

GENETIC PARAMETERS FOR STRUCTURAL TRAITS IN NEW ZEALAND BEEF CATTLE AND THEIR CORRELATIONS WITH PRODUCTION TRAITS

F. Weik^{1,2}, R.E. Hickson¹, S.T. Morris¹, D.J. Garrick¹ and J.A. Archer^{2,3}

¹School of Agriculture & Environment, Massey University, Palmerston North 4442, New Zealand

²AbacusBio Ltd, Dunedin 9058, New Zealand

³Current address: Beef + Lamb New Zealand Genetics, Dunedin 9054, New Zealand

SUMMARY

Structural soundness has the potential to affect the length of a productive life in beef cattle. The objectives of this study were to estimate genetic parameters for structural traits and to examine their relationship with production traits (mature weight, body condition score, 18-month weight and yearling hip height) measured in beef cattle in New Zealand. Heritabilities for structural traits were low to moderate ranging from 0.09 to 0.25. Genetic correlations among structural traits ranged from 0.18 to 1.00 whereas phenotypic and genetic correlations with production traits were generally low positive to moderate negative (-0.54–0.23) indicating only a limited impact on production.

INTRODUCTION

Structural soundness is believed to influence fitness of cattle in extensive pasture-based farming systems. Beef cattle may be required to walk long distances to graze so unsound structure may impact on cow performance. Scientific literature on structural traits of beef cattle is sparse and there are no previous reports from New Zealand. Research on structural soundness has been predominantly conducted in dairy cattle (Dechow *et al.* 2002) and there is some evidence that females with good conformation stay in the herd for longer (Berry *et al.* 2005). Most reports, however, have been focused on type traits other than feet and leg scores. Therefore, the objectives of this study were to estimate genetic parameters for 9 structural feet and leg traits recorded in commercially farmed beef cattle in New Zealand and to examine their relationship with mature cow weight (MWT), body condition score (BCS), 18-months weight (W18) and yearling hip height (HH).

MATERIALS AND METHODS

Dataset. The project was approved by the AgResearch Invermay Animal Ethics Committee. Data were obtained from an ongoing progeny test initiated in 2014 on 5 commercial New Zealand hill country farms to compare the performance of progeny derived from matings of Angus, Hereford, Simmental, Stabilizer and Charolais bulls over Angus or Hereford cows (Weik *et al.* 2021). The current study used data recorded between 2014 and 2020 for structural and production traits. Birth dates were not recorded, but age was assigned based on fetal age scanning.

Trait definitions. Structural traits were assessed according to the Beef Class Structural Assessment system (Breedplan 2021). Seven traits were recorded: front feet angle (FA), front feet claw set (FC), front legs front view (FF), rear feet angle (RA), rear feet claw set (RC), rear legs hind view (RH) and rear legs side view (RS). Records were available for a total of 2,294 animals for RA, 2,670 animals for RH and RS and 2,671 animals for all other structural traits at approximately 16–20 months of age by the same experienced Breedplan accredited assessor across all farms. Each trait was recorded following a linear assessment on a 1 to 9 scale, with 1 and 9 representing biological extremes with 5 as the intermediate optimum. No animals were scored at the extreme ends of the scale (1–2 or 9, respectively) and 99.6% of observations were between 5 and 7 (Table 1). Overall feet score was calculated for each animal by taking the worst score for FA and RA, or FC and RC, for overall feet angle (OA) and overall claw set (OC), respectively.

Four production traits were included in the correlation analyses, namely MWT, BCS, W18 and

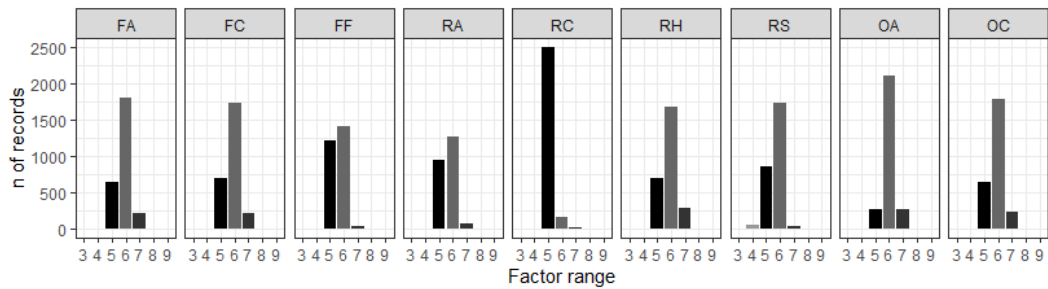


Figure 1. Distribution of scores for front feet angle (FA), front feet claw set (FC), front legs front view (FF), rear feet angle (RA), rear feet claw set (RC), rear legs hind view (RH), rear legs side view (RS), overall feet angle (OA) and overall claw set (OC)

