

BREEDS OF NEW ZEALAND SHEEP – AS RECORDED OR BY GENOMIC PREDICTION

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SUMMARY

The breed composition of the New Zealand sheep industry was examined to help understand the nature of this industry and observe recent trends. The maternal breeds of the New Zealand sheep meat industry are predominantly Romney with Coopworth, Perendale and Texel also common. The last 15 years has seen increased Perendale and Texel and decreased Coopworth numbers and a trend towards composites in ram breeding flocks. A genomic prediction method (gBLUP) was used to predict breed composition. Predicted breed composition was found to be similar to recorded breed for animals with similar breed composition to those in the training set used, and therefore is a useful method of verifying breed recording or predicting breed in unrecorded animals. Genomic prediction tended to over-predict breed components for animals of breed types not included in the training set.

INTRODUCTION

The breed composition of a population reveals the nature of that industry, and can inform research and policy decisions. The composition of the New Zealand (NZ) sheep meat industry is examined, primarily using the Sheep Improvement Limited (SIL; sil.co.nz) database. As more breeding stock are required to resource the national ewe flock than for terminal sires, these results mainly reflect the maternal breed composition.

Genotyping platforms that assay thousands of single nucleotide (SNP) markers have recently been used to predict breed composition (Sölkner *et al.* 2010, Kuehn *et al.* 2011; VanRaden *et al.* 2011; Frkonja *et al.* 2012). One such method was examined in NZ sheep populations, as it offers a method of breed designation without relying on animal recording, and may therefore be useful for validating sample origin and breed recording. It may also allow prediction of breed composition in unrecorded animals.

MATERIALS AND METHODS

Recorded breed. A file of all NZ sheep that have individual records was obtained from SIL's database. The information obtained included year of birth (BYR; 1960-2012) and breed proportions. Up to five different contributing breeds are recorded on SIL for each animal. These are determined by (preferentially): averaging the recorded breeds of the parents, direct recording by owner or by substituting the 'flock breed' for the breed of any unknown parent. The averaging process rounds values up to the nearest 0.5%.

Genomic prediction of breed. The OvineSNP50 SNP genotypes of 13,118 animals that had been genotyped by AgResearch, predominantly as part of an Ovita-funded research programme, up to August 2011 were obtained. Of these 8,705 were recorded on SIL at the time of analysis.

Genomic prediction of breed. Genomic selection (GS) methods were applied to the recorded breed proportions to develop predictions of breed proportions (VanRaden *et al.* 2011). Animals born prior to 2008, and with a recorded breed composition having more than 50% of either Romney (n=2849), Coopworth (n=1007), Perendale (n=290) or Texel (n=168), or more than 50% of Romney, Coopworth or Perendale combined (hereafter denoted "CompRCP"; n=103) were chosen for training. Prediction equations for each breed were calculated using the gBLUP method (Goddard *et al.*, 2010) using the model $y_i \sim \mu + u_i + e_i$, where y is the recorded proportion of

Romney, Coopworth, Perendale or Texel), μ is a constant, u_i is the modelled breed proportion and e_i is the residual, $\text{Var}(u)=G\sigma_a^2$, $\text{Var}(e)=I\sigma_e^2$ and G is the genomic relationship matrix calculated using the first method described by VanRaden (2008). The heritabilities ($\sigma_a^2/(\sigma_a^2+\sigma_e^2)$) of these 'traits' were fixed at 0.95. For animals not in the training set, predicted breed proportions were calculated directly from the animal's SNP data (VanRaden 2008). Principal components were calculated with the `prcomp` function of R (R Core Team, 2013) using the genomic relationship matrix (as described above) of all 13,118 genotyped animals as a similarity matrix. This was used to graphically display the results.

RESULTS AND DISCUSSION

Recorded breeds. A summary of NZ sheep breeds is shown in Table 1. SIL uses a set of breed definitions as required by its clients, and a number of these represent recent composites, but they are treated as additional 'pure' breeds here. SIL is underrepresented in fine-medium wool breeds (Merino, Corriedale and Halfbred), which use alternative genetic evaluation systems. Trends in recent years (Figure 1) are for stable numbers of Romney, decreasing Coopworth, increased Perendales and Texels (but levelled off), increased Poll Dorset and Suffolks (but now decreasing). The recorded numbers (full animal equivalents) of 'Composite' increased sharply from 2000 to 2005 and then levelled off. In recent years, less than 30% of animals with Coopworth were pure Coopworths. Corresponding figures for Romney, Perendale and Texel were around 70%, 60% and 5%, respectively.

