GENETIC COURSE OF LIVE WEIGHT AND FEED INTAKE OVER AN 8-WEEK TEST PERIOD

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INTRODUCTION

The major costs in producing pork are feed costs and the costs associated with the time taken to reach a desired slaughter weight. Pig breeding programs aim towards reducing these costs by selecting the most efficient pig. Selection of breeding pigs can be based on the ratio between growth and feed intake, where these traits are measured over a fixed weight- or time-interval. If there are any differences between animals in performance patterns during the test period, they are not taken into account when animals are selected using this strategy.

The phenotype of a pig changes during growth and ageing, pigs become heavier and eat more as they get older. There is supporting evidence that the ways in which pigs both eat and grow are partly caused by genetics. There is increasing interest in genetic parameters that describe performance patterns during growth and ageing. The use of scale-equipped electronic feeder stations enables collection of data on daily feed intake (DFI) and live weight (WT). This data provides information about performance patterns of pigs for DFI and WT, enabling the investigation of selection strategies for growth and/or feed intake patterns.

MATERIAL AND METHODS

Data. Daily feed intake and WT records were available for pigs tested over an eight-week period in 29 weekly batches between February and October 2001 at Bunge Meat Industries (BMI). On average, pigs entered the test when they were 126 d (± 3 d) of age. Based on their weight at the start of test pigs were assigned to one of seven feeding levels. Each week the daily feed allowance was incremented by 100 g. In the first week pigs had *ad lib*. access to feed, allowing them to adjust to their new environment.

Each weekly batch contained about 60 animals, which were evenly distributed over two pens. In each pen there were three electronic feeder stations (developed in-house by BMI). One of the feeder stations was equipped with a weight scale, for a further description see McSweeny *et al.* (2001). Individual records within pigs were used to derive daily records. Outliers for WT and DFI were defined as all values under or above : average ± (0.75 × average), where average is the average of all individual measurements, across pigs, at a certain day on test. Daily feed intake was determined by summing the individual records of one pig that appeared at the same day on test. Daily WT was determined by averaging the individual records of one pig that appeared at the same day on test. The data set after excluding outliers contained recordings on

1589 boars of three different lines, with 59314 WT records and 80353 DFI records. Each boar had about 37 WT records and 50 DFI records during the eight-week test period. Pedigree of animals was traced back four generations, resulting in a pedigree file of 3641 animals, including the animals with records. The animals with no records consisted of 340 sires and 1712 dams. Pigs in the data set originated from 822 litters.

Model. Different weeks on test were assumed to be different traits, resulting in eight traits. Recordings of WT and DFI within week were treated as repeated records within trait. All eight traits were bivariately analysed, using ASREML (Gilmour *et al.*, 2001). Fixed effects were modelled as a function of age using Legendre polynomials (e.g. Spiegel, 1968), where eight was the maximum order of fit for each fixed effect. A first order of fit was equal to a intercept of the fixed effect, second order of fit was equal to the interaction of age with the fixed effect, third order of fit was equal to the interaction of squared age with the fixed effect, and so on, where the age coefficients were modelled using the Legendre polynomials. Significance of the fixed effects was determined using PROC GLM (SAS, 1988). As soon as a polynomial coefficient was no longer significant, all higher order fits were considered not significant. Significant fixed effects for WT were : line with a second order of fit, week of test with a third order of fit, feeding level with a second order of fit, and weekly batch with a fourth order of fit. Significant fixed effects for DFI were : line, week of test with a third order of fit, feeding level with a third order of fit, and weekly batch with an eighth order of fit.

Table 1. Heritabilities on the diagonal, genetic correlations below the diagonal and phenotypic correlations above the diagonal for live weight recorded in different weeks [A]

Week on test	1	2	3	4	5	6	7	8	Total variance
1	**0.24**	0.62	0.59	0.54	0.47	0.45	0.41	0.36	33.4
2	0.86	**0.32**	0.70	0.59	0.52	0.47	0.45	0.38	40.8
3	0.93	0.89	**0.27**	0.72	0.62	0.57	0.54	0.49	41.9
4	0.82	0.64	0.89	**0.27**	0.69	0.67	0.62	0.58	48.4
5	0.76	0.63	0.84	0.91	**0.31**	0.67	0.61	0.56	62.7
6	0.69	0.42	0.76	0.97	0.89	**0.34**	0.69	0.67	69.5
7	0.71	0.54	0.82	0.97	0.88	0.97	**0.27**	0.69	81.1
8	0.65	0.33	0.71	0.92	0.77	0.95	0.97	**0.31**	93.7

[A] SE ranged from 0.04 to 0.06 for estimates of heritabilities, 0.02 to 0.12 for estimates of genetic correlations, and 0.01 to 0.02 for estimates of phenotypic correlations.

