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## Modelling the dynamics of ruminal acidosis

Daniel Sauvant, Sylvie Giger-Reverdin, Francois Meschy

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# Abstracts

## Proceedings of the 2009 Meeting of the Animal Science Modelling Group

Edited by  
J. France<sup>1</sup>, E. Kebreab<sup>2</sup>, C. Pomar<sup>3</sup>, and J. A. Metcalf<sup>4</sup>

<sup>1</sup>Centre for Nutrition Modelling, Department of Animal and Poultry Science, University of Guelph, Guelph, Ontario, Canada N1G 2W1; <sup>2</sup>Department of Animal Science, University of Manitoba, Winnipeg, Manitoba, Canada R3T 2N2; <sup>3</sup>Agriculture et Agroalimentaire Canada, Sherbrooke, Quebec, Canada J1M 1Z3; and <sup>4</sup>Nutreco Canada AgResearch, 150 Research Lane, Guelph, Ontario, Canada N1G 4T2.

This group meets yearly for one-day meetings. The 2009 meeting was sponsored by Nutreco Canada, Inc., Guelph, ON, Canada; Adisseo, Inc., Cambridge, ON, Canada; Evonik Degussa GmbH, Hanau, Germany; Provimi 9–11, Avenue Arago, 78190 Trappes, France and Agri-King, Inc., Fulton, IL, USA. It was held on July 11 at Pointe-à-Callière, 350 Place Royale, Vieux-Montreal, Quebec, Canada, prior to the ADSA-CSAS-ASAS Joint Annual Meeting. Summaries of the papers presented follow. Each summary has been peer reviewed and edited for clarity. The person who presented the paper is identified with an e-mail address.

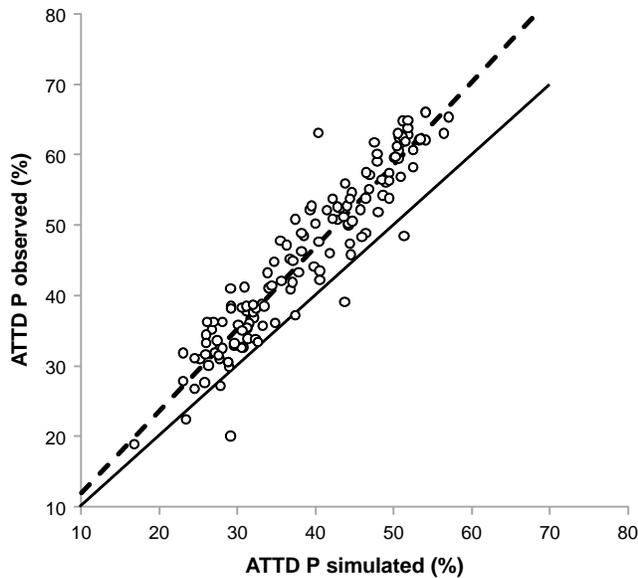
**Fate of dietary phosphorus in the digestive tract of growing pigs: A mathematical model.** M. P. Létourneau-Montminy<sup>1,5</sup>, A. Narcy<sup>1</sup>, M. Magnin<sup>2</sup>, P. Lescoat<sup>1</sup>, J. F. Bernier<sup>4</sup>, C. Pomar<sup>5</sup>, D. Sauviant<sup>3</sup>, and C. Jondreville<sup>6</sup>. <sup>1</sup>INRA, UR83, F-37380 Nouzilly, France, marieiris18@hotmail.com; <sup>2</sup>BASF Nutrition Animale, F-53200 Château-Gontier, France; <sup>3</sup>INRA, UMR791, AgroParisTech, F-75231 Paris, France; <sup>4</sup>Université Laval, Département des Sciences Animales, Québec, QC G1V 0A6, Canada; <sup>5</sup>Agriculture et Agroalimentaire Canada, Sherbrooke, QC J1M 1Z3, Canada; <sup>6</sup>INRA, USC 340, Nancy Université, F-54500 Vandoeuvre-lès-Nancy, France.

Reducing dietary phosphorus (P) without affecting performance is essential in the development of sustainable pig production systems. This requires precise understanding and quantification of the fate of the different forms of ingested P (phytic, non phytic, and mineral) along the digestive tract in interaction with the factors that can modify its utilization, mainly dietary calcium (Ca) and phytases. A mathematical model based on mechanistic concepts was developed using in vitro

and in vivo information. The stomach and the proximal and distal small intestine are the three digestive tract segments of the model. Eight pools were represented within each compartment: for P, Phytic P (PP) and non-phytic P (NPP) and for Ca, Ca originating from plants and from minerals, each subdivided into soluble and insoluble form. Relationships between pools were through solubilization, insolubilization and hydrolysis processes. Ingested P solubilization and phytic P (PP) hydrolysis occur in the stomach and result in suitable forms for absorption. Soluble P absorption by active and passive processes occurs in the small intestine and P insolubilization in the distal intestine.

The solubility of PP was parameterized according to the kinetics of maize and wheat phytate solubility related to pH (Scheuermann et al. 1989) and was fixed to 70%. Solubilized phytate could then be hydrolyzed by microbial (*Aspergillus niger* 3-phytase) and plant phytase following a Michaelis–Menten kinetic law. Solubilized and hydrolyzed PP is then available for absorption. Michaelis–Menten kinetic parameters  $V_{\max}$  and  $K_m$  were obtained from in vitro or in vivo data as previously indicated (Létourneau-Montminy et al. 2007). High dietary Ca is known to decrease PP solubility at normal stomach pH levels (Wise 1983) and was therefore included in the model. Also, considering that Ca can decrease P absorption by formation of insoluble Ca-phosphate complexes (Cromwell 1996), a P insolubilization process was also assumed to occur at the distal part of the small intestine due to increasing pH. Sensitivity analyses stressed that pH and transit time strongly modulates the extent of phytic P hydrolysis. The major constraint for gastric phytic P degradation seems to be the solubility of phytate and could be partly responsible for the incomplete phytate hydrolysis that is frequently observed at the terminal ileum in pigs. The model was also able to accurately rank exogenous phytase according to their phytate degradation efficiency (50% lower for plant than for microbial phytase). Hydrolysis level by microbial phytase was consistent with previous results (e.g., Kornegay et al. 2001) with an increase of digestible P averaging 0.70 g for 500 FTU  $\text{kg}^{-1}$ . P absorption was also sensitive to transit time in both the proximal and the distal part of the small intestine.

