EVOLUTION OF THE CNCPS - DEVELOPMENT OF V7

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INTRODUCTION

The CNCPS was first described in a conference proceedings addressing protein requirements for cattle in the 1980's (Fox et al., 1982; Van Soest et al., 1982). Ten years later, a series of manuscripts were published outlining the CNCPS in more detail including carbohydrate and protein digestion (Sniffen et al., 1992), microbial growth (Russell et al., 1992), amino acid supply (O'Connor et al., 1993) and animal requirements (Fox et al., 1992). These publications laid the foundation for a substantial R&D effort over ~30 years that has seen numerous model updates published culminating in summary papers describing new versions of the CNCPS (Fox et al., 2004; Tylutki et al., 2008). The effort continues today with the most recent updates describing v6.5 of the CNCPS (Higgs et al., 2015; Van Amburgh et al., 2015). A unique aspect of the CNCPS, which sets it apart from other modeling efforts, is its widespread commercial use and global reach. Estimates have various versions of the CNCPS being used by thousands of people in dozens of countries to formulate the rations of millions of cattle around the world every day.

The initial intention in developing v7 was to improve predictions of AA supply. Our strategy was to include estimations of protozoal and endogenous N flows from the rumen as part of v6.5. However, given the extensive cycling of N within the rumen, to the liver, and among the entire GIT, it became apparent that to adequately capture all these dynamics, a more holistic approach would be required. The entire GIT of the CNCPS has been rebuilt in v7 along with a new system to estimate post absorptive components of N metabolism such as urea recycling and AA supply. Development of v7 has changed the CNCPS from a static to a more dynamic and mechanistic model. New capability has also been included based on work from (Ross, 2013) and (Raffrenato, 2011). This provides new capability to understand variation in nutrient supply and can help refine ration formulation. A complete model description is provided by Higgs (2014). This paper will focus on aspects of the model that impact N metabolism and its subsequent flow out of the rumen.

AN OVERVIEW OF V7

Model structure

Since inception, the CNCPS has been developed for field application with care taken to ensure model inputs are routinely available on most farms (Fox et al., 2004). Practical application has remained a core philosophy in model development and v7 adheres to the same fundamental principles. While new capability is available within the model, ensuring the model would be field usable was a priority.

Version 7 is constructed in the system dynamics modeling software Vensim (2010). Vensim uses a diagrammatic interface with embedded mathematical statements and calculates iteratively over time. The time unit used in the development of this model is hour, and the model simulates for 300 h with integration every 6 minutes. The simulation time used was the shortest period needed for the model to reach dynamic equilibrium or 'steady state' (Sterman, 2000) across a range of diets. The diagrammatic interface of Vensim is convenient and allows for visual critique of the model which aids interpretation, particularly when considering biological processes. The visual nature also means the model can be more easily understood and interrogated by current and future contributors to the R&D effort.

Diets are generally balanced for the average cow in a group on a per day basis. Although v7 calculates continuously over time, and the unit used within the model is hour, the output from the model is expressed on a per day basis. To do this, the model is sampled for 24 h after simulating for 276 h (once it has reached steady state). Therefore, the format of the outputs generated are similar to those from v6.5.

Several aspects of the model have been completely rebuilt using entirely new approaches. Protein digestion is one example which is now calculated on an N basis and is reconciled by compartment to ensure N balance through the model is correct. This facilitated the construction of a mechanistic system to estimate urea recycling and simplified the estimation of AA flows through the GIT.

Intake and nutrient digestion

Digestion of nutrients in the original CNCPS (Sniffen et al., 1992) followed the system proposed by Waldo et al. (1972) where the kinetics of digestion and passage are integrated to predict substrate digestion. Assuming a single potentially digestible pool, the system can be described by the following equation:

$$\frac{dA}{dt} = -k_1 A - k_2 A$$

where,
A = the amount of potentially digestible substrate in the rumen,
k_1 = the digestion rate,
k_2 = the rate of passage,
t = time in hours.

The derivative of the previous equation gives:

$$R = Ae^{-(k1+k2)t}$$

where, assuming a single feeding,
R = the remaining potentially available substrate present in the rumen after *t* hours,
A = the amount of substrate fed.

Using this system, the ratio of $k_1/(k_1 + k_2)$ gives the fraction of substrate digested in the rumen from a single feeding and has been used to statically capture the dynamics of rumen digestion in both the CNCPS and the protein sub-model of the NRC (2001).

The new rumen sub-model follows the same general system previously used, but because the model is dynamic, rather than static, and calculates continuously, an intake term can and must be added to the model which allows the estimation of substrate pool size at steady state. The general form of the system is shown in Figure 1 and is represented by the equation:

$$\frac{dA}{dt} = k_1 A - k_2 A - k_3 A$$

where,
A = the amount of potentially digestible substrate in the rumen,
k_1 = the rate of substrate intake,
k_2 = the digestion rate,
k_3 = the rate of passage,
t = time in hours.

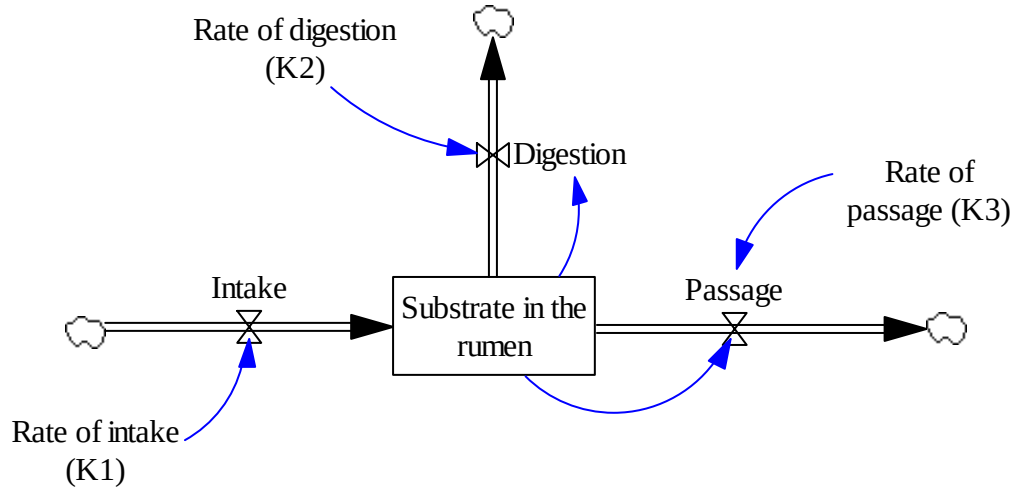

Figure 1. Diagram representing the dynamics of a single pool of substrate digestion in rumen

The pattern of intake affects many aspects of the model including, but not limited to, microbial growth, rumen N supply and rumen pool sizes. Changing the intake pattern from a constant influx to pulses that represent meals creates variation in the predicted rumen pools sizes. More frequent smaller meals result in less variation than larger, less frequent meals. Meal duration is also important with longer slower meals resulting in less variation than the same meal size over a shorter period of time. The model could also accommodate unequal meal sizes allowing for the comparison of different systems (tie-stalls, free-stalls or grazing) and different management scenarios (over-crowding, slug feeding, etc.).