HH. A total of 39,464 records were available for MWT. Data were obtained at 3 timepoints annually, prior to mating, at calf weaning and prior to calving for cows aged over 2 years. Cow BCS was recorded at the same times, generating 39,467 records based on visual assessment on a 1 to 10 scale (1=emaciated, 10=obese; Hickson *et al.* (2017)). Both traits were adjusted to a constant 6 years of age using fixed effect models with age and contemporary group (CG) as factors in the model.

A total of 7,048 progeny were recorded for weaning weight (WWT) between 110 and 228 days of age. Measures on W18 were available for 4,189 individuals measured between 455 and 752 days of age. Each animal was recorded once for WWT and W18. Linear and quadratic adjustments to 200 and 600 days of age were applied for WWT and W18 using a multiplicative approach similar to that described by Reverter *et al.* (2000). Records for HH were obtained once per animal between 277 and 417 days of age for 5,125 individuals, and adjusted to 365 days, using quadratic age adjustments.

Observations for production traits further than 3 standard deviations from the CG mean were deleted. For all structural traits, WWT and W18, CG comprised farm, sex, recording date and management group from birth until the day of recording. The CG for MWT and BCS consisted of farm, time of year, recording date and management group at the time of data collection. The HH CGs were made up of farm, sex and recording date. Individuals with missing CG information or CG containing only 1 animal were excluded from analyses. All production traits were tested for evidence of heterogeneity. Traits with a significant regression of CG mean on CG SD were scaled to homogenize the variance (Pickering *et al.* 2012).

Statistical analysis. Data quality control and pre-adjustments of phenotypes were conducted using R version 3.6 (R Core Team 2019). (Co)variance parameters were estimated using ASREML 4.1 (Gilmour *et al.* 2009). For all traits, WWT was included as a correlated trait to account for preselection. Thus, heritability estimates were obtained from bivariate animal models and genetic and phenotypic correlations from (co)variance parameters using a range of trivariate animal models.

Fixed effects included for all traits were CG, breed percentage and heterosis (purebred = 0, first-cross = 1). Age of dam was fitted as a factor for all structural traits as well as WWT, W18 and HH. Age at scoring was fitted as a linear covariate in the model for each structural trait. An animal effect and a residual error term were fitted as random effects for each trait, a permanent environmental effect was fitted for MWT and BCS due to repeated measures over time and a maternal additive genetic as well as a permanent environmental effect of the dam were fitted for WWT. Variance structures for the random effects were assumed as follows: $\text{var}(a) = \mathbf{A}\sigma_a^2$, $\text{var}(m) = \mathbf{A}\sigma_m^2$, $\text{var}(pe) = \mathbf{I}\sigma_{pe}^2$ and $\text{var}(e) = \mathbf{I}\sigma_e^2$. No covariance was fitted between direct and maternal genetic effects. The numerator relationship matrix (\mathbf{A}) included 13,325 animals with 394 sires and 4,098 dams.

RESULTS AND DISCUSSION

Means, phenotypic standard deviations and estimated heritabilities from bivariate analyses with

WWT for each structural trait are presented in Table 1. The means of all structural traits ranged from 5.1 to 6.0. The standard deviations (SD) were similar for most traits except RC. The limited number of extreme scores meant that SD were low for all structural traits.

