

## A GROWTH MODELLING APPROACH TO PREDICTING THE CORRELATED RESPONSES TO SELECTION FOR FEEDING AND GROWTH TRAITS

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### SUMMARY

Mathematical growth models, such as the Brody Growth Curve, provide a means of incorporating the information contained in a series of liveweight measurements into parameters of biological meaning. Variation that exists in these parameters was used to simulate a population of animals and examine the correlated phenotypic responses to selection in feeding, growth and carcass traits. Results are illustrative only because of the lack of model calibration. The average growth curve and daily feed intake (DFI) of a selected cohort was increased by selection on 600 day weight alone in comparison to the average of the unselected population. Conversely, selection on reduced mature weight only decreased these traits, with no apparent effect on feed conversion efficiency (FCE). Selection on combinations of 600 day weight, mature weight and mature feed intake had intermediate effects, however, efficiency increased when selection was for 600 day weight and against mature feed intake. The DFI and FCE at liveweights of 200, 400 and 600 kg were increased by selection for 600 day weight but were reduced by selection against mature weight.

**Keywords:** Growth model, correlated response, selection, food intake

### INTRODUCTION

Growth traits such as birth, weaning and yearling weights have been routinely recorded and analysed in genetic evaluations (Kaps, *et al.* 2000). The economic importance of other growth traits such as mature size, maturing rate and growth rate has led to their inclusion in genetic evaluations and increased the interest among scientists and producers in life-time age-weight relationships. However, a series of weight records taken during an animal's life are difficult to interpret in isolation, without reference to other weight records. Mathematical growth models provide a means of incorporating the information contained in such records into a few parameters of biological meaning that are easily understood (Cho, *et al.* 2002). The Brody growth curve (Brody, 1945) as formulated by Doren *et al.* (1989) is a simple example:

$$y_t = A - (A - y_o) e^{-k(t-t_o)}$$

where  $y_t$  is the weight of the animal at time  $t$ ,  $y_o$  is the weight of the animal at original time  $t_o$ ,  $A$  is the asymptotic weight (mature weight) and  $k$  characterises rate of growth. This growth model uses two parameters of biological importance to describe the growth of an animal across time. The shapes of the growth curves produced by such equations for different animals are not identical, indicating that the parameter values of the growth models vary between individuals. This variation can be used to help investigate the possible effect that selection on a particular trait(s) has on a range of other traits.

The objective of this study is to develop an approach to examine the effect selection on a single trait or index has on a range of feeding, growth and carcass traits in a selected cohort through simulation of the growth curves for a population of animals using the variation that exists in parameter values.

## MATERIALS AND METHODS

The model adopted was based on that of Kinghorn (1985). Weight at time  $t$  was defined by:

$$y_t = w(L_m(1 - e^{-kt/L_m}))^P \quad \text{or in a time step approach,}$$

$$y_t = w((y_{t-1}/w)^{1/P} + k \cdot e^{-kt/L_m})^P$$

- where  $L_m$  is mature length,  $w$  is a scaling factor,  $k$  is a constant characteristic of the rate of decrease in linear growth rate and power  $P$  relates weight to body length. Daily feed intake at time  $t$  was defined by:

$$DFI_t = NFCR \cdot (y_t - y_{t-1}) + m \cdot [(y_t + y_{t-1})/2]^{0.75}$$

- where NFCR (Net Food Conversion Ratio) is Kg feed required per Kg tissue deposited and  $m$  is maintenance cost per Kg metabolic body weight per day. Feed conversion efficiency at time  $t$  was defined by:

$$FCE_t = y_t / AccFI_t$$

- where  $AccFI_t$  is  $DFI_t$  accumulated to time  $t$ . Carcass weight was also simulated, as follows:

$$Cwt_t = ay_t^b$$

- where  $a$  and  $b$  were estimated by non-linear regression from Beef CRC carcass and weight data.

The model parameters were allocated means, standard deviations, plus correlations among them. Ideally, these parameters would be estimated reliably from data, but this has not yet been possible. Sensible values were allocated in order to be able to demonstrate the approach undertaken, and so caution is needed in interpreting current results.

The growth curve for each animal in the population was simulated by sampling a parameter set from the assumed multivariate distribution. The resulting population of animals was then selected on one or more predicted trait values and the selected group examined for correlated phenotypic responses in other traits. Table 1 shows the traits used for each round of selection, and the economic values allocated to them for illustrative purposes.