An important factor that intake pattern strongly influences is rumen NH_3-N, which in turn, impacts microbial growth. A comparison of predicted NH_3-N using continuous intake, 4 meals/d and 8 meals/d is found in Figure 2. Microbial growth in the model becomes limited when rumen NH_3-N falls below 5.0 mg/dl (Satter and Roffler, 1975). This interaction causes the behavior observed in Figure 2 when NH_3-N falls below 5.0 mg/dl when the meal pattern is 4 meal/d. The effect of N recycling within the model is evident as rumen NH_3-N slowly increases until the next meal is consumed. The same general pattern is presented by Schwab et al. (2005) using in-vivo data. With continuous feeding and with 8 meal/d rumen NH_3-N remains above 5.0 mg/dl demonstrating the importance of feeding pattern on rumen N supply.

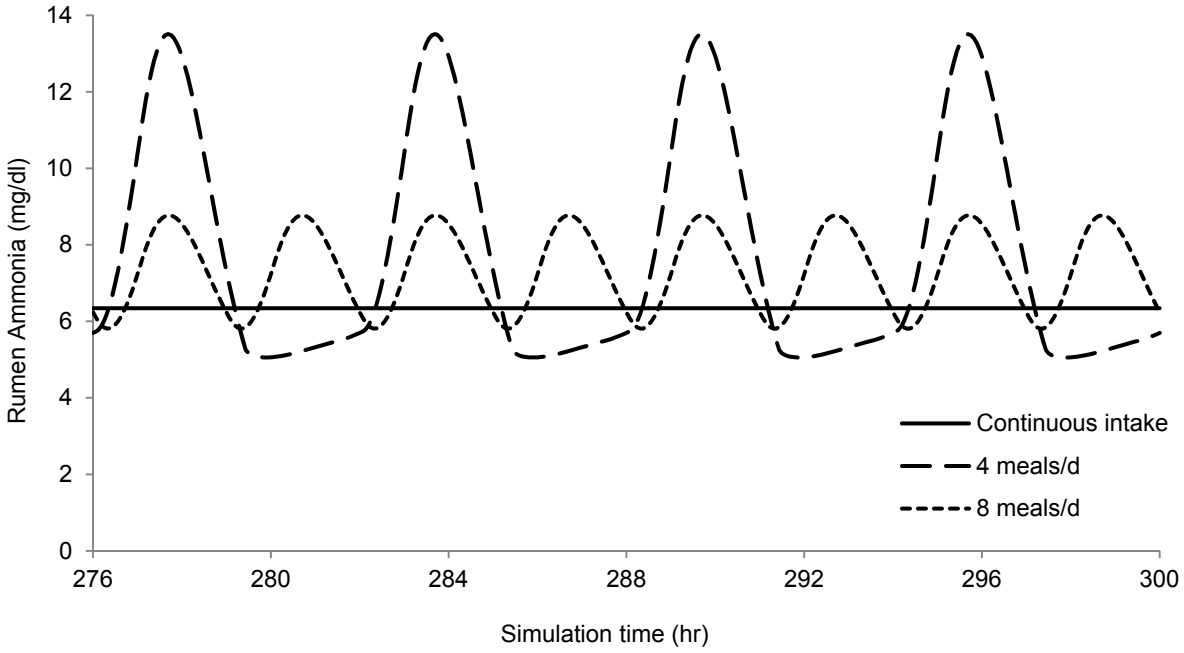

Figure 2. Variation in rumen NH_3-N (mg/dl) among three different meal distributions represented by continuous intake, four meals per day and eight meals per day. The ammonia concentration does not decrease below 5 mg/dl in this example because below that value, microbial yield is decreased thus offsetting the demand.

Protozoa

Protozoa have been accommodated in previous versions of the CNCPS by reducing the theoretical maximum growth yield of bacteria from 0.5 to 0.4 g cells per g CHO fermented (Russell et al., 1992) but do not contribute to digestion or microbial protein production. Protozoa have important effects not only on bacterial yield, but also nutrient digestion and cycling within the rumen (Firkins et al., 2007; Hristov and Jouany, 2005) and can make up 40% to 50% of the total microbial biomass (Hristov and Jouany, 2005). Further, protozoa can contribute 5-10% of the microbial flow in high producing dairy cows, and their AA profile differs to that of bacteria, particularly in Lysine content where it is greater. To capture these effects, aspects of protozoal growth and metabolism

were constructed in v7. To appropriately account for microbial growth, the bacterial growth yield was set at the maximum amount (0.5 g cells per g CHO fermented; Isaacson et al., 1975) to then allow for protozoal predation of bacteria.

An example of how predictions of microbial growth behave, with and without protozoa, are presented in Figure 3. Dietary comparisons include high and low levels of forage at high or low levels of intake. Diets were formulated to provide a 600 kg animal with enough energy and protein to support 45 kg milk at the high level of intake and 20 kg milk/d at the low level of intake. Simulations are run for 300 h which is the time required for all microbial functions to reach steady state within the rumen sub-model.

Using this example, predicted rumen pools of fiber bacteria (FB-N) and non-fiber bacteria (NFB-N) are reduced by protozoal growth. This occurs due to predation and also competition for substrate. Non-fiber bacteria are most affected as they exist in the fluid phase and are more accessible for protozoa to engulf (Dijkstra et al., 1998). Fiber bacteria are also engulfed as a collateral effect of fiber engulfment (Dijkstra et al., 1998). Protozoal pool sizes when intake was high were 4.2% and 9.2% of the microbial N for the low and high forage diets, respectively, and are within the range and follow the same trend reported by Sylvester et al. (2005). Pool sizes on the lower intake diets are higher which is due to lower predicted passage. A positive feedback exists within the model where, as the protozoal cell mass increases, more substrate can be engulfed. This is controlled by lysis, passage and also the ability of protozoa to digest engulfed material.

