10.1071/ANv54n12abstracts

8th International Workshop on Modelling Nutrient Digestion and Utilisation in Farm Animals

Extended Abstracts

The following one-page abstracts summarise papers presented at the Workshop in addition to those published as peer-reviewed research papers or reviews in the Special Issue of *Animal Production Science* Volume 54, Issues 11–12. Their sequence and organisation into four major topic areas follows the order of presentation at the Workshop. These abstracts have not been independently peer-reviewed for science quality but have been edited for form of presentation and clarity of content.

Topic: Digestion, metabolism and consequences for productivity

A model of phosphorus utilization in lactating dairy cattle

J. Dijkstra[A,E]*, J. France*[B]*, A. Bannink*[C]*, J.L. Ellis*[A]*, E. Kebreab*[D]*, R.M.A. Goselink*[C] *and G. Klop*[A]

[A]Animal Nutrition Group, Wageningen University, 6700 AH Wageningen, the Netherlands. [B]Centre for Nutrition Modelling, University of Guelph, Guelph N1G 2W1, Canada. [C]Animal Nutrition, Wageningen UR Livestock Research, 6700 AH Wageningen, the Netherlands. [D]Department of Animal Science, University of California, Davis, CA 95616, USA.

Introduction

To address global concerns about phosphorus (P) needs and P pollution, the objective of the present study was to evaluate the impact of various dietary factors and milk composition on P excretion from dairy cattle using a mechanistic model of P digestion and metabolism.

Methods

The model is a development of that by Hill *et al.* (2008). In their model, P is present in three forms (Pi, inorganic P; Pt, phytic acid P; Po, organic non-phytic acid P). Only Pi is absorbed from the gut. After absorption, Pi may be recycled to the rumen via saliva, excreted in milk and in urine, or used for bone P accretion. The major modifications to this model include: fractional fluid passage rate, salivation rate, and Pi utilization for microbial growth being related to dietary characteristics; absorption of Pi from the gut, excretion of absorbed Pi to urine, and net utilization of Pi for bone synthesis being dependent on plasma Pi concentration; and P content of milk being related to milk protein and lactose content as derived by Klop *et al.* (2014).

Results and discussion

As expected, dietary P content has a major effect on P excretion (Table 1). The Pt fraction, NDF content, fermentable OM content, and roughage proportion of the diet hardly changed P excretion. Reduced protein and lactose content of milk, and increased feed intake and milk production level, resulted in decreased and increased total tract P digestibility, respectively. These preliminary results indicate no or limited impact of diet composition (except for dietary P content) and significant impact of milk production and composition on reduction of P excretion in manure.

Table 1. Sensitivity of P digestion and excretion to changes in key model parameters

Parameter	Change	P flow (g/d)			P digestibility	Milk P output
		Faeces	Urine	Milk	(% of P intake)	
Default	-	40.4	1.6	23.0	40.9	33.6
P content (g/kg DM)	3.8 → 3.4	34.8	1.5	23.0	43.1	37.6
NDF content (g/kg DM)	380 → 480	40.7	1.6	23.0	40.5	33.6
Fermentable OM (g/g)	0.55 → 0.45	40.2	1.6	23.0	41.3	33.6
Fraction Pt of total P (g/g)	0.24 → 0.12	40.3	1.6	23.0	41.2	33.6
Milk protein / lactose (g/kg)	35 / 45 → 33 / 44	41.5	1.7	21.5	39.4	31.4
Intake / milk prod. (kg/day)	18 / 23 → 19 / 25	42.3	1.6	25.0	41.4	34.6

References

Hill SR, Knowlton KF, Kebreab E, France J, Hanigan MD (2013) A model of phosphorus digestion and metabolism in the lactating dairy cow. *Journal of Dairy Science* **91**, 2021–2032.

Klop G, Ellis JL, Blok MC, Brandsma GG, Bannink A, Dijkstra J (2014) Variation in phosphorus content of milk from dairy cattle as affected by differences in milk composition. *Journal of Agricultural Science*, DOI: 10.1017/S0021859614000082.

[E]Corresponding author: jan.dijkstra@wur.nl

Topic: Digestion, metabolism and consequences for productivity

Methane production and hydrogen dynamics in dairy cattle: a model of rumen metabolic pathways

H.J. van Lingen[A,B,E]*, L.E. Moraes*[C]*, A. Bannink*[D]*, E. Kebreab*[C] *and J. Dijkstra*[B]

[A]TI Food and Nutrition, Wageningen, The Netherlands, P.O. Box 557, 6700 AN. [B]Animal Nutrition Group, Wageningen University, Wageningen, The Netherlands, P.O. Box 338, 6700 AH. [C]Department of Animal Science, University of California, Davis, CA 95616, USA. [D]Wageningen UR Livestock Research, P.O. Box 65, 8200 AB, Lelystad, The Netherlands.

Introduction

Mechanistic models have been developed to describe fermentation and digestion in the gastrointestinal tract of cattle. Dijkstra *et al*. (1992) developed a rumen model representing microbial growth and nutrient degradation to end products such as volatile fatty acids (VFA). This model accurately predicted the total VFA production, rather than the proportions of the individual VFA. Mills *et al*. (2001) extended the model of Dijkstra *et al*. (1992) by representing methane (CH_4) production. The metabolic balance equations of Baldwin (1995) were used to predict CH_4 production from the net hydrogen (H_2) yield from among others the type and amount VFA produced. Bannink *et al*. (2011), after implementing a reconsidered approach of the VFA molar proportions, indicated a 15% uncertainty of predicted CH_4 caused by factors like the model representation. None of these models contained a fully mechanistic representation of rumen metabolic pathways and methanogenesis. The aim of this study was to develop a full mechanistic representation of VFA production pathways, H_2 yield and methanogenesis by rumen microbes.

Methods

The mechanistic model contains state variables for cellulolytic hexose, amylolytic hexose, cellulolytic pyruvate, amylolytic pyruvate, cellulolytic microbes, amylolytic microbes, acetate, propionate, butyrate, H_2 and methanogens, and a zero-pool for CH_4. Flux equations are described by Monod and mass-action forms.

Results and discussion

This model permits the interpretation and quantification of rumen metabolic pathways yielding acetate, propionate, butyrate, H_2 and CH_4. Predicted propionate and CH_4 yield per unit of feed increased and decreased, respectively, in response to higher hexose inflow, which reflects a diet with more rapid degradable carbohydrates. Further, improvement of predicted CH_4 production might be achieved to extend the model with a separate state variable for protozoa, affecting the partition of the metabolic pathways. The present modelling effort provided the integration of existing knowledge on rumen metabolic pathways and reproduced observations on VFA profile and CH_4 production.

References

Baldwin RL (1995) Modelling Ruminant Digestion and Metabolism. Chapman and Hall, London.

Bannink A, Schijndel MW van, Dijkstra J (2011) A model of enteric fermentation in dairy cows to estimate methane emission for the Dutch National Inventory Report using the IPCC Tier 3 approach. *Animal Feed Science and Technology* **166-167**, 603-618.

Dijkstra J, Neal HDSC, Beever DE, France J (1992) Simulation of nutrient digestion, absorption and outflow in the rumen: model description. *The Journal of Nutrition* **122,** 2239-2256.

Mills JAN, Dijkstra J, Bannink A, Campbell SB, Kebreab E, France J (2001) A mechanistic model of whole-tract digestion and methanogenesis in the lactating dairy cow: model development, evaluation, and application. *Journal of Animal Science* **79**, 1584-1597.

[E]Corresponding author: henk.vanlingen@wur.nl

Topic: Digestion, metabolism and consequences for productivity

Addition and evaluation of amino acid response equations in the NRC (2012) swine growth model

S. Ghimire[A,C], *C.F.M. de Lange*[B], *A.J. Myers*[A] *and M.D. Hanigan*[A]

[A]Virginia Polytechnic Institute and State University, Blacksburg, VA 24061, USA. [B]University of Guelph, Guelph, Ontario, N1G 2W1, Canada.

Introduction

The NRC nutrient requirement model for swine (NRC 2012) does not predict animal responses to varying nutrients in the diet. The amino acids (AA) requirements in the model are predicted by broken line linear plateau regression methods using amino acid requirement studies. We reconstructed the growing-finishing swine model of NRC (2012) and modified it to include AA responses. The objective of this study was to evaluate the newly revised AA response equations.

Methods

The AA response equations were derived after considering AA utilization efficiency, AA growth composition, and AA available from the diet for each AA. Gender specific equations were used to calculate maximum protein deposition (Pd_{max}) as described in NRC (2012). Predicted protein deposition was taken as the minimum of that allowable from dietary AA, energy supply, and Pd_{max}. A total of 22 publications reporting growth performance on varying lysine concentrations and energy were used to create a dataset for evaluation purposes. The publications were a subset of those used by the NRC (2012) committee for the lysine requirement model. The reported ingredient compositions of the diets for each treatment were used to predict standard ileal digestible (SID) AA and metabolizable energy (ME) based on the NRC (2012) feed ingredient library. The final dataset contained 335 treatment means. The initial body weight (BW) of the animals ranged from 5.5 to 104 kg, ME in the diet ranged from 2308 to 3733 kcal/kg BW, and the SID lysine concentrations were from 0.3 to 1.8% of diet. Evaluations were conducted with 2 scenarios: one with adjustment for bias among locations and pig lines, and the other without any adjustment.

Results and discussion

The results of evaluations revealed that the root mean squared prediction errors (RMSPE) as a percentage of the observed means for average daily gain (ADG) and final body weight were 9% and 21%, respectively, before bias adjustment and 5% and 11%, respectively, after the adjustment. Mean bias associated with final body weight prediction was reduced after the adjustment (35 to 1% of MSPE). The RMSPE for daily feed intake was 24% before the adjustment and 19% after adjustment. The residuals plotted against initial body weight did not show significant correlations indicating that the initial body weight of the animal did not affect predictions. Similarly, residuals were not significantly correlated with dietary ME content or SID lysine concentration which showed that the model predicted the nutritional response with good accuracy.

References

NRC (2012) 'Nutrient requirements of swine.' (The National Academies Press: Washington, D.C.)

[C]Corresponding author: sand72@vt.edu

Topic: Digestion, metabolism and consequences for productivity

Environmental stress effects on swine maintenance energy requirements

R.R. White[A,B] *and M.D. Hanigan*[A]

[A]Department of Dairy Science, Virginia Tech, Blacksburg, VA, USA.

Introduction

Increasing climate variability, population growth, and decreasing resource availability necessitate improvement of livestock production efficiency during environmental stress. Temperature is known to affect energy metabolism and balance; however, the NRC (2012) predictions of maintenance only account for cold stress. The objective of this study was to fit adjustment factors for the allometric energy constant used in the NRC maintenance equation to better account for the effects of cold and heat stress and animal performance on maintenance energy requirements (ME_m) of growing pigs.

Methods

A literature search was used to identify 13 studies reporting 104 treatment means measuring metabolizable energy intake (MEI), heat production (HP), temperature (T), and average daily gain (ADG). The average allometric ME_m constant (a_g) based on body weight (BW) was estimated by:

$$ln(HP)/BW^{0.6} = a_g + b*ln(MEI)/BW^{0.6}, \quad [1]$$

with parameters fitted by regression using data from the literature search. Assuming the slope was valid across studies, an estimate of the intercept value, a_i, was calculated for each treatment:

$$ln(HP)/BW^{0.6} - b*ln(MEI)/BW^{0.6} = a_i \quad [2]$$

Differences between a_i and a_g (e) represented maintenance variation among treatments including variation associated with temperature stress. These differences were regressed on T and ADG to yield different equations to predict e that could be used to adjust baseline ME_m:

$$ME_m = \exp(a_g+e)*BW^{0.6} \quad [3]$$

$$e = c1 + c2*ADG + c3*T + c4*T^2 \quad [4]$$

$$\text{IF}(T > \text{LCT}), \text{THEN } e = c1 + c2*ADG+c3*T+c4*T^2, \text{ELSE } e = c5 + c6*ADG + c7*T \quad [5]$$

Results

The estimate of a_g was 830 kJ/kg $BW^{0.6}$ which was similar to the NRC value of 824 kJ/kg $BW^{0.6}$. Residual analyses showed that ME_m was over-predicted at high T or high ADG and under-predicted at low T and ADG (slope bias). Values of e predicted by equation 4 (c1 = 0.233; c2 = -0.007; c3 = -0.019; c4 = 0.0003) eliminated the slope bias, reduced prediction error and improved concordance of the ME_m prediction. Comparing the heat-stressed and cold-stressed portions of equation 5 (c1 = 0.101; c2 = 0.012, c3 = -0.012; c4 = 0.002; c5 = 0.180; c6 = -0.108; c7 = -0.005) revealed that low-ADG animals were more prone to cold stress and less affected by heat; however, coefficients were not statistically different from 0 indicating inadequate data to identify the model.

Conclusions

The bias adjustment factors predicted by the CQ model provide a useful, practical addition to the swine NRC (2012) for researchers interesting in predicting swine responses to both heat and cold stress. Although the DQL model highlights interesting and expected interactions between production stage and ambient temperature, further data is needed to reliably specify this relationship.

References

National Research Council (NRC) (2012) 'Nutrient requirements of swine: 10th revised edition.' (National Academies Press: Washington, DC)

[B]Corresponding author: rrwhite@vt.edu

Topic: Digestion, metabolism and consequences for productivity

Determination of parameters for modelling the maintenance requirement and performance of broiler chickens challenged by enteric bacteria

A. Remus[A], *L. Hauschild*[A,B] *and I. Andretta*[A]

[A]Universidade Estadual Paulista - UNESP, Jaboticabal, São Paulo 14884-900, Brazil.

Introduction

Health challenges can directly affect production costs because they impair broiler performance. This meta-analysis was conducted to evaluate the performance responses of broiler chickens challenged by enteric bacteria (*Clostridium* spp*., Escherichia coli*, and *Salmonella* spp.) and to quantify the impact of these health challenges on their maintenance requirements and feed efficiency.

Methods

The database used for the meta-analysis included 65 articles published between 1997 and 2012 with information on feed intake, protein intake, methionine intake, and weight gain of 86,300 broilers. Treatment comparisons were classified as: (1) control or challenged with *Salmonella* spp., *Clostridium* spp., and *E. coli*; or (2) control or fed feed additives. The feed intake and weight gain results of the treated birds were transformed into values relative to those obtained in the controls (difference in %). The meta-analysis involved three sequential analyses: graphical, correlation, and variance-covariance analysis (Lovatto *et al.* 2007). Equations estimating weight gain were established as a function of nutrient intake.

Results and discussion

Variation in feed intake was explained mainly by variation in initial age (19%), average daily consumption of methionine (18%), initial weight (10%), duration of challenge (8%), and type of challenge (2%). Birds that were not challenged but received feed additives were more efficient in the use of dietary protein for weight gain compared to the controls. Comparative regression analyses modelling weight gain as a function of protein or methionine intake suggested that nutrients were diverted to the immune system in response to a challenge with enteric bacteria, in agreement with the findings of others (Klasing 2007). Compared to the controls, the challenge reduced weight gain by 15% when expressed as a function of protein intake, and 11% when expressed as a function of methionine intake. The intercepts of the regressions for each type of bacterial challenge (*Salmonella* spp., *Clostridium* spp., and *E. coli*) were different from zero and negative (-2.2, -0.70 and -3.37, respectively); indicating that all challenges types increased the maintenance requirements of the birds. Moreover, the regression responses were curvilinear indicating that all challenge types reduced the feed efficiency of the birds.

Conclusion

These data highlight the applicability of meta-analysis to the determination of parameters that could be used to model the nutritional requirements of broiler chickens challenged with enteric bacteria.

References

Klasing KC (2007) Nutrition and the immune system. *British Poultry Science* **48**, 525-537.

Lovatto PA, Lehnen CR, Andretta I, Carvalho, AdA, Hauschild L (2007) Meta-análise em pesquisas científicas - enfoque em metodologias. *Revista Brasileira de Zootecnia* **36**, 285-294.

[B]Corresponding author: lhauschild@fcav.unesp.br

Topic: Digestion, metabolism and consequences for productivity

Assessment of models of protein requirements for predicting average daily gain of goats

A.K. Almeida[A,B]*, K.T. Resende*[A]*, I.A.M.A. Teixeira*[A]*, A.P. Souza*[A] *and M.H.M.R. Fernandes*[A]

[A]Unesp/Univ Estadual Paulista, Jaboticabal-SP 14884-900, Brazil.

Introduction

The demand of nutrients for animal maintenance and production drives the animal's dry matter intake (DMI) and influences its performance (average daily gain; ADG). Given this relationship, we propose that animal DMI and ADG could be used to assess nutrient requirements' models currently used for growing goats.

Methods

We evaluated the NRC (2007) and AFRC (1998) models for estimating protein requirements of growing goats using individual data of dry matter and metabolisable protein intake (MPI) of 46 Saanen goats, with liveweight (LW) ranging from 30.4 ± 0.2 to 44.0 ± 0.5 kg. These animals were fed *ad libitum* twice a day with a total mixed diet (11.5 MJ ME/kg DM and 105 g of MP/kg DM) and gained 135 ± 34 g/day. From MPI, we deducted the predicted MP required for maintenance, according to each feeding system; the remaining MPI we divided by predicted MP required for weight gain to obtain the predicted ADG by NRC and AFRC. The predicted ADG was evaluated according to St-Pierre (2003).

Results and discussion

Both NRC and AFRC overestimate DMI (437 and 116 g/day, respectively). We used observed intake and concluded that these feeding systems also overestimate the ADG (Table 1). For the AFRC model, we also detected systematic bias of -0.426 g for each gram of increase in the predicted value.

Table 1. Statistics from regressions of residual ADG on predictions by AFRC and NRC centered on their mean values

Model	Mean bias		Linear bias[A]		s.e. (g/day)[B]	Minimum bias (g/day)[C]	Maximum bias (g/day)[C]
	Estimated (g/day)	P-value	Estimated (g/day)	P-value			
NRC	-64.4 ±21.1	<0.001	-0.195 ±0.150	0.20	29.4	-77.9	-304
AFRC	-149.0 ±20.1	<0.001	-0.426 ±0.142	<0.01	37.9	-175.0	-304

[A] Linear bias represents the change in the bias of the prediction (g/day) per unit of change in the prediction (unitless). [B] Residual standard error. [C] Bias at minimum or maximum predicted ADG (g/day).

Because we have taken into account protein recommendations, we conclude that the evaluated models show biases when describing Saanen goats' requirements from 30 to 45 kg of LW. For the future, researchers should address the source of this bias.

References

AFRC (1998) 'The nutrition of goats.' (CAB International: Wallingford, UK)

NRC (2007) 'Nutrient requirements of small ruminants: sheep, goats, cervids, and new world camelids.' (National Academy Press: Washington)

St-Pierre NR (2003) Reassessment of biases in predicted nitrogen flows to the duodenum by NRC 2001. *Journal of Dairy Science* **86** (1), 344-350.

[B]Corresponding author: almeida.amelia@gmail.com

Topic: Digestion, metabolism and consequences for productivity

Predicting biogas and methane production from goat manure

B. Biagioli[A,C]*, K.T Resende*[A]*, I.A.M.A. Teixeira*[A]*, M.H.M.R. Fernandes*[A]*, J. Lucas*[A]*, N. St-Pierre*[B] *and C.J. Härter*[A]

[A]Univ. Estadual Paulista, Department of Animal Sciences, Jaboticabal, SP 14884-900, Brazil. [B]The Ohio State University, Department of Animal Sciences, Columbus, OH 43210, USA.

Introduction

The diets of small ruminants are based on forages and on average only 70% of feed intake is actually digested by these animals (CSIRO, 2012). The 30% remained may be subjected to anaerobic fermentation and biogas production, representing a potential energy source. The manipulation of fermentation factors such as temperature, pH, total solids and shape of manure to undergo bio-digestion may optimise biogas production. Our results allowed us to develop equations capable of predicting the biogas and methane production according to a number of pre-established factors.

Methods

The experiment was conducted in the Univ. Estadual Paulista, UNESP, Jaboticabal campus. Anaerobic digestion of goats' manure was measured using 24 digesters distributed in central composite design according to the following factors: ambient temperature (temp) (20.11°C, 21.48°C, 30.24°C, 33.74°C and 34.67°C), pH condition (6.80, 6.84, 7.01, 7.15, 7.22), total solids (TS) content (2.63%, 3.53%, 4.46%, 6.85%, 6.87%), and manure processed or not. Data were analyzed as a mixed model with fixed effect variables (temperature, pH, TS, manure processing and their interactions) and random effect (day and digester), using the PROC MIXED procedure of SAS (version 9.0). The model parameters were estimated using the option of the MODEL SOLUTION OUTP. Significance was declared at $P \leq 0.02$.

Results

We found that manure processing did not affect biogas production. Biogas production was optimised at 34.67°C, pH 7 and 7% of total solids. To develop the equations, the likelihood ratio test revealed that TS and days, as well as the interaction between temperature and TS, and the interaction among TS, pH, and temperature were significant ($P<0.02$) and thus were included in our predictive equation for biogas production. $BV = -0.03075 (\pm 0.02) - 1.0205 (\pm 0.30) * TS + 0.01257 (\pm 0.001) * D - (0.00023 (\pm 0.00002) * d^2) + (0.03504 (\pm 0.01) * TEMP * TS) + (0.14 (\pm 0.04) * TS * pH) - (0.00479 (\pm 0.001) * TS * TEMP * pH)$, where: BV = biogas volume, m3; TS = total solids of manure %; D = number of days in fermentation; TEMP = room temperature, °C. We also developed an equation to predict the percentage of methane in the biogas. $CH_4 = 17.9104 (\pm 6.67) + 1.6430 (\pm 0.58) *D - 0.02301 (\pm 0.01) * D^2$, where: CH_4 = percentage of methane in biogas, %; D = number of days in fermentation.

Discussion and conclusion

The equations developed herein are potential decision tools to optimize biogas production in different environments within the temperature range of 20 to 35°C.

References

Commonwealth Scientific and Industrial Research Organisation (CSIRO) (2012) 'Nutrient requirements of domesticated ruminants.' (CSIRO Publishing: Collingwood, Australia)

[C]Corresponding author: brunobiagioli@fcav.unesp.br

Topic: Digestion, metabolism and consequences for productivity

Estimation of DM mass in the digestive tract of sheep using a compartmental digesta kinetics model

M.C. Barnett[A,D]*, I. De Barbieri*[A,B]*, R.S. Hegarty*[A]*, V.H. Oddy*[C] *and J.V. Nolan*[A]

[A]School of Environmental and Rural Science, University of New England, Armidale 2351, Australia.
[B]National Institute of Agricultural Research, Tacuarembó, TBO 45000, Uruguay. [C]Beef Industry Centre, Department of Primary Industries NSW, Trevenna Road, Armidale 2351, Australia.

Introduction

Compartmental models are frequently used to determine the retention time of digesta in the gastrointestinal tract (GIT) of sheep without surgical intervention. However, few can calculate the mass of DM in the different compartments of the GIT. Our intention was to develop such a model.

Methods

Seventeen Merino wethers, 33 months old (57.2 ± 8.3 kg) were held indoors and fed chaffed oaten/lucerne hay once daily at either 1.0X or 1.5X maintenance. Faecal samples were collected sequentially after administering a particle-phase marker (5 g of Cr-mordanted NDF). Patterns of excretion of Cr over time were fitted to a compartmental model using WinSAAM (Barnett 2013). Actual masses of DM contents in key compartments of the GIT were obtained after euthanasia.

Results

Model estimates of DM mass within the GIT were moderately correlated (Reticulorumen r=0.63, P < 0.01; Total GIT r = 0.76; P < 0.01) with actual DM mass (Fig. 1).

