Model to Predict Absorbed Amino Acid Supply at the Proximal Duodenum in Growing Beef Cattle

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ABSTRACT : Five crossbred beef cattle (Simmental×yellow cattle, Shantung Province) fitted with permanent cannulae in the rumen and T-type cannulae at the proximal duodenum and terminal ileum, were fed five different diets containing corn, cotton meal or soybean meal and ammoniated straw to determine the dry matter, crude protein and amino acid flows in duodenal and ileum digesta, and to calculate the regression equations between theoretical and experimental concentration of AA in duodenal digesta. The results showed that there was a strong correlation between experimental (g/d, y) and theoretical CP flows (g/d, x) at the proximal duodenum, the R^2-value regression equation of crude protein is very high (0.9636). The R^2-value regression equation of the limiting amino acid (such as Met or Lys) is high (0.7573 or 0.9252 respectively). This results indicated that we can formulate better diets fed to beef cattle according to the theoretical amino acid concentration. A mathematical model has been successfully constructed for predicting the supply of absorbed amino acids at the proximal duodenum in growing beef cattle. ***(Asian-Aust. J. Anim. Sci. 2005. Vol 18, No. 3 : 358-363)***

Key Words : Growing Beef Cattle, Absorbed Amino Acid, Supply, Predictive Model

INTRODUCTION

In ruminants, proteins and amino acid (AA) are first subject to microbial degradation in the rumen making it difficult to predict the quality and quantity of AA that are absorbed by the animal. A number of studies have shown that the amino acid (AA) profile of absorbable proteins can vary widely according to diet and may not always be the best adapted for optimal performance and efficiency in ruminants (see review by Rulquin and Verite,1993). In order to control the flow of metabolizable AA and so utilize feeds to the best, it is of prime importance that the AA composition of duodenal digesta be predicted. Several attempts have been made to estimate the amounts of individual AA flowing to or being absorbed in the small intestine (Gabel and Poppe, 1986; Hvelplund and Madsen, 1989).

Since ruminant production is dependent on the supply of specific limiting AAs (Clark et al., 1992; Merchen and Titgemeyer, 1992), it is of interest to evaluate the relation between feedstuff characteristics and the profile of AA flow to the duodenum. The AA passage to the duodenum can be calculated (Clark et al., 1987), assuming that the AA profile of rumen undegraded protein (RUP) reflects feedstuffs' AAs profile of duodenal CP, and by using data on the relative amounts of RUP and microbial protein (MCP) and their composition. According to our research basis, a mathematical model had been successfully constructed to estimate the amino acid requirements for growing Taihe silky fowls in early stage (Li et al., 2003). So the objectives of this experiment were to establish another predictable model of the absorbed amino acid supply at the proximal duodenum in growing beef cattle, including in experimental and in theoretical calculations of the duodenal AA profile.

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MATERIALS AND METHODS

Animals and diet

Five crossbred beef cattle fitted with permanent cannula having an internal diameter of 10 cm in the rumen and T-type cannula having an internal diameter of 2 cm at the proximal duodenum and terminal ileum, aged 4 to 5 yr, weight 590±10 kg, were used in this study. The experiment comprised five 21 d periods, each consisting of 14 d of adaptation and 7 d of sampling. Five cattles were fed the same diet at the same period, including five different feeding levels. The procedures and protocols were approved by the University animal care and use committee. The ration was offered twice daily at 08:00 and 20:00 and there was free access to water at all times. The beef cattles were fed the five different level diets (Table 1) in five experiments respectively. Briefly, the diets were formulated to contain (DM basis) 10.50% CP, 10.70% CP, 7.66% CP, 14.40% CP, 12.25% CP, and other nutrients to be short of or exceed NRC (1996) recommendations, respectively.

