

ESTIMATES OF GENETIC PARAMETERS FROM RANDOM REGRESSION ANALYSES OF SCROTAL CIRCUMFERENCE AND DAYS TO CALVING IN BRAHMANS

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SUMMARY

Serial records for scrotal circumference for bulls in a Brahman herd were analysed fitting random regressions on orthogonal polynomials of age. Up to seven 'repeated' records, measured between 300 and 800 days of age, were available. Days to Calving records were analysed assuming a simple repeatability model. Uni- and bivariate analyses were carried out, the latter estimating a genetic cross-covariance function for the two traits. Results showed that a quadratic regression on age modelled changes in variation for scrotal circumference adequately. Heritability estimates for scrotal circumference were highest around 400 days of age. There was little evidence for any changes in genetic correlation between the two traits with age at scrotal circumference measurement.

Keywords: Fertility, beef cattle, genetic parameters, random regression.

INTRODUCTION

There is growing awareness that variances and genetic parameters for growth and size related traits change with time. Random regression analyses allow such changes to be modelled and are applied to measures of reproductive performance in Brahman cattle, in order to identify potential changes in heritabilities and genetic correlations with age at recording.

MATERIAL AND METHODS

Data. Data consisted of serial scrotal circumference (SS) records for Brahman bulls in a single herd. Up to seven measurements per animal, recorded between about 300 to 800 days of age, were available. Raw data comprised 4851 records on 1533 animals. Edits eliminated animals without weaning weight management group codes, animals with less than 100% Brahman genes, and progeny of five bulls, deemed to be crossbred bulls on the basis of their progeny means for SS, although pedigree records identified them as purebred Brahmans. Records for Days to Calving (DC) in Brahmans were obtained from BREEDPLAN analyses for Brahmans. There were 5650 records, 2478 of which originated from the same herd as the SS records. Again, non-purebred records were disregarded from the analysis. Characteristics of the remaining data are summarised in Table 1.

Table 1. Characteristics of the data structure.

| | SS (cm) | DC (days) |
|--------------------------|------------|--------------|
| No. records | 3985 | 4419 |
| No. animals ... | | |
| in data | 1328 | 2402 |
| in analysis ^A | 3079 | 6767 |
| Mean | 23.93 | 389.8 |
| SD | 3.92 | 72.2 |
| No. CG ^B | 252 | 493 |
| Mean age | 537.7 | |

^A including parents

^B contemporary groups

Analysis. Uni- and bivariate analyses were carried out by restricted maximum likelihood, fitting a random regression model for SS, regressing on Legendre polynomials of age, and a repeatability model for DC. Analyses of SS considered orders of polynomial fit from $k=1$ (repeatability model) to

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$k=5$. The model of analysis fitted contemporary groups (CG), defined as weaning weight management group - date of recording subclasses, employing an age slicing of 45 days. Mean age trends were taken into account through a fixed regression on cubic, orthogonal polynomials of age. In addition, birth type and age of dam status ("heifer factor") effects were fitted as fixed effects, and age of dam was taken into account as a linear and quadratic covariable. Two sets of random regression coefficients, corresponding to animals' genetic and animals' permanent environmental effects were included for each animal, considering the same order of fit for both throughout. All pedigree information available was utilised. Analyses assumed homogeneous measurement error variances, as preliminary investigations had shown little advantage of a log-linear variance function model. Records for DC were analysed fitting a repeatability model, which is equivalent to a random regression model with an order of fit of $k=1$. The only fixed effect in the model of analysis was contemporary groups, defined as herd - service sire - bull in date - previous lactation status - age of cow subclasses. Bivariate analyses of SS and DC employed the same models as the respective univariate analyses. With records taken on distinct subsets of animals, only a genetic 'cross-covariance' function was estimated.

