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Using the reaction norm approach to investigate genotype by environment interactions in the UK Suffolk Sire-Referencing Scheme

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Background

- Artificial insemination (AI) schemes produce half-sib groups in a wide range of environments
- If genotype x environment interactions (GxE) exist then performance of offspring is less predictable
- Reaction norm approach allows a systematic investigation of GxE effects

Suffolk Sire Referencing Scheme (SRS)

- National scheme with flocks linked by common AI sires
- Selected for lean meat production using selection criteria of weight at scanning (SWT) for fat (FD) and muscle depth (MD)
- 24,308 lamb records from 1990-1997 analysed

Random model for GxE - scanning weight (kg)

Parameter	Model				
	1	6	S×F 7	S×Y 8	S×FY 9
σ_p^2	41.95	41.00	41.10	41.15	41.16
σ_e^2	28.73	28.74	29.54	29.56	29.25
h^2	0.32 ± 0.010	0.20 ± 0.011	0.15 ± 0.016	0.15 ± 0.016	0.15 ± 0.016
m^2		0.07 ± 0.008	0.05 ± 0.008	0.05 ± 0.008	0.05 ± 0.009
r_{am}		-0.26	-0.02	-0.02	-0.06
c_1^2		0.06 ± 0.009	0.06 ± 0.008	0.06 ± 0.008	0.06 ± 0.008
s^2		-	0.02 ± 0.004	0.03 ± 0.005	0.03 ± 0.004
$\Delta \log L$	-118.2	0	20.10	32.43	41.86
P	P<0.01		P<0.01	P<0.01	P<0.01

Maniatis and Pollott (2002) Animal Science 75: 3-14.

Random model for GxE in scanning weight (kg)

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m^2					0.05 ± 0.009
r_{am}		-0.26	-0.02	-0.02	-0.06
c^2_1		0.06 ± 0.009	0.06 ± 0.008	0.06 ± 0.008	0.06 ± 0.008
s^2		-	0.02 ± 0.004	0.03 ± 0.005	0.03 ± 0.004
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Can we replace SxFY with a reaction norm model?

Maniatis and Pollott (2002) Animal Science 75: 3-14.

Reaction norm model

$$Y_{ijkl} = \text{Fixed}_i + \text{Random}_i + \text{Sa}_j + \text{Sb}_j(X) + \text{Sc}_j(X^2) + \text{resid}_{ijkl}$$

Sa_j = Sire intercept

Sb_j = Sire reaction norm (linear)

Sc_j = Sire reaction norm (quadratic)

X = CG mean for the environmental variable

Model also includes covariances between the reaction norm components

Reaction norm model

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Key question: How do we measure the environment?

norm components

Reaction norm model

$$Y_{ijkl} = \text{Fixed}_i + \text{Random}_i + Sa_j + Sb_j(X) + Sc_j(X^2) + \text{resid}_{ijkl}$$

Key question: How do reaction norm models affect other random effects?

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Key question: How do we measure the environment?
norm components

Reaction norm model

$$Y_{ijkl} = \text{Fixed}_i + \text{Random}_i + S a_j + S b_j (X) + S c_j (X^2) + \text{resid}_{ijkl}$$

Key question: How do reaction norm models affect other random effects?

$S a_j$ = Sire reaction norm (linear)

$S b_j$ = Sire reaction norm (quadratic)

Key question: How does heritability change in different environments?

Key question: How do we measure the environment?
norm components

Options for measuring the environment

- Use index of factors such as climate, soil type, breed, management, husbandry skills etc
- Use contemporary group mean of trait
- Use contemporary group mean of an independent but informative trait

Looking at environmental measures for scanning weight using a fixed effect model (kg)

Environmental measure – CG mean	LogL	Resid. Var.
CG fixed effect	0	40.38
Scanning weight	2587	49.82
Fat depth	3739	54.32
Muscle depth	4015	56.11
8wk weight	5223	62.04
ADG 8wk to scanning	2183	48.15
ADG birth to scanning	797	42.9
Adjusted Scanning wt.	497	41.8
Adj. ADG birth to scanning	661	42.42

