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Original Paper

Genetics of feed intake traits in the Czech Large White pig population

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Feed represents a substantial proportion of the variable costs of pig production. Feed efficiency is traditionally expressed as the feed conversion ratio (*FCR*) and more recently as residual feed intake (*RFI*). Although feed efficiency can be generally improved indirectly by selection for increased growth rate and decreased adipose tissue, a higher genetic response could be achieved through direct selection of feed intake traits. The aim of this study was to provide a pilot analysis of feed intake data of 281 Czech Large White boars. Data were recorded individually using the Feed Intake Recording Equipment in field performance testing from 2018 to 2020. The analysed feed intake traits were average daily feed intake (*ADFI*), *FCR* and *RFI*. *RFI* was calculated as the deviation of observed *ADFI* and average population *ADFI* predicted on the basis of the model, with mid-test metabolic weight and average daily gain as regressors. The heritability estimates were 0.35 and 0.34 for *ADFI* and *FCR*, respectively, and the estimate was slightly higher (0.43) for *RFI*. The genetic standard deviations ranged from 100 to 110 g of feed per day and 103 g of feed per kg of weight gain. The amounts of explained variability by environmental effects of jointly tested animals were from 0.20 to 0.46. The sufficient amount of genetic variability and moderate heritability estimates give the possibility for selection of feed intake traits, although a larger number of animals will be essential to estimate more precise breeding values.

Keywords: animal breeding, pig selection, genetic parameters, feed conversion ratio, residual feed intake

1 Introduction

Feed represents a substantial proportion of the variable costs of pig production (Do et al., 2013). To increase profitability and produce saleable pork, producers need to follow technologies to improve feed efficiency. One of the most efficient ways is to include feed efficiency traits into pig genetic improvement programs. The economic weights of such traits are 16% to 24% of the overall economic importance of growth, reproduction, health and carcass traits in maternal and sire pig breeds (Krupa et al., 2020). In this context, decreasing the pressure of feed costs and reduction of environmental impact are the most significant challenges in the pig sector (Gillert et al., 2017).

The choice of feed intake traits to predict feed intake for production requirements differs between populations and studies. In pigs, the average daily feed intake (*ADFI*), feed conversion ratio (*FCR*) or residual feed intake (*RFI*) are commonly used. In general, *FCR* representing the ratio of feed intake (inputs) and weight gain (output) is expressed as the inverse trait of the feed intake efficiency during growth. Selection for reduced feed intake is not optimal because of the strong relationship between feed intake and body weight, body composition, and daily body weight gain (Do et al., 2013). Moreover, selection pressure oriented towards growth rate and fat content has an indirect impact on *FCR* (Gilbert et al., 2017).

Residual feed intake, also called net feed efficiency, was first introduced by Koch et al. (1963) and is defined as the difference between observed and expected feed intake for given production and maintenance needs. *RFI* does not suffer from undesirable properties that are joined to ratio traits such as *FCR* (Do et al., 2013). Selection for *FCR* reduces sow appetite and fatness which, together with increased prolificacy, has been seen as a hindrance to sow lifetime performance (Gilbert et al., 2012).

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Selection for reduced *RFI* could improve the efficiency of energy use without reducing the feed intake capacity that is required for production (Kennedy et al., 1993).

The potential of *RFI* for the improvement of feed efficiency in pigs is evaluated in studies based on commercial populations or experimentally selected lines. The establishment of experimental lines is a common strategy to evaluate the direct and correlated responses to a criterion for selection and to study the impact of the selection on animal physiology (Gilbert et al., 2017). Recent studies showed that pigs with lower *RFI* had better feed conversion efficiency and meat quality (Gilbert et al., 2007, Gilbert et al. 2017). Pigs divergently selected for *RFI* consistently demonstrate differences in carcass composition and in feed intake (Patience et al., 2015). Low *RFI* pigs have less carcass fat, consume less feed and exhibit similar or slightly slower rates of gain compared with high *RFI* pigs (Cai et al., 2008). The influence of *RFI* selection on carcass composition and catabolic activity in the liver and muscle was reported by Naou et al. (2015). Gilbert et al. (2012) stated that metabolic changes observed during growth in response to selection might explain part of the better efficiency of the low *RFI* sows, decreasing basal metabolism and favouring rapid allocation of resources to lactation.

In the Czech Republic, breeding pigs are tested in field performance tests without information about feed intake. Now, data from the pilot project started in 2018 are available. Therefore, the aims of this study were to analyse phenotypic data, investigate different feed intake traits and estimate their characteristics in the Czech Large White population.

