_y were similar to or more accurate than EBV and the index had predictivity similar to the full ssGBLUP. With the largest reference population (ref_33k), all indirect DGV_y were almost as accurate as GEBV from full ssGBLUP, with the index marginally improving predictivity for WW. This marginal improvement for WW may be caused by the use of less than optimal genetic parameters, for example, zero covariance between direct and maternal effects (to reduce computing costs). The DGV_y obtained with ref_33k reference population were more accurate than GEBV from full ssGBLUP obtained with ref_8k reference population.

Although predictivity of indirect predictions when using ref_33k was similar to predictivity from full ssGBLUP, it does not mean that predictions have the same average. The reason for that is the different sources of information used to calculate indirect predictions. Correlations between GEBV and indirect predictions are a good tool to assure that the latter can be used for interim evaluations. Correlations between

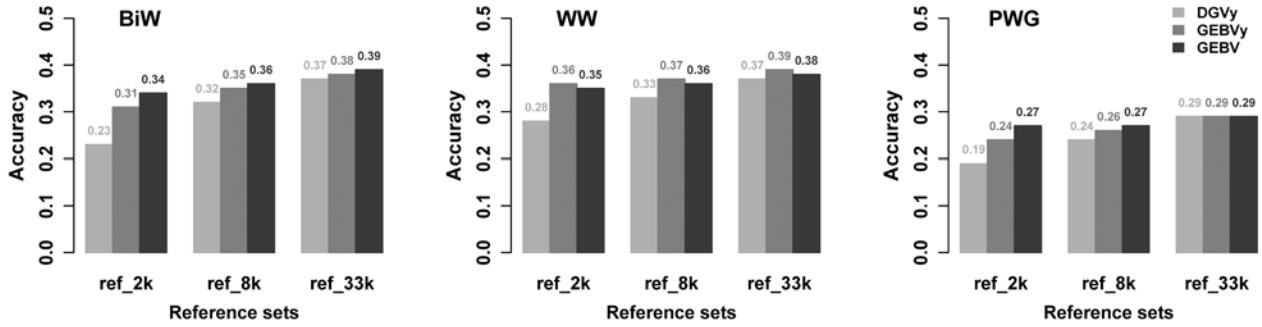

Figure 1. Predictive ability of indirect predictions on 18,721 young genotyped animals when using reference populations ref_2k (contains top bulls and top cows that had an EBV accuracy for BiW ≥0.85), ref_8k (contains all parents that were genotyped) ref_33k (contains all genotyped animals born up to 2012) animals to run single-step genomic BLUP (ssGBLUP) and derivate SNP effects. BiW = birth weight; WW = weaning weight; PWG = postweaning gain; DGV_y = direct genomic value for young genotyped animals; $GEBV_y$ = is genomic estimated breeding value obtained via indirect predictions for young animals and DGV_y. GEBV (genomic estimated breeding value, obtained directly from ssGBLUP when genotypes on reference and validation animals were considered together in evaluations are genomic predictions obtained directly from ssGBLUP when genotypes on reference and validation animals were considered together in evaluations. Predictive ability was calculated as correlation between corrected phenotypes and genomic EBV.

GEBV from full ssGBLUP and DGV_y or $GEBV_y$ from indirect predictions are shown in Table 3. On average, correlations with DGV_y were 0.73, 0.89, and 0.96 for ref_2k, ref_8k, and ref_33k, respectively. Higher correlations were observed between GEBV and $GEBV_y$, with values for the 3 reference sets being 0.89, 0.95, and 0.97, respectively. Those results endorse the use of a reference population of size close to 33,000 animals for this American Angus data set. By doing that, indirect predictions are as accurate as predictions including genotypes for young animals in the evaluation (full ssGBLUP).

For young animals, GEBV = w_1PA + w_4DGV – w_5PP, with all weights adding up to 1.0 (VanRaden and Wiggans, 1991; VanRaden et al., 2009; Aguilar et al., 2010). When the number of genotyped animals is small, w_4 is small and ignoring PA reduces predictivity. Using an index with PA improves the predictivity; however, PP is ignored and computed weights w_1 and w_4 are approximate. When the number of genotyped animals is large, w_4 is close to 1.0 and ignoring PA marginally reduces the predictivity for some traits. Therefore, the indirect prediction via DGV is accurate when SNP effects are derived from ssGBLUP with sufficient size of the reference population.

