

# **MAKING AN OLD MODEL NEW AGAIN: UPDATES TO THE CNCPS AND A PERSPECTIVE ON THE FUTURE**

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## **SUMMARY**

Nutritional models can be evolutionary. The CNCPSv6.5 is the latest evolution in the CNCPS path and the final update for this version. Among the analytical improvements, error corrections, and new research implemented within the CNCPS framework, model accuracy has been improved. These changes allow the nutrition professional to reduce dietary crude protein levels while maintaining or improving production and profitability. More importantly, the feed descriptions for AA in the feed library are now current and in a form that allows any user to make updates and additions with contemporary AA analyses methods. This step provides the next opportunity to continue to develop the model to better predict the supply and requirements of AA for lactating and growing cattle. Further, the application of a combined efficiency of use of MP AA appears to provide a more consistent approach between AA supply and requirements that should improve the ability of the model to predict limiting AA and provide more sensitivity in determining a dietary approach to overcome the limitation. Finally, the model is being reprogrammed to incorporate more dynamic approaches to modeling and data analyses and this approach appears to provide more functional comparisons for things like forage and fiber feeding, digestibility and disappearance as a starting point.

## **INTRODUCTION**

The first complete version of The Cornell Net Carbohydrate and Protein System (CNCPS) was released in 1991, and was first published in 1992 and 1993 in a series of four papers (Fox et al., 1992, O'Connor et al., 1993, Russell et al., 1992, Sniffen et al., 1992). The principal objective of CNCPS was to serve as a tool for both research development and feed formulation for cattle (Russell et al., 1992). In order to fulfill these goals, the CNCPS has been continuously under development by incorporating research outcomes into mathematical equations. As a consequence, several updated versions have been released over the last 20 years (Fox et al., 2000, Fox et al., 2004, Tylutki et al., 2008). Moreover, several implementations of the program have been used by the industry to evaluate and formulate diets. Other updates to the model have included the refining of the feed library (Higgs et al., 2012a) and an improvement in the equations to predict nitrogen excretion (Higgs et al., 2012b). The latest version, CNCPSv6.1 (Tylutki et al., 2008, Van Amburgh et al., 2010), is used as a formulation and evaluation platform by AMTS.Cattle (Agricultural Modeling and Training Systems LLC; Cortland, NY), NDS (Ruminant Management & Nutrition; Reggio Emilia, Italy), DinaMilk (Fabermatica; Ostriano, Italy), and Dalex (Dalex Livestock Solutions, Los Angeles, CA). The model is currently being updated to v6.5, the final version of this edition.

More recently, development of the CNCPS has been focused on improving the prediction of AA requirements and supply for lactating dairy cattle. This has led to a number of changes within the model including updated AA profiles in the feed library, re-characterization of protein

fractionation and pool assignments and the adoption of a combined efficiency of utilization for EAA used for maintenance and lactation.

The objective of this paper is to provide a description of changes made to CNCPS in the last few years and also to provide some discussion about the future of the model and how the current development group has incorporated more mechanistic and improved understanding of cattle biology, primarily in rumen and gut function and how it alters our approach to formulating diets. The new version has been evaluated on lactating cattle and the outcome is still being developed.

## Model updates

### *Protein Fractionation and Digestion Rates*

The information provided by the CNCPS feed library, including estimations of digestion kinetics of protein fractions within each feed, are as important as any other component of the model structure. The CNCPS feed library includes more than 800 different feeds and were recently reviewed and updated using large datasets from commercial laboratories by Higgs et al. (2012a). Updates to the feed library included a re-characterization of the non-protein nitrogen (NPN) fraction (PA) to ammonia (PA1) and the soluble true protein fraction (PB1) to soluble non-ammonia CP (PA2). A summary of the changing nomenclature in the equations used to calculate ruminal degradation, outflow and intestinal digestion are in Table 1.

**Table 1.** Equations to compute pools, rumen degradation and intestinal digestion for feed protein fractions.

| Variables <sup>1</sup> | Description                 | Equations <sup>2,3</sup>   |
|------------------------|-----------------------------|--|
| PA1 <sub>j</sub>       | Ammonia                     | ammonia <sub>j</sub> × (SolCP <sub>j</sub> /100) × (CP <sub>j</sub> /100)                            |
| PA2 <sub>j</sub>       | Soluble non-ammonia CP      | SolCP <sub>j</sub> × CP <sub>j</sub> /100 – PA1  |
| PC <sub>j</sub>        | Unavailable CP              | ADIP <sub>j</sub> × CP <sub>j</sub> /100   |
| PB2 <sub>j</sub>       | Slowly degradable CP        | (NDIP <sub>j</sub> – ADIP <sub>j</sub> ) × CP <sub>j</sub> /100                                      |
| PB1 <sub>j</sub>       | Moderately degradable CP    | CP <sub>j</sub> – PA1 <sub>j</sub> – PA2 <sub>j</sub> – PB2 <sub>j</sub> – PC <sub>j</sub>           |
| RDPA1 <sub>j</sub>     | Ruminally degraded PA1      | DMI <sub>j</sub> × PA1 <sub>j</sub>  |
| RDPA2 <sub>j</sub>     | Ruminally degraded PA2      | DMI <sub>j</sub> × PA2 <sub>j</sub> × (kdPA2 <sub>j</sub> / (kdPA2 <sub>j</sub> + kp <sub>j</sub> )) |
| RDPB1 <sub>j</sub>     | Ruminally degraded PB1      | DMI <sub>j</sub> × PB1 <sub>j</sub> × (kdPB1 <sub>j</sub> / (kdPB1 <sub>j</sub> + kp <sub>j</sub> )) |
| RDPB2 <sub>j</sub>     | Ruminally degraded PB2      | DMI <sub>j</sub> × PB2 <sub>j</sub> × (kdPB2 <sub>j</sub> / (kdPB2 <sub>j</sub> + kp <sub>j</sub> )) |
| RDPEP <sub>j</sub>     | Ruminally degraded peptides | RDPA2 <sub>j</sub> + RDPB1 <sub>j</sub> + RDPB2 <sub>j</sub>   |
| REPA2 <sub>j</sub>     | Ruminally escaped PA2       | DMI <sub>j</sub> × PA2 <sub>j</sub> × (kp <sub>j</sub> / (kdPA2 <sub>j</sub> + kp <sub>j</sub> ))    |
| REPB1 <sub>j</sub>     | Ruminally escaped PB1       | DMI <sub>j</sub> × PB1 <sub>j</sub> × (kp <sub>j</sub> / (kdPB1 <sub>j</sub> + kp <sub>j</sub> ))    |
| REPB2 <sub>j</sub>     | Ruminally escaped PB2       | DMI <sub>j</sub> × PB2 <sub>j</sub> × (kp <sub>j</sub> / (kdPB2 <sub>j</sub> + kp <sub>j</sub> ))    |
| REPC <sub>j</sub>      | Ruminally escaped PC        | DMI <sub>j</sub> × PC <sub>j</sub>   |
| DIGPA2 <sub>j</sub>    | Digestible PA2              | IntDigPA2 <sub>j</sub> × REPA2 <sub>j</sub>  |
| DIGPB1 <sub>j</sub>    | Digestible PB1              | IntDigPB1 <sub>j</sub> × REPB1 <sub>j</sub>  |
| DIGPB2 <sub>j</sub>    | Digestible PB2              | IntDigPB2 <sub>j</sub> × REPB2 <sub>j</sub>  |
| DIGFP <sub>j</sub>     | Digestible feed protein     | DIGPA2 <sub>j</sub> + DIGPB1 <sub>j</sub> + DIGPB2 <sub>j</sub>                                      |

<sup>1</sup> Subscript *j* means for the *j* th feed.

<sup>2</sup> SolCP: ; CP: Crude protein; NDIP: ; ADIP: ; NDF: Neutral detergent fiber; ADF: Acid detergent fiber; DMI: Dry matter intake; IntDig: intestinal digestibility constants

<sup>3</sup> Kp is either liquid (kpl) forage (kpf) concentrate (kpc).

Degradation rates of protein fractions were previously updated as described by Van Amburgh et al. (2007) which, along with re-assigning the soluble protein pools to flow with the liquid passage rate, represented a considerable improvement in the sensitivity of MP predictions. In this update, the PB2 pool (fiber bound protein) was linked to the CHOB3 pool (digestible NDF) and the PA1 pool was lowered to 200%/hr from 10,000%/hr. The more recent re-characterization of the PA1 pool from NPN to ammonia described by Higgs et al. (2012a) shifted a considerable amount of protein from the PA1 to the PA2 pool. In the CNCPS, the PA1 pool does not contribute MP to the animal, whereas the PA2 pool can contribute up to 15% of total amino acid flow to the small intestine (Reynal et al. 2007; Volden et al. 2002). Hence, this new configuration considerably increased the predicted MP supply. Van Amburgh et al. (2010) reported that MP predictions, prior to the most recent update were in good agreement with observed milk. Therefore, the rates associated with PA2 and PB1 pools were re-calculated to ensure MP predictions were consistent with the previous predictions. The re-calculated rates are 10-40%/hr and 3-20%/hr for the PA2 and PB1 pool, respectively, and are consistent with literature reports (Lanzas et al., 2007b).