Table 1. Breeds of sheep recorded on SIL from 2005 and estimates in the NZ population.

Breed	% (of purebreeds)	% in SIL [#]	% in genotyped subset	% in NZ*
Romney	53	44	52	58
Coopworth	7	9	23	11
Merino	<1	<1	0	8
Perendale	7	9	7	7
Corriedale	2	2	<1	6
Halfbred	NA	NA	0	4
Drysdale	<0.1	<0.1	0	1
Borderdale	<1	<1	<0.1	1
Texel	2	8	7	1

* <http://www.rarebreeds.co.nz/sheepnumbers.html>

including part contributions; Other breeds exceeding 2%: Poll Dorset (5%), Suffolk (4%), Composite (4%).

Breed Prediction. Graphical representations of the training set and the remaining animals are shown in Figures 2 and 3 respectively, using the first two principal components (PCs). These explained 66% of the variation (proportion of eigenvalues) in the relationship matrix. The predictions are not always between zero and one, but were seldom more than 0.1 from this range. When the prediction equations were applied to a subset of the SIL recorded animals (whose genotypes were available at that time, and whose SIL breed matched one of the training set breed types), the regression of predicted on recorded breed had correlations ranging from 0.92 (for proportion of Texel) to 0.98 (for proportion of Romney). The slopes of the regressions ranged from 0.96 (Coopworth) to 1.06 (Texel). These results suggest that the genomic selection method is predicting the recorded breed closely, at least within this set of breed types.

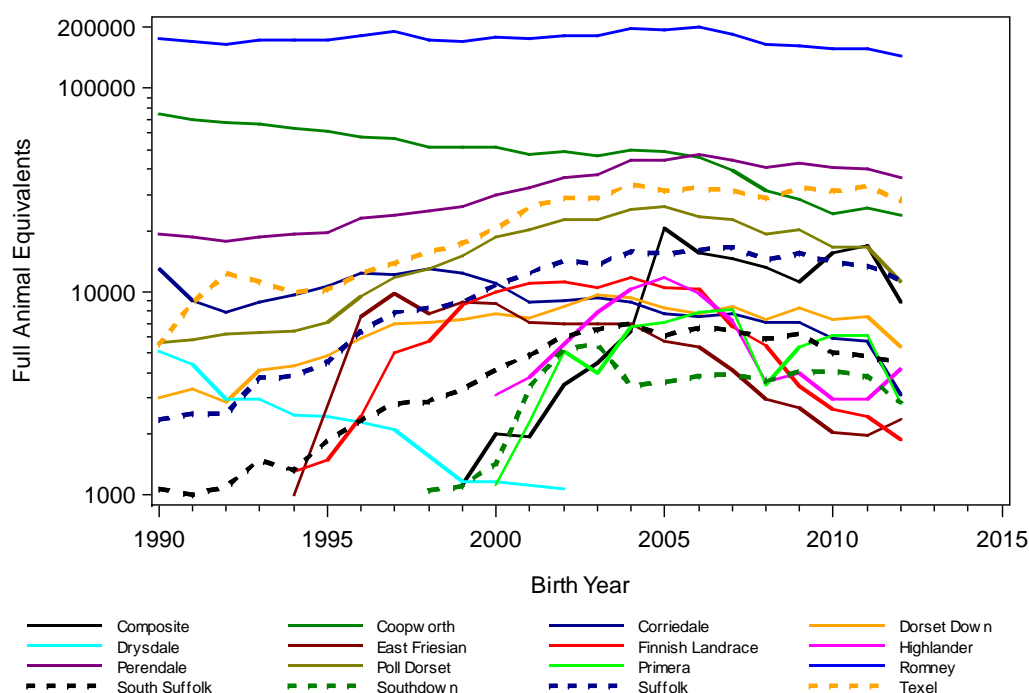


Figure 1. Full animal equivalents of each breed recorded on SIL for each birth year.