Protozoa make a significant contribution to microbial protein turnover in the rumen which increases peptides, free AA and NH_3-N (Walker et al., 2005). In situations where rumen N is deficient, the effect of protozoa in the model stimulates bacterial growth and CHO digestion through increasing the rumen N supply, although net microbial flow out of the rumen is still reduced through predation. Predicted microbial turnover ranged from ~10% to 40% which is lower than what is typically reported (Hristov and Jouany, 2005), but this might be expected in high producing animals (Firkins et al., 2007). Overall efficiencies of microbial growth in the faunated simulations ranged from 17.4 to 28.5 g microbial N kg^{-1} RD OM which is similar to the finding of Broderick et al. (2010). Values in the defaunated simulations were higher than what might be expected and demonstrates the importance of including protozoa in the model.

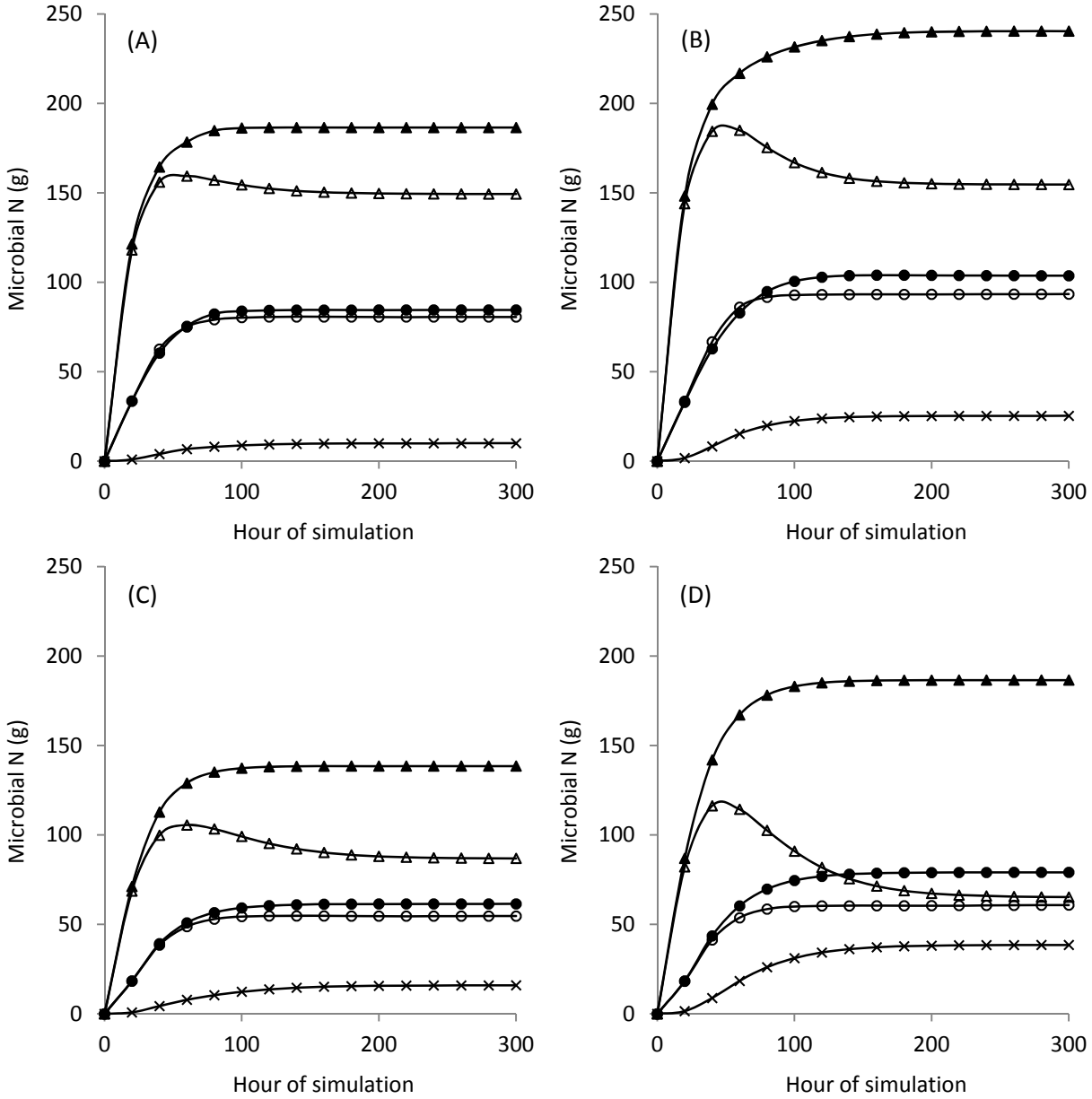

Figure 3. Rumen microbial N pools in diet simulations at high intakes with low (A) or high (B) levels of forage or low intakes with low (C) or high (D) levels of forage where the rumen was either faunated or defaunated. Microbial populations in the faunated rumen include: Non-fiber bacteria (∆), fiber bacteria (○) and protozoa (×). Microbial populations in the defaunated rumen include: Non-fiber bacteria (▲) and fiber bacteria (●).

Intestinal digestion

In previous versions of the CNCPS, material that escapes rumen digestion and arrives in the lower GIT can either be digested or passed out in the feces (Sniffen et al., 1992). This is calculated using an intestinal digestibility coefficient that represents the entire lower GIT. In reality, digestion in the small intestine and large intestine occur by

different processes with the small intestine being enzymatic and the large intestine fermentative (Van Soest, 1994). In the current model, digestion in these two compartments has been separated with digestion in the small intestine modeled using a single digestion coefficient, while the large intestine utilizes a mechanistic structure, similar to the rumen model.

Urea recycling

Ruminants have a remarkable ability to recycle N back to the GIT on order to sustain favorable conditions for microbial protein synthesis and in general, this recycling appears to be an obligate function with a low energy requirement (Reynolds, 1992). While previous versions of the model have accounted for N recycling (Fox et al., 2004), the dynamics are difficult to capture in a static model. A great deal of work has taken place to try and understand the exact mechanisms and quantitative aspects of N recycling, and while the exact mechanisms remain evasive, quantitative aspects of N fluxes are reasonably well understood and described (Lapierre and Lobley, 2001; Marini et al., 2008; Marini and Van Amburgh, 2003; Recktenwald et al., 2014).