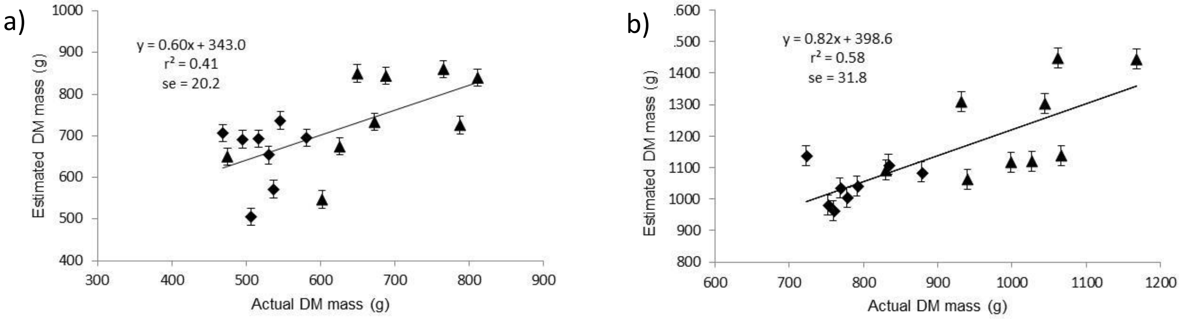

Fig. 1. Relationship between estimated DM mass by compartmental model with actual values obtained from euthanised sheep in a) reticulorumen and b) total GIT when fed either 1.0X (♦) or 1.5X maintenance (▲) (mean ± SEM).

Discussion

While estimates of digesta mass were moderately correlated with actual values, further analysis of measured DM mass in segments of the sheep GIT will allow modification of the model to improve the accuracy of DM calculation in the sheep GIT. Such information may allow better characterisation of differences in nutrient supply and methane emissions between individual ruminants.

References

Barnett MC (2013) Impact of gut kinetics on methane production within the sheep. PhD Thesis, University of New England, Armidale, NSW.

[D]Corresponding author: mbarnet3@une.edu.au

Modelling bicarbonate kinetics in the sheep

R.C. Dobos[A,D], *R.C. Boston*[B] *and J.V. Nolan*[C]

[A]Beef Industry Centre of Excellence, NSW Department of Primary Industries, Armidale, 2351 Australia. [B]School of Veterinary Medicine, University of Pennsylvania, PA 19348, USA. [C]School of Environmental and Rural Science, University of New England, Armidale 2351, Australia.

Introduction

A quantitative understanding of bicarbonate (HCO_3^-) kinetics in the body is crucial when analysing results of experiments undertaken to estimate oxidation of carbon-labelled components *in vivo* and energy expenditure. The main aim of this study was to develop a new model of HCO_3^- kinetics in ruminants capable of describing previously published data.

Methods

Data from Leng and Murray (1972) were used. On day 1, a sheep was injected intraruminally (IR) with ~50 *μCi* of $NaH^{14}CO_3$. Blood and rumen fluid samples taken at intervals over 24 h (Experiment 1) were analysed to determine specific radioactivity (SA) of HCO_3^--C (μCi/gC). Two days later the same sheep was injected intravenously (IV) with $NaH^{14}CO_3$ and a similar sampling procedure was followed (Experiment 2). We used WinSAAM to fit 3-compartment mammillary models of HCO_3^- kinetics, after a 2-compartment model was found to be inadequate to describe these SA data.

Results

The estimated compartment sizes (*M(i), gC*) and carbon flows between compartments (*R(i,j), gC/d*) for separate 3-compartment mammillary IR and IV models are shown in Table 1.

Table 1. Estimated distribution of HCO_3^- and flow kinetics. FSD (SD/mean) is shown parentheses. Compartment 1 is blood accessible, compartment 2 is rumen accessible and compartment 3 is "other" tissues

	Compartments			Flows							
Model	*M(1)*	*M(2)*	*M(3)*	*R(1,0)*	*R(2,0)*	*R(0,1)*	*R(0,2)*	*R(1,2)*	*R(2,1)*	*R(1,3)*	*R(3,1)*
IR	11.7	1.0	10.5	236.7	15.4	250.0	2.2	79.1	65.9	34.4	34.4
	(0.09)	(0.13)	(0.16)	(0.04)	(0.30)	(0.03)	(0.34)	(0.08)	(0.15)	(0.16)	(0.16)
IV	5.1	8.7	7.4	98.9	133.6	214.0	18.6	257.4	142.4	15.9	15.9
	(0.06)	(0.08)	(0.10)	(0.10)	(0.09)	(0.02)	(0.37)	(0.09)	(0.10)	(0.06)	(0.06)

Discussion

Bicarbonate kinetics in humans and other simple-stomached animals have generally been described by 3-compartment mammillary models consisting of a central compartment (accessible by sampling blood) and two other compartments with 'medium' and 'slower' rates of turnover. It seems unlikely that the rumen would exactly mirror that of compartment 2, so a 4th compartment may be needed to describe HCO_3^--C kinetics in ruminants.

References

Leng RA, Murray RM (1972). Estimation of the fermentation rate in the rumen of sheep using VFA production, carbon dioxide production and methane production. In: *Tracer studies on non-protein nitrogen for ruminants* pp.25-34. Vienna: International Atomic Energy Agency.

[D]Corresponding author: robin.dobos@dpi.nsw.gov.au

Topic: Digestion, metabolism and consequences for productivity

Kinetics of allantoin metabolism in sheep

J.V. Nolan[A,B] *and L.P. Kahn*[A]

[A]School of Environmental and Rural Science, University of New England, Armidale 2351, Australia.

Introduction

The flow of microbial nucleic acids (and microbial cells) from the rumen can be determined non-invasively by prediction from urinary excretion of purine derivatives (PD) including allantoin. Excretion of allantoin is not, however, entirely via the urine. To better understand the kinetics of allantoin in sheep, we quantified a compartmental model of allantoin-C flows in the body.

Methods

Merino x Border Leicester wethers, 2 years old, 40 kg, were given hourly meals of oaten chaff (89.3 % DM, 1.2 % N; 650 g/d) mixed with lucerne chaff (87.2 % DM, 2.8 % N; 250 g/day). Single iv injections of [^{14}C]-allantoin were administered to each sheep; samples of blood were collected for 18 h and of urine for 4 days. The specific radioactivity (SR) of blood and urine allantoin, and blood HCO_3^- was determined. Later, $H^{14}CO3^-$ was also administered iv to quantify blood HCO_3^- kinetics (Kahn and Nolan 2000). The SR data for allantoin and HCO_3^- (and tracer recovery) were fitted using WinSAAM.

Results and discussion

The model structure used to fit the SR *v.* time data from one of the sheep is given in Fig. 1A with compartment sizes (g C) and flows (g C/d). Fitted SR data and tracer recovery are given in Fig. 1B.

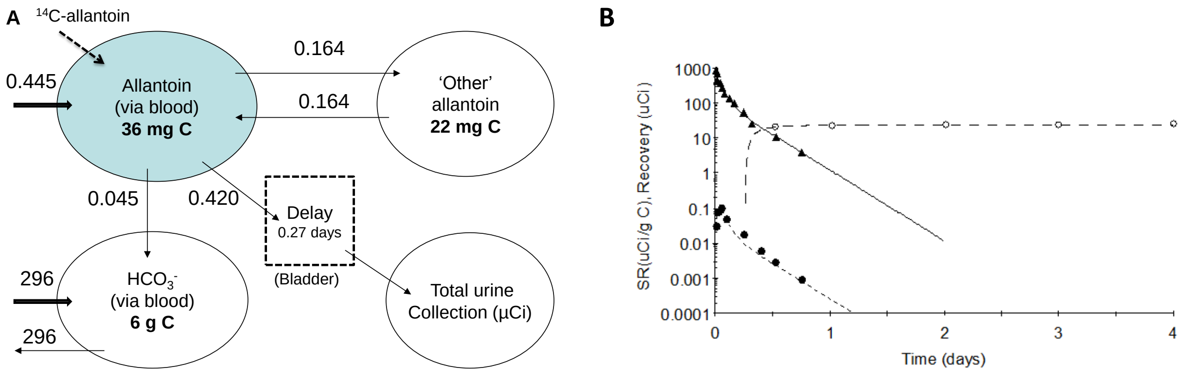

Fig. 1. A model with a central (shaded) compartment of allantoin (site of tracer injection, sampled via blood, ▲) linked to another allantoin compartment (body water) and to a HCO_3^- compartment (sampled via blood, ●). Transfer of ^{14}C-allantoin from blood to urine (µCi recovered, ○) is also shown.

Allantoin is unlikely to be degraded in the tissues of sheep but its rapid passage from blood to urine (420 mg C) is to be expected, given the limited capacity for its renal reabsorption. About 73 % of the [^{14}C]-allantoin injected was recovered in urine during the 12 h after tracer injection, increasing to 90% after 4 days. Only small amounts of allantoin entered the gut (45 mg C/d) to be metabolised by microorganisms to HCO_3^- that was then excreted, probably mostly via the lungs.

References

Kahn L, Nolan JV (2000). Kinetics of allantoin metabolism in sheep. *British Journal of Nutrition* **84**, 629-634.

[B]Corresponding author: jnolan@une.edu.au

Evaluation of a bovine VFA prediction model using data on sheep

P. Nozière[A,D], *E. Ollion*[A], *D. Pacheco*[B] *and D. Sauvant*[C]

[A]INRA-Vetagrosup, Theix, France. [B]AgResearch Grasslands, Palmerston North, New Zealand.
[C]INRA-AgroParisTech, Paris, France.

Introduction

An empirical model of volatile fatty acids (VFA) molar proportions in the rumen has been previously developed from large databases on digestion in bovines (Nozière *et al*. 2011). We aimed to perform an external validation of this model on data from experiments (exp) in sheep.

Methods

Selected treatments (trt, N = 342) covered a range of feeding contexts (DM intake level, DMI%LW = 2.11 ± 0.85; OMd = 69.6% ± 11.3; digestible NDF / digestible OM (DNDF/DOM) = 0.43 ± 0.22 g/g). Predicted VFA molar proportions were calculated from measured DNDF/DOM, ruminal starch digestibility (RStD, in g/100 g), and DMI%LW (Nozière et al., 2011). When RStD or DNDF/DOM were not measured (Ntrt = 187 and 89, respectively), they were calculated using INRA feed tables including effects of passage rates and of digestive interactions, respectively (Sauvant and Nozière, 2013). The data were processed using general linear models to dissociate within- vs inter- exp variations.

Results

The within-exp relationships between calculated (X) vs observed (Y) VFA molar proportions did not significantly differ from the bisector (Y = X) for C2, but the slope was 0.45 and 1.36 for C3 and C4, respectively (Fig. 1). The differences (Y - X) were mainly related within-exp to RStD (Nexp = 31; Ntrt = 89; slope = -0.10 ± 0.04 for C3 and +0.15 ± 0.03 for C4), and to DMI%LW (Nexp = 44; Ntrt = 142; slope = +1.61 ± 0.46 for C2, -2.85 ± 0.39 for C3 and +0.52 ± 0.22 for C4).

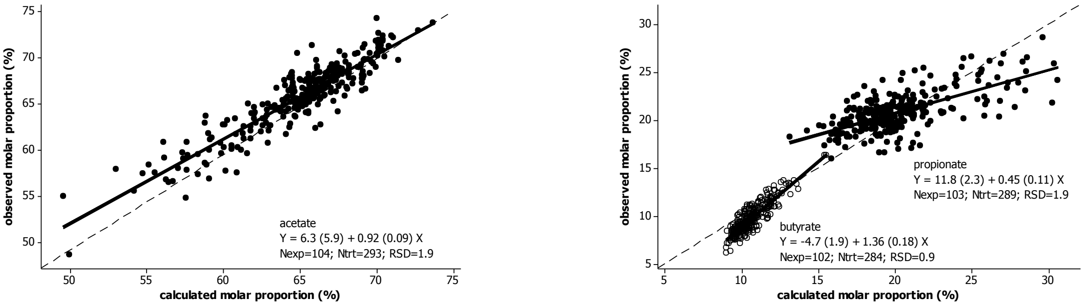

Fig. 1. Within-exp relationships between observed and calculated rumen VFA molar proportions.

Conclusions

Compared to predictions in bovines, the response of VFA molar proportions to RStD and DMI%LW in ovines appears much lower for propionate, and higher for butyrate.

References

Nozière P, Glasser F, Sauvant D (2011) In vivo production and molar percentages of volatile fatty acids in the rumen: a quantitative review by an empirical approach. *Animal* **5**, 403–414.

Sauvant D, Nozière P (2013) La quantification des principaux phénomènes digestifs chez les ruminants: les relations utilisées pour rénover les systèmes d'unités d'alimentation énergétique et protéique. *INRA Productions Animales* **26**, 327-346.

[D]Corresponding author: pierre.noziere@clermont.inra.fr

Evaluation of a mechanistic model simulating *in vitro* gas production and ammonia evolution for a variety of feedstuffs fed to ruminants

S. Giger-Reverdin[A,B,C], *A. Serment*[A,B] *and D. Sauvant*[A,B]

[A]INRA, UMR791 MoSAR, 16 rue Claude Bernard, F-75005 Paris, France. [B]AgroParisTech, UMR791 MoSAR, 16 rue Claude Bernard, F-75005 Paris, France.

Introduction

A mechanistic model (14 compartments) simulating *in vitro* fermentation of pea fractions with the HFT method proposed by Menke *et al.* (1979) was described by Serment and Sauvant (2010). This paper aimed to evaluate this model on a diversity of feedstuffs usually fed to ruminants in Europe.

Methods

Twenty one feeds were clustered in six homogeneous groups: fast degradable energy (wheat, oats, barley, sugar-beet pulp, citrus pulp), low degradable energy (maize, sorghum), high degradable meals (soyabean, rapeseed, sunflower), legume seeds (faba bean, pea, lupin), highly lignified fibre (brewers grain, coconut meal, palm kernel meal, alfalfa hay, dehydrated alfalfa), high fibre but low lignin (soyabean hulls, corn silage, corn stover). Parameters of the model were fitted to the kinetics of mean values per group for gas production (2, 4, 6, 8, 12 and 24 hours of incubation) and ammonia concentration (measured at 2, 4, 6, 8 and 24 hours) in the HFT syringes.

Results

Among the 15 “unknown” model parameters, feeds fractional degradation rates were firstly fitted and, then, N and carbohydrates soluble fractions were included in the fitting procedure. Fractional degradation rates ranged between 2 and 6%/hour for cell wall, 15 and 30%/hour for non-structural carbohydrate, 1 and 20%/hour for non-soluble protein and 15 and 60%/hour for soluble protein.

Kinetics of gas production presented systematically a global shape of sigmoid growth while ammonia kinetics varied largely from a quasi linear shape to a clear decrease, at around 10h of incubation, followed by a high rebound. Accuracy of the prediction was estimated by the residual standard deviation of the regression between modelled and observed values. For gas production, it varied from 0.740 to 2.690 ml gas in the 6 groups, and for ammonia, from 2.04 to 15.56 mg ammonia/L. The last point (24 hours) had a large influence on the regression values.

Discussion and conclusion

This mechanistic model reflects with a good accuracy the heterogeneity of kinetics of in vitro digestion across six groups of feeds representative of the diversity of byproducts and concentrates. The microbial compartment of the model, linked with available nitrogen and carbohydrates, allowed to fit correctly the large diversity of kinetics of ammonia. To be further developed, this model should be applied to kinetics of e.g. microbes and components of the substrates.

References

Menke KH, Raab L, Salewski A, Steingass H, Fritz D, Schneider W (1979) The estimation of the digestibility and metabolizable energy content of ruminant feedingstuffs from the gas production when they are incubated with rumen liquor *in vitro. Journal of Agricultural Science* **93**, 217-222.

Serment A, Sauvant D (2010). A mechanistic model of pH and gas exchanges in the rumen and its in vitro application. In '7th International Workshop on Modelling Nutrient Digestion and Utilization in Farm Animals, (Eds D Sauvant, J Van Milgen, P Faverdin and N Friggens), pp. 148-157. Wageningen Academic Publishers.

[C]Corresponding author: sylvie.giger-reverdin@agroparistech.fr

Modelling nutrient digestion and absorption in cattle by a spreadsheet integrating the NorFors digestion model

P. Nørgaard[A,C], *K.B. Andersen*[A], *L.M. Jensen*[A] *and N.I. Nielsen*[B]

[A]Department of Veterinary Clinical and Animal Sciences, University of Copenhagen, 1870 Frederiksberg C, Denmark. [B]Knowledge Centre for Agriculture, Cattle, 8200 Aarhus N, Denmark.

Introduction

The NorFor feed evaluation system models the digestion of individual nutrient fractions in individual feedstuffs in the rumen, small intestine and large intestine. The digestion of forage NDF in the rumen is predicted by a 2 pools model, whilst the residual carbohydrates, fermentation products, NDF, protein, starch in forages and concentrates are predicted by a 1 pool model (Volden 2011).

Methods

The NorFor digestion model was implemented into an Excel 97-2003 spreadsheet including prediction of methane (Nielsen *et al.* 2013), digestibility of the different feed fractions, net energy value and the absorption of amino acids (AA), fatty acids (FA) and glucose in the small intestine. The production of acetate, propionate and butyrate (SCFA) was predicted from fermented carbohydrate according to (Murphy *et al.* 1982). Methane was predicted from the dietary content of fatty acids (g/kg DM). The spreadsheet allows modelling digestion of diets with 3 forages and 4 concentrates.

Results and Discussion

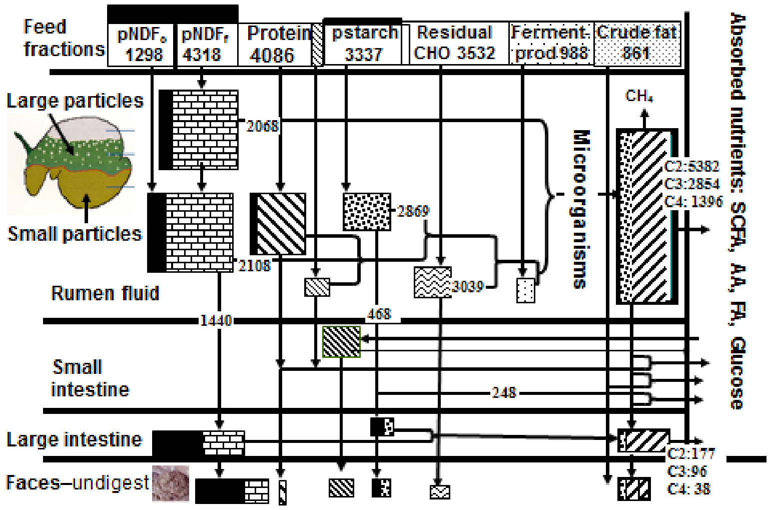

Fig. 1. illustrates the digestion routes of the NorFor feed factions. The values (g/day) in the boxes represent the predicted values from a 625 kg cow fed 12.5 kg clover grass DM, 5 kg barley DM and 4 kg rape seed meal DM. pNDF$_c$ and pNDF$_f$ are potential digestible NDF from concentrate and forage. ■ Indigestible.

Fig. 1. NorFors digestion model feed fractions and absorption of nutrients. The solid bars represent indigestible NDF, protein and starch.

References

Murphy MR, Baldwin RL, Koong LJ (1982) Estimation of Stoichiometric Parameters for Rumen Fermentation of Roughage and Concentrate Diets. *Journal of Animal Science* **55**, 411-421.

Nielsen NI, Volden H, Åkerlind M, Brask M, Hellwing ALF, Storlien T, Bertilsson J (2013). A prediction equation for enteric methane emission from dairy cows for use in Norfor. *Acta Agriculturae Scandinavica, Section A –Animal Science* **63**, 126-130.

Volden, H (2011) NorFor- The Nordic feed evaluation system. EAAP Publ. 130, Wagen. Acad. Press.

[C]Corresponding author: pen@sund.ku.dk

Topic: Digestion, metabolism and consequences for productivity

Modelling real-time individual lysine requirements in growing-finishing pigs: model update and validation

C. Pomar[A,D], *J. Rivest*[B], *I. Andretta*[C] *and L. Hauschild*[C]

[A]Agriculture and Agri-Food Canada, Sherbrooke, J1M 1Z3, Canada. [B]Centre de Développement du Porc du Québec, Québec, G1V 4M7, Canada. [C]Univ Estadual Paulista, Jaboticabal, São Paulo, Brazil.

Introduction

Feeding growing-finishing pigs with daily tailored diets using precision techniques can reduce lysine intake by more than 25% without compromising pig performance. This feeding approach is based on a mathematical model called AIPF that estimates daily amino acid requirements of individual growing-finishing pigs (Hauschild *et al.* 2012). In the following study the performance of the revised model is compared with current methods of estimating population lysine requirements.

Methods

Daily feed intake (DFI), weekly body weight (BW) and 28-days body protein (BP) data collected individually in 82 pigs raised in experimental conditions was used to estimate daily the standardized ileal digestible lysine requirements (SIDLysRe, %) with the following models: (1) polynomial functions were fitted to DFI, BW and BP data (*a posteriori*) and the smoothed data used to estimate the reference individual requirements as proposed by Hauschild *et al.* (2012). Also *a posteriori*, (2) the InraPorc model (van Milgen *et al.* 2008) was calibrated to BP data and (3) the NRC model (NRC 2012) to BW data and the average pig SIDLysRe calculated as suggested. The DFI was estimated with the same polynomial function in all *a posteriori* models. The AIPF model was used in real-time to estimate individual SIDLysRe requirements with (4) protein deposition rate assumed to be constant (16%) in BW gain or (5) adjusted based on feed conversion data.

Results and discussion

Real-time models (4 and 5) estimate daily SIDLysRe individually based on pass data while *a posteriori* models (1 to 3) estimate these requirements for the average population using the entire growing period data. Average DFI was 2% higher in real-time than in *a posteriori* models. In relation to model 1, protein deposition was higher by 1, 5, 12 and 4% in models 2 to 5, and average population SIDLysRe higher by -3, 12, 7 and 2%, respectively. The slopes between the reference and models 2 to 5 were respectively 0.97, 0.49, 0.45 and 0.86. Assuming a constant proportion of protein in BW gain, the SIDLysRe was underestimated in young and overestimated in old pigs. The difficulty of estimating SIDLysRe with the information available in real-time, which is DFI and BW, was mostly overcome by correcting the proportion of protein in BW gain with feed conversion data. Average population daily estimations of SIDLysRe of model 5 were close to the reference and InraPorc models, but were biased in relation to the NRC model. Real-time models allow the estimation of daily SIDLysRe per pig and thus lysine intake can be reduced dramatically when pigs are fed accordingly.

References

Hauschild L, Lovatto PA, Pomar J, Pomar C (2012) Development of sustainable precision farming systems for swine: Estimating real-time individual amino acid requirements in growing-finishing pigs. *Journal of Animal Science* **90**, 2255-2263.

NRC (2012) 'Nutrient requirements of swine, 11th edition'. (National Academy Press: Washington, DC)

van Milgen J, Valancogne A, Dubois S, Dourmad J-Y, Seve B, Noblet J (2008) InraPorc: A model and decision support tool for the nutrition of growing pigs. *Animal Feed Science and Technology* **143**, 387-405.

[D]Corresponding author: Candido.Pomar@agr.gc.ca

Topic: Digestion, metabolism and consequences for productivity

Predictions of digestion and methane production from fresh grass by the Molly cow model

M.D. Hanigan[A,D]*, R. Vibart*[B]*, S. Muetzel*[B]*, M. Tavendale*[B]*, P. Gregorini*[C] *and D. Pacheco*[B]

[A]Department of Dairy Science, Virginia Tech, Blacksburg, VA 24060, USA. [B]AgResearch, Grasslands Research Centre, Palmerston North 4442, New Zealand. [C] DairyNZ, Hamilton 3240, New Zealand.

Introduction

Ruminants convert forage into human edible products thus representing a vital contribution to food sufficiency. However, they also generate large quantities of methane (CH_4) and excrete more than 70% of the nitrogen they consume. Maximising human-edible food production while minimising production costs and environmental impacts, requires a robust representation of animal responses to a wide range of inputs. The Molly cow model represents key elements of digestion and metabolism and thus is potentially useful in such an exercise. However, it has not been sufficiently evaluated on fresh grass diets. The objective of this work was to assess model predictions of grass digestibility and CH_4 predictions from fresh temperate grass diets.