### *Amino Acid Profiles*

Comparison of feed AA profiles in the original CNCPS feed library with profiles of other databases used in the industry showed that there were inconsistencies among the data. Much of this can probably be attributed to the analytical methods used to generate data for the original AA CNCPS feed library (O'Connor et al., 1993). Methods used on some feeds were not adequate to correctly quantify sulfur AA and often represented only one sample. Thus, methionine concentrations of some feeds are lower than reality and the sample size used to populate the library may not best represent what is most commonly used in the industry. However, other feeds added after the original library developments, including many proprietary feeds, were analyzed using correct methodology which has led to inconsistencies throughout the library.

To improve the consistency and accuracy of AA profiles in the CNCPS feed library, profiles were updated using datasets provided by Evonik Industries AG (Hanau, Germany), Adisseo (Commentary, France) and taken from the NRC (2001). Data provided were mean values from analyses completed in the respective companies' laboratories or published in the NRC (2001). In all cases, AA analyses were completed on the whole feed and are expressed in the CNCPS on a % CP basis (equivalent to NRC 2001). This differs from previous versions of the CNCPS where AA were expressed as a % of the buffer insoluble residue (O'Connor et al., 1993). Analyzing AA on the buffer insoluble residue is analytically challenging and much larger databases exist for analyses of whole feed samples. Amino acids in the soluble fraction also contribute up to 15% of the AA flowing out of the rumen un-degraded (Reynal et al., 2005) which are not present in the buffer insoluble residue. For these reasons the AA profiles were changed to being expressed on a whole feed basis.

To update the feed library, the most appropriate profile was assigned based on data availability and was used as received by the source without alteration. If profiles for specific feeds were not available in the datasets provided, current CNCPS values were retained. Proprietary feeds were not changed and were assumed to be analyzed using appropriate methods that provided adequate AA recoveries. Table 2 has examples of AA profiles from the old and new feed library.

## Amino Acid Utilization

Another area of consideration has been the efficiency of AA utilization used by the CNCPS. Currently, AA requirements for maintenance and lactation are derived using two separate efficiencies of use as described by Fox et al., (2004).

**Table 2:** Comparison of old and new amino acid profiles from selected feeds in the CNCPS feed library. Values from the old library are expressed as % buffer insoluble residue. Values from the new library are expressed as % CP from the whole feed.

|   |            | Met        | Lys        | Arg        | Thr        | Leu         | Ile        | Val        | His        | Phe        | Trp        |
|---|------------|------------|------------|------------|------------|-------------|------------|------------|------------|------------|------------|
| Alfalfa hay 17 CP 46 NDF 20 LNDf            | Old        | 0.7        | 6.0        | 6.4        | 5.0        | 9.3         | 6.0        | 7.1        | 2.6        | 6.3        | 1.8        |
|   | <b>New</b> | <b>1.3</b> | <b>4.8</b> | <b>4.2</b> | <b>4.0</b> | <b>6.7</b>  | <b>3.9</b> | <b>5.0</b> | <b>1.9</b> | <b>4.6</b> | <b>1.4</b> |
| Mixed hay 13 CP 56 NDF 14 LNDf              | Old        | 0.7        | 4.4        | 4.6        | 3.9        | 7.4         | 4.4        | 5.5        | 1.8        | 4.9        | 1.6        |
|   | <b>New</b> | <b>1.4</b> | <b>4.3</b> | <b>4.5</b> | <b>4.0</b> | <b>6.8</b>  | <b>3.8</b> | <b>4.9</b> | <b>1.8</b> | <b>4.3</b> | <b>1.4</b> |
| Corn silage unprocessed 35 DM 45 NDF coarse | Old        | 0.8        | 2.1        | 1.9        | 2.1        | 6.4         | 2.4        | 3.2        | 1.1        | 2.9        | 0.1        |
|   | <b>New</b> | <b>1.6</b> | <b>2.8</b> | <b>2.3</b> | <b>3.4</b> | <b>8.5</b>  | <b>3.4</b> | <b>4.5</b> | <b>1.7</b> | <b>3.9</b> | <b>0.7</b> |
| Blood meal                                  | Old        | 1.1        | 9.3        | 5.0        | 4.7        | 13.4        | 0.9        | 9.1        | 6.5        | 7.9        | 1.9        |
|   | <b>New</b> | <b>1.2</b> | <b>8.7</b> | <b>4.3</b> | <b>4.6</b> | <b>12.3</b> | <b>1.1</b> | <b>8.2</b> | <b>5.9</b> | <b>6.8</b> | <b>1.4</b> |
| Soybean meal 47.5% CP solvent               | Old        | 1.3        | 6.5        | 7.7        | 4.8        | 8.7         | 4.0        | 4.4        | 2.7        | 5.2        | 1.4        |
|   | <b>New</b> | <b>1.3</b> | <b>6.1</b> | <b>7.3</b> | <b>3.9</b> | <b>7.6</b>  | <b>4.5</b> | <b>4.7</b> | <b>2.6</b> | <b>5.1</b> | <b>1.3</b> |
| Canola meal expelled                        | Old        | 1.4        | 6.7        | 6.8        | 4.9        | 8.0         | 4.9        | 6.4        | 4.0        | 4.7        | 1.2        |
|   | <b>New</b> | <b>2.1</b> | <b>5.7</b> | <b>6.1</b> | <b>4.4</b> | <b>7.0</b>  | <b>4.2</b> | <b>5.3</b> | <b>2.6</b> | <b>4.0</b> | <b>1.5</b> |
| Corn distillers light spirits               | Old        | 1.2        | 2.1        | 4.2        | 3.1        | 9.1         | 2.8        | 5.2        | 1.8        | 4.2        | 1.6        |
|   | <b>New</b> | <b>2.0</b> | <b>2.8</b> | <b>4.3</b> | <b>3.7</b> | <b>11.7</b> | <b>3.7</b> | <b>4.9</b> | <b>2.7</b> | <b>4.9</b> | <b>0.8</b> |
| Corn gluten feed dry                        | Old        | 2.1        | 1.2        | 3.2        | 2.9        | 16.2        | 4.3        | 5.0        | 2.5        | 6.5        | 0.4        |
|   | <b>New</b> | <b>1.6</b> | <b>3.1</b> | <b>4.6</b> | <b>3.6</b> | <b>8.5</b>  | <b>3.0</b> | <b>4.7</b> | <b>2.9</b> | <b>3.5</b> | <b>0.5</b> |

Lapierre et al (2007) discussed the biological correctness of this assumption and suggested when considering the distribution of enzymes for AA catabolism and the dominate role the liver plays in the modifying peripheral AA supply, using a combined efficiency of use makes more sense. Doepel et al. (2004) calculated a single efficiency of use for each essential AA using a meta-analysis of 40 published papers involving abomasal, duodenal or intravenous infusions of casein or free AA (Table 3). In this version of the CNCPS, we adopted the efficiency that represented what was considered to be 100% of MP supply from the work of Doepel et al., (2004) as described by Lapierre et al. (2007) and believe this to be a more representative efficiency that can be evaluated among variable ME allowable milk supply.

**Table 3.** Combined efficiencies of amino acid utilization for both maintenance and lactation (adapted from Doepel et al. (2004) and Lapierre et al. (2007)) based on values derived from the data set at 100% of the metabolizable protein requirement.

| AA         | Arg  | His  | Ile  | Leu  | Lys  | Met  | Phe  | Thy  | Val  |
|------------|------|------|------|------|------|------|------|------|------|
| Efficiency | 0.58 | 0.76 | 0.67 | 0.61 | 0.69 | 0.66 | 0.57 | 0.66 | 0.66 |

## EVALUATION

### *Evaluation dataset development*

Three different data sets were developed from both the literature (references not provided here), and from farm data from regional nutritionists to evaluate lysine (Lys) and methionine (Met) requirements, supply, rumen N balance and milk yield predictions.