The prediction capabilities of the model were assessed by comparing actual and simulated apparent total tract digestibility of P (ATTD) based on published data not



**Fig. 1.** Apparent total tract digestibility (ATTD) of P observed, adjusted for study effect, and simulated by the model. (Dashed line:  $\text{ATTD P observed} = -0.005 + 1.18 \text{ ATTD P simulated}$ ,  $\text{RMSE} = 0.05$ ,  $R^2 = 0.94$ , intercept and slope did not differ from 0 and 1 respectively; continuous line is  $Y = X$ ; each point represents one observation).

used for model development. The data base was composed from publications where the main sources of variation are plant and microbial (several origin) phytase and mineral P sources. The model accurately predicts pigs' apparent P digestibility, although it tends to underestimate observed values (Fig. 1). The model should be combined with a metabolic model to integrate the regulation of P and Ca metabolism before practical use.

**Key words:** Calcium, model, phosphorus, phytase, pigs

**Cromwell, G. L. 1996.** Metabolism and role of phosphorus, calcium, and vitamin D3 in swine nutrition. Pages 101–110 in M. B. Coelho and E. T. Kornegay, eds. Phytase in animal nutrition and waste management. BASF Corporation, Mount Olive, NJ.

**Kornegay, E. T. 2001.** Digestion of phosphorus and other nutrients: the role of phytases and factors influencing their activity. Pages 237–271 in M. R. Bedford and G. G. Partridge, eds. Enzymes in farm animal nutrition. CAB International, Wallingford, UK.

**Létourneau-Montminy, M. P., Jondreville, C., Lescoat, P., Pomar, C., Meschy, F., Bernier, J. F. and Sauvant, D. 2007.** First step of a model of calcium and phosphorus metabolism in growing pigs: Fate of ingested phosphorus in the stomach. *Livest. Prod. Sci.* **109**: 63–65.

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**Wise, A. 1983.** Dietary factors determining the biological activities of phytate. *Nutr. Abst. Rev.* **53**: 791–806.

**A modelling approach to evaluate the feeding of high sugar grasses to cattle: Nitrogen and methane.** J. L. Ellis<sup>1</sup>, A. Bannink<sup>2</sup>, J. Dijkstra<sup>3</sup>, A. J. Parsons<sup>4</sup>, S. Rasmussen<sup>4</sup>, G. R. Edwards<sup>5</sup>, E. Kebreab<sup>6</sup>, and J. France<sup>1</sup>. <sup>1</sup>Centre for Nutrition Modelling, Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, jellis@uoguelph.ca; <sup>2</sup>Animal Sciences Group, Animal Production, Wageningen University and Research Centre, Lelystad, the Netherlands; <sup>3</sup>Animal Nutrition Group, Wageningen University, Wageningen, the Netherlands; <sup>4</sup>AgResearch, Palmerston North, New Zealand; <sup>5</sup>Lincoln University, Lincoln, New Zealand; <sup>6</sup>Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada.

High-sugar grass varieties have received considerable attention for their potential ability to reduce nitrogen (N) excretion in cattle. However, feeding high-sugar grasses alters the pattern of rumen fermentation, and no studies to date have examined this strategy in terms of other environmental pollutants influenced by these patterns, such as methane (CH<sub>4</sub>). It is the purpose of this work to use modelling to evaluate the effect of high sugar grasses on CH<sub>4</sub> emission from dairy cattle. The data base consisted of four published studies for which high-sugar grasses were being evaluated for their effect on N excretion. Water-soluble carbohydrate (WSC) content of the diet ranged from 95 to 253 g kg<sup>-1</sup> DM, CP ranged from 115 to 263 g kg<sup>-1</sup> DM, and the WSC:CP ratio ranged from 0.4 to 2.0. The rumen model framework of Dijkstra et al. (1992) was used for this evaluation, as modified by Mills et al. (2001), Bannink et al. (2008), and Reijs (2007). Proc GLM in SAS was used to analyse the results with study as a fixed effect. Total N excretion was predicted well by the model, and decreased significantly as the WSC:CP ratio of the diet increased ( $P = 0.0002$ ). Simulated results show an increase in hexose available to amylolytic microbes, increased use of ammonia and soluble protein by these microbes, and subsequently lower loss of N from the rumen as ammonia. Simulated results also showed that predicted CH<sub>4</sub> increased from 6 to 7% of gross energy intake as the diet WSC:CP ratio increased from 0.4 to 2.0 ( $P = 0.013$ ). Simulated rumen fermentation reveals a shift in VFA profile, with an increase in acetate and butyrate and decrease in propionate (% of total VFA) ( $P < 0.05$ ) as the WSC:CP ratio increases. The predicted rumen pH (mean value 6.0) was not influenced by treatment ( $P = 0.955$ ). Predicted fractional solid and fluid passage rates increased slightly ( $P = 0.0038$ ) and decreased slightly ( $P = 0.01$ ), respectively. Increased acetate production was the result of sugar fermentation in the rumen, which VFA stoichiometry predicted to occur to a greater extent at higher rumen pH. Per gram of fermented matter, protein generates far less acetate

than WSC. The shift in VFA profile had a direct effect on the hydrogen balance sub-model used to predict CH<sub>4</sub> formation, and CH<sub>4</sub> increased as a result of this shift. Overall this project demonstrates the usefulness of modelling for hypothesis testing, and suggests that this potential N mitigation strategy may also increase CH<sub>4</sub> emission.