2 Material and methods

2.1 Data

Feed Intake Recording Equipment (FIRE) electronic feeders were used to record the field performance test data of boars of the Czech Large White breed. Growth and feed intake data were collected on the farm from 2018 to 2020. Only one pig could take feed from each feeder at the same time. Each pen contained up to 12 boars fed by one feeder. Boars were fed ad libitum with a feed of the same composition for the whole test period. At the test end, all boars were measured with an ultrasound machine (Mindray LTD.) for lean meat content (*LM*) and backfat thickness (*BF*), both adjusted to a constant weight of 100 kg.

Individual feed intake and body weight were recorded when each pig visited the feeder. In total, there were 236,530 individual feeder visits of 294 boars, with age at the test start between 80 to 90 days and feeding for the next 50 to 70 days. These data were edited using the following rules:

a) visits with feed intake less than 10 g per visit were omitted,

b) outliers in body weight which substantially differed from the line estimated by the linear regression of the average daily body weight on age for each animal were marked as dubious and were omitted from analyses (4.14% of total visit records). The procedure for the regression coefficient estimation from only reliable data and the subsequent marking outliers was performed thirty times,

c) only data up to the ultrasound measurement date were used,

d) in the case of missing reliable body weight data on the current date, the weight was computed as the linear regression of weights on adjacent dates (3.35% of total daily weight records).

All boars had records regarding feeding at each day over the test period.

Next, growth and feed intake variables were computed for each pig:

a) average daily gain (*ADG*) was calculated from FIRE data as the slope from the simple linear regression of the body weight at the start and end of the test (g/day),

b) average daily feed intake (*ADFI*) was derived as the total feed intake (*FI)* over the test period divided by the number of days in the test (g/day),

c) *FCR* was calculated as the ratio of *FI* and *ADG* (*FI/ADG*),

d) the mean body weight (*MBW*) was derived as the average of the daily body weights from the FIRE data,

e) metabolic body weight at mid-test (*MWT*) was calculated as the *MBW* raised to the power 0.75.

Only data from animals ranging between 1% and 99% quantiles for traits *ADFI*, *FCR*, and *MWT* were kept in the analysis. After editing, there were records of 281 boars fed in 35 pens (*PEN*) in the data set. The pedigree was traced back to the 1st of January, 2000, and the file contained 1,422 animals in total. A basic statistical description of the data set is shown in Table 1.

Table 1 Basic statistics description of the data set after data editing

	Abbreviation		N
Animals	-		281
Sires	-		29
Dams			81
Litters (common litters environment)	LIT		97
Pens (animals fed by one feeder together for the whole test period)	PEN		35
Year-Seasons (formed quarterly on the basis of test end date)	YS		8
Feeders (No. of apparatus)	-		8
	Abbreviation	Unit	(mean ± SD)
The total amount of feed intake in the test period	FI	kg	144.12 ± 19.38
Days in test	TL	day	60.7 ± 2.93
Average daily feed intake	ADFI	g/day	2,375 ± 303.69
Feed conversion ratio	FCR	kg/kg	2.33 ± 0.24
Body weight at the: end of the feed test	BWO	kg	104.5 ± 9.50
start of feed test	BWS	kg	42.2 ± 4.68
Age at the: start of feed test	AGES	day	85.2 ± 1.9
end of feed test	AGEO	day	144.9 ± 2.2
Average daily gain in feed test	ADG	g/day	1,043 ± 127.5
Backfat adjusted to body weight 100 kg	BF	mm	6.8 ± 0.94
Lean meat adjusted to body weight 100 kg	LM	%	59.1 ± 1.60
Mid-test metabolic weight	MWT	kg	24.9 ± 1.60
Parity	PAR	N	3.2 ± 1.7
Total number born in the litter	TNB	N	16.6 ± 2.5
Animals per: sire		N	9.7 ± 6.9
dam		N	3.5 ± 1.9
Littermates		N	2.9 ± 1.4
Animals per pen		N	8.0 ± 2.3
Sires per pen		N	2.1 ± 0.8
Dams per pen		N	2.8 ± 0.8
Pens in year-seasons		N	4.38 ± 1.3
Pens per feeder apparatus		N	4.4 ± 0.7
Residual feed intake: RFI = ADFI – (-937.8 + 0.905*ADG + 98.95*MWT)	RFI	g/day	0.00 ±179.46

2.2 Estimation of Residual Feed Intake (RFI)

RFI was computed as the difference between the observed *ADFI* and the predicted *ADFI* ($ADFI_p$). $ADFI_p$ was predicted on the basis of regression coefficients estimated by the General Linear Model implemented in statistical package SAS® (SAS Institute Inc., 2008). The model used for *ADFI* prediction (variables used are described above) was $ADFI_p = \mu + \beta_1 * MWT + \beta_2 * ADG + e$. Then, the residual feed intake values (*RFI*) were calculated as $RFI = ADFI - (\beta_1 * MWT + \beta_2 * ADG)$.