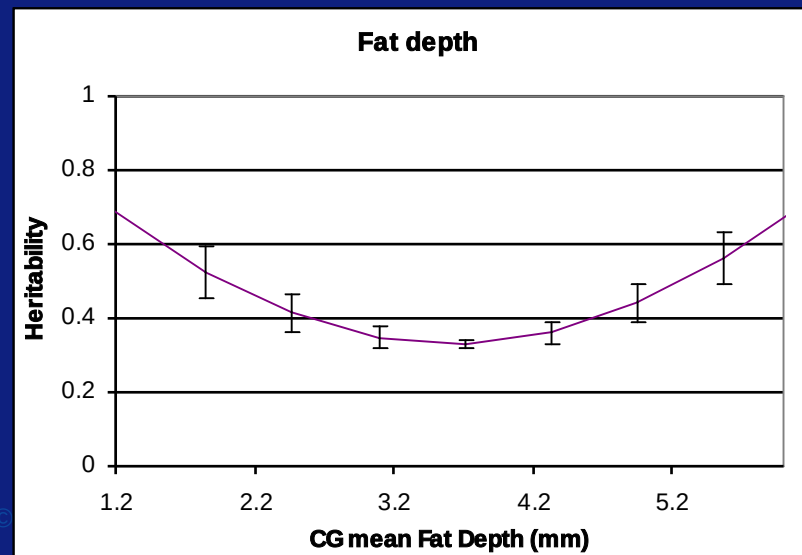
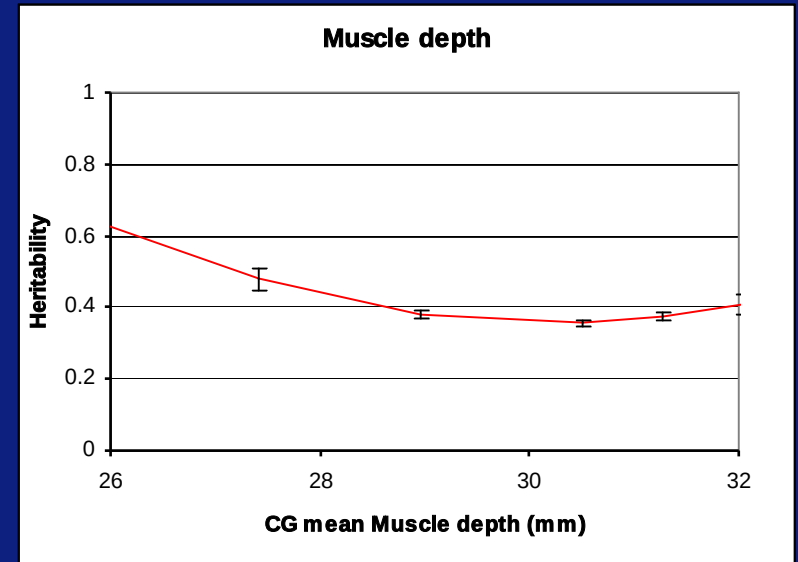
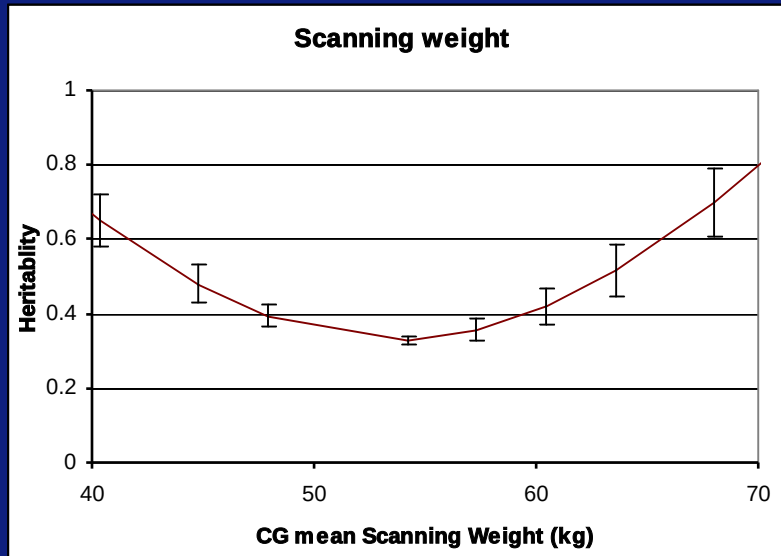
Looking at environmental measures for scanning weight using an animal model (kg)

	LogL	Resid. Var.
Simple model + CG	39	29.16
Simple model + CG + SxFY	0	28.63
Simple model + CGSWTadj	463	31.23
Simple model + CGADGBSadj	581	31.16
Simple model + linear RR CGSWTadj	388	30.37

Summary from fat depth and muscle depth

- CG trait mean always has a poorer fit than CG fixed effect
- CG trait mean always has the best fit of all the CG mean measures of the environment
- Of the others, ADG mean has the best fit

Heritability of SWT, MD and FD over the range of environments found



The effect of reaction norms on the direct - maternal genetic correlation for SWT

	LogL	r_{DM}^s
Full model (FM)	-67090	-0.25
FM + SxFY	-67017	-0.04
FM + sire, sire.CGFD	-67024	0.63
FM -CG, + CGFD, + SxFY	-68662	-0.18
FM -CG, + CGFD, + sire	-69376	0.29
FM - CG + CGFD + sire + sire.CGFD	-69209	0.27

^s Correlation between direct and maternal genetic effects

Conclusions

- Reaction norms explained some, but not all, of the Sire/Flock/Year GxE effect
- No measure of the environment was as good as the trait CG mean but ADG tended to be consistently good
- Heritability of the 3 traits varied across environments
- The direct-maternal correlation changed when reaction norms were used

Acknowledgements

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