Description and validation of a harmonised model of the growing pig for the optimisation of the utilisation and excretion of nutrients

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Introduction The proposed model may be considered as an advance upon previous models; giving a synthesis of the contemporary information base and having a structure with maximum flexibility and minimum usage of fixed coefficients. It is distinctive in that it includes: (1) linkage from dietary nutrients to tissue retention via algorithms for main-stream biochemical processes; (2) a unified driver allowing compatible calculation of (i) the nutrient costs of energy and of protein cycling, (ii) the nutrient costs of maintenance and protein retention, and (iii) the interactions between energy and protein usage; (3) prediction of the rate and composition of tissue retention during growth, and of the cost of thermoregulation; (4) reversal of the role of conventional model parameters such that they become out-turns, rather than inputs, of the model, including (i) the metabolisability of energy, (ii) the ideality of protein and the efficiency of use of ileal digested ideal protein, (iii) the efficiency of utilisation of energy (k) for maintenance (k_M), for protein (k_{Pr}) and lipid (k_{Lr}) retention, which are accepted as variables derived from calculation of efficiencies of production of ATP.

Materials and methods The elements are largely a synthesis of algorithms presented by Whittemore *et al.* (2001a, b, c), which also suggested proofs of principle. Nutrient intake is defined in terms of starch, non-starch polysaccharide, amino acids, oil and ash. The products of fore gut digestion are ileal digested starch, true ileal digested amino acids, and ileal digested lipid, which are absorbed to yield usable glucose, amino acids and lipids. Hind gut digestion yields VFA, gaseous losses and faecal excretions. Amino acids are prioritised to body protein retention, turnover and excretion; lipids are prioritised to lipid retention; while energy-containing end-products of digestion not having contributed carbon skeletons are catabolised, yielding ATP to drive tissue synthesis, support and turnover. Chemical masses are accumulated into carcass tissues and whole-body live weight by use of experimentally-derived empirical relationships. Other routines attempt quantification of the influence of climatic environment, disease and activity.

Results The efficiency of use of ME for protein retention (k_{Pr}) was found to fall from 0.55 at 5 kg pig protein mass to 0.45 at 15 kg protein mass. The maximum efficiency of use of ileal (apparently) digested ideal protein was found to be 0.86. The gross out-turns from the model were tested against data from a recently completed experiment involving 104 pigs of three types grown from 25 to 115 kg live weight and slaughtered serially for carcass and chemical analysis following daily measurement of live weight and feed intake. Model results for individual pigs were regressed upon those observed. Effective simulation is shown by target values of $y_0 = 0$ and $b = 1$ in the equations;

Modelled lipid mass = 1.95 (± 0.275) + 0.829 (± 0.0197)•Observed lipid mass $r^2 = 0.95$
Modelled protein mass = –1.05 (± 0.364) + 1.13 (± 0.027)•Observed protein mass $r^2 = 0.94$
Modelled live weight = –1.96 (± 1.31) + 1.05 (± 0.017)•Observed live weight $r^2 = 0.97$
Modelled P2 backfat depth = 3.50 (± 0.275) + 0.663 (± 0.0197)•Observed P2 $r^2 = 0.76$

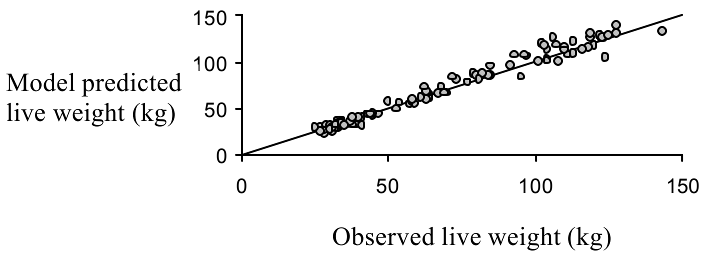

Figure 1. Chart of model predicted live weight versus observed live weight for the 104 pigs. The solid line represents the 1:1 relationship

Conclusion This model will increase the likelihood of optimising diverse production systems with regard to nutrient use and pollution control. The model will be used at the heart of an Integrated Management System for pig production that will further incorporate aspects of iteration, learning and diagnosis. The simulation of P2 backfat depth requires further sophistication, and appears sensitive to pig type.

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