2.3 Statistical analysis

Initially, the General Linear Model and Mixed Model procedures implemented in statistical package SAS® (SAS Institute Inc., 2008) were used to investigate the influence of various factors on analysed traits. Next, restricted maximum likelihood (REML) and optimisation using a quasi-Newton algorithm with analytical gradients (Neumaier and Groeneveld, 1998) as implemented in the VCE 6.0 program (Groeneveld et al., 2008) were used to estimate the variances in the univariate models as follows:

$ADFI_{ijk} = YS_i + P_j + ADG_{ijk} + MWT_{ijk} + A_{ijk} + e_{ijk}$,

$FCR_{ijk} = YS_i + P_j + MWT_{ijk} + A_{ijk} + e_{ijk}$,

$RFI_{ijk} = YS_i + P_j + A_{ijk} + e_{ijk}$,

where YS_i is the fixed effect of year-season (defined on the basis of the quarter of the year of the feed test end), P_j is the random effect of the given pen (animals fed by the feeder in whole test period together) with $p \sim N(0,I\sigma^2_p)$, A_{ijk} is a random animal genetic effect within YS_i and P_j with $A_l \sim N(0,A\sigma^2_a)$, where A is the relationship matrix, e_{ijk} is the random residual with $e \sim N(0,I\sigma^2_e)$, and ADG_{ijk} and MWT_{ijk} are linear regression covariates of average daily gain and mid-test metabolic weight.

3 Results and discussion

The analysis of factors affecting feed intake traits (*ADFI* and *FCR* phenotypes) are summarised in Table 2. Values in the table represent the decrease in R^2 when the given factor is removed from the model (R^2 of the full model – R^2 of reduced model). In our data set, the environmental conditions (*PEN*, *LIT*, *YS*), *MWT*, production and body composition (*ADG*, *BF*) explained 91.39% (*ADFI*) and 86.01% (*FCR*) of phenotypic variance. Saintilan et al. (2013), using similar models, published from 70.5% to 79.9% of explained *ADFI* phenotypic variance by models in four studied populations. Similarly, Rauw et al. (2006) published 61% to 81% of explained phenotypic variance by models with factors *MWT*, *BF*, age and body weight gain in different test periods defined on the basis of age in the Duroc population. The higher values in the current study could be explained by smaller numbers of animals.

The highest amount of phenotypic variance was explained by all environmental factors (27.91 and 44.40% for *ADFI* and *FCR* variance, respectively). The exclusion of environmental factors particularly from the full model showed almost zero influence of *PEN* and *YS* and a significant influence only of the common litter environment (P <0.001). The next most important factors were *ADG* and *MWT* with 3.72 – 6.80% and 2.12 – 3.14% of explained phenotypic variability, respectively. Both these factors were significant, with P < 0.001 for both analysed traits. *BF* explained less than 1% of the variability and was not significant for any trait. Saintilan et al. (2013) found the highest influence of environmental factors on *ADFI* (24 - 28%) and *ADG* (29 - 47%), followed by *LM* (5 - 16%), keeping the *BF* and dressing percentage below 1%. The *MWT* in their work removed only up to 1.5% of phenotypic variability due to managing feeding performance testing based on the animals' weights. Similarly, Do et al. (2013) reported that models with or without *MWT* did not lead to significantly different results. Performance testing in the Czech Republic is arranged in herds, and the test start/end are managed on the basis of the animals' age. Therefore, there are not constant weights at the beginning and end of the test, and therefore the *MWT* for animals differs. In station trials, which are managed on a weight basis, *MWT* is relatively constant and could be omitted from the models.

