Genetic parameters for measures of the efficiency of gain of boars and the genetic relationships with its component traits in Duroc pigs

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ABSTRACT: Genetic parameters for the efficiency of gain traits on 380 boars and the genetic relationships with component traits were estimated in 1,642 pigs (380 boars, 868 gilts, and 394 barrows) in 7 generations of a Duroc population. The efficiency of gain traits included the feed conversion ratio (FCR) and residual feed intake (RFI) and their component traits, ADG, metabolic BW (MWT), and daily feed intake (FI). The RFI was calculated as the difference between the actual and expected FI. The expected FI was predicted by the nutritional requirement and by the residual of phenotypic (RFIphe) and genetic (RFIgen) regressions from the multivariate analysis for FI on MWT and ADG. The means for RFIphe and RFIgen were close to zero, and the mean for nutritional RFI was negative (−0.11 kg/d). The traits studied were moderately heritable (ranging from 0.27 to 0.53). The genetic and phenotypic correlations between ADG and FI were moderate to high, whereas the genetic correlation between MWT and FI was moderate, and the phenotypic correlation between them was low. The corresponding correlations between RFIphe and RFIgen were > 0.95, implying that they can be regarded as the same trait. The genetic and phenotypic correlations of FCR with measures of RFI were high but lower than unity. The RFIphe was phenotypically independent of its component traits, MWT (rp = 0.01) and ADG (rp = 0.03). The RFIgen was genetically independent of MWT (rg = −0.04), whereas there was a weak genetic relationship (rg = 0.15) between RFIgen and ADG. Residual FI was more heritable than FCR, and the genetic and phenotypic correlations of RFIphe and RFIgen with FI were positive and stronger than that of FCR with FI. These results provide evidence that RFIphe or RFIgen should be included in breeding programs for Duroc pigs to make genetic improvement in the efficiency of gain.

Key words: Duroc pig, efficiency of gain, genetic parameter, growth

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INTRODUCTION

The cost of feeding animals is a major determinant of profitability in animal production systems, and, thus, any effort at improving the efficiency of feed use will help to reduce feed cost. This has long been recognized by the poultry and porcine industries, in which the cost of feed is readily quantified. One way to reduce feed costs is through selection of more efficient animals (Hoque et al., 2006a). It is necessary, therefore, to consider avenues for reducing feed input to improve production efficiency.

Estimates of genetic parameters for important traits are requisite for accelerating the progress of ongoing breeding programs. Selection for growth rate has received considerable attention in most pig improvement projects. For growth traits, numerous heritability and correlation estimates are available in pigs (Suzuki et al., 2005). However, there is a lack of reports on estimates of the genetic relationships among measures of the efficiency of gain and their component traits in pigs.

Selection for residual feed intake (RFI), that is, feed consumed above or below the requirements for production and maintenance, may be a useful alternative measure (Arthur et al., 2001b). This difference in intake is generally calculated as RFI by comparing the actual and predicted feed intake of an animal. The predicted feed intake is the amount of feed that the animal is expected to consume by its BW and growth rate. Variation in RFI may reflect differences in the efficiency with which animals digest and utilize energy for mainte-
nance and production. Selection against RFI might improve the efficiency of energy utilization without reducing appetite, which is needed for production of the product. Inclusion of this trait in a breeding program depends on its heritability and its relationships with other traits of interest.

The objective of this study was to estimate genetic parameters for and genetic relationships between measures of the efficiency of gain and its component traits in Duroc pigs.

**MATERIALS AND METHODS**

Animal management and research protocols were followed as stated in the guidance book for performance test at the prefectural research station for meat production of pigs in Japan.

**Animals at Performance Test**

Duroc pigs used in this study were from a line that was selected through 7 generations, from 1995 to 2001, at the Miyagi Prefecture Animal Industry Experiment Station. The average population size of each generation was 15.6 sires and 44.5 dams. A total of 1,642 pigs were tested, and the tested pigs were the progeny of 125 boars and 356 gilts. To estimate the variance components, a pedigree file was constructed. The total number of pigs in the pedigree, including test pigs, was 1,780. Description of the data structure is presented in Table 1. Gilts farrowed only once, and boars were retained for use during one 4- to 6-wk breeding period. Thereby, a new generation was obtained each year.

