

CHANGE OF FEED INTAKE CURVE OF PIGS BY USING GENETIC NON LINEAR AND RANDOM REGRESSION MODELS

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INTRODUCTION

Selection of pigs over the last decades by using selection indexes which gave higher weights to feed efficiency and lean content than growth rate has resulted in reduced feed intake (Smith *et al.*, 1991 ; Webb, 1998). Reduced feed intake is a major factor limiting higher performance levels in young pigs. Moreover, selection based on different criteria has caused large genotype differences in both mean feed intake and feed intake pattern (Schinckel, 1994).

The economic optimum of feed intake capacity occurs at the level where savings in total maintenance requirements through faster growth are offset by cost of increased fat deposition (Webb, 1995). Two remarks could be made on this definition :

- First, nutrient excretion costs have increasing importance and should be minimised by feed intake optimisation (De Vries and Kanis, 1994 ; De Lange, 1997).
- Second, the economic optimum of feed intake is not fixed but varies within the growth period: pigs from 10 - 40 kg live weight deposit a high proportion of lean and little fat, the period of peak lean growth is around 50 - 60 kg liveweight and, at maturity even with moderate energy intakes, the ratio of fat gain to lean gain increases (De Lange *et al.*, 1995).

At present, fatness levels, feed efficiency should be further improved by optimisation of daily feed intake, rather than by a reduction of backfat thickness. Webb (1995), Eissen (2000) and Schulze *et al.* (2001) suggest to increase feed intake at early stage of growth, when lean deposition is limited by feed intake capacity. On the other hand, reducing extensive feed intake at the end of the finishing period, associated with high fat deposition, will result in improved feed efficiency. Although late feed intake can be controlled by management, this may result in some higher costs (De Vries and Kanis, 1994).

The aim of this paper is to examine the change of feed intake curve of pigs by selection based on improved nonlinear two-stage genetic analysis (GTS) and linear random regression models (RRM) to analyse longitudinal data of daily feed intake.

MATERIAL AND METHODS

Material. Data on 5245 young boars from two dam lines (2938 of line 3, 2307 of line 4), tested at the central test station of PIC Germany between June 1992 and April 1998, were analysed. Animals were penned in groups of 12 and fed ad libitum during 10 weeks (100 - 170 days of age). Individual feed intakes were recorded with ACEMA 48 electronic feeding stations. The data were periodically recorded on test weeks 1, 3, 5, 7 and 9 and the first 2 days of each test week were discarded to reduce the influence of adaptation to the feeder, thus resulting in a mean of 24 daily records of feed intake per growing pig. Details of data and management strategies have been described by Schulze *et al.* (2001).

Two-stage genetic analysis (GTS). In the first step of GTS, a logistic function [$y_{ij} = \alpha_{Li}/(1+\exp(\beta_{Li}-\gamma_{Li}x_{ij}))$] or a linear-segmented model [$y_{ij} = \alpha_{Si} + \gamma_{Si}x_{ij}$ ($x_{ij} < \beta_{Si}$); $y_{ij} = \alpha_{Si} + \gamma_{Si}\beta_{Si}$ ($x_{ij} \geq \beta_{Si}$)] described the systematic relationship between daily feed intake (y_{ij}) and the day on test (x_{ij}). Functions were first fitted by Ordinary Least Squares (OLS) using Proc NLIN (SAS, 1990). It was observed that individual variability in feed intake increased with feed intake level. Therefore, the pattern of variation was characterised by defining :

$$\text{Cov}(y_i|\beta_i) = \mathbf{R}_i(\beta_i, \xi) = \sigma^2 \mathbf{H}_i(\beta_i, \theta)$$

where $\mathbf{H}_i(\beta_i, \theta) = \text{diag}(f(x_{i1}, \beta_i)^{2\theta}, \dots, f(x_{in_i}, \beta_i)^{2\theta})$ describes the variance heterogeneity according to the power-of-the-mean variance model and n_i is the number of records of the i^{th} animal.

A Generalised Least Squares (GLS) algorithm, as proposed by Davidian and Giltinan (1995), was iterated ten times in order to estimate individual function and variance parameters. Individual variance heterogeneity (θ) was estimated based on absolute residuals.

