



Single- and multiple-breed genomic evaluations for conformation traits in Canadian Alpine and Saanen dairy goats

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ABSTRACT

Conformation traits are functional traits known to affect longevity, production efficiency, and profitability of dairy goats. However, genetic progress for these traits is expected to be slower than for milk production traits due to the limited number of herds participating in type classification programs, and often lower heritability estimates. Genomic selection substantially accelerates the rate of genetic progress in many species and industries, especially for lowly heritable, difficult, or expensive to measure traits. Therefore, the main objectives of this study were (1) to evaluate the potential benefits of the implementation of single-step genomic evaluations for conformation traits in Canadian Alpine and Saanen dairy goats, and (2) to investigate the effect of the use of single- and multiple-breed training populations. The phenotypes used in this study were linear conformation scores, on a 1-to-9 scale, for 8 traits (i.e., body capacity, dairy character, fore udder, feet and legs, general appearance, rear udder, medial suspensory ligament, and teats) of 5,158 Alpine and 2,342 Saanen does. Genotypes were available for 833 Alpine and 874 Saanen animals. Averaged across all traits, the use of multiple-breed analyses increased validation accuracy for Saanen, and reduced bias of genomically enhanced breeding values (GEBV) for both Alpine and Saanen compared with single-breed analyses. Little benefit was observed from the use of GEBV relative to pedigree-based EBV in terms of validation accuracy and bias, possibly due to limitations in the validation design, but substantial gains of 0.14 to 0.21 (32–50%) were observed in the theoretical accuracy of validation animals when averaged across traits for single- and multiple-breed analyses. Across the whole genotyped population, average gains in theoretical ac-

curacy for GEBV compared with EBV across all traits ranged from 0.15 to 0.17 (32–37%) for Alpine and 0.17 to 0.19 (40–41%) for Saanen, depending on the model used. The largest gains were observed for does without classification records (0.19–0.22 or 50–55%) and bucks without daughter classification records (0.20–0.27 or 57–82%), which have the least information contributing to their traditional EBV. The use of multiple-breed rather than single-breed models was most beneficial for the Saanen breed, which had fewer phenotypic records available for the analyses. These results suggest that the implementation of genomic selection could increase the accuracy of breeding values for conformation traits in Canadian dairy goats.

Key words: genomic selection, classification, single-step genomic BLUP, single-step genomic predictions, small ruminants

INTRODUCTION

The profitability of both livestock sectors and individual farming operations is closely related to the efficiency of production. Consequently, breeding programs in many species and countries began with a focus primarily on production traits (e.g., milk, meat, fiber). However, genetic antagonisms between production traits and other functionally and economically important traits such as conformation, reproduction, and health have become apparent (Rauw et al., 1998; Brito et al., 2021). This has led to the incorporation of more traits in the breeding objectives of many species (Brown et al., 2007; Newman et al., 2009; Miglior et al., 2017). Although functional traits may not directly affect producer revenue, they are often economically important because of their relationship with longevity and cost of production (e.g., veterinary care). Antagonistic genetic relationships have been reported between milk yield and some conformation traits in dairy goats (McLaren et al., 2016), whereas some conformation traits were favorably correlated with productive and

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functional productive life (Castañeda-Bustos et al., 2014). Genetic progress for functional traits has traditionally been relatively slow because they are often less heritable than production traits, are measured at a later age, and evaluated with lower accuracy due to the challenges of data collection (e.g., low participation in phenotype recording programs and subjectivity in the trait definitions). Thus, methods to improve objective phenotyping and the accuracy of breeding values are critical to increase the rate of genetic gain for functionally relevant traits.

In Canadian dairy goats, Massender et al. (2022) demonstrated that selection accuracy for breeding candidates could be increased by 35 to 54% from the implementation of single-step genomic evaluations for milk production traits. However, they hypothesized that the benefits may be even higher for other economically important traits that are less heritable or where few phenotypic records are collected (Van Eenennaam et al., 2014; Miglior et al., 2017; Brito et al., 2021), such as conformation traits.

In dairy species, type classification programs have long been used by breed societies to provide a measure of the conformation of animals relative to a defined standard. The traits scored are related to characteristics that animals need to have long and productive lives (Sewalem et al., 2004, 2005; Miglior et al., 2017). These programs have provided a way for phenotypic information to be gathered for the genetic evaluation of conformation traits. For Canadian dairy goat breeds, the optional type classification system is managed by the Canadian Goat Society (Guelph, ON, www.goats.ca). This program is a nonselective system for registered or registerable first lactation does in participating herds. Later lactation does and bucks may also be classified at the owner's discretion (Canadian Goat Society, 2020). All traits are scored on a linear scale with 1 and 9 representing the biological extremes of the trait, similarly to the classification system for Canadian dairy cows (www.holstein.ca). The Canadian Dairy Goat Genetic Improvement Program (Sullivan, 2000) provides genetic evaluations for 8 linear conformation traits: body capacity (**BC**), dairy character (**DC**), fore udder (**FU**), feet and legs (**FL**), general appearance (**GA**), rear udder (**RU**), suspensory ligament (**SL**), and teats (**TE**). Only a doe's first classification record, scored in either first or second lactation, is used in the single-trait multiple-breed genetic evaluation models (Sullivan, 2000). The models include fixed effects of breed, parity, age class, and a covariate of DIM and random effects of herd-year-classifier and animal additive genetic effect.

Although pedigree-based genetic evaluations for conformation traits in dairy goats have been available

since the early 1990s in Canada (Sullivan, 2000), low participation in classification due to cost and challenges with administering the program have hindered the genetic evaluation of these traits. Relatively few animals are evaluated for conformation traits each year and the accuracy of genetic evaluations are, consequently, low. Given that conformation traits are the only functionally relevant traits currently evaluated for Canadian dairy goats, and that there are known negative genetic correlations between production and conformation traits in dairy goats (McLaren et al., 2016), increasing the number of animals evaluated and the accuracy of genetic evaluations would be beneficial to the Canadian dairy goat sector. Single-step genomic evaluation has been previously found to substantially increase the theoretical accuracy of breeding values for milk production traits in this population (Massender et al., 2022), and would enable more herds not currently participating in the classification program to receive genetic evaluations for these traits. Nevertheless, research is needed to determine the optimal approach for the implementation of genomic selection for type traits in this population. In this context, the objectives of this study were (1) to evaluate the potential benefits of the implementation of single-step genomic evaluations for conformation traits in Canadian Alpine and Saanen dairy goats, and (2) to investigate the effect of the use of single- and multiple-breed training populations.

MATERIALS AND METHODS

Phenotypes

The data used in this research were obtained from industry organizations or samples collected by commercial producers; thus, institutional animal care approval was not required. Records for Alpine and Saanen does collected through the Canadian Goat Society's Classification Program were obtained from the Canadian Centre for Swine Improvement (Ottawa, ON, Canada), which manages the Canadian Dairy Goat Genetic Improvement Program. Classification records included the 8 traits used in the Canadian Dairy Goat Genetic Improvement Program, as previously described. Phenotypic quality control was performed using the R software version 4.0.4 (<https://r-project.org>) to remove incomplete or duplicate records, does from contemporary groups (based on herd-year-classifier) with less than 2 animals, records collected on does less than 300 d of age, or that were not in lactation at the time of recording. Approximately 80% of records were collected on first lactation does, whereas about 20% were collected in later lactations (2 to 5). Few does had records collected in both first and later lactations, thus, only

Table 1. Descriptive statistics for linear conformation traits by breed

Breed	Trait	Abbreviation	Mean \pm SD	Range	CV (%)
Alpine (n = 5,158)	Body capacity	BC	5.8 \pm 1.2	2.0–9.0	21.3
	Dairy character	DC	6.4 \pm 1.1	2.0–9.0	17.1
	Feet and legs	FL	5.5 \pm 1.2	1.0–9.0	21.2
	Fore udder	FU	5.0 \pm 1.5	1.0–9.0	30.3
	General appearance	GA	5.8 \pm 1.3	1.0–9.0	22.2
	Rear udder	RU	5.5 \pm 1.4	1.0–9.0	26.2
	Suspensory ligament	SL	5.9 \pm 1.4	1.0–9.0	23.0
	Teats	TE	5.1 \pm 1.9	1.0–9.0	36.2
Saanen (n = 2,342)	Body capacity	BC	6.2 \pm 1.2	2.0–9.0	19.0
	Dairy character	DC	6.6 \pm 1.2	1.0–9.0	17.9
	Feet and legs	FL	5.8 \pm 1.2	1.0–9.0	20.1
	Fore udder	FU	5.6 \pm 1.4	1.0–9.0	25.2
	General appearance	GA	6.1 \pm 1.3	1.0–9.0	20.6
	Rear udder	RU	5.8 \pm 1.4	1.0–9.0	24.2
	Suspensory ligament	SL	6.3 \pm 1.4	1.0–9.0	21.8
	Teats	TE	5.5 \pm 1.7	1.0–9.0	31.4

a doe's first record was used. In routine genetic evaluations, only classification records measured in either first or second lactation are used. The final data set retained 94% of available records and included 5,158 and 2,342 Alpine and Saanen does, respectively (Table 1). The single-breed data sets were also combined for multiple-breed analyses.