Neglecting PP seems to have no considerable effect in this population, because predictivity of indirect predictions was very similar to predictivity from full ssGBLUP. Neglection of PP indirectly means adjusting PA for an average PP. VanRaden et al. (2012) used different weights for animals based on the number of genotyped parents, which better accounts for PP.

A study by Wiggans et al. (2015) used SNP effects from previous monthly genomic multistep evaluations to calculate preliminary GEBV for young genotyped animals. The objective was to have daily or weekly genomic evaluations for U.S. dairy cattle and reduce the time between having DNA samples and predictions from a monthly official evaluation. Their reference set contained all genotyped animals with phenotypes (about 597,000; corresponding to ref_33k in our study) and correlations between preliminary and official evaluations were higher than 0.99 for Holsteins but smaller for other breeds with a smaller number of genotyped animals. Further research with different species will be critical in determining the sufficient size of the reference population for indirect predictions to achieve high predictivity. It may be related to effective population size, number of independent SNP (Pintus et al., 2013), and relationships between reference and validation populations as in multistep methods. Although indirect predictions via ssGBLUP use a concept similar to multistep methods for young genotyped animals, indirect predictions via ssGBLUP may be more accurate than multistep predictions because the latter are affected by approximations involved in deregressions and possible double counting of phenotypic information.

For young animals, indirect predictions via SNP effects from ssGBLUP seems a viable alternative as it can be done separately from the full evaluation. As SNP effects are calculated based on trait GEBV or DGV, indirect predictions are easily obtained for multitrait models, as done in this study; multibreed and crossbred evaluations are possible when the **G** matrix is able to account for information on all breeds. However, if young animals and particularly full-sibs are intensively selected, selection on the Mendelian sampling will not be accounted for, leading to preselection bias (Patry and Ducrocq, 2011). Analyses by ssGBLUP with all genotypes subject to selection are expected to account for preselection (VanRaden and Wright, 2013), because selection is accounted for

Table 3. Correlations between genomic estimated breeding value from full single-step genomic BLUP and direct genomic value for young genotyped animals (DGV_y) or the genomic estimated breeding value obtained via indirect predictions for young animals ($GEBV_y$) from indirect predictions.

Trait[1]	Indirect prediction	ref_2k[2]	ref_8k[2]	ref_33k[2]
BiW	DGV_y	0.66	0.87	0.96
	$GEBV_y$	0.85	0.94	0.97
WW	DGV_y	0.75	0.89	0.95
	$GEBV_y$	0.90	0.95	0.97
PWG	DGV_y	0.78	0.90	0.96
	$GEBV_y$	0.91	0.96	0.97

[1]BiW = birth weight; WW = weaning weight; PWG = postweaning gain.

[2]ref_2k (contains top bulls and top cows that had an EBV accuracy for BiW ≥0.85), ref_8k (contains all parents that were genotyped) ref_33k (contains all genotyped animals born up to 2012).

when all information used for selection is included in the model (Henderson, 1975).

Comments on SNP Weighting and SNP Selection

The way SNP effects are calculated in ssGBLUP allows for inclusion of different weights for SNP: $\hat{\mathbf{u}} = \mathbf{D}\mathbf{Z}'\mathbf{G}^{-1}(\mathbf{DGV})$, with weights for **G** fit into the diagonal matrix **D**. Those weights can be calculated through an iterative process, or external weights can be used as input for ssGBLUP (Wang et al., 2012; Su et al., 2014). Weighting **G** seems to be a reasonable approach to achieve higher prediction accuracy, especially in the presence of "major" SNP. Sun et al. (2011) showed higher prediction accuracy when using weighted **G** in regular GBLUP compared to BayesB. For some traits, SNP weighting or SNP selection in ssGBLUP also gave additional prediction accuracy (Wang et al., 2014). In fact, when weights are different per trait, this precludes the use of multiple traits unless the model includes 1 common additive effect and specific additive effects for individual traits. In practice and especially under a selection index, gains from a multiple-trait analysis can overcome losses due to not fitting "major" SNP. Also, when the number of genotyped animals increases, the rate of gain in reliability increases at a slower pace (VanRaden et al., 2011); therefore, weighting SNP may no longer have a big impact on prediction accuracy (Winkelman et al., 2015).

