

Balancing for Amino Acids in Dairy Diets

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Abstract

Before the revision of the National Research Council system for expressing the protein needs of dairy cows, little attention was paid to protein quality in ruminant diets. Microbial protein synthesis in the rumen was assumed to provide an adequate supply of amino acids for the production of meat and milk by cattle. However, the protein requirements for milk production in high-producing cows have exceeded the ability of the rumen microbial population to synthesize some essential amino acids. The Cornell Net Carbohydrate and Protein System (CNCPS) is a dynamic, factorial model which predicts supply and requirement for amino acids.

The objectives of this study were 1) to test the ability of the amino acid submodel of the CNCPS to predict amino acid flow at the duodenum, and 2) to determine if early lactation cows would respond to rumen bypass amino acids with an increase in milk or milk protein yield. Five early-lactation Holstein cows were fitted with rumen and duodenal cannulae and utilized in a metabolism trial with a 5 x 5 Latin square design. Two diets were formulated to contain equal amounts of crude protein, degradable and undegradable protein (UIP), neutral detergent fiber, and non-structural carbohydrate. These diets used either fish meal or corn gluten meal and corn distiller's grain as sources of UIP. Bypass lysine (23 g/day) or bypass methionine (13 g/day) or both were then added to the corn protein-based diet. Diets consisted of grass silage, a barley and corn-based concentrate with the appropriate protein supplement, and whole cottonseed.

Dry matter intake, milk yield, casein yield, and microbial nitrogen flow were not affected by diet; diets supplemented with amino acids tended to have lower microbial nitrogen flow. Although agreement between measured amino acid flow and the CNCPS were generally good, the model tended to overestimate the value of FM as a bypass protein and underestimate the value of the CGD diet. Variability among cows and within feedstuffs has a large impact on the ability to predict amino acid flow to the intestine.

Introduction

Since the revision of the National Research Council¹ (NRC) system for expressing the protein needs of dairy cows, interest in the amino acid nutrition of lactating cows has grown. Previously, little attention was paid to protein quality in ruminant diets; it was assumed that microbial protein synthesis in the rumen would supply the amino acids required for production of meat and milk by cattle. However, the protein requirements for milk production in high-producing cows have exceeded the ability of the rumen microbial population to synthesize some essential amino acids. The utilization of bovine somatotropin to augment milk production will

increase the importance of protein quality in dairy cattle diets.²

When casein is abomasally infused into lactating cows, milk production, milk protein yield, or both, increase.³ Infusion studies have also shown that lysine and methionine are limiting amino acids during peak lactation, and that the extent of lysine limitation declines with advancing stage of lactation.^{4,5} In spite of these results with infusion studies, the response to supplementation of dairy cattle diets with rumen-undegradable protein (UIP) using current NRC guidelines is somewhat unpredictable. The lack of response in some instances reflects deficiencies in the amino acid profile of the UIP supplement in use, or dietary limitations in precursors for the synthesis of microbial protein. Several computer models have been developed to predict the flow of microbial protein into the small intestine and response to supplementation with various UIP sources. The ability to predict milk and milk protein response to bypass protein supplements is of value in formulating economical rations which support milk production, reproduction and growth.

The Cornell Net Carbohydrate and Protein System (CNCPS)^{6,7} is a dynamic, factorial model which predicts supply and requirement for amino acids. Supply of amino acids is based on microbial protein synthesis and on dietary protein which escapes microbial degradation. Several improvements in this model, relative to NRC, are:

- microbial protein production is based on **rates** of structural and nonstructural carbohydrate fermentation (rather than TDN)
- microbial yield is adjusted as a function of growth rate (reflecting higher microbial efficiency as the cow consumes more dry matter)
- the amount of undegraded feed protein is based on both resistance to degradation and on rate of passage through the rumen
- amino acid composition of the UIP fraction is based on analysis of the insoluble protein fraction, rather than amino acid composition of the parent feed.

The objectives of this study were 1) to test the ability of the amino acid submodel of the CNCPS to predict amino acid flow at the duodenum, and 2) to deter-

mine if early lactation cows would respond to rumen bypass amino acids with an increase in milk or milk protein yield.

Materials and Methods

Five early-lactation Holstein cows were utilized in a metabolism trial with a 5 x 5 Latin square design. Cows were fitted with ruminal and duodenal cannulae at the beginning of the preceding dry period. Two diets were formulated to contain equal amounts of crude protein, degradable and undegradable protein (UIP), fiber (NDF), and non-structural carbohydrate. However, these diets used either fish meal (FM) or corn gluten meal and corn distillers' grain (CGD) as the source of UIP. The CNCPS was used to calculate the difference in duodenal lysine and methionine flow between FM and CGD diets. Bypass lysine (23 g/day; CG-L) or bypass methionine (13 g/day; CG-M) or both (CG-LM) were then added to the CGD diet, for a total of five different diets. Zinc-lysine (Lyzin[®]) or zinc-methionine (Zinpro[®]) were used as sources of bypass amino acids. Mineral premixes were formulated such that all diets contained approximately 600 ppm zinc. Diets consisted of 42% grass silage, 7 to 9% whole cottonseed, and 49 to 51% barley and corn-based concentrate with the appropriate protein supplement (dry matter basis).

