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GENOMIC PREDICTIONS FOR MEAT COLOUR TRAITS IN NEW ZEALAND SHEEP

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SUMMARY

The aim of this study was to evaluate the accuracy of genomic prediction for lamb meat colour traits in New Zealand sheep. A total number of 7,602 animals born between 2010 and 2013 were genotyped with the High-Density Ovine BeadChip containing 606,006 single nucleotide polymorphisms. The traits included in this study were: loin redness (A24), yellowness (B24) and lightness (L24) measured 24 hours after blooming. The significance of the fixed effects and covariates were determined using general linear model. The final fixed effects models included contemporary group, sex and birthday deviation from the contemporary group mean as a covariate. The residual from the above model was used as phenotype for the genomic evaluation model development. The software GEBV was used to calculate direct genomic values (DGV), using GBLUP methodology. To evaluate the accuracy of genomic prediction, two sets of animals were formed based on birth year: training (birth years: 2010, 2011 and 2012) and validation (birth year: 2013) sets. The accuracies for the three traits ranged from 0.29 to 0.33. Even though the accuracies were low, considering the costs and difficulty to measure and to select for meat quality traits, genomic selection might be a viable alternative.

INTRODUCTION

Meat colour traits have high economic relevance for the sheep industry as it is directly related to the appearance of the product, being an indicator of freshness and quality to consumers. In order to achieve consumer satisfaction, good management practices and environmental conditions for the animals and subsequently during meat processing play a very important role in the meat colour traits. However, it is known that meat colour has also a genetic component (e.g. Payne *et al*. 2009; Mortimer et al. 2014) and the gains achieved through genetic selection are permanent and cumulative. In order to genetically improve these traits, phenotypes must be recorded. However, they can only be recorded post-slaughter and are expensive to measure. Progeny testing not only increases the cost but also the generation interval. One possible solution to genetic improvement of these traits is genomic selection (Meuwissen *et al*. 2001), which has become a routine procedure because it reduces both progeny testing costs and generation interval. It refers to selection based on genomic breeding values, calculated from high density marker data. The benefits from genomic selection depend on the generation of accurate genomic breeding values (GEBVs). GEBV accuracies have been published for many traits in sheep (e.g. Daetwyler *et al*. 2012; Auvray *et al*. 2014). However such estimates are scarce for meat colour traits. The aim of this study was to evaluate the accuracy of genomic prediction for meat colour traits in New Zealand sheep, using the GBLUP methodology.

MATERIAL AND METHODS

Phenotypic data. Pedigree and performance records were obtained from the Sheep Improvement Limited database (SIL, www.sil.co.nz). A total of 7,602 animals born between 2010 and 2013 in the FarmIQ Progeny Test flocks (www.farmiq.co.nz) were included in this study. These animals were primarily progeny from terminal sire composites and Texel mated to a variety of maternal breeds. Animals were randomly selected to be slaughtered on given dates at commercial abattoirs. There were four to five slaughters per year and processing procedures and times were kept the same for each slaughter. The traits included in this study were: loin redness (A24), yellowness (B24) and lightness (L24) measured at 24 hours after blooming.

On the day after the slaughter, the boneless loins were vacuum packed and stored at -1°C for 8 weeks (to simulate the period that takes for chilled lamb to reach the retail market). At 8 weeks post-processing, loin pH was measured on the *Longissimus dorsi* muscle and three 2-cm thick slices of the loin were placed on small plastic trays and wrapped using semi permeable cling film and stored at 4°C (to simulate retail display) for colour measurements at 24, 48, 96 and 168 hours (seven days). Measurements were taken using a Minolta Chromometer (Konica Minolta Sensing, Inc., Osaka Japan). Three replicates were collected and the average value for each were analysed. The chromometer measures colour using the standard CIE L* a* b* colour variables (CIE L* = lightness/darkness; CIE a* = redness/brownness; CIE b* = yellowness). Only measurements at 24 hours are presented in this paper and are taken to represent the maximum redness (A value) post blooming.

