

Residual feed intake as selection tool in South African Bonsmara cattle

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ABSTRACT

In South African Bonsmara cattle, feed conversion ratio (FCR) is mostly used as a measure of feed efficiency in selection programs but has the disadvantage of being a ratio trait and unfavourably correlated to weight and mature size. Residual feed intake (RFI) overcomes both these disadvantages. The purpose of this study was to evaluate RFI as a potential trait in a selection programme by determining its correlations with growth related traits as well as other efficiency traits. Data of 5981 Bonsmara bulls that participated in centralised growth tests was analysed. In this study, RFI was calculated within contemporary groups of more than ten animals. The h^2 for RFI, FCR and KR were 0.27 ± 0.02 , 0.23 ± 0.02 and 0.18 ± 0.02 respectively. The genetic correlation between RFI and FCR, and RFI and KR were 0.65 ± 0.04 and 0.12 ± 0.07 respectively. Correlations approaching zero were estimated between RFI and shoulder height (SH), body length (BL), scrotal circumference (SC), average daily gain (ADG), weaning weight (WW) and metabolic mid-weight (MMW), and a strong correlation of 0.79 ± 0.03 with daily feed intake (DFI). This study shows sufficient genetic variation for RFI to be considered by the Bonsmara breed as a measure of feed efficiency and confirms its independence from growth and size traits.

Keywords: Feed efficiency, residual feed intake, feed conversion ratio, Kleiber ratio, Bonsmara

1. Introduction

In 2010 the total number of beef cattle in South Africa was estimated to be 14.1 million, of which 60% were owned by commercial farmers. There are approximately 70 feedlots and 495 abattoirs, with the largest feedlot accommodating 120 000 cattle and processing 1 600 carcasses daily

(Department of Agriculture, Forestry and Fishery, 2010). Feed efficiency is therefore an important trait to consider as feeding costs is by far the largest expense in the beef industry, comprising about 55 to 75 % of the total costs associated with beef cattle production (Arthur *et al.*, 2001a). Selection for higher feed efficiency in beef cattle using RFI holds potential for less dry matter intakes (DMI), less manure production and less methane emissions while maintaining body weights similar to those of less efficient cattle (Nkrumah *et al.*, 2006; Hegarty *et al.*, 2007). The measures of feed efficiency used in South Africa are feed conversion ratio (FCR) and Kleiber ratio (KR). Both these measurements have the disadvantage of being ratio traits, and FCR's strong association with growth rate (Bishop *et al.*, 1991; Koots *et al.*, 1994) has partly contributed to an increase in mature size and consequently higher maintenance cost of the breeding herd (Liu *et al.*, 2000). Residual feed intake (RFI) is a linear trait and has been shown to be independent from mature weight and average daily gain (ADG) while being highly correlated to feed intake (Archer *et al.*, 1999; Herd *et al.*, 2003; Crews, 2005; Nkrumah *et al.*, 2007). Studies have reported heritability estimates for RFI varying from 0.14 to 0.58 (Fan *et al.*, 1995; Crews *et al.*, 2003). In South Africa, RFI is currently not used as a feed efficiency measure in selection programs. The purpose of this study was to determine the association of RFI with growth related traits and feed efficiency traits, with potential inclusion of RFI in a selection programme.

2. Materials and Methods

The data for this study was obtained from growth tests performed at the centralised test stations of the Agricultural Research Council (ARC) and private stations in South Africa from 1999 to 2010. The data used for this study was stored on INTERGIS, a database for South African data recording, and consisted of Bonsmara bulls that met breed standards as set by the Bonsmara breeders' society and took part in centralised testing. There was an adaptation period of 28 days and a test length of 84 days. Bulls were individually fed *ad lib* with a standard, complete growth ration prescribed for all stations as described by Archer & Berg (2000). Each bull had a transponder around its neck which opens a specific trough, making it possible to determine individual feeding. Weekly intakes were determined by subtracting the weight of feed remaining in the bunk from the total weight of feed given during that week. Body weight was taken at weekly intervals after a 12 hour overnight fast.

