

CHANGE IN ACCURACY OF ESTIMATED BREEDING VALUES FOR VIAscan LEAN-MEAT YIELD WHEN ESTIMATED FROM HALF-SIB RECORDS.

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SUMMARY

In-plant sheep carcass grading systems offer ram breeders the opportunity to use carcass yield data from culls in genetic evaluations. This is a special case of two-stage selection where the second-stage measurement is not made on selection candidates in the nucleus, but on half-sib relatives that have been slaughtered. Carcass yield data from ~ 11,500 progeny of 257 sires in the Beef + Lamb New Zealand Central Progeny Test were used to investigate the loss in breeding value accuracy in this scenario. All animals had pedigree recorded, weaning weight and weight of lean in the hindleg, loin and shoulder primal cuts measured by VIAscan. Datasets were prepared where VIAscan measurements were retained for a random 5%, 10%, 20%, 30%, 40% and 50% of animals, each replicated five times. Breeding values were estimated for each dataset, along with datasets comprising 0% and 100% of VIAscan records retained. Breeding values for all individuals without VIAscan records were regressed against their breeding value in the 100% dataset to determine the loss of accuracy from having records on a proportion of half-sibs rather than their own (plus their half-sibs) records. Results indicate an asymptotic increase in EBV accuracy with increasing VIAscan records. When the proportion of animals with records reaches 50%, accuracy increases to 76.0%, 67.6% and 72.8% for VIAscan leg, loin and shoulder meat yield, respectively.

INTRODUCTION

There are limitations in selection programmes for carcass traits due to the fact that many traits can only be measured post-slaughter, or in the live animal with expensive technologies such as CT scanning (Young *et al.* 1996). Measurement at slaughter is problematic because slaughter obviously precludes the animal from being a selection candidate. Meat processors in New Zealand are using carcass grading systems like VIAscan (Hopkins *et al.* 2004) which routinely give estimates of lean meat yield for carcass primal cuts. There is potentially useful carcass data collected on ram breeders' culls at slaughter that could improve meat yield breeding values. This is a special case of two stage selection (Jopson *et al.* 2004), where the primary measures are ultrasonic eye muscle dimensions, and second-stage carcass measurements are not made on highly-ranked selection candidates in the nucleus, but on half-sib relatives sent for slaughter. The accuracy of an individual's breeding value (EBV) is influenced by, amongst other things, whether the animal or its relatives were measured for a trait, the number of relatives measured and the relationship with relatives (Falconer and Mackay, 1996). The loss of accuracy in meat yield EBVs due to half-sibs of selection candidates being measured rather than candidates themselves is not known. The aim of this research was to simulate differing proportions of culls with meat yield measurements and investigate the effect on EBVs in the individuals remaining in the flock

MATERIAL AND METHODS

A progeny test dataset comprising 11,500 progeny, from 257 sires, born between 2005 and 2013, was used. Pedigree and trait data were obtained from the Beef + Lamb New Zealand Central Progeny Test (McLean *et al.* 2006). VIAscan traits analysed were weight of lean in the hindleg, loin and shoulder primal cuts (VSLEG, VSLOIN and VSSHLD, respectively; Payne *et al.* 2009); and correlated traits fitted in the Sheep Improvement Limited (SIL) meat yield module,

namely live weight at weaning and eight months of age, ultrasonic eye muscle measurement and fat depth over the eye muscle at the 12th rib (WWT, LW8, EMA and FD, respectively; Jopson *et al.* 2009).

Slaughter progeny included all the progeny of terminal sire rams and the male progeny of dual purpose rams. Slaughter animals were drafted at monthly intervals from weaning at 12 weeks of age to achieve an 18 kg carcass weight. All lambs were slaughtered at Alliance Group Plants, and evaluated using VIAscan (Hopkins *et al.* 2004) for VSLEG, VSLOIN, VSSHLD and carcass weight (CWT). The retained ewe progeny from dual purpose sires were weighed for LW8 and ultrasound scanned to measure eye muscle area (EMA) and fat depth over the eye muscle (FD) approximately 180 days after the mean lambing date of each flock.

