ACCOUNTING FOR RUMINAL DEFICIENCIES OF NITROGEN AND BRANCHED-CHAIN AMINO ACIDS IN THE STRUCTURE OF THE CORNELL NET CARBOHYDRATE AND PROTEIN SYSTEM

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EFFECTS OF A RUMINAL DEFICIENCY OF NITROGEN

The rumen typically operates as an energy-limited, nitrogen-excess system, but diets can be so low in degradable crude protein that microbial growth is limited by N. Ruminal bacteria respond differently to N sources and N-limitation. Cellulolytic ruminal bacteria need ammonia as an N source, have little capacity to utilize amino-N, are unable to ferment fiber when ammonia is depleted, and do not produce ammonia from amino-N sources (1, 2, 3). Some hemicellulose-digesting ruminal bacteria are stimulated by amino-N, but even these species are primarily dependent on ammonia as an N source (4). Many nonfiber digesting ruminal bacteria prefer amino-N to ammonia (2, 5), and some can even produce ammonia from amino-N source (6).

The Cornell Net Carbohydrate and Protein System (CNCPS) model uses rates of carbohydrate fermentation to estimate microbial growth in the rumen (7). Growth yields are adjusted to accommodate maintenance energy expenditures, peptide availability, and pH, but previous versions of the CNCPS did not account for N-limitation per se. Ruminal N-limitation can decrease microbial flow (g bacteria/d) from the rumen (8, 9, 10), depress fiber fermentation (7), and reduce DMI (10, 11, 12, chapters 18 and 21), but the CNCPS did not have equations to accommodate these effects.

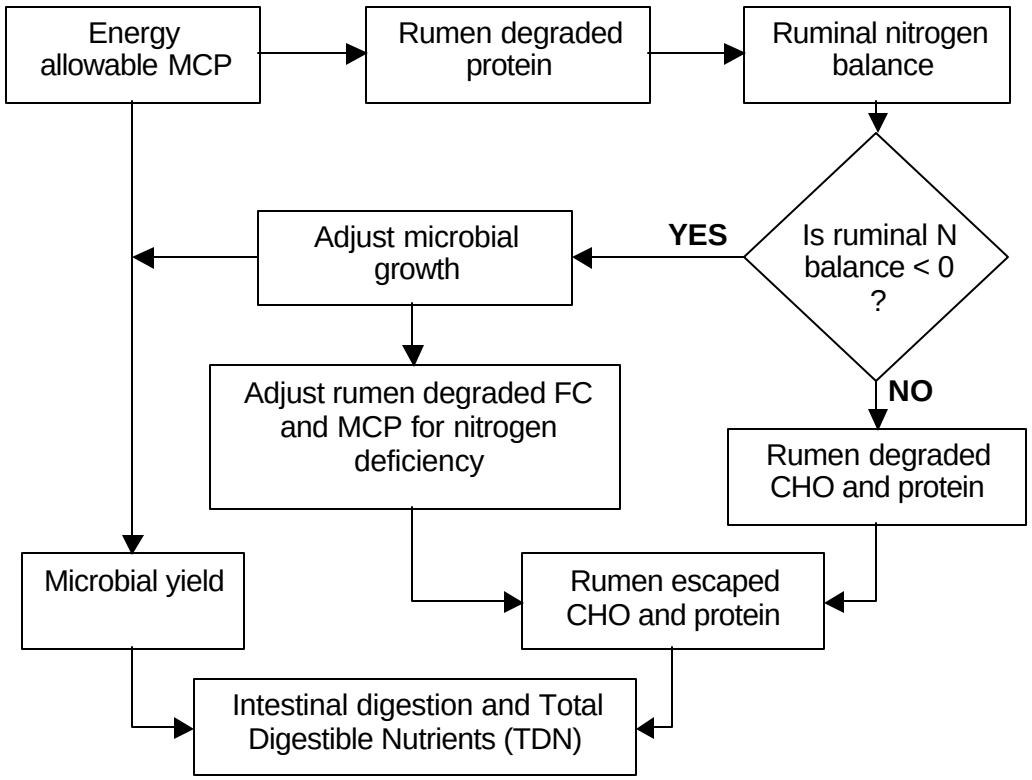
Most systems of ration formulation for cattle (ARC, 13; NRC, 14; CSIRO, 15; INRA, 16; AFRC, 17; NRC, 18) acknowledge the importance of supplying adequate N as well as energy. However, none of them have a systematic method of discounting ruminal activity, microbial growth, and DMI when ruminal N is depleted.

The objectives of this first study were 1) to devise equations for CNCPS version 4 that could quantify the impact of N-limitation on microbial protein production, fiber digestion, and DMI, and 2) validate these CNCPS adjustments with experimental data with cattle responses to added dietary N.

Ruminal Nitrogen Deficiency Model Development

Figure 1 shows the algorithmic adjustments developed for CNCPS version 4.0 to account for reductions in microbial yield and cell wall digestion when ruminal N is deficient. The CNCPS microbial growth equations and their definitions as published by level 2 of the NRC (18) model were used to adjust the rumen submodel. Definitions used for this submodel are shown in Table 1. The equations as published by Tedeschi et al. (19) are listed in Table 2.