The significance of the fixed effects and covariates were determined using the general linear model (GLM) procedure of SAS (SAS Inst., Inc., Cary, NC). The final fixed effects models included contemporary group, sex and to offset the differences in age of measurement, birthday deviation from the mean of the contemporary group was used as a covariate in the analysis. Contemporary group was defined by flock, birth year, sex, weaning mob (management group) and trait measurement/slaughter mob. The residual for each animal after adjusting for the above effects was used as the phenotype for the GEBV model development.

Genomic data. Marker genotypes were obtained using the Illumina High-Density Ovine BeadChip (Illumina Inc., San Diego, CA, USA), containing 606,006 single nucleotide polymorphisms (SNPs). SNPs were excluded from the analysis if minor allele frequency was less than one percent, call rate less than 90%, if they were located on the sex chromosomes, did not have known chromosome and/or position on the genome, had duplicated map positions (2 SNPs with the same position but with different names) or an extreme departure from Hardy Weinberg equilibrium ($p < 10^{-15}$). A total of 519,186 SNPs were retained for further analyses after filtering.

The software GEBV (Sargolzaei *et al*. 2009), was used to calculate direct genomic values (DGV), using the GBLUP methodology. The following model was used in genomic analysis:

$\boldsymbol{y} = \mathbf{1}\mu + \boldsymbol{Wa} + \boldsymbol{e}$, where **y** is the vector of phenotypes adjusted for fixed effects, **μ** is the overall mean, **a** is the vector of random animal DGVs, $\boldsymbol{e}$ is the vector of random residual effects, **1** is a vector of 1s and **W** is the design matrix linking records to animal DGVs. The DGVs were assumed normally distributed with mean zero and variance equal to $\mathbf{G}*\boldsymbol{\sigma}_g^2$, where **G** is the genomic relationship matrix based on the SNP markers and $\boldsymbol{\sigma}_g^2$ is the genetic variance. The random residual effects were assumed normally distributed with mean zero and variance equal to $\mathbf{I}*\boldsymbol{\sigma}_e^2$, where **I** is an identity matrix and $\boldsymbol{\sigma}_e^2$ is the residual variance.

To evaluate the accuracy of genomic prediction, two sets of animals were formed based on year of birth: training (birth years: 2010, 2011 and 2012) and validation (birth year: 2013) sets. For each trait, 10 runs were performed where each time a randomly selected group of approximately 300 animals born in 2013 (validation set) were taken as the validation set and all the animals from

the training. The youngest cohort of animals were used in validation to mimic what would happen in practice and the number of 300 was chosen in order to keep a practical number of animals in the validation set. The genomic prediction accuracy in the validation set was calculated as the Pearson correlation between DGV and adjusted phenotypes divided by the square root of heritability. The heritability was estimated from the same dataset using Restricted Maximum Likelihood (REML) procedures fitting an animal model and the same fixed effects described before, using ASReml 3.0 (Gilmour *et al.* 2009).

RESULTS AND DISCUSSION

Number of observations, trait means (± SD), trait range, coefficient of variation and the estimated heritabilities (± SE) are given in Table 1. The traits included in this study had low heritability estimates. Despite the variation in heritabilities, the DGV accuracy estimates were similar and ranged from 0.29 to 0.33 (Table 2). L24 presented the highest Pearson correlation between DGVs and adjusted phenotypes; however B24 presented a lower heritability and consequently the accuracy estimates were similar (0.32 and 0.33, respectively).

Table 1. Trait statistics and heritability estimates

Trait[1]	N	Mean ± SD	Range	CV (%)	h^2 ± SE
A24	7,602	16.79 ± 2.51	9.62 – 24.44	14.98	0.17 ± 0.03
B24	7,601	12.82 ± 2.65	5.68 – 20.31	20.68	0.11 ± 0.02
L24	7,601	40.45 ± 3.43	29.09 – 51.25	8.47	0.16 ± 0.03

[1]A24: redness/brownness; B24: yellowness; L24: lightness/darkness; N=number of animals; SD=standard deviation; CV=coefficient of variation; h^2=heritability; SE= standard error.