Measurements taken at the end of the test are shoulder height (SH), body length (BL), skin thickness and scrotal circumference (SC). Data entries with weekly intakes outside three standard deviations were deleted, and the same applied for age, initial weight, ADG, SC, SH, BL and weaning weight (WW). Animals had to comply with requirements for all traits to be included. Contemporary groups included a concatenation between test station, test year, season (test number) and test phase (C1, C2 and C3). The calculation of RFI depends on the predicted feed intake that was determined by regressing actual feed intake against metabolic mid-weight and ADG (Koch *et al.*, 1963). Contemporary groups with less than 10 animals were discarded to be able to obtain a more representative regression. The remaining 270 groups (total of 5981 animals) had an average size of 22 and were available for further analysis. Pedigree information and recordings covered four generations, a total of 20 398 animals, with 3 851 sires and 14 520 dams.

To calculate RFI, metabolic mid-weight (MMW), ADG, actual DFI and expected DFI were required. Measurements for DFI were on as is basis. These traits were calculated using the following formulas:

$$\text{MMW} = ((\text{Initial weight} + \text{Final weight}) / 2)^{0.75}$$

$$\text{ADG} = (\text{Final weight} - \text{Initial weight}) / \text{Test length}$$

$$\text{DFI} = \text{Total Feed Intake} / \text{Test length}$$

Actual DFI was regressed against MMW and ADG for each contemporary group using PROC REG of SAS 9.1.3 (2006). The fitted model to calculate expected DFI was $Y_i = \beta_0 + \beta_1 \times \text{ADG}_i + \beta_2 \times \text{MMW}_i + e_i$ (Koch *et al.*, 1963), where Y_i is the expected daily feed intake of animal i , β_0 is the regression intercept, β_1 is the partial regression coefficient of feed intake on ADG of animal i , β_2 is the partial regression coefficient of feed intake on MMW and e_i is the error. RFI was calculated by subtracting expected DFI from actual DFI (Koch *et al.*, 1963), KR by dividing ADG with MMW (Kleiber, 1947) and FCR by dividing DFI by ADG.

The phenotypic Pearson correlations between all traits were determined using PROC CORR of SAS 9.1.3 (2006). The PROC GLM procedure was used to identify fixed effects for the estimation of estimated breeding values (EBV). Effects tested to include in the model (at significant level of $P < 0.05$) were contemporary group (270 levels), herd (123 levels), age, age², (dam age), and (dam age)².

All effects were included as fixed effects in the model for WW, BL, SC and MMW. All but age² were included for DFI, ADG and SH. Herd and age were included for RFI. Animal was included as a random effect in all models and random maternal effects were assumed to be zero. Variance components, heritabilities and genetic correlations for all traits were estimated by multitrait restricted maximum likelihood (REML) procedures using VCE 6 (Groeneveld *et al.*, 2010), and EBV's estimated using PEST 2 (Groeneveld *et al.*, 2010). The animal model used is described as $Y_i = X\beta_i + Z\mu_i + e_i$, where Y_i is the vector of trait i (RFI, FCR, KR, ADG, DFI, WW, MMW, SH, BL, SC), X is the matrix relating observations to fixed effects, B_i is the vector of fixed effects associated with trait i , Z is the matrix relating observations to random effects (which is animal for all traits), μ_i is the vector of random effects associated with trait i and e_i is the unexplained residual effects for trait i .

3. Results

The descriptive statistics is presented in table 1, and genetic parameters and phenotypic correlations estimated for the different traits in table 2. The heritability estimate for RFI in this study was 0.27 ± 0.02 , which is similar to estimates reported by Koch *et al.* (1963) (0.28), Fan *et al.* (1995) (0.28) and Mujibi *et al.* (2011) (0.29). The heritability of RFI was higher than that estimated for KR (0.18 ± 0.02), but similar to that of FCR (0.23 ± 0.02). Heritability for KR was slightly less than 0.23 ± 0.09 found in South African Herefords by Köster *et al.* (1994) for KR based on growth from 205-365 days.