Table 1. Raw means, phenotypic standard deviations (σ_P) and heritabilities (h^2) for structural traits with standard errors shown in brackets

	FA	FC	FF	RA	RC	RH	RS	OA	OC
Mean	5.8	5.8	5.6	5.6	5.1	5.9	5.7	6.0	5.8
σ_P	0.53	0.52	0.50	0.53	0.26	0.57	0.53	0.43	0.51
	(.09)	(.09)	(.08)	(.09)	(.04)	(.10)	(.09)	(.07)	(.09)
h^2	0.23	0.10	0.09	0.17	0.09	0.22	0.12	0.25	0.11
	(.05)	(.04)	(.04)	(.05)	(.04)	(.05)	(.04)	(.06)	(.04)

*For structural trait abbreviations see Figure 1

Table 2. Genetic (below diagonal) and phenotypic (above diagonal) correlations (se) from trivariate animal models among structural and production traits in New Zealand beef cattle

	FA	FC	FF	RA	RC	RH	RS	OA	OC	MWT	BCS	W18	HH
FA		0.38	0.22	-0.03	0.07	0.14	0.12	0.74	0.36	-0.07	-0.06	-0.09	0.00
		(.02)	(.02)	(.02)	(.02)	(.02)	(.02)	(.01)	(.02)	(.03)	(.03)	(.02)	(.02)
FC	0.99		0.17	0.02	0.02	0.12	0.14	0.27	0.95	-0.03	-0.04	-0.03	0.04
	(.12)		(.02)	(.02)	(.02)	(.02)	(.02)	(.00)	(.00)	(.03)	(.03)	(.02)	(.02)
FF	0.54	0.66		0.08	0.04	0.21	0.12	0.15	0.16	-0.06	-0.08	-0.13	0.01
	(.20)	(.27)		(.02)	(.02)	(.02)	(.02)	(.02)	(.02)	(.03)	(.03)	(.02)	(.02)
RA	0.24	0.19	0.69		0.15	0.09	0.08	0.39	0.04	-0.07	0.00	-0.12	-0.06
	(.20)	(.26)	(.24)		(.02)	(.02)	(.02)	(.02)	(.02)	(.03)	(.04)	(.02)	(.03)
RC	0.33	0.57	0.27	0.36		0.04	0.03	0.12	0.20	-0.05	-0.04	0.01	0.01
	(.23)	(.32)	(.32)	(.26)		(.02)	(.02)	(.02)	(.02)	(.03)	(.03)	(.02)	(.02)
RH	0.21	0.38	0.61	0.50	0.43		0.29	0.11	0.12	-0.08	-0.14	-0.17	0.07
	(.17)	(.21)	(.21)	(.18)	(.24)		(.02)	(.02)	(.02)	(.03)	(.03)	(.02)	(.02)
RS	0.42	0.60	0.18	0.72	0.53	0.26		0.12	0.13	-0.06	-0.14	-0.14	-0.02
	(.19)	(.25)	(.28)	(.21)	(.30)	(.20)		(.02)	(.02)	(.03)	(.03)	(.02)	(.02)
OA	0.92	0.76	0.79	0.53	0.32	0.27	0.56		0.26	-0.10	0.00	-0.11	-0.03
	(.04)	(.15)	(.19)	(.16)	(.23)	(.16)	(.18)		(.02)	(.03)	(.03)	(.02)	(.03)
OC	0.91	1.00	0.61	0.22	0.66	0.34	0.59	0.69		-0.05	-0.05	-0.02	0.04
	(.12)	(.02)	(.26)	(.24)	(.26)	(.21)	(.25)	(.15)		(.03)	(.03)	(.02)	(.02)
MWT	-0.19	-0.10	-0.21	-0.16	-0.16	-0.16	-0.16	-0.20	-0.13				
	(.07)	(.11)	(.12)	(.09)	(.12)	(.08)	(.10)	(.07)	(.11)				
BCS	-0.07	-0.14	-0.27	-0.10	-0.09	-0.54	-0.35	-0.03	-0.12				
	(.09)	(.13)	(.14)	(.11)	(.14)	(.10)	(.12)	(.09)	(.12)				
W18	-0.17	-0.04	-0.30	-0.53	-0.27	-0.09	-0.06	-0.32	-0.08				
	(.12)	(.17)	(.17)	(.13)	(.18)	(.12)	(.16)	(.11)	(.16)				
HH	0.07	0.15	0.23	-0.19	-0.07	0.19	-0.12	-0.03	0.14				
	(.12)	(.17)	(.18)	(.15)	(.18)	(.12)	(.16)	(.12)	(.16)				

*For structural trait abbreviations see Figure 1; MWT=mature cow weight, BCS=body condition score, W18=18-month weight, HH=yearling hip height

The estimated heritabilities for structural traits were in the low-to-mid range from 0.09 to 0.25, consistent with Jeyaruban *et al.* (2012) and Vallee *et al.* (2015). Heritabilities for front feet observations were higher than their rear counterparts. The highest heritabilities were estimated for FA, RH and OA. Production traits were moderately to highly heritable with 0.57 (0.03) for MWT, 0.54 (0.04) for W18 and 0.52 (0.04) for HH and the estimated heritability was lowest for BCS at

0.25 (0.03). Those values are consistent with estimates from the literature.