The first dataset (AA set), was compiled from studies where Lys, Met, or both were increased either by intestinal infusion or by feeding in ruminally protected form. In total 19 studies were selected and concentrations of digestible Lys (8 studies forming 43 treatments) and Met (11 studies forming 50 treatments) in protein truly digested were calculated for control and treatment groups. A dose-response approach was used to define required Lys and Met concentrations in MP for maximal protein synthesis according to Rulquin et al. (1993). Reference values of 6.80 and a 2.43 percent were identified intermediate to the lowest and highest concentrations values for Lys and Met in MP, respectively. Predicted concentrations of Lys in MP varied between 4.99 and 9.30 % of MP and for Met between 1.69 and 2.85 % of MP. Positive and negative values for production responses were calculated using the reference values for control and treatment groups. Responses of milk protein yield (g/day) and the predicted concentrations of Lys and Met (% of MP) were evaluated by regression procedures.

The second dataset (rumen set) was compiled from studies where post-ruminal N flows were assessed with the omasal sampling technique (Ahvenjärvi et al., 2000, Huhtanen et al., 1997, Reynal and Broderick, 2005). A recent meta-analysis (Broderick et al., 2010, Huhtanen et al., 2010) on omasal sampling suggested that it is a reliable alternative to measuring nutrient flows via duodenal cannula. Moreover, the use of a triple marker system is more robust and reduces variation caused by the multiple and diverse markers used with post-ruminally cannulated animals. Therefore, to avoid inducing variation due to cannula position and the variety of marker use we included only studies with the omasal sampling technique. In total, 19 peer-review studies with 74 treatments were included.

The third data set (lactation set) was compiled from studies published in the Journal of Dairy Science between 2001 and 2012. Lactation trials were included for dairy cows in different stages of lactation (early, mid and late). Studies with cross over design (Latin square, Box-Behnken, etc.) and with few experimental units ( $n < 6$ ) were excluded from the data set. In total, 103 lactation studies were pre-selected, by which 55 with 200 treatments met the criteria for incorporation into the data set. The criteria for each study were: (a) description and chemical analysis of the ration fed for each treatment, (b) inclusion of each feed included into the ration, (c) information of actual dry matter intake (DMI), (d) information on milk yield and milk composition for each treatment. This dataset was enhanced by incorporating farm data from nutritionists in the Northeast U.S. that were willing to share their data. From the regional nutritionists 15 farms with 50 different diets were included.

A spreadsheet version of the CNCPS was used to conduct the model simulations for this study. Information on feed chemistry required by the CNCPS to run a simulation was used as reported by the study. When incomplete information was presented, values were predicted using the procedures described by Higgs et al., (2012a). Animal information required to run a simulation in the CNCPS included a description of housing conditions, body weight (BW) and BW change for period studied, body condition score (BCS) and BCS change during the period studied, stage of lactation, and stage of pregnancy. If stage of pregnancy, BW and BCS were not provided, CNCPS default values were used. When BW change was available, but BCS change was not, the final BCS (in CNCPS as the target BCS) was calculated from BW change assuming that empty BW (EBW) changes on average 13.7% for each unit of BCS change (Fox et al., 1999, NRC, 2001). To calculate EBW from BW the following equations were used:

$$EBW = 0.851 * \text{Shrunk BW (SBW)}, \text{ and } SBW = 0.96 * BW$$

$$\text{Therefore, } EBW = 0.81696 * BW$$

### Statistical Analysis

Statistical analysis was conducted with JMP (SAS). To describe the relationships between increasing concentrations of Lys and Met in MP and protein yield responses, a broken line model with a plateau was used. According to the NRC (2001), this linear model was either equal to or superior to other models for describing protein content and protein yield responses to increasing amounts of both Lys and Met in MP. The model consisted from a linear regression line to a break point followed by a plateau:

$$Y_{ij} = \beta_0 + \beta_1 X_{ij}, \text{ when } X \leq C$$

$$Y_{ij} = \beta_0 + \beta_1 C, \text{ when } X > C$$

Where,  $Y_{ij}$  = the expected outcome for the dependent variable Y observed at repetition  $j$  of the continuous variable X in study  $i$ ,  $\beta_0$  = the overall intercept across all studies,  $\beta_1$  = the overall slope of Y on X across all studies, C = the break point.

For the lactation and rumen datasets, a mixed effects model using the restricted maximum likelihood (REML) procedure was used to analyze the data as proposed by St-Pierre (2001):

$$Y_{ij} = \beta_0 + \beta_1 X_{ij} + s_i + b_{1i} X_{ij} + \varepsilon_{ij},$$

Where,  $Y_{ij}$  = the expected outcome for the dependent variable Y observed at repetition  $j$  of the continuous variable X in study  $i$ ,  $\beta_0$  = the overall intercept across all studies,  $s_i$  = the random effect of study  $i$ ,  $\beta_1$  = the overall slope of Y on X across all studies,  $b_{1i}$  = the random effect of study  $i$  on the slope of Y on X,  $X_{ij}$  = the data associated with repetition  $j$  of the continuous variable X in study  $i$ , and  $\varepsilon_{ij}$  = random variation.

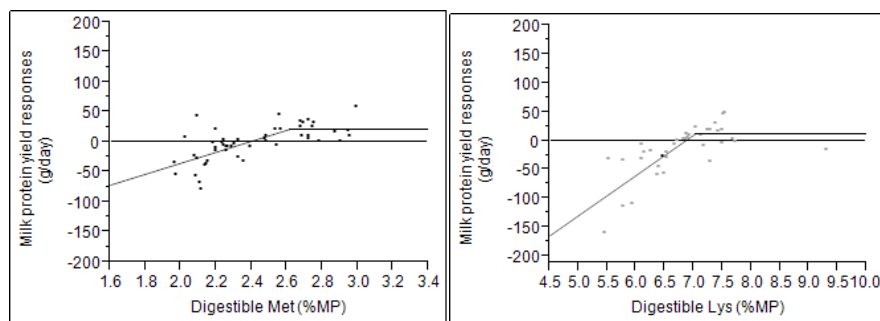
To evaluate the performance of the model several statistics were calculated. The squared sample correlation coefficients reported were based on either the BLUP ( $R^2_{BLUP}$ ) or model predictions using a mean study effect ( $R^2_{MP}$ ). The Bayesian information criterion (BIC) was used as the statistical criterion to indicate the goodness of model fit, where lower values indicate a better fit. The residuals (predicted – observed) were visually examined for any patterns as well as for any potentially confounding factors. Additional model adequacy statistics were calculated to give further insight into the accuracy, precision, and sources of error in each model (Tedeschi, 2006).

Mean square prediction errors (MSPE) were used to indicate accuracy. A decomposition of the MSPE was also performed to give an estimation of the error due to central tendency (mean bias), regression (systematic bias), and random variation. Concordance correlation coefficients (CCC) were used to simultaneously account for accuracy and precision. Concordance correlation coefficients can vary from 0 to 1, with a value of 1 indicating that no deviation from the  $Y = X$  line has occurred.

## RESULTS & DISCUSSION

### *Lys and Met requirements*

The plots of model predicted concentrations of Lys and Met (%MP) and the corresponding responses of milk protein yield are presented in Figure 1. The breakpoint estimates for Lys and Met for maximal milk protein yield were 7.00 and 2.60 % of MP, respectively. Similar breakpoint estimates were reported for NRC (2001) and the previous version of CNCPS. The CNCPSv6.1 estimated Lys breaking point at 6.93 % of MP and that of Met at 2.34 % of MP (Whitehouse et al., 2013). Current estimations require slightly higher Lys, and 11% higher Met supply to optimize protein yield responses which can be attributed to the updated AA profiles in the feed library.



A.

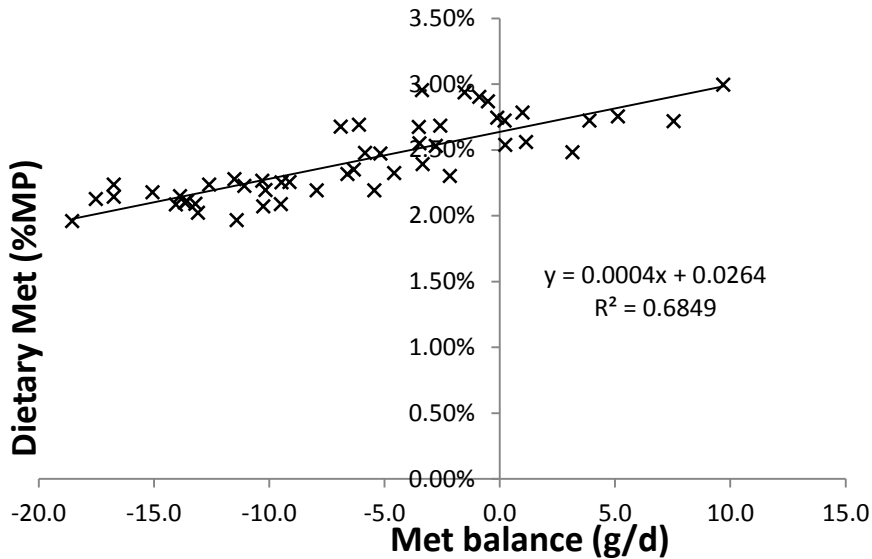
B.