The reproductive trait under investigation was scrotal circumference (SC) and showed a genetic correlation of -0.08 ± 0.04 with RFI. The genetic correlations between RFI and weight traits were low, such as 0.10 ± 0.07 with ADG, -0.01 ± 0.09 with WW and 0.02 ± 0.07 with MMW. The genetic correlation with DFI was high (0.79 ± 0.03), which is similar to previously published estimates, such as 0.79 by Arthur *et al.* (2001b), 0.75 by Nkrumah *et al.* (2004) and 0.81 by Schenkel *et al.* (2004). There was a weak genetic correlations with SH (-0.05 ± 0.07). Genetic correlations between FCR and weight traits were medium to high, including -0.66 ± 0.04 with ADG, -0.21 ± 0.08 with WW, and -0.44 ± 0.06 with MMW, while the correlation with DFI (0.11 ± 0.06) was weak. The genetic correlation with size traits, SH (-0.35 ± 0.06) and BL (-0.39 ± 0.06), were medium. A weak genetic correlation of

0.12 \pm 0.07 between KR and RFI was estimated, as well as a strong correlation of -0.64 \pm 0.05 between KR and FCR. The correlation between RFI and FCR was estimated to be 0.65 \pm 0.04, which is similar to previously published estimates ranging from 0.57 to 0.85 (Arthur *et al.*, 2001a, 2001b; Nkrumah *et al.*, 2004; Van der Westhuizen *et al.*, 2004)

Table 1 Means, standard deviations (SD), minimums and maximums for age, dam age, growth, body measurements and efficiency traits

| Trait | Mean | SD | Min | Max |
|----------------------------|-------|------|-------|-------|
| Age (days) | 329 | 23 | 261 | 392 |
| Dam age (days) | 2209 | 1059 | 676 | 6080 |
| Average daily gain (g) | 1744 | 267 | 760 | 2654 |
| Weaning weight (kg) | 237 | 32 | 140 | 376 |
| Metabolic mid-weight (kg) | 78 | 7 | 57 | 102 |
| Daily feed intake (kg) | 10.2 | 1.3 | 5.3 | 14.7 |
| Shoulder height (mm) | 1168 | 29 | 1030 | 1300 |
| Body length (mm) | 1362 | 45 | 1140 | 1550 |
| Scrotal circumference (mm) | 334 | 28 | 200 | 470 |
| Residual feed intake (kg) | 0 | 0.63 | -3.09 | 3.49 |
| Kleiber ratio (g/kg) | 22.34 | 3.10 | 12.01 | 32.74 |
| Feed conversion ratio (kg) | 5.93 | 0.84 | 3.34 | 10.86 |

4. Discussion

The participation in central growth tests by Bonsmara stud breeders in South Africa has a cost implication and it is important to measure traits that will contribute to their selection programs for more efficient animals. The results indicate that the heritability estimates for RFI and FCR are similar, which suggests that rate of genetic improvement will not be decreased with the replacement of FCR with RFI. The genetic correlations estimated in this study showed that selecting for feed efficiency

Table 2 Heritabilities (on diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) for RFI, SH, LE, SC, ADG, DFI, WW, FCR, MMW and KR, with standard errors, of Bonsmara cattle as determined with the use of VCE 6