Table 2 Percentage of the variability of feed intake traits (*ADFI* and *FCR)* explained[1] by the factors or traits included in the linear regression models and their levels of significance[3] (SAS GLM procedure)

Factor[2]	ADFI	FCR
PEN (R)	0.11	0.03
LIT (R)	5.67 ****	7.98 **
YS (F)	0.00	0.00
ADG (C)	6.80 ****	3.72 ****
BF (C)	0.30	0.50
MWT (C)	2.12 ****	3.14****
R^2 of the full model	91.39 %	86.01 %
LIT (R) + PEN (R) + YS (F)	27.91	44.40

[1] The difference in % between the R^2 of the full model and the R^2 of the reduced model obtained by deleting this trait/factor from the full model.

[2] For further information about factors see Table 1, type of factors in the model (in parenthesis): F – fixed, R – random, C – linear regression of covariate.

[3] Levels of significance of factors in the full model: ** P <0.05, *** P <0.01, **** P <0.001.

There are several different ways to calculate *RFI* in pigs and other species. Hoque and Suzuki (2009) summarised models for *RFI* prediction in beef cattle populations and recommended an equation with covariates *ADG* and *MWT*. This equation seems to be the best choice for the studied data set, due to the insignificant influence of *BF* on *ADFI*. The prediction of *ADFI* was based only on linear regression of covariates (SAS GLM procedure) and did not take into account the other environmental factors. It could be argued that a relatively low number of boars and tested pens in the study disrupt assumptions about the average influence of other factors and resulted in overestimation or underestimation of regressors. On the other hand, *RFI* values computed via regression coefficients estimated with the model shown in Table 2 resulted in highly correlated (92.0%) *RFI* values (not shown).

Heritability, additive genetic variances and the fractions of phenotypic variances explained by pen effects are shown in Table 3. For all studied feed intake traits (*ADFI*, *FCR*, *RFI*), heritabilities were moderate with the highest value estimated for *RFI* (0.43) and values of 0.35 for ADFI and 0.34 for FCR. Similar results were found in Yorkshire pigs and other populations. Heritabilities ranged from 0.30 to 0.45, 0.41 to 0.66 and 0.10 to 0.39 for *FCR*, *ADFI* and *RFI*, respectively (Kadarmideen et al., 2004, Cai et al., 2008, Hoque et al., 2009, Do et al., 2013, Jiao et al., 2014, Gilbert et al., 2017). Although heritability estimates in our study are significant, levels of estimated standard errors were higher than in other studies. The values of the standard errors are about twice those in other previously cited studies (taking into account the level of heritability estimate).

Table 3 Variance components and proportion of variances with approximate standard errors estimated by univariate models

Trait	Variances		The proportion of variances ± SE	
	Animal	Pen	Animal (h^2)	Pen
ADFI	10.674	6.231	0.346 ± 0.138	0.202 ± 0.083
FCR	0.012	0.016	0.343 ± 0.126	0.467 ± 0.093
RFI	11.850	6.232	0.429 ± 0.147	0.274 ± 0.092

Although the pen variance in the phenotypic analysis seemed to be not significant, the inclusion of additive animal factor into the animal model changed the previously reported ratio of explained variance of LIT and *PEN*. In animal models, there were found estimations of common litter environment close to zero and not significant for any of the traits. On the other hand, the estimations of the environment of jointly tested animals (*PEN*) were high and significant (0.20, 0.21 and 0.46 for *ADFI*, *RFI* and *FCR*, respectively).

Saintilan et al. (2013) reported the ratio of the variance of the common litter environment on the phenotypic variance as 0.0 to 0.13 in populations of three breeds, and some of these variance estimations were significant. *PEN,* for Czech data, described from 20% to 47% of phenotypic variability. These values are much higher than values reported by Do et al. (2013), from 2% to 5%, although phenotype variabilities of feed efficiency traits in that study are similar. This high ratio of phenotypic variability explained by the *PEN* factor is probably due to little experience with feeders in the herd (the data are from the pilot project) and the smaller amount of data in the current study.

4 Conclusions

In the current study, variance components for feed intake traits *ADFI*, *FCR* and *RFI* were estimated using univariate animal models. Investigated traits were moderately heritable. The heritability estimates were 0.35 and 0.34 for *ADFI* and *FCR*, respectively, and slightly higher for *RFI* (0.43). The genetic standard deviations from 100 to 110 g of feed per day and 103 g of feed per kg of weight gain were found. A high amount of phenotypic variation was explained by pen effect, probably due to an unstable herd environment, which could be resolved in the future with an increased number of animals tested and higher accommodation and standardisation of the feed Intake Recording Equipment during the performance testing.

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