**Figure 1.** Milk protein yield responses as a function of digestible methionine (A) (Met;  $y = -219 + 92.65 \cdot \text{Met}$  and  $y = -219 + 92.65 \cdot 2.60$  for the linear and the plateau part of the model, respectively) and lysine (B) (Lys;  $y = -478 + 70.02 \cdot \text{Lys}$  and  $y = -478 + 70.02 \cdot 7.00$  for the linear and the plateau sections of the model, respectively).

### *Efficiency of AA use*

To evaluate the updated efficiency of AA use included in the CNCPS, the data set used to determine the optimum proportion of Met and Lys in MP was used to perform a regression of model predicted AA balance (g Met/d) against the concentration of Met in the diet (Met % MP). Using the new efficiencies (Table 3), the regression line intercepted the Y axis at approximately 2.6 % dietary Met relative to total MP (Figure 2), similar to the breakpoint derived in Figure 1 A. The studies used to perform this analysis were specifically designed to be both sufficient and limited in Met supply in order to observe a dose response. Hence, one would expect the model to predict both positive and negative Met balance. Using the old efficiencies of AA use, the regression line intercepts the Y axis at 2.0 % dietary Met (% MP) and no diets are predicted to have negative Met balance, contrary to expectations. Using the new efficiencies (Figure 2), there

is a balance of both positive and negative Met balance among the data set. This suggests the new efficiencies of use allow the model to more adequately represent the true gram per day requirements of essential amino acids.



**Figure2.** Model predicted Met balance (MP Met supply less requirement; g Met/d) versus dietary Met (%MP).

### *Rumen degradation*

Updates to the digestion rates, passage rate assignments (Van Amburgh et al., 2010), and pool characterization (Higgs et al 2012a; Lanzas et al., 2007a) have made MP predictions by the CNCPS more sensitive than previous versions of the model (Van Amburgh et al., 2010). The ability of the model to predict the various nitrogen fractions leaving the rumen was evaluated against omasal flow data. Studies in the compiled dataset reported measures of ruminal undegraded N (RUN), non-ammonia nitrogen (NAN) and bacterial N (BactN) flows. The dataset represented a wide range diets and nutrient compositions (Table 4). The omasal flow of BactN and RUN ranged from 78 to 480 and from 7 to 326 g/day, respectively (Figure 3). The model predicted post-ruminal flows of non-ammonia nitrogen NAN ( $R^2 = 0.97$ ; RMSE = 24.57) and RUN ( $R^2 = 0.91$ ; RMSE = 21.93) well, but with the current rates and pools size descriptions, underestimates BactN ( $\beta_1 = 1.55$ ) and overestimates RUN ( $\beta_1 = 0.73$ ). However, there is a uniform offset which provides a prediction of NAN that is robust with little bias (NAN;  $R^2 = 0.98$ ; RMSE = 26.77;  $\beta_1 = 1.17$ ). The variance component analysis indicated that most of the variance is attributed to the study effect and not residuals, even though residual influence was higher for BactN (Table 6).



**Table 4.** Input variables used for the rumen sub-model evaluation dataset.

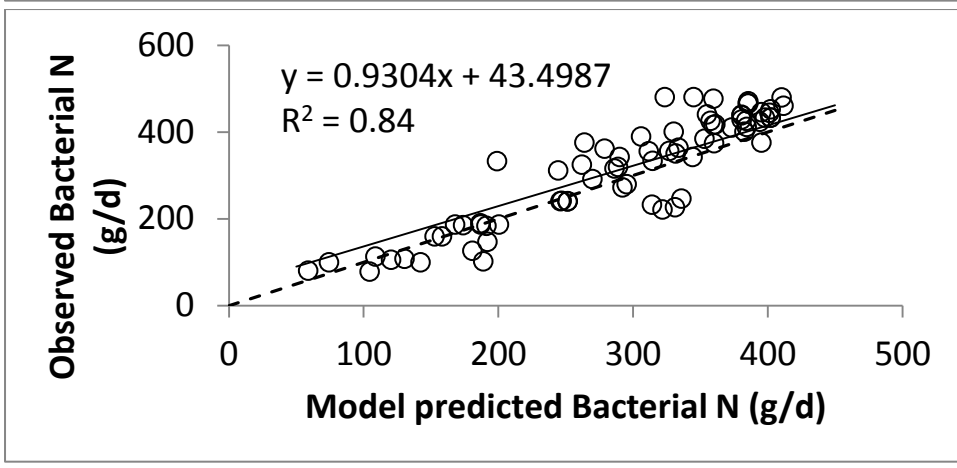
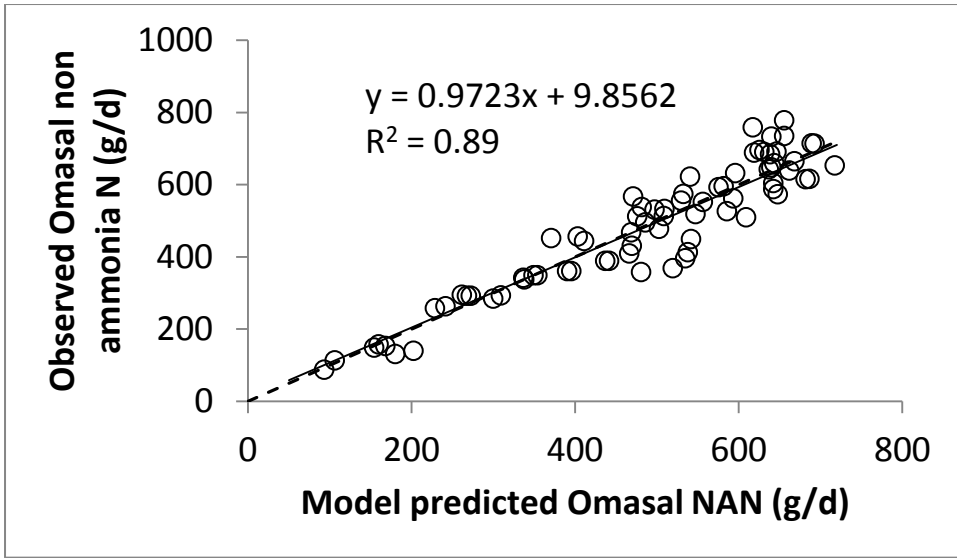
|                                      | Mean | SD    | Min  | Max  |
|--------------------------------------|------|-------|------|------|
| <b><i>Diet Composition (%DM)</i></b> |      |       |      |      |
| CP                                   | 16.1 | 2.55  | 9.9  | 20.7 |
| RUP                                  | 5.9  | 1.33  | 2.9  | 9.2  |
| RDP                                  | 10.2 | 1.81  | 6.2  | 14.5 |
| NDF                                  | 34.6 | 9.02  | 22.7 | 59.5 |
| Starch                               | 23.8 | 11.66 | 44.1 | 1.1  |
| Fat                                  | 4    | 0.84  | 2.6  | 6.2  |
| <b><i>Omasal flows (g/day)</i></b>   |      |       |      |      |
| Non ammonia nitrogen (NAN)           | 481  | 176.8 | 87   | 778  |
| Bacterial nitrogen (BactN)           | 316  | 123.8 | 78   | 480  |
| Rumen undegraded nitrogen (RUN)      | 164  | 65.1  | 7    | 326  |