Genotypes

The tissue sample collection procedures and genotypes used in this study were previously described by Massender et al. (2022). In total, 1,707 animals were genotyped, of which 833 were Alpine (78 bucks, 755 does) and 874 were Saanen (97 bucks, 777 does) animals. There were 289 Alpine and 291 Saanen does with both conformation phenotypes and genotypes (Table 2). Genotypic quality control was performed within breed, as described in Massender et al. (2022). The quality control procedures retained 45,221 (84.8%) SNP for the multiple-breed data set, and 44,598 (83.6%) and 43,598 (81.7%) SNP for the Alpine and Saanen breeds, respectively.

Pedigree

Pedigree information was obtained from the Canadian Livestock Records Corporation (Ottawa, ON, Canada, www.clrc.ca). The pedigree was trimmed to only include ancestors of animals with records or genotypes and a pedigree analysis was performed with the *pedigree* package (Coster, 2013) available in the R software. The pedigrees for Alpine and Saanen had 11,486 and 6,270 animals, respectively, whereas the multiple-breed pedigree had 17,362 animals. Few ancestors were shared between the 2 breeds, and genotyped animals had a deeper pedigree on average than phenotyped ani-

mals (17.8–20.3 vs. 12.9–15.3 generations on average; Table 2). The average pedigree depth (in generations) was higher for Saanen than Alpine. Almost all animals (>94%) with records or genotypes had known parents. The *seekparentf90* package from the *blupf90* family of programs (Misztal et al., 2014) was used to identify and correct pedigree errors found in 59 genotyped parent-progeny pairs by searching for matching animals among all genotyped individuals. The parents of animals with a pedigree conflict were then set to missing if no better match was found (45 of 59).

Statistical Analyses

Genetic parameters and breeding values were estimated using single-trait animal models, through the *airemlf90* and *blupf90* programs (Misztal et al., 2014), respectively. Genetic parameters were estimated using a single-step genomic BLUP (**ssGBLUP**) approach with all available genomic and pedigree data and default scaling and blending parameters for the

Table 2. Number of animals with phenotypes, genotypes, and both genotypes and phenotypes; average pedigree depth (generations); and number (%) of animals with known sires and dams, by breed

Item	Alpine	Saanen
Animals with phenotypes	5,158	2,342
Average pedigree depth	12.9	15.3
Known sires	1,090 (99.9%)	597 (98.5%)
Known dams	3,401 (98.6%)	1,572 (97.1%)
Animals with genotypes	833	874
Average pedigree depth	17.8	20.3
Known sires	227 (99.4%)	203 (97.1%)
Known dams	640 (98.8%)	587 (96.7%)
Animals with both	289	291
Average pedigree depth	18.7	20.3
Known sires	90 (100.0%)	90 (95.9%)
Known dams	236 (100.0%)	226 (94.8%)

H matrix (Misztal et al., 2009, 2020; Aguilar et al., 2010; Lourenco et al., 2020). The **H** matrix is a hybrid relationship matrix combining both pedigree (**A**) and genomic (**G**) relationship matrices (Legarra et al., 2009). The model for each trait included fixed effects of parity (first or later), and linear covariates of doe age (d) and DIM, similarly to the models currently used in the official genetic evaluations (Sullivan, 2000). The random effects included contemporary group (herd-year-classifier), and animal additive genetic effect. The **H** matrix included all available pedigree information and accounted for inbreeding in \mathbf{A}^{-1} . For the multiple-breed analyses, the phenotypes recorded on Alpine and Saanen animals were considered a single-trait with a pooled training population. In such analyses, the breed effect (Alpine or Saanen) was added to the model and multiple-breed genetic parameter estimates were used. Therefore, the general model used for the analysis of each trait is described as follows:

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}_u\mathbf{u} + \mathbf{Z}_w\mathbf{w} + \mathbf{e},$$

where \mathbf{y} is a vector of phenotypes, \mathbf{b} is a vector of fixed effects, \mathbf{u} is a vector of random animal additive genetic effects, \mathbf{w} is a vector of random contemporary group effects, and \mathbf{e} is a vector of random residuals. The **X**, **Z_u**, and **Z_w** design matrices relate observations to fixed, animal additive genetic, and contemporary group effects, respectively. It was assumed that the animal additive genetic effects were normally distributed with a mean of zero and a variance equal to $\mathbf{H}\sigma_u^2$, where σ_u^2 is the additive genetic variance. As described in Massender et al. (2022), the optimal blending (α and β) and scaling (τ and ω) factors were defined based on validation accuracy and bias. The optimal values for the blending and scaling factors were the same as found in Massender et al. (2022) for the milk production traits (i.e., $\alpha = 0.95$, $\beta = 0.05$, $\tau = 1.0$, and $\omega = 0.8$) and only the results from the analyses predicted with the optimal parameters are presented. The random contemporary group and residual effects were assumed to be normally distributed with a mean of zero and variance $\mathbf{I}\sigma_w^2$ and $\mathbf{I}\sigma_e^2$, respectively, where **I** is an identity matrix, and σ_w^2 and σ_e^2 are the estimated contemporary group and residual variances.

Validation Analyses

Genotyped animals were divided into training and validation populations based on their year of birth and average theoretical accuracy of their pedigree-based EBV across all traits, calculated with multiple-breed analyses and all available data (**EBV_full**). Animals

born after 2012 with an average EBV_full theoretical accuracy ≥ 0.40 were eligible for the validation population, whereas all other animals were retained in the training population. Using a lower threshold compared with that reported in Massender et al. (2022) was necessary to ensure a sufficient validation population size, due to the lower heritability of the conformation traits compared with the production traits and the limited number of phenotypic records available. In total, 225 Alpine and 268 Saanen animals were eligible for the validation populations.

The same validation approaches as described in Massender et al. (2022) were used in this study. Briefly, forward validation included all eligible animals for each breed in the validation population, whereas for forward cross-validation, 10 random subsets of the eligible validation animals were taken, and the validation analyses were replicated 10 times. After animals were assigned to either training or validation populations, reduced data sets were created by removing all phenotypes of validation animals and their descendants. Thereafter, genomically enhanced breeding values (**GEbV**) and EBV were predicted using both full (**GEbV_full** and **EBV_full**) and reduced (**GEbV_val** and **EBV_val**) data sets. For the traditional BLUP analyses, the **H** matrix described in the model above was replaced by **A**. The validation and theoretical accuracy analyses used the *tidyverse* packages (Wickham et al., 2019) available in the R software.

