ESTIMATES OF GENETIC PARAMETERS FOR SCAN MEASUREMENTS IN AUSTRALIAN BRAHMANS AND SANTA GERTRUDIS ADJUSTING FOR AGE VERSUS ADJUSTING FOR WEIGHT AT SCANNING

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SUMMARY

Records for scanned eye muscle area, P8 fat depth, fat depth at 12/13th rib and scanning weight for Brahman and Santa Gertrudis cattle were analysed fitting age at scanning as a linear covariable within sex in the model of analysis, pre-adjusting records for age, and pre-adjusting records for weight at scanning. Heritability estimates were moderate, higher at older ages, and tended to be higher when adjusting for weight than for age. High correlations between the two fat depth measures were unaffected by the method of adjustment, while genetic correlations between eye muscle area and weight were reduced from moderate when adjusting for age to zero when adjusting for weight.
Keywords : Scan records, *Bos indicus*, genetic parameters

INTRODUCTION

BREEDPLAN gives breeding value estimates for carcass traits at a common market weight using scan records, adjusted for age at scanning, as auxiliary information. Recently, adjustment of scanned records to a common weight rather than a common age has been advocated. This paper presents estimates of genetic parameters for scan traits in *Bos indicus* cattle, and examines the effect of alternative adjustment methods on estimates.

MATERIAL AND METHODS

Data. Records for P8 fat depth (P8), 12/13th rib fat depth (RIB), eye muscle area (EMA) and scanning weight (SWT), collected until August 1996, were obtained for Australian Santa Gertrudis (SG) and Brahman (BR) cattle. There were 5,587 and 3,634 records with at least one scan trait measured, respectively. No live muscles scores were available. Most animals had records for all 4 traits. Data were subdivided according to age at recording, 400 (301-500) days and 600 (501-700) days, eliminating any double records per animal within age class. Table 1 summarises characteristics of the data structure.

Scan measurements were pre-adjusted to the mean weight within each data set by first predicting the animal's age at the mean and then adjusting each trait to the mean for this trait using the predicted age. This yielded traits P8*, RIB* and EMA*. Adjustments were carried out using the X-intercept approach used in BREEDPLAN, and generalised least squares estimates of linear regressions on age within sex, obtained from univariate REML analyses of P8, RIB and EMA. For comparison, all three traits were pre-adjusted for age using these estimates and the X-intercept approach. The resulting

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measures are denoted as $P8^+$, RIB^+ and EMA^+. Table 2 gives means and standard deviations for adjusted records.

Analyses. Analyses were carried out by restricted maximum likelihood, fitting a simple animal model. Fixed effects fitted were contemporary groups, defined as herd-sex-management group-date of scanning subclasses, and age status of the dam (Heifer *vs.* cow), age of dam as a linear and quadratic covariable and, for P8, RIB, EMA and SWT age at recording as a linear covariable within sex. Other univariate analyses (not shown) fitted a maternal genetic or permanent environmental effect in addition. While they identified some maternal effects they were not statistically significant and thus disregarded in further analyses. Multivariate analyses (4 traits) considered P8, RIB, EMA, SWT, and $P8^*$, RIB^*, EMA^* and SWT, respectively.

RESULTS AND DISCUSSION

Results from univariate analyses are given in Table 3. Generally, there was little difference in heritability (h^2) estimates between traits pre-adjusted for age (superscript +) and adjusted for age within the model of analysis. Pre-adjustment to a common weight tended to increase h^2 estimates