Figure 1. Process for adjusting microbial crude protein (MCP) yield and ruminal degradation of fiber carbohydrate predictions for a ruminal N deficiency. CHO is carbohydrate and FC is fiber carbohydrate.



In order to determine the total ruminal N balance, the first step is to compute microbial growth from ruminally degraded FC (EFCBact, g bacteria/d) and NFC (ENFCBact, g bacteria/d) when energy is limiting bacterial growth (EAllowableBact, g bacteria/d; Eq. 1) (7).

Since in the CNCPS model the FC and NFC bacteria are assumed to contain 10% N (7), EAllowableBact multiplied by 0.1 gives the bacteria requirement for N. If the ruminal N balance is negative (the requirement is higher than the sum of dietary supply and recycled N), microbial growth is decreased (13). Nitrogen-allowable bacterial growth (NAllowableBact, g bacteria/d; Eq. 2) is the sum of ruminally degraded true protein N (PeptideUptakeN, g N/d), non-protein N from the diet (DegradedDietN, g N/d), and recycled N (RecycledN, g N/d) divided by the bacterial nitrogen concentration.

If fermentable energy is the first limiting nutrient, microbial protein production is dictated by energy, not N available in the rumen, and there is no need to reduce microbial yield. However, if N is limiting then microbial yield is reduced (BactRed, g bacteria/d) by the difference between the energy allowable and the protein allowable bacterial growth (Eq. 3).

Some ruminal bacteria can continue to ferment carbohydrates even if N is limiting and growth is not possible (5). Energy spilling can be caused by futile cycles of potassium, ammonium, or protons through the cell membrane (20). Continuous culture studies with N-limited mixed ruminal bacteria indicated NFC bacteria fermented abnormally large amounts of glucose or starch, but FC bacteria could not spill energy

(21). Because NFC bacteria can “spill energy” when N is limiting, NFC digestion is not affected, but N-limitation has a negative effect on FC digestion (22).

Table 1. Description of the acronyms used in the nitrogen adjustment submodel.

Acronyms	Description
BactRed	Total amount of bacteria growth reduction due to ruminal N deficiency, g of bacteria/d
$BactRed_j$	Amount of bacteria growth reduction due to ruminal N deficiency for the j^{th} feed, g of bacteria/d
DegradedDietN	Amount of ruminally-degraded nitrogen provided by the diet, g of N/d
EAllowableBact	Total bacteria growth allowable by ruminal available energy, g of bacteria/d
$EBactRatio_j$	Proportion of fiber carbohydrate and nonfiber carbohydrate bacteria for the j^{th} feed to the total diet bacteria based on energy availability in the rumen
EFCBact	Total diet energy allowable fiber carbohydrate bacteria growth, g of bacteria/d
$EFCBact_j$	Energy allowable fiber carbohydrate bacteria growth for the j^{th} feed, g of bacteria/d
$EFCBactRatio_j$	Proportion of fiber carbohydrate bacteria to the total bacteria growth for the j^{th} feed based on energy availability in the rumen
ENFCBact	Total diet energy allowable nonfiber carbohydrate bacteria growth, g of bacteria/d
$ENFCBact_j$	Energy allowable nonfiber carbohydrate bacteria growth for the j^{th} feed, g of bacteria/d
$FCBactRed_j$	Amount of fiber carbohydrate bacteria growth reduction for the j^{th} feed, g of bacteria/d
FCRed	Total fiber carbohydrate not degraded due to fiber carbohydrate bacteria reduction growth, g of fiber carbohydrate/d
$FCRed_j$	Fiber carbohydrate not degraded due to fiber carbohydrate bacteria reduction growth for the j^{th} feed, g of fiber carbohydrate/d
FCRedRatio	Proportion of fiber carbohydrate not degraded because of N limitation, %
NAllowableBact	Total bacterial growth allowable by diet ruminal degradable N intake, g of bacteria/d
$NAllowableBact_j$	Bacterial growth allowable by ruminal degradable nitrogen intake for the j^{th} feed, g of bacteria/d
PeptideUptakeN	Amount of nitrogen from degraded peptide used by ruminal bacteria, g of N/d
$RDCB2_j$	Rumen degraded carbohydrate B2 for the j^{th} feed, g of carbohydrate/d
$RECB2_j$	Rumen escaped carbohydrate B2 for the j^{th} feed, g of CHO /d
RecycledN	Amount of nitrogen recycled through the blood as ammonia, g of N/d
Y_{1j}	Microbial yield for fiber carbohydrate bacteria for j^{th} feed, g bacteria/g fiber carbohydrate digested in the rumen

Within the CNCPS, the overall FC digestion is dependent on FC digestion rate of each feed; therefore, the effect of the nitrogen deficiency must be determined for each feed in the diet. The reduction in bacterial yield for the j^{th} feed (Eq. 4) is computed using the $EBactRatio_j$ (Eq. 5).

Table 2. Equations to adjust microbial growth and fiber digestion for a ruminal N deficiency.

