

## Genetic relationship between feed efficiency and profitability traits in beef cattle

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### Abstract

Genetic selection to improve feed efficiency aims to reduce the cost of feeding costs in beef cattle production and thereby improve profitability. The aim of this study was to estimate genetic (co)variances to compare residual feed intake (RFI) and feed conversion ratio (FCR) with growth, reproductive and profitability traits measured in growth tests of young bulls. The heritability estimated for FCR was 0.34 and for RFI 0.31 with a genetic correlation estimate of 0.75 between the traits. The estimated genetic correlation between profitability and FCR and RFI were  $-0.92$  and  $-0.59$ , respectively. The genetic correlations and expected correlated responses between RFI and FCR with post-wean profitability (M-value) suggest that indirect selection for M-value through the direct selection for FCR and/or RFI will result in slower genetic progress in M-value than direct selection for M-value. However, where the M-value cannot be calculated and/or direct selection for M-value is not possible, it would be better to select indirectly for M-value through the use of FCR rather than RFI.

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### Introduction

High feeding costs of animals are a major constraint in profitability in livestock production enterprises. Feed costs represent approximately one-half the total cost of production for most classes of livestock and improvement of feed efficiency should be a major consideration in most breeding programs (Kennedy *et al.*, 1993). Genetic selection to improve feed efficiency aims to reduce the cost of feeding in beef cattle production and thereby improve profitability.

Koots *et al.* (1994b) reported highly negative weighted genetic correlation estimates between feed conversion ratio (FCR) and growth rate and size. These correlations indicate that selection to reduce FCR, and thus improve efficiency, would be accompanied by an increase in growth rate, and an increase in mature cow size. A second disadvantage of selection for FCR related to problems inherent with selection on ratio measurements (Gunsett, 1986), involving two different traits (feed intake and growth) with different variances within them.

Considerable variation in feed intake, independent of size and growth rate, exists in beef cattle and this trait is defined as residual (or nett) feed intake (RFI) (Archer *et al.*, 1998). The advantage of using RFI as an efficiency trait instead of FCR is that RFI is not defined as a ratio trait and that selection to reduce RFI offers an opportunity to reduce feed intake, without compromising growth performance, and also without the possible correlated response in maturity type (Archer *et al.*, 1998; Herd & Bishop, 2000). RFI is however more difficult to calculate than FCR and the energy required for growth and maintenance, assumed in the calculations of RFI, can be differing in different environments and climates.

The aim of this study was to estimate genetic (co)variances (and ratios) to compare RFI and FCR with growth, reproductive and especially with profitability trait(s) measured in growth tests of young bulls.

### Materials and Methods

The data analysed in this study was collected from the centralised growth test stations of South Africa's Agricultural Research Council (ARC). Records from Bonsmara bulls, tested in centralised growth tests between 1989 and 2001 were used. The data set consists of the individual feed intake and weights of 6 738 bulls.

Traits measured in a centralised growth test are feed intake, weekly weights (growth), scrotum circumference (SCR) and shoulder height (SHD). Individual feed intakes and weekly weights make it possible to calculate an average daily gain (ADG), feed conversion ratio (FCR), residual (or nett) feed intake as well as a feedlot profitability value for each bull. Feed conversion ratio is the amount of feed consumed

by the animal in order to gain a kilogram in body (live) weight. Residual (or nett) feed intake is defined as the amount of feed consumed by an animal less or more than what would be expected for the growth of the animal and its body weight (used as an indicator of maintenance requirements). A post-weaning growth monetary value, calculated in Rand (M-value), for each bull was simulated as if the tested bull was fed under feedlot conditions and sold to an abattoir. The M-value was calculated as income at the end of the test period minus all variable expenses during the growth test period.

Variance components, heritabilities and genetic correlations for and between weaning weight (WW), ADG, SCR, SHD, FCR, RFI and M-value were estimated simultaneously by multitrait restricted maximum likelihood (REML) procedures using the VCE package developed by Groeneveld (1994).

The importance of non-genetic sources of variation on the traits was determined by the PROC GLM procedure of SAS (2000). Non-genetic sources that were included in the models for WW were the linear and quadratic regressions of the age of the dam, the linear and quadratic regression of the age of the animal at weaning and the contemporary group for weaning weights (herd, weaning date, treatment code and sex) as fixed effects (1 246 levels). The linear regression of the age of the dam and the contemporary group fixed effect for the growth test (which include test centre, test year, test phase and test number) were included in the model (514 levels) for ADG only. For SCR and SHD the linear and quadratic regression of the age of the animal at the end of the growth test, the linear regression of the age of the dam and the contemporary group fixed effect for the growth test were included as non-genetic sources. The linear regression of the age of the animal at the end of the growth test and age of the dam were included and the contemporary group effect as a fixed effect for FCR, RFI and M-value. These non-genetic sources were significant ( $P < 0.001$ ) and were therefore included in the models for FCR, RFI and M-value.