RESULTS

Univariate analyses of SS. Figure 1 shows numbers of records together with means and standard deviations for individual ages at recording in 10-day intervals. Variability tended to increase with age, but this increase was much reduced after correcting records for fixed effects. Estimates of measurement error variances from univariate analyses of SS and corresponding maximum log likelihood values are given in Table 2. Likelihood ratio tests indicated that an order of fit of $k=3$, i.e. a quadratic regression on orthogonal polynomials of age was sufficient to model changes in variation for SS with age adequately. Standard deviations for the ages in the data, derived from estimated covariance functions are shown in Figure 2. Phenotypic (not shown) variation increased slowly and steadily with age, along with an increase in mean. Estimates of genetic variances, increased more steeply up to about 500 days of age, and then levelled off. This resulted in high heritability (h^2) estimates of more than 60% for the youngest ages (Figure 3). Scrotal size is generally considered a

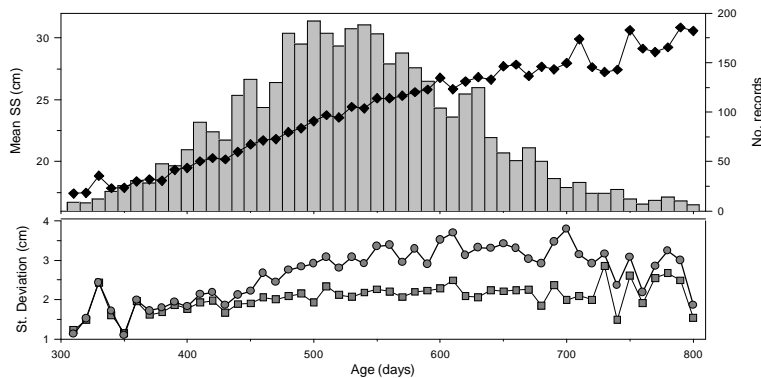


Figure 1. Number of records (bars), means (◆) and standard deviations (● : raw data, ■ : data adjusted for fixed effects) for scrotal circumference (10 day intervals)

highly heritable trait; h^2 estimates of order of magnitude 0.5 have been reported repeatedly. In a review, Koots *et al.* (1994) give an average value of 0.48. However, as shown in Figure 2, an increase in estimates of genetic variances in these data was accompanied by a decline in estimates of variance due to animals' permanent environmental effects. This resulted in the sum of the two components changing

Table 2. Log likelihood values (log L), numbers of parameters (p) and estimates of error variances (σ^2 , SS : scrotal circumference, DC : days to calving) for orders of polynomial fit k.

| k | Univariate analyses SS | | | | | Bivariate analyses SS+DC | | | |
|---------------|------------------------|-------|-------|-------|------|--------------------------|--------|--------|--------|
| | 1 | 2 | 3 | 4 | 5 | 1 | 2 | 3 | 4 |
| p | 3 | 7 | 13 | 21 | 31 | 6 | 10 | 16 | 24 |
| log L | -146.8 | -56.7 | -18.5 | -12.9 | -9.6 | -216.6 | -127.9 | -87.7 | -82.4 |
| σ^2 SS | 1.13 | 0.91 | 0.85 | 0.84 | 0.82 | 1.14 | 0.91 | 0.85 | 0.84 |
| σ^2 DC | | | | | | 2494.3 | 2489.6 | 2491.1 | 2490.7 |

comparatively little across ages, and changing more or less proportionally to the total, phenotypic variance. Hence repeatability (t) estimates were close to 0.8, ranging from 0.75 to 0.86 (Figure 3). This pattern suggests that the high estimates of genetic variance for ages up to 500 days may, in part at least, reflect sampling variation in the partitioning of the total variance.

Univariate analysis of DC. Estimates from a univariate analysis of DC were 0.176 ± 0.051 for h^2 and 0.026 ± 0.055 for the proportion of variance due to permanent environmental effects of the animal (p^2), resulting in t of 0.202, with estimates for the phenotypic and residual variance of 3129 and 2496, respectively. Johnston and Bunter (1996) reported a somewhat higher value for t of 0.25 for DC in Angus, with a substantially higher p^2 of 0.13. Of the 2402 animals with records in this analysis, however, 1425 had only a single record, i.e. there was limited scope for reliable partitioning of genetic and environmental effects due to the animal. An additional analysis including records for cows with at least 75% Brahman genes increased the data to 5214 records on 2689 cows, and yielded more comparable estimates of 0.136 ± 0.036 for h^2 , 0.124 ± 0.038 for p^2 and 0.250 for t. This emphasises the sensitivity of a small data set to selection of records and the resulting sampling errors of estimates.

