

## **A PRELIMINARY EVALUATION OF A METHOD FOR INCORPORATING GENETIC INFORMATION INTO PHENOTYPIC PREDICTION MODELS**

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### **SUMMARY**

Genetic merit and phenotypic performance are generally predicted independently. Achieving further gains in production efficiency requires genetic and non-genetic fields of expertise work in an integrated manner to deliver new technologies. A study was undertaken using beef cattle to examine a method for incorporating genetic information into phenotypic prediction models. Relationships between fat deposition parameters in a modified version of the Meat Animal Research Centre (MARC) model and Rib Fat EBVs from the Angus cattle breed were explored. These relationships were incorporated into the MARC model and subsequent predictions of P8 fat depth were compared to a scenario where Rib Fat EBVs were not used. Generally small improvements in most measures of predictive accuracy were found. The full commercial benefit of integrating genetic information into phenotypic prediction models will be gained when genetic information is delivered across multi-breed platforms.

### **INTRODUCTION**

The importance of matching animal genotype and management practices with the prevailing production environment has been evident for quite some time. However, the prediction of genetic merit (breeding value) and phenotypic performance still occur relatively independently. Bourdon (1998) suggested predictions of genetic merit are presented without context making it difficult for breeders to effectively use them, particularly in diverse environments. Generally, simulation modelling designed to predict phenotypic performance suffers from the limitation of not giving due consideration to genetic merit. Most simulation models consider genetic merit is described by either breed or breedtype. Both represent impediments to increasing production efficiency. Recognising this Oddy (2009) argued genetics and nutrition need to be more integrated in their approach to delivering new technologies for use in animal production. Bourdon (1998) coined the term 'physiological breeding value' to describe genetic values for inclusion in simulation modelling. Kinghorn (2012) has described various ways genetic information can be used to assist livestock management beyond breeding decisions.

The purpose of this paper is to describe a method for incorporating genetic information into phenotypic prediction models. This will increase the utility of such tools for on-farm decision making and increase the acceptance of phenotypic and genetic prediction in animal production.

### **MATERIALS AND METHODS**

**Data.** Data used in this study originated from the New South Wales Department of Primary Industries muscling selection herd. This herd is described further elsewhere (McKiernan and Robards 1996, 1997; Walmsley and McKiernan 2011). Briefly, this herd originates from a group of Hereford cows mated to Angus bulls selected from industry herds in 1991 (McKiernan and Robards 1996, 1997) based on visual muscle score (McKiernan 1990). Heifer selection in subsequent generations was based on visual muscle score and single-sire matings were made to Angus bulls selected from industry for high or low muscling to increase/maximise divergence in muscle score between lines.

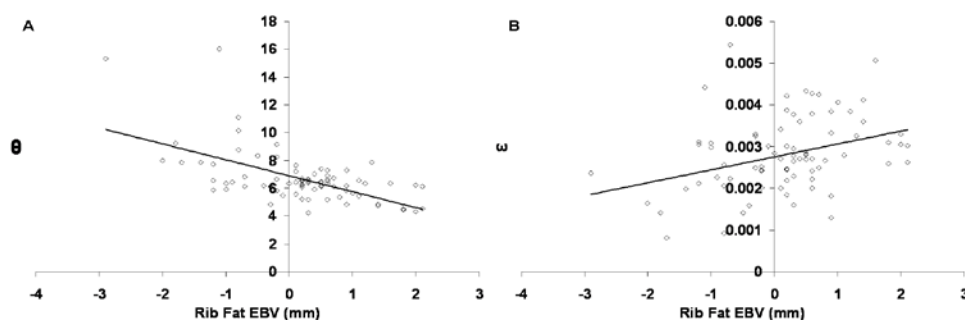
All progeny have had regular live weights, scanned fatness (P8, rib and IMF) and eye muscle areas recorded by a BREEDPLAN accredited scanner using real-time ultrasound following BREEDPLAN protocols (Graser *et al.* 2005). All pedigree information and recorded data have been submitted to the Angus group BREEDPLAN database and been used to estimate breeding values using the national genetic evaluation system, BREEDPLAN (Graser *et al.* 2005). Data were taken from steer cohorts born in 2006 and 2007 to evaluate the inclusion of EBVs in phenotypic prediction models. The 2006 cohort were used to develop and evaluate relationships between model parameters and EBVs with the 2007 cohort only being used to evaluate these relationships.

