

Genetic analysis of digestibility traits in pigs measured by near-infrared spectroscopy

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Abstract

The aim of this study was to estimate genetic parameters for apparent total tract digestibility of nitrogen (ATTDn) and dry matter (ATTDdm) and to investigate their genetic relationship to other relevant production traits in pigs. Near infrared spectroscopy was used for prediction of nitrogen content in feces. The estimated heritabilities of ATTDdm and ATTDn were 0.22 and 0.20, respectively. The genetic correlations between ATTDdm and ATTDn and feed intake from 40 to 120 kg were -0.5 and -0.65, respectively. No significant genetic correlations were found between any of the digestibility traits and growth and carcass quality traits. The results suggested that the current selection strategy is improving the digestibility of nitrogen and dry matter, but that selection for improved digestibility would reduce the feed consumption from 40 to 120 kg.

Introduction

Protein is a costly nutrient in feed and efficient use of proteins from the feed is therefore important due to global issues such as increasing human population and need for proper nutrition, climate changes, greenhouse gas emissions and profit in pork production.

Less than 1% of the greenhouse gas emissions from Norway is from the pork production. The largest source of emissions from pig production systems is nitrous oxide from manure storage (Bonesmo and Enger 2021). This emission represents a nutrient loss from the animal and by improving nutrient efficiency in pigs, emissions and production efficiency can be improved.

Since 1958, Norsvin Landrace has been bred for improved efficiency (Gjerlaug-Enger *et al.*, 2012). This has led to a reduction in carbon dioxide equivalents per kg carcass weight (kg CO₂-eq./kg CW) from 3.5 to 2.3 kg CO₂-eq./kg CW. This reduction is a result of more weaned piglets, lower mortality, shorter growth period and improved feed efficiency (Bonesmo and Enger 2021). To further improve genetic selection for efficiency to reduce carbon footprint and improved efficiency, nitrogen digestibility can be a trait of interest. However, measuring digestibility on a large-scale can be challenging, as this previously has been measured by using respiratory chambers and total excreta collection. Nirea *et al.* (2018) concluded that near-infrared spectroscopy (NIRS) can be used for prediction of chemical composition in feces and is a cost-effective method for measuring digestibility in large-scale, and Déru *et al.* (2021) showed that additive genetic variation existed for digestibility of different nutrients in Large White pigs measured by NIRS. The aim of this study was therefore to estimate genetic parameters for apparent total tract digestibility (ATTD) of nutrients measured by NIRS.

Materials & Methods

The data material for the study was collected at Norsvins boar testing station in Norway. The test period was between 40 to 120 kg live weight of the boars. The data recording was conducted from June 2019 to April 2021 on randomly selected Norsvin Duroc boars, fed *ad libitum* on conventional concentrate containing 9.15 g SID lysine/kg and 9.55 MJ NE/kg.

Fecal sampling. To determine ATTD of nutrients, individual fecal samples were sampled at 120 kg live weight. The samples were stored at -20°C before processing and chemical analysis. The samples were freeze dried, homogenized and ground (1 mm sieve) prior to chemical analyses and NIRS analyses. In total, fecal samples were collected from 1895 boars.

Near-infrared spectroscopy. All NIR spectra were acquired using an XDS Rapid Content Analyzer (Foss, Hilleroed, Denmark) over the spectral region of 400–2500 nm. For all samples, triplicate measurements were obtained. A total of 300 fecal samples were used to make a calibration model for nitrogen content (Kjeldahl-N) in the fecal samples. Partial least squares regression was used for calibration and prediction (cross-validation $R^2 = 0.73$, estimation error (RMSECV) = 1.6 g nitrogen/ kg dry matter). Subsequently, this calibration model was used to predict nitrogen contents in the remaining samples. Prior to regression and prediction, all NIR spectra were pre-processed employing 1-order derivatization and subsequent normalisation using the Standard Normal Variate approach (Barnes *et al.*, 1989).

Traits. All animals had individual records of the following traits: feed consumption from 40 to 120 kg (F40120), days from 40 to 120 kg (D40120), loin depth at 100 kg (LDP) and back fat at 100kg (BF). Apparent total tract digestibility of nitrogen (ATTDn) and apparent total tract digestibility of dry matter (ATTDdm) was calculated by the model described in Maynard and Loosli (1969), using an indigestible marker (acid insoluble ash) occurring naturally in the feed. Descriptive statistics for the traits are shown in Table 1.

Table 1. Descriptive statistics for feed consumption from 40 to 120 kg (F40120), days from 40 to 120 kg (D40120), loin depth at 100 kg (LDP) and back fat at 100kg (BF). Apparent total tract digestibility of nitrogen (ATTDn) and apparent total tract digestibility of dry matter (ATTDdm).

	n¹	Mean	SD¹	Min¹	Max¹
ATTDdm (%)	1895	73.2	4.6	47.2	84.4
ATTDn (%)	1608	71.3	6.2	31.3	85.6
F40120 (kg)	13922	171.4	13.7	100.3	274.7
D40120 (days)	14030	75.4	8.7	50.9	114.8
BF (mm)	9306	5.7	1.5	2.9	13.0
LDP (mm)	9526	58.3	4.7	41.2	77.6

¹ Number of animals (n), standard deviation (SD), minimum value (min), and maximum value (max).

Genetic analyses. The traits were analysed using multivariate animal models, and estimation of variance components and genetic correlations were performed using the DMU software package (Madsen and Jensen, 2013).