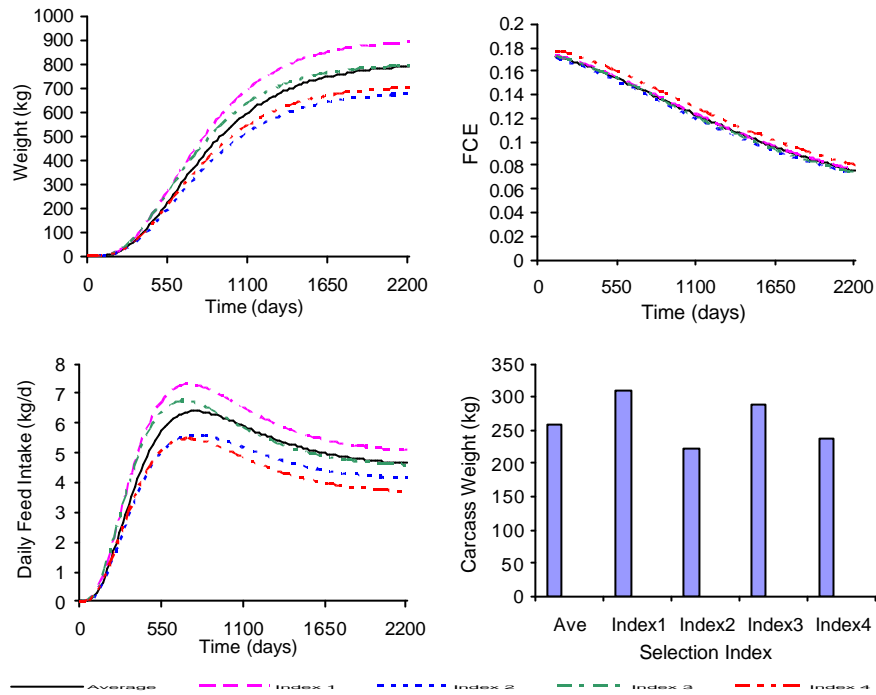
**Table 1. Traits and economic values (EV) used for selection**

Index	Index traits <sup>A</sup>		
	600D Wt	M Wt	M FI
1	1		
2		- 1	
3	1	- 0.5	
4	1		-0.1

<sup>A</sup> Index traits: 600D Wt, liveweight 600 days postpartum; M Wt, mature liveweight measured at 5yrs of age; M FI, cumulative feed intake to 5 yrs of age.

**RESULTS AND DISCUSSION**

The average phenotypic responses to selection on the economic indexes described above are presented in Figure 1 in comparison to the unselected population average.



**Figure 1. The correlated phenotypic response of growth, daily feed intake, feed conversion efficiency (FCE) and carcass weight to selection.**

Selection for increased 600 day weight (index 1) increased the average growth curve of the selected cohort in comparison to the unselected population (figure1). The opposite occurred when selection was against mature weight (index 2) with the average growth curve being reduced. The other indexes produced intermediate results. Interestingly, selection using index 3 increased liveweight at marketable ages whilst not increasing liveweight at maturity. The daily feed intake (DFI) curves followed the same pattern, with index 1 increasing DFI and index 2 decreasing DFI. However, index 4 reduces DFI below that of index 2 thus increasing efficiency. This is reflected in figure 1 with index 4 having a higher FCE than the average population and the other indexes. Carcass weights (figure 1)

follow the same pattern as the growth curves primarily because they are derived from predicted liveweight.

The correlated responses of FCE and DFI at different liveweights are presented in Table 2. Index 1 increased DFI and FCE whilst index 2 decreased both traits. Index 4 also reduced DFI however the FCE of this index remained in close proximity to that of the average population. The DFI and FCE of index 3 remained relatively close to that of the average population, with a slightly higher DFI at smaller liveweights.

The results above can be interpreted to indicate selection for larger genotypes is desirable because they can reach higher body weights on a given quantity of feed. However, this does not mean they are more efficient (Kinghorn, 1985), which the results indicate (Table 2). Taking into account the maternal costs of production, which this simulation does not, would result in animals being selected on their level of maturity and fit to the production and market system (Kinghorn, 2000) and increasing the efficiency of the production system as a whole.

The correlated phenotypic responses in growth, feeding and carcass traits to selection using different criteria were able to be investigated by utilising the variation that exists in the parameter values of a growth model. However, there are two important limitations of the current study to note. Firstly, the growth model used has not been calibrated to appropriate data. Secondly, simple calibration to phenotypic data will only make the approach proposed reliable for predicting the mean merit of the selected group, not of their progeny. However, suitable calibration, and estimation of genetic parameters for growth curve parameters, could make the approach proposed here useful for predicting genetic responses to selection in breeding programs.

## REFERENCES

- Brody, S. (1945) "Bioenergetics and Growth" Reinhold Publishing Corporation, New York.
- Cho, Y.M., Yoon, H.B., Ahn, B.S. and Park, Y.I. (2002) Proc. 7<sup>th</sup> World Congr. Genet. Appl. Livest. Prod., Montpellier CD-ROM Communication n° 11-02. ISBN 2-7380-1052-0
- Doren, P.E., Baker, J.F., Long, C.R. and Cartwright, T.C. (1989) *J. Anim. Sci.* 67:1432.
- Kaps, M., Herring, W.O. and Lamberson, W.R. (2000) *J. Anim. Sci.* 78:1436.
- Kinghorn, B. (1985) *J. Anim. Breed. Genet.* 102:241.
- Kinghorn, B. (2000) In "Animal Breeding. Use of New Technologies", p. 265, editors B. Kinghorn, J. van der Werf and M. Ryan, The Post Graduate Foundation in Veterinarian Science of the University of Sydney, Sydney.

**Table 2: Correlated response of daily feed intake (DFI) and feed conversion efficiency (FCE)**

		Liveweight (kg)		
Trait	Index	200	400	600
DFI	Average	5.60	6.41	5.90
	Index 1	+0.65	+0.86	+1.04
	Index 2	-0.41	-0.84	-1.20
	Index 3	+0.38	+0.33	+0.15
	Index 4	-0.48	-0.99	-1.39
FCE	Average	0.155	0.140	0.122
	Index 1	+0.004	+0.007	+0.010
	Index 2	-0.004	-0.007	-0.017
	Index 3	+0.003	+0.004	+0.003
	Index 4	+0.005	+0.004	-0.003