| Trait | RFI | SH | LE | SC | ADG | DFI | WW | FCR | MMW | KR |
|-------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| RFI | 0.27 ± 0.02 | -0.05 ± 0.07 | 0.01 ± 0.07 | -0.08 ± 0.04 | 0.10 ± 0.07 | 0.79 ± 0.03 | -0.01 ± 0.09 | 0.65 ± 0.04 | 0.02 ± 0.07 | 0.12 ± 0.07 |
| SH | -0.01 | 0.39 ± 0.03 | 0.77 ± 0.03 | 0.32 ± 0.04 | 0.54 ± 0.04 | 0.33 ± 0.05 | 0.41 ± 0.06 | -0.35 ± 0.06 | 0.62 ± 0.04 | 0.35 ± 0.06 |
| LE | -0.01 | 0.65* | 0.28 ± 0.02 | 0.23 ± 0.05 | 0.66 ± 0.04 | 0.47 ± 0.05 | 0.58 ± 0.06 | -0.39 ± 0.06 | 0.77 ± 0.03 | 0.43 ± 0.06 |
| SC | 0.02 | 0.36* | 0.37* | 0.36 ± 0.03 | 0.20 ± 0.04 | 0.12 ± 0.04 | 0.31 ± 0.07 | -0.14 ± 0.05 | 0.35 ± 0.05 | 0.07 ± 0.05 |
| ADG | 0.00 | 0.35* | 0.39* | 0.32* | 0.25 ± 0.02 | 0.67 ± 0.04 | 0.35 ± 0.07 | -0.66 ± 0.04 | 0.75 ± 0.03 | 0.91 ± 0.02 |
| DFI | 0.48* | 0.39* | 0.39* | 0.35* | 0.57* | 0.31 ± 0.03 | 0.28 ± 0.08 | 0.11 ± 0.06 | 0.55 ± 0.05 | 0.57 ± 0.05 |
| WW | -0.04* | 0.46* | 0.52* | 0.36* | 0.19* | 0.26* | 0.21 ± 0.02 | -0.21 ± 0.08 | 0.66 ± 0.05 | 0.08 ± 0.08 |
| FCR | 0.43* | -0.05* | -0.09* | -0.05* | -0.62* | 0.27* | 0.03 | 0.23 ± 0.02 | -0.44 ± 0.06 | -0.64 ± 0.05 |
| MMW | 0.00 | 0.63* | 0.68* | 0.53* | 0.44* | 0.56* | 0.69* | 0.01 | 0.30 ± 0.02 | 0.40 ± 0.07 |
| KR | 0.00 | 0.01 | 0.02 | 0.04* | 0.84* | 0.30* | -0.20* | -0.69* | -0.11* | 0.18 ± 0.02 |

* Significant, with significance level set at $P < 0.01$

using RFI will not influence growth performance and size but will decrease feed intake, while FCR will increase growth and weight traits. The genetic correlation between RFI and DFI was high, while the genetic correlation between FCR and DFI was considerably lower. Therefore the change in feed intake can be expected to be higher when using RFI instead of FCR as a selection tool.

A weak genetic correlation between KR and RFI, and a high correlation between KR and FCR showed that selecting for KR might lead to similar results as when selecting for FCR, while results might differ greatly from those obtained when using RFI. The correlation between RFI and FCR was estimated to be high, but using RFI as a selection tool may deliver more desirable results as it will not increase the maintenance requirements of the herd.

The large number of small contemporary groups found in practice would require a different approach to the calculation of RFI. Small groups will decrease the reliability of the regression used to calculate expected feed intake. A solution is to calculate RFI on one regression including all the animals in the dataset, and including contemporary group in the model for EBV estimation. Another approach by MacNeil *et al.* (2011) to increase the number of animals with values is to analyse DFI, ADG and MMW and use these EBV's to predict genetic RFI.

RFI shows potential as a trait to be included in a selection program, especially for breeders in areas that cannot support large animals. Its ability to identify animals that consume less without a decrease in growth performance has the potential to increase profitability. However, a previous study on centrally tested South African Bonsmara bulls reported that selecting for RFI will not necessarily be more profitable, with the genetic correlations between post-wean profitability and FCR being -0.92, but only -0.59 with RFI (Van der Westhuizen *et al.*, 2004). A recent study by Berry & Crowley (2012) also questioned the profitability of RFI and proposed different feed efficiency measurements, namely residual gain (RG) and residual intake and body weight gain (RIG) to address this issue. Further studies are needed to investigate other potentially useful feed efficiency measures in South African Bonsmara cattle.

5. Conclusions

This study on South African Bonsmara cattle has shown that selection for RFI will decrease DFI without increasing growth, weight or size, while selection for FCR will lead to an increase in growth,

weight and size. The moderate heritability of RFI makes it a potential trait to be included in a selection program. The small contemporary groups presented a limitation for the calculation of RFI.

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