The EBV_full and GEbV_full, predicted from the full data sets, were used as an approximation of the animal's true breeding value in the validation analyses. Validation accuracy (**VAL_ACC**) was calculated for the validation animals as in Equation 1, as proposed by Legarra and Reverter (2018):

$$\text{VAL_ACC}_i = \sqrt{\frac{\text{cov}((\text{G})\text{EBV}_{i\text{full}}, (\text{G})\text{EBV}_{i\text{val}})}{(1 - \bar{F})\sigma_{ui}^2}}, \quad [1]$$

where VAL_ACC_i is the estimated validation accuracy for the i th trait, calculated using the covariance between EBV or GEbV analyzed with full, $(\text{G})\text{EBV}_{i\text{full}}$, and reduced, $(\text{G})\text{EBV}_{i\text{val}}$, data sets for the i th trait, the average inbreeding coefficient for animals in the validation population within each scenario (\bar{F}), and the estimated additive genetic variance for the i th trait (σ_{ui}^2). Bias, defined as the inflation or deflation of breeding values computed from reduced data sets relative to the full data sets, was calculated as the regression coefficient (b_1) of the regression of **GEbV_full** or **EBV_full** on **GEbV_val** or **EBV_val** [i.e., $(\text{G})\text{EBV}_{\text{full}} = b_0 + b_1(\text{G})\text{EBV}_{\text{val}}$], respectively, minus one. For the forward

cross-validation approach, average validation accuracies and biases and their corresponding standard deviations are presented from across the 10 replicates.

Theoretical Accuracy Analyses

The amount of information gained from the inclusion of genomic information was quantified by comparing average theoretical accuracies of EBV and GEBV calculated with both reduced and full data sets. This was assessed as individual accuracies are the ones used by breeders for selection decisions. Theoretical accuracies (**THE_ACC**) for breeding values of individual animals were calculated from the standard errors of prediction, obtained from the blupf90 software (Misztal et al., 2014), using the formula (Equation 2) proposed by Van Vleck (1993):

$$\text{THE_ACC}_{i,j} = \sqrt{1 - \frac{(s_{i,j})^2}{(1 + f_j)\sigma_{ui}^2}}, \quad [2]$$

where $\text{THE_ACC}_{i,j}$ is the estimated theoretical accuracy for the i th trait EBV of the j th animal, f_j is the inbreeding coefficient for the j th animal, σ_{ui}^2 is the estimated additive genetic variance for the i th trait, and $(s_{i,j})$ is the standard error of prediction for the i th trait EBV of the j th animal. After the theoretical accuracies were calculated for all animals in both pedigree and genomic scenarios, the population was divided into various population subsets (e.g., validation animals, does with or without records, bucks with or without daughter records) and average theoretical accuracies within these subsets were calculated for each trait and averaged across traits. It should be noted that the theoretical accuracy calculation used ignores the effect of selection-induced gametic phase disequilibrium (Bijma, 2012). Consequently, the absolute theoretical accuracy values presented may overestimate the selection response that would be observed in practice and it is the difference between scenarios that is of interest in this study.

RESULTS AND DISCUSSION

Genetic Parameters

Heritability estimates for the conformation traits were low to moderate, ranging from 0.11 ± 0.03 for BC and FL in Saanen to 0.31 ± 0.03 for GA in Alpine (Table 3). The heritability estimates were consistently the same or lower for Saanen as they were for Alpine, whereas the multiple-breed heritability estimates

Table 3. Heritability estimates ($h^2 \pm \text{SE}$) for Alpine, Saanen, and Alpine and Saanen combined

Trait ¹	Alpine	Saanen	Alpine and Saanen
BC	0.22 ± 0.03	0.11 ± 0.03	0.19 ± 0.02
DC	0.16 ± 0.02	0.16 ± 0.04	0.17 ± 0.02
FL	0.17 ± 0.03	0.11 ± 0.03	0.16 ± 0.02
FU	0.28 ± 0.03	0.23 ± 0.04	0.26 ± 0.02
GA	0.31 ± 0.03	0.21 ± 0.04	0.27 ± 0.02
RU	0.22 ± 0.03	0.14 ± 0.03	0.19 ± 0.02
SL	0.18 ± 0.02	0.13 ± 0.04	0.15 ± 0.02
TE	0.18 ± 0.03	0.12 ± 0.04	0.16 ± 0.02

¹Traits: body capacity (BC), dairy character (DC), feet and legs (FL), fore udder (FU), general appearance (GA), rear udder (RU), suspensory ligament (SL), and teats (TE). Genetic parameters were estimated using the single-step method with default parameters.

tended to be intermediary. The intermediary results were expected, given the differences in heritability estimates and number of phenotypic records between the 2 breeds. The conformation traits recorded, and their definitions, differ between countries, which makes comparisons challenging. It is worth noting, as shown in Supplemental Table S1 (<https://doi.org/10.7910/DVN/KHHVPT>; Massender, 2022a), that the conformation traits evaluated in Canada are composite major category scores that incorporate multiple linear conformation traits. This differs from other countries, such as France, the United Kingdom, and the United States, where the component traits are usually evaluated directly (Manfredi et al., 2001; Wiggans and Hubbard, 2001; McLaren et al., 2016).

In multiple-breed analyses of American dairy goats, Luo et al. (1997) reported that conformation traits, scored on a 1-to-50 scale, were moderately to highly heritable, including traits related to GA (0.27 for rump width to 0.52 for stature), DC (0.24), rear legs (0.21), FU attachment (0.25), RU (0.19 for RU arch to 0.25 for udder depth and RU height), SL (0.33), and teats (0.36 for teat placement to 0.38 for teat diameter). The heritability estimates reported in this research followed similar trends with traits related to stature (i.e., GA) being the most heritable, although the heritability estimates for DC, SL, and TE were lower than reported by Luo et al. (1997). In French Alpine and Saanen animals, heritability estimates for structure related traits, such as GA and BC, ranged from 0.03 for back in Saanen to 0.50 for thoracic perimeter in Alpine with standard deviations (**SD**) lower than 0.05 (Manfredi et al., 2001). For mammary system related traits, heritability estimates in French Alpines and Saanen have been reported to be moderate to high by Manfredi et al. (2001), ranging from 0.15 for teat angle to 0.52 for teat length (**SD** <0.05); Rupp et al. (2011), ranging from 0.20 for teat angle to 0.50 for teat length (**SE**

<0.02); and Carillier et al. (2014), ranging from 0.40 for udder shape to 0.57 for udder floor position (SE <0.02). Interestingly, the relative heritability of traits for the Alpine and Saanen breeds seems to be trait-specific in the French populations, unlike the present results where the heritability estimates for Saanen were consistently lower. In a composite population designed by crossing Alpine, Saanen, and Toggenburg animals, McLaren et al. (2016) reported that heritability estimates (\pm SE) for feet and leg traits (0.02 ± 0.02 for front legs to 0.25 ± 0.05 for back feet set) were generally lower than for mammary system traits (0.15 ± 0.04 for udder attachment to 0.38 ± 0.05 for udder depth). In Italian Alpine and Saanen goats, heritability estimates for mammary system traits estimated with a Bayesian approach were moderate but tended to be lower than some of the other studies described (Bifani et al., 2020), ranging from 0.12 (lower and upper bounds of the 95% highest posterior density region: 0.07–0.17) for udder floor position in Saanen to 0.38 (0.31–0.46) for teat length in Alpine. Overall, it can be concluded that heritability estimates for conformation traits of dairy goat breeds vary considerably, depending on trait, statistical model, and population. However, the heritability estimates reported in the present study tended to be on the lower end of results reported in the literature.

It should be noted that the results of the validation and theoretical analyses, here after described, are both dependent on the genetic parameter estimates. Given the low number of phenotypic records available, the results should be interpreted with caution, as bias in the genetic parameter estimates would influence these results. Although this study represents a first step in the implementation of genomic evaluations for conformation traits in Canadian dairy goats, this highlights the importance of repeating these analyses in the future to validate the results as more phenotypic and genotypic information becomes available for analysis.

Validation Accuracy

On average, validation accuracies for both EBV (0.31 ± 0.02 to 0.38 ± 0.02 ; Table 4) and GEBV (0.18 ± 0.02 to 0.35 ± 0.02 ; Table 4) were relatively low, indicating that predictions from validation data sets were not highly correlated with predictions using the full data sets. This result could be due to the small number of phenotyped individuals in the population and low to moderate heritability of the traits, such that the inclusion of own or offspring phenotypes causes substantial changes in EBV and GEBV. Trends observed for both forward cross-validation and forward validation approaches were similar, as also reported in Massender et

al. (2022). The low SD across replicates also suggests that the accuracy estimates were similar regardless of replicate. Therefore, there was little benefit to the inclusion of additional animals in the training population by using the forward cross-validation approach. However, it is possible that the differences in training population sizes in this study were not large enough to observe a benefit from the forward cross-validation approach.