Pigs were weaned at 4 wk of age. At 8 wk of age, 1 to 2 male piglets (total of 50 piglets) and 2 to 4 female piglets (total of 100 piglets) from each litter were selected as candidates for boars and gilts based on their individual BW at 8 wk. At that time, about 80 piglets in all, composed mainly of boars with some gilts (when boars were not available) from each litter, were selected for full-sib testing in each generation. This first stage of selection was conducted within litters. Boars for full-sib tests were subsequently castrated. Performance tests began when the BW reached 30 kg and ended at 105 kg. Pigs were provided ad libitum access to a specially ordered formula feed (15% CP, 78% TDN, 0.76% Lys on a DM basis) during the testing period. The same diet was fed throughout the 7 generations. Pigs had free access to water. Boars were reared individually in performance-testing pens. Gilts and barrows were reared in growing pens, with group feeding in a concrete-floored building with 8 pigs per pen, which allowed 1.2 m² of floor area per pig.

**Selection Method**

The detailed procedure for selection has been described by Suzuki et al. (2005). The selection was conducted without a control line. The first and second generations of selection were performed using an index selection method based on the relative desired gains (Yamada et al., 1975). Traits as selection criteria were ADG from 30 to 105 kg of BW, LM area (EMA), backfat thickness (BF) at 105 kg of BW, and i.m. fat (IMF).

Genetic and phenotypic parameters used to derive the selection criteria were obtained from the performance test data of the first and second generations. The means of ADG, EMA, BF, and IMF at the first generation were 850 g, 36.1 cm², 2.34 cm, and 4.3%, respectively. Relative desired gain was 135 g, 3.9 cm², −0.54 cm, and 0.7%, for ADG, EMA, BF, and IMF, respectively, established from the performance test data of the first generation. Consequently, the selection index equation was as follows:

\[
I = (0.038 \times ADG) + (1.38 \times EMA) - (15.10 \times BF) + (12.63 \times IMF) - 56.68.
\]

Breeding values of ADG, EMA, BF, and IMF were estimated using multiple-trait, animal-model BLUP from the third generation onward. The breeding values were calculated using the prediction and estimation program after estimating genetic parameters using the variance component estimation (VCE) program (version 4.2.5; Neumaier and Groeneveld, 1998), with the models of generation and sex as fixed effects and random effects of the individual additive genetic effect and error. Relative economic weights of selection traits were calculated from the relative desired gains of ADG, EMA, BF, and IMF, respectively, established from performance test data of the first generation, as described above. The aggregate breeding values were calculated by multiplying the relative economic weights by the EBV of
each trait; then, selection was executed. To avoid rapid disappearance of the genes of the base generation from the population, selection was made within sires for boars and within litters for gilts at the first generation. Approximately 15 boars and 50 gilts were selected at each generation. In each generation, inbreeding coefficients for individual pigs were computed. Based on inbreeding information, all matings were planned to minimize the rate of increase in inbreeding.

**Traits in Study**

The weekly BW of the individual pig during the test period was recorded and the ADG for each animal was calculated individually from the difference between beginning and end test BW divided by the number of days. The BW at midtest (MBW) for each animal was computed as the average of the beginning and end of test BW. Metabolic BW at midtest (MWT) was calculated as MBW raised to the power of 0.75 (i.e., MBW$^{0.75}$). Daily feed intake (FI) was measured only for individual boars as the difference between supplied and leftover feed. The FI was then combined with ADG and MWT to compute measures of the efficiency of gain-feed conversion ratio (FCR) and RFI for individual boars. The FCR was calculated as FI divided by ADG. The RFI was estimated as nutritional RFI ($\text{RFI}_{\text{nut}}$), phenotypic RFI ($\text{RFI}_{\text{phe}}$), and genetic RFI ($\text{RFI}_{\text{gen}}$). The $\text{RFI}_{\text{nut}}$ was estimated using the following method from JFSS (2005):

$$\text{RFI}_{\text{nut}} = \text{FI} - (\text{DE}/3,495),$$

where $\text{DE} = \text{the daily energy requirement} = (140 \times \text{MWT}) + (\text{PR}/0.42) + (\text{FR}/0.71)$; $\text{PR} = \text{protein accumulation} = (0.121 \times \text{MBW}) + [119.2 \times (\text{ADG} + 25.5)] \times 5.66$; $\text{FR} = \text{fat accumulation} = (-0.268 \times \text{MBW}) - (0.0015 \times \text{MBW}^2) + (99.65 \times \text{ADG}) + (42.43 \times \text{ADG}^2) + [3.45 \times (\text{ADG} - 21.4)] \times 9.46$; and 1 kg of feed contained 3,495 kcal of GE.