**Key words:** Methane, mechanistic modelling, nitrogen, sugar grass

**Bannink, A., France, J., López, S., Gerrits, W. J. J., Kebreab, E., Tamminga, S. and Dijkstra, J. 2008.** Modelling the implications of feeding strategy on rumen fermentation and functioning of the rumen wall. *Anim. Feed Sci. Technol.* **143**: 3–26.

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**Development and evaluation of a tool to sort feedlot beef cattle into uniform outcome groups.** R. D. Sainz<sup>1</sup>, L. G. Barioni<sup>2</sup>, F. R. C. Araujo<sup>3</sup>, and J. W. Oltjen<sup>1</sup>. <sup>1</sup>University of California, Davis, CA, USA, rdsainz@ucdavis.edu; <sup>2</sup>Embrapa Cerrados, Planaltina-DF, Brasil; <sup>3</sup>Aval Serviços Tecnológicos, Uberaba, MG, Brasil.

Feedlots allow beef cattle producers to “finish” animals, i.e., deposit primarily fat on and in the carcass, prior to harvest. Typically, this involves feeding high-energy (grain) diets for periods of 60 to 180 d. Ideally the final product is an animal that meets market specifications of weight and finish perfectly. Due to variability in genotype, previous nutrition, health status, etc., cattle entering and leaving the feedlot are often a heterogeneous lot. Therefore, producers market some animals that are too light and thin, and others that are too heavy and fat. In practice, feeders must sort heavy cattle, at a high cost of labour, stressed animals and lost productivity. We have developed a decision aid program that uses available starting information (breed type, sex, frame score, weight and fatness) and the Davis Growth Model (Oltjen et al. 1986; Sainz and Hasting 2000) to simulate each animal’s growth curve to achieve one or more pre-determined endpoints. This allows producers to sort cattle at the start of the feeding period based on expected days on feed. Recent field testing has shown that pens sorted in this manner upon feedlot entry are

more uniform and command higher prices at slaughter than cattle sorted visually.

**Key words:** Beef cattle, decision aid program, growth model

**Oltjen, J. W., Bywater, A. C., Baldwin, R. L. and Garrett, W. N. 1986.** Development of a dynamic model of beef growth and composition. *J. Anim. Sci.* **62**: 86–97.

**Sainz, R. D. and Hasting, E. 2000.** Simulation of the development of adipose tissue in beef cattle. Pages 175–182 in J. P. McNamara, J. France and D. Beever eds. *Modelling nutrient utilization in farm animals*. CABI Publishing, Wallingford, UK.

**Mechanistic model of methane emissions from anaerobic manure storage systems.** Q. Huang and E. Kebreab. National Centre for Livestock and Environment, Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada R3T 2N2, qiangh@cc.umanitoba.ca.

The Intergovernmental Panel on Climate Change (IPCC 2007) recommended an empirical model for estimating the amount of GHG emissions worldwide. However, due to its static nature and low resolution in geographic region and management practice, IPCC (2007) encourages countries and regions to develop their own country or region-specific models. This study develops a mechanistic model for estimating methane emissions from anaerobic manure storage systems. The model describes five biochemical steps, hydrolysis, acetogenesis, hydrogenogenesis, homoacetogenesis, hydrogen methanogenesis, and acetate methanogenesis, performed by four bacterial groups, acetogenic, hydrogenogenic, homoacetogenic, and methanogenic bacteria. The model was coded using the acsIX computer language (AEGIS Technologies Group Inc. AL). Most initial pool sizes were based on experimental values, but some were estimated through the optimization feature of acsIX. A fourth-order Runge-Kutta method with an integration step size of 0.05 d was used for numerical integration. An experiment with swine manure using batch reactors was conducted to generate data for evaluation and initial pool size estimation. The model simulated the time series of CH<sub>4</sub> production and VFA concentration of two batch anaerobic digesters well, which in both cases had a correlation coefficient higher than 0.90. Mean square prediction errors of CH<sub>4</sub> production and VFA concentrations were mainly due to random variation of observed data, confirming the good fit of the model. The model was sensitive to parameters describing the hydrolysis process and kinetics of acetogenic and acetate methanogenic bacteria. The measured experimental value of CH<sub>4</sub> emissions from the batch reactors was 78.3 g kg<sup>-1</sup> volatile solid (VS) over 146 d. Simulation based on the IPCC (2007) model predicted 260 g CH<sub>4</sub> kg<sup>-1</sup> VS (assuming

methane-producing potential ( $B_0$ ) = 0.48,  $T = 25^\circ\text{C}$ , and methane conversion factor = 80%), whereas a mechanistic model predicted 74.8 g  $\text{CH}_4 \text{ kg}^{-1}$  VS for the same period. Further work is being conducted to develop the model in order to account for periodic influx of substrate into the system.

**Key words:** Greenhouse gases, manure management, mechanistic model

**Intergovernmental Panel on Climate Change 2007.** 2006 IPCC guidelines for national greenhouse gas inventories: Volume 4, agriculture, forestry and other land use. IGES, Japan.

**Modelling the dynamics of ruminal acidosis.** D. Sauvant<sup>1,2</sup>, S. Giger-Reverdin<sup>1</sup>, and F. Meschy<sup>1</sup>. <sup>1</sup>INRA, UMR791 Physiologie de la Nutrition et Alimentation, 16 rue Claude Bernard, 75231 Paris Cedex 05, France, sauvant@agroparistech.fr; <sup>2</sup>AgroParisTech, 16 rue Claude Bernard, 75231 Paris Cedex 05, France.