	Equations
[1]	$\text{EAllowable Bact} = \text{EFCBact} + \text{ENFCBact}$
[2]	$\text{NAllowable Bact} = (\text{PeptideUptakeN} + \text{DegradedDietN} + \text{RecycledN}) / 0.1$
[3]	$\text{BactRed} = \text{EAllowable Bact} - \text{NAllowable Bact}$
[4]	$\text{NAllowable Bact}_j = \text{NAllowable Bact} \times \text{EBactRatio}_j$
[5]	$\text{EBactRatio}_j = (\text{EFCBact}_j + \text{ENFCBact}_j) / (\text{EFCBact} + \text{ENFCBact})$
[6]	$\text{BactRed}_j = (\text{EFCBact}_j + \text{ENFCBact}_j) - \text{NAllowable Bact}_j$
[7]	$\text{FCBactRed}_j = \text{BactRed}_j \times \text{EFCBactRatio}_j$
[8]	$\text{EFCBactRatio}_j = \text{EFCBact}_j / (\text{EFCBact}_j + \text{ENFCBact}_j)$
[9]	$\text{FCRed}_j = \text{FCBactRed}_j / Y_{1j}$
[10]	$\text{Adjusted RDCB2}_j = \text{RDCB2}_j - \text{FCRed}_j$
[11]	$\text{Adjusted RECB2}_j = \text{RECB2}_j + \text{FCRed}_j$
[12]	$\text{FCRedRatio} = 100 \times \text{FCRed} / \text{RDCB2}$

Then, the bacterial yield reduction for each feed ($BactRed_j$, g bacteria/d) is computed for each feed from its energy allowable growth of FC ($EFCBact_j$) and NFC ($ENFCBact_j$), and N allowable growth ($NAllowableBact_j$) (Eq. 6).

The reduction in FC bacterial yield ($FCBactRed_j$, g bacteria/d) due to a ruminal N deficiency is then computed (Eq. 7) for each feed from the reduction in bacteria produced allocated to the feed and the $EFCBactRatio_j$ when N is not limiting (Eq. 8).

As discussed before, N-limitation is likely to decrease carbohydrate fermentation as well as FC bacterial growth. *F. succinogeses* was unable to ferment “excess cellobiose” when N was limiting (23), and mixed culture studies indicated that organic matter digestion was also reduced by N-limitation (24, 25). To account for this effect, $FCBactRed_j$ is multiplied by the inverse of its yield (Y_{1j}, g bacteria/g FC digested) to estimate the amount of FC for each feed that is not degraded ($FCRed_j$, g FC/d) (Eq. 9).

In this case, we have simply used the reduction in FC bacteria to estimate additional FC passage from the rumen. The reduction in FC bacteria was computed in Eq. 7, and it dictates the FC escape (not the converse).

The last step is to adjust the ruminally degraded carbohydrate B2 ($RDCB2_j$, g/d; Eq. 10) and ruminally escape carbohydrate B2 ($RECB2_j$, g/d; Eq. 11). The $RDCB2_j$ and $RECB2_j$ were calculated as described by Pitt et al. (26). No feedback adjustment is performed in the EAllowableBact calculation due to the change in RDCB2 because the submodel calculates microbial growth based on the first limiting nutrient in the rumen for bacteria growth.

The percentage of carbohydrate B2 not degraded in the diet as a result of the ruminal N deficiency (FCRedRatio, %; Eq. 12) is predicted by dividing the sum of FC reduction of all feeds by the total RDCB2 estimated from passage and degradation rates (27). This value is used to predict the reduction in DMI due to a reduction in fiber degradation, consequently decreasing fiber passage rate (12, Chap. 21).

Ruminal Nitrogen Deficiency Model Evaluation

The model used in this evaluation was the CNCPS version 4.0 (28), which contains rumen fermentation and animal growth equations similar to the version used in the development of the NRC (27) model level 2 and also contains the nitrogen deficiency model described here. Five published studies, as described by Tedeschi et al. (19), were identified that had adequate information (animal and feed composition descriptions) and in which the design provided a sensitive test (unsupplemented controls and incremental additions of N resulting in animal growth responses) to evaluate this model.

The statistical analysis and model evaluation were described by Tedeschi et al. (19). The model bias was calculated by dividing the mean of the Y-variate minus the mean of the X-variate by the mean of the X-variate if the intercept (b) was different from zero; otherwise it was calculated as the slope (a) of the regression through the origin minus 1. As shown below, they are equivalent only if b = 0.

$$\text{Model bias} = a - 1 = \frac{\bar{y} - \bar{x} - b}{\bar{x}}$$

Results and Discussion

Regressions of observed versus predicted ADG (first limiting of ME or MP allowable gain) without adjustment for rumen N deficiency had an intercept value that was significant ($P < 0.05$), and the mean bias was 0.16 kg/d. When the N-limitation adjustment was added, the intercept was no longer significant ($P > 0.05$), the r^2 value was higher (0.825 versus 0.875, respectively), and the MSE was lower (0.025 versus 0.018, respectively).