Experimental periods were two weeks long. The last five days of each period were used for sampling of feces, urine, ingesta, and milk. Ingesta flow was determined using ytterbium-labeled grass particles as a particulate-phase marker. Duodenal ingesta was dried in a 55° oven and ground through a 1 mm screen. Amino acid content of duodenal ingesta was measured by ion-exchange HPLC. Ytterbium was measured by neutron activation.

Results and Conclusions

The results of the study are shown in Table 1. Dry matter intake, milk yield, and casein yield were not affected by diet. Microbial nitrogen (N) flow also was not significantly affected by diet, although diets supplemented with bypass amino acids tended to have lower microbial N flow. Presumably, gains in the bypass amino acids due to supplementation were offset by decreases in amino acids of microbial origin. In this study, utilization of a relatively high-quality source of UIP (fish meal) did not result in improved milk or milk protein yields as compared to plant sources of UIP.

Table 2 shows a comparison of the predictions of the CNCPS predictions with several measured amino acid flows at the duodenum. Many of the predictions are very close to measured values; in general, the CNCPS tended to overestimate the value of FM as a bypass protein and underestimate the value of the CGD

Table 1. Dry Matter Intake, Milk Measures, and Duodenal Amino Acids Using Bypass Amino Acids in the Diets of Lactating Cows.

	Diet ¹					SEM ²
	FM	CG-L	CG-M	CG-LM	CGD	
Dry matter intake, kg/d	22.5	23.3	23.7	23.4	22.7	1.52
Milk yield, kg/d	30.9	33.3	32.3	32.7	34.2	4.90
Casein yield, g/d	130.4	126.3	129.7	131.1	133.5	21.2
Bacterial N flow at duodenum, g/d	369	302	241	320	382	23.8
Lysine flow at duodenum, g/d	194	169	132	171	197	12.5
Methionine flow at duodenum, g/d	54.3	61.1	46.8	61.5	68.3	4.54

¹ FM, Fish meal; CGD, corn gluten/corn distillers; CG-L, lysine-supplemented, CG-M, methionine-supplemented; CG-LM, both lysine and methionine-supplemented.

² Standard error of the mean; there were no significant effects due to diet.

Table 2. Comparison of Cornell Net Protein Carbohydrate System (CNCPS) Predictions and Estimated Amino Acid Flow.

Amino Acid, g/day	FM Diet			CGD Diet		
	CNCPS	Measured	% Difference	CNCPS	Measured	% Difference
Lysine	216	194	-10.2	189	197	+4.2
Methionine	75	54	-28.0	66	68	+3.0
Leucine	235	256	+8.9	271	381	+40.6
Isoleucine	162	146	+9.9	156	178	+14.1
Valine	180	172	+4.4	184	211	+14.7

Figure 1. Duodenal flow of lysine (solid line) and methionine (dashed line) as predicted by CNCPS with increasing dry matter intake of fish meal-supplemented diet. Actual measurements of duodenal lysine (■) and methionine (●) flow from cannulated cows are superimposed.

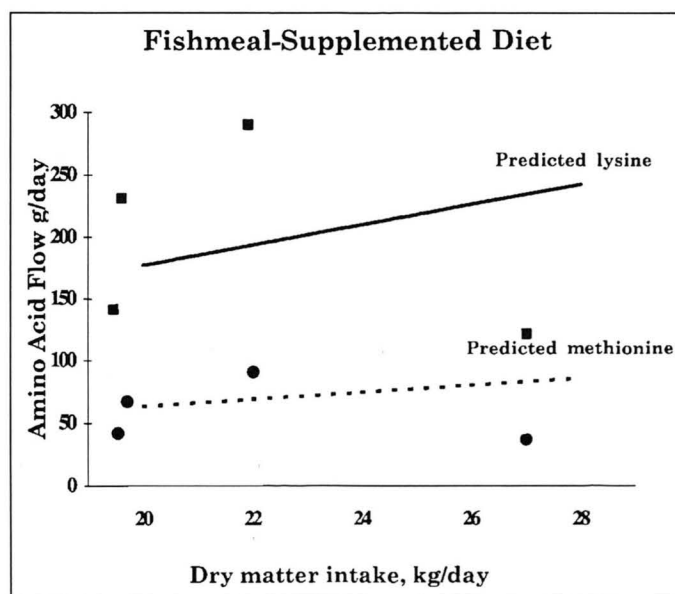
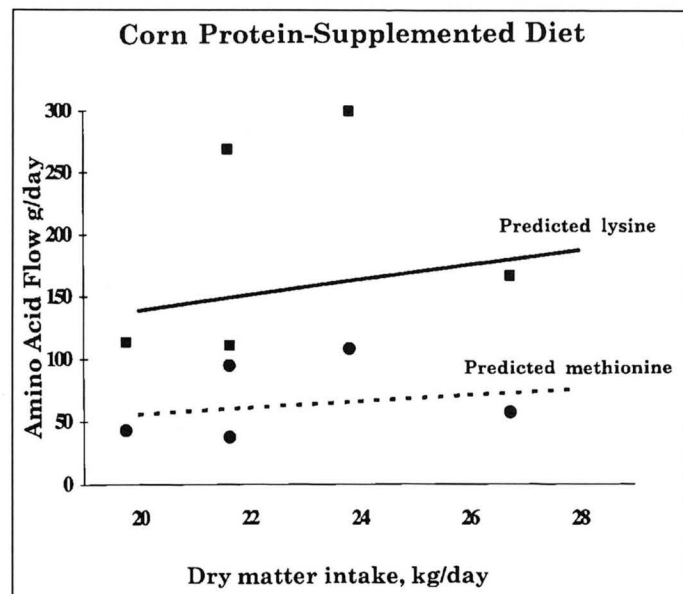