**Predicting Phenotypes.** A dynamic growth modelling system, called ‘BeefSpecs’, is used to predict animal phenotypes; specifically P8 fat depth (mm). A description of the development of BeefSpecs can be found in Walmsley *et al.* (2010a; 2011). BeefSpecs uses easy to obtain on-farm inputs (e.g. breed type, sex, frame score, live weight, P8 fat depth) in combination with differential equations to describe the pattern of lean and fatty tissue deposition in the empty body of animals (MARC model; Williams and Jenkins 1998). Total body fat is used to predict rib fat depth (mm) and in turn P8 fat depth (mm) (Walmsley *et al.* 2010b).

**Integrating Genetic Information.** The inclusion of genetic information in phenotypic prediction models was explored using the method outlined by Doeschl-Wilson *et al.* (2007) and Kinghorn (2012). In brief, this involves using differential evolution (DE; Price and Storn 1997) to manipulate parameters in the modified MARC model to achieve the best agreement between observed and predicted P8 fat depths. The first parameter modulates the impact weight gain has on body composition ( $\theta$ ; Keele *et al.* 1992) and the other term describes the relationship between total body fat and rib fat depth ( $\omega$ ; Williams *et al.* 1992). Regressions of estimated growth model parameters on Rib Fat EBV were then developed for inclusion in the modified MARC model.

**Statistical Analysis.** Sums of squares of difference are used by DE to compare observed and predicted P8 fat depths. Regressions between Rib Fat EBVs and model parameters were developed using the linear model function in the R statistical package (R Development Core Team 2011). Model predictions were evaluated using a customised procedure in R that included mean bias,  $[\sum(\text{observed} - \text{predicted})/n]$ , mean square error of prediction (MSEP) and the decomposition of MSEP into bias, slope and random components as proportions (Tedeschi 2006), as well as the regression slope and correlation between observed and predicted values. The root of MSEP (RMSEP) is used to present the prediction error on the same scale as fat depth.

## RESULTS AND DISCUSSION



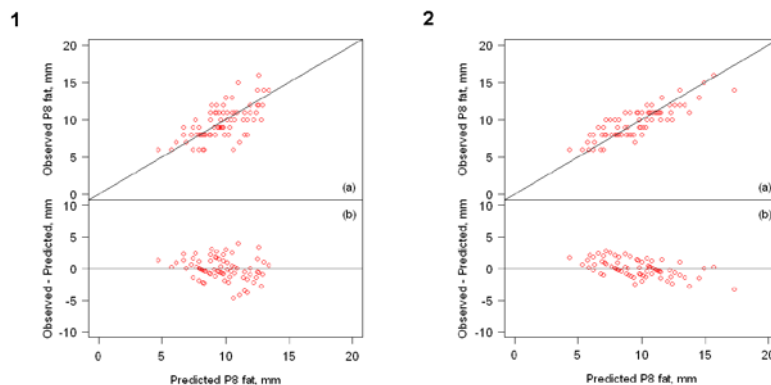
**Figure 1. Rib Fat EBV relationship with fat deposition parameters ( $\theta$  and  $\omega$ ) in the modified Meat Animal Research Centre model for the 2006 steer cohort from the New South Wales Department of Primary Industries muscling herd.**

Fat deposition parameters ( $\theta$  and  $\omega$ ) that produced the highest agreement with observed P8 fat depths in the 2006 steer cohort were determined using DE. The relationships Rib Fat EBVs have with these parameters are demonstrated in Figure 1. The regression of  $\theta$  on Rib Fat EBV was:  $\theta = 6.90$  (s.e. = 0.18) - 1.15\*EBV (s.e. = 0.18) ( $R^2 = 0.34$ ). The regression of  $\omega$  on Rib Fat EBV was:  $\omega = 2.75e^{-3}$  (s.e. =  $9.55e^{-5}$ ) + 3.10e<sup>-4</sup>\*EBV (s.e. = 9.64e<sup>-5</sup>) ( $R^2 = 0.12$ ). Regressions containing both Rib and Rump Fat EBVs were tested and resulted in similar accuracy.

**Table 1. Assessment of differences between observed and predicted P8 fat depths when not using (base) and using (EBV) Rib Fat EBVs to assist predictions in the 2006 and 2007 steer cohorts from the New South Wales Department of Primary Industries muscling herd.**

Descriptor	2006 Cohort		2007 Cohort	
	Base	EBV	Base	EBV
n	80		78	
Observed (O) P8 fat, mm	9.68		3.68	
Predicted (P) P8 fat, mm	9.61	9.69	4.09	4.06
Mean Bias, mm	0.06	-0.01	-0.41	-0.38
Slope of O vs. P, b	0.78	0.71	0.56	0.63
Correlation between O and P, r	0.65	0.87	0.37	0.45
RMSEP, mm	1.72	1.35	1.48	1.41
Bias, %	0.13	0.01	7.56	7.35
Slope, %	5.77	32.65	8.47	7.13
Random, %	94.10	67.34	83.97	85.51

The predictive accuracy of including Rib Fat EBVs in the MARC model is demonstrated in Table 1 in comparison to base scenarios where EBVs were not used. In the 2006 cohort there was a slight improvement in mean bias, correlation between observed and predicted, RMSEP and MSEP due to bias. However, the base scenario had a slope between observed and predicted that was closer to 1 and a lower proportion of MSEP was due to errors in the slope component. All measures of predictive accuracy improved slightly in the 2007 cohort compared to the base scenario when Rib Fat EBVs were incorporated to make predictions of P8 fat depth.