The CNCPS 4.0 model without the ruminal N deficiency adjustment tended to overpredict ADG at low and high observed ADG (Figure 2A). Therefore, the proportion of deviation points lying within –0.1 and 0.1 kg/d was only 37.9% (Figure 2B). In contrast, the CNCPS model with the ruminal N deficiency adjustment had an even distribution of points along the unity line and, therefore, did not have any systematic prediction error (Figure 2C). Consequently, the proportion of deviation points lying within –0.1 and 0.1 kg/d was higher (62.1%; Figure 2D) than without adjustment.

Figure 3 summarizes the relationship between ruminal N balance (A) and FCRedRatio (B) on ADG (g/d).

Figure 3A indicates that animal performance (ADG, g/d) was improved with increasing levels of urea in the diet until the ruminal N balance was close to zero (Y_{max} occurred at 0.6% of required ruminal N). The pattern of the regression suggests that a further increase in ruminal N would not increase animal performance. This lack of animal response is likely to occur due to the lack of available ruminal degraded carbohydrate to support microbial growth in forage based diets, not dietary N (12, Chap. 18).

In a similar fashion, Figure 3B results were obtained regressing ADG (g/d) on the reduction in fiber digestibility (Eq. 12). This figure indicated that increasing the amount of fiber not degraded (decreasing fiber digestibility), had a negative impact on animal

performance (ADG, g/d), which is expected once less energy is being obtained from fiber degradation (12, Chap. 18).

Figure 2. Prediction of ADG (kg/d) by the Cornell net carbohydrate and protein system (CNCPS) without (A and B) and with (C and D) the N deficiency adjustment. (A) Relationship between observed (o) ADG and predicted (p) first limiting metabolizable energy or metabolizable protein allowable ADG (kg/d) not adjusted for a negative ruminal N balance. The regression is ADGo = 1.07×ADGp – 0.2288, and r^2 = 0.83. (B) Deviation (CNCPS predicted minus observed ADG) versus observed ADG indicated 37.9% of the points are within the range –0.1 and 0.1 kg/d. (C) Relationship between observed (o) ADG and predicted (p) first limiting of metabolizable energy or metabolizable protein allowable gain (kg/d) adjusted for a negative ruminal N balance. The regression is ADGo = 0.9147×ADGp + 0.035, and r^2 = 0.88. The regression through the origin is ADGo = 0.9487×ADGp. (D) Deviation (CNCPS predicted minus observed gain) versus observed ADG indicated 62.1% of the points are within the range –0.1 and 0.1 kg/d. The data points are Lomas et al. (29), ◊; Boin and Moura (30), ; Abdalla et al. (31), Δ; Fox and Cook (32), ×; and Danner at al. (33), o.