Methods

A version of the Molly cow model with particle passage described as a function of liquid passage was used for the work. Digestibility predictions were assessed using a perennial ryegrass data set assembled from the literature, while CH_4 predictions were compared to data from a respiration chamber experiment assessing diet and physiological state.

Results

Ruminal degradation rates for protein, starch, and fiber are scaled in the model using observed dietary *in situ* rates which have been previously calibrated to North American diets. The approach worked well for grass protein; however, fiber digestibility was dramatically under predicted when using observed *in situ* measurements necessitating recalibration of the model. After calibration, root mean square prediction errors expressed as a percent of the observed values (RMSPE) were 11.8, 12.9, 39.5, 12.6, 8.2, and 26.2% for NDF passage, ADF passage, non-ammonia, non-microbial nitrogen (NANMN) passage, fecal NDF output, fecal ADF output, and fecal N output, respectively. More than half of the NANMN error was associated with slope bias indicating that the representation of ruminal N degradation did not fully capture the true process. The model predicted CH_4 production for dry and lactating cows fed alfalfa pellets and fresh grass with concentrate, respectively with an RMSPE of 25%. There was no prediction bias with respect to predicted CH4 production, intake rate, or dietary NDF content.

Conclusions

Fiber digestibility of fresh grass appears to be much greater than predicted from *in situ* data. The model predicted grass digestion with reasonable accuracy after recalibration to the data except for NANMN flow. The model predicted the effects of dry matter intake and feed composition on CH_4 production with no apparent bias.

MDH was supported by a Global Research Alliance Senior Scientist (GRASS) Award, funded by the New Zealand Government.

[D]Corresponding author: mhanigan@vt.edu

Topic: Digestion, metabolism and consequences for productivity

Biopara-Beef a whole animal simulation model: methane predictions

V. Ambriz-Vilchis[A,B,D]*, R.H. Fawcett*[B]*, J.A. Rooke*[C] *and N.S. Jessop*[B]

[A]Royal (Dick) School of Veterinary Studies and the Roslin Institute, The University of Edinburgh, Easter Bush Veterinary Centre, Roslin, Midlothian, EH25 9RG, Scotland, UK. [B]Bioparametrics Ltd. SRUC Building, West Mains Road, Edinburgh, Lothian, EH9 3JG, Scotland UK. [C]Future Farming Systems Group, SRUC, West Mains Road, Edinburgh EH9 3JG, UK.

Introduction

Global climate change research requires animal models that accurately predict discharges to the environment from animal feeding regimes. Bioparametrics models have been shown to accurately predict intake, rumen pH and milk yield from livestock. The aim of the present study was to evaluate Biopara-Beef CH_4 output predictions by comparing them with data from on-farm trials.

Methods

A trial was conducted at the Beef Research Centre of SRUC, UK, in summer 2012. Steers (39 Charolais and 39 Luing) were fed concentrate-based (dry matter basis; barley 70%, barley straw 8%, molasses 2%, wheat distillers dark grains 18%, minerals 1%) or forage based (barley 38%, wheat distillers dark grains 10%, minerals 1%, whole crop barley silage 28% and grass silage 22%) diets. Indirect open-circuit respiration chambers were used to measure CH_4 concentrations by infrared absorption spectroscopy. Animal and feed characteristics were used as inputs for Biopara-Beef and daily CH_4 emissions were predicted. CH_4 outputs were compared: for individual animal's correlation coefficient and concordance correlation coefficient (CCC) were performed; at the whole herd level t-test was used to compare observed and predicted means (Mean ± SEM).

Results

Individual animal predictions were acceptable (Fig. 1a. $r = 0.59$, CCC = 0.50, $P < 0.01$, $n = 69$). When compared at a herd level observed CH_4 emissions 167.2 ± 5.0 g/day were not different to that predicted by Biopara-Beef 162.3 ± 2.8 (Fig. 1b. $P = 0.40$, $n = 69$).

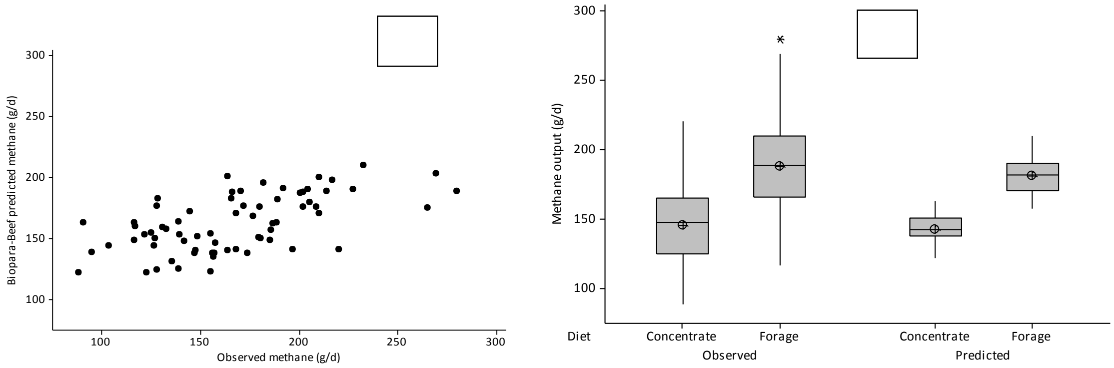

Fig. 1. Relationship between observed and predicted methane output a) per individual animal b) at the herd level and with different diet.

Conclusions

Given an adequate description of the animal and the diets consumed, Biopara-Beef can successfully predict CH_4 emissions and be used as a tool to evaluate CH_4 discharge to the environment as CH_4 output at a herd level for different breeds and diets.

[D]Corresponding author: V.Ambriz-Vilchis@sms.ed.ac.uk

Topic: Digestion, metabolism and consequences for productivity

Biopara-Milk a whole cow simulation model: rumen pH predictions

V. Ambriz-Vilchis[A,B,D], *A.I. Macrae*[A], *R.H. Fawcett*[B], *D.J. Shaw*[C] *and N.S. Jessop*[B]

[A]DHHPS, Royal (Dick) School of Veterinary Studies and the Roslin Institute, The University of Edinburgh, EH25 9RG, Scotland, UK. [B]Bioparametrics Ltd., EH9 3JG, Scotland UK. [C]Royal (Dick) School of Veterinary Studies and the Roslin Institute, The University of Edinburgh, EH25 9RG, Scotland, UK.

Introduction

Nutrition has a profound influence on production, health and welfare, and simulation models can be used as a tool to understand those interactions. Biopara-Milk (Bioparametrics Ltd.) is a model which can predict milk yield, feed intake and rumen pH. Rumen pH predictions are derived from continuous estimates of bicarbonate concentration in the rumen (Kohn and Dunlap 1998). The aim of the present study was to compare Biopara-Milk rumen pH predictions with those obtained from rumen pH boluses in cubicle housed commercial dairy cows.

Methods

A trial was carried out at Langhill Dairy Farm (The University of Edinburgh, Midlothian, Scotland, UK) during spring 2013. Fourteen multiparous cows were administered a rumen bolus (WellCow, Ltd, Scotland, UK) to measure pH. The cows were fed a partial mixed ration (dry matter basis): 1st cut grass silage 44.9%, wheat silage 17.6%, 2nd cut grass silage 15.6%, dairy meal 18.5%, molasses 3.4% and parlour concentrate fed to yield. Details on the animals (BCS, BW, milk yield, lactation week) and on the feed were used as inputs for Biopara-Milk. Rumen pH values per hour were obtained. Limits of agreement method for repeated measures explored the relationship between observed and predicted pH. Statistical analyses were carried out using R Core Team (2013).

Results and conclusions

Circadian pH dynamics per cow were obtained (Fig. 1). Biopara-Milk predicted pH values that were on average 0.13 (95% C.I. -0.34 to 0.61 pH) lower than those recorded by the boluses.

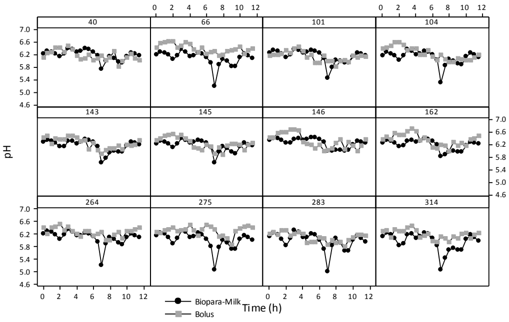

Fig. 1. Predicted and observed circadian pH dynamics.

With adequate description of the animal and the feed consumed, Biopara-Milk can accurately predict circadian rumen pH dynamics and be used to evaluate the effect different feeding regimes have on it.

References

Kohn RA, Dunlap TF (1998) Calculation of the buffering capacity of bicarbonate in the rumen and in vitro. *Journal of Animal Science* **76**, 1702-1709

R Core Team (2013) A language and environment for statistical computing. In: R foundation for Statistical Computing, Vienna, Austria

[D]Corresponding author: V.Ambriz-Vilchis@sms.ed.ac.uk

A mechanistic model of casein synthesis in mammary tissue based on the phosphorylation of mTOR

S.I. Arriola Apelo[A,B] *and M.D. Hanigan*[A,C]

[A]Department of Dairy Science, Virginia Tech, Blacksburg, VA, 24061, USA. [B]Current address:
Department of Medicine, University of Wisconsin, Madison, WI, 53705, USA.

Introduction

The mammalian target gene of rapamycin, mTOR, regulates rates of mRNA translation, initiation and elongation. Specific essential amino acids (EAA) increase mTOR phosphorylation in mammary epithelial cells and this has been correlated with increased rates of casein synthesis. The objective of the present work was to expand an existing model of EAA effects on mTOR phosphorylation, described by Appuhamy and Hanigan (2010), to include individual EAA and to incorporate the effect of mTOR phosphorylation on synthesis rates of α-S1-casein ($SR_{(Csn)}$) in the mammary gland of lactating dairy cows.

Methods

Data to estimate model parameters were obtained from Arriola Apelo *et al.* (2014a, 2014b). Modelling work was completed using acslX software (Aegis Tech, Huntsville, AL, USA). The model was fitted against mTOR phosphorylated:total ratios ($Q_{P(mTOR)}$) and $SR_{(Csn)}$ (% h^{-1}) using the NL2SOL algorithm to minimize the error sum of squares.

Results and discussion

Isoleucine and phenylalanine were the EAA with the most explanatory power for mTOR phosphorylation (RMSPE, 20% of the observed mean). Casein synthesis, which was originally represented as a function of EAA, had reduced prediction errors when represented as a mass action function of predicted mTOR phosphorylation.

Contrary to muscle, which is most sensitive to leucine, casein synthesis was best explained by the effects of isoleucine and phenylalanine on mTOR phosphorylation. This means that strategies which enhance the supply of metabolisable isoleucine and phenylalanine could enhance the efficiency of milk protein synthesis in lactating dairy cows.

References

Appuhamy JADRN, Hanigan MD (2010) Modeling the effects of insulin and amino acids on the phosphorylation of mTOR, Akt and 4EBP1 in mammary cells. In "Modelling nutrient digestion and utilization in farm animals". (Eds D Sauvant, JV Milgen, P Faverdin, and N Friggens) pp 225-232. (Wageningen Academic Publishers, Wageningen)

Arriola Apelo SI, Singer LM, Lin XY, McGilliard ML, St-Pierre NR, Hanigan MD (2014a) Isoleucine, leucine, methionine, and threonine effects on mammalian target of rapamycin signaling in mammary tissue. *Journal of Dairy Science* **97**, 1047-1056.

Arriola Apelo SI, Singer LM, Ray WK, Helm RF, Lin XY, McGilliard ML, St-Pierre NR, Hanigan MD (2014b). Casein synthesis is independently and additively related to individual essential amino acid supply. *Journal of Dairy Science* **97**, 2998-3005.

[C]Corresponding author: mhanigan@vt.edu

Topic: Digestion, metabolism and consequences for productivity

Calibration of a dynamic model of the sheep mammary gland by using experimental data

A.S. Atzori[A,C], *R.A. Molina*[B], *C. Dimauro*[A], *M. Cellesi*[A], *A. Cannas*[A] *and G. Pulina*[A]

[A]Sezione di Scienze Zootecniche, Dipartimento di Agraria, University of Sassari, Italy. [B]Departamento de Ciencias Agrarias, Universidad Nacional de Colombia, Palmira, Colombia.

Introduction

A dynamic model of the sheep mammary gland was developed and parameterized employing an object-oriented simulation environment, and evaluated by using only DNA/RNA data as indicators of mammary cell dynamics (Dimauro *et al*. 2010). This work aimed to calibrate the model by using morphometric parameters measured on Sarda dairy ewes.

Methods

The calibration was performed with Vensim®PLE 6.0 using individual data from sheep slaughtered at the end of pregnancy and during lactation (Castanares-Castro *et al*. 2013). Values observed at the end of pregnancy for mammary volume and N of alveoli were used for initial model setting. Average values of milk secretion rate per alveolus and alveolar volume were set at $4x10^{-4}$ MJ/h and at $4x10^{-4}$ L, respectively. The calibration was made adjusting N of progenitor alveoli and constant fractional rates until model predictions matched the N of differentiated alveoli observed during the lactation.

Results and conclusions

Predicted N of active alveoli (thin lines; Fig. 1. showed an oscillatory behavior, with maximum frequency in darkest areas. Quiescence induced by the feedback inhibitor of lactation caused short term oscillations between milkings. The predicted highest values indicate the max N of active alveoli at each time, which matched observed N of alveoli (bold line; Fig. 1). For this prediction, the initial N of progenitor alveoli was estimated equal to $1x10^6$; estimated constant fractional rates were: 0.12/h, $7x10^{-6}$ and $7x10^{-5}$ MJ/h for alveoli quiescence, alveoli senescence and reserve mobilization during negative energy balance, respectively. Predictions of alveoli dynamics and milk yield agreed with observed data.

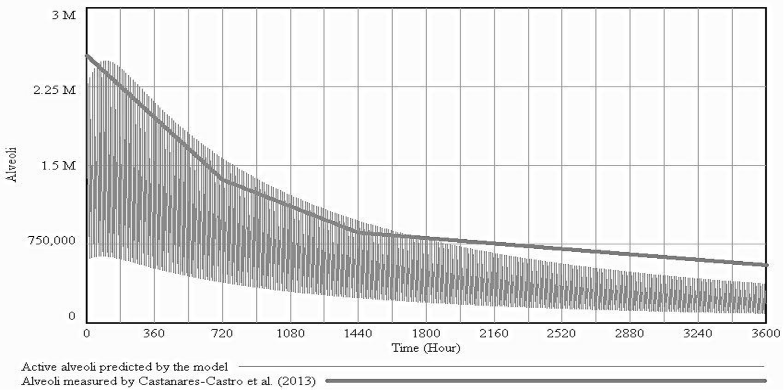

Fig. 1. Predicted and measured N of mammary gland alveoli from 0 to 150 days in milk.

References

Dimauro C, Atzori AS, Pulina G (2010) Assessing and optimizing the performance of a mechanistic mathematical model of the sheep mammary gland. In: Modeling Nutrient Utilization in Farm Animals (Ed. D Sauvant et al.) pp 72-82. (Wageningen Academic Press, Wageningen, The Netherlands).

Castanares-Castro N, Colitti M, Nudda A, Stefanon B, Pulina G (2013) Dynamics of secretory cells in lactating ewes. *Small Ruminant Research* **113**, 251-253.

[C]Corresponding author: asatzori@uniss.it

Topic: Digestion, metabolism and consequences for productivity

Mechanistic model for quantifying nitrogen excretions from Mediterranean dairy goats

C. Fernández[A,C], J.A.D.R.N. Appuhamy[B], J.G. Fadel[B] and E. Kebreab[B]

[A]Institute for Animal Science and Technology, Polytechnic University of Valencia, Spain. [B]Department of Animal Science, University of California, Davis 96516, USA.

Introduction

Small ruminants make up around 52% of domesticated ruminants globally (FAO 2008), and their contribution to water and air pollution has not been studied. Small ruminants have higher intake per unit body weight than large ruminants, leading to a potential higher nitrogen (N) excretion. Nitrogen conversion efficiency ranges 5 to 20%. (Allard *et al*. 2003). Thus small ruminants can have a significant environmental impact that needs quantifying.

Model development

A mechanistic, dynamic and deterministic model was developed by representing major body-N kinetics. Mass and time units to the model were in grams and days, respectively. Dry matter intake (DMI), and dietary crude protein (CP), rumen degradable and undegradable protein, and ash contents were input variables. The model includes 3 N pools; N in rumen (Q_R), N in post-rumen compartments (Q_PR) and blood plasma-N (Q_P, Fig. 1). All fluxes were represented by mass action equations. Fractional rates of plasma-N flux to the rumen, duodenal-N passage, and N excretion in urine were adjusted for dietary CP content, DMI and dietary ash content, respectively (Fig. 1). The model was optimized by solving for all the parameters simultaneously and internally evaluated using 73 measured fecal, urinary and milk-N output observations from mid-lactation Mediterranean dairy goats fed total mixed rations (forage, 40%; CP, 14-20% DM; DMI, 1400-2300 g/day).

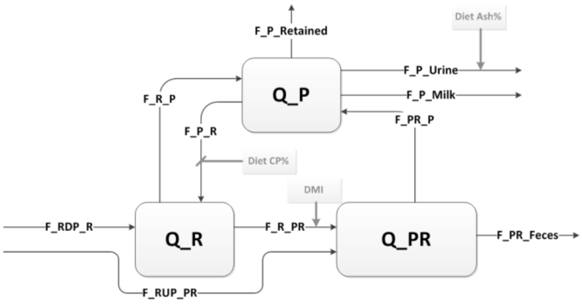

Fig. 1. Schematic representation of N kinetics in the model.

Results and discussion

Standard deviations of model parameter estimates were <25% of the estimates suggesting that the data were adequate to describe the model. The optimised model predicted fecal- and urinary-N excretions with root mean square prediction error of 17.4 and 23.5% of the average observed values, respectively. In both cases, less than 5% of the prediction error was systematic indicating good representation and parameterization of N kinetics in the model.

References

Allard V, Newton PC, Lieffering M, Clark H, Matthew C. Soussana JF, Gray YS (2003) Nitrogen cycling in grazed pastures at elevated CO_2: N returns by ruminanats. *Global Change Biology* **9**, 1731-1742.

FAO (2008) FAOSTAT, http://faostat.fao.org/site/569/default.aspx

[C]Corresponding author: cjfernandez@dca.upv.es

Topic: Digestion, metabolism and consequences for productivity

Direct *in vitro* measurement of indigestible neutral detergent fibre to improve the prediction of milk production from subtropical forages

K.J. Harper[A,B] and D.M. McNeill[A]

[A]The University of Queensland, Gatton Campus, Gatton 4343, Australia.

Introduction

The Cornell Net Carbohydrate and Protein System (CNCPS) model derives indigestible neutral detergent fibre (iNDF) values by acid detergent lignin x 2.4 (iNDF2.4). However, this relationship is questionable in subtropical forages. The objective of this study was to compare the CNCPS estimated available metabolisable energy (ME) and potential milk yield from forages using the model derived iNDF2.4 values, with iNDF values determined by long term fermentation (iNDF240).

Methods

Forage groups and their chemical compositions, determined from a survey of the Queensland dairy industry (C4Milk project) were recorded into the CNCPS library. The location and animal inputs were standardised for all simulations. For ease of comparison no other feed ingredients were included in the diet. Simulations predicting available ME (MJ/day) and milk yield (kg/day) were compared with forages formulated with iNDF2.4 or iNDF240 values. The iNDF240 values were determined by long term (240 h) *in vitro* fermentation.

Results and discussion

The CNCPS simulation showed considerable variation in predicted ME supply due to iNDF input, leading to differences in milk production ranging from +1.3 to -6.3 kg (Table 1).

Table 1. Milk yield (kg/day) and total ME supply (MJ/day) estimates from the CNCPS, based on predicted iNDF2.4 or *in vitro* iNDF240 of forage groups relevant to dairy diets in Queensland

Forage	iNDF2.4 (%DM)	iNDF240 (%DM)	Kd (%/hour)	ME iNDF2.4	Milk NDF2.4	ME iNDF240	Milk iNDF240	Δ Milk
				Silages				
Barley	13.13	10.48	7	135.1	12.2	140.2	13.5	+1.3
Sorghum	12.73	22.44	5	116.7	6.9	99.2	0.6	-6.3
				Pastures				
Tropical mix	12.16	21.39	5	126.4	9.5	110	4.4	-5.1
Ryegrass	7.87	10.3	9	146.4	12.5	141.4	11.2	-1.3

Inputs were: continuously grazed, 45 month old dairy cows, shrunk LW 576 kg, 120 days in milk, milk fat 4%, DMI 15 kg/day. The iNDF240 was inputted by adjusting the ADL content as determined by iNDF240/2.4

The CNCPS model's estimates of iNDF from ADL were reliable for the two temperate forage groups. By contrast, CNCPS over-predicted milk yield in the subtropical forage groups if iNDF2.4 were used. This helps to explain why models such as the CNCPS can perform sub-optimally for subtropical feeding systems. Directly measured iNDF240 values should be included in diet formulation models.

Funded by Dairy Australia, QDAFF and The University of Queensland.

[B]Corresponding author: karen.harper@uq.edu

Remodelling the interaction between probiotic *Bacillis subtilis* and rumen microbiota of black and white breed calves

R.V. Nekrasov[A,D], *N.A. Ushakova*[B], *G.Y. Laptev*[C] *and L.A. Il'ina*[C]

[A]All-Russian Research Institute of Animal Husbandry, Russian Academy of Sciences, Dubrovitsy, Moscow region, Russia. [B]Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences, Moscow, Russia.[C]BIOTROF Ltd., Kolpino, St. Petersburg, Russia.

Introduction

Supplementing the ration for ruminants with probiotics improves health status of the animals including reduction in incidence of diarrhoea and lowering the number of pathogenic microorganisms in the rumen (Gaggìa *et al*. 2010). Composition of the rumen microbiota and its interaction with probiotics can be investigated using modern molecular biology techniques such as Terminal Restriction Fragment Length Polymorphism (T-RFLP)(Hartman and Widmar 2008).

Methods

Ten black and white breed calves aged 4 weeks were randomly divided into two groups to study the effect of biofilm-protected probiotic *B. subtilis* B-8130 on a phyto-carrier. The control group was fed milk plus concentrates and did not receive probiotic. The experimental group was fed a forage-based ration supplemented with 0.1% of the probiotic. The species composition of the microbial community from the rumen fluid of calves (age 4.5 mo, N = 3) was investigated using T-RFLP. Samples of rumen fluid were collected 3 h after feeding.

Results

After changing the ration from dairy to plant, the rumen fluid of the control group was dominated by *Firmicutes* bacteria, including *Clostridia*, *Lachnospiraceae* and *Clostridiaceae*. Other microorganisms were *Bacteroidetes*, *Actinobacteria* and uncultured *Bacillaceae*. Addition of probiotic *B. subtilis* B-8130 to the ration of the experimental animals increased the number of *Thermoanaerobacteriaceae*, *Peptostreptococcaceae*, *Alicyclobacillaceae* and *Pseudomonadaceae*, *Burkholderiaceae*, and uncultured *Bacteroidetes* in the rumen. This restructured rumen microbiota contributed to an increase in average daily gain of 13%. Correlation coefficient analysis of distinct *Ruminococcaceae* microorganisms showed that their genome has 250 bp long products corresponding to the phylotype of *Faecalibacterium* that correlates negatively with digestion and productivity of the animals. The probiotic-based ration facilitated a significant 53% reduction in their number ($P<0.05$).

Conclusions

We demonstrate that productivity of calves can be improved during transition from dairy to plant-based rations using the probiotic *B. subtilis* B-8130. T-RFLP analysis is useful for monitoring the development of the rumen microbial population.