**Figure 2. Plot of (a) observed vs. predicted and (b) residual P8 fat depth when (1) not using and (2) using Rib Fat EBVs to assist predictions of P8 fat depth in the 2006 steer cohort from the New South Wales Department of Primary Industries muscling herd.**

Differences between observed and predicted P8 fat depth in the 2006 cohort are shown in Figure 2. The improvements in mean bias and RMSEP due to the inclusion of Rib Fat EBVs in predictions of P8 fat depth seen in Table 1 are evident in Figure 2. The slight change in the slope between observed and predicted P8 fat depth seen in Table 1 is also recognisable. These results suggest there is scope for EBVs to be incorporated into phenotypic prediction models. However, some issues have arisen during this process. Some  $\theta$  values obtained from the linear regressions between  $\theta$  and Rib Fat EBV are beyond the parameter range considered realistic and thus these regressions need further investigation. Another important issue hindering the inclusion of EBVs in phenotypic prediction models is EBVs are currently derived on a breed specific basis. The modified MARC model functions across breeds by specification of breed type (British, European, *Bos Indicus*). Generation of EBVs applicable across breeds would compliment this and simplify their inclusion in phenotypic prediction models not only in beef cattle but other livestock species.

## CONCLUSIONS

The inclusion of Rib Fat EBVs in a modified MARC model slightly increased the accuracy of predicting P8 fat depth. This result indicates that EBV inclusion in phenotypic prediction models should be further explored over a wider range of EBVs. Some consideration should however be given to which model parameters are involved and their biological interpretation as well as the method of EBV delivery to industry (i.e. multibreed EBVs in preference to breed-specific EBVs).

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## REFERENCES

- Bourdon R.M. (1998) *J. Anim. Sci.* **76**: 2308
- Doeschl-Wilson A.B., Knap P.W., Kinghorn B.P. and van der Steen H.A.M. (2007) *Anim.* **1**: 489
- Graser H-U., Tier, B., Johnston D.J., and Barwick S.A. (2005) *Aust. J. Exp. Agric.* **45**: 913
- Keele J.W., Williams C.B. and Bennett G.L. (1992) *J. Anim. Sci.* **70**: 841
- Kinghorn B.P. (2012) *Anim. Prod. Sci.* **52**: 78
- McKiernan W.A. (1990) *Proc. Ass. Adv. Anim. Breed. Genet.* **9**: 447
- McKiernan W.A. and Robards G.E. (1996) *Proc. Aust. Soc. Anim. Prod.* **21**: 151
- McKiernan W.A. and Robards G.E. (1997) *Proc. Ass. Adv. Anim. Breed. Genet.* **12**: 77
- Oddy V.H. (2009) *Rec. Adv. Anim. Nut.* **17**: 103
- Price K. and Storn R. (1997) *Dr Dobb's J.* **264**: 18
- R Development Core Team (2011) R Foundation for Statistical Computing, Vienna, Austria. URL: <http://www.R-project.org>
- Tedeschi L.O. (2006) *Ag. Sys.* **89**: 225
- Walmsley B.J. and McKiernan W.A. (2011) *Proc. Ass. Adv. Anim. Breed. Genet.* **19**: 123
- Walmsley B.J., Oddy V.H., McPhee M.J., Mayer D.G. and McKiernan W.A. (2010a) *Aust. Farm Bus. Man. J.* **7**: 29
- Walmsley B.J., Wolcott M.L. and McPhee M.J. (2010b) *J. Anim. Sci.* **88**: 1848
- Walmsley B.J., Oddy V.H., McPhee M.J., Mayer D.G. and McKiernan W.A. (2011) *ODSIM2011, 19<sup>th</sup> International Congress on Modelling and Simulation* **19**: 898
- Williams C.B. and Jenkins T.G. (1998) *J. Anim. Sci.* **76**: 980
- Williams C.B., Keele J.W., and Bennett G.L. (1992) *J. Anim. Sci.* **70**: 858