Sub-acute ruminal acidosis (SARA) is one of the major nutritional disorders occurring in intensive ruminant production, particularly in high producing cows. Beyond experimentation, modelling is a way to progress in integration, updating and renewal of knowledge. Prediction of mean values of rumen pH is a well-studied issue. In contrast, SARA and the dynamics of pH (Pitt and Pell 1997) have been rarely modelled. The present aim was to underline the major issues dealing with modelling kinetics of pH and episodes of SARA.

*Dynamic empirical modelling.* Postprandial kinetics of pH have frequently been presented in the literature. In contrast, they have only seldom been modelled. A meta-analysis of 219 published kinetic curves, fitted by a 3rd degree polynomial, was performed and followed by a principal component analysis (Dragomir et al. 2008). Most of the curves were accurately fitted. The major cause of differences between pH kinetics was mean pH values which appeared closely related to items such as time under a given threshold, i.e., 6.0, or the area under it. The rate of pH decrease is also an important factor to be considered. The results of this meta-analysis are of interest. However they are limited by the diversity of the objectives of the selected publications and by the lack of consistent factors of variation and predictors among them.

*Dynamic mechanistic modelling.* Several levels of organisation and time scales can be chosen to build mechanistic models of dynamic aspects of acidosis (Sauvant et al. 2006). Three levels are proposed: (1) At the underlying level, the physico-chemical one, the major difficulty rests on the large differences in size and fractional turnovers between, on one hand, compartments of VFA and carbonates (0.05 to 0.15 mol  $\text{L}^{-1}$ ) and, on the other hand, the compartment of protons (around  $10^{-7}$  mol  $\text{L}^{-1}$ ). Therefore, except in the paper of Offner and Sauvant (2006), this last

compartment has been neglected, and published models are limited to capture of flows of  $\text{H}^+$  by  $\text{HCO}_3^-$  (Pitt and Pell 1997; Imamidoost and Cant 2005). Moreover, action of  $\text{HCO}_3^-$ , which is generally considered as the major buffering driving force in the rumen, is shared with the buffer action of VFA when acidosis becomes marked ( $\text{pH} < 5.6$ ). This dual control of pH has so far not been specifically modelled. (2) Postprandial kinetics of pH are largely determined by patterns of intake and rumination. As this principle has rarely been modelled (Sauvant et al. 1996; Imamidoost and Cant 2005), a dynamic model was developed to associate kinetics of DMI, chewing activities and rumen pH (Giger-Reverdin et al. 2009). This model is based on a simple compartment structure of digestion in the rumen and is controlled by a chewing behaviour sub-model, which controls buffer recycling through saliva. Preliminary results, obtained with dairy goats receiving an acidogenic diet, are promising despite difficulties in accurately representing individual variations. (3) Episodes of SARA, which last several days, have not been modelled until recently. A compartment model was built to fit kinetics of spontaneous SARA bouts using various factors measured on dairy goats receiving an acidogenic diet (rumen pH, DMI, milk yield, chewing activities, etc.). A first version of this model, recently published (Desnoyers et al. 2009), provided a dynamic description of SARA bouts over 20 d. These results indicate that pH kinetics in the rumen following a sudden load of rapidly fermentable carbohydrates do not match those of spontaneous SARA episodes. This piece of work demonstrates the possibilities and limits in modelling pH kinetics and episodes of SARA. However more work is needed before obtaining a mechanistic and integrated model of SARA.

**Key words:** Empirical modelling, mechanistic modelling, pH, sub-acute ruminal acidosis

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**Sauvant, D., Baumont, R. and Faverdin, P. 1996.** Development of a mechanistic model of intake and chewing activities in sheep. *J. Anim. Sci.* **74**: 2785–2802.

**Development of a linear programming model to estimate distribution of protozoa in the reticulo-rumen.** S. E. Hook<sup>1</sup>, J. Dijkstra<sup>2</sup>, and J. France<sup>1</sup>. <sup>1</sup>Centre for Nutrition Modelling, Department of Animal and Poultry Science, University of Guelph, Guelph, Ontario, Canada N1G 2W1, shook@uoguelph.ca; <sup>2</sup>Animal Nutrition Group, Wageningen University, PO Box 338, 6700 AH Wageningen, the Netherlands.

The flow of protozoa out of the reticulo-rumen is much less than expected from the total number of rumen protozoa present. This is due to selective retention of protozoa in the reticulo-rumen, which is necessary to maintain their numbers in the organ. Protozoa may be retained on feed particles (Orpin, 1985), as well as on the epithelium of the reticulo-rumen (Abe and Iriki, 1989). Although mathematical models of microbial contribution to rumen functioning have been developed (Dijkstra, 1994; Dijkstra et al. 2002), few have been designed to model protozoa in both the attached and free-living phases.

Czerkawski (1987) presented a model of protozoal flow from the rumen and suggested that the majority of protozoa are lost in the omasum, explaining the reduced numbers found in hindgut flow. Others have shown that this is not the case though (e.g. Leng, 1989; Towne and Nagaraja, 1990). In order to provide a more accurate representation of protozoa in the reticulo-rumen, taking into account the recent literature on sequestration, distribution, and generation times, a linear programming model was developed, of similar complexity to the model for enumerating anaerobic rumen fungi by France et al. (1990).