In the second step of GTS, the following model was fitted to individual estimated function parameters :

$$\beta_i^* = \mathbf{X}_i \mathbf{b}_i + \mathbf{Z}_i \mathbf{a}_i + \mathbf{e}_i$$

where \mathbf{X}_i is the design matrix for fixed effects \mathbf{b}_i , \mathbf{Z}_i is the design matrix for additive genetic effects \mathbf{a}_i , and \mathbf{e}_i is a vector of residuals. The vector \mathbf{b}_i contains the overall means, the birth farm, the effect of year-season-pen and the regression coefficients for animal weight at the beginning of the test. It was assumed that $\text{var}(\mathbf{a}_i) = \mathbf{A} \otimes \mathbf{G}_0$ and $\text{var}(\mathbf{e}_i) = \mathbf{R}$, where \mathbf{A} is the numerator relationship matrix, \mathbf{G}_0 the covariance matrix for additive genetic effects and \mathbf{R} is the residual covariance matrix. The uncertainty of estimation in β_i^* was incorporated by means of the estimated asymptotic covariance matrices (Steimer *et al.*, 1984) :

$$\mathbf{C}_i^{*-1} = \mathbf{X}_i'(\beta_i^*) \mathbf{H}_i^{-1}(\beta_i^*; \theta) \mathbf{X}_i(\beta_i^*),$$

constructed by substituting the estimated variance and function parameters, where $\mathbf{X}_i(\beta_i)$ was the $(n_i \times 3)$ matrix with j^{th} row equal to $\mathbf{f}'_j(\beta_i)$.

Routines from NAG-Fortran90-Library were used to implement the GLS algorithm and population parameters were estimated using ASREML (Gilmour *et al.*, 1999).

Linear random regression (RRM). The following RRM was fitted :

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{a} + \mathbf{W}\mathbf{p} + \mathbf{e}$$

where \mathbf{y} is a vector containing daily data of feed intake, \mathbf{b} is a vector of fixed effects and covariates, \mathbf{a} and \mathbf{p} contain random coefficients of intercept, days on test and days on test squared for additive genetic effects and permanent environmental effects, respectively, and \mathbf{e} is a vector of residual terms. \mathbf{X} , \mathbf{Z} and \mathbf{W} are the corresponding incidence matrices. The vector \mathbf{b} contains the overall mean, the birth farm, the effect of year-season-pen, a linear regression on individual start weight, the day on test and the day on test squared (25 different days) as well as the interactions of day on test and day on test squared with birth farm, year-season-pen effect and regression on start weight.

The variance was $\text{Var}(\mathbf{y}) = \mathbf{Z}\mathbf{G}\mathbf{Z}' + \mathbf{W}\mathbf{P}\mathbf{W}' + \mathbf{R}$, where $\mathbf{G} = \mathbf{A} \otimes \mathbf{G}_0$, $\mathbf{P} = \mathbf{I} \otimes \mathbf{P}_0$ and $\mathbf{R} = \mathbf{I} \otimes \mathbf{R}_0$. \mathbf{A} is the numerator relationship matrix. Covariance matrix \mathbf{G}_0 was assumed unstructured. Based on Akaike's Information Criterion, \mathbf{P}_0 was diagonal with element (1,1) equal to σ_{pe}^2 and remainder elements equal to 0, and \mathbf{R}_0 was heterogeneous autoregressive-moving average of order (1,1). Variance components were estimated with ASREML.

RESULTS AND DISCUSSION

The mean estimated day on test corresponding to maximum increment in feed intake (β_L) varied from 75 to 81 days on test. The mean estimated day on test at which the feed intake plateau was reached (β_S) varied from 45 to 48 days on test. Individual estimates of variance heterogeneity (θ) varied considerably from pig to pig, proving that daily feed intake shows high differences not only in systematic variation but also in the variation pattern. Significant differences in θ were observed between lines: mean value was 1.10 (1.18) for line 3 using logistic function (segmented function) and a mean value was 0.74 (0.88) for line 4 using logistic function (segmented function). Mean values and standard deviations for estimates of nonlinear function and variance parameters are presented in table 1.

Table 1. Mean values and standard deviations (SD) for estimates of nonlinear functions and variance parameters^A

		Line 3		Line 4	
		Mean	SD	Mean	SD
Logistic	α_L (kg/day)	6.40	1.70	6.41	1.54
	β_L (day)	75	37.43	81	41.11
	γ_L (kg/kg*day)	0.0292	0.07483	0.0278	0.09165
	θ_L	1.102	3.25	0.737	2.71
Segmented	α_S (kg/day)	1.41	0.58	1.32	0.56
	β_S (day)	45	33.76	48	27.18
	γ_S (kg/day ²)	0.0596	0.08062	0.0560	0.06782
	θ_S	1.18	2.65	0.878	2.22

^A α_L : asymptotic feed intake ; β_L : day of maximum increment in feed intake ; γ_L : logistic feed intake rate ; θ_L : power of logistic variance function ; α_S : intercept of linear-segmented function ; β_S : estimated day at which feed intake plateau is reached ; γ_S : slope of linear-segmented function ; θ_S : power of linear-segmented function.