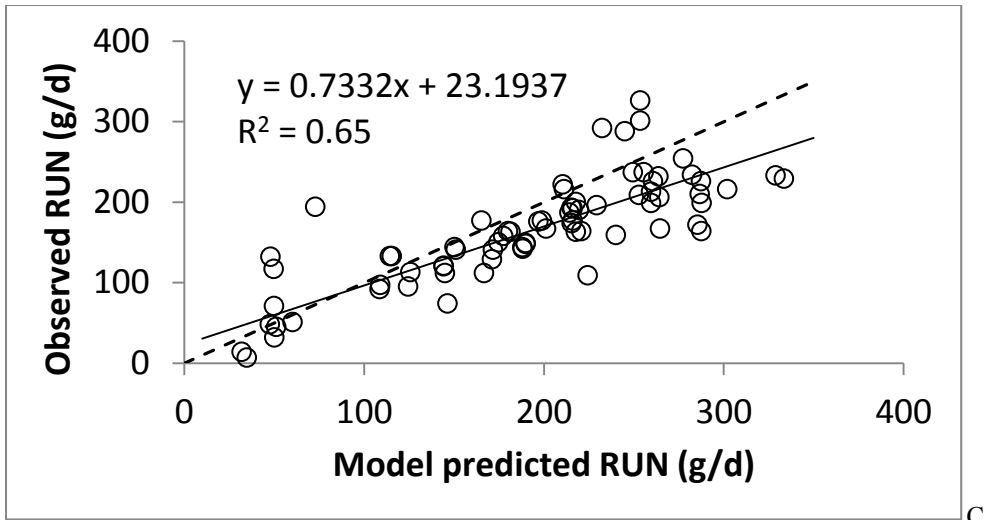
***Milk yield prediction***

Diets with a wide range of nutrients were included in the evaluation data set (Table 5). Previous evaluations of the CNCPS were conducted using specific experimental datasets of a few studies conducted at Cornell University (Fox et al., 2004, Tylutki et al., 2008). The first limiting nutrient (MP or ME) was regressed on the observed milk yield, and results demonstrated the capability of CNCPS to predict the first limiting nutrient. The current evaluation reinforced the ability of the latest version to accurately predict the most limiting nutrient: the first limiting nutrient (MP or ME) was predicted with an  $R^2 = 0.95$  and a RMSE = 1.77. Further, the development of a large dataset provided the opportunity to evaluate the model over a wide range of production and dietary conditions.

Results of the evaluation of ME and MP allowable milk yield are presented in Figure 4 and Table 6. Both MP and ME allowable milk were predicted with reasonably well with an overall  $R^2$  of 0.76 and a RMSE of 1.59 kg. In this evaluation, MP allowable milk was predicted with greater accuracy than ME allowable milk ( $R^2 = 0.82$  and RMSE= 1.12 kg;  $R^2 = 0.76$  and RMSE = 1.96 kg, respectively). An early attempt to evaluate CNCPSv6.0 when MP was the first limiting nutrient resulted in low precision ( $R^2 = 0.29$ ; Van Amburgh et al. (2007). Since then, several updates to the model have been made (Higgs et al., 2012b, Van Amburgh et al., 2010, Van Amburgh et al., 2007) and among them, the updates to the protein fractionation and degradation rates have resulted in improved predictions and sensitivity of the model.

Within the data sets evaluated, it is more difficult to evaluate energy balance because typically information on BCS change and body weight change are not reported. Also, body weight change, depending on stage of lactation, is not a good indicator of energy balance due to changes in rumen fill and dry matter intake, and body water vs body fat changes, and changes in physiological state (e.g. pregnancy related BW changes). Thus, the ability to describe ME allowable milk or ME balance among published data sets is more difficult and that outcome is reflected in the partitioning of error in the MSPE (Table 6) where the majority of the error is random and due to study and not systematic within the model.



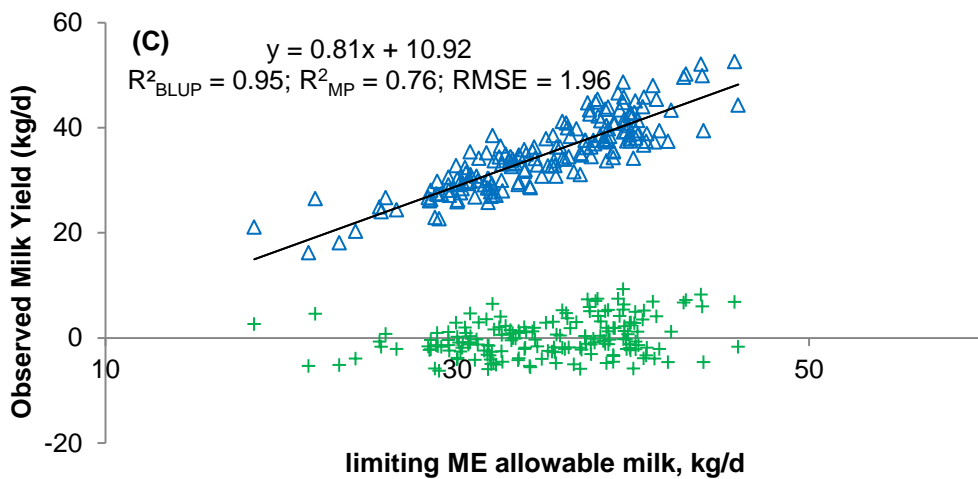
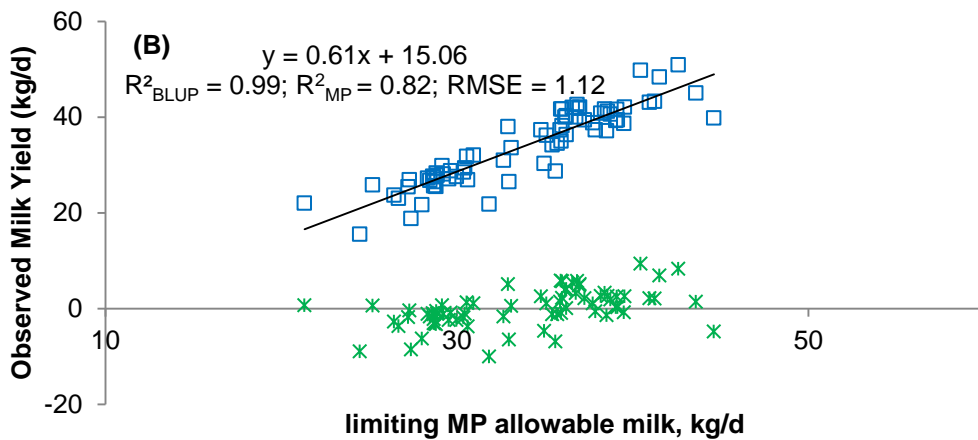


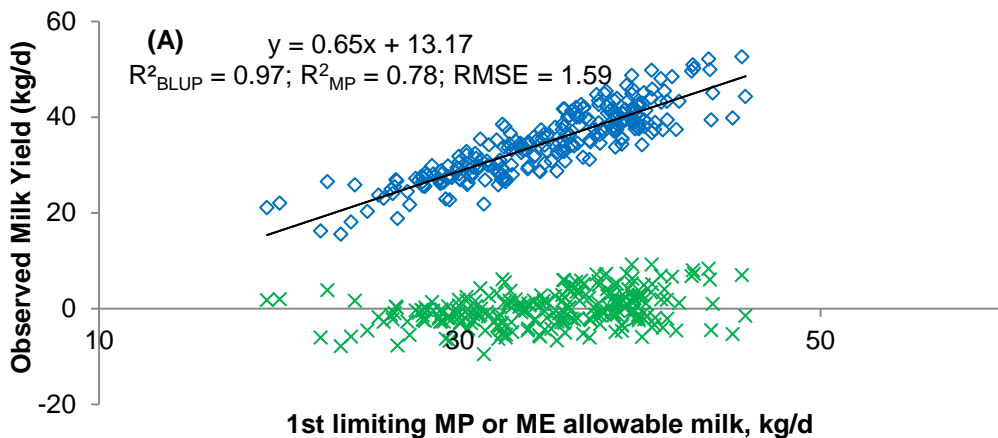
**Figure 3.** Observed versus model predicted values of: (A) non-ammonia nitrogen (NAN), (B) bacterial nitrogen (BactN) and (C) rumen undegradable nitrogen (RUN), assessed with a mixed effects model.

**Table 5.** Cattle and production characteristics for the lactation evaluation dataset.

|                                      | Mean | SD    | Min  | Max   |
|--------------------------------------|------|-------|------|-------|
| <b><i>Diet Composition (%DM)</i></b> |      |       |      |       |
| CP                                   | 16.9 | 2.35  | 9.4  | 29.5  |
| RUP                                  | 7.2  | 1.55  | 3.3  | 16.7  |
| RDP                                  | 9.7  | 1.38  | 6.08 | 14.6  |
| NDF                                  | 33.8 | 5.4   | 25.3 | 52.7  |
| Starch                               | 23.1 | 7.2   | 2.1  | 37.8  |
| Fat                                  | 4.8  | 1.3   | 2.0  | 13.1  |
| <b><i>Animal Inputs</i></b>          |      |       |      |       |
| Initial body weight, kg              | 623  | 44.4  | 525  | 737   |
| Final body weight, kg                | 632  | 46.1  | 532  | 748   |
| Initial BCS, 1-5 scale               | 2.92 | 0.374 | 1.1  | 3.6   |
| Final BCS, 1-5 scale                 | 2.96 | 0.384 | 1.2  | 4.4   |
| DMI, kg                              | 22.3 | 2.73  | 13.5 | 29.1  |
| <b><i>Production inputs</i></b>      |      |       |      |       |
| Milk Yield, kg/d                     | 34.6 | 7.14  | 15.5 | 52.6  |
| ECM <sup>1</sup> , kg/d              | 32.3 | 6.18  | 14.9 | 47.15 |
| Milk protein, %                      | 3.02 | 0.194 | 2.51 | 3.61  |
| Milk fat, %                          | 3.67 | 0.479 | 2.06 | 5.06  |

<sup>1</sup>ECM: energy corrected milk (Kirchengessner, 1997)





**Figure 4.** Observed versus model predicted values of: (A) first limiting MP or ME (◇) and residuals (×), (B) MP limiting (□) and residuals (\*) and (C) ME limiting (Δ) and residuals (+), assessed with a mixed effects model.