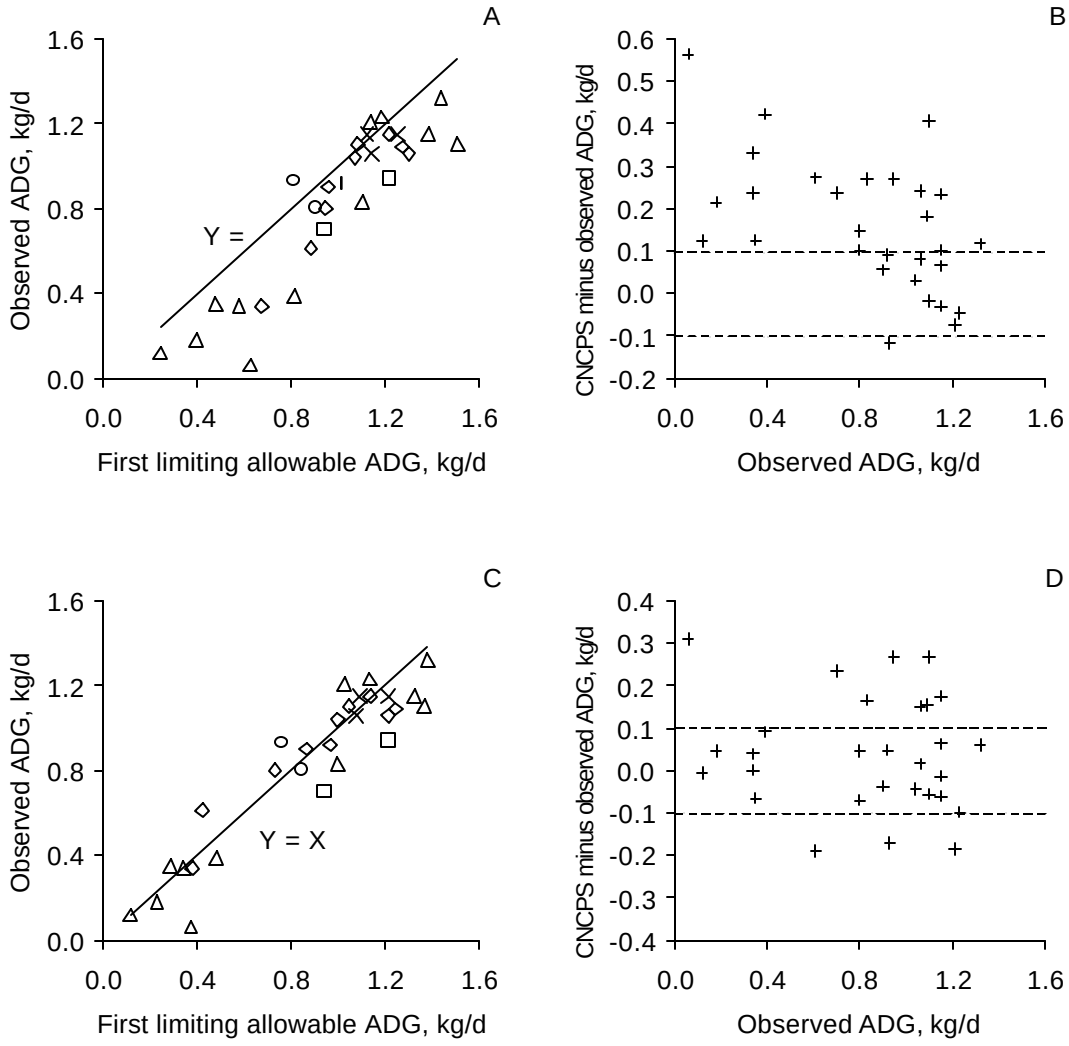
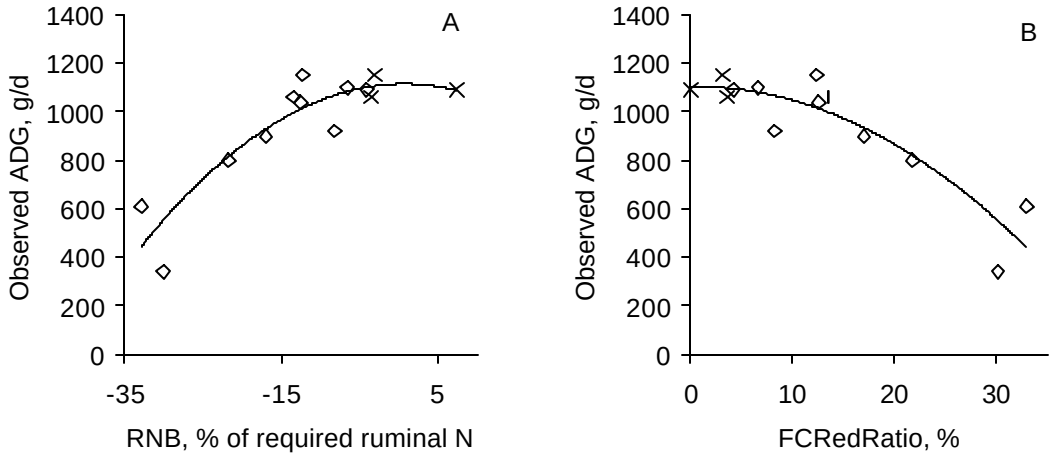


Figure 3. Relationship of observed (o) ADG (g/d) and (A) predicted (p) ruminal N balance (RNB, % of required ruminal N to attain balance of zero) and (B) reduction in fiber digestibility (%) by the Cornell net carbohydrate and protein system (CNCPS) for animals fed corn silage diets only. (A) The equation is Y = 1114 + 0.79X - 0.595X2 with an R2 of 0.82. (B) The equation is Y = 1102 + 0.83X - 0.636X2 with an R2 of 0.82. The data points are from Lomas et al. (29), ◊; and Fox and Cook (32), ×. FCRedRatio is the fiber carbohydrate digestion reduction ratio (%).



Overall, the N-limitation adjustment reduced the overprediction of the animal ADG and DMI by the CNCPS 4.0, but the bias was not completely eliminated. The present ruminal N deficiency adjustment assumed that all other required nutrients for microbial growth were adequate, and this assumption may not always be valid (34). Ruminal cellulolytic bacteria require branched-chain fatty acids (isovaleric, isobutyric, and 2-methylbutyric) as well as N (2). Microbial growth might be initially reduced by BCAA instead of N, when BCAA is below the adequate level.

EFFECT OF A RUMINAL DEFICIENCY OF BRANCHED-CHAIN AMINO ACIDS

Branched-chain volatile fatty acids (BCVFA: isobutyric, isovaleric, and 2-methylbutyric) are derived from dietary sources or recycling of bacterial protein by ruminal oxidative deamination and decarboxylation of valine, leucine, and isoleucine, respectively (35, 36, 37, 38, 39). The BCVFA are essential nutrients and increase growth of rumen cellulolytic as well as some non-cellulolytic bacteria (37, 40, 41, 42, 43, 44, 45).

After their absorption, cellulolytic and many non-cellulolytic bacteria use them to synthesize either essential amino acids (valine, leucine, and isoleucine) via reductive carboxylation pathways (46) or long-chain fatty acids and aldehydes (42).

Previous studies have shown that BCVFA can improve feed intake (47, 48), cellulose digestion (34, 49), microbial growth (49, 50), and weight gain (51, 52) of growing animals fed high fiber diets. For lactating dairy cows, enhancement of N

retention (51, 53, 54, 55, 56, 57), milk production (58, 59, 60), and milk persistency (51, 60) has also been observed.