References

Gaggìa F, Mattarelli P, Biavati B (2010) Probiotics and prebiotics in animal feeding for safe food production. *International Journal of Food Microbiology* **141**, 15-28.

Hartman N, Widmar F (2008) Reliability for detecting composition and changes of microbial communities by T-RFLP genetic profiling. *FEMS Microbiology Ecology* **63**, 249-260.

[D]Corresponding author: nek_roman@mail.ru

Topic: Digestion, metabolism and consequences for productivity

Estimating the energetic cost of feeding excess nitrogen to dairy cattle

K.F. Reed[A,C]*, D.P. Casper*[B] *and E. Kebreab*[A]

[A]Department of Animal Science, University of California, Davis, CA, USA. [B]Dairy Science Department, South Dakota State University, SD, USA.

Introduction

Tyrrell *et al.* (1970) found that digestible N (DigN) fed above the animal's requirement had a negative effect on the energy balance (EB) of the lactating cow. However, little effort has been made to further quantify the energetic cost of overfeeding N or to incorporate excess N excretion into nutrient requirement models. Our objectives are to re-evaluate the results reported by Tyrell *et al.* (1970) and re-estimate the effect of excess DigN on energy balance using a larger and newer data set and a cross-classified mixed-model framework.

Methods

A data set containing 1,094 indirect calorimetry observations on lactating dairy cattle was subset to obtain the 330 observations collected before 1970. This data subset was then split into observations having a positive and negative N balance (*ExN*) and fit to the following linear model: $\boldsymbol{EB} = \beta_0 + \beta_1 \times \boldsymbol{EI} + \beta_2 \times \boldsymbol{MBW} + \beta_3 \times \boldsymbol{ExN} + \beta_4 \times \boldsymbol{EC}$ where *EB* (MJ) is the difference between energy intake and expenditure (Tyrrell *et al.* 1970); *EI* is the digestible energy (DE, MJ) or metabolizable energy (ME, MJ) intake; *MBW* is metabolic body weight ($\text{kg}^{3/4}$); *ExN* (g) is DigN above requirement (Tyrrell *et al.* 1970); and *EC* is the energy content of the feed in either DE or ME (MJ/kg).

Similarly, the full data set was split according to observations having positive and negative *ExN* and fitted to the above linear model with the addition of cross-classified random effects for animal and study. *EB*, and *ExN* were calculated according to NRC (2001) recommendations.

Results and discussion

Re-evaluation of Tyrrell *et al.* (1970) gave qualitatively similar estimates for all parameters (Table 1). Using DE but not ME as the energy unit, positive *ExN* has a significant negative effect on *EB*, suggesting that this effect is due to the energy in urine. However, further investigation into the relationship of *EB* and the different forms of DigN (i.e. true protein vs. non-protein N) is required.

Table 1. Parameter estimates of the linear mixed model fit to observations from the full data set with positive or negative nitrogen balance using digestible or metabolizable energy

Model	β_0	β_1	β_2	β_3	β_4
Positive ExN, ME	-9.1 (0.95)	6.6e-4 (6.9e-6)	-8.0e-2 (5.6e-3)	1.3e-3 (1.13e-3)	3.1 (0.27)
Negative ExN, ME	-4.6 (2.22)	6.1e-4 (2.22e-5)	-9.1e-2 (1.34e-2)	8.0e-4 (7.60e-3)	2.8 (0.70)
Positive ExN, DE	-14 (1.16)	6.1e-4 (7.0e-6)	-9.2e-2 (6.1e-3)	-3.5e-3 (1.28e-3)	4.2 (0.31)
Negative ExN, DE	-4.6 (2.70)	5.5e-4 (2.25e-5)	-0.10 (1.56e-2)	-1.5e-3 (8.97e-3)	2.6 (0.77)

References

National Research Council (2001) 'Nutrient Requirements of Dairy Cattle' 7th rev. edn. (National Academy of Sciences: Washington, DC).

Tyrrell HF, Moe PW, Flatt WP (1970) 'Influence of Excess Protein Intake on Energy Metabolism of the Dairy Cow' In 'Proceedings of the 5th EAAP Symposium on Energy Metabolism of Farm Animals'. (Ed A Schürch and C Wenk) pp. 69-72. (Juris Verlag, Zurich).

[C]Corresponding author: kfreed@ucdavis.edu

Topic: Digestion, metabolism and consequences for productivity

Representing interconversion among volatile fatty acids did not improve prediction of their production in the Molly cow model

S. Ghimire[A,D]*, R.A. Kohn*[B]*, P. Gregorini*[C] *and M.D. Hanigan*[A]

[A]Virginia Polytechnic Institute and State University, Blacksburg, VA 24061, USA. [B]University of Maryland, College Park, MD 20742, USA. [C]DairyNZ Ltd., Hamilton, New Zealand.

Introduction

The Molly cow model uses three sets of coefficients for forage, concentrate and mixed diets to predict volatile fatty acid (VFA) production (Murphy *et al.* 1982) which, from our recent study, showed large prediction errors. In the present study, these errors were evaluated by rederiving parameters with and without including VFA interconversion equations based on thermodynamics.

Methods

Equations based on thermodynamics were derived to represent interconversion among VFA with pH and VFA concentration as driving variables. Rate constants were calculated from mean observation of a dataset including eight studies with reported pH, VFA production and concentration. For parameter estimation, this dataset was combined with another dataset with 62 studies reporting VFA concentrations. The parameters for *de novo* acetate, propionate and butyrate production from individual dietary fractions within forage and concentrate diets were utilised to create equations which weighed parameters in a continuous manner based on forage to concentrate ratio. The base parameters were bounded to ensure complete carbon balance and estimated along with VFA absorption constants, both before (5V) and after (5W) inclusion of interconversion equations.

Results and discussion

The final parameters did not improve predictions of VFA production in either model (Table 1). Propionate and butyrate concentration predictions were improved by ~10% but with increased errors for production. Parameters for VFA absorption changed (+33 to +46 %) significantly (>30%) in both 5V and 5W. When the residuals of VFA production were plotted against predicted pH there was significant slope bias for acetate and propionate which suggests the potential for improvement if effects of pH on VFA production were better represented in the model.

Table 1. Root mean squared prediction errors (% of mean) of concentration and production of volatile fatty acids (VFA) before (Initial) and after (Final) re-derived VFA coefficient in unaltered (5V) and an altered (5w) to represent interconversion between VFA in the Molly cow model

Models	Concentration						Production					
	Acetate		Propionate		Butyrate		Acetate		Propionate		Butyrate	
	Initial	Final	Initial	Final	Initial	Final	Initial	Final	Initial	Final	Initial	Final
5V	23	21	42	30	35	26	66	69	65	71	52	56
5W	20	20	55	31	28	26	69	70	66	76	66	53

Reference

Murphy MR, Baldwin R, Koong LJ (1982) Estimation of stoichiometric parameters for rumen fermentation of roughage and concentrate diets. *Journal of Animal Science* **55**, 411-21.

[D]Corresponding author: sand72@vt.edu

Adjusting energy use by Molly using mitochondrial respiration data

H.A. Rossow[A,C] *and C.C. Calvert*[B]

[A]Dept of Population Health and Reproduction, Veterinary Medicine Teaching and Research Center, University of California, Tulare CA 93274, USA. [B]Department of Animal Science, University of California, Davis CA 95616, USA.

Introduction

The model of a dairy cow, Molly (Baldwin 1995), was developed using ATP yields that did not account for decreased ATP yields due to proton leak. The objective of this research is to use data from isolated liver mitochondria from dairy cows to determine the impact of proton leak.

Methods

Liver P/O ratio (PO), maximal substrate oxidation and production parameters were measured on 50 lactating Holstein dairy cows at approximately 80 days in milk. Liver mitochondria were isolated to measure oxygen consumption due to ATP synthesis, proton leak and estimate PO (Ramsey *et al*. 2004). Using the Advanced Continuous Simulation Language (ACSLX v. 2.5.0.6, 2012), simulations of measured data were used to predict the impact of different PO based on measures of mitochondrial succinate oxidation as a proxy for glucose oxidation.

Results and discussion

Low PO ratios, as observed from isolated mitochondria, decrease predicted body fat, milk fat and increase acetate, glucose and fatty acid oxidation. These results indicate that isolated mitochondria could be used to estimate maximal velocities of substrate oxidation and PO and the assumption of equivalent maximal velocities for substrate oxidation may not be valid.

Table 1. Measured cow parameters vs. estimated parameters using Molly

Parameters	Measured (PO = 1.34)	Molly theoretical max (PO = 2.65)[A]	Molly No proton leak (PO = 3)
Milk, kg/day	47 (7.3)	46	46
Milk fat, kg/day	1.6 (0.77)	1.7	1.8
Milk protein, kg/day	1.4 (0.54)	1.4	1.5
Body fat kg	82	140	146
Acetate oxidation, mol/day	39	27	25
Glucose oxidation, mol/day	10	8.7	8.5
Fatty acid oxidation, mol/day	2.8	1.3	1.1

[A]Theoretical maximum PO based on calculations from Kennedy (personal communication, 2014).

[B]Standard deviations are in parentheses and represent cow measurements.

References

Baldwin RL (1995) Modeling Ruminant Digestion and Metabolism. Chapman & Hall, London, UK.

Ramsey JJ, Hagopian K, Kenny TM, Koomson EK, Bevilacqua L, Weindruch R, Harper, ME (2004) Proton leak and hydrogen peroxide production in liver mitochondria from energy- restricted rats. *American Journal of Physiology Endocrinology Metabolism* **286**, E31-E40.

[C]Corresponding author: Heidi.Rossow@gmail.com

Effect of body weight on protein requirements for maintenance in growing *Bos indicus* cattle

M.L. Chizzotti[A,B,C], *D.Heiderich*[A], *M.M. Ladeira*[A], *P.T da Silva*[A]

[A]Department of Animal Science, Universidade Federal de Viçosa, Viçosa, Brazil. [B]Department of Animal Science, Universidade Federal de Lavras, Lavras, Brazil.

Introduction

This work was conducted to evaluate the physiological stage of Nellore cattle over the requirements of protein for maintenance, determined in g/kg of body weight or g/kg of metabolic weight ($kg^{0.75}$).

Methods

Eighteen non-castrated bulls of the Nellore breed were used in 3 consecutive trials at different stages of maturity (at 320, 400 or 480 kg bodyweight (BW)). In each trial, eight 3x3 Latin squares design trials were used, with 3 treatments (10, 14 or 18% crude protein), 3 experimental periods and 3 animals. The forage:concentrate ratio was 60:40. Each experimental period lasted 14 days, being 9 days for adaptation and 5 days for total collection of feces and urine. Nitrogen balance was evaluated in each maturity stage. The total endogenous losses were estimated by regressing the N balance on N intake, expressed in g N/kg BW or g N/kg $BW^{0.75}$, considering the intercept as the net requirements of protein for maintenance. The slope coefficient of the regression of absorbed N on N intake was used to determine the efficiency of utilization of metabolisable protein for maintenance (MPm). The requirement for MPm was determined by dividing the net protein for maintenance (NPm) by the efficiency of utilization of metabolisable protein. The experimental data was analysed using the MIXED procedure of SAS 9.3, considering the fixed effect of the 3 weight groups (above), the 3 diets (10, 14 or 18% CP) with random effects of experimental period and animal nested within each experimental period. The solution procedure was used to adjust the linear regressions. A critical level of probability of type I error of 0.05 was used. The AIC and BIC criteria were used to evaluate the best fitted model, comparing the regressions based on liveweight versus metabolic BW to estimate the protein requirements.

Results and discussion

A decrease in N retention per unit body weight with increasing BW was observed. The net nitrogen loss, in g N/kg BW.day, decreased with increasing BW, as did the efficiency of use of absorbed amino acids. The requirements for MPm decreased ($P < 0.05$) as BW increased, according to the following equation: MPm (g CP/kg BW.day) = 2.2441 - 0.0034 x BW (kg). This decrease in requirements for MPm can be explained by the fact that with increasing age/weight there is decreased lean tissue deposition and increased carcass fat, which reduces protein synthesis and degradation and consequently the loss of endogenous-N. The prediction equations to estimate NPm and MPm provided a better fit when expressed in relation to BW compared to metabolic weight, and therefore we suggest expressing the requirements for protein in g/kg BW and adjust those requirements for the BW of the animals. In conclusion, the endogenous losses of nitrogen, the net and metabolisable requirements of protein for maintenance in g/kg BW, and the efficiency of utilization of metabolisable protein decrease with advancing stage of maturity.

The authors thank CAPES and CNPq.

[C]Corresponding author: mariochizzotti@ufv.br

Overview of the Methane Prediction Module in the AusBeef Rumen Model

H.C. Dougherty[A,F], *E. Kebreab*[A], *B.A. Little*[B], *A.B. Ingham*[B], *R.S. Hegarty*[C]. *D. Pacheco*[D] *and M.J. McPhee*[E]

[A]Department of Animal Science, University of California, Davis, CA 95616, USA. [B]Animal, Food, and Health Sciences, CSIRO, St. Lucia, QLD 4067, Australia. [C]School of Env. Rural Science, University of New England, Armidale, NSW 2351, Australia. [D]AgResearch Grasslands, Palmerston North 4442, New Zealand. [E]Department of Primary Industries, Armidale, NSW 2351, Australia.

Introduction

Improved livestock nutrition modelling can enable better description and prediction of the physiological and environmental effects of specific production processes, thereby improving productivity and efficiency. Although there are several models of livestock methane emissions (e.g., Ellis *et al.* 2007) few mechanistic whole-animal models exist. The AusBeef rumen model, initially proposed and developed by Nagorcka and Zurcher (2002), is one of the few whole-animal dynamic and mechanistic models that can be used to predict both productivity and enteric fermentation from ruminants.

Methods

The AusBeef model is an integration of several sub-models including those for body growth, voluntary feed intake, rumen, and lower gut. Each of these models contains additional sub-models, allowing for more accurate prediction of a variety of biological processes. The methane (CH_4) module within the rumen submodel of AusBeef is discussed below.

Results and discussion

There are seven equations that explicitly deal with CH_4 production. The main equation relates rumen hydrogen (H_2) balance to CH_4 production. Hydrogen is produced from rumen fermentation of hexose and amino acids and from microbial growth. Hexose is fermented to volatile fatty acids (VFAs) by cellulolytic and amylolytic bacteria, as well as by protozoa, with some VFAs produced by the fermentation of protein. Hydrogen is produced by fermentation of hexose and amino acids as well as by microbial growth; H_2 production from microbial growth is related to soluble protein uptake in the rumen. Hydrogen is also consumed by VFA production, biohydrogenation of dietary lipids, and microbial growth, with uptake into microbes related to ammonia utilised for growth by amylolytic and cellulolytic bacteria.The model requires improvement in dealing with the effect of nitrates and dietary lipids in reducing enteric methane production. A major redevelopment of the AusBeef rumen sub-model is underway, so that the sub-model will run within AusFarm, a software tool to analyse whole-farm simulation studies.

References

Ellis JL, Kebreab E, Odongo NE, McBride BW, Okine EK, France J (2012) Prediction of methane production from dairy and beef cattle. *Journal of Dairy Science* **90**, 3456-3466.

Nagorcka BN, Zurcher EJ (2002) The potential gains achievable through access to more advanced mechanistic models of ruminants. *Animal Production in Australia* **24**,455-561.

[F]Corresponding author: hdougherty@ucdavis.edu

Topic: Digestion, metabolism and consequences for productivity

Prediction of body composition based on body protein mass in growing goats

C.J. Härter[A], *N. St-Pierre*[B], *and I.A.M.A. Teixeira*[A,C]

[A]Univ. Estadua Paulista, Department of Animal Sciences, Jaboticabal, SP 14884-900, Brazil. [B]The Ohio State University, Department of Animal Sciences, Columbus, OH 43210, USA.

Introduction

Accurate body composition prediction is fundamental in feeding systems, primarily because nutrient requirements of growing animals are based on it. Allometric equations based on empty body weight (EBW) are often applied to predict body composition in growing small ruminants. However, previous studies with poultry and swine recommended use of estimates of water and ash body composition based on protein mass (PM) because environmental changes exert less influence on body protein mass (NRC 2012). There is a lack of information on whether the approach of using allometric equations based on protein mass to predict body composition can also be applied to growing goats and the current study evaluated this aspect.

Methods

Allometric equations based on EBW and on body PM to predict ash and fat body composition were compared using data from 32 F1 Boer × Saanen and 25 Saanen male kids from 5 to 25 kg of body weight. The data were obtained using the comparative slaughtered methodology. The parameters of the equations based on EBW and PM were compared between breeds. For this the allometric equations were jointly fitted for the two breeds studied using the PROC NLIN and the MARQUARDT methods of SAS v9.2. This statistical analysis allows testing the effect of breed on the function parameters using a straightforward t-test. The HOUGAARD option of the PROC NLIN was used to estimate the skewness of the parameters estimated and it was also used to ensure that the t-tests were valid.

Results and discussion

Our results showed that ash and fat body composition can be predicted using allometric equations based on EBW or PM. Ash and fat body composition estimates based on EBW were different between breeds; however this difference disappeared when they were estimated based on PM. Ash accretion based on PM for both breeds was constant (212 g of ash/kg of PM), but fat accretion increased from 361 to 954 g/kg of PM gain when body weight increased from 5 to 25 kg. Protein mass seems a better predictor of body composition, as shown here, because PM excluded the effect of the proportion of mature weight (i.e., breed effect). These findings are in accordance with current knowledge that potential body protein is less influenced by environmental changes because it is a genetic characteristic primarily under homeorhetic control. In addition, mature weight of a given breed is directly related to the rate of tissue deposition in the body, and these rates determine the differences in body composition between breeds (Owens *et al.* 1993). Therefore, allometric equation based on PM should be used to predict ash and fat body deposition in intact male goats at pre-pubertal ages from different breeds.

References

Owens FN, Dubeski P, Hanson CF (1993) Factors that alter the growth and development of ruminants. *Journal of Animal Science* **71**(11), 3138-3150.

NRC (2012) 'Nutrient requirements of swine.' Eleventh revised edition. (The National Academy Press: Washington, DC)

[C]Corresponding author: izabelle@fcav.unesp.br

Topic: Digestion, metabolism and consequences for productivity

Estimating intramuscular fat content from CT scan images

Y.C.S.M. Laurenson[A,C] *and M.J. McPhee*[B]

[A]School of Environmental & Rural Science, University of New England, Armidale, NSW 2351, Australia. [B]NSW Department of Primary Industries, Beef Industries Centre of Excellence, Trevenna Rd, Armidale, NSW 2351, Australia.

Introduction

Intramuscular fat (IMF) content is an important attribute determining meat quality, with higher contents of IMF resulting in the improved palatability of beef. Currently, IMF content is subjectively determined by visual appraisal of intramuscular fat deposits within the *longissimus dorsi* (i.e. marbling score). Chemical analysis (ether extraction) provides an objective determination of IMF content. However, this method is destructive and incurs significant financial and diuturnal costs. A number of automated image analysis systems for determining tissue composition from CT scan images have previously been proposed (Thompson and Kinghorn 1992; Alston *et al*. 2005), but as yet none are capable of estimating IMF content. This abstract outlines a framework for the quantification of IMF from CT scan images of deboned beef primal cuts.

Method and validation

A histogram of the frequency of greyscale pixel values was used to summarise CT scan images of a beef primal cut. The typical bimodal pattern was assumed to represent the differing densities of fat and muscle. Otsu thresholding was implemented to provide the pixel value boundary between fat and muscle, however, it should be noted that the density distributions of fat and muscle are not discrete. Thus, a Gaussian mixture model was fitted to the frequency plot by using the corrected Akaike's information criterion to determine the number of Gaussian distributions, as well as their means, standard deviations and weightings. This resulted in a number of overlapping normal distributions, which were assigned as fat or muscle depending upon whether their means were above or below the boundary previously determined. Normal distributions falling into each category were then summed to give the density distributions of fat and muscle. The weights (g) of the fat and muscle components were subsequently estimated by using standards to determine the relationship between greyscale pixel value and density, resulting in an R^2 of 0.997 between estimated and observed primal weights.

CT scan images containing only lean muscle and IMF were generated by carrying out a particle analysis on pixel values less than the boundary determined by Otsu thresholding (i.e. fat). Particles greater than 0.15% of the total area of fat and muscle were removed from the image (i.e. assumed to be subcutaneous and intermuscular fat). The total weight of the resultant images were then estimated as previously described. By subtracting the previously calculated weight of muscle from the estimate of muscle and IMF, we were able to quantify the IMF content of beef primal cuts.

A validation study is currently being carried out to compare the estimated weight of IMF determined by this methodology and the chemical analysis of IMF.

References

Alston CL, Mengersen KL, Thompson JM, Littlefield PJ, Perry D, Ball AJ (2005) Extending the Bayesian mixture model to incorporate spatial information in analysing sheep CAT scan images. *Australian Journal of Agricultural Research* **56**, 373-388.

Thompson JM, Kinghorn B (1992) CATMAN – A program to measure CAT scans for prediction of body components in live animals. *Proceedings of the Australian Association of Animal Breeding and Genetics* **10**, 560-564.

[C]Corresponding author: ylaurens@une.edu.au

Topic: Digestion, metabolism and consequences for productivity

Dynamic mechanistic modelling of feed efficiency in *Bos indicus* beef cattle

R.D. Sainz[A,B] *and J.W. Oltjen*[A]

[A]University of California, Davis, CA 95618 USA.

Introduction

The NRC (2000) concluded that maintenance requirements of *Bos indicus* cattle are about 10 percent lower than those of *B. taurus* cattle; however there is no mention of variation within breeds. This study aimed to examine maintenance and protein metabolism relative to feed efficiency.

Materials and methods

Individual data on feed intakes and weight gains from 20 residual feed intakes (RFI) trials with a mean duration of 73.6 ± 6.2 days, conducted with male (n=1058) and female (n=358) Nelore (n=1245), Guzerat (n=145) and Brahman x Nelore cattle (n=26) were used to fit the parameters for protein synthesis (K2) and degradation (K3), and maintenance (alpha) of the Davis Growth Model (Oltjen *et al*. 1986) in a two-stage process. First, mean values of K2 and alpha were fitted, leaving K3 fixed. Then individual values of K3 and alpha were fitted, fixing K2 at the mean value. Data and parameter values were subjected to analysis of variance, with Trial and Animal as random and Breed, Sex and RFI Group as fixed effects, with interactions included when significant.

Results and discussion

After data cleaning, 1485 records remained. Differences among RFI groups were as expected, with Low RFI cattle having lower DMI, similar ADG, greater gain:feed, and lower RFI values than High RFI cattle (Table 1). Parameters for protein degradation and maintenance energy requirements were greater and lower, respectively, in Low vs High RFI cattle. Values of K3 and alpha were correlated (r = 0.822), although this is not explicit in the model. The difference in maintenance requirements between the most and least efficient groups was > 38%, indicating that variation in maintenance requirements within breed types is much greater than the variation among breed types.

Table 1. Performance of *Bos indicus* cattle in different efficiency categories

Variable	RFI group			SD[A]	*P* value[B]
	Low	Medium	High		
n	*463*	*576*	*444*		
Dry matter intake, kg/day	8.78	9.58	10.36	0.801	< 0.0001
Average daily gain, kg/day	1.329	1.356	1.362	0.2077	0.107
Gain:feed	0.149	0.0141	0.132	0.0180	< 0.0001
Residual feed intake, kg/day	-0.756	0.007	0.750	0.308	< 0.0001
Protein degradation rate coeff.[C] (K3), $kg^{0.27}/d$	0.1375	0.1436	0.1477	0.00703	< 0.0001
Maintenance coefficient, $Mcal/kg^{0.75}\cdot day$	0.0620	0.0737	0.0860	0.0130	< 0.0001

[A]Pooled standard deviation; [B]Probability of a Type I error; [C]K3 estimated with K2 fixed at 0.05592.

References

National Research Council (2000) 'Nutrient requirements of beef cattle, 7th revised edition.' (National Academy Press: Washington, DC)

Oltjen JW, Bywater AC, Baldwin RL, Garrett WN (1986) Development of a dynamic model of beef cattle growth and composition. *Journal of Animal Science* **62**, 86-97.

