# RANDOM REGRESSION ANALYSES OF FEED INTAKE OF INDIVIDUALLY TESTED BEEF STEERS

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## INTRODUCTION

Feed intake has been used for assessing feed conversion, feed efficiency, and residual feed intake of beef cattle. However, little information is available on the optimum period to evaluate feed intake of beef cattle. Studies by Archer *et al.* (1997) and Archer and Bergh (2000), for instance, investigated the minimum duration of test required to provide an accurate measure of feed intake through several analyses with progressively increased test lengths obtained by including extra feed intakes. The optimum length of test and genetic and environmental parameters of feed intake could be assessed using random regression (RR) models. Recently, two publications by Schnyder *et al.* (2001a) and Schnyder *et al.* (2001b) have demonstrated the feasibility of applying RR models to feed intake of pigs.

The objectives of this study were: 1) to apply a RR model to feed intake data of beef steers; 2) to quantify genetic, environmental, and phenotypic parameters; and 3) to assess the optimum period of test.

## MATERIAL AND METHODS

**Data**. Data were daily dry matter intakes of crossbred steer calves born from 1996 to 1999 in three research herds in Ontario, Canada. Steers were placed into the Elora Beef Research Center feedlot after weaning. Steers were submitted to an adjustment period of 28 days. Steers born in 1996 and 1997 were fed one diet of high percentage of corn grain. Steers born in 1998 and 1999 were fed one of four diets: high percentage of corn grain (from starting on feed to finish) or one of three types of corn silage for 112 days followed by high percentage of corn grain. Steers were fed *ad libitum* and individual daily feed intakes were recorded up to when steers reached the carcass finish point of 8 mm of subcutaneous fat evaluated via ultrasound. The data set consisted of 49,609 daily dry matter intakes up to 224 days of test on 293 steers from 39 sires. Test group was defined as steers tested in the same year and under the same diet. Minimum number of steers per test group was 12.

**Random regression models**. The RR models included fixed linear regression effect on breed composition and fixed regressions on third order orthogonal Legendre polynomials of the actual days on test for starting age and herd of origin effects and third (model 1) or fifth (model 2) order Legendre polynomials for test group effect. Random regressions on third order polynomials were included for permanent environment (PE) and additive genetic animal effects. Residuals were assumed independently distributed with heterogeneous variance for each week (32 weeks in total).

**Gibbs sampler**. The Bayesian procedure, via Gibbs sampling, used in this study was similar to that described by Jamrozik and Schaeffer (1997) for milk production curves. Prior inverted Wishart distributions were assumed for PE and additive genetic variances and prior independent scaled inverted Chi-Square distributions were assumed for residual variances. Flat improper priors were used for location parameters. Two chains of 170,000 samples were generated for each model with a burn-in period of 5,000. Means of the marginal posterior distributions of (co)variance components for genetic ($\mathbf{K_g}$), permanent environmental ($\mathbf{K_p}$) and residual effects were computed as averages of samples after the burn-in from the two chains.

**Daily and cumulative feed intake**. (Co)variance components of the r-th random effect for daily and cumulative feed intake at a given day of test were obtained as a function $\mathbf{K}_r$. For instance, the genetic variance for feed intake on the 112$^{th}$ day of test was obtained as $\mathbf{k}_{112}'\mathbf{K}_g\mathbf{k}_{112}$, where $\mathbf{k}_{112}$ was the vector of Legendre polynomial coefficients for the 112$^{th}$ day of test. The genetic variance for cumulative feed intake up to 112 days on test was obtained as $\mathbf{k}^{*}{}'\mathbf{K}_g\mathbf{k}^{*}$, where $\mathbf{k}^{*} = \sum_{t=1}^{112}\mathbf{k}_t$.

**Eigenfunctions and eigenvalues**. Genetic eigenvalues and eigenvectors were calculated from the additive genetic covariance matrix $\mathbf{K}_g$. Eigenvectors were multiplied by the vector $\mathbf{k}_t$ of Legendre polynomial coefficients to obtain eigenfunctions evaluated at the t$^{th}$ day of test.

**Model comparison**. The $R^2$ of each model was calculated as the square of the product-moment correlation between observed and adjusted observations given by each model, using the estimated location and dispersion parameters.

## RESULTS AND DISCUSSION

**Gibbs sampling**. The samples were strongly correlated for both additive genetic and PE effects. For the two models, most elements of $\mathbf{K}_g$ and $\mathbf{K}_p$ had an effective sample size between 200 and 300 samples. The sample sizes for residual variances ranged from 213,365 to 296,772 samples for both models.

**Model fitting**. Models had similar overall $R^2$ (0.49 vs 0.50, for model 1 and 2, respectively). When $R^2$ was calculated within test groups, model 2 showed an increase in $R^2$ over model 1 for test groups that had diet changed from corn silage to high percentage of corn grain.

**Genetic parameters**. Genetic ($\sigma^2_g$), permanent environmental ($\sigma^2_p$), residual ($\sigma^2_e$), and phenotypic ($\sigma^2_t$) variances of daily and cumulative feed intake at different days of test and their corresponding ratios with respect to $\sigma^2_t$ were estimated (Figure 1). The $h^2$ of daily feed intake ranged from 2 % to 23 % for day 1 to day 168 of test for both models. After 168 days, $h^2$ substantially increased, reaching 33 % and 42 % at 224 days of test for model 1 and 2, respectively. This increase in the $h^2$ after 168 days should be looked at with caution, as few steers (< 162) were on test in the last eight weeks. In general, $h^2$ of cumulative feed intake increased as more daily feed intake records were cumulated. However, cumulative feed intake

of short periods of 28 days around the middle of the test period showed similar or higher $h^2$ than cumulative feed intakes that started from the initial weeks of the test. This happened due to the reduction of PE effects. As expected, residual variance substantially reduced as more daily feed intakes were cumulated. Estimates of genetic correlations of cumulative feed intakes in short periods of 28 days around the middle of the test with the feed intake in the entire test period and in the period from 1 to 168 days were similar or higher than of cumulative feed intakes that started from initial weeks of the test (Figure 1). These results suggest that a short period of 28 days, starting between 57 and 85 days on feed, would be practicable and sufficient for evaluating feed intake of beef cattle.

