ESTIMATES OF PARAMETERS FOR SCAN RECORDS OF AUSTRALIAN BEEF CATTLE TREATING RECORDS ON MALES AND FEMALES AS DIFFERENT TRAITS

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SUMMARY

Age adjusted field scanning records for eye muscle area, P8 fat depth, fat depth at 12/13th rib and scanning weight for Australian Angus, Hereford, Polled Hereford and Santa Gertrudis were analysed treating measurements for heifers/steers and bulls as different traits. Estimates of variances, heritabilities and genetic correlations are given. Average genetic correlations between sexes (across breeds) were 0.92, 0.69, 0.77 and 0.93 for the four traits, respectively. Results have been implemented into BREEDPLAN (V4.1) using scan records of heifers and bulls as different traits.

Keywords: Scan records, genetic parameters, correlation between sexes

INTRODUCTION

There are distinct differences in growth pattern between sexes, bulls not only tending to grow faster but also to remain leaner than heifers, raising the question whether records on males and females should be considered as the same trait in genetic evaluation systems. This is particularly relevant for traits related to carcass composition and the fact that our main beef production products are slaughter steers and heifers and not bulls. This paper examines the genetic correlation between sexes for ultrasound scan records taken in the field.

MATERIAL AND METHODS

Data. Data consisted of ultrasound scan records taken by proficiency tested commercial scanners from Australian Angus (A), Hereford (H), Polled Hereford (PH) and Santa Gertrudis (SG) cattle between the age of 300 to 700 days. Traits considered were 12/13th rib eye muscle area (EMA, in cm^2), P8 fat depth (P8, in mm), fat depth over the 12/13th rib (RIB, in mm) and weight at scanning (SWT, in kg). The data was recorded between 1987 and 1997 and came from 188, 83, 58 and 7 herds of the four breeds, respectively.

Analysis. Bivariate analyses were carried out for each of the four measures by restricted maximum likelihood, assuming records on heifers and steers (H/S) represented a different trait to records on bulls (B). The model of analysis was similar to the BREEDPLAN model (Graser *et al.* 1995). Fixed effects fitted were contemporary groups (CG), defined as herd-date of scanning-management group subclasses, with a 60 day 'age slicing' within subclasses, the so-called "heifer factor", ie. an age of dam class (heifer : " 28 months at calving, cow : > 28 months , unknown), and birth type (single, twin, unknown). Age at scanning and age of dam at calving were taken into account as linear and quadratic covariables. Random effects fitted were animals' additive genetic effects and sire x herd

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interaction effects. Pedigree information up to two generations back was considered, while sire x herd effects were assumed to be independently distributed.

RESULTS

Characteristics of the data structure are summarised in Table 1. Means and standard deviations show clear differences between sexes, with bulls being heavier and having correspondingly larger EMA but being leaner and showing considerably less variation in fat depth than heifers and steers.

Table 1. Characteristics of the data structure

	EMA		P8		RIB		SWT	
	H/S	B	H/S	B	H/S	B	H/S	B
				Angus				
No. records	14,124	18,583	14,056	18,523	14,128	18,602	14,004	18,222
Mean	54.85	75.07	5.772	4.209	4.412	3.236	369.3	500.0
SD	9.73	13.78	3.435	2.364	2.526	1.671	73.7	102.3
Mean age	495.8	503.9	496.3	504.2	495.8	503.8	495.2	502.8
No. CG[A]	1189	1751	1187	1755	1187	1755	1175	1720
No. animals[B]	64,606		64,441		64,644		63,463	
No. SxH[C]	3321		3323		3333		3287	
				Hereford				
No. records	10,499	15,064	10,536	15,069	10,537	15,071	10,374	14,761
Mean	51.90	74.11	6.111	4.616	3.938	3.180	367.54	516.36
SD	9.76	13.71	3.820	2.686	2.116	1.535	69.35	103.32
Mean age	514.2	527.7	514.1	527.7	514.1	527.7	514.9	528.2
No. CG	936	1618	940	1625	940	1625	919	1580
No. animals	47,087		47,159		47,170		46,349	
No. SxH	2446		2457		2457		2404	
	Polled Hereford							
No. records	4385	4824	4377	4790	4384	4807	4354	4822
Mean	52.20	74.58	5.797	5.053	3.940	3.451	356.9	514.0
SD	10.25	12.91	3.337	2.848	2.018	1.679	63.0	101.8
Mean age	504.9	515.4	504.9	515.3	505.0	515.3	504.8	515.5
No. CG	488	701	487	699	487	700	483	697
No. animals	20,466		20,432		20,451		20,430	
No. SxH	1042		1043		1043		1042	
				Santa Gertrudis				
No. records	3165	3547	3260	3598	3255	3597	3316	3662
Mean	55.06	68.98	5.29	2.59	3.30	1.88	360.1	440.0
SD	10.56	12.87	3.55	2.07	1.99	1.16	83.8	98.7
Mean age	528.0	530.2	522.2	526.9	522.1	527.0	521.5	525.4
No. CG	196	225	210	239	211	238	216	243
No. animals	11,203		11,131		11,112		11,543	
No. SxH	684		700		699		703	

[A] Contemporary Groups, [B] In the analysis, including parents without records
[C] Sire x herd interaction effects

Estimates of phenotypic variances (σ_P^2), heritabilities (h^2), the variance due to sire x herd effects expressed as a proportion of σ_P^2 (s^2), and the corresponding correlations between sexes, r_G and r_S, respectively, are given in Table 2 and corresponding estimates of regression coefficients are summarised in Table 3. Note that with traits measured on distinct subsets of animals, residual covariances are zero, ie. there is no phenotypic correlation in the usual sense. Distinct differences in σ_P^2 between sexes and breeds could largely be attributed to scale effects. While coefficients of variations tended to be highest for SG, they were very similar for B and H/S for fat measures (32-46 %) and only slightly higher for H/S (8-11 %) than B (7-9 %) for EMA and SWT. For fat depths, h^2 for H/S were consistently higher than for B, presumably because higher fat levels in H/S allowed better expression of genetic variation. Estimates for s^2 were consistently low, but significant in the two larger data files, ranging from 0 to 0.05.