Bivariate analyses of SS and DC. Estimates of the genetic covariance between SS and DC for different orders of fit for SS are shown in Figure 2. Again, a quadratic regression ($k=3$) sufficed. For ages with reasonable numbers of records, i.e. 400 to 700 days, estimates of the corresponding genetic correlation varied little with age, and were of similar magnitude to the estimate from a repeatability model analysis for both traits ($k=1$) of -0.30. Previous estimates for this correlation were -0.25, -0.28 and -0.41 in Herefords, Angus and Zebu cross cattle, respectively (Meyer *et al.* 1991). Estimates of genetic parameters for both traits were almost identical to those from corresponding univariate analysis; estimates for SS are shown in Figure 3 and estimates for DC were $h^2=0.178$ and $p^2=0.035$, respectively.

CONCLUSIONS

Variances of SS records increase with age and mean value. Hence random regression models fit the data better than a repeatability model. Records taken prior to 500 days of age are evidently more heritable and thus more informative than those recorded later. A single SS measurement taken around 400 days of age appears adequate for genetic evaluation. With limited data available, there is no evidence for a change in genetic correlation between SS and DC between 400 and 700 days of age. Whilst the estimate of about -0.3 is favourable, it is low, suggesting that both traits need to be

measured to maximise scope for genetic improvement of reproductive performance in both sexes.

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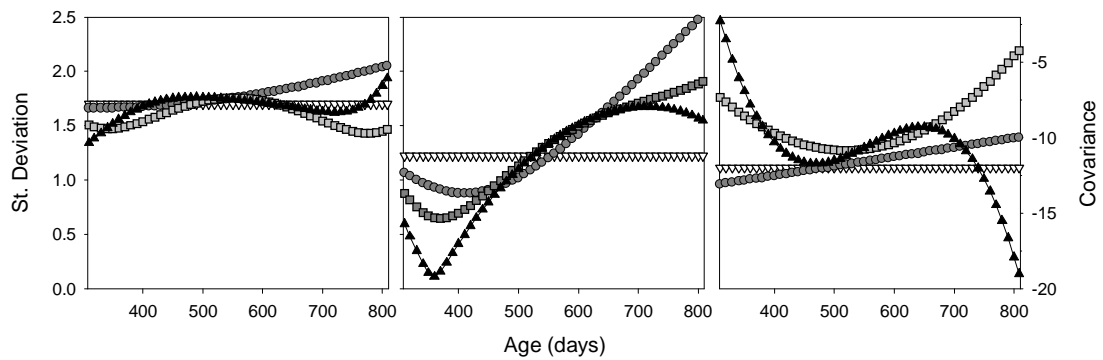


Figure 2. Estimates of genetic (left) and permanent environmental (middle) standard deviations for scrotal circumference and covariances between scrotal circumference and days to calving (right) for different orders of fit (∇ : k=1, \bullet : k=2, \blacksquare : k=3 and \blacktriangle : k=4)

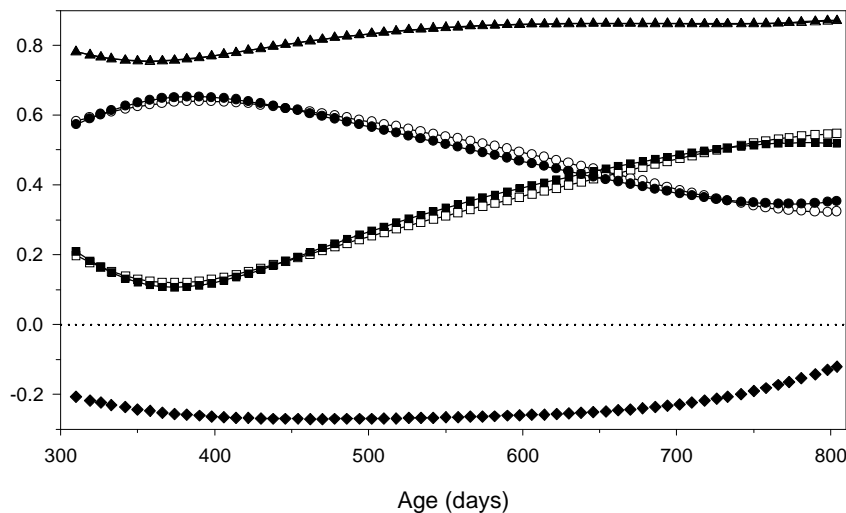


Figure 3. Estimates of heritability (\bullet), permanent environmental effects (\blacksquare) and repeatability (\blacktriangle) for SS, and genetic correlation between SS and DC (\blacklozenge) (open symbols : univariate, closed symbols : bivariate analyses)