The proportion of urea returned to the GIT relative to urea production is remarkably uniform among experiments when animals are fed diets at, or in moderate excess of MP requirements (Lapierre et al., 2004, Ouellet et al., 2004, Recktenwald, 2007, Valkeners et al., 2007). However, recycling increases when N supply is limited (Reynolds and Kristensen, 2008, Valkeners et al., 2007) and decreases when N supply is greatly in excess (Lapierre et al., 2004, Reynolds and Kristensen, 2008). To estimate the proportion of urea returned to the GIT in v7, the equations presented in Recktenwald et al. (2014) and Reynolds and Kristensen (2008) were used in combination. Recktenwald et al. (2014) showed a linear relationship between urea production and urea recycling in high producing cows fed diets ranging from 15% - 17% CP, while, Reynolds and Kristensen (2008) showed an increase in the proportion of urea recycled at very low N intakes. Therefore, using the equations in combination allowed for a wider range in dietary conditions to be represented. Recycled urea is distributed to either the rumen, large intestine or small intestine and continues to cycle through the system at steady state. To integrate these transactions, a new system of N recycling was constructed in v7.

A summary of the pools and flows of N in v7 once absorbed from the GIT is found in Figure 4. The model assumes non-ammonia N absorbed in the small intestine (NAN Ab to PDV) has two general fates: 1) it is utilized for a function of maintenance or production (Liver-NAN Utilized) or, 2) it is converted to urea in the liver (Liver-NAN to Urea). Nitrogen requirements for maintenance or production include milk, growth, reserves, fetal growth, scurf, metabolic urinary losses and gut secretions. Absorbed NH_3-N from either the rumen (R-NH3 N to PDV), large intestine (LI-NH3 N to PDV) or small intestine (SI-NH3 N to PDV) is assumed to be completely converted to urea in the liver (PDV-NH3 to Urea). Nitrogen converted to urea can either be returned to the GIT (Urea-N Liver Recycled to the GIT), or excreted in the urine (Urea-N Liver Irreversible Loss).

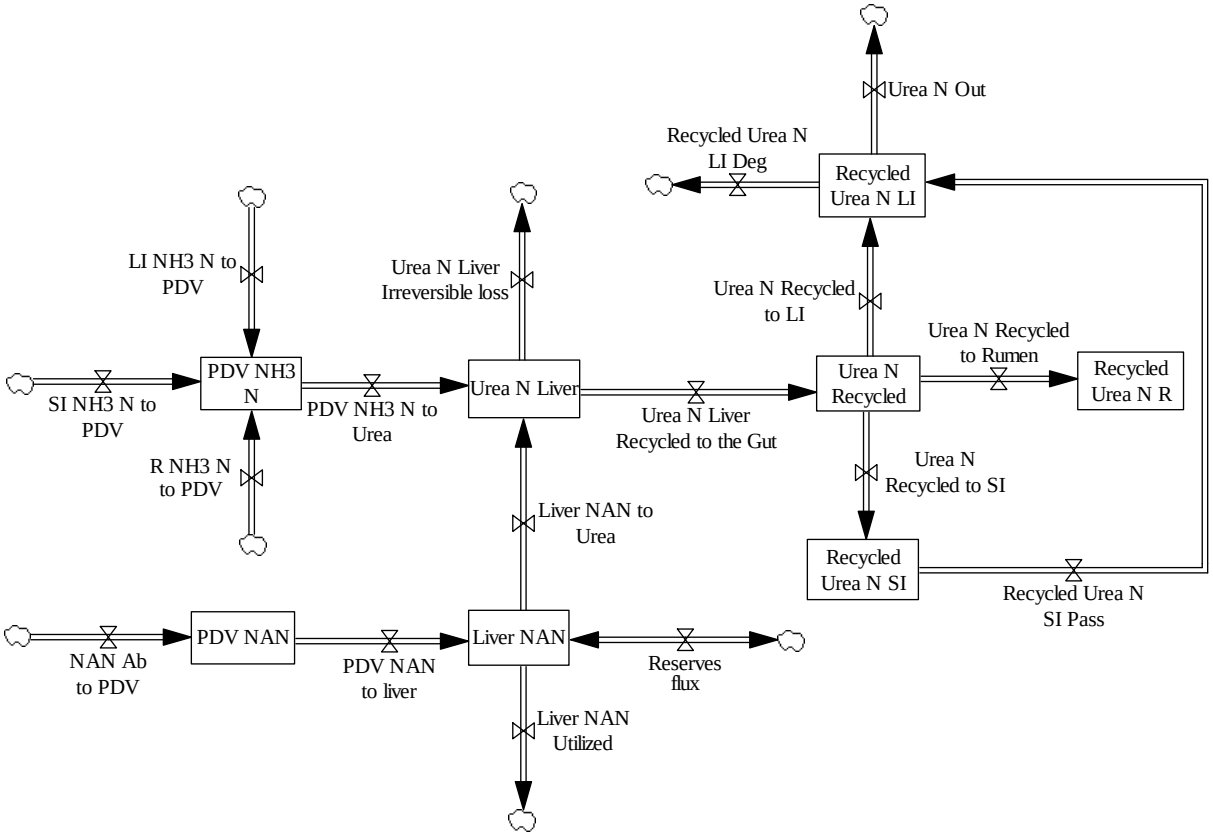

Figure 4. Post absorptive N transactions in the model. Boxes represent pools and arrows represent flows.

Endogenous nitrogen

The contribution of endogenous AA to total AA flows were recognized by O'Connor et al. (1993) when the original CNCPS was being described, but at the time, it was deemed there was not enough quantitative information available to include them in the model. A great deal of work has been conducted since the 90's which has improved the quantitative understanding of endogenous N transactions along the GIT (Marini et al., 2008; Ouellet et al., 2010; Ouellet et al., 2004; Ouellet et al., 2002). Using these data, endogenous N (EN) losses into the GIT were modeled mechanistically in v7 to capture the various transactions along the GIT and between microbial pools.

Endogenous secretions occur at various places along the GIT. Important sources include saliva, gastric juices, bile, pancreatic secretions, sloughed epithelial cells and mucin (Tamminga et al., 1995). Gross EN to the forestomach and intestines were estimated according to Ouellet et al. (2002) and Ouellet et al. (2010) which were subsequently partitioned into individual components (Table 1) using estimates reported in Egan et al. (1984). Endogenous contributions are reasonably consistent among diets when expressed relative to DMI or OMI (Marini et al., 2008; Ouellet et al., 2010; Ouellet et al., 2002; Tamminga et al., 1995). Thus, the model expresses each component as g

EN per kg DMI. A summary of the EN contributions to various points in the GIT are in Table 1.

Table 1. Endogenous contributions used to predict endogenous AA requirements and supply in v7 of the CNCPS.