RESULTS AND DISCUSSION

Heritabilities, genetic correlations and phenotypic correlations for WT recorded in different weeks are in table 1. Heritability of WT was around 0.3 for all weeks on test, except for the first week were heritability was lower. Genetic correlations between weeks on test for WT ranged from 0.33 to 0.97, and were highest when weeks were adjacent and lower when weeks were further apart. Phenotypic correlations between weeks on test for WT ranged from 0.36 to 0.72, and decreased when weeks were further apart. Huisman *et al.* (2002) estimated a heritability of around 0.17 for WT for a longer test period using a random regression model,

while correlations showed the same pattern as the correlations estimated in this analysis. The second part of the test period in the study of Huisman *et al.* (2002) was similar to the test period in this study.

Table 2. Heritabilities on the diagonal, genetic correlations below the diagonal and phenotypic correlations above the diagonal for daily feed intake in different weeks [A]

Week on test	1	2	3	4	5	6	7	8	Total variance
1	**0.11**	0.19	0.11	0.05	0.07	0.07	0.06	0.10	0.405
2	0.80	**0.10**	0.16	0.07	0.10	0.09	0.06	0.09	0.205
3	0.55	0.54	**0.11**	0.14	0.09	0.07	0.08	0.08	0.197
4	-0.22	0.14	0.47	**0.09**	0.17	0.09	0.09	0.08	0.236
5	-0.11	0.38	0.54	0.80	**0.10**	0.20	0.12	0.11	0.237
6	-0.21	0.38	0.48	0.61	0.63	**0.09**	0.21	0.12	0.272
7	-0.08	0.22	0.29	0.42	0.35	0.64	**0.15**	0.22	0.306
8	0.45	0.45	0.12	0.05	0.33	0.26	0.56	**0.20**	0.346

[A] SE ranged from 0.02 to 0.03 for estimates of heritabilities, 0.10 to 0.19 for estimates of genetic correlations, and 0.01 for estimates of phenotypic correlations.

Heritabilities, genetic correlations and phenotypic correlations for DFI recorded in different weeks are in table 2. Heritability of DFI was about 0.10 for the first six weeks, increased to 0.15 in the seventh week on test, and increased even further to 0.20 in the last week. Genetic correlations between weeks on test for DFI ranged from –0.22 to 0.80, and were highest when weeks were adjacent and lower when weeks were further apart. Phenotypic correlations between weeks on test for DFI ranged from 0.05 to 0.22, and decreased when weeks were further apart. Von Felde *et al.* (1996) divided a test period into five sub-periods and estimated variance components for these sub-periods. The heritability they found for DFI was higher (0.25) than the heritability found in this study. This is probably due to the fact that pigs in this study were feed restricted while Von Felde *et al.* (1996) studied pigs that had *ad lib.* access to feed. The higher heritability at the end of test may indicate that pigs were less restricted in the last two weeks of test. The daily feed allowance increased by 100 g each week. However, the average actual DFI increased by 350 g from week two to week eight on test.

While the genetic and phenotypic correlations for WT show a steady decline when weeks are further apart, this was not the case for DFI. Genetic correlations between first and other weeks on test for DFI were different from the genetic correlations between the other weeks. Daily feed intake had a higher total variance in the first week on test, and the heritability estimate for WT in the first week is somewhat lower than the estimates for the other weeks. One explanation for these results could be the adjustment period. In the first week pigs have to get used to the electronic feeders, and this might add noise to the weight measurements, resulting in a lower genetic variance and a higher error variance. Another explanation for the shift in correlations early on test could be the onset of puberty (Rydhmer *et al.*, 1993), although if it is puberty, it is early onset of puberty.

Genetic correlations between WT and DFI ranged from 0.25 to 0.52 (table 3), and were lowest in the first week and highest in the fifth week. Phenotypic correlations between WT and DFI did not change over test, and had a value of approximately 0.21 (table 3). Von Felde *et al.* (1996) estimated a genetic correlation between gain on test and DFI of 0.5, which is similar to the genetic correlation we found, phenotypic correlation between gain on test and DFI estimated by Von Felde *et al.* (1996) was the same as the value we found

Table 3. Genetic and phenotypic correlations between live weight and daily feed intake at weeks on test [A]

	week on test							
	1	2	3	4	5	6	7	8
genetic	0.25	0.30	0.41	0.48	0.52	0.42	0.37	0.51
phenotypic	0.20	0.20	0.22	0.22	0.21	0.22	0.21	0.22

[A] SE for estimates of genetic correlations ranged from 0.11 to 0.16, SE for estimates of phenotypic correlations was 0.02

CONCLUSION

The estimated parameters for WT do not really change over the eight-week period, all genetic correlations between weeks on test for WT were high (table 1). Genetic correlations between weeks on test indicate that DFI is changing during the eight-week period (table 2). Daily feed intake measured in the first week on test was different from DFI measured in weeks two through eight on test. The trend in genetic correlations between WT and DFI was an increase in genetic correlation within weeks between WT and DFI during test (table 3). Phenotypic correlations between WT and DFI within weeks were stable during test. Estimated parameters for WT and DFI and between WT and DFI do not change after week 4 on test, implying that the test period can be shortened for these two traits.

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