Carillier et al. (2013) reported validation accuracies for udder conformation traits, calculated as the Pearson correlation between daughter yield deviations (DYD) and GEBV, ranging from 0.33 for FU to 0.43 for RU attachment for French bucks of the Alpine and Saanen breeds using a multiple-step GBLUP approach. Using a ssGBLUP approach, Carillier et al. (2014) reported higher validation accuracies, calculated as the Pearson correlation between GEBV and DYD, across both breeds ranging from 0.50 to 0.66 in French Alpine and Saanen goats. Teissier et al. (2019) reported validation accuracies ranging from 0.36 to 0.62 with the same statistic in the same population. The use of weighted single-step GBLUP provided a small gain in validation accuracy for traits in Saanen previously associated with a major QTL, whereas validation accuracies were lower for Alpine using the weighted ssGBLUP approach (Martin et al., 2018; Teissier et al., 2019). Recently, Teissier et al. (2020) reported some further gains in validation accuracy from the use of haplotypes rather than single SNP in a weighted ssGBLUP approach in the same population. These methodologies could be explored in the Canadian population to improve validation accuracies in the future. Mucha et al. (2018) reported generally lower validation accuracies, calculated as the correlation between de-regressed proofs and ssGEBV, for conformation traits in a UK composite population created by crossing Alpine, Saanen, and Toggenburg animals. Validation accuracies ranged from 0.18 for teat shape to 0.48 for teat placement for mammary system traits and 0.04 to 0.55 for FL traits (Mucha et al., 2018). The results reported by Mucha et al. (2018) were more similar to the present results, suggesting that size of the training population as well as the number of phenotyped animals may be factors contributing to the lower validation accuracies observed in these results. The UK population had a similar number of phenotyped animals (6,723) to the present study and training and validation populations were comprised predominantly of does (Mucha et al., 2018). In contrast, the French dairy goat breeding scheme has greater use of artificial insemination and participation in phenotype recording than the Canadian dairy goat populations (e.g., 150,676 records for conformation traits reported in Teissier et al., 2019) enabling the development of

Table 4. Average validation accuracy \pm SD of single-step genomic breeding values (GEBV) and pedigree-based EBV estimated using either single- or multiple-breed training populations and alternative validation designs¹

Breed	Trait ²	Forward cross-validation						Forward validation					
		Single-breed		Multiple-breed		Multiple-breed		Single-breed		Multiple-breed		Multiple-breed	
		EBV	GEBV	EBV	GEBV	EBV	GEBV	EBV	GEBV	EBV	GEBV	EBV	GEBV
Alpine	BC	0.39 \pm 0.02	0.35 \pm 0.02	0.37 \pm 0.02	0.35 \pm 0.02	0.37 \pm 0.02	0.35 \pm 0.02	0.37	0.33	0.37	0.33	0.35	0.33
	DC	0.31 \pm 0.03	0.24 \pm 0.02	0.31 \pm 0.03	0.23 \pm 0.02	0.23 \pm 0.02	0.23 \pm 0.02	0.28	0.21	0.28	0.21	0.28	0.20
	FL	0.27 \pm 0.02	0.23 \pm 0.02	0.27 \pm 0.02	0.22 \pm 0.02	0.22 \pm 0.02	0.22 \pm 0.02	0.26	0.22	0.26	0.22	0.27	0.21
	FU	0.45 \pm 0.02	0.44 \pm 0.02	0.42 \pm 0.02	0.42 \pm 0.02	0.42 \pm 0.02	0.42 \pm 0.02	0.45	0.44	0.45	0.44	0.42	0.42
	GA	0.37 \pm 0.02	0.36 \pm 0.03	0.36 \pm 0.02	0.35 \pm 0.03	0.36 \pm 0.02	0.35 \pm 0.03	0.36	0.34	0.36	0.34	0.36	0.33
	RU	0.44 \pm 0.03	0.43 \pm 0.03	0.44 \pm 0.03	0.41 \pm 0.03	0.41 \pm 0.03	0.41 \pm 0.03	0.43	0.40	0.43	0.40	0.43	0.39
	SL	0.34 \pm 0.02	0.30 \pm 0.02	0.31 \pm 0.01	0.27 \pm 0.01	0.27 \pm 0.01	0.27 \pm 0.01	0.33	0.29	0.33	0.29	0.30	0.24
	TE	0.49 \pm 0.02	0.42 \pm 0.02	0.52 \pm 0.02	0.44 \pm 0.02	0.44 \pm 0.02	0.44 \pm 0.02	0.47	0.41	0.47	0.41	0.50	0.43
	Average	0.38 \pm 0.02	0.35 \pm 0.02	0.38 \pm 0.02	0.34 \pm 0.02	0.34 \pm 0.02	0.34 \pm 0.02	0.37	0.33	0.37	0.33	0.36	0.32
	BC	0.26 \pm 0.01	0.17 \pm 0.01	0.25 \pm 0.02	0.22 \pm 0.01	0.22 \pm 0.01	0.22 \pm 0.01	0.24	0.15	0.23	0.15	0.23	0.20
Saanen	DC	0.33 \pm 0.03	0.20 \pm 0.03	0.35 \pm 0.03	0.22 \pm 0.03	0.27 \pm 0.02	0.22 \pm 0.03	0.32	0.17	0.32	0.17	0.34	0.19
	FL	0.25 \pm 0.02	0.13 \pm 0.01	0.27 \pm 0.02	0.17 \pm 0.01	0.17 \pm 0.01	0.17 \pm 0.01	0.24	0.13	0.24	0.13	0.26	0.16
	FU	0.40 \pm 0.03	0.28 \pm 0.02	0.45 \pm 0.03	0.37 \pm 0.03	0.37 \pm 0.03	0.37 \pm 0.03	0.38	0.25	0.38	0.25	0.42	0.34
	GA	0.31 \pm 0.02	0.18 \pm 0.02	0.31 \pm 0.02	0.23 \pm 0.02	0.23 \pm 0.02	0.23 \pm 0.02	0.27	0.15	0.27	0.15	0.27	0.19
	RU	0.38 \pm 0.02	0.24 \pm 0.02	0.36 \pm 0.02	0.28 \pm 0.02	0.28 \pm 0.02	0.28 \pm 0.02	0.37	0.22	0.37	0.22	0.36	0.26
	SL	0.27 \pm 0.02	0.11 \pm 0.02	0.28 \pm 0.02	0.18 \pm 0.02	0.18 \pm 0.02	0.18 \pm 0.02	0.25	0.09	0.25	0.09	0.26	0.16
	TE	0.26 \pm 0.02	0.17 \pm 0.02	0.29 \pm 0.02	0.24 \pm 0.02	0.24 \pm 0.02	0.24 \pm 0.02	0.23	0.15	0.23	0.15	0.27	0.21
	Average	0.31 \pm 0.02	0.18 \pm 0.02	0.32 \pm 0.02	0.24 \pm 0.02	0.24 \pm 0.02	0.24 \pm 0.02	0.29	0.16	0.29	0.16	0.30	0.21

¹The GEBV used in this analysis were predicted using the optimal scaling factors for the **H** matrix (i.e., 0.95, 0.05, 1.0, and 0.8 for α , β , τ , and ω , respectively).²Traits are body capacity (BC), dairy character (DC), fore udder (FU), rear udder (RU), suspensory ligament (SL), and teats (TE).

a training population consisting of bucks with highly accurate EBV.

