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INCORPORATING GENOMIC INFORMATION IN EVALUATIONS FOR FARMED DEER IN NEW ZEALAND

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SUMMARY

The New Zealand deer industry has made notable genetic progress in the last decades. Initially based around velvet antler and venison, deer are now selected based on several traits including carcass composition, reproduction, and disease resistance within DEERSelect, the industry performance recording system in New Zealand. Due to its low cost and manageable logistics for deer, the genotyping-by-sequencing (GBS) technology was chosen to replace microsatellites for parentage assignment and has allowed a national genetic evaluation across flocks since 2015. Genomic information, however, is not yet fully exploited as evaluations currently only use a traditional pedigree-based, best linear unbiased prediction (BLUP) approach, to estimate the genetic merit of an animal. To assess the benefits of using genomic information in the evaluations, here we compare BLUP, genomic BLUP (GBLUP) and single-step genomic BLUP (SSGBLUP) evaluations for several production traits in the NZ deer industry. Using forward-validation, we estimate the prediction accuracy and bias for these three approaches in 19,863 red animals born between 2018 and 2020. We show that regardless of the approach, GBLUP or SSGBLUP, incorporating genomic information explicitly improves prediction accuracy and reduces bias. Across all traits, we estimate gains in accuracy of 16% for GBLUP and 18% for SSGBLUP on average for red deer. We therefore recommend the incorporation of genomic information in the evaluations performed by DEERSelect and propose a computational pipeline to support the medium to long-term growth of this dynamic livestock industry in New Zealand.

INTRODUCTION

The New Zealand deer industry has made substantial genetic progress in the last decades (Ward *et al*. 2016). Initially based around velvet antler and venison, deer are now selected based on several traits including carcass composition, reproduction, and disease resistance within DEERSelect, the deer industry performance recording system in New Zealand (Gudex *et al.* 2013; Ward *et al.* 2016).

Since 2015, the AgResearch deer genomics program has developed and implemented genotyping-by-sequencing (GBS) methods for deer parentage (Dodds *et al.* 2019; Rowe *et al.* 2018), gender and breed assignment (Bilton *et al.* 2019). Deer are routinely genotyped by GenomNZ (https://www.agresearch.co.nz/genomnz) using these GBS methods (Rowe *et al.* 2018). Genomic information, however, is not yet fully exploited in current evaluations as they only use the theoretical relationships between animals contained in the pedigree to estimate their genetic merit (A matrix). This approach to generate breeding values (BVS) is also known as best linear unbiased prediction (BLUP) approach. In contrast to that, the genomic BLUP (GBLUP) approach uses the realized relationships between animals (Genomic Relationship Matrix - GRM) and thus allows a more accurate estimation of their breeding values. Under the GBLUP approach, the actual relatedness for between animals is estimated using genomic markers (realized relationships).

The SSGBLUP approach is intermediate between the latter two, as it weights both genomic (GRM) and pedigree (A) contributions to construct a unified relationship matrix known as H matrix. The SSGBLUP approaches thus requires an extra parameter α ($0 \leq \alpha \leq 1$) to weight the GRM and A matrices. The main advantage of the SSGBLUP approach is to allow the direct incorporation of animals with either pedigree or genomic information in the genetic evaluation.

Here we investigate ways to incorporate genomic information in routine deer evaluations of genetic merit. We use production traits related to growth, meat and carcass yield, health, and reproduction to compare the performance of genomic prediction using pedigree (BLUP), genomic BLUP (GBLUP) and single-step genomic (SSGBLUP) relationships among animals.

MATERIALS AND METHODS

Animals and Phenotypes. We used phenotypes for red animals born between 2018 and 2020. Phenotypic data from six production traits related to growth, meat and carcass yield, health, and reproduction was retrieved from DEERSelect. Production traits analysed were weaning live weight (WWT), 12-month live weight (W12), carbohydrate larval antigen-specific immunoglobulin A levels at 10 months of age (CARLA10), ultrasound measured eye muscle area at 10 months of age (EMA), velvet weight at 2 years (VW2), and conception date at 2 years (CD2). Table 1 details the number of records per trait and their corresponding summary statistics.

Table 1. Number of records and summary statistics by trait for New Zealand red deer

	n records	Mean	SD	Min.	Max.
WWT	18,649	55	7	22.2	89.4
W12	15,894	90	8.5	51.4	130.3
CARLA10	6,962	2.4	1.2	-2.3	6.6
EMA	6,205	25.9	2.9	12.7	36.3
VW2	1,031	3.1	1	0.7	8.1
CD2	2,163	103.7	12.4	73	130

GBS Genotypes. We used genotypic information from 19,863 animals and 55,784 SNPs mapped using GBS data. Genomic relationship matrices (GRM) were constructed using the KGD software (Dodds *et al.* 2015). Principal components (PCs) were obtained from the GRM in GCTA (Yang *et al.* 2011).

Population structure. The deer population in New Zealand is composed of several crosses from two species of the genus Cervus: C. elaphus (red deer) and C. canadensis (wapiti deer/elk), which have notable phenotypic differences. Given that the inclusion of genetically divergent breeds can reduce prediction accuracy in genomic evaluations (Calus *et al.* 2014; Makgahlela *et al.* 2013), analyses are conducted separately for each breed. Birth herd codes were used as a proxy for breed. Only red analyses are presented here.