**Table 6.** Model adequacy statistics for the prediction of the first limiting nutrient (metabolizable protein or/and metabolizable energy; MP and ME, respectively) and of post ruminal flow of non-ammonia nitrogen (NAN), bacterial nitrogen (BactN) and rumen undegradable nitrogen (RUN).

|                                | n   | RMSE <sup>1</sup> | BIC <sup>2</sup> | Variance Component <sup>3</sup> |       |          | CCC <sup>4</sup> | MSPE <sup>5</sup> | MSPE partitioned <sup>6</sup> (%) |                |                |
|--------------------------------|-----|-------------------|------------------|---------------------------------|-------|----------|------------------|-------------------|-----------------------------------|----------------|----------------|
|                                |     |                   |                  | Study                           | Slope | Residual |                  |                   | U <sup>M</sup>                    | U <sup>S</sup> | U <sup>R</sup> |
| <i>Lactation</i>               |     |                   |                  |                                 |       |          |                  |                   |                                   |                |                |
| MP or ME                       | 250 | 1.56              | 1192             | 77.7                            | 0.5   | 21.8     | 0.83             | 12.8              | 0.05                              | 21.75          | 78.20          |
| ME                             | 177 | 1.77              | 870              | 67.0                            | 0.6   | 32.4     | 0.84             | 11.8              | 0.55                              | 16.33          | 83.12          |
| MP                             | 73  | 1.12              | 360              | 91.5                            | 0.4   | 8.1      | 0.83             | 14.2              | 0.45                              | 26.91          | 72.64          |
| <i>Post-ruminal flow (g/d)</i> |     |                   |                  |                                 |       |          |                  |                   |                                   |                |                |
| NAN                            | 74  | 24.97             | 767              | 84.6                            | NS    | 15.4     | 0.68             | 14011             | 83.35                             | 3.52           | 13.13          |
| BactN                          | 74  | 24.55             | 743              | 86.1                            | NS    | 13.9     | 0.31             | 17762             | 91.08                             | 6.16           | 2.76           |
| RUN                            | 74  | 21.73             | 726              | 66.9                            | NS    | 33.1     | 0.71             | 1141.6            | 24.41                             | 7.68           | 67.91          |

<sup>1</sup> Root mean square error

<sup>2</sup> Bayesian information criterion

<sup>3</sup> Percentage of variance related to the effect of study and random variation

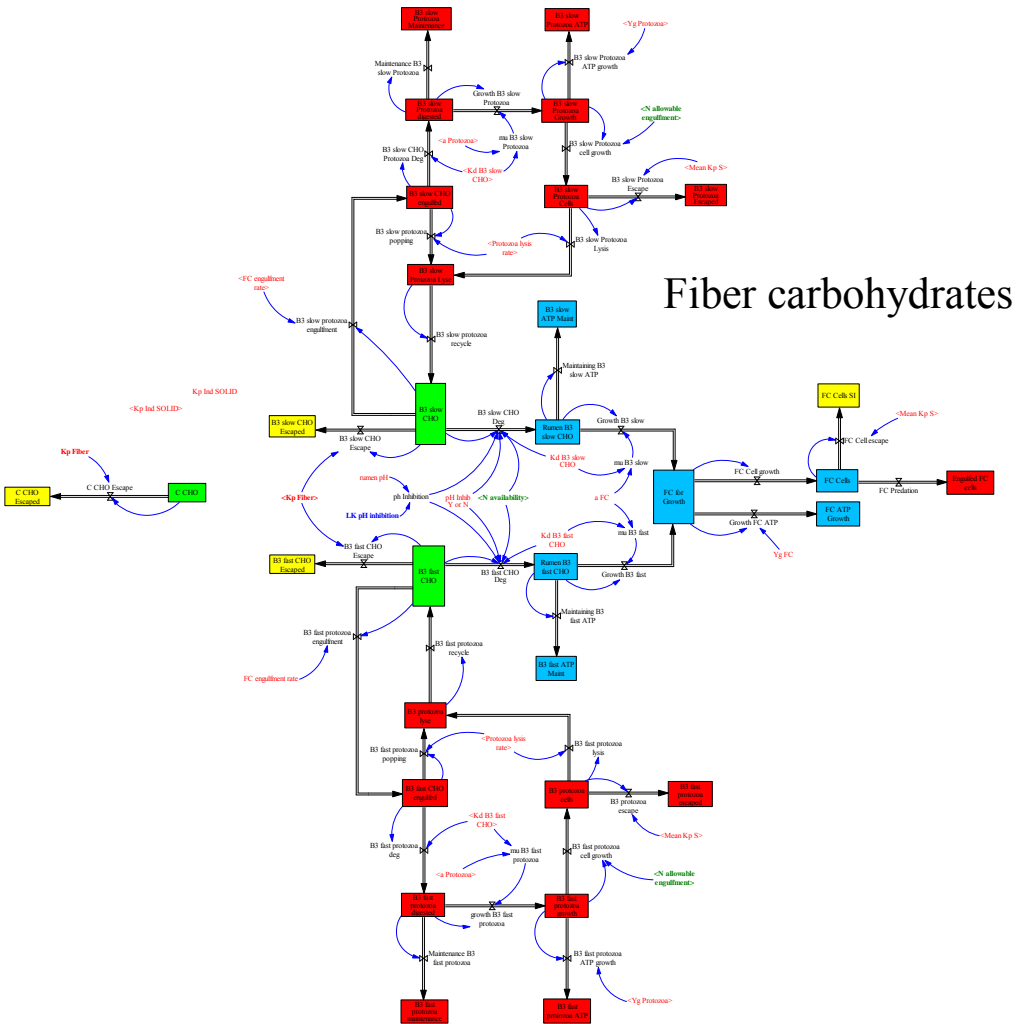
<sup>4</sup> Concordance correlation coefficient.

<sup>5</sup> Mean square prediction error.

<sup>6</sup> U<sup>M</sup> = percentage of error due to mean bias, U<sup>S</sup> = percentage of error due to systematic bias, U<sup>R</sup> = percentage of error due to random variation (U<sup>M</sup> + U<sup>S</sup> + U<sup>R</sup> = 100).

## Moving the CNCPS to a dynamic platform

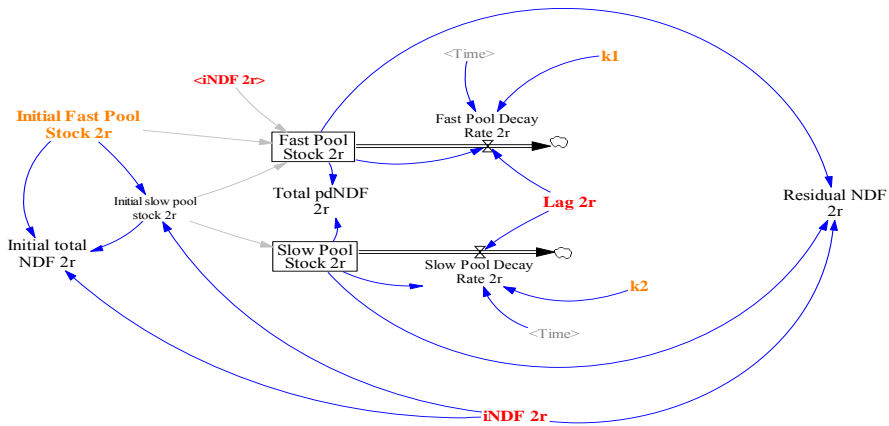
Work is ongoing in the modeling group at Cornell to move the CNCPS to a more dynamic framework in order to more effectively capture the interactions of nutrient digestion, intake and microbial growth. Figure 5 is a schematic representation of the fiber carbohydrate section of the model. The model has three fiber fractions: rapidly degrading, slowly degrading, and indigestible. Fractionating the fiber out in this manner allows for more precise estimations of digestion, and also estimations of pool sizes in the rumen when the model reaches dynamic equilibrium.