The use of single- or multiple-breed models had little effect on validation accuracy estimates for Alpine (0.38 ± 0.02 and 0.38 ± 0.02 for EBV, and 0.35 ± 0.02 and 0.34 ± 0.02 for GEBV; Table 4) or Saanen EBV (0.31 ± 0.02 and 0.32 ± 0.02). However, interestingly, there was an average gain in accuracy of 0.06 points (33%) across traits from the use of multiple-breed analyses relative to single-breed analyses for GEBV in Saanen. It follows that the Saanen breed would benefit more from the use of multiple-breed models, given that there were substantially fewer phenotypic records available for this breed when compared with Alpine. This result was only observed for the GEBV analyses and not the EBV analyses, which indicates that the inclusion of additional genotypes in the multiple-breed models was beneficial for the Saanen breed, rather than gains being attributable to the higher heritability estimates from the multiple-breed models or the inclusion of additional phenotypic records. The Alpine and Saanen breeds share a common history and were managed together until a few decades ago (Carillier et al., 2013; Brito et al., 2015, 2017), which is not reflected in the pedigree information available, as demonstrated by the few ancestors shared between the 2 pedigrees. Thus, the genomic relationship matrix could be capturing relationships that are not reflected in the pedigrees to increase the information contributing to the prediction of GEBV. When comparing GEBV in the French Alpine and Saanen breeds, Carillier et al. (2014) reported very similar results from single and multiple-breed analyses with trait-specific differences of less than or equal to 0.02.

The observed validation accuracies for GEBV predicted with either single or multiple-breed analyses were the same or lower than EBV for both Alpine and Saanen when averaged across traits, ranging from 0.16 to 0.35 for GEBV and 0.29 to 0.38 for EBV, depending on the analyses (Table 4). The average validation accuracy across traits was similar for both EBV and GEBV for Alpine and lower for Saanen GEBV, but the differences in validation accuracies varied considerably by trait, breed, and statistical approach used (Table 4). Previously, Carillier et al. (2013) reported percent gains in validation accuracy for GEBV predicted using a multiple-step GBLUP approach relative to EBV ranging from 7 to 21% for mammary system traits. The lack of gain in validation accuracy for GEBV compared with EBV in the present results was also observed for the milk production traits (Massender et al., 2022), and is likely attributable to the structure of the training population and limitations of the validation design. Previously, Vermette et al. (2013) reported gains in

validation accuracy relative to EBV across conformation traits to be about 0.32 points in Canadian Alpine goats using a multiple-step GBLUP approach. However, the gains varied across traits, ranging from decreases of 0.35 points for DC to gains of up to 0.57 points for BC. The authors noted that the results of the analysis should be interpreted with caution due to the very small validation population used in that report (Vermette et al., 2013), similarly to the present results. Consequently, these validation analyses should be replicated with larger training populations in the future to more accurately estimate the realized benefits of the inclusion of genomic information in the Canadian Dairy Goat Genetic Improvement Program.

Validation Bias

The level of bias observed varied considerably by breed and trait but was similar for both EBV and GEBV, ranging from an average across all traits of -0.07 ± 0.09 to -0.02 ± 0.06 for EBV and -0.19 ± 0.10 to -0.04 ± 0.07 for GEBV using the forward cross-validation approach (Table 5). The negative values for bias estimated for most traits indicate that there was inflation of breeding values predicted from reduced data sets relative to full data sets. The SD between replicates for the forward cross-validation approach were large, often larger than the estimates, indicating that the magnitude of the bias estimates depended substantially on the specific subset of the validation population that was used in a replicate. This was also demonstrated by the larger bias estimates from the forward validation approach (Table 5). Although the size of the validation population was restricted by the small number of genotyped animals, this finding demonstrates that the size of the validation populations may have been too small to obtain consistent estimates of the level of bias. The bias estimates in the present study are within the wide range reported in literature for mammary system conformation traits. Carillier et al. (2013, 2014) reported regression coefficients ranging from 0.73 to 0.92 and 0.60 to 1.51, respectively, equivalent to bias estimates of -0.27 to -0.08 and -0.40 to 0.51 as defined in the present study, across breeds. The wide range of bias estimates reported in the literature are likely attributable to the small genomic training population sizes that are common in dairy goat populations, limiting the design of validation analyses, but could also reflect differences in selection intensity between various goat populations.

The use of multiple-breed rather than single-breed analyses, once again was of benefit for Saanen, but also had a small benefit for Alpine when averaged across traits. Comparing GEBV relative to EBV, absolute values for bias decreased by an average of

Table 5. Average validation bias (regression coefficient minus 1) \pm SD of single-step genomic breeding values (GEBV) and pedigree-based EBV estimated using either single- or multiple-breed training populations and alternative validation designs¹

Breed	Trait	Forward cross-validation						Forward validation					
		Single-breed		Multiple-breed		Single-breed		Single-breed		Multiple-breed			
		EBV	GEBV	EBV	GEBV	EBV	GEBV	EBV	GEBV	EBV	GEBV		
Alpine	BC	0.03 \pm 0.06	-0.02 \pm 0.05	-0.03 \pm 0.06	0.01 \pm 0.05	0.02	0.08	0.04	0.11	0.04	0.11		
	DC	-0.05 \pm 0.11	-0.10 \pm 0.15	-0.02 \pm 0.11	-0.06 \pm 0.14	-0.12	-0.19	-0.08	-0.13	-0.08	-0.13		
	FU	-0.04 \pm 0.05	-0.12 \pm 0.07	-0.04 \pm 0.05	-0.07 \pm 0.06	-0.06	-0.09	-0.08	-0.02	-0.08	-0.02		
	FL	-0.02 \pm 0.05	-0.06 \pm 0.03	-0.07 \pm 0.05	-0.07 \pm 0.04	-0.06	-0.08	-0.11	-0.11	-0.11	-0.11		
	GA	-0.02 \pm 0.05	-0.06 \pm 0.05	-0.05 \pm 0.05	-0.11 \pm 0.04	-0.10	-0.21	-0.17	-0.26	-0.17	-0.26		
	RU	-0.07 \pm 0.03	-0.04 \pm 0.05	-0.07 \pm 0.04	-0.01 \pm 0.05	-0.15	-0.05	-0.14	-0.03	-0.14	-0.03		
	SL	-0.04 \pm 0.06	-0.13 \pm 0.10	-0.01 \pm 0.05	-0.03 \pm 0.10	-0.09	-0.18	-0.05	-0.13	-0.05	-0.13		
	TE	0.02 \pm 0.03	-0.04 \pm 0.05	0.03 \pm 0.03	0.00 \pm 0.05	0.03	-0.03	0.05	0.02	0.05	0.02		
	Average	-0.02 \pm 0.06	-0.07 \pm 0.07	-0.03 \pm 0.06	-0.04 \pm 0.07	-0.07	-0.09	-0.07	-0.07	-0.07	-0.07		
	BC	0.07 \pm 0.11	-0.05 \pm 0.07	0.05 \pm 0.13	0.00 \pm 0.10	0.20	0.05	0.11	0.05	0.11	0.05		
Saanen	DC	-0.06 \pm 0.11	-0.13 \pm 0.08	-0.09 \pm 0.10	0.05 \pm 0.14	-0.11	-0.18	-0.14	-0.04	-0.14	-0.04		
	FU	-0.02 \pm 0.05	-0.30 \pm 0.09	-0.03 \pm 0.05	-0.09 \pm 0.06	-0.09	-0.37	-0.08	-0.07	-0.08	-0.07		
	FL	-0.09 \pm 0.04	-0.17 \pm 0.08	-0.05 \pm 0.05	-0.01 \pm 0.05	-0.14	-0.16	-0.04	0.03	-0.04	0.03		
	GA	-0.11 \pm 0.08	-0.15 \pm 0.10	-0.13 \pm 0.09	-0.15 \pm 0.07	-0.22	-0.28	-0.21	-0.29	-0.21	-0.29		
	RU	-0.14 \pm 0.07	-0.36 \pm 0.06	-0.19 \pm 0.07	-0.19 \pm 0.07	-0.20	-0.42	-0.26	-0.18	-0.26	-0.18		
	SL	-0.09 \pm 0.09	-0.59 \pm 0.13	-0.14 \pm 0.11	-0.23 \pm 0.13	-0.17	-0.66	-0.22	-0.23	-0.22	-0.23		
	TE	-0.02 \pm 0.11	0.22 \pm 0.19	0.00 \pm 0.12	0.16 \pm 0.13	-0.03	0.08	0.01	0.25	0.01	0.25		
	Average	-0.06 \pm 0.08	-0.19 \pm 0.10	-0.07 \pm 0.09	-0.06 \pm 0.09	-0.10	-0.24	-0.10	-0.06	-0.10	-0.06		

¹The GEBV used in this analysis were predicted using the optimal scaling factors for the \mathbf{H} matrix (i.e., 0.95, 0.05, 1.0, and 0.8 for α , β , τ , and ω , respectively).