In order to compare the effectiveness of response in M-value based on selection for RFI or FCR, expected correlated responses were estimated (Falconer & Mackay, 1996).

## Results and Discussion

The average ( $\pm$  s.d.) age of bulls at wean was  $205 \pm 23$  days with an average weaning weight of  $234 \pm 30$  kg. The average age at the end of the growth test was  $410 \pm 26$  days. The mean FCR ( $6.44 \pm 0.81$ ) corresponds with the mean FCR of  $6.5 \pm 0.9$  obtained by Arthur *et al.* (2001). The range in RFI between  $-3.73$  and  $3.56$  correlates well with the corresponding range estimated for Bonsmara cattle by Archer & Bergh (2000) of between  $-3.76$  and  $3.72$ . The least profitable animal in the growth tests made a loss of R824.78, while the most profitable animal achieved a profit of R494.36. The average M-value was a loss of R223.93 with a standard deviation of R141.28.

**Table 1:** Heritability (on diagonal) and genetic correlation estimates (above diagonal) for and among traits

|         | WW          | ADG         | SCR         | SHD         | FCR         | RFI         | M-value     |
|---------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|
| WW      | <b>0.32</b> | 0.28        | 0.15        | 0.50        | -0.03       | -0.05       | -0.24       |
| ADG     |             | <b>0.37</b> | 0.21        | 0.48        | -0.69       | -0.09       | 0.65        |
| SCR     |             |             | <b>0.42</b> | 0.09        | -0.06       | 0.05        | 0.01        |
| SHD     |             |             |             | <b>0.52</b> | -0.24       | -0.02       | 0.10        |
| FCR     |             |             |             |             | <b>0.34</b> | 0.75        | -0.92       |
| RFI     |             |             |             |             |             | <b>0.31</b> | -0.59       |
| M-value |             |             |             |             |             |             | <b>0.36</b> |

The heritability for and genetic correlation estimates between WW, ADG, SCR, SHD and FCR (Table 1) are of the same order as those reported by Koots *et al.* (1994a; b). A difference in heritability and genetic correlations estimates for and between WW and other traits as compared to Koots *et al.* (1994a; b), can be ascribed to the exclusion of additive maternal effect in the current study and the fact that the estimates reported by Koots *et al.* (1994b) were obtained from two trait (bivariate) analyses.

The heritability estimate of 0.34 for FCR corresponds well with the mean estimate reported by Koots *et al.* (1994a), as well as those obtained by Archer *et al.* (1999) and Herd & Bishop (2000), but is lower than the 0.42 obtained by Arthur *et al.* (2001). The heritability estimate of 0.31 for RFI corresponds to that of 0.32 estimated by Arthur *et al.* (2001).

The correlation estimates between RFI and the other traits (except for the correlation of 0.75 between RFI and FCR) were close to zero. This confirms that RFI is genetically independent of ADG and SHD. Selection for growth rate (ADG) has been repeatedly associated with an increase in mature cow size, and its benefit to overall herd productivity has been questioned seriously (Archer *et al.*, 1998).

The advantage in the use of RFI is therefore its independence of ADG and SHD, and therefore, genetic selection for lower RFI has the potential to improve feed efficiency in young animal without increasing cow size. FCR on the other hand, is lowly correlated with SHD (-0.24). This indicates that selection for lower FCR will have only a small positive effect on SHD and that it is possible to select animals with a low FCR without a marked increase in SHD.

The high genetic correlation estimate of -0.92 between FCR and M-value indicate that these two traits are practically the same. RFI is also genetically correlated with the M-value (-0.59), but to a lesser degree than FCR.

The expected correlated response in M-value through indirect selection for FCR was 0.87, while the expected correlated response in M-value through indirect selection for RFI was 0.55. These results suggest that it would be more efficient to select directly for M-value than through indirect selection on either FCR or RFI. Where the M-value cannot be calculated and direct selection is not possible, it would be better to select indirectly for M-value through the use of FCR rather than RFI.

## Conclusion

For Bonsmara cattle, under South African conditions, genetic correlations indicate that RFI is independent of ADG and SHD. The genetic correlation between FCR and SHD are also small, indicating that it is possible to select animals with favourable breeding values for FCR and not necessarily increase SHD. The genetic correlations and expected correlated responses between RFI and FCR with M-value suggest also that indirect selection for M-value through the direct selection for FCR and/or RFI will result in slower genetic gain in M-value than direct selection for M-value. However, where the M-value cannot be calculated and/or direct selection for M-value is not possible, it would be better to select indirectly for M-value through the use of FCR rather than RFI.

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