

76. Protein efficiency is heritable but not genetically correlated with meat quality in pigs

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Abstract

The improvement of protein efficiency (PE) is an essential component in the development of a sustainable pig production. This study aims to estimate the heritability of PE when dietary protein is reduced, and to estimate its genetic correlations with meat quality and production traits. A total of 682 pigs were used in estimating the heritability of PE, and 512 pigs in estimating genetic correlations. The results from this study showed potential for selective breeding of PE in Large White pigs with a heritability of 0.40. Meat quality, except meat redness, is not expected to be influenced by genetic improvement of PE, as there were no significant genetic correlations between PE and meat quality traits. Favourable relationships exist between PE and feed conversion ratio, and with average daily feed intake, which means that protein-efficient pigs fed under a reduced-protein diet consume less feed and efficiently convert the feed to lean mass.

Introduction

In the past, the focus of animal breeding had been on improving production traits, but today, sustainability concerns are gradually gaining importance. An essential component to consider in the development of sustainable pig production is the reduction of nitrogen excretion in fattening pigs. The inefficient use of dietary protein by the animals results in the excretion of excess nitrogen, thereby contributing to pollution (Notarnicola *et al.*, 2017). Therefore, considering the environmental and ecological impact of pig production, it is essential to improve protein efficiency (PE) in pigs. In addition to nutritional strategies to improve PE, a genetic solution can be sought. Feed conversion ratio (FCR) and residual feed intake (RFI) are used to characterize feed efficiency. Although FCR and RFI are expected to correlate with PE, selection for improved FCR and RFI would likely increase energy efficiency rather than PE (Kasper *et al.*, 2020; Millet *et al.*, 2018) since energy intake is the main factor driving feed intake. Moreover, it has been shown that selecting for improved FCR and RFI with the aim of reducing nutrient excretion may not be as efficient as selecting for the nutrient trait itself (de Verdal *et al.*, 2011). In contrast to FCR and RFI, very few studies have investigated the possibility to improve PE, which may be due to a number of factors such as difficulties in phenotyping animals for this trait and the lack of approved and validated proxies. The heritability of PE reported in the studies of Saintilan *et al.* (2013) and Kasper *et al.* (2020) indicate the potential to select genetically for improved PE in pigs. However, knowledge of genetic correlations of PE with other traits of importance such as meat quality and growth performance traits is important to account for possible trade-offs. The aim of this study was therefore to estimate the heritability for PE and its genetic correlations with meat quality and growth performance traits.

Materials & methods

A total of 682 Swiss Large White pigs were used in this study, which all had *ad libitum* access to feed and water. Once a pig reached a body weight (BW) of ≥ 20 kg (average \pm standard deviation: 22.5 ± 1.6 kg), it was allocated to a pen where it remained until slaughter. The automatic feeder dispensed the grower diet to pigs until an average BW of 63 ± 2 kg, and thereafter a finisher diet until an average BW of 106 ± 5 kg when the pigs were slaughtered. The levels of digestible protein and essential amino acids for the grower and finisher diets were 20% lower than the recommended levels, with the same digestible energy. The automatic feeders

(Schauer Maschinenfabrik GmbH & Co. KG, Prambachkirchen, Austria) recorded all daily visits to the feeder and the quantity of feed consumed per visit for each animal.

Protein efficiency. After slaughter, the left carcass including the whole head was scanned with dual-energy X-ray (DXA) absorptiometry to determine lean tissue content, which was used in the following prediction equation to estimate the protein content retained in the carcass (Kasper *et al.*, 2021).

$$\text{Protein content carcass (g)} = -482.745 + 0.23 (\text{g lean tissue DXA} \times 2) \quad (1)$$

PE of the carcass was calculated as the ratio of protein deposited in the carcass minus the protein content in the carcass at 20 kg BW to the total dietary protein intake. The protein content of the carcass at 20 kg BW was estimated based on data from the experiment of Ruiz-Ascacibar *et al.* (2017).

Other traits in the study. Loin muscle area and backfat thickness were assessed on the left carcass side at the 10th to 12th ribs' level. A picture of the loin muscle was taken and the area was measured. Backfat thickness was measured with a ruler. Intramuscular fat content was determined by the Soxhlet method. A 2 cm thick chop was cut from the loin muscle at the 10th to 12th ribs' level and freed from adhering adipose and connective tissues. After 20 min in the cooling room, CIE Lab-values (lightness, redness and yellowness), were recorded using the Minolta CR-300 colorimeter. Subsequently, the chops were weighed, suspended in sealed plastic bags at 2 °C for 48 h and re-weighed to determine the drip loss. The same chops were then vacuum-sealed and cooked in a water bath at 72 °C for 45 min, then cooled in cold water for 15 min, rinsed to remove coagulated sarcoplasmic protein, dabbed dry and weighed to determine cooking loss. The cooked chops were frozen at -20 °C and shear force was measured on four cores of 13 mm diameter using a Warner Bratzler Shear Force machine.