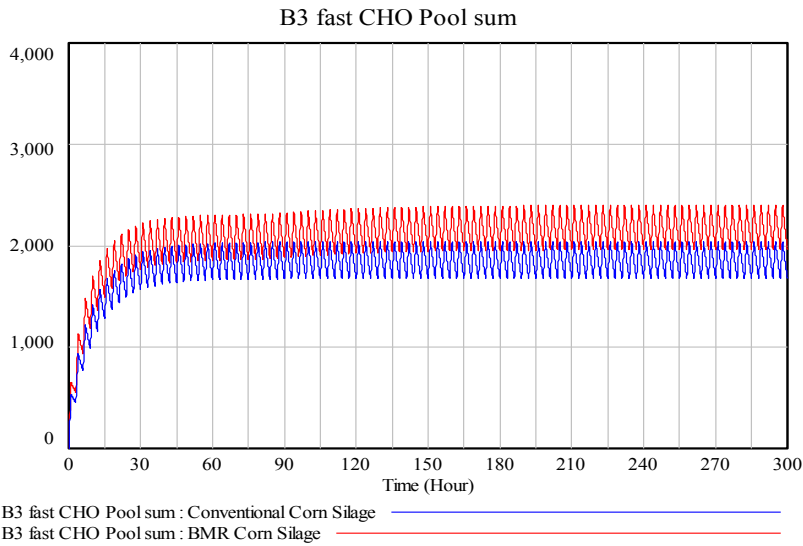
**Figure 5.** Schematic representation of a dynamic, three pool NDF digestion model in version 7.0 of the CNCPS.

### Calculating NDF digestion rates and pool sizes

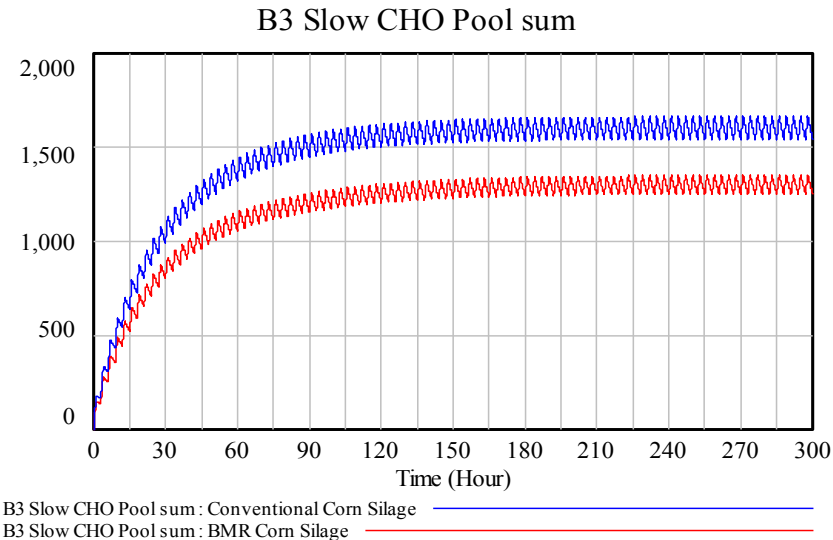
The model shown in Figure 6 requires more sophisticated inputs than previous versions of the CNCPS. These include estimations of the relative size of the rapidly degrading, slowly degrading and undigestible fiber pools for each feed in the ration along with the rate of digestion for each pool. These inputs can be calculated using the model shown in Figure 4. This model was first described by Raffrenato, Nicholson and Van Amburgh, (2010) and Raffrenato,( 2011) and uses *in vitro* NDFD data taken at 30, 120 and 240 hours to describe the three pool characteristics of NDF degradation. Any material remaining after 240 hours is considered indigestible within the context of feeding dairy cattle. Examples of simulated digestion and rumen fill curves for typical dairy cattle diets fed 58% forage diets consisting of a base of conventional corn silage or BMR corn silage are in Figures 5, 6 and 7, respectively.



**Figure 6.** Schematic representation of a model designed to estimate the relative size of rapidly degrading NDF (Fast Pool Stock 2r), slowly degrading NDF (Slow Pool Stock 2r), indigestible NDF (*i*NDF 2r; measured as remaining NDF after a 240hr *in vitro* fermentation), and the rate of digestion associated with each fraction ( $K_1$  and  $K_2$ ).

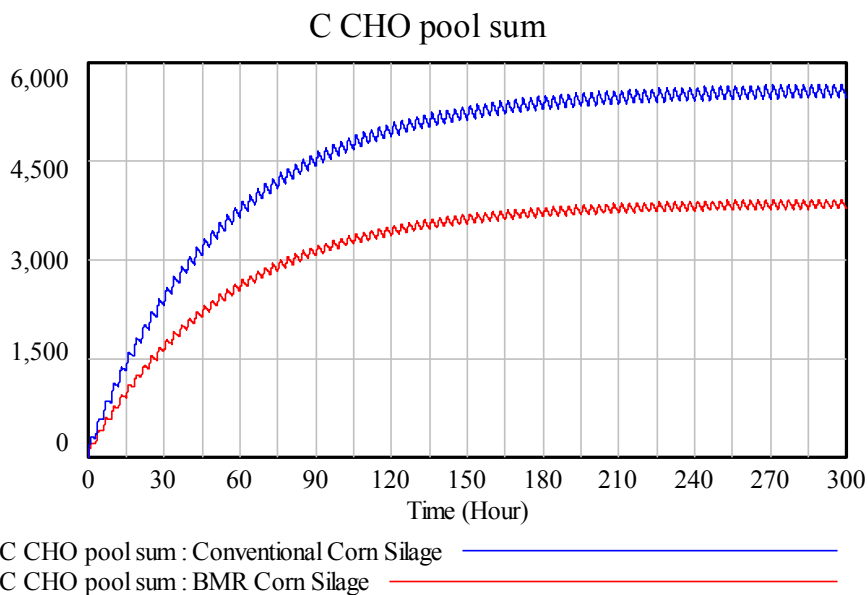


**Figure 7.** Predicted rumen content of the fast pool NDF (Raffrenato et al., 2010; Raffrenato, 2011) supplied by either conventional corn silage (blue line) versus bmr corn silage (red line). The oscillations are feeding periods versus rumen outflow or degradation. Y axis is grams of fast pool NDF.

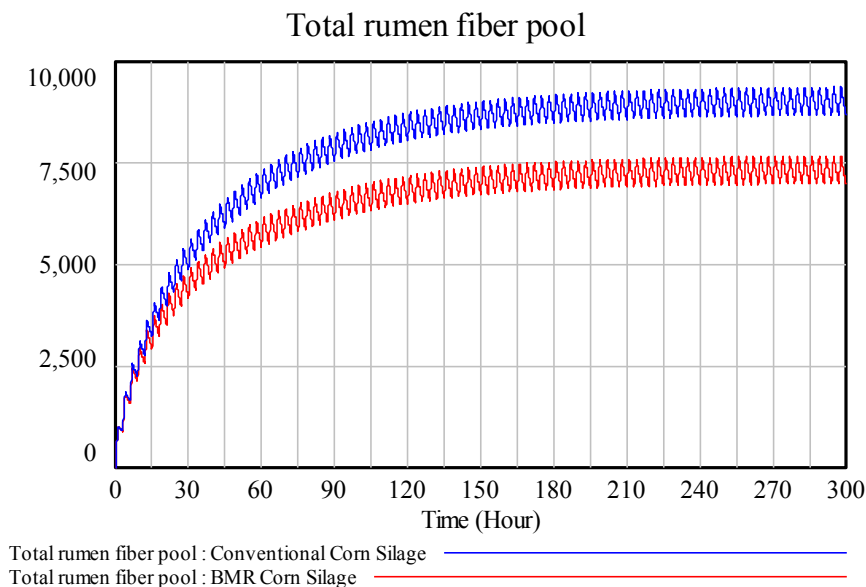


**Figure 8.** Predicted rumen content of the slow pool NDF (Raffrenato et al., 2010; Raffrenato, 2011) supplied by either conventional corn silage (blue line) versus bmr corn silage (red line). The oscillations are feeding periods versus rumen outflow or degradation. Y axis is grams of slow pool NDF.





**Figure 9.** Predicted rumen content of the undigestible NDF determined from 240 hr in vitro digestibility (Raffrenato et al., 2010; Raffrenato, 2011) supplied by either conventional corn silage (blue line) versus bmr corn silage (red line). The oscillations are feeding periods versus rumen outflow or degradation. Y axis is grams of undigestible NDF content in the rumen.