Endogenous component	Secretion (g N/kg DMI)
Saliva	0.9
Rumen sloughed cells	4.3
Omasum/abomasum sloughed cells	0.3
Omasum/abomasum secretions	0.2
Pancreatic secretions	0.4
Bile	0.1
Small intestine sloughed cells[1]	0.7
Small intestine secretions[1]	0.7
Large intestine sloughed cells	0.3

[1] Includes secretions past the pancreatic and bile duct and prior to the terminal ileum

The mechanistic framework of v7 enabled EN to be modeled in all parts of the GIT including the microbial transactions in the rumen and large intestine. Endogenous N transactions through each compartment in the model are summarized in Figure 5 using the 'Hay' treatment in the study of Ouellet et al. (2010) as an example. Endogenous N in the rumen has three potential fates: 1) It is degraded to ammonia; 2) escapes the rumen and can be digested in the SI 3) or is incorporated into microbial protein. In the example used, total EN secretions into the GIT were 135.4 g/d of which 46.4 g/d was recovered as either free EN in the duodenum or incorporated in microbial protein. The balance (89.0 g/d) was considered lost by the animal and part of the maintenance requirements for protein. Of the 89.0 g/d lost, 31.8 g/d appeared in the feces and 57.2 g/d was degraded in the GIT to NH_3. The total estimated requirement (89.0 g/d) when expressed relative to DMI is 5.1 g EN/ kg DMI which, interestingly, is similar to estimates of metabolic fecal N for the same diet (5.0 g MFN/kg DMI) in v6.5. Metabolic fecal N is the major MP requirement for maintenance in v6.5. Therefore, although v7 estimates these losses in an entirely different way and accounts for their reutilization (microbial incorporation), the maintenance requirements for protein are similar to v6.5.

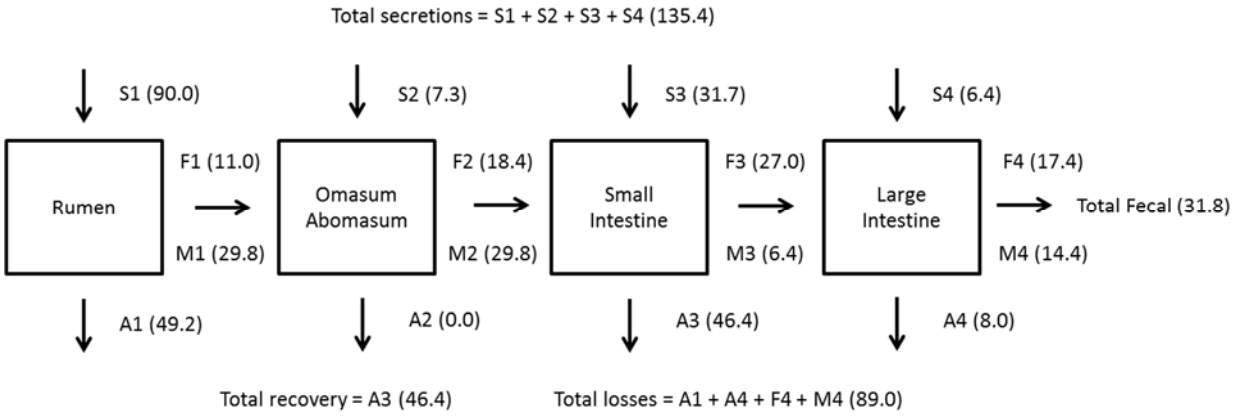

Figure 5. Model predicted endogenous transactions (g endogenous N/d) by compartment for the hay treatment presented in Ouellet et al. (2010). S1-S4 are the endogenous secretions into the gut; F1-F4 are the flows of free endogenous N; M1-M4 are the flow of endogenous N in bacteria; A1-A4 is the endogenous N absorption at different sites. Recovery is only possible in the small intestine (A3) where the N can be absorbed as AA.

AMINO ACID REQUIREMENTS

Requirements for each individual EAA in the CNCPS are predicted for processes that are quantified by the model (maintenance, lactation, pregnancy, growth) and subsequently divided by the efficiency of transfer to that process to give the total AA requirement (O'Connor et al., 1993; Fox et al., 2004). The efficiency of transfer could also be thought of as the additional requirement for each AA relative to the requirements quantified by the model. Such processes include oxidation across the gut or in other tissues, anaplerotic requirements, synthesis of non-essential AA, gluconeogenesis etc. (Lapierre et al., 2005; Lapierre et al., 2006; Lemosquet et al., 2010; Lobley, 2007). The apparent efficiency of AA use for any given diet can be calculated by dividing model predicted amino acid requirement (AAR) by amino acid supply (AAS), which can be variable, and typically decreases as AAS increases relative to AAR and also energy (Hanigan et al., 1998). This decrease in apparent efficiency of AA use represents AA being increasingly used for purposes other than those quantified or described by the model. If the utilization of each AA for every process in metabolism could be adequately quantified, the term ‘efficiency of use’ would become obsolete as it would be 100% (there would be no additional requirement above model predictions). The ability of cows to direct AA to other uses demonstrates the interactions among different nutrients and is an example of the metabolic flexibility that allows productivity to be maintained across a wide range of nutrient inputs and supply (Lobley, 2007). The pertinent question for ration balancing is: what level of additional AA supply is required above the predicted requirements for milk protein synthesis and body protein requirements to maximize productivity and minimize AA wastage? The answer to this question is going to differ among models as supply and requirements are calculated in different ways.

The optimum supply of EAA in v7 was estimated similarly to Doepel et al. (2004) using a dataset of studies that infused AA into the abomasum, duodenum, or

