Longitudinal analysis of residual feed intake in mink using random regression with heterogeneous residual variance

M. Shirali[*], V.H. Nielsen[*], S.H. Møller[†] and J. Jensen[*]
[*]Center for Quantitative Genetics, Department of Molecular Biology and Genetics, Aarhus University, Denmark;
[†]Department of Animal Science Epidemiology and management, Aarhus University, Denmark.

ABSTRACT: Heritability of residual feed intake (RFI) increased from moderate to high over the growing period in male and female mink. The lowest heritability for RFI (male: 0.18 ± 0.03 standard deviation (SD); female: 0.18 ± 0.03 SD) was in early and the highest heritability (male: 0.49 ± 0.02; female: 0.46 ± 0.02 SD) was achieved at the late growth stages. The genetic correlation between different growth stages for RFI showed a high association (0.86 to 0.98) between early and late growing periods. However, phenotypic correlations were lower from 0.5 to 0.90. The residual variances were substantially higher at the end compared to the early growing period suggesting that heterogeneous residual variance should be considered for analyzing feed efficiency data in mink. This study suggests random regression methods are suitable for analyzing feed efficiency and that genetic selection for RFI in mink is promising.
Keywords:
longitudinal analysis
feed efficiency
heritability

Introduction

Feed efficiency in farmed mink is dependent on the stages of growth due to the changes in biological requirements of the animals. Berg and Lohi (1992) reported low to medium correlation for feed conversion ratio (feed:gain) between growth stages. Sørensen (2002) reported high heritability (0.30) for feed efficiency (gain:feed) in mink and suggested that a high selection response is possible for this trait. However, selection for feed conversion ratio has shown to result in disproportional or unpredictable genetic gain for feed intake and body weight gain (Gunsett (1984) and (1986)); therefore, in this study residual feed intake (RFI) has been estimated as a measure of feed efficiency. Furthermore, to our knowledge no study has put the context of feed efficiency in longitudinal aspect using random regression in mink. Random regression method can be advantageous by adjustment for temporary environmental effect on the traits and taking into account changes in the genetic variances during growth. Bayesian analyses have shown to improve the inference of model parameters and facilitating large scale analyses (Jensen (2001)). Therefore, in this study Gibbs sampling algorithm was used to estimate parameters of the posterior distribution of each (co)variance parameter.

The objective of this study was to estimate genetic parameters for feed efficiency and growth traits during entire growing-furring period using random regression models involving orthogonal polynomial regression for multiple random effects along with heterogeneous residual variances.

Materials and Methods

Animals. The data were available from previous experiment by Møller et al. (2007) and Nielsen et al. (2011). Four lines (FF, AL, RF and FC) were used. Three lines (FF, AL and RF) each with 100 female and 20 male breeders were established for experiment. Line FF was a control line where breeding animals were chosen at random. A maximum of two males from the same sire and two offspring from the same litter were used for breeding. The AL line was fed *ad libitum* and the RF line was fed about 80% of *ad libitum* feeding. The FC line was established in generation two from the AL line. After the normal selection AL line in generation one, 10 males and 50 females with the lowest feed conversion ration were selected for breeding in the FC line. The data of current study was collected from 2003 to 2005 as part of the above experiment. Animals were kept in pairs of one male and one female per cage. In total, body weight of 4278 juvenile mink were available of which half were male and half female; and feed intake was measured per cage and records of 2139 mink cages were available.

Data. Body weight was measured 8 times during the growth period from 9 to 30 weeks of age. Individual weights were recorded over two days, every third week. The daily feed intake was calculated based on the feed allowance (from a Palm Pilot controlling the feeding machine) and feed left-overs (removed daily) (Møller et al. (2007); Nielsen et al. (2011)). However, the accumulated feed intake from 6 periods of 3 weeks between weighing's from 12 to 30 weeks of age is used in the current study.

Statistical analyses. The genetic parameters for RFI were estimated using a univariate random regression model for cumulative feed intake of each cage that included, besides other systematic effects, body weight of the male and female mink. The following random regression model was fitted:

$$y_{ijklm} = YL_i + b_1(BWM_k) + b_2(BWF_l) + l_{q1}(t)'r_i + l_{q2}(t)'a_k + l_{q2}(t)'a_l + l_{q2}(t)'p_k + l_{q2}(t)'p_l + e_{ijklm}$$

where y_{ijklm} is the feed intake record for each cage with animal k and l on day j in year and line of i; YL_i is the effect of year and line interaction; b_1 is the regression coefficient for body weight of male mink of k; BWM_k is the body weight for male mink k; b_2 is the regression coefficient for body weight of female mink of l; BWF_l is the body weight for female mink l; t is the average of age for male and