²Traits are body capacity (BC), dairy character (DC), feet and legs (FL), fore udder (FU), general appearance (GA), rear udder (RU), suspensory ligament (SL), and teats (TE).

0.03 points (43%) for Alpine and 0.13 points (68%) for Saanen across traits, however, the difference was trait dependent. Carillier et al. (2014) also observed trait-dependent differences in validation bias between single-breed and multiple-breed models. Identifying the levels of bias allows genomic evaluations to be rescaled to ensure that GEBV of young breeding candidates are not inflated or deflated relative to older animals. However, the bias observed in the present study was only moderate, on average, possibly due to the use of optimal scaling parameters in the \mathbf{H} matrix.

Theoretical Accuracy Analyses

Validation Population. The animals in the validation population in the reduced data sets represent possible selection candidates (i.e., young animals without own or daughter records), thus, the average theoretical accuracy of validation animals provides an indication of selection accuracy. It should be noted that these theoretical accuracies may overestimate the selection response that could be observed in practice due to selection-induced gametic phase disequilibrium (Bijma, 2012). However, given the limitations of the validation analyses, comparing average theoretical accuracies between EBV and GEBV provides an indication of the potential benefits of genomic selection.

Average theoretical accuracies by trait and breed are presented in Table 6 for the validation animals used in the forward cross-validation approach and in Supplemental Table S2 (<https://doi.org/10.7910/DVN/4S56HC>; Massender, 2022b) for all eligible animals using the forward validation approach. Comparing the average theoretical accuracies between EBV_val and GEBV_val shows the amount of information gained from the inclusion of genomic information. Gains in average theoretical accuracy of GEBV relative to EBV for validation animals ranged from 0.11 to 0.23 (22–58%), depending on the trait and breed, with average gains of 0.14 (32%) and 0.18 (43%) for Alpine, and 0.18 (46%) and 0.21 (50%) for Saanen in single and multiple-breed analyses, respectively. However, it should be noted that the use of optimal scaling parameters (i.e., $\omega = 0.8$) may have inflated the gains observed in theoretical accuracy of GEBV relative to EBV.

The multiple-breed predictions had higher average theoretical accuracies for validation animals for all traits. Across all traits there were average gains of approximately 0.04 for Alpine and 0.03 for Saanen from the use of multiple-breed analyses relative to single-breed analyses. Previously, Massender et al. (2022) reported that gains in average theoretical accuracy were similar for single and multiple-breed analyses of milk produc-

tion traits in the same population. The differences in these results between trait groups may be attributable to the fact that the number of phenotyped animals and trait heritability estimates are both considerably lower for the conformation traits when compared with the milk production traits. Consequently, these results suggest that the multiple-breed models had greater information contributing to the predictions from the inclusion of both additional phenotypes and genotypes.

Full Population. Average theoretical accuracy across all traits for various genotyped and nongenotyped subsets of the population are presented in Table 7. Across the whole genotyped population, average gains in selection accuracy for GEBV_full relative to EBV_full were 0.15 to 0.17 (32–37%) for Alpine and 0.17 to 0.19 (40–41%) for Saanen in single and multiple-breed analyses, respectively (Table 7). The SD of theoretical accuracy across animals within each subset also decreased for GEBV compared with EBV, indicating that the GEBV estimates were more consistent than the EBV estimates. In line with the results reported by Massender et al. (2022), the largest gains in average theoretical accuracy were observed for the subsets of the population with the least information contributing to their EBV, does without records (0.19–0.22 or 50–55% gain) and bucks without daughter records (0.20–0.27 or 57–82% gain). This shows the gains in selection accuracy that could be expected from the implementation of genomic selection for conformation traits in the Canadian dairy goat populations. Once again, limited gains in theoretical accuracy (<0.02) were observed for nongenotyped animals of any population subset, highlighting the need for producers to genotype more animals to observe the full benefits of genomic selection.

The gain in average theoretical accuracy of GEBV_full relative to EBV_full by trait in both points and percentages are presented in Table 8 for both single- and multiple-breed analyses. The gains in accuracy were consistently higher for multiple-breed analyses in Alpine but were slightly more variable for Saanen. The gains in accuracy were generally highest for the least heritable traits (i.e., DC, FL, SL, TE) and lowest for the most heritable traits (i.e., FU and GA). It is well accepted that the implementation of genomic selection is most beneficial to lowly heritable traits, as can be observed in these results.

Future Research and Recommendations. The results of the present study for conformation traits, and as previously described by Massender et al. (2022) for milk production traits, demonstrate that an increase in selection accuracy could be expected from the use of single-step GEBV relative to traditional EBV in the

Table 6. Average theoretical accuracy of single- and multiple-breed single-step genomic breeding values (GEBV) and pedigree-based EBV for validation animals with full and reduced data sets assessed through forward cross-validation¹

Breed	Trait ²	EBV (full)			EBV (reduced)			GEBV (full)			GEBV (reduced)		
		Single-breed	Multiple-breed	Multiple-breed	Single-breed	Multiple-breed	Multiple-breed	Single-breed	Multiple-breed	Multiple-breed	Single-breed	Multiple-breed	
Alpine	BC	0.53 ± 0.01	0.51 ± 0.01	0.41 ± 0.01	0.44 ± 0.01	0.41 ± 0.01	0.65 ± 0.01	0.64 ± 0.01	0.65 ± 0.01	0.58 ± 0.01	0.60 ± 0.01		
	DC	0.47 ± 0.01	0.49 ± 0.01	0.41 ± 0.01	0.40 ± 0.01	0.41 ± 0.01	0.63 ± 0.01	0.61 ± 0.01	0.63 ± 0.01	0.56 ± 0.01	0.59 ± 0.01		
	FL	0.48 ± 0.01	0.47 ± 0.01	0.40 ± 0.01	0.41 ± 0.01	0.40 ± 0.01	0.63 ± 0.01	0.61 ± 0.01	0.63 ± 0.01	0.56 ± 0.01	0.58 ± 0.01		
	FU	0.56 ± 0.01	0.53 ± 0.01	0.44 ± 0.01	0.47 ± 0.01	0.44 ± 0.01	0.66 ± 0.01	0.66 ± 0.01	0.66 ± 0.01	0.59 ± 0.01	0.61 ± 0.01		
	GA	0.58 ± 0.01	0.56 ± 0.01	0.47 ± 0.01	0.49 ± 0.01	0.47 ± 0.01	0.68 ± 0.01	0.68 ± 0.01	0.68 ± 0.01	0.60 ± 0.01	0.62 ± 0.01		
	RU	0.53 ± 0.01	0.52 ± 0.01	0.44 ± 0.01	0.44 ± 0.01	0.44 ± 0.01	0.65 ± 0.01	0.64 ± 0.01	0.65 ± 0.01	0.58 ± 0.01	0.60 ± 0.01		
	SL	0.50 ± 0.01	0.49 ± 0.01	0.41 ± 0.01	0.42 ± 0.01	0.41 ± 0.01	0.63 ± 0.01	0.63 ± 0.01	0.63 ± 0.01	0.57 ± 0.01	0.59 ± 0.01		
	TE	0.49 ± 0.01	0.47 ± 0.01	0.40 ± 0.01	0.41 ± 0.01	0.40 ± 0.01	0.62 ± 0.01	0.62 ± 0.01	0.62 ± 0.01	0.56 ± 0.01	0.58 ± 0.01		
	Average	0.52 ± 0.01	0.50 ± 0.01	0.42 ± 0.01	0.44 ± 0.01	0.42 ± 0.01	0.64 ± 0.01	0.64 ± 0.01	0.64 ± 0.01	0.58 ± 0.01	0.60 ± 0.01		
	BC	0.44 ± 0.01	0.52 ± 0.01	0.40 ± 0.03	0.36 ± 0.02	0.40 ± 0.03	0.67 ± 0.01	0.61 ± 0.01	0.67 ± 0.01	0.56 ± 0.01	0.63 ± 0.01		
Saanen	DC	0.50 ± 0.01	0.50 ± 0.01	0.41 ± 0.03	0.40 ± 0.03	0.41 ± 0.03	0.66 ± 0.01	0.63 ± 0.01	0.66 ± 0.01	0.57 ± 0.01	0.62 ± 0.01		
	FL	0.43 ± 0.01	0.49 ± 0.01	0.40 ± 0.03	0.36 ± 0.02	0.40 ± 0.03	0.65 ± 0.01	0.60 ± 0.01	0.65 ± 0.01	0.56 ± 0.01	0.62 ± 0.01		
	FU	0.55 ± 0.01	0.52 ± 0.01	0.43 ± 0.03	0.44 ± 0.03	0.43 ± 0.03	0.70 ± 0.01	0.66 ± 0.01	0.67 ± 0.01	0.59 ± 0.01	0.64 ± 0.01		
	GA	0.54 ± 0.01	0.58 ± 0.01	0.46 ± 0.03	0.43 ± 0.03	0.46 ± 0.03	0.68 ± 0.01	0.66 ± 0.01	0.68 ± 0.01	0.59 ± 0.01	0.64 ± 0.01		
	RU	0.48 ± 0.01	0.53 ± 0.01	0.43 ± 0.03	0.39 ± 0.03	0.43 ± 0.03	0.68 ± 0.01	0.62 ± 0.01	0.68 ± 0.01	0.57 ± 0.01	0.63 ± 0.01		
	SL	0.48 ± 0.01	0.50 ± 0.01	0.41 ± 0.03	0.39 ± 0.03	0.41 ± 0.03	0.66 ± 0.01	0.63 ± 0.01	0.66 ± 0.01	0.57 ± 0.01	0.62 ± 0.01		
	TE	0.44 ± 0.01	0.49 ± 0.01	0.40 ± 0.03	0.37 ± 0.02	0.40 ± 0.03	0.65 ± 0.01	0.61 ± 0.01	0.65 ± 0.01	0.56 ± 0.01	0.62 ± 0.01		
	Average	0.48 ± 0.01	0.52 ± 0.01	0.42 ± 0.03	0.39 ± 0.03	0.42 ± 0.03	0.67 ± 0.01	0.63 ± 0.01	0.67 ± 0.01	0.57 ± 0.01	0.63 ± 0.01		