The model predicts relative proportions of protozoa in the free-living and attached phases of the reticulo-rumen in a quasi-steady state system. Inputs included specific growth rate and specific death rate of protozoa in the free-living and attached phase, rate of passage of protozoa from to the omasum in the free-living and attached phase, rate of transfer between the two phases, and mean retention time of protozoa in the free-living and attached phase. Bounds on each parameter were determined based on a thorough examination of the literature, focusing on protozoa in the rumen of healthy cattle and sheep consuming commonly fed diets, and other constraints

imposed. Anticipated application of this model is to determine the distribution of protozoa in the reticulo-rumen when ruminants are fed hay-based and grain-based diets, with differences between the diets being reflected in the number of protozoa found in each phase.

**Key words:** Linear programming, protozoa, reticulo-rumen, sequestration

**Abe, M. and Iriki, T. 1989.** Mechanism whereby holotrich ciliates are retained in the reticulo-rumen of cattle. *Br. J. Nutr.* **62**: 579–587.

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**Multi-criteria models for estimating nutrient requirements in young pigs.** A. B. Strathe<sup>1</sup>, J. Vinther<sup>2</sup>, and E. Kebreab<sup>3</sup>. <sup>1</sup>Section of Nutrition, Department of Basic Animal and Veterinary Sciences, Faculty of Life Sciences, University of Copenhagen, DK-1870, Frederiksberg, Denmark, strathe@life.ku.dk; <sup>2</sup>Danish Pig Production Association, Axelborg, Denmark. <sup>3</sup>Department of Animal Science, University of Manitoba, Winnipeg, Manitoba, Canada R3T 2N2.

The essential amino acid tryptophan (TRP) is known to play important biological roles. Apart from its incorporation into body proteins, TRP is the precursor for synthesis of serotonin, an important neurotransmitter associated with mood, sleep and appetite regulation (Le Floch and Seve 2007). Moreover, utilization of growth rate as the single criterion for setting the TRP requirement may not give the full picture due to multiple effects of TRP. The objective of the present study was to develop multi-criteria models for estimating TRP requirements for young pigs that use information in

multiple responses simultaneously. Average daily gain (ADG) and feed intake (FI) data from 21 studies (92 treatment means) on TRP requirements in young pigs weighing from 5–40 kg BW were collated in a data base. The dosage variable was expressed as the ratio of TRP to lysine. In the current study, linear (LBL) and quadratic (QBL) broken-line functions were used to estimate the TRP requirement (Robbins et al. 2006). The multi-criteria models were fitted by stacking the responses into a common vector and constructing an indicator variable flagging the different responses. Furthermore, it is also necessary to have a statistical model with different residual variances because different responses may have different variances. The study effect was considered random, which was included by adding a study effect to the plateau parameter in the statistical models. The BW variable is dichotomized because the studies were conducted in BW ranges 5–11 and 22–38 kg BW and thus BW was expressed as a categorical variable. The statistical models were implemented in the %NLINMIX macro (SAS Institute, Inc.), where GROUP option in the REPEATED statement is used to specify different residual variances for the responses (Thiébaud et al. 2002). The results of the analysis are presented in Table 1. Single-criteria analyses reveal that there was no effect of BW on the requirement ( $P > 0.05$ ) and thus the requirements presented in Table 1 are for the entire BW range. Furthermore, it was also shown that the requirement depends on both the biological response and the model used to estimate the requirement. Table 1 shows the sum of  $-2\log$  likelihood ( $1043.6 + 1150.5 = 2194.1$ ) for QBL single-criteria models, which equals the multi-criteria QBL1 model (2194.2) when no correlation between the responses and random effects are modelled. Thus, the estimation scheme for the multi-criteria models behaved as expected. Introducing covariance between random plateaus estimates (ADG and FI) further improves the fit to data ( $-2\log$  likelihood = 2182.7). Under practical feeding conditions multiple requirements are not possible and thus a

combined requirement can be estimated by introducing a common requirement parameter in the QBL multi-criteria model (QBL3). The TRP requirement amounts to 20% (SE: 1.2) of lysine.

**Key words:** Multi-criteria models, nutrient requirements

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**Fractional protein synthesis and degradation rates in jejunal epithelial cells along the crypt-villus axis are simultaneously measured in vitro after an intraperitoneal injection of a flooding dose of L-[ring- $^2$ H $_5$ ]phenylalanine in fed weanling piglets.** X. Yang, L. Liu, D. Lackeyram, T. C. Rideout, Y. Shen, K. Swanson, J. France, and M. Z. Fan. Centre for Nutrition Modelling, Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada N1G 2W1, yang@uoguelph.ca.

Gut mucosal protein turnover, including protein synthesis and degradation, contributes significantly to whole body energy and nitrogen homeostasis and requirements. Primary intestinal epithelial cells are isolated and incubated in vitro for investigation of amino acid metabolism and target gene and protein expressions. This study measured in vivo fractional protein synthesis rates (FSR) in the proximal and the distal jejunum as well as FSR and fractional protein degradation rates (FDR) in vitro in epithelial cells during incubation for the cell isolation from the small intestinal crypt-villus axis in piglets. Six post-weaning gilts at the age of 28 d were given an intraperitoneally flooding dose of phenylalanine (Phe) containing L-[ring- $^2$ H $_5$ ]Phe in saline (Bregendahl et al. 2008). Harvested proximal and distal jejunal segments were incubated and 12 epithelial cell fractions were isolated along the crypt-villus axis from the gut segments with the distended sac method (Fan et al. 2004). Viability of the isolated cells was monitored (90%) by the trypan blue exclusion method. Isotopic Phe enrichments in samples were analyzed with gas chromatography-mass spectrometry (Fan et al. 2006). The isotopic Phe enrichments in the plasma and the jejunal tissue free pools were flooded at 25–27 molar%. The in vivo FSR (%/d, mean  $\pm$  SE,  $n = 6$ ) was lower in the proximal ( $30.03 \pm 2.97$ ) than in the distal jejunal ( $39.72 \pm 2.61$ ) segment. Intracellular isotopic Phe enrichments in the bound pool ( $E_{\text{Bound } t}$ , molar%) of the 12 collected cell fractions increased with time ( $t$ , min) during the in vitro incubation and isolation and could be described by  $E_{\text{Bound } t} = a + b \times (1 - e^{(-\text{FSR} \times t)})$