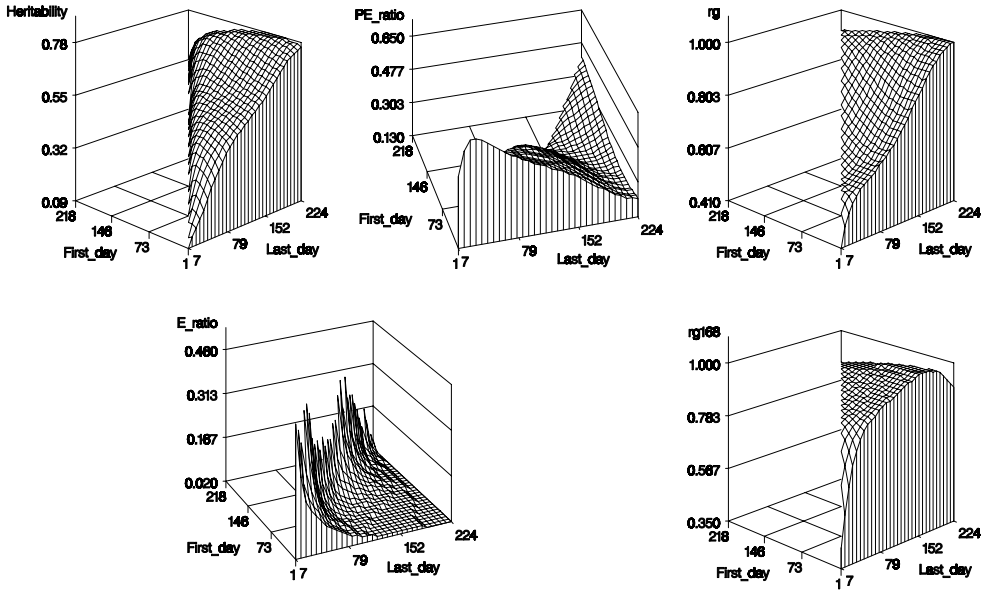


**Figure 1. Heritability, permanent environmental (PE_ratio) and residual (E_ratio) variance ratios, and genetic correlation with cumulative feed intake in the entire test period (rg) and in the period from 1 to 168 days of test (rg168) of cumulative daily feed intakes in different test lengths (Last_day), starting to cumulate daily feed intakes from different weeks (First_day). Results from model 2**

**Genetic eigenfunctions**. The estimated genetic eigenfunctions from each model are presented in Figure 2. The first eigenfunction explained more than 75 % of the genetic variance of daily feed intake for both models. It was positive and increased during the test. This means that selection for overall level of daily feed intake in one direction, at any time during the testing period, would cause a response in that same direction over the entire test period and response would be larger towards the end of test. The size of the first eigenvalue indicated that selection would produce rapid changes if this kind of alteration in the mean trajectory was favored

(Kirkpatrick *et al*., 1990). The second eigenfunction, which explained more than 22 % of the genetic variance for both models, changed sign around 175 days of test. This means that changes in the slope of genetic curve to increase daily feed intake from the beginning to around 175 days would cause the feed intake to decrease after 175 days and vice-versa. The size of the second eigenvalue indicated that the response to selection involving the second eigenfunction would be slower than for changes involving the first eigenfunction. The third eigenfunction explained less than one percent of the genetic variance. Schnyder *et al*. (2001b) also found that changes of the overall level of feed intake are easier to achieve than changes of slope or inflexion of the feed intake curve of growing pigs.

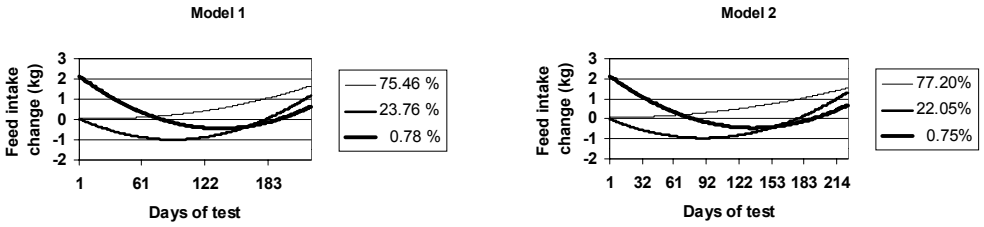


**Figure 2. Eigenfunctions for daily feed intake of steers. Percent scaled eigenvalues are presented in the legend, indicating the importance of each eigenfunction**

## CONCLUSIONS

Random regression analysis of daily feed intake of beef cattle provides genetic and environmental parameters useful for examining the optimum duration of test. Estimates of genetic and environmental parameters and genetic eigenfunctions indicated that a short period of 28 days, starting between 57 and 85 days on feed, would be sufficient for evaluating feed intake. Further studies with larger data sets on the advantages of using random regression models to analyze feed intake and feed efficiency of beef cattle are warranted and planned.

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