Estimated heritabilities for parameter β_L were 0.03 for line 3 and 0.16 for line 4. Estimated heritabilities for parameter β_S were 0.04 for line 3 and 0.05 for line 4. Heritabilities for the remainder function parameters (not presented) were low or should be interpreted with care, since the corresponding correlations were very high. This shows that GTS methods needs high quality data of feed intake (continuously recorded over a long test period at later age).

Genetic correlations between intercept and linear regression coefficients from RRM were positive and ranged from 0.57 to 0.55, between intercept and quadratic regression coefficients were negative and ranged from -0.77 to -0.79, and between linear and quadratic coefficients ranged from -0.48 to -0.61 for lines 3 and 4, respectively. The second major eigenfunction obtained from the additive genetic (co)variance matrix explained about 10 % of the genetic variation of daily feed intake. Individual breeding values for daily feed intake were weighted by coefficients of this second eigenfunction, which permitted to select for high feed intake at early stage of growth and decreased feed intake at the end of the test period.

In order to examine the change in feed intake curve after selection based on GTS and RRM, a reference population was formed with boars that had at least five tested descendants. Figures

1a (line 3) and 1b (line 4) show the differences between mean daily feed intake of reference population and mean daily feed intake of offspring of the best 5 % boars ranked according to (1) breeding values of daily feed intake weighted by the coefficients of the second eigenfunction from RRM, (2) breeding values of function parameter β_L (logistic function) and (3) breeding values of function parameter β_S (linear-segmented function).

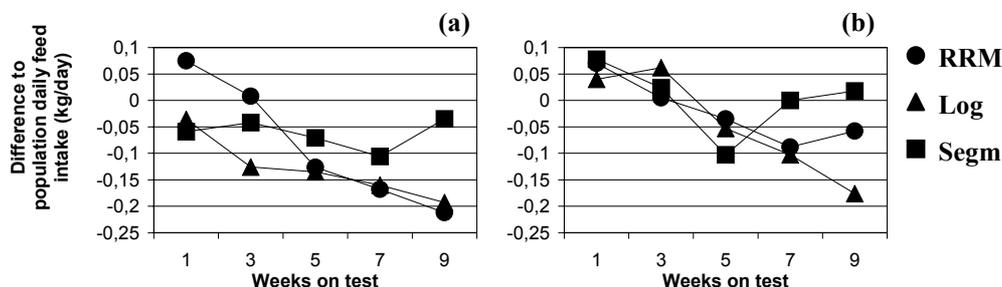


Figure 1. Weekly means of daily feed intake from offspring of 5 % best boars selected according to Random Regression Models (RRM), logistic (Log) and linear-segmented (Segm) functions for line 3 (a) and line 4 (b)

Breeding objectives, i.e. the modification of feed intake curve in each period of test, are determined by the pattern of feed intake of tested animals, which can be largely different among genotypes. From all methods used, selection on parameters estimated by RRM increased mostly early feed intake. By using linear-segmented function, feed intake was reduced at the middle of the test with slight changes at the end of the test period. Extensive feed intake at the end of the finishing period was mostly reduced (-200 g/day) by selection based on logistic function. From viewpoint of data, RRM are preferred if individual observations on daily feed intake are sparse.

REFERENCES

- Davidian, M. and Giltinan, D.M. (1995) «Nonlinear models for repeated measurement data». Chapman and Hall, London, UK.
- De Lange, C.F.M., Mohn, S. and Nyachoti, M. (1995) *Can. Soc. of Anim. Sci.*
- De Lange, C.F.M. (1997) *Proc. of swine production*, Shakespeare, Ontario, Canada.
- De Vries, A.G. and Kanis, E. (1994) *Proc. 5th WCGALP XVII* : 390-397.
- Eissen, J. (2000) PhD Thesis, Wageningen Agricultural University, The Netherlands.
- Gilmour, A., Cullis, B.R., Welham, S.J. and Thompson, R. (1999) «ASREML».
- SAS (1990) «SAS/STAT[®] User's guide». SAS Inst. Inc., Cary, USA.
- Schinckel, A.P. (1994) «Swine Nutrition Guide». Univ. of Nottingham, U.K.
- Schulze, V., Roehle, R., Lorenzo Bermejo, J., Looft, H. and Kalm, E. (2001) *Livest. Prod. Sci.* **73** : 199 - 211.
- Smith, W.C., Ellis, M., Chadwick, J.P. and Laird, R. (1991) *Anim. Prod.* **52** : 193-199.
- Steimer, J.L., Mallet, A. and Golmard, J.L. (1984) *Drug Metab. Rev.* **15** : 265-292.
- Webb, A.J. (1995) *Anim. Breed. Abstr.* **63** : 731-736.
- Webb, A.J. (1998) *Dairy Sci.* **81** (Suppl. 2) : 36-46.