The $\text{RFI}_{\text{phe}}$ and $\text{RFI}_{\text{gen}}$ were estimated by the residual of phenotypic and genetic regression, respectively, from the multivariate analyses of FI on MWT and ADG, fitting a model with fixed terms for the overall mean plus random terms for the generation and the animal effects (including pedigree). Then, $\text{RFI}_{\text{phe}}$ was estimated as:

$$\text{RFI}_{\text{phe}} = \text{FI} - (\beta_\text{wiphe} \times \text{MWT}) - (\beta_\text{gphe} \times \text{ADG}),$$

where the phenotypic regression coefficients, $\begin{bmatrix} \beta_\text{wiphe} \\ \beta_\text{gphe} \end{bmatrix}$, are

$$\begin{bmatrix} \beta_\text{wiphe} \\ \beta_\text{gphe} \end{bmatrix} = P^{-1}c; \ P = \text{the phenotypic covariance matrix of 2 production traits (MWT and ADG)}; \text{and } c = \text{the vector of the phenotypic covariance of FI with production traits.}$$

$\text{RFI}_{\text{gen}}$ was estimated as:

$$\text{RFI}_{\text{gen}} = \text{FI} - (\beta_\text{wigen} \times \text{MWT}) - (\beta_\text{ggen} \times \text{ADG}),$$

where the genetic regression coefficients, $\begin{bmatrix} \beta_\text{wigen} \\ \beta_\text{ggen} \end{bmatrix}$ = $G^{-1}c$; $G =$ the genetic covariance matrix of MWT and ADG and $c =$ the vector of the genetic covariance of FI with production traits estimated using the REML method.

**Statistical Analysis**

The covariance components for all traits were estimated by the REML method with the VCE program (Neumaier and Groeneveld, 1998). Standard errors of the heritability estimates and genetic correlations were also estimated using the same program. The (co)variance components for the efficiency of gain traits ($\text{RFI}_{\text{nut}}, \text{RFI}_{\text{phe}}, \text{RFI}_{\text{gen}}, \text{and FCR}$) were estimated using a 4-trait model. The corresponding components for FI, growth, and the efficiency of gain traits were also estimated in a series of 4-trait models (FI, ADG, and MWT were common, with I the efficiency of gain trait). The optimization in VCE was done with a quasi-Newton procedure and included setting up the mixed model equations, numerical factorization, solving the triangular system, computing the sparse inverse, and assembling the gradients. The convergence criterion (i.e., the variance of the simplex values) for all runs was $10^{-9}$. The following multitrait animal model, in matrix notation, was used to estimate the genetic parameters:

$$\mathbf{y} = \mathbf{X}\beta + \mathbf{Za} + \mathbf{e},$$

where $\mathbf{y} =$ a vector of observations; $\beta$, $\mathbf{a}$, and $\mathbf{e}$ = the vectors of fixed, additive genetic, and residual effects, respectively; and $\mathbf{X}$ and $\mathbf{Z} =$ the known incidence matrices. Fixed effects were sex and selection generation for all traits. The selection generation included the genetic effect of selection and the environmental effect at each generation. Assumptions for random effects were:

$$\mathbf{a} \sim \mathcal{N}(0, \mathbf{A}\sigma_a^2) \text{ and } \mathbf{e} \sim \mathcal{N}(0, \mathbf{I}\sigma_e^2),$$

where $\mathbf{A} =$ the matrix of additive relationships among pigs; $\mathbf{I}_e =$ the identity matrix of appropriate order; and $\sigma_a^2$ and $\sigma_e^2 =$ the additive genetic and residual variances, respectively. All pigs in the pedigree were used in the analysis to establish the numerator relationship matrix of the pigs.

**RESULTS**

The means, heritabilities, and genetic and phenotypic correlations among FI and growth traits (ADG and MWT) are presented in Table 2. The mean values for FI and ADG were consistent with other reports (Mrode and Kennedy, 1993; Suzuki et al., 2005) in the same breed. Estimated heritabilities for growth traits were moderate to high, ranging from 0.44 to 0.53. Appetite,
as measured by FI, was moderately heritable (0.53). The genetic correlations of ADG with FI (0.60) and MWT (0.77) were high and were moderate (0.26) between FI and MWT, whereas the phenotypic correlations among all of them were low to moderate, ranging from 0.14 to 0.51.