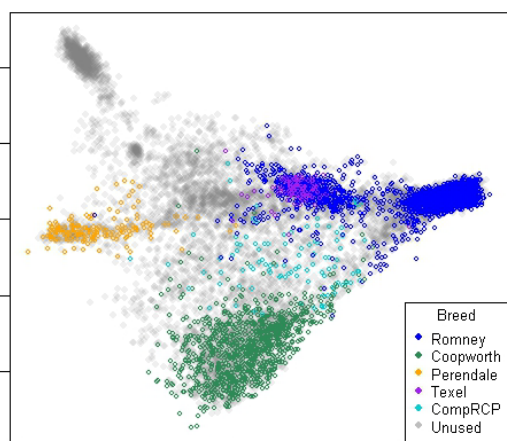


Figure 2. Plot of the first two principal components (PC2 v PC1) of the training set (coloured) for the genomic selection method.

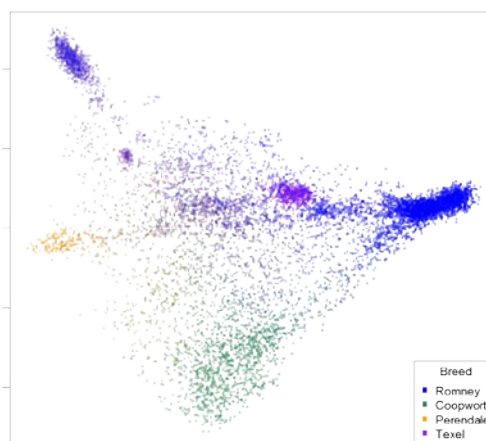


Figure 3. Predicted breed composition of 8776 animals (PC2 v PC1) not in the training set. Points increase in transparency as predicted breed proportions decrease.

The graphs show that breeds cluster together. Coopworths are more spread out than the other breeds, possibly reflecting that a relatively smaller percentage of Coopworth animals are recorded as pure. It may also reflect that the Coopworth breed has allowed some introgression of other breeds, and therefore they are likely to be more diverse than a closed breed. The Romney breed is

mainly located in one region, but some extend across the position of the Perendales (in PC2-PC1 space). This substructure may be a result of differing breeding priorities within this breed.

Animals in the upper left quadrants (Figure 3) are predicted to have a low proportion of each breed being predicted. The animals in this region tend to be meat breeds or composites (mainly Primera, Poll Dorset, Suffolk, and Wiltshire; see Table 2). Therefore the predicted breed proportions are likely to be overestimates. This suggests that the prediction method does not work so well in regions that did not contain any training set animals. It remains to be seen if these predictions would drop if some of these animals were included in training. An intriguing result is the estimated proportions in the four Cheviots genotyped, being about 140% Perendale and -40% Romney, which points to the Romney x Cheviot origins of Perendales.

Table 2. Mean predicted proportions, for Romney (pRom), Coopworth (pCoop), Perendale (pPere) and Texel (pTex) in animals that are recorded as purebred and that were not used for training. Results are shown for Cheviots and breeds with at least 10 animals genotyped.

Breed	n	pRom	pCoop	pPere	pTex
Romney	1496	0.985	0.007	0.003	0.002
Coopworth	286	0.022	0.937	0.011	0.021
Perendale	262	0.036	0.017	0.933	0.009
Texel	57	0.025	0.041	0.037	0.869
Corriedale	42	0.084	0.403	0.212	0.145
Poll Dorset	39	0.333	0.090	0.099	0.054
Suffolk	25	0.241	0.127	0.318	0.140
Finnish Landrace	12	0.123	0.167	0.217	0.134
Marshall Romney	10	0.709	0.110	0.116	0.015
Cheviot	4	-0.444	-0.033	1.389	0.046

CONCLUSIONS

NZ meat sheep are predominantly Romney with recent increases in Perendale and Texel and decreases in Coopworth. There is also a trend towards composites. Genomic methods offer a novel method for predicting breed or breed composition, without animal recording. There is a need for additional samples from the base breeds not currently sampled.

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