All slaughtered progeny in the dataset had VIAscan records. New datasets were created where VIAscan records (VSLEG, VSLOIN, VSSHLD and CWT) were set to missing for a randomly selected proportion of the dataset. Datasets were produced where only a random 5%, 10%, 20%, 30%, 40% and 50% (referred to as P5 to P50, respectively) had VIAscan records present, with each dataset replicated five times. Datasets where 0 and 100% (P0 and P100, respectively) of VIAscan measurements were present were also produced, this provides datasets with EBVs estimated from correlated traits only and a dataset where EBVs are estimated from the true measurement of every animal.

EBVs were calculated using the SIL genetic engine (Young and Wakelin 2009), which are produced using a multi-trait animal model in ASReml (Gilmour *et al.* 1999). The models included terms for age of dam, birth and rearing rank, contemporary group (flock, birth year, sex, weaning mob and slaughter mob) and birthday deviation (as a covariate) for the traits WWT, LW8, FD, EMA, VSLEG, VSLOIN and VSSHLD, respectively, and a random animal effect. Breeding values were then compiled in a master dataset, and analysed in SAS (2013) with binary indicators to identify if the animal had its own VIAscan phenotypic records included or excluded for each iteration. Animals with EBVs predicted solely from relatives (i.e. their own VIAscan records were set to missing) were then regressed against the EBVs for the same animals from the P100 dataset, to produce Pearson correlation (accuracy relative to the EBV when all animals are measured for the trait).

RESULTS

The accuracy of EBVs for the three VIAscan traits estimated when no VIAscan data were present (i.e. based solely on live weight and ultrasound scanning data) ranged from 75.9 to 78.4% relative to EBVs when all animals have VIAscan records (Table 1). The average progeny per sire with VIAscan records ranged between 2.3 and 20.0 for P5 and P50, respectively. Some sires with small numbers of progeny were not represented with VIAscan records in the P5 and P10 datasets, but effectively all sires had progeny with records present for the P20 to P50 datasets.

Table 1. Mean accuracy (r) of EBVs for animals based on a proportion of half-sib relatives having VIAscan records relative to EBVs when all animals had records.

	P0	P5	P10	P20	P30	P40	P50
VSLEG	0.784	0.793	0.808	0.835	0.851	0.863	0.872
VSLOIN	0.766	0.764	0.771	0.786	0.798	0.809	0.817
VSSHLD	0.759	0.777	0.794	0.819	0.836	0.846	0.855
Sires	NA	205	239	253	255	255	257
Progeny/sire	0	2.3	4.1	7.9	12.0	16.1	20.0

The addition of VIAscan data increased the accuracy values for all three EBVs, increasing accuracy to between 81.7 and 87.2% for the P50 datasets. The majority of the improvement in accuracy was observed in the P5 to P30 datasets, with the response appearing to be heading for an asymptote in the P50 datasets. There was very good agreement in accuracy results across replicates as can be seen for VSSHLD in Figure 1.

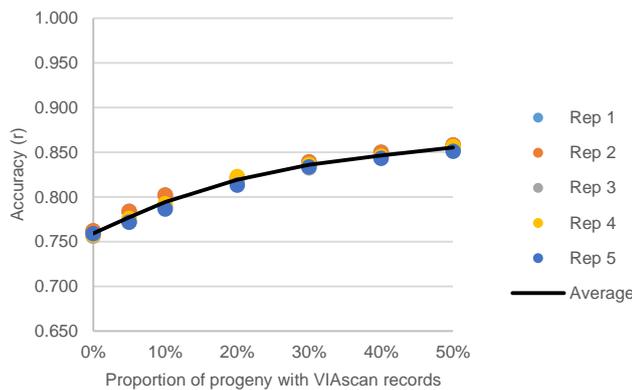


Figure 1. Accuracy of VIAscan shoulder EBVs relative to the true breeding value (TBV).

DISCUSSION

Ram breeders have a range of technologies available for prediction of meat yield to incorporate into their breeding programmes. This includes ultrasound scanning, CT scanning, and now VIAscan carcass grading as an in-plant measurement of meat yield in the hindleg, loin and shoulder primal cuts. Meat yield breeding values that use data from all three are available through SIL. However, the gains that can be made using data collected in plant have not been quantified. Some loss of EBV accuracy is expected due to the fact that the animals must be slaughtered to gather the measurement so selection candidates are not measured, compared to a situation where it is possible to measure the selection candidate itself.