**Figure 10.** Predicted rumen content of the total NDF intake supplied by either conventional corn silage (blue line) or bmr corn silage (red line) estimated from the three pool model of

Raffrento (2011) and implemented in the CNCPS. The oscillations are feeding periods versus rumen outflow or degradation. Y axis is grams of total NDF rumen content. Application of the multi-pool model of NDF digestion within the structure of the CNCPS provides a new perspective on the differences in potential feed intake between diets based on conventional and bmr corn silages. This is illustrated in Figures 7 through 10, where the prediction for the fast pool of NDF content is greatest in the bmr corn silage compared to the conventional corn silage (Fig. 7). Conversely, the slow pool and indigestible NDF pools are the greatest for the conventional (Fig. 8 and 9) and when integrated with passage rate in the overall model, the difference in total rumen NDF content at a fixed intake is approximately 1,500 grams. If the rumen content of NDF is a limiting factor total dry matter intake, then under the conditions of the simulation, the cattle fed the bmr corn silage diet should have the capacity to consume approximately 1.5 kg (3.31 lbs) additional dry matter to equal the fill effect of the conventional corn silage based diet. This approach would allow the user to visualize and explain why dry matter intakes are greater in cattle fed bmr corn silage based diets. Most likely it is related to the total volume of NDF in the rumen at any one time and the larger the slow and indigestible pools, the greater the rumen fill and overall DMI would decrease accordingly.

### **Acknowledgements**

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### **REFERENCES**

- Ahvenjärvi, S., A. Vanhatalo, P. Huhtanen, and T. Varvikko. 2000. Determination of reticulo-rumen and whole-stomach digestion in lactating cows by omasal canal or duodenal sampling. *Br. J. Nutr.* 83:67-77.
- Broderick, G. A., P. Huhtanen, S. Ahvenjärvi, S. M. Reynal, and K. J. Shingfield. 2010. Quantifying ruminal nitrogen metabolism using the omasal sampling technique in cattle—a meta-analysis. *J. Dairy Sci.* 93:3216-3230.
- Doepel, L., D. Pacheco, J. J. Kennelly, M. D. Hanigan, I. F. Lopez, and H. Lapierre. 2004. Milk protein synthesis as a function of amino acid supply. *J. Dairy Sci.* 87:1279-1297.
- Fox, D. G., C. J. Sniffen, J. D. O'Connor, J. B. Russell, and P. J. Van Soest. 1992. A net carbohydrate and protein system for evaluating cattle diets: Iii. Cattle requirements and diet adequacy. *J. Anim. Sci.* 70:3578-3596.
- Fox, D. G., T. P. Tytlutki, M. E. Van Amburgh, L. E. Chase, A. N. Pell, T. R. Overton, L. O. Tedeschi, C. N. Rasmussen, and V. M. Durbal. 2000. The net carbohydrate and protein system for evaluating herd nutrition and nutrient excretion. Cncps version 4.0.: Model documentation. Department of Animal Science, Cornell University, Ithaca, New York.
- Fox, D. G., L. O. Tedeschi, T. P. Tytlutki, J. B. Russell, M. E. Van Amburgh, L. E. Chase, A. N. Pell, and T. R. Overton. 2004. The cornell net carbohydrate and protein system model for evaluating herd nutrition and nutrient excretion. *Anim. Feed Sci. Tech.* 112:29-78.
- Fox, D. G., M. E. Van Amburgh, and T. P. Tytlutki. 1999. Predicting requirements for growth, maturity, and body reserves in dairy cattle. *J. Dairy Sci.* 82:1968-1977.
- Higgs, R., L. Chase, D. Ross, and M. Van Amburgh. 2012a. Evaluating and refining the cncps feed library using commercial laboratory feed databases. Pages 146-156 in Proc. 74<sup>th</sup> Cornell Nutrition Conference For Feed Manufacturers. Cornell University, Syracuse, NY.

- Higgs, R. J., L. E. Chase, and M. E. Van Amburgh. 2012b. Development and evaluation of equations in the cornell net carbohydrate and protein system to predict nitrogen excretion in lactating dairy cows. *J. Dairy Sci.* 95:2004-2014.
- Huhtanen, P., S. Ahvenjärvi, G. A. Broderick, S. M. Reynal, and K. J. Shingfield. 2010. Quantifying ruminal digestion of organic matter and neutral detergent fiber using the omasal sampling technique in cattle—a meta-analysis. *J. Dairy Sci.* 93:3203-3215.
- Huhtanen, P., P. G. Brotz, and L. D. Satter. 1997. Omasal sampling technique for assessing fermentative digestion in the forestomach of dairy cows. *J. Anim. Sci.* 75:1380-1392.
- Lanzas, C., C. J. Sniffen, S. Seo, L. O. Tedeschi, and D. G. Fox. 2007a. A revised cneps feed carbohydrate fractionation scheme for formulating rations for ruminants. *Anim. Feed Sci. Technol.* 136:167-190.
- Lanzas, C., L. O. Tedeschi, S. Seo, and D. G. Fox. 2007b. Evaluation of protein fractionation systems used in formulating rations for dairy cattle. *J. Dairy Sci.* 90:507-521.
- NRC. 2001. Nutrient requirements of dairy cattle. 7th rev. Ed. National Academy Press, Washington, D.C.
- O'Connor, J. D., C. J. Sniffen, D. G. Fox, and W. Chalupa. 1993. A net carbohydrate and protein system for evaluating cattle diets: Iv. Predicting amino acid adequacy. *J. Anim. Sci.* 71:1298-1311.
- Reynal, S. M. and G. A. Broderick. 2005. Effect of dietary level of rumen-degraded protein on production and nitrogen metabolism in lactating dairy cows. *J. Dairy Sci.* 88:4045-4064.
- Reynal, S. M., I. R. Ipharraguerre, M. Liñeiro, A. F. Brito, G. A. Broderick, and J. H. Clark. 2007. Omasal flow of soluble proteins, peptides, and free amino acids in dairy cows fed diets supplemented with proteins of varying ruminal degradabilities. *J. Dairy Sci.* 90: 1887-1903.
- Rulquin, H., P. M. Pisulewski, R. Vérité, and J. Guinard. 1993. Milk production and composition as a function of postruminal lysine and methionine supply: A nutrient-response approach. *Liv. Prod. Sci.* 37:69-90.
- Russell, J. B., J. D. O'Connor, D. G. Fox, P. J. Van Soest, and C. J. Sniffen. 1992. A net carbohydrate and protein system for evaluating cattle diets: I. Ruminal fermentation. *J. Anim. Sci.* 70:3551-3561.
- Sniffen, C. J., J. D. O'Connor, P. J. Van Soest, D. G. Fox, and J. B. Russell. 1992. A net carbohydrate and protein system for evaluating cattle diets: Ii. Carbohydrate and protein availability. *J. Anim. Sci.* 70:3562-3577.
- St-Pierre, N. R. 2001. Invited review: Integrating quantitative findings from multiple studies using mixed model methodology. *J. Dairy Sci.* 84:741-755.
- Tylutki, T. P., D. G. Fox, V. M. Durbal, L. O. Tedeschi, J. B. Russell, M. E. Van Amburgh, T. R. Overton, L. E. Chase, and A. N. Pell. 2008. Cornell net carbohydrate and protein system: A model for precision feeding of dairy cattle. *Anim. Feed Sci. Technol.* 143:174-202.
- Van Amburgh, M., L. Chase, T. Overton, D. Ross, E. Recktenwald, R. Higgs, and T. Tylutki. 2010. Updates to the cornell net carbohydrate and protein system v6. 1 and implications for ration formulation. Pages 144-159 in Proc. 72<sup>nd</sup> Cornell Nutrition Conference For Feed Manufacturers. Cornell University, Syracuse, NY.
- Van Amburgh, M. E., A. Recktenwald, D. A. Ross, T. R. Overton, and E. S. Chase. 2007. Achieving better nitrogen efficiency in lactating dairy cattle: Updating field usable tools to improve nitrogen efficiency. Pages 25-37 in Proc. 69<sup>th</sup> Cornell Nutrition Conference For Feed Manufacturers. Cornell University, Syracuse, NY.
- Volden, H., L. T. Mydland, and V. Olaisen. 2002. Apparent ruminal degradation and rumen escape of soluble nitrogen fractions in grass and grass silage administered intraruminally to lactating dairy cows. *J. Animal Sci.* 80: 2704-2716.

Whitehouse, N. L., C. G. Schwab, T. P. Tylutki, and B. K. Sloan. 2013. Optimal lysine and methionine concentrations in metabolizable protein for milk protein production as determined with the latest versions of dairy NRC 2001 and AMTS. *Cattle. J. Dairy Sci.* 96. E-Suppl. 1.