¹The GEBV used in this analysis were predicted with optimal scaling factors for the **H** matrix (i.e., 0.95, 0.05, 1.0, and 0.8 for α , β , τ , and ω , respectively).²Traits are body capacity (BC), dairy character (DC), feet and legs (FL), fore udder (FU), general appearance (GA), rear udder (RU), suspensory ligament (SL), and teats (TE).

Table 7. Average theoretical accuracy (\pm SD) of pedigree-based EBV and genomic breeding values (GEBV) for specific nongenotyped and genotyped subsets of the population, estimated across traits, using single- or multiple-breed training populations and full data sets¹

Group	Alpine						Saanen					
	EBV (full)			GEBV (full)			EBV (full)			GEBV (full)		
	Single-breed	Multiple-breed		Single-breed	Multiple-breed		Single-breed	Multiple-breed		Single-breed	Multiple-breed	
Whole population												
Nongenotyped	0.49 \pm 0.16	0.47 \pm 0.16		0.49 \pm 0.16	0.48 \pm 0.16		0.40 \pm 0.15	0.44 \pm 0.16		0.41 \pm 0.15	0.45 \pm 0.16	
Genotyped	0.47 \pm 0.15	0.46 \pm 0.15		0.62 \pm 0.08	0.63 \pm 0.07		0.43 \pm 0.13	0.46 \pm 0.14		0.60 \pm 0.07	0.65 \pm 0.06	
Bucks												
Nongenotyped	0.42 \pm 0.18	0.41 \pm 0.18		0.43 \pm 0.18	0.42 \pm 0.17		0.35 \pm 0.15	0.38 \pm 0.16		0.37 \pm 0.16	0.40 \pm 0.17	
Genotyped	0.46 \pm 0.16	0.45 \pm 0.15		0.61 \pm 0.09	0.62 \pm 0.07		0.38 \pm 0.19	0.41 \pm 0.20		0.58 \pm 0.10	0.63 \pm 0.10	
Does												
Nongenotyped	0.50 \pm 0.16	0.49 \pm 0.15		0.51 \pm 0.16	0.50 \pm 0.15		0.41 \pm 0.15	0.45 \pm 0.16		0.42 \pm 0.15	0.46 \pm 0.16	
Genotyped	0.47 \pm 0.14	0.46 \pm 0.14		0.62 \pm 0.08	0.63 \pm 0.07		0.44 \pm 0.11	0.47 \pm 0.12		0.60 \pm 0.07	0.65 \pm 0.06	
Does with records												
Nongenotyped	0.60 \pm 0.06	0.59 \pm 0.06		0.61 \pm 0.06	0.59 \pm 0.06		0.53 \pm 0.06	0.57 \pm 0.06		0.53 \pm 0.07	0.58 \pm 0.06	
Genotyped	0.61 \pm 0.04	0.60 \pm 0.04		0.69 \pm 0.03	0.69 \pm 0.03		0.54 \pm 0.04	0.58 \pm 0.04		0.65 \pm 0.04	0.69 \pm 0.03	
Does without records												
Nongenotyped	0.36 \pm 0.14	0.35 \pm 0.14		0.37 \pm 0.14	0.36 \pm 0.14		0.30 \pm 0.12	0.32 \pm 0.13		0.31 \pm 0.13	0.34 \pm 0.14	
Genotyped	0.38 \pm 0.11	0.38 \pm 0.10		0.57 \pm 0.06	0.59 \pm 0.05		0.38 \pm 0.09	0.41 \pm 0.10		0.58 \pm 0.06	0.63 \pm 0.05	
Bucks with daughter records												
Nongenotyped	0.53 \pm 0.14	0.51 \pm 0.14		0.53 \pm 0.14	0.52 \pm 0.14		0.45 \pm 0.12	0.49 \pm 0.12		0.47 \pm 0.13	0.51 \pm 0.13	
Genotyped	0.56 \pm 0.09	0.55 \pm 0.09		0.66 \pm 0.06	0.67 \pm 0.05		0.51 \pm 0.09	0.55 \pm 0.10		0.64 \pm 0.06	0.69 \pm 0.06	
Bucks without daughter records												
Nongenotyped	0.30 \pm 0.14	0.29 \pm 0.14		0.32 \pm 0.14	0.31 \pm 0.14		0.27 \pm 0.13	0.30 \pm 0.14		0.29 \pm 0.14	0.32 \pm 0.14	
Genotyped	0.35 \pm 0.14	0.35 \pm 0.13		0.55 \pm 0.08	0.58 \pm 0.06		0.31 \pm 0.19	0.33 \pm 0.20		0.55 \pm 0.11	0.60 \pm 0.10	

¹The GEBV used in this analysis were predicted using the optimal scaling factors for the **H** matrix (i.e., 0.95, 0.05, 1.0, and 0.8 for α , β , τ , and ω , respectively).