The accuracy values from the P0 dataset for hindleg, loin and shoulder yield EBVs are 78.4%, 76.6% and 75.9% respectively. This level of accuracy illustrates that LW8, WWT, EMA, and FD are relatively highly correlated with the VIAscan traits (Payne *et al.* 2009) and therefore contribute significantly to the prediction of meat yield breeding values (Thompson and Meyer 1986). The results also show that a significant improvement in EBV accuracy can be made by using in-plant VIAscan measurements compared to not collecting any data at slaughter (i.e. compared to the P0 treatment). The majority of the improvement in accuracy was achieved by sampling between P20 and P30 treatments (i.e. a random 20 to 30 percent of animals slaughtered and measured). The economic benefit has not been considered, and so the cost of not having the slaughtered animals available for use in the nucleus or as rams for sale to commercial farmers has not been accounted for. This would need to be estimated to optimise the use of VIAscan measurement in a nucleus flock.

The asymptotic curve observed in Figure 1 indicates that 100% accuracy would not be achieved if it were in fact possible to collect VIAscan records on all individuals and still have selection candidates available. While this appears somewhat counter-intuitive, half-sibs only have around 25% of their alleles in common (Falconer and Mackay 1996) so 100% accuracy can never be achieved where the selection candidate is not measured for a goal trait, but some of its half-sib relatives were measured for the trait.

There are two practical factors that need to be considered in interpreting these results. Firstly, the Central Progeny Test dataset is not typical of a nucleus flock in that it is a progeny test design where a large proportion of progeny are slaughtered. In a breeder's nucleus flock, there will be many genetic connections between the rams used in the flock, all of which would be expected to improve the accuracy of breeding values, especially over time as the depth of pedigree increased (Falconer and Mackay 1996) .

Secondly, the simulated culling was based on random selection of animals. In practice farmers are likely to select a biased sample of lower-ranked animals based on live weight and ultrasonic scanning data. While some animals with high EBVs may be culled for physical faults, these are expected to be a minority. This results in truncated selection within the flock, rather than random selection. Truncated selection would also introduce unbalanced representation of sire lines in the animals sent for slaughter measurement. Thus the accuracy figure presented here may be higher than would be achieved in practice through truncated selection (Weigel 2001). However, the extent of this is unknown, but could be determined through further simulation.

CONCLUSION

Meat yield breeding values for selection candidates estimated using data collected from half-sib relatives give EBV accuracy levels intermediate between not collecting VIAscan measurements and having a technology that can measure meat yield in the live animal. Collecting measurements on a random 12 progeny per sire (P30) gives close to the maximum improvement in EBV accuracy, but an economic analysis is needed to determine the optimum level.

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REFERENCES

- Falconer D.S. and Mackay T.F.C. (1996) *Introduction to Quantitative Genetics*. 4th Ed. Pearson Prentice Hall.
- Gilmour A.R., Cullis B.R., Welham S.J. and Thompson R. (1999) ASREML Reference Manual. NSW Agriculture.
- Hopkins D.L., Safari, E., Thompson, J.M. and Smith, C.R. (2004) *Meat Sci.* **67**: 269.
- Jopson N.B., Amer P.R. and McEwan J.C. (2004) *Proc. N.Z. Soc. Anim. Prod.* **64**: 212.
- Jopson N.B., Newman S-A.N., McEwan J.C. (2009) *Proc. N.Z. Soc. Anim. Prod.* **69**: 158.
- McLean N.J., Jopson N.B., Campbell A.W., Knowler K., Behrent M., *et al.* (2006) *Proc. N.Z. Soc. Anim. Prod.* **66**: 368.
- Payne G.M., Campbell A.W., Jopson N.B., McEwan J.C., Logan C.M. and Muir P.D. (2009) *Proc. N.Z. Soc. Anim. Prod.* **69**: 210.
- SAS Institute Inc. (2013) SAS/STAT 9.3 Users Guide. Cary, NC: SAS Institute Inc.
- Thompson R. and Meyer K. (1986) *Livest Prod Sci* **15**: 299.
- Weigel K.A. (2001) *J Dairy Sci.* **84**: E177
- Young M.J. and Wakelin R. (2009) *Proc. N.Z. Soc. Anim. Prod.* **69**: 148.
- Young M.J., Nsoso S.J., Logan C.M. and Beatson P.R. (1996) *Proc. N.Z. Soc. Anim. Prod.* **56**: 205.