**Table 1.** Fit statistics ( $-2\log L$ :  $-2$  log likelihood and BIC: Bayesian information criteria) for linear (LBL) and quadratic (QBL) broken line functions, which are used either as single or multi-criteria models. The requirement for tryptophan, which is expressed as the ratio of tryptophan to lysine, is also given

Model	Criteria	$-2\log L$	BIC	Requirement, [est; SE]
Single-LBL	ADG	1049.7	1071.0	[0.172; 0.0056]
Single-QBL	ADG	1043.6	1064.9	[0.208; 0.0111]
Single-LBL	FI	1150.6	1171.9	[0.159; 0.0069]
Single-QBL	FI	1150.5	1171.9	[0.190; 0.0131]
Multi-QBL1	ADG + FI	2194.2	2236.8	[0.208; 0.0111], [0.190; 0.0130]
Multi-QBL2	ADG + FI	2182.7	2228.3	[0.210; 0.0111], [0.190; 0.0131]
Multi-QBL3	ADG + FI	2185.9	2228.5	[0.202; 0.0119]

for each of the pigs. Curve fitting (parameter estimate mean  $\pm$  SE,  $n=6$ ) showed  $E_{\text{Bound } t} = 0.5546 + 0.4616 \times (1 - e^{(-0.0168 \times t)})$  for the proximal and  $E_{\text{Bound } t} = 0.5463 + 1.3640 \times (1 - e^{(-0.0136 \times t)})$  for the distal segment, with FSR (%/d, mean  $\pm$  SE,  $n=6$ ) being  $24.19 \pm 4.84$  and  $19.58 \pm 11.67$  for the proximal and the distal intestinal segments, respectively. The model of  $E_{\text{Free } t} = c + d \times e^{(-\text{FDR} \times t)}$  was used to describe isotopic Phe enrichments ( $E_{\text{Free } t}$ , molar%) in the free pools of the 12 collected cell fractions that decreased with time ( $t$ , min) for each of the pigs [for the proximal segment:  $E_{\text{Free } t} = 4.7721 + 16.6540 \times e^{(-0.0286 \times t)}$ ; for the distal segment:  $E_{\text{Free } t} = 6.5243 + 11.1961 \times e^{(-0.0306 \times t)}$ ; parameter estimate mean  $\pm$  SE,  $n=6$ ]. The FDR (%/d, mean  $\pm$  SE,  $n=6$ ) was estimated to be  $41.11 \pm 4.12$  and  $44.02 \pm 5.12$  in the proximal and the distal jejunal segments, respectively. Epithelial FDR estimates were about twofold higher than ( $P=0.0541$  and  $P=0.0346$ ) the FSR estimates in vitro in both intestinal segments. In conclusion, intestinal epithelial FSR and FDR can be measured simultaneously in vitro from individual test animals when isotopic amino acid enrichment in both the free and bound pools is monitored continuously for a suitable length of time for kinetic analysis. Gut epithelial FSR and FDR estimated in vitro were associated with a large variability among individual test animals. Isolated intestinal epithelia are likely associated with enhanced protein catabolism during their isolation and incubation in vitro.

**Key words:** Fractional protein degradation rates, fractional protein synthesis rates, intestinal epithelia, stable isotopes, weanling pigs

**Bregendahl, K., Yang, X., Liu, L., Yen, J. T., Rideout, T. C., Shen, Y., Werchola, G. and Fan, M. Z. 2008.** Fractional protein synthesis rates are similar when measured by intraperitoneal or intravenous flooding doses of L-[ring- $^2\text{H}_5$ ]phenylalanine in combination with a rapid regimen of sampling in piglets. *J. Nutr.* **138**: 1976–1981.

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**Fan, M. Z., Matthews, J., Etienne, N. M. P., Stoll, B., Lackeyram, D. and Burrin, D. G. 2004.** Expression of brush border L-glutamate transporters in epithelial cells along the crypt-villus axis in the neonatal pig. *Am. J. Physiol.* **287**: G385–G398.

**A global sensitivity analysis using Advanced Continuous Simulation Language to assess parameters in a rodent model of protein turnover.** H. A. Johnson, C. C. Calvert, and J. G. Fadel. Department of Animal Science, University of California, Davis, CA 95616, USA, hajohnson5@aim.com.

The measurement of protein fractional synthesis rate is based on the measured specific radioactivities of tracer