female mink in each cage; $l_q(t)$ is a vector valued function that yields the vector of standardized Legendre polynomials of order q for each cage; q_1 is the second order and q_2 is the first order Legendre polynomial; r_i is the vector of regressions on Legendre polynomials for YL_i; a_k is a vector of order $(q_2 + 1)$ of additive genetic effects of animal k; a_l is a vector of order $(q_2 + 1)$ of additive genetic effects of animal l; p_k is a vector of order $(q_2 + 1)$ of permanent environmental effect of litter for animal k; p_l is a vector of order $(q_2 + 1)$ of permanent environmental effect of litter for animal l; and e_{ijklm} is the residual of the model fitted with heterogeneous variance in 6 classes. The genetic (co)variance matrix (**G**) and the permanent environmental (co)variance matrix (**P**) each had order of $2 \times (q_2 + 1)$ because the effects are estimated for both males and females. Heterogeneous residual variance was estimated in 6 classes, effectively for each time period that feed intake was accumulated. The model allows prediction of separate effects for each animal even though records were based on cages containing two animals.

Bayesian estimation method via Gibbs sampling was used to estimate **G** and **P** and the residual variance for the six classes. The Gibbs sampling was performed for 2M rounds with first 50k considered as burn-in and every 500th sample saved for posterior analysis. Coda package (Plummer et al. (2006)) of R program was used to evaluate convergence to the posterior distribution of the (co)variance parameters. Furthermore, covariance functions were used to obtain genetic parameters for RFI from 90 to 216 days of age. DMU software package (Madsen and Jensen (2010)) was used for the univariate random regression model using Gibbs sampling.

Results and Discussion

Heritability of RFI. The results showed that heritability of RFI increases substantially with age. The lowest heritability for male (0.18 ± 0.03 standard deviation (SD)) and female (0.18 ± 0.03 SD) were achieved at early stages of growth and highest heritabilities for male (0.49 ± 0.02 SD) and female (0.46 ± 0.02 SD) were achieved at the end of the growth period from 168 to 210 days of age. The results indicate higher genetic variance at the end of the growth period which could be due to different underlying factors such as different QTL with different mode of inheritance influencing the trait along with more pronounced animal's genetic effect compared to the early growth. This suggests that higher selection response can be achieved by selecting for feed efficiency in furring period. The heritability patterns for male and female mink were similar (Figures 1 and 2). This indicates similar pattern for genetic variance for male and female minks. In addition, lower genetic variance in the early stage of growth can be due to the fact that animal performance in this time period can be mostly regulated by its dam maternal ability. This was observed by high permanent environmental effect (0.71 to 0.61) at this time period compared to the end of the growth period (0.47 to 0.37). Furthermore, the genetic variance can be low as the variation in body weight is lower in this time period compared to the later stages. To our

knowledge no heritability for RFI has been reported in mink. However, Sørensen (2002) reported 0.30 heritability for feed efficiency (gain:feed) in growing period of mink. In addition, the range of heritability for RFI in pigs is $0.10 - 0.44$ (Cai et al. (2008); Gilbert et al. (2007); Shirali (2014)). Moreover, Drouilhet et al. (2013) and Larzul and De Rochambeau (2005) reported heritability of 0.16 ± 0.05 and 0.45 ± 0.11 for RFI in rabbits, respectively.

Correlation between RFI at different stages of growing-furring period. The genetic correlation for RFI between growing and furring period were high ranging from 0.86 to 0.98, suggesting that animals with better feed efficiency at early growth period tend to be efficient at the end of the growth period (Figure 3 and 4). However, correlations lower than unity suggests that extra genetic gain can be obtained by selecting for feed efficiency at the end of the growth period. Furthermore, feed efficiency has shown to have different genetic background at different stages of growth in other species, e.g. in pigs (Shirali, (2014)). However, the phenotypic correlations between early and late growth periods were low to moderate ranging from 0.50 to 0.90. This suggests that the environmental factors substantially affect feed efficiency at the end of the growth period. The residual variances obtained considering heterogeneous residual variance analysis showed that the residual variances at the end of the growth period were high ranging from 0.41 ± 0.02 SE to 1.39 ± 0.08 SE compared to the residual variances in the growing period ranging from 0.15 ± 0.01 standard error (SE) to 0.25 ± 0.01 SE. This further confirms the environmental influences on the phenotype of feed efficiency. The phenotypic correlations in this study were in agreement with Pearson correlation of 0.28 for feed conversion ratio (feed:gain) between early and late growth periods in minks reported by Møller et al. (2007).

Conclusion

Heritability of feed efficiency in mink is low in early growth and increases to high with age. Results show that RFI can be substantially improved by genetic selection later in the growth period. Feed efficiency in mink should be analyzed longitudinally and random regression models have shown to be suitable for dissecting the genetic background of RFI.

Literature Cited

Berg, P., and Lohi, O. (1992). Acta Agric. Scand., Sect. A, Animal Sci. 43:151-157.

Cai, W., Casey D.S., and Dekkers J.C.M. (2008). J. Anim. Sci. 86:287-298.