Table 1 . Characteristics of the data structure

	Santa Gertrudis				Brahman			
	SWT	P8	RIB	EMA	SWT	P8	RIB	EMA
					400 days			
No. records	1,230	1,152	1,152	1,211	745	751	788	791
No. animals[A]	4,486	4,097	4,097	4,430	3,147	3,257	3,329	3,336
No. of sires[B]	131	120	120	124	119	121	130	130
No. of dams	1,037	959	959	1,024	586	613	629	632
No. CG[C]	120	113	113	117	75	84	88	88
Mean	343.2	3.390	2.303	54.09	303.5	3.495	2.317	52.92
SD	81.4	3.087	1.796	12.24	58.3	2.037	1.212	9.64
Mean age	419.5	422.0	422.0	419.5	417.7	417.1	418.6	418.7
SD age	49.5	49.4	49.0	49.8	53.5	54.1	53.4	53.4
					600 days			
No. records	3,688	3,684	3,688	3,685	2,177	2,249	2,302	2,303
No. animals	7,834	7,829	7,831	7,828	6,922	7,112	7,181	7,184
No. of sires	171	171	170	170	201	196	205	205
No. of dams	2,067	2,063	2,067	2,066	1,584	1,645	1,656	1,658
No. CG	239	238	239	239	118	123	130	130
Mean	453.7	4.499	2.894	65.60	389.5	4.128	2.710	63.18
SD	83.3	3.579	1.927	1.862	90.1	2.457	1.438	13.32
Mean age	592.2	595.2	595.1	595.2	585.7	587.5	587.0	587.1
SD age	44.2	44.2	44.2	44.2	50.9	51.4	51.3	51.3

[A] Including parents without records [B] With progeny in the data [C] Contemporary groups

compared to adjustment to a common age (except for EMA in BR). Phenotypic variances (σ_P^2) for EMA^* and RIB^* were markedly smaller, and those for $P8^*$ somewhat smaller than corresponding estimates for traits adjusted to a common age. As exhibited in Table 2, the adjustment procedure produced predicted ages with much larger standard deviations (and ranges; not shown) than on the original scale. Traits adjusted for predicted ages (superscript *), however were considerably less variable than unadjusted traits or traits adjusted for age (superscript +). Records taken at older ages (600 days) were generally more heritable than those taken earlier, with differences most pronounced for fat depths in BR.

Table 2. Means (μ) and standard deviations (sd) for adjusted records and ages (μ_a and sd_a)[A]

	Santa Gertrudis						Brahman					
	$P8^*$	$P8^+$	RIB^*	RIB^+	EMA^*	EMA^+	$P8^*$	$P8^+$	RIB^*	RIB^+	EMA^*	EMA^+
						400 days						
μ	3.149	3.361	2.179	2.292	54.35	54.11	3.349	3.537	2.242	2.325	52.37	52.39
sd	2.336	2.997	1.322	1.742	9.69	11.92	1.645	2.174	1.000	1.286	7.08	8.88
μ_a	437.3	422.0	437.3	422.0	433.1	419.4	427.1	416.1	427.1	417.8	426.3	417.7
sd_a	73.1	49.4	73.1	49.4	73.3	49.7	77.1	54.2	75.7	53.5	73.7	53.5
						600 days						
μ	4.337	4.492	2.821	2.888	65.78	65.56	4.075	4.123	2.662	2.699	62.82	62.72
sd	3.173	3.455	1.667	1.862	9.19	11.28	2.211	2.390	1.174	1.361	10.27	12.65
μ_a	609.8	595.2	610.1	595.2	610.1	595.2	607.1	586.2	606.0	585.7	604.8	585.8
sd_a	99.4	44.2	99.5	44.2	99.5	44.2	128.0	51.0	127.0	50.9	125.3	50.9

[A] P8 : P8 fat depth, RIB : fat depth at 12th/13th rib, EMA : eye muscle area; superscript '*' denotes traits adjusted for predicted age at mean weight, '+' denotes traits adjusted for (actual) age

Table 3. Estimates of heritabilities (h^2) and phenotypic variances (σ_P^2) from univariate analyses