intravenously and fitted a logistic curve (Higgs, 2014). The optimum supply of each EAA was defined as the point in which a logistic curve was approaching plateau most rapidly (Lysine example; Figure 6). This point is similar to the break-point in the segmented linear model used in the NRC (2001). The optimum ratio of model predicted AAR to AAS (efficiency of use) for each AA in v7 are in Table 2. The impact of energy supply on the utilization of AA was also investigated by regressing the ratio of AAR and AAS against AA supply relative to total ME (Lysine example; Figure 7). Interestingly, the optimum supply of Met and Lys estimated using this approach was 15.1% and 5.7% of EAA, respectively, which is similar to results found in other studies that used different approaches (Rulquin et al., 1993; Schwab, 1996; Schwab et al., 1992). However, under these circumstances, no relationship was observed between the 'efficiency' of AA use when AA supply was expressed relative to MP supply but a strong relationship was observed when AA were expressed relative to ME supply which is in agreement the findings of Van Straalen et al. (1994). These data suggest when balancing rations it might be more appropriate to consider AA supply relative to ME which is the approach used in swine (NRC, 2012). Establishing requirements for monogastrics is less complicated than in ruminants as the true AA supply is more easily determined (Lapierre et al., 2006). And to extend the comparison, the predicted Lys requirement for a lactating sow in the NRC (2012) model is 2.72 g Lys/Mcal ME which is similar to the 3.03 g Lys/Mcal ME calculated in this study for dairy cows. Likewise, the recommended ratios for each EAA and Lys are similar in the dairy cow and sow with the exception of Met and His (Table 2). These data suggest, as improvements are made to the predictions of true AA supply in dairy cows, consideration of the approach used to balance AA in other species where AA supply is more easily determined could provide opportunities to improve productivity and the efficiency of nutrient use. The data in Table 2 do not represent recommendations for v6.5 of the CNCPS. Those recommendations are provided by Van Amburgh et al. (2015).

Table 2. Efficiency of use and optimum supply of each EAA relative to total EAA, ME and Lys.

AA	Efficiency of use	% EAA	g AA/ Mcal ME	Lys:AA Dairy[1]	Lys:AA Swine[2]
Arg	0.55	10.2%	2.04	1.49	1.85
His	0.70	4.5%	0.91	3.33	2.50
Ile	0.61	10.8%	2.16	1.40	1.78
Leu	0.67	17.1%	3.42	0.89	0.89
Lys	0.62	15.1%	3.03	1.00	1.00
Met	0.53	5.7%	1.14	2.66	3.71
Phe	0.53	10.7%	2.15	1.40	1.82
Thr	0.53	10.7%	2.14	1.41	1.49
Trp	0.58	2.9%	0.59	5.16	5.33
Val	0.62	12.4%	2.48	1.22	1.15

[1] Optimum Lys:EAA ratio for the data set used

[2] Optimum Lys:EAA ratio for a lactating sow (NRC, 2012)

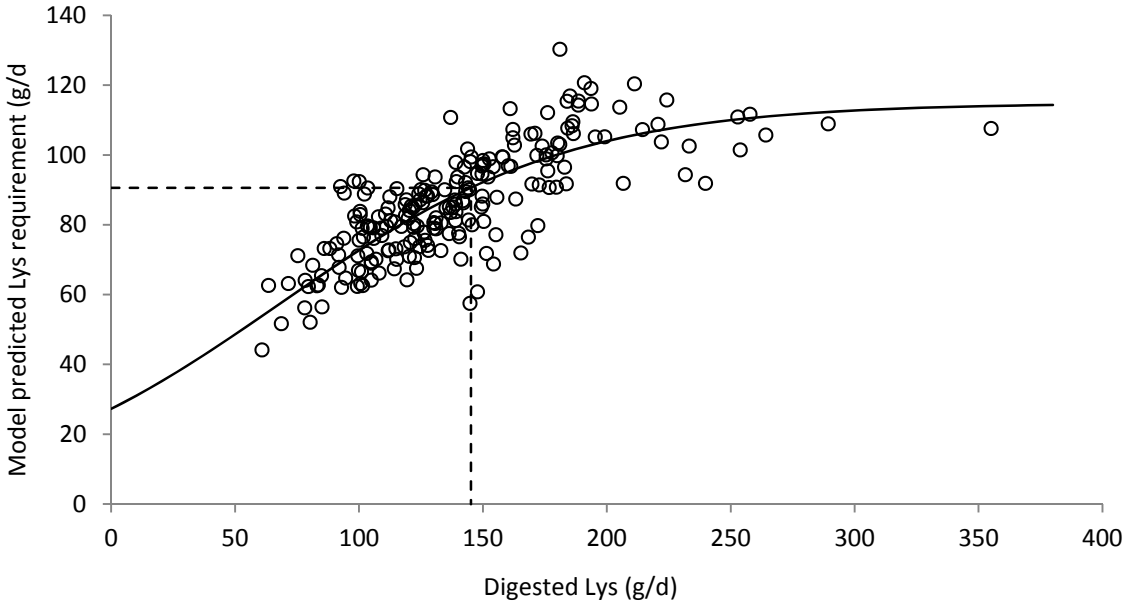

Figure 6. Logistic fit of model predicted Lys requirement and Lys supply. The dashed line represents the optimum ratio of Lys requirement and Lys supply

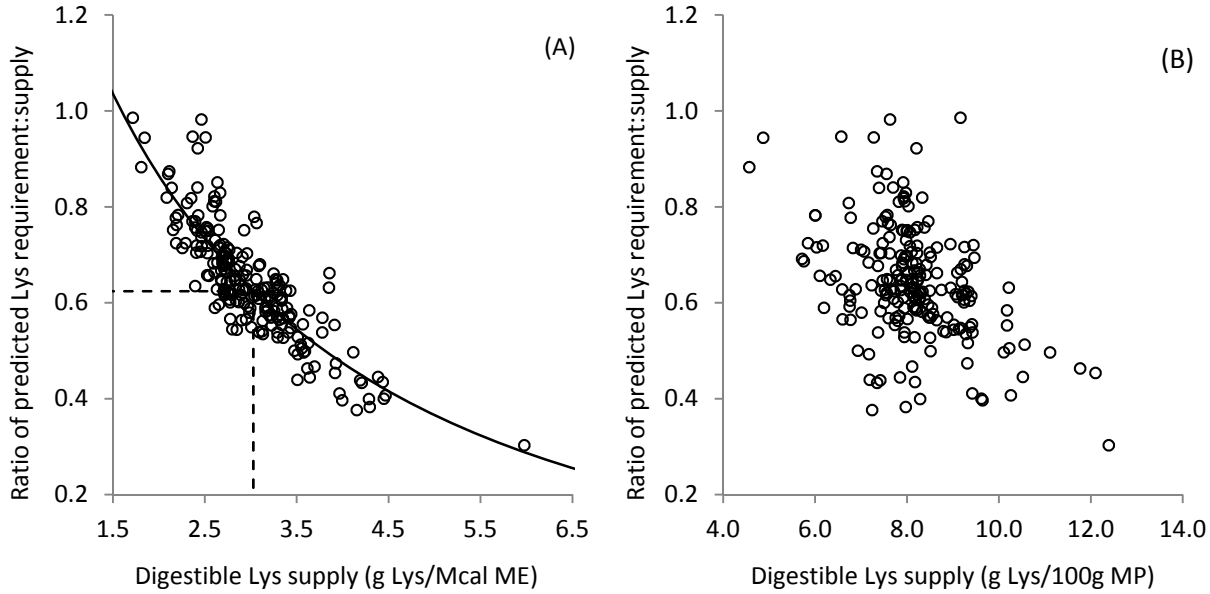

Figure 7. Relationship between model predicted Lys requirement:supply and Lys supply relative to ME (A) or MP (B). The dashed line in (A) represents the Lys supply at the optimum ratio of model predicted Lys requirement and supply. No significant relationship was determined in (B).