The means, variance components, and heritabilities for the efficiency of gain traits are presented in Table 3. Lower values of RFI or FCR indicate better efficiency of an animal. The mean values for RFI不只是(phe and RFI只是(gen were close to zero and was negative for RFI不只是(nut. All 3 estimates of RFI were moderately heritable (0.34, 0.41, and 0.42 for RFI不只是(nut, RFI不只是(phe, and RFI只是(gen, respectively), indicating that variation in RFI of Duroc pigs contains genetic components, which should respond to selection. However, the heritability of FCR was moderate (0.27).

The genetic and phenotypic correlations among different measures of the efficiency of gain are shown in Table 4. The genetic and phenotypic correlations between RFI不只是(phe and RFI只是(gen were greater than 0.95, implying that they may be regarded as the same trait. Corresponding correlations between FCR and different RFI estimates were large but less than 0.90, indicating that FCR should be regarded as a distinct trait. The phenotypic correlations of RFI不只是(nut with the other 2 RFI estimates were close to unity (>0.95), whereas their genetic correlations were large but less than unity. The positive genetic correlations between RFI and FCR indicate that lower RFI (greater efficiency) was associated with improved FCR.

The correlation coefficients between different measures of the efficiency of gain and their component traits are presented in Table 5. Feed intake was positively correlated with all measures of the efficiency of gain but was more strongly correlated with RFI不只是(phe and RFI只是(gen than with RFI不只是(nut and FCR. By definition, RFI不只是(phe should not be phenotypically correlated with its component traits, and the results confirmed this [i.e., rp with MWT (0.01) and ADG (0.03) were close to zero]. In addition, the results show that RFI只是(gen was genetically independent of MWT (rp = −0.04), whereas a weak genetic correlation was observed between RFI只是(gen and ADG (rp = 0.15). The RFI不只是(nut was weakly genetically correlated with growth traits. Favorable (negative) genetic and phenotypic correlations were observed between FCR and its component traits. These estimates indicated that as ADG increased, the FCR decreased (greater efficiency).

**DISCUSSION**

The estimated heritability for ADG was very similar to that (0.43) reported by Mrode and Kennedy (1993) using pen averages of Yorkshire, Landrace, and Duroc boars and to literature averages (0.44) reported by Hutchens and Hintz (1981). However, the present estimate for ADG was greater than the estimate (0.24) by Johnson et al. (1999) in Large White pigs. With Duroc and Landrace pigs, Lo et al. (1992) found a heritability estimate of 0.36 for ADG from 39.5 to 103.6 kg of BW, which was close to the present estimate. Robison and Berruecos (1973) indicated that greater values of heritability for ADG can be expected when pigs are individually fed. Jungst et al. (1981) suggested that differences in estimates of heritability for rate of gain might be due to feeding method (restricted or ad libitum). Differences in source of data and sampling error may be other causes of the differences. Appetite, as measured by FI, appeared highly heritable. Our estimate was comparable to, but slightly greater than, the estimate of 0.45 reported by Mrode and Kennedy (1993) and the esti-
mate of 0.34 for boars fed ad libitum as reported by Cameron et al. (1990). Our study has shown that considerable genetic variation exists in FI, ADG, and MWT in Duroc pigs and that these variations could be exploited in selection programs for the improvement of feed utilization and growth performance.

The genetic and phenotypic correlations between ADG and FI in the current study are in agreement with the findings of Mrode and Kennedy (1993) and Johnson et al. (1999). Mrode and Kennedy (1993) estimated genetic and phenotypic correlations between ADG and FI to be 0.80 and 0.74, respectively. Corresponding correlations estimated by Johnson et al. (1999) for Large White swine were 0.82 and 0.72, respectively. The large estimated genetic and phenotypic correlations between ADG and FI indicate that faster-growing pigs had greater daily feed consumption.