Drouilhet, L., Gilbert, H., Balmisse, E., et al. (2013). J. Anim. Sci. 91:3121-3128.

Gilbert, H., Bidanel, J.P., Gruand, J., et al. (2007). J. Anim. Sci. 85:3182-3188.

Gunsett, F.C. (1984). J. Anim. Sci. 59: 1185-1193.

Gunsett, F.C. (1986). Proc. 3rd WCGAL Nebraska, Lincoln, Nebraska, USA. 11, 437-442.

Jensen, J. (2001). J. Dairy Sci. 84:2803:2812.

Larzul, C., and De Rochambeau H. (2005). Livest. Prod. Sci. 95:67–72.

Madsen, P., and Jensen, J. (2010). Faculty of agricultural sciences, Tjele, Denmark. (http://www.dmu.agrsci.dk/)

Møller, S.H., Hansen, B.K., Nielsen, V.H. (2007). NJF Seminar, Kolding, Denmark. No. 403.

Nielsen, V.H., Møller, S.H., Hansen, B.K., et al. (2011). Can. J. Anim. Sci. 91:231-237.

Plummer, M., Best, N., Cowles, K., et al. (2006). R News, vol 6, 7-11.

Shirali, M. (2014). PhD thesis. Wageningen Press.

Sørensen, K. (2002). PhD thesis. Aarhus University.

Figure 1: Heritability (h^2) of RFI with 1SD above (USD) and below (LSD) average for male minks during growing period (90 to 216 days)
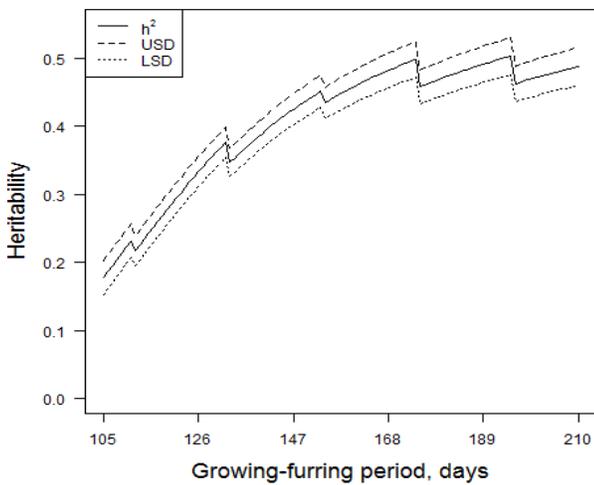

Figure 2: Heritability (h^2) of RFI with 1SD above (USD) and below (LSD) average for female minks during growing period (90 to 216 days)
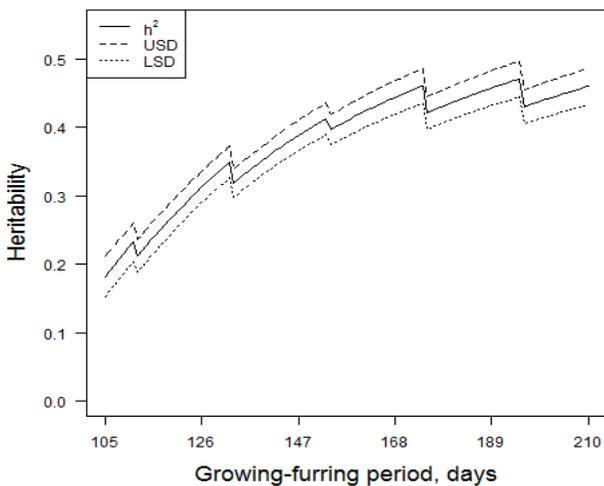

Figure 3: Genetic correlations (r_g) for RFI in male minks between different days of growing period (90 to 216 days)
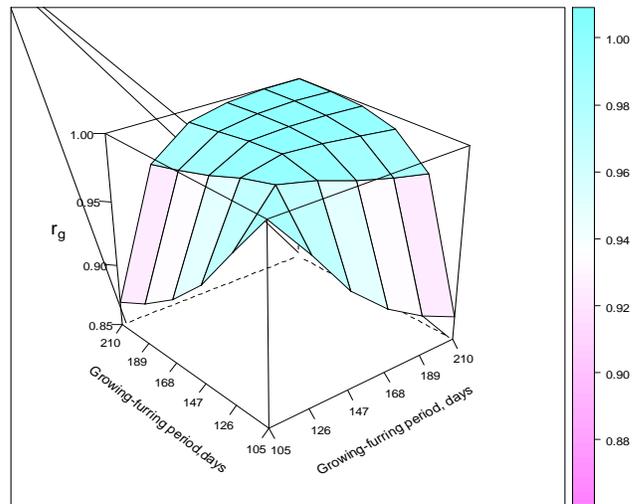

Figure 4: Genetic correlations (r_g) for RFI in female minks between different days of growing period (90 to 216 days)