Figure 2. Duodenal flow of lysine (solid line) and methionine (dashed line) as predicted by CNCPS with increasing dry matter intake of corn gluten/corn distillers' grains-supplemented diet. Actual measurements of duodenal lysine (■) and methionine (●) flow from cannulated cows are superimposed.



diet. Figures 1 and 2 demonstrate the impact of dry matter intake on amino acid flow as predicted by the model for FM and CGD diets. Scattered over the model's regression lines are individual cow measurements from this study. In addition to differences in dry matter in-

take, variability among cows and within feedstuffs has a large impact on the ability to predict amino acid flow to the intestine.

Computer models of amino acid flows can help in the prediction of response to UIP and to amino acid supplements. This may be particularly true in high-producing herds or herds treated with bovine somatotropin. At the present time, reliability may be hindered by variability in feedstuffs and among cows, and by unanticipated effects on microbial protein production.

References

1. National Research Council, 1989. Nutrient requirements of dairy cattle, 6th revised edition. National Academy Press, Washington, D.C.
2. McGuffey, R.K., and J.I.D. Wilkinson, 1991. Nutritional implications of bovine somatotropin for the lactating dairy cow. *J. Dairy Sci.*:74(Supl. 2):63-71.
3. Choung, J. and D.G. Chamberlain. 1992. Protein nutrition of dairy cows receiving grass silage diets. The effects of post-ruminal supplements of proteins and amino acids. *J. Sci. Food Agric.* 60:25-30.
4. Schwab, C.G., C.K. Bozak, N.L. Whitehouse, and M.M.A. Mesbah, 1992. Amino acid limitation and flow to duodenum at four stages of lactation. 1. Sequence of lysine and methionine limitation. *J. Dairy Sci.* 75:3486-3502.
5. Schwab, C.G., C.K. Bozak, N.L. Whitehouse, and V.M. Olson. 1992. Amino acid limitation and flow to the duodenum at four stages of lactation. 2. Extent of lysine limitation. *J. Dairy Sci.* 75:3503-3518.
6. 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.
7. 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.

Postpartum Pathologic Changes Associated With a Palpable Uterine Lumen in Dairy Cattle

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Abstract

Clinicians at the Veterinary Teaching Hospital at Colorado State University have determined that approximately 5% of all dairy cows have a palpable uterine lumen (PUL) at 28-42 days postpartum. The tubular structure of these uteri is collapsible and the inner walls of the uterine horns are distinguishable by palpation; however, fluid accumulation is not apparent. Delayed involution or subclinical endometritis is suspected. Fifteen Holstein cows with a PUL at first postpartum reproductive exam were matched for parity and stage of lactation with 15 cows with normal reproductive tracts during the same postpartum exam. Blood samples were collected from all cows and all uteri were cultured, flushed with lactated Ringer's solution, and biopsied. Complete blood counts

revealed that all cows were in normal health during the trial. Aerobic and/or facultative anaerobic bacteria were isolated from 14 of 15 cows with PUL and 13 of 15 cows with normal uteri. Nonhemolytic streptococci, coliforms and *A. pyogenes* were the most common isolates; however, the incidence of uterine infection did not differ ($P>0.50$) between the two groups. Uterine flush samples from 6 cows (5 PUL, 1 normal) contained elevated mixed populations of degenerative and nondegenerative neutrophils, evidence of an inflammatory response. Uterine tissue specimens were scored according to a modified grading system based on a mare endometrial biopsy scoring system. Scores $\geq 2A$ were assigned to 9 cows with a PUL and only 4 cows with normal uteri. These data indicate that diagnosis of PUL at postpartum examination is likely to identify cows with severe inflammatory changes.