The heritability estimate for FCR in the present study was consistent with previous estimates (Cameron et al., 1990; Mrode and Kennedy, 1993). We are not aware of any published studies on genetic parameters for RFI in pigs. However, Fan et al. (1995) estimated heritability for RFI (calculated from feeding standard formulas) to be 0.23 in Angus cattle. The heritability estimates for RFIphe and RFIgen obtained in the current study are within the range of previous studies. Foster et al. (1983) found a pooled estimate, across breeds, of 0.30 for RFI adjusted for ADG and backfat, and Haer (1992) reported a heritability of 0.45 for RFI adjusted for ADG and lean growth. Mrode and Kennedy (1993) reported a heritability of 0.30 for RFI when adjusted for ADG and backfat and of 0.38 when adjusted for lean growth rate. The genetic variation found in RFI suggests that opportunities exist to select against RFI as a means of improving the efficiency of gain.

There are few reports in the literature of genetic and phenotypic correlations among different estimates of the efficiency of gain, but those available are in general agreement with the findings of this study. Estimated genetic and phenotypic correlations between RFIphe and RFIgen were greater than 0.95, implying that they can be practically regarded as the same trait. No published literature was found on estimates of the relationships between different measures of the efficiency of gain in pigs. However, Hoque et al. (2006b) reported very large genetic (0.97) and phenotypic (0.98) correlations between RFIphe and RFIgen in beef cattle, concluding that selection for RFIgen would give results similar to selection for RFIphe. The genetic correlations of RFIphe and RFIgen with FCR in the current study were large, which is in agreement with the findings of Herd and Bishop (2000) and Arthur et al. (2001a) in beef cattle.

Calculation of RFI requires estimation of expected FI, which can be obtained through regression or through use of feeding standard formula. Kennedy et al. (1993) showed that when expected FI is obtained by phenotypic regression, RFIphe is expected to be phenotypically independent of the component traits and, when expected FI is obtained by genetic regression, RFIgen is expected to be genetically independent of its component traits. They also mentioned that even when RFI is calculated by genetic regression, there is no guarantee that genetic correlations with component traits will be close to zero. In our study, both MWT and ADG were phenotypically independent of RFIphe, and MWT was genetically independent of RFIgen, whereas there was a weak genetic correlation between RFIgen and ADG. However, when RFI is estimated using expected FI calculated from feeding standard formulas, it is not automatically independent of production traits and is, in fact, usually correlated with these traits, as observed in the current study and in the studies by Fan et al. (1995) and Arthur et al. (2001b) in beef cattle.

The low to moderate, but favorable, negative genetic correlations between FCR and growth traits observed in present study are in agreement with the estimates by Suzuki et al. (2005) and Hoque et al. (2006b). Suzuki et al. (2005) reported the genetic correlation between FCR and ADG to be -0.09 in Duroc pigs, whereas the corresponding correlation was highly negative (-0.52) when estimated by Hoque et al. (2006b) in beef cattle. The estimates from this study suggest that selection for ADG will also lead to slight improvement in FCR, and this has been demonstrated in many selection experiments (Kennedy, 1984). The effect of selection for improved growth rate on appetite is not clear. Some studies have shown a correlated reduction in appetite

### Table 4. Genetic (above the diagonal) and phenotypic (below the diagonal) correlations among the efficiency of gain traits of boars

<table>
<thead>
<tr>
<th>Traits</th>
<th>RFI_{nut}</th>
<th>RFI_{phe}</th>
<th>RFI_{gen}</th>
<th>FCR</th>
</tr>
</thead>
<tbody>
<tr>
<td>RFI_{nut}</td>
<td>—</td>
<td>0.76 ± 0.12</td>
<td>0.74 ± 0.11</td>
<td>0.67 ± 0.18</td>
</tr>
<tr>
<td>RFI_{phe}</td>
<td>0.97 ± 0.09</td>
<td>—</td>
<td>0.98 ± 0.09</td>
<td>0.86 ± 0.13</td>
</tr>
<tr>
<td>RFI_{gen}</td>
<td>0.96 ± 0.09</td>
<td>0.97 ± 0.08</td>
<td>—</td>
<td>0.84 ± 0.12</td>
</tr>
<tr>
<td>FCR</td>
<td>0.94 ± 0.10</td>
<td>0.88 ± 0.11</td>
<td>0.84 ± 0.11</td>
<td>—</td>
</tr>
</tbody>
</table>

1RFI_{nut} = the residual feed intake calculated from the nutritional requirement; RFI_{phe} = the phenotypic residual feed intake; RFI_{gen} = the genetic residual feed intake; FCR = the feed conversion ratio.

