# GENETIC PARAMETERS FOR GROWTH OF TROPICAL BEEF CATTLE

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## INTRODUCTION

Accurate estimates of genetic parameters arc required for the efficient application of mixed model methodology to the estimation of breeding values. Yet the number and quality of parameter estimates for tropical cattle genotypes, even for growth traits, are limited (e.g. see Plasse 1978; Iloeje 1986). Estimates for genotypes used in the Australian tropics are particularly scarce, the study by Seifert (1975) being the most recent. Accordingly, the objective of the study reported here was to estimate direct and maternal genetic components for a number of growth traits recorded on a range of cattle genotypes in a tropical environment.

## MATERIALS AND METHODS

### (i) Data

Da[illegible] collected at the National Cattle Breeding Station, Belmont, near Rockhampton, Australia. The physical environment and general management of the herd is described by Seifert (1975). Weaning age ranged from six to seven months. Data on three crossbred genotypes were analysed. The Brahman cross (BX) /Africander cross (AX) genotypes contained on average 50% Brahman/Africander, 25% Hereford and 25% Shorthorn genes. The Hereford x Shorthorn (HS) genotype was nominally composed of 50% of each breed. All animals were $F_3$ and subsequent generation crosses. During the period of this study, all genotypes were under selection largely for a combination of weaning weight, tick resistance and final weight at two years of age in males using independent culling levels (Seifert, 1975). Female selection was generally restricted to culling for reproductive failure. Within the HS genotype, a randomly selected line was also maintained (Frisch 1981a).

Records were collected on 16 calf crops between 1966 and 1983. However because of experimental treatments, data on two calf crops of BX and HS animals were not used. Because of sequential culling of bulls from weaning, only female post-weaning records were analysed.

### (ii) Statistical analysis

Firstly, a fixed effects analysis was performed within genotypes (BX, AX and HS) to estimate the effects of dam age at calving (DA) and lactation status of the dam at conception (PLS) on birth weight, preweaning gain (weaning weight - birth weight) and post weaning gain (final weight at two years of age - weaning weight). Since the two effects are confounded in maiden heifers, the factors were fitted in combination. The number of levels of DA/PLS was reduced until the residual mean square increased. Other factors in the model were calf year of birth, sex and all first order interactions. Calf day of birth was fitted as a covariate. Gains were adjusted to a common age period.

Secondly, variance components for direct and maternal genetic effects on birth weight and preweaning gain and for direct genetic effects on post-weaning gain were estimated using Henderson's Method III (Henderson, 1973). Data were pre-adjusted for DA/PLS using multiplicative adjustment factors calculated from the first analysis. Since, with few exceptions, bulls were used for only one year, sires were nested within years and dams were nested within both sires and maternal grandsires. A number of models were fitted to the data. These included models with fixed effects only (year of birth and sex of calf), fixed plus sire effects, fixed plus maternal grandsire effects, fixed plus sire plus dam effects, and fixed plus sire plus dam plus maternal grandsire effects. Reductions in sums of squares associated with fitting each effect were equated to expectations to yield estimates of the variance components. Covariances were calculated from analyses of the sum of pairs of traits.

All analyses were carried out within genotypes. Variance components for gains and birth weight were also averaged across genotypes to give pooled estimates. Variances for weaning weight and final weight were derived from variance and covariance estimates for birth weight and gains.

Table 1 Multiplicative adjustment factors for dam age/ previous lactational status classifications on birth weight and pre-weaning gain in the three genotypes

| | Genotype | | | | | |
|---|---|---|---|---|---|---|
| | AX | | HS | | BX[1] | |
| Dam age/previous lactational status | Birth weight | Pre-weaning gain | Birth weight | Pre-weaning gain | Birth weight | Pre-weaning gain |
| No. records | 1696 | 1696 | 1331 | 1331 | 1070 | 1070 |
| 3 years (maiden) | 1.044 | 1.084 | 1.052 | 1.112 | 1.055 | 1.054 |
| 4 years lactating | 1.013 | 1.015 | 1.037 | 1.056 | 1.010 | 1.007 |
| 4 years dry | 0.994 | 0.972 | 1.001 | 0.979 | | |
| 5(+) years lactating | 1.015 | 0.969 | 1.011 | 1.000 | 0.950 | 0.968 |
| 5(+) years dry | 0.964 | 0.960 | 0.979 | 0.920 | | |
| 6+ years lactating | | | 0.973 | 0.984 | 0.986 | 0.971 |
| 6+ years dry | | | 0.950 | 0.954 | | |

[1]No significant effects of lactational status were observed for BX.

## RESULTS AND DISCUSSION

Dam age effects on birth weight and pre-weaning gain were greatest and persisted longest in the HS and were shortest in the BX (Table 1). Effects of lactation in the previous year (PLS) were highest in HS, intermediate in AX and not significant ($P \geq 0.05$) in BX animals. DA/PLS effects were generally non significant on post weaning gain. The magnitude of the maternal (DA/PLS) effects was inversely proportional to the general level of tropical adaptation of the genotypes (see Frisch, 1981b) i.e. the effects were least in the BX genotype which is best equipped to cope with the stresses of heat, parasites and poor nutrition. However, given that the environment in this study was relatively benign compared with some environments in northern parts of Australia, PLS effects should still be considered in genetic evaluation programs for Brahman cross animals in the northern tropics.