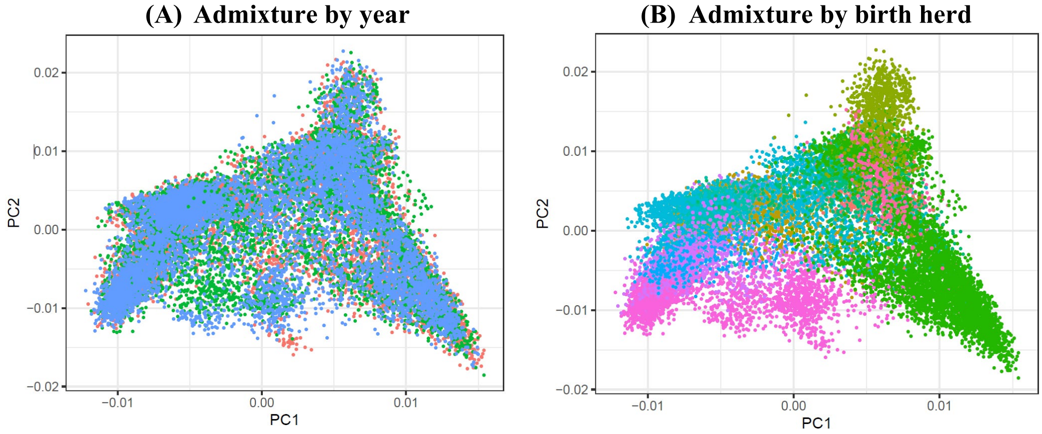
Statistical Analyses. Phenotypes were modelled using a univariate genetic model for each trait. Genetic models include relevant covariates for each trait, including contemporary group, age of dam, birth date deviation, and breed proportions measured with PCs from the GRM (PC1 to PC3).

Genetic parameters and breeding values were estimated using pedigree (BLUP), genomic BLUP (GBLUP) (VanRaden 2008) and single-step genomic BLUP (SSGBLUP) (Misztal *et al.*, 2009) relationships among animals in MTG2 (Lee and van der Werf 2016). This software tool was also used to construct the H matrix. In absence of any prior information, we used α=0.5, equal weights for pedigree and genomic relationships, to construct H.

Genomic prediction accuracy. We assessed the prediction quality of the three relationship matrices using a forward-validation scheme. This was done by removing the phenotypes of the last cohort (target population, animals born in 2020), estimating the genetic models again using the older cohorts (training population, animals born 2018 and 2019), and comparing the breeding value predictions with actual phenotypes for the last cohort of animals. Prediction quality was assessed using two measures: prediction accuracy and prediction bias. Prediction accuracy (acc) is defined as correlation between predicted breeding values and phenotypes adjusted by fixed effects divided by the squared root of the heritability (SSGBLUP model). Bias (bias) as the regression's slope between predicted breeding values and phenotypes adjusted by fixed effects.

RESULTS AND DISCUSSION

Population structure. Figure 1 shows the first two PCs by birth year (A) and birth herd (B). In the figure A, we observe that animals are spread out evenly across the plot, suggesting that there is little change in the genetic composition of the animals over time. In contrast to that, figure B shows that birth herds form clearly defined clusters in specific regions which do not mix with each other. We can thus conclude that there is more variation between birth herds than across time.


(A) Admixture by year

(B) Admixture by birth herd

Figure 1. Genetic admixture by birth year (A) and birth herd (B) for deer born between 2018-2020. Principal components (PC) 1 and 2 are shown in the x and y-axis

Table 2. Accuracy and bias of genomic prediction using pedigree (BLUP), genomic (GBLUP) and single-step SSGBLUP) approaches for red deer

		BLUP		GBLUP		SSGBLUP	
	n target	**acc**	**bias**	**acc**	**bias**	**acc**	**bias**
WWT	6,476	0.33	0.41	0.34	0.57	0.28	0.87
W12	5,382	0.36	0.50	0.47	0.65	0.49	0.62
CARLA10	2,548	0.29	0.46	0.47	0.71	0.46	0.64
EMA	2,152	0.34	0.72	0.42	0.77	0.45	0.78
VW2	343	0.40	1.42	0.43	1.02	0.46	1.11
CD2	733	0.31	1.20	0.22	0.62	0.27	0.78
	Average	**0.34**	**0.79**	**0.39**	**0.72**	**0.40**	**0.80**

Genomic Prediction accuracy. The prediction accuracy and bias for the six production traits in red deer are presented in Table 2. Across all traits the prediction accuracy from BLUP, GBLUP and SSGBLUP approaches are 0.34, 0.39 and 0.40. This implies that incorporating genotypic information in the genetic evaluation could provide much more accurate breeding values, on average 16% and 18% more accurate for GBLUP and SSGBLUP, respectively. Similarly, bias is also reduced when using genotypic information (SSGBLUP) H, although variation by trait is still present.

Our analyses have some caveats. First, for computational easiness we focus only on red animals born between 2018 and 2020. This strategy reduces the computational time for the genetic evaluation but also limits the number of phenotypic records included for velvet weight (VW2) and conception date (CD2) as these are recorded at two years of age. Secondly, this strategy also reduces the number of deer with genotypes entering the evaluation. Despite these caveats, the prediction accuracy of the breeding values is improved, and the bias is consistently smaller across all traits as shown in the validation (Table 2).

CONCLUSIONS

We show that incorporating genomic information explicitly, either by using GBLUP or SSGBLUP, improves prediction accuracy and reduces bias. Across all traits, we estimate average gains in accuracy of 16% for GBLUP and 18% for SSGBLUP for red deer, the breed with the highest numbers of phenotypic records. In addition, breeding values that use genotype information are also less biased than those based on pedigree alone. We therefore recommend the incorporation of genomic information in the genetic evaluations performed by DEERSelect for red deer. Methods for joint evaluations for wapiti, red and red x wapiti cross animals are currently under investigation.

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