### Table 5. Genetic (r_g) and phenotypic (r_p) correlations between measures of the efficiency of gain of boars and their component traits in all pigs (boars, gilts, and barrows)

<table>
<thead>
<tr>
<th>Traits</th>
<th>Correlations</th>
<th>FI</th>
<th>MWT</th>
<th>ADG</th>
</tr>
</thead>
<tbody>
<tr>
<td>RFI_{nut}</td>
<td>r_p</td>
<td>0.42 ± 0.05</td>
<td>-0.14 ± 0.06</td>
<td>-0.07 ± 0.05</td>
</tr>
<tr>
<td></td>
<td>r_g</td>
<td>0.24 ± 0.03</td>
<td>0.25 ± 0.02</td>
<td>0.28 ± 0.01</td>
</tr>
<tr>
<td>RFI_{phe}</td>
<td>r_p</td>
<td>0.78 ± 0.08</td>
<td>0.01 ± 0.07</td>
<td>0.03 ± 0.09</td>
</tr>
<tr>
<td></td>
<td>r_g</td>
<td>0.81 ± 0.09</td>
<td>0.02 ± 0.11</td>
<td>0.23 ± 0.12</td>
</tr>
<tr>
<td>RFI_{gen}</td>
<td>r_p</td>
<td>0.82 ± 0.06</td>
<td>0.02 ± 0.04</td>
<td>0.22 ± 0.06</td>
</tr>
<tr>
<td></td>
<td>r_g</td>
<td>0.86 ± 0.02</td>
<td>-0.04 ± 0.13</td>
<td>0.15 ± 0.04</td>
</tr>
<tr>
<td>FCR</td>
<td>r_p</td>
<td>0.57 ± 0.08</td>
<td>-0.13 ± 0.09</td>
<td>-0.25 ± 0.09</td>
</tr>
<tr>
<td></td>
<td>r_g</td>
<td>0.46 ± 0.07</td>
<td>-0.36 ± 0.14</td>
<td>-0.10 ± 0.07</td>
</tr>
</tbody>
</table>

1RFI_{nut} = the residual feed intake calculated from the nutritional requirement; RFI_{phe} = the phenotypic residual feed intake; RFI_{gen} = the genetic residual feed intake; FCR = the feed conversion ratio; FI = the daily feed intake; MWT = the metabolic BW.
(Sather and Fredeen, 1978), and others have shown small increases in FI (Ollivier, 1986; Mrode and Kennedy, 1993). Theoretical arguments have been made that selection for ADG under ad libitum feeding would have a nominal effect on FI, at least initially, but that increases in intake might follow in later generations (Fowler et al., 1976). Heritability and genetic correlation estimates from this study suggest that selection for ADG would increase FI. However, direct selection for FCR has not been very effective (Webb and King, 1983), and selection programs that give emphasis to efficiency, rather than growth rate, on ad libitum feeding have led to a reduction in FI (Webb and King, 1983; Smith et al., 1991), which may be detrimental in the long run.

The efficiency of gain is routinely measured as the ratio of FI to product (or the reciprocal). Gunsett (1984) compared the efficiency of direct selection for a 2-component trait with a linear index trait derived from the same 2 components and concluded that the use of a linear index increases selection responses as compared with direct selection on the ratio trait (FCR). Also, selection against FI reduces appetite, which may be undesirable (Ollivier et al., 1990). The RFI, which is a linear index, is derived from the combination of feed consumption and production traits. Results from this study indicate that RFI is heritable. Selection against RFI may provide a means of reducing feed consumption that does not go to a productive purpose. Our study has shown that RFI reduces appetite, which may be undesirable (Ollivier et al., 1990). The RFI, which is a linear index, is determined only by biological (co)-variances. However, profitability will be maximized when index weights on FI (or RFI), growth, and other traits are determined by both biological and economic parameters, which need to be investigated.

Estimates of heritability reported here indicate that sufficient additive genetic variance exists in RFI, FI, and growth traits, which should lead to response from selection. Genetic correlations indicate that it should be possible to select for reduced RFI without adversely affecting growth performance. The RFI was more heritable than FCR, and FI was more strongly genetically correlated with RFI than FCR and RFI with FI. For RFI, the weights of the component traits in the selection index are determined only by biological (co)-variances. However, profitability will be maximized when index weights on FI (or RFI), growth, and other traits are determined by both biological and economic parameters, which need to be investigated.

LITERATURE CITED