If most of the feed protein consumed is ruminally degraded, and the ruminally-degraded protein is mostly true protein, the CNCPS ruminal nitrogen balance is a reasonable indicator of the potential for a BCVFA deficiency. However, when diets are high in non-protein nitrogen (e.g. urea) and much of the dietary true protein escapes the rumen, there can be enough ammonia to meet microbial growth requirements, but BCVFA can be limiting.

Thus, objective of this second study was to develop an adjustment procedure for a ruminal deficiency of branched-chain amino acids using a structure similar to the adjustment for a ruminal N deficiency described previously.

BCAA Model Development

Figure 4 describes the process of adjustment for a ruminal deficiency of branched-chain volatile fatty acids. Microbial growth is driven by the first limiting of ruminal N or the lowest BCVFA deficiencies with a consequent reduction in fiber degradation.

Figure 4. The process developed for adjusting microbial growth and ruminal degradation of fiber carbohydrate predictions for a ruminal deficiency of branched-chain volatile fatty acids (BCVFA). CHO is carbohydrate and FC is fiber carbohydrate.

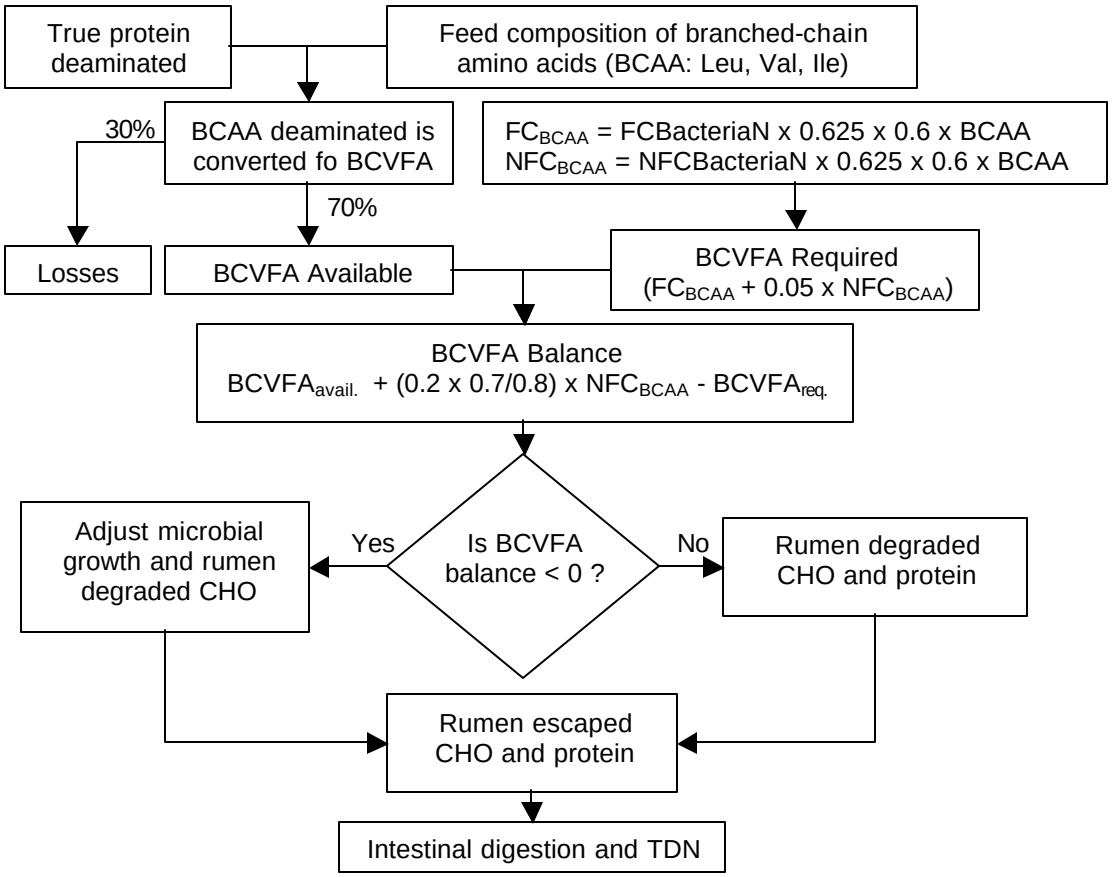


Table 3 contains definitions for variables used to adjust microbial growth and fiber digestion for a ruminal deficiency of BCAA. Table 4 lists equations developed to adjust for a BCAA deficiency.

Several assumptions are made in this adjustment process: **1)** the rate of ruminal degradation of each BCAA is similar regardless the diet, **2)** the profile of BCAA in each protein fraction (B1, B2, and B3) is constant and on average they are equal to the BCAA profile of the diet, **3)** the oxidative deamination and decarboxylation of BCAA to BCVFA and synthesis of BCAA from absorbed BCVFA via reductive carboxylation has an efficiency of 70%, **4)** BCAA synthesis by FC bacteria is directly proportional to BCVFA availability but NFC can synthesize (*de novo*) 95% of their BCAA when BCVFA is not available, and **5)** some BCVFA can also be derived from the turnover of NFC bacteria, but this production alone does not always sustain the FC bacteria.

Table 3. Description of the acronyms used in the nitrogen adjustment submodel.