Statistical Analysis. Bayesian animal models were performed using MCMCglmm (Hadfield 2010) in R. The genetic and common environmental variance components of PE were estimated using a univariate animal model (corrected for the effects of sex, slaughter weight, slaughter age, and farrowing series) and genetic correlations were estimated using bivariate models. Both univariate and bivariate models were performed with a Markov Chain Monte Carlo algorithm, using the model formula

$$y = \mu + Xb + Za + Z_c c + e \quad (2)$$

where y is a vector of observations of PE, b is a vector of fixed effects of farrowing series, sex, slaughter weight and slaughter age. X is an incidence matrix relating records to fixed effects. a is a vector of random additive genetic effects, and Z is the corresponding incidence matrix. c is a vector of random litter effects, and Z_c is the corresponding incidence matrix. Heritability was thereafter computed as the ratio of genetic variance to the phenotypic variance ($h^2 = V_A / V_p$), where phenotypic variance (V_p) is the sum of genetic variance (V_A), litter (common environmental) effect (V_{CE}) and residual variance (V_R). The litter effect was calculated as the ratio of the litter effect to the phenotypic variance ($CE^2 = V_{CE} / V_p$). A non-informative prior with an inverse Wishart distribution for the random effects and normal distribution for the fixed effects were used. The model was run with 2 million iterations, 100,000 burn-in and 1000 thinning intervals.

Results

The posterior distributions of the variance decomposition of PE is presented in Figure 1 (posterior distributions of the respective variance components are shown in the upper part, points representing single estimates are shown together with a box plot, where whiskers represent the 95% credible interval). The PE of the carcass is clearly heritable ($h^2=0.40$, 95% credible interval = (0.22, 0.59)). The common environment

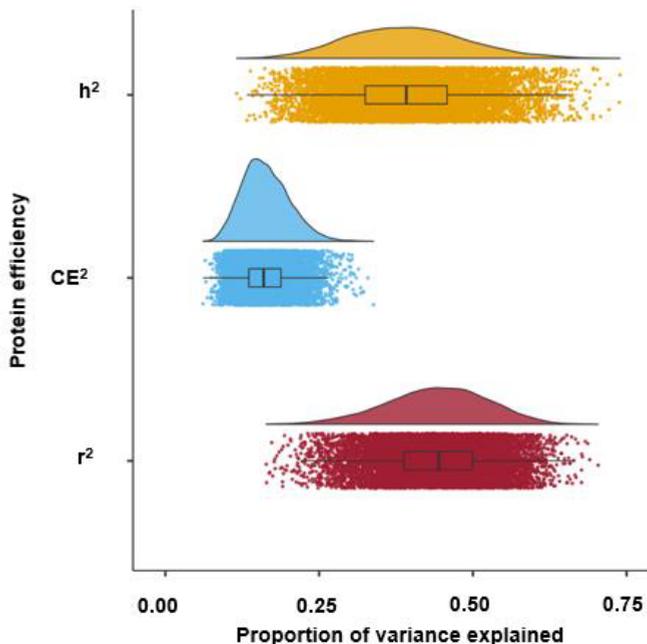


Figure 1. Posterior distributions of heritability (h^2), common environment effect (CE^2) and residual variance (r^2) of protein efficiency of the carcass.

(litter effect) also contributed to the phenotypic variation with a variance of 0.16 (0.09, 0.24), showing that pigs in the same litter performed similarly compared to others in different litters. The genetic correlations between PE and meat quality traits were generally non-significant with wide credible intervals that included zero (Table 1). However, meat redness trait showed a significant negative and moderate genetic correlation. There were high and negative genetic correlations between PE and production traits, with favourable relationships between PE and average daily feed intake and FCR (Table 1).

Table 1. Genetic correlations of protein efficiency with meat quality and production traits.

Group	Trait	r_g^1 [95% credible interval]
Meat quality traits	Loin muscle area	0.06 [-0.44, 0.60]
	Cooking loss	0.04 [-0.34, 0.39]
	Drip loss	0.03 [-0.17, 0.17]
	Shear force	0.05 [-0.20, 0.28]
	Intramuscular fat	-0.07 [-0.29, 0.16]
	Backfat thickness	-0.21 [-0.43, 0.08]
	Meat yellowness	-0.28 [-0.47, 0.03]
	Meat lightness	-0.42 [-0.88, 0.29]
	Meat redness	-0.35 [-0.59, -0.08]
	Production traits	Average daily gain
Feed conversion ratio		-0.96 [-0.97, -0.95]
Average daily feed intake		-0.93 [-0.95, -0.91]

¹ Genetic correlation.

Discussion

In this study, we showed that PE is heritable, and an improvement in PE when dietary protein is reduced is not expected to influence the quality of meat, except for the redness of meat. The favourable genetic correlations between PE and average daily feed intake (ADFI) and feed conversion ratio (FCR) show that protein-efficient pigs are expected to consume less feed and efficiently convert the feed to meat. This suggests that breeding for more protein-efficient, i.e. more sustainable pigs, could lower the cost of production, but special attention should be paid to the genetic correlation with growth rate to actually enable economic pig production. In addition, this could help decrease the competition between humans and livestock for plant-protein sources such as soybean. However, breeding for protein-efficient pigs, under a reduced dietary protein condition, may decrease average daily gain. The heritability estimate here was higher than that reported by Kasper *et al.* (2020), which may be due to higher sample size in the current study or to the experimental design. While all pigs in this study were slaughtered at 100 kg BW, pigs in the study of Kasper *et al.* (2020) were slaughtered between 40-100 kg BW, though differences in slaughter weight were corrected for statistically. A weak but significant effect of litter was observed on PE, in contrast to the study of Kasper *et al.* (2020), where the litter effect estimate was 0.002. This might be also a consequence of the larger sample size. Kasper *et al.* (2020) also reported the same relationship between PE and FCR. Although a strong negative (but favourable) genetic correlation was observed between PE and FCR, selection for FCR does not necessarily equate to selection for PE in terms of selection response. Unravelling this relationship should be the focus of future studies.

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