[B] Corresponding author: rdsainz@ucdavis.ed

Topic: Enterprise and systems models for production and environmental impact

Quantifying the impact of nutritional, animal and farm management factors on variation in milk urea content as a proxy for N excretion

A. Bannink[A,D]*, J.W. Spek*[A]*, J.L. Ellis*[B]*, J. France*[C]*, and J. Dijkstra*[B]

[A]Animal Nutrition, Wageningen UR Livestock Research, Netherlands. [B]Animal Nutrition Group, Wageningen University, Netherlands. [C]Centre for Nutrition Modelling, University of Guelph, Canada.

Introduction

Urea excreted in urine is the primary and most variable source of undesirable nitrogen (N) emissions from dairy systems. The minor fraction of urea N transported through blood ending up in milk (MUN) is in an indicator of urea N excreted in urine (UUN). For the whole range of observed MUN values the relationship between MUN and UUN is strong. Such information would be useful were it not for a far narrower range of MUN being relevant in practice and for variation in MUN being mainly due to factors other than UUN. This work aimed to quantify the influence of these other factors on MUN.

Methods

The dynamics of urea entry in blood and urea exchange between blood, udder and kidney were quantified using a mechanistic model. The model consists of variables representing urea pools in blood, kidney and milk. Flux equations are described by Michaelis-Menten kinetics or mass action forms. Model inputs are daily patterns of rate of protein and cation digestion, ammonia absorption, milk synthesis and milking. Model outputs are urea N concentration in blood plasma (PUN), MUN, urine volume and UUN.

Results and discussion

The MUN depends on PUN. Any parameter that affects PUN dynamics may hence affect MUN in collected milk. Therefore, quantifying variation in MUN that is unrelated to variation in UUN requires a quantitative understanding of PUN dynamics as affected by nutritional, management and animal factors. Nutritional factors quantified were types of carbohydrates and proteins fed (affecting the dynamics of ammonia entry in blood plasma and amino acid catabolism), and dietary effects on water dynamics and kidney function (urea reabsorption from glomerular filtrate) and on urea recycling to the gastrointestinal tract (Spek *et al.* 2013). Management factors quantified were the moment and frequency of milking and feeding. Net urea transfer between blood and milk appeared to depend on the urea concentration gradient. Changes in MUN followed those in PUN with a lag because of the time involved with urea transfer between milk and blood and between milk compartments in the udder, and recovery of labelled urea injected into the udder cistern depended on the time period between infusion and milking (Spek *et al.* 2012). MUN is a heritable animal characteristic, but this heritability appeared unrelated to variation in N utilisation and UUN at equal N intake. Using MUN as an indicator of UUN would benefit from a representation of physiological factors that underlie this heritability.

References

Spek JW, Dijkstra J, van den Borne JJGC, Bannink A (2012) Short communication: Assessing urea transport from milk to blood in dairy cows. *Journal of Dairy Science* **95**, 6536–6541.

Spek JW, Dijkstra J, van Duinkerken G, Bannink A (2013) A review of factors influencing milk urea concentration and its relationship with urinary urea excretion in lactating dairy cattle. *Journal of Agricultural Science* **151**, 407-423.

[D]Corresponding author: andre.bannink@wur.nl

Topic: Enterprise and systems models for production and environmental impact

Towards resilient livestock systems: a modelling approach to explore the combination of different genetic selection and herd management solutions

F. Douhard[A,B,C,D,F], *M. Tichit*[B,D], *P.R. Amer*[E] *and N.C. Friggens*[A,C]

[A]INRA, UMR 791 MoSAR, F-75005 Paris, France. [B]INRA, UMR 1048 Sad-APT, F-75005, Paris, France.
[C]AgroParisTech, UMR 791 MoSAR, F-75005 Paris, France. [D]AgroParisTech, UMR 1048 Sad-APT,
F-75005 Paris, France. [E]AbacusBio Limited, 442 Moray Place, Dunedin 9058, New Zealand.

Introduction

Locally, farm managers can influence the genetic selection process to better match herd genotype to environment. This study focused on selection according to extended lactation (EL), in dairy goat herds. Extended lactation is when females are not re-bred after parturition, but continue their lactation until the next breeding season. This implies changes in survival and reproduction rates at the herd level, which may then shape different long-term selection responses.

Methods

An animal model was developed to predict changes in the genetic composition of a dairy goat herd as affected by feeding level and the genetic selection pressure applied by the farm manager. The model incorporates different resource allocation coefficients between biological functions as heritable traits. It simulates short-term animal performance for different management options and long-term selection responses resulting from the transmission of traits between generations.

Results and discussion

In a herd subject to variations in the achieved feeding level, different selection strategies were explored to improve milk yield and longevity (as measured by the age of animals). Under standard management conditions (no EL) long-term selection responses to an increasing emphasis on longevity caused a trade-off at the herd level between increasing milk yield and improving survival (Fig. 1, grey line). When selection was combined with EL management for a part of the herd, the previous trade-off was alleviated (Fig. 1, arrow).

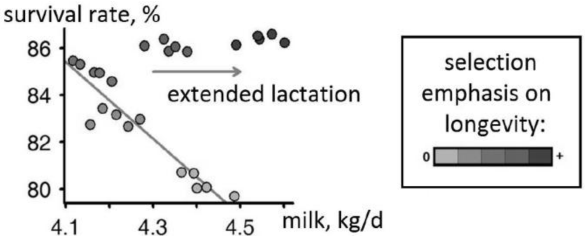

Fig. 1. Herd survival and production responses to selection for milk yield, successful reproduction and an increasing emphasis on longevity (age of animals; increasing density of shading). Selection was simulated for 40 years and the last 5 years are shown for each case.

The synergy between selection and management resulted from a complex interaction between the temporal changes of individual performance during EL and the transmission of allocation traits between generations due to herd replacement. Combining selection and management within the herd represents an effective approach to exploit genotype-by-environment interactions. Further research will be needed to assess the practical implications of this approach and the new methodology presented may well be a basis for this.

[F]Corresponding author: frederic.douhard@agroparistech.fr

Topic: Enterprise and systems models for production and environmental impact

Integrating forage supply and livestock demand models to analyse farm feed system performance

L.W. Bell[A,D]*, A.D. Moore*[B] *and D.T. Thomas*[C]

CSIRO Agriculture Flagship: [A]Toowoomba, Qld 4350, Australia; [B]Black Mountain, ACT 2601; Australia; [C]Wembley, WA 6014, Australia.

Introduction

Year-to-year variability and seasonality in forage supply cause a mismatch between forage supply and animal demand in many livestock production systems in Australia. This induces inefficiencies in production in terms of excess feed wasted or unmet animal demand. Producers often adopt more conservative stocking rates to manage this risk. Developing simple tools that capture dynamics of feed supply and demand over time can enable the risk associated with a range of strategic choices of forage mixes, livestock enterprise and stocking rates to be evaluated.

Methods

A combination of the forage simulation models, APSIM (Forage crops, crop residues, Lucerne), Grassgro (temperate pastures) and GRASP (tropical grass pasture) predicted growth of key forage sources over the long-term at a range of locations across Australia's crop-livestock zone. Livestock demands for typical enterprises were calculated based on animal energy requirements for each class of stock accounting for annual growth and lactation cycles. By combining the predicted growth and quality of various forages the whole-farm feed supply can be compared against monthly feed demand for the whole livestock enterprises on a metabolisable energy basis.

Results and discussion

Fig. 1a demonstrates how such an simple approach can be used to examine how different farm feed-base mixes can fill feed gaps and reduce the frequency and size of a farm feed deficit. For example, utilising crop residues is found to be very valuable at reducing the risk of farm feed deficits and can enable farm stocking rates to be increased by 40% without increasing the frequency of feed gaps. Scenarios of trade-offs between risk and increasing potential farm livestock productivity within given feed systems can then be evaluated (Fig. 1b).

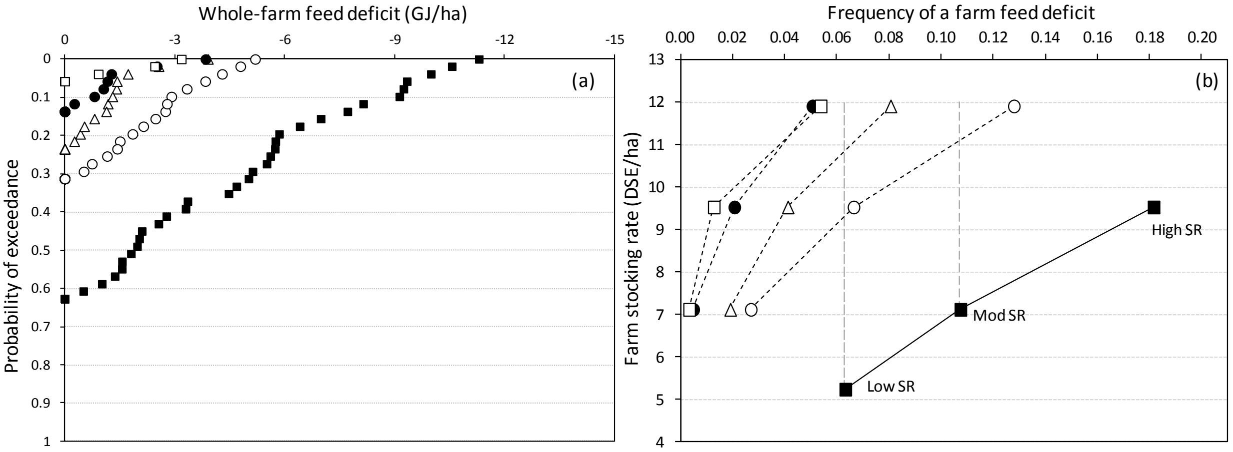

Fig. 1. Frequency and size of whole farm energy deficits (a) and effects of farm stocking rate (SR, per pasture ha) on risk of farm feed deficits for different farm feed base mixes (b); Annual pasture only (■), + 25% wheat stubble (○), + 25% dual-purpose cereal (Δ), + 25% phalaris (●), + 25% lucerne (□).

[D]Corresponding author: lindsay.bell@csiro.au

Management practices can improve feedbase use and reduce the risk of low ground cover and erosion in mixed-farming regions of southern Australia

D.T. Thomas[A,D], *A.D. Moore*[B] *and L.W. Bell*[C]

[A]CSIRO, Wembley, WA 6014, Australia. [B]CSIRO, Black Mountain, ACT 2601, Australia. [C]CSIRO, Toowoomba, Qld 4350, Australia.

Introduction

A biophysical simulation study was designed to investigate effects of implementing farming management practices on farm production and resilience in mixed cropping and livestock systems of southern Australia. Eight areas of intervention were applied based on farming systems options and innovations prioritised within the national 'Grain and Graze' research program. Whole farm effects of each intervention, and the "best practice" combination of interventions, were examined.

Methods

For each location, a mixed farming systems model was constructed by linking the APSIM soil water, soil nutrient cycling, annual crop and surface residue simulation models to the GRAZPLAN pasture and ruminant simulation models, using AusFarm® modelling software. In addition to production of crops, pastures and livestock, the model predicted the effects of ground cover management on the water balance (including runoff and potential water erosion) and inputs of carbon to the soil. Producers and industry professionals were consulted, together with land use and production statistics from the Australian Bureau of Statistics' 2011 Agricultural Census, to compile a description of soils and enterprise characteristics, land use allocation and management practices in a well-run mixed farm at seven locations (representing different regions) in southern Australia.

Results

The simulation results identified interventions that had consistent effects across locations, and those that were important at specific locations. For example, pasture utilization increased by 5 percentage units on average when stock were excluded from grazing crop residues. Pasture use increased at some locations, but not others, when confinement feeding was reduced or excluded. The removal of pasture legumes or lower pasture soil fertility resulted in an increase by 5 days in the number of days where ground cover was < 50% across locations. However, this effect was quite variable among locations (-1 to +14 days). Provision of confinement feeding reduced greatly wind erosion risk at 2 of the 7 locations (2 and 5-fold; Minnipa, SA and Temora, NSW), with less effect at other sites. Not burning crop residues had the most consistently effect on erosion risk across all sites, reducing water erosion risk by 16-41% and wind erosion risk (excluding 1 site) by 16-86%.

Discussion

This study demonstrated that the environmental outcomes of a range of management interventions can be examined using this agricultural systems modelling method. Interventions that were associated with improved pasture productivity and the direct management of cover (e.g. stubble burning and confinement feeding) had the largest effects on reducing the frequency of low ground cover and high erosion risk. Location X land use system X intervention interactions were apparent, indicating that various interventions would be of greater value when location and land use system is considered. The arbitrary "best practice" combination of interventions generally performed well across the range of indicators we evaluated, suggesting that additive improvements in ground cover and reduced erosion risk on mixed farms are likely by implementing multiple interventions.

[D]Corresponding author: dean.thomas@csiro.au

Topic: Enterprise and systems models for production and environmental impact

Evaluation of the Small Ruminant Nutrition System model (SRNS) for goat production in Vietnam

N.H. Quan[A,B], D. Parsons[A,D], N.H. Van[B], N.X. Ba[B], P.A. Lane[A], A.E.O. Malau-Aduli[A], and L.O. Tedeschi[C]

[A]School of Land and Food, Tasmanian Institute of Agriculture, University of Tasmania. [B]Faculty of Animal Sciences, Hue University of Agriculture and Forestry, Hue City, Vietnam. [C]Department of Animal Science, Texas A&M University, College Station, TX 77845-2471, United States.

Introduction

Applied nutrition models that can accurately predict goat performance under different feed intake regimes play a crucial role in developing improved feeding strategies. The primary objective of this study was to evaluate the ability of the SRNS model to predict the dry matter intake (DMI), average daily gain (ADG), nutrient digestibility, and faecal output characteristics of Vietnamese goats.

Methods

The SRNS version 1.9.4468 (http://nutritionmodels.tamu.edu/srns.html) was used to simulate animal intake and performance of two local Vietnamese goat breeds for four feeding experiments.

Results

The model under-predicted DMI (kg/d) for most treatments (R^2 = 0.70) and under-predicted ADG (g/d) for all treatments (R^2 = 0.69) (Table 1). Nutrient digestibility and faecal outputs were generally under-predicted. Coefficients of determination for DM (0.94) and CP digestibility (0.93) were high.

Table 1. Coefficient of determination (R^2), root mean square error (RMSE), slope (b), and y-intercept (a) for regression of observed and model-predicted outputs (four experiments)

Parameter	R^2	RMSE	Slope			Intercept		
			b	SD_b	Prob. b = 1	a	SD_a	Prob. a = 0
Growing period								
Dry matter intake	0.70	0.10	1.48	0.29	0.12	-0.09	0.11	0.44
Average daily gain	0.69	29.9	0.81	0.21	0.39	46.86	13.3	0.01
Digestibility period								
Dry matter digestibility	0.94	5.06	1.31	0.24	0.23	-12.18	15.4	0.45
Digestible organic matter	0.47	6.64	1.01	0.34	0.97	5.87	21.9	0.79
Digestible crude protein	0.93	6.45	1.15	0.10	0.17	0.03	5.84	0.99
Faecal output								
Dry matter	0.61	25.3	0.76	0.19	0.25	7.58	30.6	0.80
Organic matter	0.60	19.7	0.74	0.19	0.21	12.11	24.1	0.63
Crude protein	0.63	3.67	0.76	0.18	0.22	0.84	3.60	0.82

Conclusions

Our evaluation indicated that the SRNS model can predict the DMI and ADG of Vietnamese goats when nutritive values of the feeds are known. The regression equations developed in this study could be used to adjust the outputs of the SRNS model to predict the results of feeding systems.

[D]Corresponding author: david.parsons@utas.edu.au

Topic: Enterprise and systems models for production and environmental impact

Modelling methane emissions from northern beef production systems

G.J. Bishop-Hurley[A,D]*, E. Charmley*[B] *and J. Baldock*[C]

[A]CSIRO Agriculture, St Lucia, QLD 4067, Australia. [B]CSIRO Agriculture, Townsville, QLD 4811, Australia.
[C]CSIRO Land & Water, Glen Osmond, SA 5064, Australia.

Introduction

While methane emissions from grazing livestock in the rangelands of northern Australia are poorly understood, they account for approximately half of all cattle emissions. Physical measurement of methane (CH_4) is difficult so estimates are based on models. An energy-based individual animal model has been developed to model CH_4 production for northern beef production systems. The model accurately estimates the CH_4 production of beef cattle in northern Australia for accounting purposes. Limitations of knowledge and available data are discussed in relation to determining CH_4 production at the regional level.

Methods

A model based on the metabolisable energy (ME) system as described in SCA (2007) with a daily time step was developed. Dry matter intake (DMI) is driven by live weight (LW) and LW gain, diet quality and availability, and grazing pressure. Consumed energy is partitioned into maintenance and production, with the level of production related to the surplus/deficit of energy after accounting for essential processes (maintenance, pregnancy, locomotion, etc.). Total daily or annual CH_4 production (g/d; DMI X 19.6 – Kennedy and Charmley 2012) is estimated for each animal in a class and the classes summed to provide herd CH_4 emissions. Data collected at the CSIRO Lansdown Research Station were used for validation.

Results

Predicted annual growth performance was markedly lower than observed (13 kg versus 163 kg). However, modelling the data produced CH_4 emissions data similar to those obtained using open path laser from similar animals and pastures at Lansdown (127 versus 119 g/d). The model data are also consistent with results obtained using respiration chambers (Kennedy and Charmley 2012).

Discussion and conclusions

An energy-based individual animal model successfully predicted northern Australian beef cattle CH_4 emissions, but underestimated LW gain. Current energy-based models under-predict the growth achieved by beef cattle in the tropics. This could be related to differences in metabolism between tropically derived cattle breeds or the quality of the diet. Modellers need better data on free-ranging grazed cattle that relate maintenance and production to energy consumed, the quality and quantity of pasture available and the level to which cattle in extensive systems select higher quality forage in their diet. At the regional level, supplementation is poorly understood and there are few data on how and when it is used in extensive grazing systems. When calculating regional CH_4 production values, it also is vital to have accurate data on the numbers of the different classes of livestock.

References

Kennedy PM, Charmley E (2012) Methane yields from Brahman cattle fed tropical grasses and legumes. *Animal Production Science* **52**, 225-239.

SCA (2007) 'Nutrient requirements of domesticated ruminants.' CSIRO Publishing, Australia. pp 270

This work was partially funded by the Department of Climate Change and Energy Efficiency.

[D]Corresponding author: greg.bishop-hurley@csiro.au

Topic: Enterprise and systems models for production and environmental impact

The Australian national livestock methane database project

J. Hill[A,E], *E. Charmley*[B], *P. Fitch*C, Q. *Bai*[C] *and S. Cox*[D]

[A]Ternes Agricultural Consulting Pty Ltd, Upwey 3158, Australia and RMIT University, Bundoora 3083, Australia. [B]CSIRO Agriculture, Townsville 4814, Australia; [C] CSIRO Land & Water, Canberra 2601, Australia. [D]CSIRO Land & Water, Highett 3190, Australia.

Introduction

Large amounts of data have been, or are anticipated to be, generated by national research and development projects funded by the Australian Department of Agriculture, Meat & Livestock Australia, Australian Wool Innovation and Dairy Australia. Currently there is no national repository or systematic infrastructure to effectively store the data from these projects, or to allow access and interchange of data between institutes or the researchers within a program, or to international audiences.

A scoping study of the data management requirements of the Australian Government funded Reducing Emissions from Livestock program was undertaken in 2011. This study made a number of recommendations concerning the structure and meta-data requirements of a national database. These included the implementation of the standard vocabulary across datasets, the development of readily understandable metadata descriptors and use of open knowledge and secure web-enabled interfaces that facilitate searching and access by the research community.

Methods

An open source data portal has been developed using comprehensive knowledge archive network (CKAN). This data management system has the key attributes of accessibility, search and discovery, sharing and ability to federate. The infrastructure of the database was developed using information and data from the Reducing Emissions from Livestock Research Program (RELRP) and the recommendations from the scoping study. The RELRP has 39 projects representing 124 individual experiments focused on mitigation and abatement of methane production from ruminant livestock.

Results and discussion

The CKAN data management system allows users to publish datasets (numerical, text, images) through a web-interface that provides a full history of publishing. This flexibility in uploading not only allows authors to review and track changes but also notifies the research community of potential changes. Both raw data and metadata are stored within the database allowing users to search using both facetted and fuzzy matching. This facility is linked to tagged vocabulary which allows the user to narrow and enrich the search function. The approach adopted in the database also should allow the information held to be federated with other similar databases in the international arena. Federation is an important national and international issue in climate science and policy. The ability to federate datasets provides opportunities to aggregate science data to assist the development of robust national policy.

Conclusion

The Australian National Livestock methane database is one example of CKAN data management systems that may provide federated data sets for the international science community. The final management system will be available in mid-2015.

[E]Corresponding author: upweyag@optusnet.com.au

Topic: Enterprise and systems models for production and environmental impact

Using weather variables to estimate the productivity of Palisade grass

V.L.N. Brandão[A], M.I. Marcondes[A], G.O. Rocha[A] and F.H.M. Chizzotti[A,B]

[A]Department of Animal Science, Universidade Federal de Viçosa, Viçosa, MG, Brazil.

Introduction

The modelling of pasture dry matter production could be used as a management tool to make the process of working with the increasingly erratic precipitation and temperature patterns of climate-change easier and more accurate. This study aimed to define models to determine dry matter, leaf, and stem, production associate to climatic variables of Palisade grass (*Brachiaria brizantha* cv. Piatã).

Methods

Four treatments consisted of two levels of light interception (95% and 100%) and two residue heights (15 and 20 cm) were applied. Data were collected between January 2012 and November 2013. Dry matter production/day (DMPd), leaf production/day (LPd) and stem production/day (SPd) were regressed against precipitation (PCT, mm/day), minimum temperature (MIT, ^{o}C), average temperature (AVT, ^{o}C), maximum temperature (MAT, ^{o}C), base temperature (BT, ^{o}C), humidity (UM, %), evaporation (EVP, mm/d), degree-day (DD), sunlight (SL, hours/day) rain intensity (RI, mm/h), evaporation power (EP, mm), vapor pressure deficit (VPD, mm) and real evapotranspiration (REVT, mm). The weather variables were corrected by relationship: real evapotranspiration/potential evapotranspiration and multiplied by each variable, generating their corrected value. The backward procedure was used to determine the most significant variables to estimate production, and then a multivariate equation was fit. When the corrected variables presented best values of AIC (Akaike's information criterion), they replaced original variables.

Results and discussion

Multivariate equations to estimate DMPd, LPd, and SPd were determined and each showed strong correlation with variables of precipitation and temperature (Table 1).

Table1. Multivariate equations to estimate DMPd, LPd and SPd associated with climate variables

Equation	*P value*	*R²*	AIC	CRMSE
$DMPd = -59.56 + 0.27 \times MATc^2 + 36.78 \times RI - 9.05 \times RI^2 + 2.01 \times DDc^2$	0.005	0.83	801.7	15.19
$LPd = -292.50 + 73.16 \times MITc - 3.52 \times MITc^2 - 9.41 \times SL + 2.22 \times DDc^2$	0.001	0.79	857.9	15.35
$SPd = -31.03 + 4.47 \times PCT - 0.28 \times PCT^2 + 1.11 \times MAT$	0.003	0.48	722.2	6.58

CRMSE = Root mean square error generated by cross-validation; MATc = corrected maximum temperature; DDc = corrected degree-day; MITc = corrected minimum temperature.

Water was the first limiting factor of plant production, because it determines stomatal opening and closure. Cellular reactions demand an ideal range of temperature, so it could be seen that when temperature is outside this range these reactions are disabled, consequently plant productivity declined. It is concluded that climate variables are adequate to estimate DMP in Palisade grass cv. Piatã.

Sponsored by FAPEMIG and Capes.