Acronyms	Description
$AABalance_k$	Difference between available and required BCAA, g/d
$AABCW_k$	Content of the k^{th} amino acid in the bacteria cell wall, % CP
$AABNCW_k$	Content of the k^{th} amino acid in the bacteria noncell wall, % CP
$BactAAConc_k$	Content of the bacterial k^{th} BCAA (Leu, Ile, or Val), % CP
$BactAAConc_L$	Content of the 1^{st} limiting bacterial BCAA, % CP
$BactAA_k$	Amount of the bacterial k^{th} BCAA (Leu, Ile, or Val), g of BCAA/d
$BactAA_L$	Amount of the 1^{st} limiting bacterial BCAA, g of BCAA/d
BCAAAllowableBact	Bacteria growth allowable by ruminal BCAA degradation, g/d
$BCAAAllowableBact_j$	BCAAAllowableBact for the j^{th} feed, g/d
DMI_j	Dry matter intake of the j^{th} feed, kg/d
$FeedAA_{jk}$	Content of the k^{th} BCAA of the j^{th} feed, % CP
$FeedAA_L$	Content of the 1^{st} limiting BCAA in the diet, % CP
$FeedCP_j$	Content of CP of the j^{th} feed, % DM
LowestAABalance	The lowest value of AABalance among Leu, Ile, and Val, g/d
PeptidePassing	Amount of degraded peptide escaping the rumen, g/d
$RDPB1_j$	Amount of ruminally degraded B1 true protein in the j^{th} feed, g/d
$RDPB2_j$	Amount of ruminally degraded B2 true protein in the j^{th} feed, g/d
$RDPB3_j$	Amount of ruminally degraded B3 true protein in the j^{th} feed, g/d
TrueProtDeg	Total amount of true protein degraded in the rumen, g/d

Equations 5 and 8 were modified from those presented in table 2 to reflect the fourth assumption. The fifth assumption is reflected in equations 16 and 18.

Regarding the first assumption, few studies have compared the degradation rate of Leu, Val, and Ile. Varvikko (61) and Von Keyserlingk et al. (62) found that these amino acids are degraded more slowly than other amino acids. However, other authors (63, 64, 65, 66) have suggested that the degradation rate is similar for all amino acids. Because of these inconsistencies, and limitations in data available, we assumed the BCAA have similar degradation rate.

The second assumption assumes BCAA profile is uniform across different protein fractions that are ruminally degraded. Our recent studies (67) indicate the BCAA in the original plant and borate-phosphate buffer residue (insoluble protein) have similar content, but BCAA values in the cell wall (NDF residue) were 40% higher than the original forage. This suggests that adjusting for each degraded protein fraction might be a better approach than assuming homogeneity of BCAA across protein fractions.

Published data that can be used to support or challenge the third assumption is not available. However, it is likely that some BCVFA are absorbed across the rumen wall or pass out of the rumen in the fluid phase before the bacteria can convert them to BCAA. To account for this effect, we assumed 70% BCVFA ruminal availability, but it should be stressed that this value is arbitrary.

The fourth assumption is supported by the observation that none of the predominant cellulolytic ruminal bacteria can growth in the absence of BCVFA (68) and the observation that mixed ruminal bacteria from cows fed on hay had a 4-fold greater response to BCVFA than mixed bacteria from cows fed 60% grain (69). When the bacteria were obtained from cattle fed 60% grain the enhancement in microbial protein synthesis was only 5%. This observation supports the assumption that NFC can synthesize 95% of their BCAA *de novo*.

Table 4. Equations developed to adjust microbial growth and fiber digestion for a ruminal N and a ruminal branched chain amino acids deficiency.

	Equations
[5]	$EBactRatio_j = \frac{EFCBact_j + 0.05 \times ENFCBact_j}{EFCBact + 0.05 \times ENFCBact}$
[8]	$EFCBactRatio_j = EFCBact_j/(EFCBact_j + 0.05 \times ENFCBact_j)$
[13]	$TrueProtDeg = \sum_{j=1}^{n}(RDPB1_j + RDPB2_j + RDPB3_j) - PeptidePassing$
[14]	$BactAAConc_k = (0.2 \times AABCW_k + 0.8 \times AABNCW_k)/100$
[15]	$BactAA_k = (0.05 \times ENFCBact + EFCBact) \times (0.625 * 0.6) \times BactAAConc_k$
[16]	$AABalance_k = \left(\frac{\sum_{j=1}^{n} FeedAA_{jk} \times FeedCP_j \times DMI_j}{\sum_{j=1}^{n} FeedCP_j \times DMI_j} \right) \times TrueProtDeg \times 0.7 + (0.2 \times 0.7/0.8) \times (ENFCBact \times 0.625 \times 0.6 \times BactAAConc_k) - BactAA_k$
[17]	$LowestAABalance = Min(AABalance_k)$
[18]	$BCAAAllowableBact = \frac{FeedAA_L \times TrueProtDeg \times 0.7}{0.625 \times 0.6 \times BactAAConc_L} + \frac{0.2 \times 0.7 \times ENFCBact}{0.8}$
[19]	$BactRed = EAllowableBact - BCAAAllowableBact + 0.95 \times ENFCBact$
[20]	$BCAAAllowableBact_j = BCAAAllowableBact \times EBactRatio_j + 0.95 \times ENFCBact_j$
[21]	$BactRed_j = (EFCBact_j + ENFCBact_j) - BCAAAllowableBact_j$

