



Estimation of residual energy intake and its genetic background during the growing period in pigs



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ABSTRACT

The aims of this study were to (i) compare models estimating residual energy intake (REI) using either lean and fat tissue growth or their proxy traits (average daily gain (ADG) and backfat thickness (BF)); (ii) determine genetic characteristics of REI at different growth stages and the entire test period; and (iii) examine 9 genetic and phenotypic relationships of REI with other production traits. Data from 315 pigs of an F₂ generation were used which originated from crossing Pietrain sires with a commercial crossbred dam population. Average daily protein (APD) and lipid deposition (ALD), as measurements of lean and fat tissue growth, were obtained using the deuterium dilution technique on live animals. During growth from 60 to 140 kg, REI was estimated using 4 different models for energy intake that included, besides other systematic effects, (1) ADG and BF; (2) APD and ALD; (3) and (4) incorporated the same covariables as the first two models, respectively, but pre-adjusted for systematic effects. Genetic parameters and estimated breeding values were obtained based on univariate animal models using REML analysis. Over the entire growing period, heritabilities of different REI using different models were all estimated at 0.44 and their genetic correlations were at unity. At different growth stages heritabilities for REI were greater ranging from 0.47 to 0.50. Genetic correlations between REI estimates at different stages of growth, obtained using genetic model 4, indicated that REI at 60 to 90 kg was non-significantly ($P > 0.05$) associated with REI at 90–120 kg (0.32 ± 0.29) and 120–140 kg (0.28 ± 0.28), but REI of the latter growth stages showed a significant ($P < 0.05$) moderate genetic correlation (0.58 ± 0.21). REI had favourable genetic correlations with feed conversion ratio (FCR, 0.84 ± 0.13) and total nitrogen excretion (TNE, 0.85 ± 0.11). The results indicate that REI estimated based on models using proxy traits for lean and fat tissue deposition resulted in slightly lower accuracies compared to models fitting APD and ALD, which explained a greater variation of energy intake. There is great potential for improvement of REI due to its large heritability. Genetic selection for REI should consider the stages of growth, because of their differences in genetic background.

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REI explained a large portion of variance in FCR and TNE, therefore selection for REI is expected to result in, besides improvement of feed efficiency, a substantial reduction in the environmental pollution of pig production.

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1. Introduction

Improvement of feed efficiency is of great economical interest and currently one of the main goals within pig breeding programs. Residual feed intake (RFI) has been extensively discussed as an alternative trait to improve feed efficiency (de Haer et al., 1993). Differences in models used to estimate RFI have been shown to result in different relationships between RFI and production traits (Mrode and Kennedy, 1993; Johnson et al., 1999), which can influence genetic gain. In pigs, RFI has been mostly estimated using models adjusting feed intake for average daily gain (ADG) and backfat thickness (BF), often together with metabolic body weight (Gilbert et al., 2007; Cai et al., 2008). Changes in the energy content of diets during the growing period are common practice, and may have an effect on the accuracy of RFI estimation. Therefore, in the present study, metabolizable energy intake was used to estimate residual energy intake (REI). This efficiency trait (REI) has been studied extensively in dairy cattle (e.g. Mäntysaari et al., 2012).

Traits used to estimate RFI in the above referenced studies are proxies for lean and fat tissue growth, which are available in practical pig breeding programs. In the present study, however, measures of protein and lipid deposition at different stages of growth were obtained, which will likely improve on the accuracy of REI estimation. Furthermore, information about the genetic characteristics of REI, including REI estimated at different stages of the growing period, is lacking in the literature. Shirali et al. (2012) previously demonstrated the large impact improving feed conversion ratio (FCR) had on nitrogen emissions. This may be due to inter-relationships of growth and feed efficiency traits. Therefore, the association between REI and nitrogen excretion is of considerable interest in mitigating the environmental pollution of pig production.

The aims of the present study were to (i) compare REI-estimating models based on unique measurements of lean and fat tissue growth obtained from live animals with the more commonly used models based on their proxy traits; (ii) determine genetic characteristics of REI at different growth stages; (iii) examine the genetic and phenotypic relationships of REI with production traits, and (iv) investigate the genetic background of residual energy intake.

2. Materials and methods

2.1. Animals

The animals recorded for productivity traits used in this study were from a three-generation full-sib design. The founder generation (F_0) consisted of 7 unrelated Pietrain grandsires and 16 unrelated grand-dams bred from a 3-way

cross of Leicoma boars with Landrace \times Large White dams. All grand-sires were heterozygous (Nn) at the *ryanodine receptor 1* (*RYR1*) locus. Of the F_1 generation, 8 boars and 40 sows were selected to produce the F_2 generation. The F_2 generation consisted of 315 pigs from the first two parities of the F_1 sows. The pedigree was traced back from the F_2 to the F_0 generation, and contained 386 individuals in total. All animal care and handling procedures in the federal testing station were reviewed and approved by the Landwirtschaftskammer Schleswig-Holstein, Rendsburg, Germany.

2.2. Data

The REI estimates are based on 315 animals from the F_2 generation. Forty eight gilts and 46 barrows from the F_2 generation were single-housed in straw-bedded pens and fed manually. The remaining 117 gilts and 104 barrows were housed in mixed-sexed groups of up to 15 pigs in straw-bedded pens. Animals housed in groups were fed using electronic feeders (ACEMA 48, ACEMO, Pontivy, France) which recorded individual animal intakes. Pigs started the performance test at approximately 30 kg body weight (BW) and were weighed on a weekly basis. For this study, only the test period from 60 kg BW onwards was considered because at this stage the animals were entirely adapted to the electronic feeders. Pigs were weighed at target BW of 60, 90, 120 and 140 kg. Average BW (SD) at each target weight was 61 kg (2.58), 91 kg (2.60), 120 kg (2.69) and 140 kg (2.80), respectively. During growth from 60 to 90 kg, and from 90 to 140 kg BW, pigs were fed ad libitum with a diet containing 13.8 MJ of ME/kg, 17% CP and 1.1% lysine, and a diet containing 13.4 MJ of ME/kg, 16.5% CP and 1.0% lysine, respectively. The diet was changed at approximately 90 kg BW for the individually housed pigs and approximately 90 kg BW for average of all pen mates in the group-housed environment. The energy and nutrient content of the diet was analysed by the feed company and checked within the trial by analysing samples taken at the performance test station. The diets consisted of adequate nutrient supplies to permit maximum protein deposition. For a more detailed description of the data see Landgraf et al. (2006) and Mohrmann et al. (2006).

The deuterium dilution technique was used to determine chemical body composition at the target BW of 60, 90, 120 and 140 kg. This technique is an *in vivo* method predicting empty body water content of the pigs. Using this method, the percentage of fat-free substance of pigs was estimated from the empty body water content. Protein and ash content of the empty body were estimated based on the percentage of the fat-free substance. Percentage of lipid content was the deviation of the percentage of fat-free substance from 100%. The accuracy of this technique to determine body composition has been verified using magnetic resonance imaging on live animals and chemical

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