[B]Corresponding author: fernanda.chizzotti@ufv.br

A simple carbon offset scenario tool (COST) for assessing sheep enterprise intervention options to reduce greenhouse gas emissions

K.M Christie[A,C], *N.A. Doran-Browne*[B], *R.P. Rawnsley*[A], *M.T. Harrison*[A] *and R.J. Eckard*[B]

[A]Tasmanian Institute of Agriculture, University of Tasmania, Burnie, TAS 7320, Australia. [B]Melbourne School of Land and Environment, University of Melbourne, Melbourne, VIC 3010, Australia.

Introduction

The sheep Carbon Offset Scenario Tool (COST) was developed to explore the influence of various diet manipulations and flock management intervention strategies on greenhouse gas (GHG) emissions for Australian sheep farms. It is a temporally-static spreadsheet-based tool that uses Australian GHG inventory methodologies, algorithms and emission factors to estimate carbon dioxide (CO_2), methane (CH_4) and nitrous oxide (N_2O) emissions, as CO_2 equivalents (CO_2e). The sheep COST calculator provides a baseline farm and allows ten intervention strategies to compare and contrast. Each intervention strategy contains four sections: 1) baseline farm data specific to the strategy explored, 2) strategy-specific key variables, 3) productivity changes and 4) GHG and economic-related results. It also presents a carbon income estimated on the premise that the intervention strategy being examined qualifies as a carbon offset. Users can easily explore the sensitivity of several key variables using spin buttons.

Methods

As an example, we explored the intervention option *Effect of supplementary feeding of mature ewes and/or lambs on GHG emissions* using the two options available; A) match the lamb baseline sale liveweight (COST determines lamb retention time) and B) match the baseline lamb retention time (COST determines lamb sale liveweight). The baseline farm system was a self-replacing prime lamb enterprise consisting of 8800 July-born lambs with 6600 of these sold at target slaughter liveweight of 45 kg. For the strategy farm, grain with a metabolisable energy concentration of 12.6 MJ/kg dry matter (DM) and crude protein (CP) concentration of 13% was fed at an average daily rate of 250 g DM/head during the second quarter of the year (Oct to Dec). This grain displaced an equal amount of pasture (9.7 MJ/kg DM and 17% CP).

Results and conclusions

The additional energy from the grain in (A) resulted in the lambs reaching the target slaughter liveweight 18 days sooner than in the baseline farm system. Greenhouse gas emissions were reduced by 11.8 t CO_2e per annum and at a carbon price of \$10/t CO_2e, this reduction was valued at \$119/annum. However the cost of the grain, when valued at \$200/ t DM, was \$26,550/annum. The net result was a reduction in partial gross margin, relative to the baseline, of \$26,430/annum. In option B, the additional grain meant that lambs were sold 5kg liveweight heavier but at the same age as those in the baseline, which increased GHG emissions by 27.7 t CO_2e/annum. With the additional liveweight valued at \$4.00/kg carcase weight, estimated farm income increased by \$59,160/annum. While implementation costs also increased due to additional grain, this option showed an estimated increase in partial gross margin, relative to the baseline farm system, of \$27,060/annum. The sheep COST calculator can be used as a first review of the potential changes in GHG emissions associated with implementing any of the ten intervention strategies currently available. However, the marginal economic analysis is only a guide and therefore a full farm systems and economic analysis is recommended to better inform the productivity and profitability implications on farm, especially if capital investment is required to implement a strategy.

[C]Corresponding author: Karen.Christie@utas.edu.au

Topic: Enterprise and systems models for production and environmental impact

Modelling egg production of broiler breeder hens

N.T. Ferreira[A,C]*, N.K. Sakomura*[A]*, R.M. Gous*[B]*, J.C.DeP. Dorigam*[A]*, L. Soares*[A] *and E.P. da Silva*[A]

[A]Department of Animal Science, University of Agrarian and Veterinary Sciences of UNESP,
Jaboticabal, SP 14884900, Brazil. [B]University of KwaZulu-Natal, Pietermaritzburg, South Africa.

Introduction

Broiler breeder hens exhibit a peculiar characteristic, when compared to laying hens, of a non-normal distribution in egg laying frequency. This characteristic is important when predicting the daily amount of amino acids and energy required by each hen in a flock to produce each gram of egg because the amino acid and energy contents of yolk and albumen differ and the egg´s component proportions change with age. This study aimed to model egg production of a flock of broiler breeder hens, using non-isometric equations.

Methods

An assay was conducted with 60 broiler breeder hens to observe the egg production from hens aged 24 to 60 weeks. The potential rate of lay of each hen was estimated according to her rate of yolk production, whilst albumen and shell weights were predicted from yolk weight, as a function of age of hen, according to the model proposed by Johnston and Gous (2007). The rate of egg production was determined from oviposition sequences and the number and length of pauses between sequences. Non-isometric functions were applied to predict the weight of the eggs. Egg weight was obtained from the sum of yolk, albumen and shell (Emmans and Fisher, 1986). In addition, soft-shelled and double-yolk eggs were also measured.

Results and discussion

The model to predict the egg production (y) was: y (g/day) $=19.924 \times e^{(0.0006 \times t)} \times e^{(-e^{(-0.638-0.015 \times t)})}$, where y is yolk output and t is time from first egg. The yolk weight (YW) was determined by equation: $YW = 18.028 \times (1-e^{-0.015 \times (t-103.39)}) \times e^{(0.001 \times t)}$, where YW is the yolk weight (g) and is predicted based on age of the bird (t, days). The weight of albumen (AW) and shell (SW) were predicted based on YW and egg component (C, yolk + albumen) by the equations: $AW = 14.377 \times YW^{0.375}$ and $SW = 0.358 \times C^{0.687}$, respectively. The rate of double-yolk egg (DY) production is described by: $DY = 2.275 \times e^{(0.209 \times TFE)}$ and soft shell egg (SE) production is described by: $SE = 1.126 + 0.148/(1-0.024 \times TFE) - 0.056 \times TFE$, as a function of time from first egg. Based on the results achieved, the simulation models used here reflect well the egg and component weights of broiler breeders for a given age and even over the entire laying period. These models can be used in prediction of the nutrient requirements of broiler breeder hens.

References

Emmans GC, Fisher C (1986) Problems in nutritional theory. In “Nutrient requirements of poultry and nutritional research”. (Eds C Fisher, KN Boorman) pp 9-40. (Butterworths: London)

Johnston SA, Gous RM (2007) Modelling the changes in the proportions of the egg components during a laying cycle. *British Poultry Science* **48**, 347–353.

[C]Corresponding author: nayaratf@hotmail.com

Topic: Enterprise and systems models for production and environmental impact

Modelling the egg components of laying hens

H.C. Palma Bendezu[A,B], *N.K. Sakomura*[A], *E.G. Malheiros*[A], *J.C.DeP. Dorigam*[A], *E.P. da Silva*[A]
and L. Soares[A]

[A]Department of Animal Science, University of Agrarian and Veterinary Sciences of UNESP,
Jaboticabal, SP 14884900, Brazil.

Introduction

Modelling of egg components over time provides useful information for the prediction of egg weight as a function of hen age. It is also an important tool for nutritionists as it provides information about potential changes in nutrient requirements of the hen. In this context, the aim of this study was to model changes in egg components during the egg production period.

Methods

Sixty Isa Brown laying hens were used from 15 to 50 weeks of age, with each hen as an experimental unit. Feed and water were available *ad libitum* throughout. Egg weight was recorded daily and weight of egg components was recorded three times per week. The eggs were broken, the yolk separated from the albumen and immediately weighed, and the shell was washed and air-dried for two weeks prior to final weighing. All the variables had their residuals tested for normality and homoscedasticity using a Cramer-von Mises and Levene test (PROC GLM procedure, SAS software, v. 9.0). The model used was: $y=a \times e(-ct) \times e\text{-}(e(G_0\text{-}bt))$, where y is the rate of yolk production, a is an scalar parameter, c is a decay parameter, t is age at first egg, G_0 the initial state parameter at t=0 and b a growth rate parameter. Normally, albumen weight and shell weight are related to yolk output and egg contents weight, respectively. For this reason, allometric relationships between them were used to estimate albumen and shell weight (Emmans and Fisher 1986).

Results and discussion

The R^2 of the yolk production model was close to unity, indicating a good fit. Rate of yolk production (y) was described as: $y=11.7473 \times e(0.00092\times t) \times e\text{-}(e(-0.7992\text{-}0.0551\times t))$ where t is age at first egg (days) and e is the Euler number. The albumen weight (a) and shell weight (s) were described as: $a = 10.3370 \times y^{0.5213}$ and $s = 0.0808 \times (a + y)^{1.0974}$, respectively. Egg weight can be calculated from the sum of its components. The results of this study allow prediction of changes in egg components during the egg production period and are in agreement with results reported by Johnston and Gous (2007). The proportionality of egg components changed over time. Hence, the nutrient requirements of the hen may also change over the egg production period.

References

Emmans GC, Fisher C (1986) Problems in nutritional theory. In 'Nutrient requirements of poultry and nutritional research'. (Eds C Fisher, KN Boorman) pp 9-40. (Butterworths: London)

Johnston SA, Gous RM (2007) Modelling the changes in the proportions of the egg components during a laying cycle. *British Poultry Science* **48**, 347–353.

[B]Corresponding author: hldplm@gmail.com

Topic: Enterprise and systems models for production and environmental impact

A multiphase feeding program for broilers to replace the traditional system

L. Hauschild[A,B]*, C.F.D. Bueno*[A]*, A. Remus*[A]*, J. Gobi*[A]*, R.G. Isola*[A] *and N.K. Sakomura*[A]

[A] Universidade Estadual Paulista - UNESP, College of Agrarian and Veterinary Sciences, Jaboticabal, São Paulo 14884-900, Brazil.

Introduction

Previous research on the effect of multiphase feeding programs (MFP) on performance of broiler chickens did not consider the logistical shortcomings associated with the need to formulate a diet for every phase. Therefore, in this study we investigated whether a MFP (14 phases) of broilers based on the optimal mix of two feeds (Létourneau-Montminy *et al.* 2005) could replace a traditional (4 phases) system without reducing feed conversion efficiency (FCE).

Methods

Day-old chicks (n = 480) of the Cobb strain with an average weight of 44.74 ± 0.16 g (females) and 44.71 ± 0.11 g (males) were distributed in a completely randomized 2x2 factorial design (feeding program: 4 or 14 feeding phases; sex). Each treatment consisted of six replicates with 20 birds per experimental unit. Two premixed diets (A and B) were formulated to meet the requirements for the first and last day of the experimental period with reference to the lysine requirement. To obtain the average requirement of this amino acid in the various phases of each program, both diets were mixed in different proportions. Average daily feed intake (g/day), average daily body weight gain (g/day), FCE, and carcass yield (breast as a % of total carcass), were determined in response to feeding program. Results were analysed for the entire growth period (1–42 days).

Results and discussion

For the entire growth period, feed intake and body weight gain were 2% higher in the MFP whilst FCE was unaffected. Breast yield was 3% higher in the MFP ($P<0.05$). The effect of the MFP was similar for males and females. Thus, MFP improves the productivity of broilers without compromising FCE. The proposed 14 phase mixing method enables the use of more complex multiphase programs in broiler systems by removing the need to formulate a complete diet for each phase.

Table 1. Mean performance of broiler chickens fed a multiphase (14 phases) program based on the mixing of two feeds or a traditional (4 phases) feeding program over a 42 day growth period

Variables	*Traditional (4 phases)*		*Multiphase (14 phases)*		*Sex*	*Pr*[A]	*Int*[B]	*SEM*
	Male	Female	Male	Female				
ADFI, g/d	115.18	100.04	118.85	101.70	0.00	0.08	0.49	3.13
ADG, g/d	71.12	57.04	72.92	57.98	0.00	0.04	0.50	1.31
FCE	1.63	1.76	1.63	1.77	0.00	0.41	0.32	0.02
Breast (% of carcass)	40.06	39.37	40.75	41.16	0.75	0.01	0.21	1.35

[A]Pr = program; [B]Int = interaction; SEM = Standard error mean; F test with 90% with a confidence interval; ADFI = average daily feed intake; ADG = average daily gain; FCE = feed conversion efficiency.

References

Létourneau-Montminy MP, Boucher C, Pomar C, Dubeau F, Dussault J (2005) Impact de la méthode de formulation et du nombre de phases d'alimentation sur le coût d'alimentation et les rejets d'azote et de phosphore chez le porc charcutier. *Journal Recherche Porcine* **37**, 25-32.

[B]Corresponding author: lhauschild@fcav.unesp.br

Topic: Enterprise and systems models for production and environmental impact

PigGas calculator and national extension

I. Kruger[A,C] *and G. Mills*[B]

[A]Ian Kruger Consulting, Kootingal 2352, NSW. [B] GoAhead Business Solutions, Moree 2400, NSW.

Introduction

The Pork Industry Greenhouse Gas Calculator (PigGas) is a Microsoft® Excel graphical spreadsheet model which uses annual farm data from any Australian piggery to yield baseline greenhouse gas (GHG) emission profiles and mitigation scenarios. It is currently being used in the National PigGas Extension Program funded by Ian Kruger Consulting, the Australian Government and Australian Pork Limited and is delivering excellent practical results through workshops and one-on-one consultations.

Methods

The PigGas Calculator (Kruger *et al.* 2013, Mills and Kruger 2014) was developed to provide a simple tool for pork producers and their advisers. PigGas follows the Australian methodology for estimating GHG emissions for piggeries DCCEE (2012) and provides capacity to fine tune production activities and emissions at the individual enterprise level and perform 'what-if' mitigation scenarios.

PigGas inputs required are annual averages of: numbers, ages and weights in and out of each pig group; diet formulations, feed consumption and wastage for each group; waste management systems and types of land application used for each group; transport and energy used in the piggery; and pig movements and sale weights.

A nutrient mass balance approach, using the dry matter digestibility approximation of manure production from individual feed ingredients, predicts the amount of excreted volatile solids and nitrogen from which methane and nitrous oxide are determined respectively for each emissions source. For piggeries, emissions sources are: enteric (methane), manure management system (methane, nitrous oxide – direct and from volatilized from ammonia) and land application (nitrous oxide – direct and from leaching and runoff). PigGas includes energy in on-farm emissions results.

Results

As at June 2014, PigGas has been used to model on-farm baseline GHG emissions and mitigation scenarios on 34 piggeries representing 16.9% of Australia's pig herd. Results shown in Table 1 are from 26 farrow-to-finish piggeries representing 13.7% of Australia's pig herd.

Table 1. On-farm GHG emissions intensities for different types of piggery farrow to finish systems

Pig production system	Emissions intensity (kg CO_2-e/kg carcass wt)	Emissions reductions (%)
Conventional flushed	1.1 - 5.8 (av. 3.8)	14-81 (av. 54)
Conventional & deep litter	1.2 - 3.8 (av. 2.4)	1 – 70 (av. 38)
Deep litter	1.2 - 1.7 (av. 1.4)	0 - 5 (av. 3)

References

DCCEE (2012) Australian National Greenhouse Accounts - National Inventory Report 2010 Volume 1. The Australian Government Submission to the UN Framework Convention on Climate Change April 2012. DCCEE, C'wealth of Australia, Canberra ACT, April 2012. ISBN: 978-1-922003-28-7.

Kruger, I.R., Mills, G.W. & Madden, P.F. (2013) PigGas - Pork industry greenhouse gas calculator and case studies. *Final Report APL Project 2009/1011.335, Jan. 2013, Australian Pork Limited, ACT.*

Mills, Greg and Kruger Ian (2014) Pork Industry Greenhouse Gas Calculator Version 1.02.04 http://www.australianpork.com.au/industry-focus/environment/greenhouse-gases/

[C]Corresponding author: iankrugerconsulting@gmail.com

Topic: Advances in modelling methodology

Development of a generator of virtual pigs based on a generic covariance pattern for modelling growth performance to account for variability among individual pigs in deterministic growth models

L. Brossard[A,B,D], *B. Vautier*[A,B,C], *J. van Milgen*[A,B] *and N. Quiniou*[C]

[A]Unité Mixte Technologique "Ingénierie des Systèmes de Production Porcine" INRA, UMR1348 PEGASE, 35590 Saint-Gilles, France. [B]Agrocampus Ouest, UMR1348 PEGASE, 35000 Rennes, France. [C]IFIP- Institut du Porc, BP 35104, 35651 Le Rheu cedex, France.

Introduction

Most pig growth models are deterministic and consider only the average pig and not individuals within a group. Inclusion of variability among individuals in modelling approaches is required to better understand the effects of feeding strategies on mean growth, economic and environmental performance, but also the variability of these traits. The aim of this study was to obtain and to use the information of the covariance structure of model parameters, such as those used in InraPorc, and to propose a generator to create virtual pig populations.

Methods

Data for daily feed intake and live weight of 1288 gilts and barrows from 10 terminal crossbreeds reared in France and 10 batches (IFIP, Romillé, France) were collected from 70 days of age to 110 kg body weight. Each individual pig was characterized using the InraPorc model by 5 parameters (2 for daily feed intake and 3 for growth) (Vautier *et al.* 2013). The effects of crossbreed, sex, batch, and their interactions on the mean values of parameters were analysed. To investigate whether covariance structures share common tendencies, the covariance relationships among parameters were analysed according to the Flury hierarchy (1988) by a comparison of covariance matrices depending on the level of animals grouping (i.e., crossbreed, sex, batch, and their interactions).

Results and discussion

The mean values of parameters depended on sex and batch. The covariance structure of parameters differed from one group to another, a group being defined as a combination of crossbreed, sex and batch. A generic covariance matrix of parameters was calculated as the median matrix from all 40 groups' matrices. It appeared to be a better estimator of the observed covariance than a raw covariance matrix (computed from the 1288 individuals) for 72% of the 40 group matrices. A generic covariance pattern was then proposed to represent a group of pigs by combining this generic covariance matrix, observed probability distributions of parameters, and a specific vector of parameters means. As multivariate generators based on classical distributions and independency of parameters were not able to reproduce the population, a generator of virtual pigs was developed based on this covariance pattern with specific steps to take into account dependencies between probability distributions of parameters.

This work allows the inclusion of stochasticity aspects in models and decision support tools, such as InraPorc®. This will help users to study and propose innovative and realistic feeding strategies to meet performance and environmental goals and to consider variability among individual pigs.

References

Flury B (1988) 'Common principal components and related multivariate models'. (Wiley: New York)

Vautier B, Quiniou N, van Milgen J, Brossard L (2013) Accounting for variability among individual pigs in deterministic growth models. *Animal* **7**, 1265-1273. doi:10.1017/S1751731113000554

[D]Corresponding author: ludovic.brossard@rennes.inra.fr

Topic: Advances in modelling methodology

Successful use of the deletion method to determine the essential amino acid requirements of juvenile Nile tilapia (*Oreochromis niloticus*)

A.F. Diógenes,[A,C,D]*, N.K. Sakomura*[B] *and J.B.K. Fernandes*[C]

[A]Department of Biology, Faculty of Sciences, University of Porto, Portugal. [B]Animal Science Department, São Paulo State University (UNESP) Brazil. [C]Aquaculture Center São Paulo State University (CAUNESP). Via Ac. Prof. Paulo Donato Castellane, s/n 14884-900 Jaboticabal, SP, Brazil.

Introduction

This method relies on the assumption that the reduction of a non-limiting essential amino acid (EAA) has no effect on nitrogen (N) retention. However, if a single EAA is limiting in the diet, the rate of body N retention is directly related to the reduction in levels of that individual AA. This method has been shown to be fast and accurate (Rollin *et al.* 2003). Using the deletion method, we determined the optimal EAA ratio for juvenile Nile tilapia (*Oreochromis niloticus*).

Methods

Quadruplicates each consisting of 34 juvenile Nile tilapia (20 g) were randomly distributed to 1500 L tanks where they were held for 58 d. They were hand fed with one of 11 experimental diets: a balanced diet (BD) formulated to meet nutritional requirements, and ten other diets that were formulated by the deletion technique in which each EAA was reduced by 45% of the required level.

This analysis was used to determine nitrogen deposition using the equation proposed by Rollin *et al*. (2003). Statistical significance was tested using the Dunnett's test; values of $P<0.05$ were deemed to be statistically significant (R statistical package, version 0.1).

Results

Considering the linear response that exists between nitrogen deposition and EAA intake when feeding an amino acid-deficient diet, and assuming that each AA is equally limiting, the ideal dietary EAA profile relative to lysine (=100%) was estimated as: met + cys 64, thr 93, trp 24, arg 125, val 76, ile 57, leu 96, his 34, and phe + tyr 101. The optimal balance was estimated as: (g/16 g N): lys 5.01, met + cys 3.19, thr 4.67, trp 1.19, arg 6.27, val 3.78, ile 2.84, leu 4.83, his 1.72, and phe + tyr 5.03.

Conclusion

The optimal amino acid profile will help in formulating diets with high nutritional density and, with optimisation of the dietary energy:protein ratio, will reduce pollution by reducing excretion of excess N.

References

Rollin X, Mambrini M, Abboudi T, Larondelle Y, Kaushik S.J. (2003) The optimum dietary indispensable amino acid pattern for growing Atlantic salmon (*Salmo salar L.*) fry. *British Journal of Nutrition* **90**, 865-876.

Acknowledgement

National Council of Technological and Scientific Development (CNPq) and the Ajinomoto®

[D]Corresponding author: alexandre_diogenes@hotmail.com

Logistic model to fit the angelfish (*Pterophyllum scalare*) growth curve

C.H. Espitia-Manrique[A] *and J.B.K. Fernandes*[B,C]

[A]Laboratory of Tilapiculture, Aquaculture Center at São Paulo State University (UNESP). Via de Acesso Prof. Paulo Donato Castellane, s/n 14884-900 Jaboticabal, SP, Brazil. [B]Laboratory of Ornamental Fish, Aquaculture Center at São Paulo State University (UNESP), Brazil.

Introduction

The angelfish *Pterophyllum scalare* is a neotropical freshwater fish (Gómez-Laplaza and Morgan 2005), considered one the most important species in the global fish market. The relationship between weight and age is an empirical method to reduce the number of variables describing growth, showing interesting points for a productive system. Five nonlinear mathematical models (Logistic, Gompertz, Bertalanffy, Brody and Richards) were compared to fit the growth curve for six hundred angelfish fry (*P. scalare*).

Methods

Weight measurements were collected from 30 days post-hatching (0.2422 ± SD 0.055 g) every two weeks for 33 weeks. The animals were housed in twelve 200 L indoor circular tanks. Estimates of the parameters were calculated with Gauss-Newton iterative procedure using SAS® Proc Nlin. Comparisons were made among these models for Akaike Information Criterion (AIC), Bayesian Information Criterion (BIC), biological interpretability, average residual mean square, less iterations number, coefficient determination, smaller parameter range and goodness of fit.

Results

The most appropriate model to describe the *Pterophyllun scalare* growth was the Logistic model $Y=13.98/(1+100.29e^{-0.02505t})$.

Biological interpretation of growth curve parameters were 13.98 g mature weight; 0.025 g/day rate of maturing (growth rate relative to mature weight); 0.086 g/day rate of gain (first derivative with respect to time (dy/dt) measure of absolute growth rate). The maximal theoretical rate of gain was reached at age 184 days, after which began a gradual decrease until 575 days when there was minimal growth (0.000021 g/day).

Discussion

The intrinsic characteristics of models other than the Logistic did not adequately fit the growth curve data, even though sensible intervals of initial parameters were approximated for the analyses. In each of these four cases, parameters such as predicted mature weight were overestimated making these models inappropriate for this species. Selection of appropriate growth models and their variables will depend upon nature of the research problem and application of the results.

Conclusion

The Logistic model adequately described *P. scalare* growth, and with this parameterisation provided new information on an important productive trait in angelfish.

Reference

Gómez-Laplaza LM, Morgan E (2005) Time-place learning in the cichlid angelfish, *Ptherophyllum scalare*. *Behavioural Processes* **70**, 177-181.