Age		SWT	P8	$P8^*$	$P8^+$	RIB	RIB^*	RIB^+	EMA	EMA^*	EMA^+
						Santa Gertrudis					
400	h^2	0.24	0.14	0.20	0.13	0.28	0.34	0.27	0.18	0.28	0.19
	σ_P^2	908	2.173	1.667	2.070	0.860	0.648	0.819	26.71	22.53	27.22
600	h^2	0.30	0.21	0.31	0.21	0.22	0.29	0.22	0.33	0.32	0.33
	σ_P^2	1428	3.717	3.780	3.745	1.216	1.154	1.219	33.55	25.74	33.54
						Brahman					
400	h^2	0.51	0.02	0.17	0.09	0.02	0.06	0.01	0.48	0.33	0.50
	σ_P^2	732	1.480	1.525	1.673	0.583	0.547	0.628	22.98	15.24	22.61
600	h^2	0.53	0.45	0.49	0.45	0.34	0.44	0.34	0.42	0.32	0.39
	σ_P^2	1095	2.630	2.388	2.417	0.975	0.849	0.902	34.88	23.48	30.56

Table 4 gives estimates of genetic (r_G) and phenotypic (r_P) correlations from multivariate analyses. As for univariate analyses, estimates for 400 day records for BR were somewhat erratic, presumably largely due to a small sample size. There was a close genetic and phenotypic association between P8 and RIB, both on the original scale and for pre-adjusted data, and little relationship with the other traits. Adjusting for SWT resulted in slightly negative r_G between adjusted fat depths and SWT, particularly for 600 day records for SG. EMA showed a moderate correlation with SWT, while EMA^* and SWT were virtually unrelated. Estimates of h^2 and σ_P^2 from multivariate analyses (not shown) agreed closely with corresponding univariate estimates (except for 400 day measures in BR), i.e. inclusion of SWT had little effect on estimates for unadjusted traits (P8, RIB and EMA).

Table 4. Estimates of genetic (r_G) and phenotypic (r_P) correlations from multivariate analyses

Age		P8			RIB		EMA	P8*			RIB*		EMA*
		RIB	EMA	SWT	EMA	SWT	SWT	RIB*	EMA*	SWT	EMA*	SWT	SWT
							Santa Gertrudis						
400	r_G	0.90	0.25	-0.06	0.02	-0.02	0.06	0.90	-0.11	-0.21	0.08	-0.17	-0.47
	r_P	0.79	0.13	0.26	0.18	0.28	0.46	0.77	0.02	0.17	0.05	0.17	-0.03
600	r_G	0.83	0.08	0.13	0.21	0.19	0.52	0.86	-0.09	-0.39	0.06	-0.29	0.10
	r_P	0.77	0.13	0.24	0.17	0.26	0.50	0.77	0.03	-0.11	0.06	-0.06	0.07
							Brahman						
400	r_G	0.38	0.67	0.56	0.76	0.36	0.78	0.49	0.20	-0.11	0.63	-0.16	0.45
	r_P	0.73	0.14	0.24	0.18	0.26	0.59	0.72	-0.02	-0.14	0.04	-0.03	0.12
600	r_G	0.88	0.21	0.04	0.18	0.04	0.64	0.89	0.23	-0.03	0.20	-0.12	0.08
	r_P	0.75	0.14	0.12	0.16	0.15	0.50	0.75	0.11	0.04	0.12	-0.01	0.01

CONCLUSIONS

Scan records for *Bos indicus* cattle, in particular those taken at later ages, have moderate h^2 similar to those found in Australia for *Bos taurus* (e.g. Johnston *et al.* 1997, Meyer and Graser, 1999). Adjusting to a common weight instead of a common age slightly increased h^2 estimates but tended to reduce σ_P^2. High correlations between fat measures were unaffected by adjustments for weight, but moderate correlations between EMA and SWT were reduced to close to zero while adjustment of fat measures tended to induce a slight negative association with weight. Hence use of weight adjusted scan records in a genetic evaluation scheme where numerous animals do not have scan information should be regarded with caution.

REFERENCES

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