amino acids. To examine the impact of three dosing methods on changes in specific radioactivities of free amino acids (S14Aa) and protein (S14Pb), a mechanistic, theoretical model of protein turnover for a non-growing 30 g mouse has been developed for the flooding dose, continuous infusion and pulse dose methods. The model consists of three protein pools turning over at fast (49  $\mu\text{moles Leu}$ ,  $t_{1/2} = 1.2$  h), medium (440  $\mu\text{moles Leu}$ ,  $t_{1/2} = 6$  h) or slow (490  $\mu\text{moles Leu}$ ,  $t_{1/2} = 24$  h) rates and small (0.13  $\mu\text{moles Leu}$ ) and large (4.1  $\mu\text{moles Leu}$ ) amino acid pools which exchange amino acids. Using the Fourier amplitude sensitivity test (FAST; Saltelli et al. 1999) and a local sensitivity analysis in ACSL, sensitivity analyses were performed to assess the impact of the three protein pools that turnover at different rates on estimated S14Aa and S14Pb. Local and global sensitivity analyses yielded different results. For the flooding dose method, S14Aa and S14Pb were more sensitive to the rate of protein synthesis in the fast and medium protein turnover pools (sensitivity coefficients ranging from 0.05 to 0.5) using the FAST method. However local sensitivity analysis suggested that S14Aa and S14Pb were more sensitive to the protein synthesis rate of the slow protein pool. For the continuous infusion method using FAST, S14Aa was most sensitive to the medium rate protein pool and S14Pb was most sensitive to the fast turnover pool in the first 8 min until both specific radioactivities reached plateau (sensitivity coefficients ranging from 0.03 to 0.22 for FAST). Sensitivity coefficients using local sensitivity analysis for the continuous infusion method implied that S14Aa and S14Pb were most sensitive to protein synthesis rate of the slow protein pool also in the first 8 min until both specific radioactivities reached plateau. For the pulse dose method using FAST, S14Aa and S14Pb were most sensitive to the medium protein synthesis rate (sensitivity coefficients ranging from 0.025 to 0.5) whereas using the local sensitivity analysis, S14Aa and S14Pb were most sensitive to the slow protein pool turnover rate. Based on this analysis, global sensitivity analysis does yield different results from local sensitivity analyses and S14Aa and S14pb are sensitive to different parameters when using different dosing methods. Sensitivity analysis can help identify measurements critical to understanding protein turnover.

**Key words:** Global sensitivity, local sensitivity, Fourier amplitude sensitivity test, rodent, protein turnover

**Saltelli, A., Tarantola, S. and Chan P. S. 1999.** A quantitative model-independent method for global sensitivity analysis of model output. *Technometrics* **41**: 39–56.

**Reconstruction of metabolic pathways for the cattle genome: Toward bovine systems biology.** S. Seo<sup>1</sup> and H. A. Lewin<sup>2, 1</sup>. Division of Animal Science and Resource, Chungnam National University, Daejeon 305–764,

Korea, swseo@cnu.kr; <sup>2</sup>Department of Animal Sciences, University of Illinois at Urbana-Champaign, Urbana, IL 61801, USA.

Understanding the biology of cattle, particularly the unique features of ruminant metabolism, is a prerequisite to be able to work on the sustainability of the cattle industry. However, many gaps still exist in our understanding of ruminant metabolism and economic traits including milk and meat production, disease resistance, feed efficiency and reproductive performance. The recent sequencing of the cattle genome (Bovine Genome Sequencing and Analysis Consortium 2009) provides the first opportunity to systematically link genetic and metabolic traits of cattle. Metabolic reconstruction of a sequenced genome is a necessary step toward understanding the metabolism and underlying mechanism of metabolic regulation. The aims of this study were, thus, to reconstruct conserved metabolic pathways in the cattle genome and to identify metabolic pathways with missing genes and proteins. For this purpose, an amalgamated cattle genome data base was created using the NCBI and Ensembl cattle genome data bases (based on build 3.1) as data sources. The MetaCyc data base and Pathway-Tools were used to create a cattle-specific pathway genome data base, which was followed by comprehensive manual curation for the reconstruction of metabolic pathways. The curated database, CattleCyc (<http://biocyc.org/CATTLE/>) 1.0, consists of 217 metabolic pathways (Table 2). A total of 64 mammalian-specific metabolic pathways were modified from the reference pathways in MetaCyc, and two pathways previously identified but missing from MetaCyc were added. Comparative analysis of metabolic pathways revealed the absence of mammalian genes for 22 metabolic enzymes whose activity was reported in the literature. Comparative metabolic analysis of the cattle, *E. coli* and human demonstrated a strong degree of conservation among the comprehensive set of genes involved in core metabolism, which includes tRNA charging, nucleotide sugar biosynthesis, pyrimidine ribonucleotide biosynthesis, fatty acid  $\beta$ -oxidation and biosynthesis, glycogen degradation, co-enzyme A biosynthesis, and non-oxidative pentose phosphate pathway. We also identified six human

metabolic protein-coding genes for which the cattle ortholog is missing from the sequence assembly. In conclusion, CattleCyc is a powerful tool for understanding the biology of cattle and other ruminants. Having well-annotated genomes from many mammalian species hosted in BioCyc will facilitate the comparative analysis of metabolic pathways among different species and a systems approach to comparative physiology.

**Key words:** Bovine genome, metabolic reconstruction, systems biology

**Bovine genome sequencing and analysis consortium. 2009.** The genome sequence of Taurine cattle: a window to ruminant biology and evolution. *Science* **324**: 522–528.

**Using bioeconomic modelling to assess two distinct group-housing systems for breed-to-wean sow operations.** M. A. Fynn<sup>1</sup>, N. J. Lewis<sup>2</sup>, M. L. Connor<sup>2</sup>, and G. V. Johnson<sup>1</sup>. Departments of <sup>1</sup>Agribusiness and Agricultural Economics, <sup>2</sup>Animal Science, University of Manitoba, Winnipeg, MB, Canada R3T 2N2, umfynn@cc.umanitoba.ca.