The fifth assumption considers the possibility that bacterial turnover in the rumen leads to an increased deamination of amino acids and BCVFA availability for FC bacteria. CNCPS 4.0 does not attempt to model the dynamics of bacterial protein turnover, but the theoretical maximum growth yield is decreased 20% (50 to 40 g bacteria/g carbohydrate fermented) to account for protozoal predation and turnover. Thus we divided the NFC bacteria by 0.80 in order to estimate the amount of this microbial pool (predation and turnover), multiplied by 20% (turnover), and then

multiplied this turnover pool by their BCAA content to account for this additional source of BCVFA. Then this available pool was multiplied by 70% to compute rumen availability of this source of BCVFA.

If LowestAABalance is less than zero then the BCAA that is first limiting is used to calculate the BCAA allowable bacteria growth excluding the 95% from NFC bacteria, using Eq. 18. If BCVFAAllowableBact (Eq. 18) is lower than NAllowableBact (Eq. 2) then BCAA is first limiting (not ruminal N) for bacterial growth. In this case, Eq. 19-21 is used to calculate the bacterial mass reduction instead of Eq. 3-5, followed by equations 7 to 12 to calculate the adjusted bacteria yield and fiber digestion.

BCAA Model Evaluation

Data from a study with grazing dual-purpose cows (60% of bacterial yield from FC) (70) and from a study with high-producing Holstein cows (40% of bacterial yield from FC) (71) were used to simulate the effect of BCVFA deficiency on milk production (Table 5). In each case, the leucine concentration in feeds was reduced until the desired deficiency was achieved. When leucine was deficient, microbial growth and fiber digestibility declined and there was less ME and MP allowable milk.

Table 5. Sensitivity analysis of the effect of a branched-chain amino acid (BCAA) deficiency on milk production[1].

	BCAA Deficiency, %					
	0	10	20	30	40	50
Dual-purpose cow						
ME allowable milk, kg/d	7.1	5.9	4.7	3.4	1.9	0
MP allowable milk, kg/d	6.6	5.4	4.2	3.0	1.9	0.7
BCAA balance, g/d	0	-2.6	-5.2	-7.9	-10.5	-13.1
Holstein cow						
ME allowable milk, kg/d	37.0	35.3	33.8	32.2	30.5	29.0
MP allowable milk, kg/d	37.2	35.4	33.8	32.1	30.5	28.7
BCAA balance, g/d	0	-4.3	-8.5	-12.8	-17.0	-21.3

[1] The requirement of the first limiting BCAA (leucine) was 26.2 and 42.5 g/d for dual-purpose and dairy cow scenarios, respectively. Dual-purpose cow had 79% of forage and Holstein cow had 60% of forage in the diet.

Results indicated that the BCVFA deficiency would have had a greater proportional impact on the grazing dual-purpose cows than on the Holstein cows (6.9 and 1.1% reduction in milk for each gram of BCAA deficiency, respectively; Table 5).

This difference could largely be explained by bacterial turnover and the relative amounts of NFC and FC bacteria. When forage was the main dietary ingredient (79%), there was little NFC and the NFC bacteria turnover supplied approximately 3.1 g of leucine (656 g $\times$ 0.625 %CP $\times$ 0.6 %TP $\times$ 0.072 %Leu $\times$ 0.2 $\times$ 0.7 $\div$ 0.8), and the diet supplied 88% of the leucine requirement. When the diet had 40% concentrates, NFC bacterial turnover supplied 10.6 g of leucine (2250 g $\times$ 0.625 %CP $\times$ 0.6 %TP $\times$ 0.072 %Leu $\times$ 0.2 $\times$ 0.7 $\div$ 0.8), and the diet only needed to supply 75% of the requirement.

Diet simulations indicated that BCAA-BCVFA deficiencies could be offset by added soybean meal, which has a high proportion of ruminally-degraded true protein. In the grazing dual-purpose cow, when soybean meal was substituted for 0.77 kg/day of Pangola grass, MP allowable milk increased from 4.7 to 10.0 kg/d. This difference in milk (5.3 kg/d) could be 47% explained by a less negative balance of BCAA in the rumen. When Holstein dry cows were fed a forage-based diet (corn silage, 45%; alfalfa haylage, 39%; and orchardgrass hay, 16%) there was a deficiency of ruminal valine, and this deficiency could be eliminated by adding 0.6 kg of soybean meal.

CONCLUSIONS

When the CNCPS rumen submodel was modified to include equations to account for a ruminal N-deficiency, the ability to predict average daily gain in growing/finishing steers was significantly improved. Data for lactating dairy cows was lacking, but we are currently conducting lactation trial to valid these modifications. This study indicates that the model can also be improved by accounting for BCVFA and BCAA deficiencies. BCVFA deficiencies are less common than N-deficiencies, but they can have a significant impact on animal performance if the diet is primarily forage.

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