Single-Step Genomic BLUP with G Inverted by a Recursive Algorithm

Predictive ability of GEBV when the inverse of **G** was computed with the APY is shown in Fig. 2. When the recursions were conditioned on ref_2k, ref_4k, ref_8k, and ref_33k, the procedure accounted for 67, 88, 97, and 100%, respectively, of predictivity gains of ssGBLUP over BLUP. Therefore, in ssGBLUP, using genomic recursion to invert **G** while conditioning on enough number of animals, in this case about 8,000, has the same prediction power as **G** using direct inversion. The amount of memory necessary for the APY $\mathbf{G}^{-1}$ using ref_2k, ref_4k, ref_8k, and ref_33k was approximately 0.8, 1.6, 3.2, and 13.7 GB, respectively, whereas the amount of memory for the regular $\mathbf{G}^{-1}$ is 21.6 GB. Therefore, using the APY $\mathbf{G}^{-1}$ makes computations less costly and faster.

Tests involving 100,000 genotyped Holsteins with recursions conditioned on more than 15,000 animals resulted in practically identical GEBV compared to the regular inversion but with a better convergence rate (Fragomeni et al., 2015), indicating that the APY has good predictive and numerical properties. Those authors suggested that the necessary number of animals being conditioned is proportional to the number

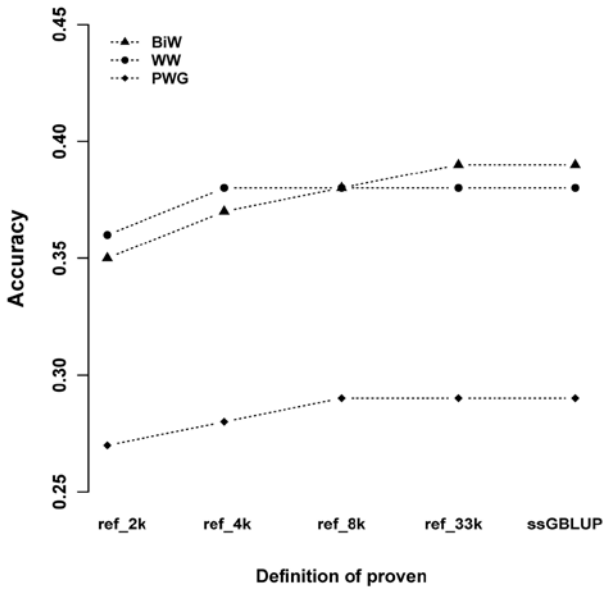

Figure 2. Predictive ability of genomic estimated breeding value for 18,721 young genotyped animals when using the algorithm for proven and young animals to invert the **G** matrix (genomic-based relationship matrix) with different definitions of proven animals: ref_2k (contains top bulls and top cows that had an EBV accuracy for BiW ≥0.85), ref_4k (contains genotyped parents of genotyped animals), ref_8k (contains all parents that were genotyped) ref_33k (contains all genotyped animals born up to 2012). Predictive ability was calculated as correlation between corrected phenotypes and genomic EBV. Predictions in single-step genomic BLUP (ssGBLUP) are obtained through direct inversion of **G**. BiW = birth weight; WW = weaning weight; PWG = postweaning gain.

of independent chromosome segments, which is a function of the effective population size.

The main advantages of the APY are low computing costs and numerical stability. With conditioning on 8,000 animals, for example, the only inverse required is for a block of **G** for 8,000 animals and additional genotypes require only linear storage and computations. Subsequently, computations with a large number of genotyped animals may be feasible with similar predictivity as in the regular inversion. The APY would be the algorithm of choice for regular evaluations with very large number of genotyped animals.

Conclusions

Genomic evaluation in beef cattle using ssGBLUP is feasible for either linear or categorical traits. Gains in predictive ability over BLUP are dependent on the size and composition of the reference population and are large for growth traits and small for CE. With a sufficient number of animals in the reference population, indirect prediction for young animals via SNP effects provides predictivity similar to full ssGBLUP, allowing for quick genomic predictions without running a complete evaluation. Use of the algorithm for proven and young animals in ssGBLUP allows for incorporation of large number of genotyped animals at low cost without compromising the predictive ability.

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