Table 2 Variance estimates ($kg^2$) for growth traits in the three genotypes

| | | Genotype | | | |
|---|---|---|---|---|---|
| | | AX | HS | BX | Pooled |
| No. records - pre-weaning | | 1406 | 1346 | 1081 | |
| - post-weaning | | 638 | 544 | 515 | |
| No. sires | | 81 | 96 | 85 | |
| Phenotypic variance | | | | | |
| Birth weight | | 17.4 | 18.4 | 21.2 | 19.0 |
| Pre-weaning gain | | 281 | 309 | 323 | 304 |
| Weaning weight | | 315 | 363 | 374 | 350 |
| Post-weaning gain | | 560 | 672 | 687 | 639 |
| Final weight | | 865 | 1187 | 1059 | 1037 |
| Genetic variance | | | | | |
| Birth weight | - direct | 8.1 | 4.2 | 9.5 | 7.2 |
| | - maternal | 0.9 | 0.6 | 3.0 | 1.5 |
| Pre-weaning gain | - direct | 30 | 66 | 34 | 43 |
| | - maternal | 94 | 46 | 28 | 56 |
| Weaning weight | - direct | 47 | 71 | 46 | 55 |
| | - maternal | 93 | 42 | 29 | 55 |
| Post-weaning gain | | 184 | 231 | 233 | 216 |
| Final weight | | 341 | 381 | 277 | 333 |
| Permanent environmental variance | | | | | |
| Birth weight | | 1.2 | 3.3 | 0 | 1.5 |
| Pre-weaning gain | | 18 | 47 | 64 | 43 |
| Weaning weight | | 18 | 70 | 79 | 55 |

Phenotypic variances were lowest in the AX but similar in the other two genotypes (Table 2). Pre-weaning direct genetic variances were similar for AX and BX but pre-weaning maternal genetic and post-weaning genetic variances were variable across genotypes. Permanent environmental variances were negligible for birth weight but sizeable for pre-weaning gain. Heritabilities for growth traits were generally similar for all three genotypes (Table 3). There was little evidence that the pooled heritabilities for the zebu cross genotypes (AX and BX) were different from HS estimates. Greatest differences were for birth weight (0.46 vs 0.23) and direct pre-weaning gain (0.11 vs 0.21) respectively. Accordingly, it was concluded that the pooled estimates reflect the best estimates for each genotype.

Table 3 Estimates of heritability (%) for growth traits, pooled across genotypes

| Trait | | Heritability |
|---|---|---|
| Birth weight | - direct | 38 |
| | - maternal | 8 |
| Pre-weaning gain | - direct | 14 |
| | - maternal | 18 |
| Weaning weight | - direct | 16 |
| | - maternal | 16 |
| Post-weaning gain | | 34 |
| Final weight | | 32 |

Table 4 Percentage estimates of genetic correlations (below diagonal) and phenotypic correlations (above diagonal) amongst growth traits and pooled across genotypes

| Trait | Birth weight | Pre-weaing gain | Post-weaning gain |
|---|---|---|---|
| Birth weight | - | 18 | 19 |
| Pre-weaning weight | 13 | - | 1 |
| Post-weaning gain | 29 | 19 | - |

The pooled estimates of heritability are notably lower than most estimates for direct effects for Bos indicus cattle (reviewed by Plasse 1978) and also lower than those reported by Seifert (1975), especially for birth weight and final weight. However they fall within the range of literature estimates. They are also in close agreement with recent estimates from zebu cross populations in the same environment (Mackinnon, M.J., Meyer, K. and Hetzel, D.J.S. unpublished) except for birth weight and maternal pre-weaning growth where the present estimates are lower.

Although phenotypic correlations were similar in the three genotypes, estimates of the genetic covariances and genetic correlations varied greatly (Table 4). This is to be expected from the relatively small size of the data set for each genotype in this study. Pooled estimates showed that both phenotypic and genetic correlations among birth weight, pre- and post-weaning gains were low though positive. This suggests that pre-weaning and post-weaning growth are lowly genetically related. The phenotypic correlations are in agreement with studies on these genotypes cited earlier and the genetic correlations are similar to post 1983 estimates. Reasons for the low genetic relationship between pre- and post-weaning growth presumably relate to the influence of genes associated with resistance to heat, parasites and poor nutrition which have a large effect on post-weaning growth in tropical environments. Estimates of both phenotypic and genetic correlations amongst these traits in temperate environments are moderate i.e. around +0.5 (see Woldehawariat et al. 1977). Thus this study supports the contention that the genetic and phenotypic covariances between traits will differ in magnitude between temperate and tropical environments. Precise estimates of genetic parameters in tropical genotypes and environments could fine tune genetic evaluation programs for these areas.

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