With the North American pork industry moving away from the use of individual sow stalls, it becomes critical to investigate the economic feasibility of various group-housing systems. This ensures that sow operation managers can make informed decisions regarding barn design and management. The objective of this research was to compare profitability between two distinct group-housing systems for gestating sows, and to formulate a profit function that accurately simulates and compares these operations. Data were collected from two 144-head farrow-to-finish sow barns in southern Manitoba, one barn housing their pigs on partially-slatted concrete flooring (CONV) and the other on straw-based solid floors (ALT). Sixty dams were followed in each respective barn from entry as gilts until culling (or the end of the trial period); the trial ran from March 2006 until April 2009. Data included production records – parity, weaned litter weights, medication application, feed intake, and insemination usage – reflecting production inputs and outputs. From these data, an entire breed-to-wean barn model was aggregated from an individual sow model – estimated using regression analysis in SAS – and simulated using STELLA software:

$$\pi = \sum_i \sum_t (\beta^t [p \cdot q^i(t) - c^h \cdot x^{ih} - k^i(t) \cdot c^r(t)]) - c^j \cdot x^j$$

where  $\pi$  is the operation's profit,  $\beta^t$  is the discrete discount factor, i.e.  $(1/1+r)^t$ ,  $r$  is the discrete discount rate,  $p$  is the market price of weanlings,  $q^i(t)$  is the production function of weanlings (at time  $t$ ) from individual sow  $i$ ,  $c^h$  cost of input  $h$ ,  $x^{ih}(t)$  is the quantity of input  $h$  for dam  $i$ ,  $k^i(t)$  is the (binary) cull factor for dam  $i$ ,  $c^r(t)$  is the cost of replacement (purchase/rearing

**Table 2. Comparison of selected organism-specific pathway genome databases**

Database statistics	CattleCyc	EcoCyc	HumanCyc
Metabolic pathways	217	194	178
Enzymatic reactions	1,419	1,245	1,253
Enzymes	1,544	1,323	2,594
Compounds	1,021	1,202	975
Pathway holes (missing enzymes)	–	–	–
Number of pathway holes	113	35	246
Pathway holes as a percentage of total reactions in pathways	14%	5%	36%

of gilt minus sow salvage value),  $c^j$  is the cost of the fixed input  $j$ , and  $x^j$  is the quantity of the fixed input  $j$  incl. purchase and rearing costs of initial gilts.

The production function was estimated in a squared flexible form with independent variables: dams' parity, medications, inseminations, and feed intake. Biological condition data were also collected on the individual animals including backfat depths, body condition scores (BCS), gait scores, and functional teats to estimate the binary cull factor using PROC PROBIT. The entire model allowed for a relative economic comparison between the two barns. Culling was strongly influenced by parity in both barns ( $P < 0.05$ ), and by backfat and gait score in CONV ( $P < 0.05$ ). Poor-condition sows were less likely to recover in CONV as compared with ALT due to harsher living conditions. The production function was explained most strongly by the barn type as well as the feed intake during the lactation period ( $P < 0.05$ ). Profitability had a higher trend in ALT as compared with CONV when considering endogenous inputs and culling rates as the production costs ( $P < 0.1$ ). Since average production per sow per time period in both barns is similar ( $P > 0.1$ ), the difference in profitability can be attributed to increased culling in earlier parities in CONV. Early culling prevents otherwise productive sows from reaching their peak production potential at around three to four parities. The ALT system seems to be more profitable than the CONV system, but a more-thorough simulation model that considers manure management, risk, and environmental components would benefit these analyses.

**Key words:** Bioeconomic modelling, breed-to-wean sow operations, group-housing systems, production function

**Evaluation of functions to predict phosphorus retention in post-weaned pigs.** R. S. Dias<sup>1</sup>, J. Chen<sup>1</sup>, J. L. Ellis<sup>1</sup>, S. Lopez<sup>2</sup>, D. M. S. S. Vitti<sup>3</sup>, E. Kebreab<sup>4</sup>, M. Z. Fan<sup>1</sup>, and J. France<sup>1</sup>. <sup>1</sup>Centre for Nutrition Modelling, Department of Animal and Poultry Science, University of Guelph, Guelph, Ontario, Canada N1G 2W1, rsouza@uoguelph.ca; <sup>2</sup>Dept. Produccion Animal, Facultad de Veterinaria, Universidad de León, 24007 León, Spain; <sup>3</sup>Centro de Energia Nuclear na Agricultura,

Piracicaba, SP, Brazil; <sup>4</sup>Department of Animal Science, University of Manitoba, Winnipeg, Manitoba, Canada R3T 2N2.

A data base on P balance was built up using 376 observations from 23 experiments with weanling piglets of initial weight between 6 and 17 kg. The data base contained information on diet, dietary P intake, BW, P excreted in faeces and P retention. The parameter estimates obtained by Schulin-Zeuthen et al. (2007) for the functions straight line (SI), monomolecular (M), Gompertz (G) and Richards (R) after fitting P retention (Pret) vs. total or available P intake were used to predict P retention in the piglet data set and the functions were further evaluated. The P retentions predicted from total P intake were compared with observed values using mean square prediction error (MSPE) and concordance correlation coefficient (CCC). The MSPE values were 0.008, 0.063, 0.014 and 0.014 whereas CCC values were 0.78, 0.31, 0.64 and 0.57 for SI, M, G and R, respectively. Both statistics showed that the straight line equation resulted in the best relationship between predicted and observed values. When P retention was predicted from available P intake, comparison between predicted and observed P retention values resulted in MSPE values of 0.005, 0.121, 0.016 and 0.014 and CCC of 0.89, 0.06, 0.59 and 0.67 for SI, M, G and R, respectively. These results confirmed that SI was the best equation to predict P retention from available P intake. In conclusion, the monomolecular equation obtained by Schulin-Zeuthen et al. (2007) was not a suitable predictor of P retention in weanling piglets, whereas the straight-line provided a feasible prediction of P retention from total or available P intake and may be used as a starting point when studying P utilization in post-weaned pigs.

**Key words:** Growth functions, P balance, post-weaned pigs

**Schulin-Zeuthen, M., Kebreab, E., Gerrits, W. J. J., Lopez, S., Fan, M. Z., Dias, R. S. and France, J. 2007.** Meta-analysis of phosphorus balance data from growing pigs. *J. Anim. Sci.* **85**: 1953–1961.