[C]Corresponding author: jbatista@caunesp.unesp.br

Topic: Advances in modelling methodology

Neural network models for predicting the response of broilers to threonine

A. Faridi[A,D], *N.K. Sakomura*[A], *D.D.Z. Donato*[A], *A. Gitoee*[B], *and J. France*[C]

[A]Department of Animal Science, College of Agrarian and Veterinary Sciences, University Estadual Paulista, Jaboticabal, Sao Paulo, Brazil. [B]Department of Animal Science, University of Kurdistan, Iran. [C]Centre for Nutrition Modelling, Department of Animal & Poultry Science, University of Guelph, Guelph, Ontario, N1G 2W1, Canada.

Introduction

Neural networks (NNs) are a relatively new option for modelling biological systems. The ability of these models in poultry nutrition has been demonstrated previously (Faridi *et al.* 2013). Here, results from NN models developed to predict average daily gain (ADG) and feed conversion ratio (FCR) in response to dietary protein (CP) and threonine (Thr) in broiler chickens are presented.

Methods

An experiment was conducted to evaluate the effects of CP and Thr (8 levels each) on ADG and FCR of broilers during the starter, grower, and finisher phases. The data obtained were imported into NN software to construct the prediction models. Starting with 64 datalines (38 and 26 datalines for training and testing, respectively), 6 separate NN models were developed to predict ADG and FCR in the 3 phases. Models with highest accuracy of prediction were subjected to a random search optimization process to find the optimal values of CP and Thr that result in maximum ADG and minimum FCR.

Results and discussion

Prediction performance of the models developed, along with optimization results, for ADG and FCR in each phase are shown in Table 1. It illustrates that NN models predicted the outputs precisely. Except in the grower phase, Thr requirement to achieve minimum FCR is higher than that for maximum ADG. Similar results have been reported earlier for lysine (Faridi *et al.* 2013).

Table 1. Prediction performance (R^2) and optimization results from the neural network models developed for three phases of growth in broiler chickens

	Performance		Optimization		
	Train	Test	Threonine (g/kg)	Protein (g/kg)	Expected output
Phase 1 (1-14 d)					
ADG (g/bird/day)	0.98	0.94	7.8	211	21.2
FCR	1.00	1.00	8.1	217	1.37
Phase 2 (15-28 d)					
ADG	0.96	0.94	7.4	196	62.4
FCR	0.98	0.99	7.1	209	1.59
Phase 3 (29-42 d)					
ADG	0.88	0.86	6.9	190	95.6
FCR	0.96	0.98	7.1	195	1.67

References

Faridi A, Golian A, France J, Heravi Musavi A (2013) Study of broiler chicken responses to dietary protein and lysine using neural network and response surface models. *British Poultry Science* **54**, 524-530.

[D]Corresponding author: ako.faridi@posgrad.fcav.unesp.br

A multinomial logit mixed model to examine the incidence of white striping in broiler breast

L.E. Moraes[A], *L. Kindlein*[A,B] *and R.D. Sainz*[A,C]

[A]University of California, Davis, CA 95618, USA. [B]Federal University of Rio Grande do Sul, Porto Alegre, Brazil.

Introduction

Genetic selection of broilers for breast muscle yield has resulted in the appearance of a myopathy known as white striping (Kuttapan *et al.* 2012). The objective of this study was to develop a generalised linear mixed model to examine occurrence due to body weight and diet nutrient density.

Methods

Broiler chicks (n = 572) fed two diets of high or low nutrient density were weighed and harvested at 10, 20, 30, 40 and 50 d of age. The response Y_{ijk} denotes the kth record (k = 1, …, n_{ij}) on the ith treatment (i = 1, 2) and jth bin (j = 1, …, 22) and represents a realisation of a multinomial sampling model with probabilities $\{\pi_{ijk1}, \pi_{ijk2}, \pi_{ijk3}\}$ of being classified in one of the three categories of white striping, i.e. $\pi_{ijk1} = P(Y_{ijk} = \text{Normal})$, $\pi_{ijk2} = P(Y_{ijk} = \text{Moderate})$ and $\pi_{ijk3} = P(Y_{ijk} = \text{Severe})$. The incidence of white striping was examined using a multinomial baseline logit mixed model (Agresti 2002): $\log\left(\frac{\pi_{ijkr}}{\pi_{ijk1}}\right) = \beta_{0r} + \beta_{1r}X_{ijk} + \alpha_{ir} + \gamma_{jr}$, r = 2, 3, where β_{0r} is the intercept, β_{1r} is the slope describing the change in the log odds with body weight, X_{ijk} is the centered body weight (kg), α_{ir} is the fixed effect of the ith dietary treatment on the log odds and γ_{jr} is the random effect associated with the jth bin on the log odds of category r.

Results and discussion

The odds of having severe rather than normal white striping multiply by 51X for each kg increase in body weight, and the odds of having severe rather than normal white striping was 3X greater on high compared to low nutrient diets. Therefore, white striping in broiler chicken breast increased with age, body weight and diet nutrient density.

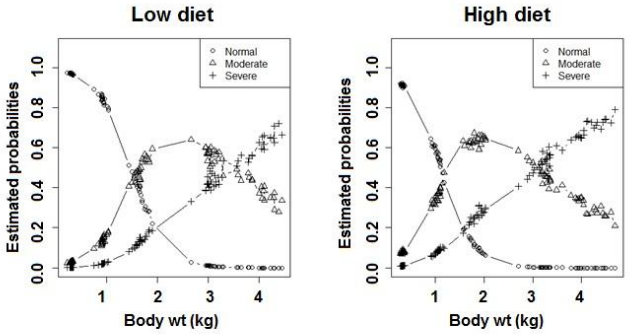

Fig. 1. Probability of occurrence of degrees (o, Normal; Δ, Moderate; +, Severe) of white striping during broiler growth as affected by age and diet nutrient density.

References

Agresti A (2002) Categorical Data Analysis (2nd ed.), New York: Wiley.

Kuttappan VA, Brewer VB, Apple JK, Waldroup PW, Owens CM (2012) Influence of growth rate on the occurrence of white striping in broiler breast fillets. *Poultry Science* **91**, 2677-2685.

[C]Corresponding author: rdsainz@ucdavis.edu

Topic: Advances in modelling methodology

Comparison of models for *in vitro* fermentation with different blank corrections

F. Garcia[A,B,E], J. Martínez Ferrer[C], A. Cora[C], M.A. Brunetti[C], M.V. Moreno[C], E. Lucini[B], M.J. Martínez[C] and D. Colombatto[A,D]

[A]Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET), Argentina. [B]Facultad de Ciencias Agropecuarias, UNC, Córdoba, Argentina. [C]Instituto Nacional de Tecnología Agropecuaria (INTA) – EEA Manfredi, Manfredi, Argentina. [D]Facultad de Agronomía, UBA, Buenos Aires, Argentina.

Introduction

Mathematical modelling of gas production profiles (GPP) allows detailed analysis of data to evaluate ruminal fermentation modifiers. *In vitro* GPP techniques usually use blanks (vessels without substrate) and discussion arises as to whether to use a common blank, a treatment-specific blank or no blank. The aim of this work was to compare the ability of different models to describe GPP using different blanks.

Methods

In three incubations (blocks), essential oils (EO) from *Lippia turbinata* (Lt): 30, 60, 120 and 240 mg/L and *Tagetes minutas* (Tm): 5, 50, 125 and 250 mg/L, and a control (no additive), were tested using the *in vitro* GPP technique. A specific blank (ruminal fluid + buffer + EO treatment) was included in the absence of substrate (80:20 alfalfa hay:corn grain). Head-space pressure was measured regularly throughout 72 hours, and the GPP calculated. To generate the GPP, three sets of data were used: no blank correction, correction for same blank (control) and correction for specific blank (corresponding EO). Five mathematical models were fitted to the 180 GPP using CurveExpert Professional 2.0.4 (Table 1).

Results

No single model could describe all GPP (Table 1). The GPP were best described by the Logistic model. By contrast, the best curve-fitting was achieved with the least descriptive models (MM and GM).

Table 1. Comparison of models to describe generated GPP

Model	%	Position	SE	AIC
L: A/(1 + b*exp(-c*x))	69.4	3.3	10.8	95
GR: A*exp(-exp(b - c*x))	61.7	2.3	6.5	72
GF: A*(1-exp((-b/c)*(e^c*(x-lag)) - 1)))	9.4	2.1	4.1	65
MM: (A*(x - lag)^c)/((x - lag)^c+K^c)	30.6	1.1	2.6	39
GM: A*(1 - exp(-b*(x - lag)-c*(sqr(x)-sqr(lag))))	24.4	1.9	3.5	52

L: logistic; GR: Gompertz Relation; GF: Gompertz Function; MM: Michaelis Menten; GM: Generalized Mistcherlich.

Conclusions

It is concluded that when different GPP are generated by adding EO, independently of which blank correction is chosen, obtaining parameters with these models to describe and compare treatments to evaluate effects of additives on ruminal fermentation will be difficult to achieve.

[E]Corresponding author: fgarcia@agro.unc.edu.ar

Topic: Advances in modelling methodology

An investigation of a linear model for the transport of markers through the digestive system of a monogastric

J.A. Belward[A]*, J. Hanan*[A,B]*, B.A. Williams*[A]*, and M.J. Gidley*[A]

[A]Centre for Nutrition and Food Science, Queensland Alliance for Agriculture and Food Innovation,
The University of Queensland, St Lucia 4072, Queensland, Australia.

Introduction

Through the use of computational and mathematical modelling we hope to integrate the understanding of digesta behaviours in the gastro-intestinal tract (GIT) to help identify properties that lead to nutritional benefits. To capture how the digesta moves through the gut, we incorporated inert marker compounds into the diet of 6 pigs, and used a slaughter-based experiment to enable measurements of material and biochemical properties at all locations in the GIT, at one point in time. We aim to develop a compartment-based model that will simulate digesta behaviour. We focus on how to translate "one time" data into a dynamic linear model, and then use 2 and 4 hour pulse marker data to refine and verify it.

Methods

As a first step, progression of digesta through the small intestine is modelled by a 6 compartment serial arrangement of mass action stages, extending one section of the 2 stage model of Bastianelli *et al*. (1996). The equations of a mass action model are linear, thus a coupled set of differential equations is obtained whose parameters are the mass action rates of each component (Belward *et al.* 2012). Analysis of the equations facilitates a heuristic argument that relates the steady state marker masses to the mass reaction rates. The task is to estimate these rates from the experimental data of the marker compounds. Once a set of rates is postulated, a plot of the masses in each stage can be calculated over the feeding cycle. The argument only provides the rates in ratio, i.e. they are determined up to a scale factor. This can be found by fitting the plot of the stage masses to the masses of a pulse marker at its specified time.

Results and discussion

We use a set of rates inversely proportional to the steady state mass of an in-feed marker to generate a plot of the masses for each stage. For each stage there is a collection of masses over a notional time, at each time there is a vector of masses and the set of masses is an array over the stages and time steps. By determining the closest match between the given data set of pulse masses and the sets of masses in a row in the array, a particular time is established which provides the scale factor to be applied to the notional times. This is applied, and mass transfer rates scaled accordingly. When the 4 hour data are used we find a reasonable fit to the 2 hour data and vice versa. We can fit both 4 and 2 hour data simultaneously to be more accurate. Future work will extend the model to the complete GIT, modify rates based on digesta properties, and include other digestion processes.

References

Bastianelli D, Sauvant D, Rerat A (1996) Mathematical modelling of digestion and nutrient absorption in pigs. *J. Anim. Sci.* **74**, 1873-1887.

Belward JA, Hanan JS, Williams BA, Gerrits WJJ, Gidley MJ (2012) On the use of marker data to determine the kinetics of the digestive behaviour of feeds. *ANZIAM J.* ***54*** *(CTAC2012).*

[B]Corresponding author: j.hanan@uq.edu.au

Topic: Advances in modelling methodology

Mathematical modelling of the plasticity of energy stores at cellular scale

M. Taghipoor[A,B], *J. van Milgen*[A], *L. Brossard*[A] *and F. Gondret*[A]

[A]INRA-UMR 1348 PEGASE, Physiology, Environment and Genetics for the Animal
and Livestock Systems, F-35590 Saint-Gilles, France.

Introduction

Farm animals, as for any living organism, need energy for their basal metabolism and physical activities. When dietary energy intake exceeds energy expenditure (on a short-term or long-term basis), the surplus is stored, particularly in the form of glycogen and triacylglycerols. The energy supply and need by the organism regulates the degradation and synthesis of these stocks. Moreover, when faced with environmental constraints (nutritional, health, heat, etc.), the animal modifies its metabolism at the cellular scale in order to guarantee its homeostasis. For example, in the case of nutritional challenges, the energy stocks are mobilized to produce the required energy for the animal. In this work we have used mathematical modelling to study the influence of the energy reserves and the animal's energetic state on energy metabolism at cellular scale.

Methods

A system of ordinary differential equations represents the dynamics of energy reserves (glycogen and lipids) as well as intermediate substrates of energy metabolism. Thus, based on regulators of enzyme activity, the dynamics of storage and use of energy reserves in a cell have been described by mathematical equations. Regulators of enzyme activity include intracellular (e.g. ATP/ADP ratio) and extracellular (e.g. hormone secretions) signals. The numerical method Runge-Kutta has been used to solve the model equations using free software Scilab.

Results

The evolution in time of energy reserves, energy level as well as all intermediate substrates for a generic cell has been simulated. Because of its generic aspect, this model can be used for different research questions and different cell types by changing the basic parameters. For example, we use the model to illustrate the energy metabolism and the plasticity of energy reserves for three levels of ATP requirement to simulate (i) a toy model (when ATP need is zero) which allows observing the model behavior, (ii) an adipocyte (when ATP need is low), and (iii) a contracting muscle fibre (when ATP need is high). The results show how the variations in energy consumption affect the dynamics of energy stores. In fact, for the same amount of nutrients absorbed by a cell, when energy consumption (ATP requirement) increases, the energy stores (glycogen and lipids) release more substrates to meet this increased energy demand.

The model has the capacity to integrate additional phenomena such as protein metabolism in a muscle fibre and it can also be used to simulate tissue growth. For example, adipose tissue may be represented in the simplest way as a sum of adipocytes; the model then allows simulation of adipose tissue growth at a macroscopic scale as the sum of the lipids produced by each cell.

Discussion

The model is generic and phenomenological; however it provides a basis to investigate relevant hypotheses in farm animal production. It allows, for example, studies of postprandial metabolism (fast dynamics) and energy stock management in lactation/gestation (slow dynamics). Furthermore, it allows understanding and predicting of the effects of diets containing different sources of energy (carbohydrates/lipids) on the energy stocks in the animal.

[B]Corresponding author: masoomeh.taghipoor@rennes.inra.fr

Topic: Advances in modelling methodology

Evolution of parameter changes for beef cattle growth in the Davis Growth Model over 40 years

J.W. Oltjen[A,D], R.D. Sainz[A], L.G. Barioni[B], D.P. Lanna[C] and T.Z. Albertini[C]

[A]Department of Animal Science, University of California, Davis, USA. [B]EMBRAPA Agricultural Informatics, Campinas, Brazil. [C]ESALQ University of Sao Paulo, Piracicaba, Brazil.

Introduction

Experience with use of the Davis Growth Model (Oltjen *et al*. 1986b) since its development has revealed its strengths and weaknesses (Oltjen *et al*. 1986a, Garcia *et al*. 2008, McPhee *et al*. 2009). Improvements have been made both within the model structure and to parameter estimates.

Model structure

Originally, the DNA (deoxyribonucleic acid) equation was an interpolation based on body fatness between DNA of a reference well-fed animal and an animal at that same protein content fed near maintenance. However, DNA estimates diverge from the model's continuous simulated DNA at heavier weights. Subsequently, initial DNA is estimated by the following equation which requires both body protein (PROT) and previous rates of protein accretion and energy intake (NUT2):

$$DNA = \left(\frac{K3 \cdot PROT^{0.73} + \frac{dPROT}{dt}}{NUT2 \cdot K2}\right)^{1/0.73}$$

where K2 (protein synthesis rate constant), K3 (protein degradation rate constant) and NUT2 are defined as in the original model. This equation provides estimates of initial DNA that are within 1 g of simulated DNA across the entire growth path for both implanted and non-implanted steers.

Model parameters

Because the newer DNA estimates differ from the original ones, other parameters in the model were re-estimated (original parameter values from Oltjen *et al*. (1986) in parenthesis):

K1 = 0.00493 (0.00429) K2 = 0.0444 (0.0461) Alpha = 0.0841 (0.0858)

Also, the increase in protein synthesis due to implant became 3.9% instead of the original 4.2%. Additional work with Nellore found lowered K1, K3 and alpha in these slower growing *Bos indicus* cattle (Sainz *et al*. 2006). Also, fits show decreased K3 with use of beta-agonists.

References

Garcia F, Sainz RD, Agabriel J, Barioni LG, Oltjen JW (2008) Comparative analysis of two dynamic mechanistic moles of beef cattle growth. *Animal Feed Science and Technology* **143,** 220-241.

McPhee MJ, Oltjen JW, Fadel JG, Mayer DG, Sainz RD (2009) Parameter estimation and sensitivity analysis of fat deposition models in beef steers using acslXtreme. *Mathematics and Computers in Simulation* **79,** 2701–2712.

Oltjen JW, Bywater AC, Baldwin RL (1986a) Evaluation of a model of beef cattle growth and composition. *Journal of Animal Science* **62**, 98-108.

Oltjen, JW, Bywater AC, Baldwin RL, Garrett WN (1986b) Development of a dynamic model of beef cattle growth and composition. *Journal of Animal Science* **62**, 86-97.

Sainz RD, Barioni LG, Paulino PV, Valadares Filho SC, Oltjen JW (2006) Growth patterns of Nellore vs. British beef cattle breeds assessed using a dynamic, mechanistic model of cattle growth and composition. In 'Nutrient digestion and utilisation in farm animals: modelling approaches'. (Eds E Kebreab, J Dijkstra, A Bannink, WJJ Gerrits, J France) pp. 160-170. (CAB International: Wallingford, UK)

[D]Corresponding author: jwoltjen@ucdavis.edu

Topic: Advances in modelling methodology

Updates and evaluation of the Cornell Net Carbohydrate and Protein System

A. Foskolos[A]*, E.A. Collao-Saenz*[A]*, R.J. Higgs*[A]*, D.A. Ross*[A]*, E.B. Recktenwald*[A] *and M.E. Van Amburgh*[A,B]

[A]Department of Animal Science, Cornell University, Ithaca, NY 14853, USA.

Introduction

The first version of the Cornell Net Carbohydrate and Protein System (CNCPS) was released in 1991 and has been under continuous evolution since. Our objective was to describe the latest updates of the model (version 6.5) and evaluate it against both literature and on-farm data.

Methods

The first set of updates is related to feed fractionation: the protein A fraction in the CNCPS, formally classified as non-protein nitrogen, was re-classified to ammonia (PA1) and soluble protein (PA2). The model includes a library of ~ 800 different ingredients which provide the platform for describing the chemical composition of the ration. Each feed in the feed library was evaluated against data from 2 commercial laboratories and updated where required to enable more precise predictions of dietary energy and protein supply. A multi-step approach was developed to predict uncertain values using linear regression, matrix regression and optimization. Further, amino acid (AA) profiles were updated using contemporary datasets and now represent the profile of AA in the whole feed rather than the insoluble residue. Degradation rates of protein and carbohydrate fractions were adjusted according to the new fractionation scheme, and corresponding changes to equations used to calculate rumen outflows and post-rumen digestion were defined. The link between BCS and NEm for growing cattle was eliminated. Moreover, a combined efficiency of essential AA use was adopted instead of separate efficiencies for maintenance and lactation. Three different datasets were developed to evaluate lysine (Lys) and methionine (Met) requirements (AA dataset), rumen N balance (rumen dataset) and most limiting (metabolisable energy or protein; ME or MP, respectively) predictions (lactation dataset). In total, 96 peer-reviewed studies with 367 treatments and 15 regional farms with 50 different diets were included.

Results and discussion

The AA dataset was used to indicate the concentration of Lys and Met that maximizes milk protein yield and content according to the broken line model with plateau: results suggested concentrations of 7.00 and 2.60% MP for Lys and Met, respectively, for maximal protein yield and 6.77 and 2.85% MP for Lys and Met, respectively, for maximal protein content. Proposed concentrations are slightly higher for Lys and 11-18% higher for Met compared with CNCPSv6.0 and are attributed to the changes in feed AA profile. The model predicted accurate and precise post-rumen flows of rumen degradable ($R^2_{BLUP} = 0.98$; $R^2_{MP} = 0.79$; CCC = 0.89) and undegradable N ($R^2_{BLUP} = 0.92$; $R^2_{MP} = 0.65$; CCC = 0.80), bacterial N ($R^2_{BLUP} = 0.97$; $R^2_{MP} = 0.84$; CCC = 0.87) and provided a uniform offset of non-ammonia N that is robust with little bias ($R^2_{BLUP} = 0.98$; $R^2_{MP} = 0.89$; CCC = 0.94). For the lactation dataset, the model predicted milk yield accurately and precisely according to the first limiting nutrient (MP or ME) with a $R^2_{BLUP} = 0.95$, $R^2_{MP} = 0.78$ and CCC = 0.83). Further, in this evaluation, MP-allowable milk was predicted with greater accuracy than ME-allowable milk ($R^2_{BLUP} =$ 0.99 and 0.95; $R^2_{MP} =$ 0.82 and 0.76; CCC = 0.83 and 0.84, for MP and ME, respectively), suggesting there are limitations in data describing energy use by the cow or digestibility of diets and ingredients. Results suggest a significant improvement of the model due to current updates.

[B]Corresponding author: mev1@cornell.edu

Topic: Advances in modelling methodology

Deriving estimates of individual variability in genetic potentials for three dairy breeds using a model of lifetime nutrient partitioning

H.N. Phuong[A,D], *O. Martin*[A], *I.J.M. de Boer*[B], *K.L. Ingvartsen*[C], *Ph. Schmidely*[A],
and N.C. Friggens[A]

[A]INRA-AgroParisTech, UMR791 Modélisation Systémique Appliquée aux Ruminants, Paris, France.
[B]Animal Production Systems group, Wageningen University, Wageningen, The Netherlands. [C]Faculty of Science and Technology, Aarhus University, Tjele, Denmark.

Introduction

Predicting the productive response of cows to a change in nutritional environment is essential for simulating lifetime efficiency. We explored the ability of a nutrient partitioning model to predict lifetime performance and to derive estimates of individual variability in genetic potentials.

Methods

The details of the nutrient partitioning model have been described by Martin and Sauvant (2010). Data of 102 cows (180 lactations) of 3 breeds: Danish Red, Danish Holstein, and Jersey were used. Individual cow performance through sequential lactations was used to derive genetic parameters for each by calibrating the model to achieve best fit, cow by cow. Animal performance data included milk yield (kg/d), milk fat, milk protein, milk lactose content (kg/kg), body weight (kg/cow), and dry matter intake (kg/d). Model quality was evaluated using root mean square error, and correlations between parameters in the model were explored using principal component analysis.

Results and discussion

The model predicted body weight and milk fat, protein and lactose with a high degree of accuracy. Milk yield and dry matter intake were satisfactorily predicted in early and mid-lactation, but under-predicted in in late lactation (Fig. 1). The extent to which the model's genetic parameters were correlated was consistent with those reported in the literature. In conclusion, the model is suitable for simulating the effects of genetic selection strategies on lifetime performance of individual cows.

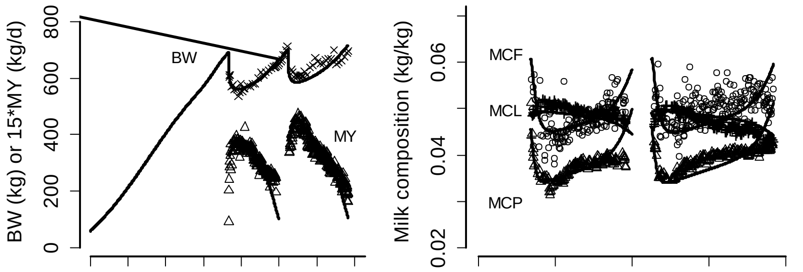

Fig. 1. Model simulations (solid line) of milk yield (MY), body weight (BW), milk fat content (MCF), milk protein content (MCP), milk lactose content (MCL). MY is presented as MY×15.