One reason that may contribute to the moderately low accuracies may be the low heritabilities of the traits. The accuracy estimates presented are global accuracies and robust accuracies could differ in various breed subgroups. Although our reference set appears large, almost all animals are crossbreds and/or composites from a variety of breeds. According to Saatchi *et al*. (2011) the validation is sensitive to the choice of the validation sample and to the pedigree relationships between the animals contributing to the validation and training sets, and the accuracies of DGVs are dependent on the strength of genetic relationships between the training and validation sets. It highlights the importance of maintaining an approximately constant average genetic relationship between animals in the training set and younger animals available for selection. One alternative is to define training and validation sets that are more related and also to evaluate other methodologies such as genomic evaluations using a single step procedure (Misztal *et al*. 2009) that would allow including phenotypes of non-genotyped individuals in the predictions.

In general, low accuracies of genomic breeding values limit the benefit from genomic selection. However, for traits such as meat color that are difficult to improve by traditional selection, genomic selection will be an important tool. The genomic values would help to predict breeding value of young selection candidates (without their own performance). It would result to reduced costs, shorten generation intervals, and hence accelerate the rate of genetic gain. However, future investigations are needed in order to find alternatives to increase the genomic breeding values accuracies for meat colour traits.

It is also important to highlight the need for the industry to continue investing in phenotyping and genotyping animals to create and maintain good reference and validation sets to develop accurate genomic predictions.

Table 2. Number of individuals in training and validation populations and accuracy of genomic prediction for meat colour traits

Trait	N in training	N in validation	Mean accuracy[1] (± SD)
A24	5,980	1,622	0.29 ± 0.08
B24	5,979	1,622	0.33 ± 0.11
L24	5,979	1,622	0.32 ± 0.04

[1]Mean accuracy estimated via 10 groups of around 300 animals. N=number of animals; SD=standard deviation; A24=redness/brownness; B24=yellowness; L24=lightness/darkness.

CONCLUSION

Genomic selection is likely to be a valuable tool to help in the improvement of difficult to measure phenotypes and low heritability traits such as meat colour. The findings in this study show that it is possible to generate molecular breeding values for rams at an early age for selection and breeding, thus reducing both generation interval and the costs of progeny testing. Further research will help to improve the accuracies of genomic breeding values for meat colour traits.

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REFERENCES

Auvray B., McEwan J.C., Newman S.-A. N., Lee M. and Dodds K.G. (2014) *J. Anim. Sci.* **92**: 4375.

Daetwyler H.D., Swan A.A., van der Werf J.H.J and Hayes B.J. (2012). *Genet. Sel. Evol*. **44**: 33.

Gilmour A.R., Gogel B.J., Cullis B.R. and Thompson R. *ASReml user guide release 3.0.* VSN International Ltd, Hemel Hempstead, UK, 2009.

Meuwissen T.H., Hayes B.J. and Goddard M.E. (2001). *Genetics*. **157**: 1819

Misztal I., Legarra A.and Aguilar I. (2009) *J. Dairy Sci.*, **92**: 4648

Mortimer S.I., van derWerf J.H.J., Jacob R.H., Hopkins D.L., Pannier L., *et al*. (2014) *Meat Sci.*, **96**(2 Pt B): 1016

Payne G., Campbell A.W., Jopson N.B., McEwan J.C., Logan C.M., *et al*. (2009). *Proc. NZ Soc. Anim. Prod*. **69**: 210

Saatchi M., McClure M.C., McKay S., Rolf M., Kim J., *et al*. (2011). *Genet. Sel. Evol*. **43**: 40.

Sargolzaei M., Schenkel F.S. and VanRaden P.M. (2009). in *Dairy Cattle Breeding and Genetics Meeting. 7(1).*