The following models were used to analyse the different traits.

For ATTDdm and ATTDn:

$$y_{ijklmno} = \text{MOB}_i + \text{OP}_j + \text{DAY}_k + \text{HYS}_l + \text{LITT_NO}_m + \text{animal}_n + \text{pen}_o + e_{ijklmno} \quad (1)$$

For F40120, D40120, LDP and BF:

$$y_{ijklm} = \text{MOB}_i + \text{HYS}_j + \text{LITT_NO}_k + \text{animal}_l + \text{pen}_m + e_{ijklm} \quad (2)$$

The sampler (OP), day of sampling (DAY), herd-year-season born (HYS), birth month (MOB) and dams litter number (LITT_NO) were included as fixed effects, whereas animal and pen were included as random effects. Pedigree information was traced 10 generations back and in total there were 24706 animals in the pedigree.

Results

Estimates of variance components and heritability for ATTDdm and ATTDn are presented in Table 2. Both additive genetic variance components were significantly different from zero. The estimated heritability for ATTDdm was higher than the heritability for ATTDn. The genetic correlation between ATTDdm and ATTDn was estimated to 0.80.

Table 2. Variance components, heritabilities (h^2)¹ and the genetic correlation (r_g) for apparent total tract digestibility of dry matter (ATTDdm) and nitrogen (ATTDn).

	Additive genetic variance (σ_a^2)	Pen variance (σ_{pen}^2)	Residual variance (σ_e^2)	h^2	r_g
ATTDdm (%)	2.9	1.8	10.0	0.22	0.80
ATTDn (%)	5.5	3.2	22.0	0.20	

$$^1 h^2 = \sigma_a^2 / (\sigma_a^2 + \sigma_e^2)$$

The genetic correlations between ATTDdm and ATTDn to production traits are presented in Table 3. The genetic correlations between the digestibility traits (ATTDdm and ATTDn) and F40120 were -0.50 and -0.65, respectively. The genetic correlations between the ATTDdm and ATTDn and D40120, LDP and BF were not significantly different from zero.

Table 3. Genetic correlations (SE) between apparent total tract digestibility of dry matter (ATTDdm) and nitrogen (ATTDn) and production traits.

	F40120 ¹	D40120 ²	LDP ³	BF ⁴
ATTDdm	-0.50 (0.12)	-0.11 (0.15)	-0.18 (0.12)	-0.15 (0.15)
ATTDn	-0.65 (0.11)	-0.10 (0.15)	-0.22 (0.15)	-0.19 (0.15)

¹ Feed consumption from 40 and 120 kg live weight

² Days from 40 to 120 kg live weight

³ Loin depth at 100 kg

⁴ Back fat at 100 kg

Discussion

This study has shown that genetic variation exists in apparent total tract digestibility traits, when chemical components were predicted by NIRS, and digestibility was estimated based on an internal marker in the feed. Improved digestibility of nutrients will increase the resource utilization of the animal. Selection for changed body composition, such as carcass leanness and reduced backfat has been a strategy to obtain feed efficient animals in pig breeding. Other traits, such as gross feed intake, feed conversion ratio and residual feed intake has also been used (Patience, 2012). Some of these traits might provide selection responses that are related to the allocation of feed resources to different tissues. This has ensured that feed is used for production. However, to improve feed efficiency further, it is important to know how well the intestines utilize the nutrients in the feed. The trait, ATTDn, can therefore further improve the efficiency of the animals, and hence reduce nitrogen loss in the environment, which is becoming an increasing global problem. To predict ATTDdm and ATTDn based on a spot fecal sample as an alternative to total collection method, acid insoluble ash was used as a marker. Brestenský *et al.* (2017) suggested that acid insoluble ash was a suitable marker to use in digestibility studies for pigs. However, caution must be made with the sampling, to avoid contamination. In the current study, rooting material was held back for three days prior to sampling to avoid the pigs getting acid insoluble ash from other sources than the feed. The method for chemical analysis could influence the level of digestibility estimates, but not the variation. Bastianelli *et al.* (2015) proposed to use direct prediction of digestibility of different nutrients using NIRS. Then, the need for a marker would be minimized, as it is only needed for the fecal samples used for developing the calibration models. The variance components

estimated in this study suggested that both digestibility traits are heritable and can be selected for. Few studies have previously carried out genetic analyses of digestibility traits in pigs. However, Déru *et al.* (2021) estimated a heritability for digestibility coefficients for nitrogen to be 0.27. This result is higher than the current study, but on a smaller dataset, different breed and conventional diet. The same study found an even higher heritability for nitrogen digestibility on a high-fibre diet (0.56), due to higher genetic variation. Increasing fibre content in the diet might increase the genetic variation in the trait but could at the same time reduce the digestibility of nutrients (Déru *et al.*, 2021; Zhang *et al.*, 2013). Genetic correlations between the digestibility traits and production traits were identified and suggested that the current selection strategy is improving the digestibility of nitrogen and dry matter. The results are in accordance with Déru *et al.* (2021), which estimated a high negative genetic correlation between nitrogen digestibility and daily feed intake (-0.59) in animals on conventional diet. The current study did not find any significant genetic correlations between ATTD_{dm}, ATTD_n and D40120, BF or LDP. This highlights that digestibility traits are heritable, but mainly related to feed intake and general function of the intestines, as opposed to allocation of feed resources to different tissues in the body. However, the results suggested that the current selection strategy is improving the digestibility of nitrogen and dry matter.

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