

Estimation of Breeding Values for Footrot in New Zealand Merino Sheep

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Summary

Footrot affects all aspects of sheep production and has substantial welfare and economic impacts, particularly for the fine-wool industry in New Zealand (NZ), which is largely dominated by Merino sheep and high rainfall environments. Genetic selection provides an opportunity to improve resistance to footrot and in turn reduce the production loss and management costs associated with footrot outbreaks. Footrot was recorded on 2,196 yearling wethers in a Central Progeny Test (CPT) environment with a further 1,081 phenotypes available for industry animals. The heritability of average footrot score was 0.20 ± 0.05 in the CPT. However, ultimately the successful provision of industry breeding values for footrot will rely on a larger pool of phenotypes across environments and genotypes. The inclusion of phenotypes scored in five industry flocks, linked to the CPT via pedigree, led to a small decline in variances and heritability for average footrot score, relative to CPT data. Transitioning phenotypes based on the biological progression of footrot resulted in similar residual variance estimates when industry data was included, indicating breeding values are likely to be more comparable across challenge events. We propose that incorporating industry phenotypes will provide breeders with greater capacity to obtain estimates of the genetic potential of young animals to resist footrot.

Keywords: single-step, transition matrix, disease resistance, MERINOSELECT

Introduction

Footrot is a highly contagious and difficult to manage hoof disease in sheep and other ungulates that begins with interdigital dermatitis and progresses to separation of the hard horn from the foot (Mulvaney, 2013). Both infection and the progression of footrot within the flock are heavily influenced by the prevailing weather conditions and the presence of the infective bacteria *Dichelobacter nodosus* (Egerton & Raadsma, 1991). Several studies have also found footrot resistance to be heritable, with estimates ranging from 0.10 to 0.30 in populations of Romney (Skerman *et al.*, 1988), Merino (Raadsma *et al.*, 1994), and Scottish Black Face and Mule breeds (Nieuwhof *et al.*, 2008). Previous estimates of the heritability of footrot resistance in the New Zealand Merino population range from 0.17 to 0.39 (Walkom *et al.*, 2017; Raadsma *et al.*, 2018). This paper aims to estimate breeding values for footrot, using the New Zealand Merino Central Progeny Test (CPT) database along with records provided by industry Merino flocks from across New Zealand.

Material and Methods

The CPT flock mated approximately 2,000 commercial fine wool NZ Merino ewes to 40 Merino type rams via AI per year (one link ram between each year) from 2013 to 2015 (half the 2015 matings were natural). Rams were perceived as trait leaders for footrot or other key production traits, and were widely used in the NZ Merino industry. The commercial ewe flock (no pedigree available) were aged between 2 and 6 years and were declared free of footrot at the start of the trial. The ewes and resulting progeny were managed in Waipara, New Zealand. The 2014 and 2015 progeny did not have dam, birth type and rear type recorded, but sire pedigree was known.

Along with the CPT, five Merino industry flocks within New Zealand contributed phenotypes for genetic evaluation (Table 1). All animals analysed were submitted to the MERINOSELECT database (Brown *et al.*, 2007) with sire and dam pedigree of varying depths available for all flocks. The industry flocks were considered moderately linked to the CPT and the other flocks, based on a calculated accuracy of comparison between flocks ranging from 0.33 to 0.56, as described by Huisman *et al.* (2006).

The footrot phenotypes were scored after the footrot challenge was deemed to be sufficient and prior to any treatment: that is, when a proportion of subsampled animals were exhibiting underrun feet. Each foot was then scored on a 5 point scale by trained NZ Merino Pty. Ltd staff, with 0 being not affected and 1 to 5 representing different degrees of severity of foot damage, from water maceration (1) to chronic footrot (5) (Mulaney, 2013). The established protocol was that animals were not foot bathed within the previous 1-2 months and not vaccinated in the previous 12 months before scoring. All individuals with data were naturally challenged by relocation to a footrot affected site as yearlings (from 290 – 430 days of age). From the CPT, 2,196 footrot phenotypes were included from each of the three year drops exposed to separate challenge events with the proportion of sheep expressing under-run feet in the three challenges ranging from 25% to 78% (Table 1). Industry flocks contributed 1,081 phenotypes, with the proportion of sheep with underrun feet varying across challenges from 16 to 69% (Table 1). The trait analysed in this study was the footrot score averaged across all four feet (0-5).

Footrot records from all data were collected as a result of uncontrolled natural footrot challenges. Consequently, the incidence of footrot (affected vs unaffected) and the distribution of scores for affected animals, which affects means and variances, varied across and within the CPT and industry challenges (Table 1). Pre-analysis adjustment has been done in this study using a transition matrix as per Walkom *et al.* (2017) to adjust for differences in disease incidence and transform the data to a similar incidence based on the biological progression through the footrot scores. Using data from the 2014 and 2015 CPT progeny challenges where the animals were scored multiple times a 6 x 6 transition matrix for a single day was calculated as per Stromquist (1996). Each foot were represented by a 1 x 6 matrix, representing the proportion of the foot in each score. The foot was then progressed to the n^{th} day, to achieve a common incidence (affected vs. unaffected) across challenges, by multiplying the 1x6 matrix by the transition matrix to the n^{th} power. This generated for each foot a transformed score (rounded to an integer) that was then averaged (across 4 feet) to produce a transformed average footrot record for each animal. Each challenge was transitioned forward until at least 40% of individual feet were underrun (Score 3 or higher). Challenge data with a higher incidence of under-running were not transformed.