MODEL PERFORMANCE

The sections of v7 described here, and in Higgs (2014), represent an implementation of advancements that have been made in the understanding of N availability to the animal, including improvements in the characterization of feed chemistry (Higgs et al., 2015), multiple pool NDF digestion (Raffrenato, 2011), quantification of endogenous N flows (Ouellet et al., 2010; Ouellet et al., 2002), estimates of N availability in the small intestine (Ross, 2013) and changes to estimates of microbial growth to include protozoa. The broad goal of these updates has been to improve the ability of the CNCPS to predict N flows out of the rumen, to the small intestine, and the availability of AA to the animal. Validating the changes to the model against animal data is an important step in establishing the efficacy of the model updates. The data used to evaluate the N flows from the rumen were sourced from studies that measured microbial N (MN), rumen undegraded feed N (which would include endogenous N; RUN) and total non-ammonia N (NAN) flows at the omasum (16 publications; 61 treatment means). This dataset has previously been used by Van Amburgh et al. (2015) to evaluate v6.5.

Incorporation of protozoa into the dynamic structure of v7 represents a considerable change in the system used to estimate microbial growth in the CNCPS. Compared to omasal sampling data, predictions of microbial N flows were more accurate and had less bias than v6.5, particularly when intake was high (Figure 8; Van Amburgh et al., 2015).

Prediction of RUN was more variable than MN and tended to be over-predicted when RUN flows were high (Figure 9). What is generally reported in the literature as feed N will typically also include endogenous secretions as feed N is calculated as the difference between total NAN and MN (Broderick et al., 2010). Any error in the prediction of MN or NAN will be pooled in the estimates of RUN and, therefore, more variability might be expected. Also, the predictions of RUN rely on library values to estimate the rate of N digestion of the various N fractions which can vary within and among feeds (Broderick, 1987; NRC, 2001). Estimating digestion rates of feed N *in vitro* is challenging due to contamination with microbial protein (Broderick, 1987). However, relying on library values is no doubt one of the major limitations to improving predictions of AA supply in ration formulation models. Although some bias was observed in this version of the CNCPS, the slope and intercept were closer to unity than observed for the NRC (2001) by Broderick et al. (2010) and v6.5 by Van Amburgh et al. (2015).

Total NAN was predicted accurately, precisely and with little bias (Figure 10). The relationship was similar to v6.5 (Van Amburgh et al., 2015), however, earlier versions of the CNCPS do not include direct predictions of endogenous N or protozoa. Therefore, the apparent accuracy of v6.5 suggests an over-prediction of undegraded dietary protein flow out of the rumen. Given that endogenous N, feed N, bacterial N and protozoal N have different AA concentrations, profiles and intestinal digestibility, an important first step in improving predictions of AA supply is to accurately estimate the source of N. Version 7 accounts for each N component individually and appears to predict total N flows more accurately than previous version of the model. The subsequent prediction of individual

AA flows is beyond the scope of this paper, but has also been improved. The evaluation can be found in Higgs (2014).

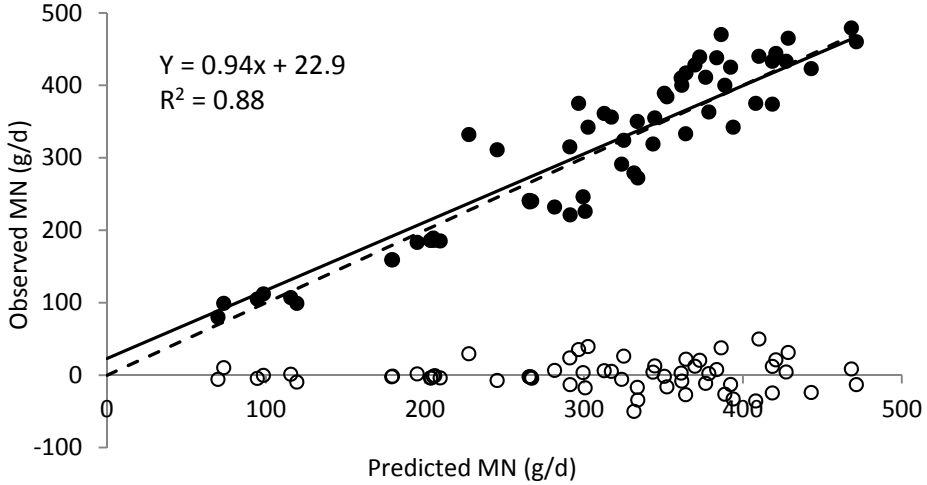

Figure 8. Predicted and observed microbial N (MN) flows at the omasum (●) and residual error (○) from the mixed model regression analysis. The solid line (—) represents the linear regression and the dashed line (- - -) is the unity line.

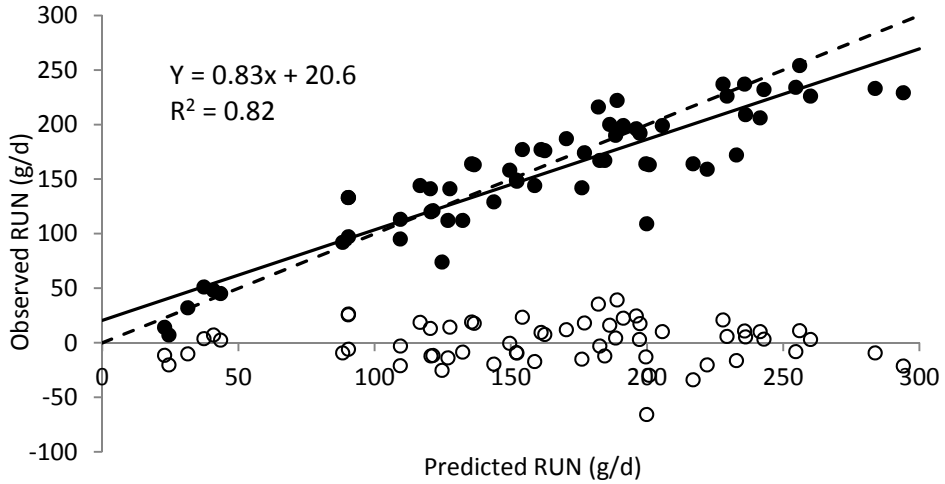

Figure 9. Predicted and observed rumen un-degraded and endogenous N flows (RUN) at the omasum (●) and residual error (○) from the mixed model regression analysis. The solid line (—) represents the linear regression and the dashed line (- - -) is the unity line.