Table 2. Estimates[3] from bivariate analyses of scan traits, treating measurements on heifers and steers (H/S) and bulls (B) as different traits

Sex	EMA		P8		RIB		SWT	
	H/S	B	H/S	B	H/S	B	H/S	B
Angus								
σ_P^2	27.75	44.55	3.950	2.509	1.952	1.142	831.7	1328.8
h^2	0.27	0.27	0.41	0.28	0.34	0.23	0.46	0.36
s^2	0.03	0.03	0.05	0.03	0.06	0.05	0.05	0.05
r_G	0.89		0.80		0.83		0.93	
r_S	1.00		0.32		0.30		0.66	
Hereford								
σ_P^2	32.1	48.4	4.662	2.765	1.562	0.942	1003	1576
h^2	0.32	0.22	0.31	0.24	0.25	0.21	0.39	0.31
s^2	0.02	0.03	0.02	0.03	0.02	0.03	0.04	0.02
r_G	0.91		0.87		0.79		0.89	
r_S	0.60		0.37		0.34		0.38	
Polled Hereford								
σ_P^2	30.30	45.51	3.806	2.998	1.521	1.076	881.3	1457.0
h^2	0.22	0.32	0.44	0.32	0.28	0.23	0.34	0.45
s^2	.02	0.00	-	-	0.01	0.00	0.05	0.00
r_G	0.88		0.73		0.80		0.90	
r_S	1.00		-		-1.00		1.00	
Santa Gertrudis								
σ_P^2	25.47	35.72	4.411	1.413	1.530	0.502	927.5	1453.6
h^2	0.35	0.13	0.37	0.11	0.32	0.08	0.28	0.15
s^2	0.01	0.04	0.02	0.02	0.04	0.03	0.03	0.01
r_G	1.00		0.35		0.65		1.00	
r_S	0.92		1.00		0.51		0.77	

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[3] σ_P^2 : Phenotypic variance, h^2 : heritability, s^2 : sire x herd interaction effect (expressed as proportion of phenotypic variance), r_G : genetic correlation, r_S : correlation between sire x herd effects

Table 3. Estimates of linear (L) and quadratic (Q) regression coefficients (multiplied by 10^4) on dam age (DA, in years) and age at scanning (A, in days)

		EMA		**P8**		**RIB**		**SWT**	
		H/S	B	H/S	B	H/S	B	H/S	B
					Angus				
DA	L	2253.65	1484.59	859.13	156.92	594.61	93.91	20,614.6	20,804.8
	Q	-335.76	-239.01	-114.03	-23.21	-94.35	-22.15	-4512.5	-4747.7
A	L	629.23	699.14	198.06	94.55	128.45	51.99	5513.9	7535.2
	Q	-0.72	-0.88	0.10	-0.06	0.06	-0.03	-3.1	-4.4
Hereford									
DA	L	2489.18	2051.97	989.71	391.97	654.89	228.99	17,502.3	22,855.5
	Q	-480.03	-372.13	-116.37	-43.11	-83.02	-23.12	-3566.1	-5360.5
A	L	492.71	675.65	185.42	89.19	83.62	52.13	5146.7	7428.0
	Q	-0.78	-0.63	0.18	0.07	0.01	0.04	-19.9	-42.5
					Polled Hereford				
DA	L	3469.90	2265.14	996.12	417.17	725.07	247.29	25100.0	31934.3
	Q	-587.53	-398.00	-126.29	-84.93	-99.79	-40.69	-4608.6	-6386.7
A	L	660.42	774.19	209.61	65.03	134.12	32.87	5303.8	8344.3
	Q	-0.52	-1.09	0.05	-0.12	0.05	-0.11	-6.2	-7.9
					Santa Gertrudis				
DA	L	1058.79	30.72	9.00	-22.67	156.15	31.20	7811.7	8741.2
	Q	-450.32	-245.81	-70.53	10.03	-59.47	-8.74	-461.5	-468.7
A	L	566.81	759.09	167.67	38.64	98.49	27.92	5811.7	8311.5
	Q	-0.29	-0.25	0.16	-0.12	0.14	-0.06	-3.9	-1.7

Estimates of r_G for EMA and SWT were close to unity, averaging 0.92 and 0.93 respectively. Corresponding averages across breeds for P8 and RIB were 0.69 and 0.77, with lowest values found for SG, the breed with the lowest phenotypic fat averages and very low heritabilities for the two fat traits when recorded on bulls. In the literature only correlations between scan records on bulls or heifers and carcase data from steers are reported. Moser *et al* (1998) found correlation of between 0.66 and 0.69 between the same traits by name recorded on the two different groups of animals.

Estimates of the correlation between sire x herd effects (r_S) were commonly lower than the genetic correlation between the sexes, however in some cases, low values of s^2 lead to spurious estimates of r_S for the two smaller data sets.(e.g RIB in PH).

Results indicate that accuracy of genetic evaluation can be improved by treating fat depth for males and females (+steers) as different traits this is now been done in BREEDPLAN. In addition, it should be ensured that males are scanned at a sufficient fat level, ie. typically at older ages, to allow genetic variation in fatness to be expressed.

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