Genetic and phenotypic correlations are shown in Table 2. Phenotypic correlations among structural traits were generally positive and lower than genetic correlations. The estimated genetic correlations were positive among all structural traits ranging from 0.18 to 1.00. The highest correlations were observed between FA and FC (0.99) and the part-whole correlations FA and OA (0.92) and FC and OC (1.00). Correlations between both rear feet traits and the overall foot scores, however, were lower with 0.53 between RA and OA and 0.66 between RC and OC, indicating that overall foot scores are primarily driven by the condition of the front feet. Jeyaruban *et al.* (2012) reported high genetic correlations between FA and RA, which were considerably lower in the current study (0.24). The correlation between FC and RC (0.57) in this study, however, was consistent with their reported estimate of 0.63. Genetic correlations were generally higher among traits measured on the front feet (0.54–0.99) than on the rear feet (0.26–0.72).

The phenotypic correlations were generally low between structural and production traits, indicating that there is no evidence that structural traits in this study have a substantial impact on those production traits measured later in life. Genetic correlations between structural and production traits were similar for MWT, BCS and W18 and were generally low and negative and this may be attributable to low variation of the observed structural traits. The only moderate genetic correlations further than 2 standard errors from 0 were the negative correlations between BCS and RH (-0.54), BCS and RS (-0.35), W18 and RA (-0.53) and between W18 and OA (-0.32). Given the distribution of scores above the optimum these suggest that selecting for BCS and W18 is unlikely to increase the frequency of animals with unsound structure. The genetic correlation between structural traits and HH were low overall with the highest genetic correlation estimated for HH and FF (0.23).

CONCLUSIONS

Low to moderate heritabilities for structural traits exist in commercially farmed beef cattle in New Zealand. Genetic and phenotypic correlations among structural and production traits were generally low to moderate and negative, indicating only weak associations and, thus, a limited impact of structural traits on the recorded production traits in this study.

ACKNOWLEDGEMENTS

This research was funded by Beef+Lamb NZ Genetics.

REFERENCES

- Berry D.P., Harris B.L., Winkelman A.M. and Montgomerie W. (2005) *J. Dairy Sci.* **88**: 2962.
- Breedplan. (2021) <https://breedplan.une.edu.au/media/1zhdxy51/recording-structural-soundness-information.pdf>; accessed 15 January 2021.
- Dechow C.D., Rogers G.W. and Clay J.S. (2002) *J. Dairy Sci.* **85**: 3062.
- Gilmour A.R., Gogel B., Cullis B., Thompson R. and Butler D. (2009) VSN Int. Ltd, UK.
- Hickson RE, Morris ST and Thomson BC. (2017) 'Beef cow body condition scoring.'
- Jeyaruban G., Tier B., Johnston D. and Graser H. (2012) *Anim. Prod. Sci.* **52**: 1.
- Pickering N.K., Dodds K.G., Blair H., Hickson R.E., Johnson P. and McEwan J. (2012) *J. Anim. Sci.* **90**: 1411.
- R Core Team. (2019). R: A language and environment for statistical computing. R Foundation for Statistical Computing. Vienna, Austria.
- Reverter A., Johnston D.J., Graser H.U., Wolcott M.L. and Upton W.H. (2000) *J. Anim. Sci.* **78**: 1786.
- Vallee A., Breider I., Van Arendonk J.A.M. and Bovenhuis H. (2015) *J. Anim. Sci.* **93**: 4277.
- Weik F., Archer J.A., Morris S.T., Garrick D.J., Miller S.P., Boyd A.M., Cullen N.G. and Hickson R.E. (2021) *New Zeal. J. Agr. Res.* 1.