Parameter estimates and breeding values were estimated from a single-step genomic BLUP model incorporating genomic and pedigree information with a lambda of 0.5 (Legarra *et al.*, 2014), using the WOMBAT linear model program (Meyer, 2007). Genomic

information was available for the CPT sires (50k SNP Illumina ovine panel), the 2014 and 2015 CPT wethers (15k Illumina ovine panel), and 600 industry rams with no phenotype (a mixture of 50k and 15k). After removal of SNP based on QC checks, a combined imputed SNP genotype for 51,713 markers was constructed for all animals. Accuracy of breeding values were estimated as per Li *et al.* (2017) using the diagonal of the H matrix.

The fixed effects model fitted included birth type (1, 2, 3, 4+), rearing type (1, 2, 3+), age of dam (linear and quadratic covariates), and age (linear of animal), (when these were unknown default values for a single lamb born to a 4.5yr-old ewe were assumed). Contemporary group was also fitted as a fixed effect, defined by breed, flock, sex, date of measurement and management group (Huisman *et al.*, 2008). To account for genetic diversity between sires, sire breed (Merino (70% of progeny), Poll Merino (22%), Corriedale (4%), Polworth (3%), Dohne (1%), and South African Meat Merino (1%)) and dam breed were fitted as a fixed effect. The analysis was first undertaken using only the footrot records from the CPT wethers, before replicating the analysis with a larger data set that incorporated the industry recorded phenotypes and associated pedigree (Table 1). For both data sets the analysis was run with observed and transitioned phenotypes.

Table 1. Summary of the observed footrot scores recorded in the Central Progeny Test and provided by industry flocks.

Flock	Drop	Sex	Animals	Sires	Dams	Mean	Percentage of feet in Category						
							0	1	2	3	4	5	
Central Progeny Test Data													
1	CPT	2013	wethers	732	42	628	1.98	9	48	18	5	4	16
2	CPT	2014	wethers	657	41	0	2.92	3	12	7	45	33	0
3	CPT	2015	wethers	807	47	0	1.85	16	37	8	24	14	1
Industry Supplied Data													
4	SX	2016	rams	48	9	46	1.73	2	50	22	27	0	0
5	S	2016	rams	125	13	72	1.57	2	56	23	18	0	0
6	C	2016	rams	303	16	259	2.00	7	28	37	19	7	3
7	M	2016	rams	357	12	313	1.73	5	36	42	14	2	0
8	G	2016	rams	113	5	102	2.81	0	18	24	29	16	13
9	G	2016	ewes	135	5	114	3.46	0	7	23	16	23	30

Results and Discussion

Parameter estimates for footrot are presented in Table 2. Estimates for fixed effects (when known) were significant, but more complete data is needed before robust estimates are obtained. The heritability of average footrot (observed phenotypes) was 0.20 ± 0.05 from the CPT data, consistent with estimates reported in Merinos (Raadsma *et al.*, 1994) and other breeds (Skerman *et al.*, 1988, Nieuwhof *et al.*, 2008). The addition of industry data had no significant impact on the heritability estimate, but resulted in a small decline in the estimates of residual, genetic, and in turn phenotypic variances when the observed phenotypes were used. The difference in variance estimates between the CPT vs. CPT + Industry data analyses for observed phenotypes were likely in part due to differences in the severity of footrot challenges and the point of disease progression at which animals were scored during the challenge.

Transitioning the data to a standard level of underrunning reduced the residual and

genetic variances overall, although the resulting slightly higher heritability was not significantly different from the heritability for observed phenotypes. In contrast to observed (unadjusted) phenotypes, the addition of industry data to the analysis did not reduce the residual variance when the transition phenotypes were used (CPT; $v_e = 0.268 \pm 0.020$, CPT + Industry; $v_e = 0.276 \pm 0.015$). Transitioning the phenotypes to a similar level of under-running was previously shown by Walkom *et al.* (2017) to result in breeding values more comparable across challenge events.

Table 2. Phenotypic (V_p), additive genetic (V_a), and residual (V_e) variances and heritability (h^2) estimates for average footrot score (standard error in parentheses).