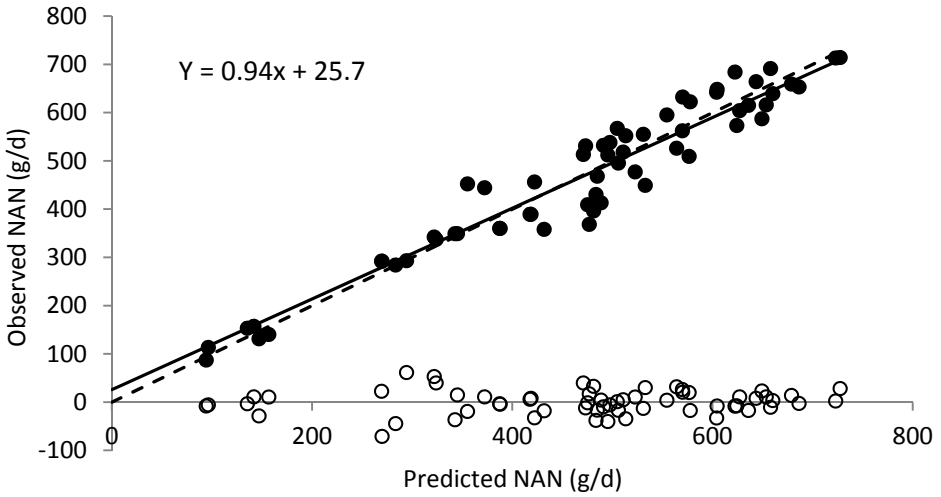

Figure 10. Predicted and observed non-ammonia N (NAN) flows at the omasum (●) and residual error (○) from the mixed model regression analysis. The solid line (—) represents the linear regression and the dashed line (- - -) is the unity line.

SUMMARY

The development of v7 has seen a shift from the original structure of the model that calculates statically, to a dynamic structure that calculates over time. A summary of the major updates to the CNCPS since version 6.0 (Tylutki et al., 2008) that have resulted in v6.1, v6.5 and v7.0 is found in Table 3. Updates that have resulted in v7.0 are described in detail by Higgs (2014).

FUTURE DIRECTION

The development of v7 of the CNCPS represents a progression from a static factorial model to a more dynamic mechanistic system. This has been possible through advancements in computing power, software availability, new laboratory techniques and a better understanding of the biological systems. For example, it is noteworthy to recognize the reason non-essential AA were not included in the original version of the CNCPS was not because the data weren't available, rather because there were not enough columns available in spreadsheets at the time (Sniffen, pers. comm.). However, the singularity effect being observed with the advancement of computing power and technology suggests that these factors are unlikely to constrain future progress, rather, biological understanding and our ability to keep pace will be first limiting.

Practical areas to target for advancement that have high value involve improving model inputs. Examples of recent advancements include the work of Ross (2013) and Raffrenato (2011). Areas of particular future importance include:

- Assays to predict rates of protein degradation.
- Simple ways to quantitatively estimate tissue accretion or mobilization.

- Further refinement of lab assays to reduce variation, particularly *in vitro* assays.

Target areas for new capability within the model include:

- Predicting the size and pattern of meals.
- Further developing the rumen model to estimate VFA production and pH.
- Rebuilding and updating the fatty acid sub-model of Moate et al. (2004) in the v7 framework which would allow for the prediction of milk components as well as yield.
- Behavioral models that better capture activity and general aspects of the farm system that effect maintenance and possibly revisiting metabolic body size related to energy partitioning.

Other, more advanced areas to target could involve optimization and automation techniques that allow rations to be formulated that satisfy a multitude of economic, farm system, compliance, and animal based constraints simultaneously and instantly. Linking this model to other models that describe other farm resource allocations such as manure to fields to minimize fertilizer use while optimizing forage yields and then allocating forages based on digestibility and nutrient profile to the appropriate groups would provide new insights into nutrient utilization related to both economics and environmental sustainability. The computational power and optimization methods already exist to achieve this.

With new model developments, the fundamental principles of the CNCPS need to stay intact and field usability needs to remain the priority. Complexity might be required in the background to improve capability or to acquire the needed inputs, but this should be carefully scrutinized, and a clean simple user experience prioritized at all times.

Table 3. Major developments in the CNCPS after the description of version 6.0 by Tylutki et al. (2008) resulting in v6.1 (Van Amburgh et al., 2007), v6.5 (Van Amburgh et al., 2015) and v7.0 (Higgs, 2014).

v6.1 (Van Amburgh et al., 2007)	v6.5 (Van Amburgh et al., 2015)	v7.0 (Higgs, 2014)
• Re-organization of passage rate assignments so soluble protein fractions flow with the liquid passage rate (Van Amburgh et al., 2007) • Reduction the digestion rates of A and B1 protein fractions to be more consistent with literature reports (Van Amburgh et al., 2007) • Reduction in the digestion rates of sugars to better reflect gas	• Updated feed chemistry in the feed library. • Updated pool structure for the protein fractions in the model where the A pool, previously defined as non-protein N, was changed to ammonia and is now defined as the A1 pool. • Updated AA profiles of feeds in the feed library. • Combined efficiency of AA use for milk production and	• New dynamic structure for the entire gastro-intestinal model. • Expansion of the post-rumen model to include a separate large and small intestine. • Development of a mechanistic large intestine. • Inclusion of protozoa in the microbial sub-model. • New system to mechanistically estimate N recycling.

	production data (Van Amburgh et al., 2007)	maintenance (Lapierre et al., 2007) • Capability to use $uNDF_{240}$ rather than lignin × 2.4 to characterize unavailable fiber (Raffrenato, 2011)	• Capability to model different meal patterns. • Capability to estimate N digestibility using an in vitro estimate of indigestible N (Ross, 2013) • Inclusion of endogenous N transactions along the gastro-intestine tract. • Revised efficiencies of AA use. • Expansion of potentially digestible NDF from 1 to 2 pools (Raffrenato, 2011) and the implementation of new passage rates for NDF from (NorFor, 2011)

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