Canadian dairy goat populations. Although the results presented here, and in Massender et al. (2022), suggest there are advantages to the implementation of genomic evaluations, they should be interpreted with caution due to the small genomic training population sizes. It is well established that the size and structure of ge-

Table 8. Theoretical accuracy gain in points (percent) of single-step genomic breeding values (GEBV) relative to pedigree-based EBV by trait for subsets of the genotyped population, predicted with single- or multiple-breed analyses and full data sets¹

Trait ²	Alpine		Saanen	
	Single-breed	Multiple-breed	Single-breed	Multiple-breed
Whole population				
BC	0.15 (32)	0.17 (37)	0.18 (45)	0.18 (38)
DC	0.16 (37)	0.18 (41)	0.17 (39)	0.19 (42)
FL	0.16 (36)	0.18 (42)	0.19 (49)	0.20 (45)
FU	0.14 (28)	0.17 (36)	0.14 (29)	0.18 (38)
GA	0.13 (25)	0.16 (32)	0.15 (31)	0.17 (33)
RU	0.15 (32)	0.16 (34)	0.17 (40)	0.18 (38)
SL	0.16 (36)	0.18 (41)	0.17 (40)	0.19 (42)
TE	0.16 (36)	0.18 (42)	0.19 (48)	0.19 (43)
Average	0.15 (32)	0.17 (37)	0.17 (40)	0.19 (41)
Does with records				
BC	0.08 (13)	0.10 (17)	0.13 (27)	0.11 (19)
DC	0.10 (18)	0.10 (17)	0.10 (18)	0.12 (21)
FL	0.09 (16)	0.11 (20)	0.14 (29)	0.13 (24)
FU	0.06 (9)	0.09 (15)	0.08 (13)	0.11 (19)
GA	0.05 (7)	0.07 (10)	0.09 (15)	0.08 (12)
RU	0.08 (13)	0.09 (15)	0.12 (23)	0.10 (17)
SL	0.08 (13)	0.10 (17)	0.11 (20)	0.13 (23)
TE	0.09 (16)	0.11 (20)	0.13 (27)	0.13 (24)
Average	0.08 (13)	0.09 (15)	0.11 (20)	0.11 (19)
Does without records				
BC	0.18 (46)	0.21 (55)	0.21 (58)	0.22 (54)
DC	0.19 (53)	0.21 (57)	0.18 (45)	0.22 (55)
FL	0.20 (56)	0.22 (61)	0.22 (63)	0.23 (59)
FU	0.17 (41)	0.21 (54)	0.17 (40)	0.21 (50)
GA	0.17 (40)	0.20 (49)	0.18 (43)	0.19 (42)
RU	0.18 (46)	0.21 (55)	0.20 (53)	0.21 (50)
SL	0.18 (47)	0.21 (57)	0.20 (53)	0.22 (55)
TE	0.19 (51)	0.22 (61)	0.21 (58)	0.23 (59)
Average	0.19 (50)	0.21 (55)	0.20 (53)	0.22 (54)
Bucks with daughter records				
BC	0.10 (18)	0.11 (20)	0.15 (32)	0.14 (25)
DC	0.11 (21)	0.13 (25)	0.13 (25)	0.15 (28)
FL	0.11 (21)	0.13 (25)	0.15 (33)	0.15 (29)
FU	0.08 (13)	0.10 (17)	0.10 (17)	0.13 (23)
GA	0.07 (11)	0.10 (16)	0.11 (20)	0.11 (18)
RU	0.10 (18)	0.11 (20)	0.14 (28)	0.13 (23)
SL	0.10 (18)	0.13 (25)	0.14 (28)	0.15 (28)
TE	0.11 (21)	0.13 (25)	0.15 (32)	0.15 (29)
Average	0.10 (18)	0.12 (22)	0.13 (25)	0.14 (25)
Bucks without daughter records				
BC	0.19 (53)	0.23 (66)	0.25 (86)	0.27 (82)
DC	0.21 (64)	0.23 (68)	0.23 (72)	0.27 (84)
FL	0.21 (64)	0.24 (73)	0.26 (93)	0.27 (84)
FU	0.18 (47)	0.22 (61)	0.22 (63)	0.26 (76)
GA	0.18 (46)	0.21 (54)	0.22 (65)	0.25 (69)
RU	0.19 (53)	0.22 (61)	0.24 (77)	0.26 (76)
SL	0.20 (59)	0.23 (68)	0.24 (77)	0.27 (84)
TE	0.20 (59)	0.24 (73)	0.25 (86)	0.27 (84)
Average	0.20 (57)	0.23 (66)	0.24 (77)	0.27 (82)

¹The GEBV used in this analysis were predicted using the optimal scaling factors for the \mathbf{H} matrix (i.e., 0.95, 0.05, 1.0, and 0.8 for α , β , τ , and ω , respectively).

²Traits are body capacity (BC), dairy character (DC), feet and legs (FL), fore udder (FU), general appearance (GA), rear udder (RU), suspensory ligament (SL), and teats (TE).

genomic training populations is one of the major factors influencing the accuracy of genomic evaluations (e.g., Goddard, 2012).

Additionally, the size of the training population limited the design of the validation analyses. The small training and validation populations, low average accuracy of the proxies of true breeding values (i.e., EBV_{full} and GEBV_{full}), and high completeness of pedigree may all have contributed to the limited gains in validation accuracy observed for GEBV relative to EBV, contrary to expectations. These analyses should be repeated as more genotypic and phenotypic information becomes available. Although considerable benefits were observed from the use of GEBV relative to EBV in terms of average theoretical accuracy, it is important to remember that the actual values may overestimate the accuracy that would be observed in selected populations (Bijma, 2012). Nevertheless, based on the results of this research, as well as the substantial international results demonstrating the benefits of genomic selection for countless traits and species, the implementation of genomic selection is recommended to accelerate genetic improvement for these traits.

The implementation of genomic selection will also enable herds that have not traditionally participated in phenotype recording programs to receive genetic evaluations and will hopefully increase producer involvement in the Canadian Dairy Goat Genetic Improvement Program. However, the implementation of genomic selection and its continued success will depend on the ability of the industry to invest resources into phenotype recording programs and the genotyping of animals to further expand the genomic training population. Phenotyping and genotyping are often viewed as a great expense relative to the value of the individual animal by Canadian dairy goat producers, which is a barrier to the successful implementation of this tool. However, new animals with phenotypic information (i.e., individual or daughter records) must be added to the genomic training population to reestimate marker effects and maintain the relationship between the training population and the population under selection or less gains in accuracy may be observed in the future (Muir, 2007; Habier et al., 2013).

Traditionally, pedigree-based genetic evaluations in the Canadian Dairy Goat Genetic Improvement Program have been predicted across breeds. Massender et al. (2022) observed no advantage to the use of multiple-breed models for more highly heritable milk production traits. However, the results of this study support the continued analysis of genetic evaluations across breeds for conformation traits as the multiple-breed analyses were found to have similar or higher validation accuracies, lower validation biases, and higher average theo-

retical accuracies than the single-breed analyses. The use of multiple-breed models will also be simpler to implement for routine genetic evaluations, allow comparisons between breeds, and will increase the size of the genomic training population.

International collaboration is another method to increase the size of genomic training populations. However, conformation trait genetic evaluations are not easily comparable between Canada and other countries because the traits evaluated, and the trait definitions, often differ between countries. Furthermore, the conformation traits evaluated in the Canadian Dairy Goat Genetic Improvement Program are inconsistent with the traits currently scored on farm. This may cause confusion for producers and reduce confidence in the genetic evaluations, especially for newer producers that are unfamiliar with the older system. It is recommended that the conformation traits evaluated be reviewed to improve consistency with the current on-farm classification system and facilitate international genetic evaluations, given the emphasis on sharing phenotypes and genotypes from various countries.

Although conformation traits are the only functionally relevant traits currently evaluated for Canadian dairy goats, the implementation of genomic selection offers great potential to expand the breeding objective to include even more traits (e.g., fertility and health traits) that are difficult or expensive to measure across the whole population. The research of additional traits requires time and resources; however, it may help to build interest in the genetic evaluation system and increase the number of herds using genetic evaluations to inform their selection decisions. This would increase the rate of genetic improvement for economically important traits across the industry, and ultimately, lead to a more productive, healthy, and sustainable dairy goat population.

CONCLUSIONS

This study evaluated the potential benefits of the implementation of genomic evaluations for linear conformation traits in Canadian Alpine and Saanen dairy goats. The results suggest that with the limited number of phenotypic records available and small genomic training population size, multiple-breed rather than single-breed analyses generally maintained or increased validation accuracy, decreased validation bias, and increased average theoretical accuracy. The differences between the single- and multiple-breed analyses were more evident for Saanen than Alpine. Gains in theoretical accuracy for GEBV relative to EBV were observed, especially for breeding candidates (e.g., does without records and bucks without daughter records). Thus, the

implementation of genomic evaluations would be expected to increase the rate of genetic improvement for functionally relevant conformation traits in Canadian dairy goats.

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