Data Set	Scale	V_p		V_a		V_e		h^2	
CPT	Observed	0.74	(0.02)	0.15	(0.04)	0.60	(0.04)	0.20	(0.05)
CPT + industry	Observed	0.66	(0.02)	0.12	(0.03)	0.53	(0.03)	0.19	(0.04)
CPT	Transitioned	0.36	(0.01)	0.09	(0.02)	0.27	(0.02)	0.26	(0.06)
CPT + industry	Transitioned	0.35	(0.01)	0.07	(0.02)	0.28	(0.02)	0.20	(0.04)

The objective of the CPT was to provide breeding values for footrot to the NZ Merino industry. The breeding values for average footrot ranged from -0.60 to 0.60 (Figure 1). Whilst the CPT provided breeding values for the progeny tested sires (Figure 1) the phenotypes were recorded on wethers. Therefore, selection could only be based on older sire breeding values (range = -0.47 to 0.61, mean accuracy = 0.66) and, without their own records, progeny could only be selected based on sire breeding values.

The single-step genomic BLUP model allowed for young selection candidates with genomic information to receive breeding values (range = -0.26 to 0.27). However, the accuracy of these estimates is heavily influenced by the animal's genomic relationship with the resource population resulting in a range in accuracies (0.07 to 0.49). By incorporating phenotypes from young industry animals recorded outside the CPT flock, selection decisions could be made on young rams and ewes which now have diverse breeding values (-0.43 to 0.69), with high accuracy (mean accuracy = 0.57, Figure 1).

Conclusions

Footrot is a heritable trait that is of commercial importance to the NZ Merino industry. Results from this study suggest that phenotypes recorded in industry flocks can be combined with CPT data to provide a basis to exploit the heritable variation and generate breeding values for a larger number of animals within the NZ Merino industry. Using single-step techniques allows the industry to take advantage of the genomic relationships which along with increased industry phenotyping is expected to improve the accuracy of selection within industry flocks.

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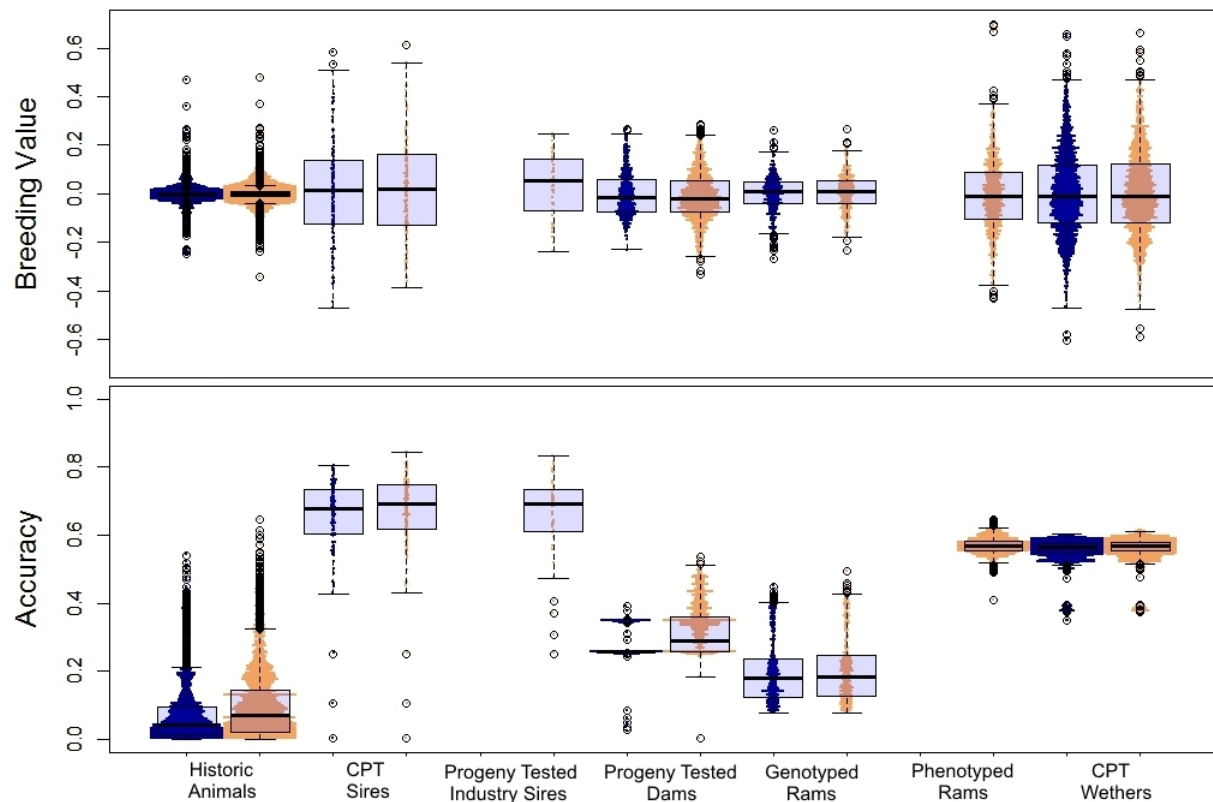


Figure 1. Distribution of estimated breeding values for Average footrot score (top) and accuracy of breeding values (bottom) when the analysis was based on CPT data (dark blue) and CPT + Industry data (orange) (data transitioned).

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