References

Martin O, Sauvant D (2010). A teleonomic model describing performance (body, milk and intake) during growth and over repeated reproductive cycles throughout the lifespan of dairy cattle. 1. Trajectories of life function priorities and genetic scaling. *Animal* **4**, 2048-2056.

[D]Corresponding author: phuong.hongoc@agroparistech.fr

Topic: Advances in modelling methodology

A mechanistic model of methanogen-hydrogen dynamics

Y. Wang[A,B]*, P.H. Janssen*[B]*, T.A. Lynch*[A]*, B. van-Brunt*[A] *and D. Pacheco*[B,C]

[A]Institute of Fundamental Sciences, Massey University, Palmerston North 4442, New Zealand.
[B]AgResearch, Grasslands Research Centre, Palmerston North 4442, New Zealand.

Introduction

Improvements in enteric methane (CH_4) prediction require a mechanistic representation of the interactions between dissolved hydrogen (H_2) and methanogens (Janssen 2010). Although methanogens are responsible for the formation of CH_4 in the rumen, the existing mechanistic models of rumen function do not include an explicit representation of their metabolism. This means that the effect of mitigation options being developed to target methanogens directly (e.g. vaccines and chemical inhibitors; Buddle *et al.* 2011) cannot be modelled mechanistically. Thus, a model to represent the relationship between methanogens and H_2 has been developed.

Methods

We developed a model of methanogen growth based on a model of microbial growth kinetics (Monod 1949). The key concept represented is that methanogens use H_2 to reproduce and survive wash-out from the rumen, producing CH_4 as a by-product (Janssen 2010). The rates of change of the methanogen population (X': 1) and H_2 concentration (S'_h: 2) are defined as:

$$X'_m = \Delta_h E X_m - \alpha X_m \qquad (1) \qquad\qquad S'_h = -\frac{q_m}{K_m+S_h} S_h X_m - \alpha S_h + \beta \qquad (2)$$

where:

$$\Delta_h(S_h) = \frac{n_m q_m}{K_m+S_h} S_h - m_m \quad (3) \qquad \text{and } E = \begin{cases} Y_m, & \text{if } \Delta_h(S_h) \geq 0 \qquad (4.1) \\ \frac{d_m}{m_m}, & \text{if } \Delta_h(S_h) < 0 \qquad (4.2) \end{cases}$$

is a function representing methanogen growth (4.1) or decay (4.2) depending on H_2 concentration. Methane production is $0.25(\beta - \alpha S_h)$. The parameters q_m, K_m, m_m, Y_m and d_m represent biological properties of the methanogen cells, being maximal rate of H_2 utilization, H_2 concentration at half q_m, maintenance requirement, yield of cells (i.e., reproduction) and decay coefficients, respectively. Input parameters are α and β, which represent the rumen outflow rate and the rate of H_2 production from fermentation, respectively.

Results and discussion

The model has been tested for its ability to replicate the relationships between methanogen growth, rumen H_2 concentrations and passage rate (Janssen 2010). Simulations indicate that it meets biological expectations and provides stable solutions with constant or intermittent inputs of H_2. The model appropriately predicts that for a given H_2 input, accelerating passage (α) will lead to increases in the H_2 concentration. This model, linked to an explicit dynamic representation of H_2 production, provides a stepping stone to improve our ability to predict ruminal CH_4 production.

References

Buddle BM, Denis M, Attwood GT, Altermann E, Janssen PH, Ronimus RS, Pinares-Patiño CS, Muetzel S, Neil Wedlock D (2011) Strategies to reduce methane emissions from farmed ruminants grazing on pasture. *Veterinary Journal* **188**, 11-17.

Janssen PH (2010) Influence of hydrogen on rumen methane formation and fermentation balances through microbial growth kinetics and fermentation thermodynamics. *Animal Feed Science and Technology* **160**, 1-22.

Monod J (1949) The growth of bacterial cultures. *Annual Review of Microbiology* **3**, 371-394.

[C]Corresponding author: david.pacheco@agresearch.co.nz

Topic: Advances in modelling methodology

Using selection trajectories to optimise energy acquisition and allocation according to nutritional environment

L. Puillet[A,B,C], D. Réale[C] and N. Friggens[A,B]

[A]INRA, UMR 791 MoSAR, F-75005 Paris, France. [B]AgroParisTech, UMR 791 MoSAR, F-75005 Paris, France. [C]UQAM, Département des Sciences Biologiques, Montréal, Canada.

Introduction

Nutrient partitioning is the study of nutrient-flow trade-offs among biological functions. Our current interest is to incorporate genetic drivers and their effects on animal fitness into nutrition partitioning models. A focus of the following study was on formalising genetics as energy acquisition and allocation parameters rather than as phenotypic traits (production potential). Our objective was to study these parameters in different nutritional environments.

Methods

An energy-based model for female ruminants was developed. It comprised a control sub-model, incorporating genetic parameters for acquisition (AQ) and allocation (AL), and an operating sub-model, converting energy into biological traits. The levels of three compartments directly determine the proportion of energy allocated to growth, reproduction and survival. A genotype (G) corresponds to a strategy of AQ and AL, defined by 4 parameters: 3 fractional rates (driving transfer in AL compartments) and 1 for acquisition (kJ/day). Simulations were run to compute the fitness of 784 G in 4 nutritional environments (NE), combining two types of competition for resources (dominance effect proportional to AQ or equal access) and two temporal profiles (stable or seasonal).

Results and discussion

In all NE, a minimal energy investment for growth was necessary, based on two contrasted strategies: a high AQ combined to a low growth AL or a medium AQ combined to a medium growth AL. Aquisition was constrained by competition: dominance favoured a high AQ (highest energy intake) while equal access favoured a medium AQ (optimising AQ costs). In stable NE, strategies were based on reproductive investment while in seasonal NE, strategies were based on survival.

Table 1. Description of the fittest genotypes obtained in 4 simulated nutritional environments

NE[B]	Fittest[A] genotype parameters			Longevity (years)	Lifetime energy for growth		Lifetime energy for survival		Lifetime energy for reproduction	
	Growth AL	Reproduction AL	AQ		MJ	%	MJ	%	MJ	%
NE1	Low	High	High	17	2262	1.6	131339	90.1	12111	8.3
NE2	Med	High	Med	15	2219	2.1	95522	90.5	7784	7.4
NE3	Low	Low	High	9	1756	3.6	45038	93.0	1643	3.4
NE4	Med	Low	Low	9	1812	4.3	37123	89.1	2719	6.5

[A]Highest number of young weaned alive; [B]NE1: stable with dominance; NE2: stable without dominance; NE3: seasonal with dominance and NE4: seasonal without dominance.

Strategies maximising fitness were strongly affected by NE. Both acquisition and allocation were levers to cope with nutritional constraints. Understanding trade-offs allows well defined fitness criteria to be maximised and to disentangle the role of acquisition and allocation. The model here is a theoretical tool, inspired from ecology, and should be tested for domestic species. It opens perspective to enrich the conceptual basis of existing nutrition models.

[C]Corresponding author: laurence.puillet@agroparistech.fr

Modelling the metabolic fate of dietary phosphorus and calcium in growing pigs and the dynamics of body composition: model evaluation and inversion

M.P. Létourneau-Montminy[A,B,F]*, A. Narcy*[C]*, T.D. Crenshaw*[D]*, J.Y. Dourmad*[E] *and C. Pomar*[A]

[A]Agriculture and Agri-Food Canada, Sherbrooke, J1M 1Z3, Canada. [B]Present address: Laval University, Quebec, G1V 0A6, Canada. [C]INRA, UR83 Recherches Avicoles, F-37380 Nouzilly, France. [D]University of Wisconsin-Madison, Madison 53706. [E]INRA, UMR1348 Pegase, F-35590 Saint-Gilles, France.

Introduction

Several phosphorus (P) response criteria are required, depending on the objective of production (e.g. profitability, welfare and environment). To meet this challenge, a robust multi-criteria model aiming to simulate calcium (Ca) and P retention within the body protein, lipid and ash of the growing pig, according to growth potential and dietary Ca and P intake, has been developed.

Material and methods

A mechanistic model was built in which parameter values were estimated using experimental data and the most relevant model mechanisms driving Ca and P metabolism were evaluated. Evaluation included a sensitivity analysis, simulation using specific experimental situations, and by comparing model predictions to observed data. The model was inversed to estimate P requirements and the estimated values were compared with existing P requirement standards for pigs (INRA, 2005; NRC, 2012).

Results and discussion

When varying model parameters from -1.5 to 1.5 times, the most influential predictor of P deposition in soft tissue was the percentage of P in body protein (observed standard deviation of ±16%) whilst the apparent total tract digestibility (ATTD) of different dietary P sources were the most influential predictors of P deposition in ash (observed standard deviation of -6 to +1%). Simulations using a balanced diet (NRC 2012) or diets low in lysine, imbalanced for Ca and P, or fed according to different depletion-repletion sequences, indicated that the model adequately represented critical aspects of P and Ca metabolism in growing pigs. Simulated Ca, P, and body protein and ash compositions were close (rMSPE, 4 to 9%; error disturbance between 83 and 97%) to experimental results, but P and Ca ATTD retention efficiencies were less accurate (rMPSE = 11 to 21%).

Model recommendations for dietary P requirements were close to those of INRA (2005) for young pigs and to those of NRC (2012) for older pigs. The evolution of dietary P requirements is modulated in the proposed model by the amount of P associated with body protein, lipid and ash, and the retention of these over time. Model recommendations for digestible Ca:P in the diet were close to INRA (2005) (2.7:1) but higher than that recommended by NRC (2012) (2.15:1).

Conclusion

The proposed mechanistic model of P and Ca metabolism adequately simulated the impact of a variety of feeding strategies on the metabolic fate of P and Ca and adequately estimated dietary P and Ca requirements over time in growing pigs.

[F]Corresponding author: Marie-Pierre.letourneau@fsaa.ulaval.ca

Modelling herbage intake of part-time grazing dairy sheep

G. Molle[A,C], *A.S. Atzori*[B] , *V. Giovanetti*[A] , *M. Decandia*[A], *M. Sitzia*[A] *and A. Cannas*[B]

[A]Agris Sardegna, Dipartimento per la Ricerca nelle Produzioni Animali, 07040 Olmedo, Italy.
[B]Dipartimento di Agraria, Università di Sassari, 07100 Sassari, Italy.

Introduction

Current models for predicting herbage intake of dairy sheep do not account for the effect of time of access to pasture (Pulina *et al*. 2013). The restriction of access to pasture (TA, h/day) to 2, 4 or 6 h/day was the focus of two experiments (E1 and E2) in which intake and performance response of lactating dairy ewes were measured while rotationally grazing Italian ryegrass (*Lolium multiflorum* Lam, E1) or Berseem clover (*Trifolium alexandrinum* L , E2) pastures. The objective of this study was to model the results gathered in E1 and E2 to define the main explanatory variables of herbage intake (HDMI, g/ewe.day) when time access to pasture is restricted.

Materials and methods

A database was set up using mean data of pasture plots (625 m^2 each) and animal groups (4 to 8 ewes per group, 3 core animals being used to measure intake and performance). Methods are detailed in Molle *et al.* (2014). Pastures were in vegetative condition and ewes were in mid-lactation, with milk yields (MY) ranging between 700 and 2200 g/ewe.day. The ewes were supplemented with 400 g/ewe of a pelleted concentrate, split into two meals/day, at each milking, and 300 g/ewe.day of lupin seed (E1) or maize (E2) and 700 g/ewe ryegrass hay fed at turn out from pasture.

A total of 144 records were used for all the variables, except for some pasture variables such as LAI (LAI = 96). A mechanistic framework model was used for *ex ante* screening of the regressors of interest. Then a stepwise regression analysis was undertaken to select the variables that best explained HDMI. In a third step, the regressors selected by the stepwise regression analysis were further screened in or out the model, taking into account variance inflation factor, squared condition number and Pearson correlation coefficients as multicollinearity criteria.

Results and conclusions

The best explanatory model for HDMI was: HDMI (g/ewe.day) = 814 (± 411, P <0.001) + 32.69 BW (± 9.44 kg/ewe, P<0.001) – 36.97 NDFE (± 2.7 % DM, P<0.001) + 125.5 TA (± 14.8 hours/day, P<0.001); N= 144, P<0.001, adjusted R^2 = 0.0.694, RMSE = 256 g/d; where BW is body weight, NDFE is content of NDF in hand-plucked herbage samples and TA is time access to pasture. Multicollinearity was low with a variance inflation factor <1.3 for all variables. Although MY increased significantly with increased TA, it did not improve prediction of HDMI suggesting that MY was more a result than a cause of variations in HDMI. It is also relevant that NDFE affected HDMI even when time access to pasture was restricted to a maximum of 6 hours, suggesting a very tight short term effect of pasture NDF on HDMI. The next step will be to develop a mechanistic model accounting for the filling effect of pasture and regulation of feeding behaviour when access to pasture is limited.

References

Molle G, Decandia M, Giovanetti V, Manca C, Acciaro M, Epifani GP, Salis L, Cabiddu A, Sitzia M, Cannas A (2014) Effects of restricted time allocation to pasture on feeding behaviour, intake and milk production of dairy sheep rotationally grazing Italian ryegrass (*Lolium multiflorum* Lam) in spring. *Animal Production Science* **54**: 1233-1237.

Pulina G, Avondo M, Molle G, Francesconi AH, Atzori AS, Cannas A (2013) Models for estimating feed intake in small ruminants. *Revista Brasileira de Zootecnia* **42**:675-690.

[C]Corresponding author: gmolle@agrisricerca.it

Topic: Modelling feed intake

Prediction of voluntary dry matter intake of growing goats

I.A.M.A. Teixeira[A,B] *and A.K. Almeida*[A]

[A]Unesp, Univ Estadual Paulista, Jaboticabal-SP 14884-900, Brazil.

Introduction

An accurate estimate of volutary dry matter intake (I_{DM}) allows researchers and producers to predict the input of nutrients and therefore animal performance. Teixeira *et al.* (2011) reported bias in current models for predicting I_{DM} of growing goats. Our objective was to develop models for predicting I_{DM} for growing goats based on their metabolic live weight (W) and weight gain (G)

Methods

We used linear mixed-effect models to associate I_{DM} and W (kg) and/or G (kg/d). We used daily individual records of 60 growing Saanen goats [18 intact males (♂), 19 castrated males (⊖) and 23 females (♀)] weighing from 14.4 to 46.6 kg and age varying from 3 to 17 months old. These animals were fed *ad libitum* twice a day, with a total mixed diet with 50:50 concentrate:roughage ration (In DM basis: 18 MJ GE/kg, 160 g of CP/kg and 318 g of NDF). In average, the observed I_{DM} and G were 978 ± 234.6 g/day and 125 ± 55.5 g/day, respectively. Also evaluated was the effect of maximum daily temperature record on I_{DM} by linear regression over the range 21.4 to 41.1 °C. Data were analysed considering repeated measurements in time (days) with the fixed effects of sex (df = 2), random effects of study (σ^2_S; df = 2) and a residual error term (σ^2_e; df = 6135). Chosen covariance structure was the Compound Symmetry, which minimised Bayesian Information Criterion. Statistical analyses were performed using the MIXED procedure of SAS V9.3. When sex was found significant ($P < 0.10$), three CONTRAST statements were used to conduct pairwise comparisons of sex.

Results and Discussion

The estimate of daily I_{DM} (g/ $LW^{0.75}$) were different for males and females goats (Eq. 1.1 and 1.2; $\sigma^2_e = 176.9$; $\sigma^2_S = 44.9$). In general, throughout the live weight range evaluated, males showed greater I_{DM} than females.

♂⊖ $I_{DM} = 105\ (9.81) + 0.0641\ (1.30) \times W - 0.1634\ (0.054) \times W^2$ [1.1]

♀ $I_{DM} = 127.5\ (8.65) - 4.57 (1.18) \times W + 0.0269\ (0.0445)\ \times W^2$ [1.2]

Since growth rate plays an important role in intake, we also developed a model accounting for effect of W and G. We estimated equations for each sex (Eq. 2.1, 2.2 and 2.3; $\sigma^2_e = 156.3$; $\sigma^2_S = 57.8$). The I_{DM} diminished with the increase of W, at same rate for females and intact males.

⊖ $I_{DM} = 115\ (5.14) - 3.99\ (0.174) \times W + 93.6\ (7.24)\ \times G$ [2.1]
♂ $I_{DM} = 115\ (5.14) - 3.54\ (0.154) \times W + 69.7\ (4.69)\ \times G$ [2.2]
♀ $I_{DM} = 105.7\ (4.94) - 3.54\ (0.154) \times W + 119.2\ (5.98)\ \times G$ [2.3]

We also verified the effect of temperature on the I_{DM} and observed that I_{DM} was reduces by 0.623 g/ $LW^{0.75}$ for each increase of 1 degree Celsius in the observed maximum daily temperature.

References

Teixeira IAMA, St-Pierre N, Resende KT, Cannas A (2011) Prediction of intake and average daily gain by different feeding system by goats. *Small Ruminant Research* **98**, 93-97.

[B]Corresponding author: izabelle@fcav.unesp.br

Topic: Modelling feed intake

New findings on dry matter intake prediction in dairy calves

A.L. da Silva[A]*, M.I. Marcondes*[A]*, J.P. Pacheco Rodrigues*[A] *and M.L. Chizzotti*[A,B]

[A]Department of Animal Science, Universidade Federal de Viçosa, Viçosa, MG, Brazil.

Introduction

Dry matter Intake (DMI) is a multifactorial variable. For suckling calves, the amount of milk offered and age are the main factors determining the intake of starter DM (Valadares Filho *et al*. 2010).

Methods

A joint analysis on DMI data from three trials was conducted, where calves where offered 2 to 8 L/day of milk for a period of 60 days, totaling 3316 observations. The DMI was expressed as a function amount of milk offered and age of calf (Eq. 1): $\mathrm{DMI} = 0.125 \times \mathrm{M} \times e^{[k \times (D - c)]}$, where: DMI (kg/day); M = milk offered (L/day); D = age (days); k = intake increment rate (day^{-1}); c = adjustment parameter.

Results

Starter intake (SI) tended to increase exponentially with calf age (Fig. 1a). Calves that had greater amounts of milk offered had lower rates of increase in starter intake (Fig. 1b). Thus, it was not possible to adopt one single equation, as SI is different for high or low amounts of milk offered.

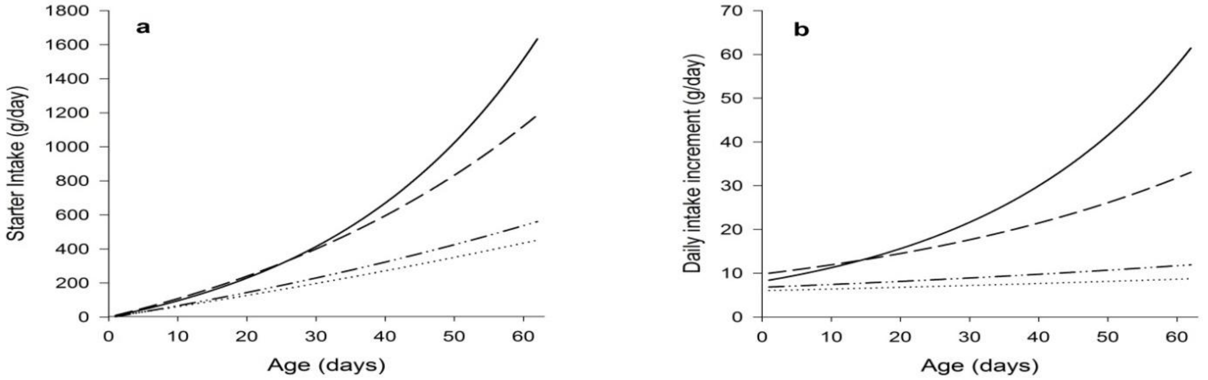

Fig. 1. a) Exponential relationship between starter intake and age of animals receiving 2 (—); 4 (– –); 6 (··–) or 8 (···) litres of milk per days. b) Daily intake increment rate for the starter feed according to age and milk amount.

After obtaining independent models for each milk level, regression techniques were applied, and two different models to predict DMI (kg/day) were created, one for calves receiving less than 5 L/day of milk (Eq 2), or for calves recieving 5 to 8 L/day (Eq. 3)

Eq. 2; R^2=0.5813; RMSE=0.2434, $\mathrm{DMI}_{<5} = 0.125 \times \mathrm{M} \times e^{\{(-0.0065 \times M + 0.0456) \times [D - (-0.0154 \times M + 0.0856)]\}}$

Eq. 3; R^2=0.6013; RMSE=0.1768, $\mathrm{DMI}_{>5} = 0.125 \times \mathrm{M} \times e^{\{(-0.0015 \times M + 0.0183) \times [D - (-0.0273 \times M + 0.2311)]\}}$

where M=amount of milk offered (L/day); D = age (days).

References

Valadares Filho SC, Marcondes MI, Chizzotti ML, Paulino PVR (2010) 'Nutrient Requirements of Zebu Beef Cattle – BR-Corte, (2nd edn).' (Viçosa - MG: Suprema Gráfica e Editora LTDA, Brazil).

[B] Corresponding author: mariochizzotti@gmail.com

Environmental stress effects on swine intake

R.R. White[A,B] *and M.D. Hanigan*[A]

[A]Department of Dairy Science, Virginia Tech, Blacksburg, VA 24060, USA.

Introduction

The changing global climate highlights the importance of identifying livestock responses to variable ambient temperatures. Swine exhibit significant production losses during environmental stress. A recent meta-study (Renaudeau *et al*. 2011) suggests a 10 to 15% decrease in intake at high temperatures but the swine NRC (2012) predicts a 35 to 40% decrease. The objective of this study was to evaluate the growing swine NRC (2012) equations for feed intake against a literature dataset and to develop a series of new equations modelling the influence of environmental stress on intake.

Methods

A literature survey identified studies assessing intake responses to temperature. The resulting dataset included 120 comparisons to thermoneutral intake from 35 studies. Intake as a fraction of thermoneutral intake (FFI) was the primary response variable. The NRC predicted FFI was compared to observed values. Residual analyses were used to identify mean and slope biases with respect to the predicted values and across temperatures. The root mean squared error of prediction (RMSPE) and the concordance correlation coefficient (CCC) for each comparison was calculated. New parameters for this equation (NRC2) were then fitted to the data, and new equations incorporating duration of exposure (TD), temperature cycling (TC), publication year (TY) and location (TL) were also derived. These new equations were also evaluated with residual analyses, RMSPE and CCC.

Results

The NRC model exhibited significant mean and slope bias across predicted values and temperatures; NRC2 substantially reduced these biases and improved RMSPE and CCC.

Table 1. Temperature model RMSPE and CCC

Model:	NRC	NRC2	TD	TC	TY	TL
RMSPE, % of Observed	257.0	149.2	143.2	144.5	144.0	129.6
CCC	0.499	0.555	0.61	0.60	0.61	0.70

The TD, TC and TY models marginally improved RMSPE and CCC compared with the NRC2 model. The TL model had the greatest improvement in predictive capacity suggesting substantial location-based differences in responses to environmental stress.

Conclusions

The new equations derived in this study provide useful additions to the NRC (2012) model for users interested in simulating swine responses to ambient temperature fluctuations.

References

National Research Council (NRC) (2012). Nutrient Requirements of Swine: 11th Revised Edition. National Academies Press, Washington, DC.

Renaudeau D J, Gourdine J L, St-Pierre N (2011). A meta-analysis of the effects of high ambient temperature on growth performance of growing-finishing pigs. *Journal of Animal Science* **89**, 2220-2230.

[B]Corresponding author: rwhite14@vt.edu

Author index