Sample collection and analyses

Feed samples were collected twice weekly before the morning feeding (i.e. 08:00). Samples were stored at -20°C until analyzed. Acid-insoluble ash (AIA) was determined as an indigestible marker of digesta flow. Duodenal and ileal

Table 1. Ingredients and nutrient composition of diets at five different feeding levels (percentage of DM)

Item	Exp. 1	Exp. 2	Exp. 3	Exp. 4	Exp. 5
Ingredient (% DM basis)					
Corn	66.99	44.38	9.06	41.85	42.00
Cotton meal	7.31	10.36	-	-	-
Soybean meal	-	-	-	13.67	9.00
Additive[a]	0.70	0.70	0.70	0.70	0.70
Aminated straw	25.00	44.56	90.24	43.78	48.30
Chemical composition					
ME(MJ/kg DM)	11.50	10.04	6.92	11.41	10.94
CP (% DM basis)	10.50	10.70	7.66	14.40	12.25
NDF (%DM basis)	28.50	40.40	63.90	43.41	45.75
OM (% DM basis)	91.40	88.95	84.95	83.64	83.02
Feed intake (kg DM/d)	7.92	6.49	6.36	7.18	8.97

[a] Containing: 95.40% NaCl, 2.50% $ZnSO_4$, 1.25% $MnSO_4$, 0.85% $CuSO_4$.

samples were taken on the last 3 d of the experimental period at 3 h intervals with collection times advanced 1 h each day to provide one sample for every 1-h interval in a 24 h period. The digesta were immediately frozen at -20°C and composited by steer within period. Prior to analysis, digesta samples were thawed and homogenized using an Ultra-Torrax (Germany) homogenizer for 2 min and representative samples were lyophilized and ground (1 mm screen). Fecal grab samples (approximately 200 g) were collected on d 19 to 21 at 6 h intervals, immediately frozen (-20°C), and composited by steer. Fecal samples were oven-dried at 55°C at least 72 h and ground (1 mm screen).

Experimental parameters measurement

The amount of DM in feedstuffs was determined by drying at 105°C for 24 h. The OM, NDF, and CP (6.25×N) (AOAC, 1984) were measured for all dried samples. All residues were analyzed for essential amino acids (EAA: methionine, lysine, threonine, arginine, isoleucine, leucine, valine, histidine and phenylalanine) and nonessential amino acids (NEAA: cysteine,glycine, serine, proline, alanine, aspartate and glutamate) based on the AOAC method number 994.12 (Llames and Fontaine, 1994). Methionine and cysteine were analyzed after oxidation according to AOAC method number 994.12 (Llames and Fontaine, 1994). AIA contents of feedstuff and duodenal and ileal and feces were determined as AOAC (1984) described and nutrient flows within the gastrointestinal tract were calculated by reference to AIA and nutrient concentrations (grams/gram of DM) at respective site.

Statistical analysis

Calculation of DM flow in duodenal or ileal digesta :

DM flow=(the whole AIA weight in feedstuff×the rate of AIA callback in fecal)/the whole AIA weight in digesta DM

Table 2. CP and TAA intakes (g/d) and TAA composition (g/100 g TAA) of five different feeding levels

	Exp. 1	Exp. 2	Exp. 3	Exp. 4	Exp. 5
CP (g/d)	830.70±15.32	694.56±13.24	487.22±17.52	1,033.89±20.68	1,089.67±16.56
TAA[1] (g/d)	729.92±11.52	594.80±9.86	302.51±7.45	802.79±16.53	766.93±13.58
TAA/CP	0.88	0.86	0.62	0.78	0.70
TAA composition (g/100 g TAA)					
TAA	100	100	100	100	100
TEAA	42.71	42.42	38.62	41.40	41.38
NEAA	57.29	57.58	61.38	58.60	58.62
Asp	8.28±0.86[a]	9.68±0.44[a]	9.81±0.53[a]	9.26±0.73[a]	9.18±0.72[a]
Ser	5.53 ±0.45[a]	6.06±0.65[a]	6.44±0.46[a]	4.68±0.43	4.71±0.50[a]
Glu	19.23±0.96[a]	18.19±0.98[a]	17.91±0.88[a]	19.14±1.21[a]	18.92±0.93[a]
Thr	4.06±0.32 [a]	4.12±0.32[a]	5.03±0.29	3.85±0.44[a]	3.95±0.40[a]
Gly	4.26±0.43 [a]	4.39±0.44[a]	5.64±0.37[a]	4.45±0.45[a]	4.52±0.59[a]
Arg	5.98±0.66[a]	7.21±0.54[a]	4.36±0.49[a]	5.45±0.59[a]	5.11±0.68[a]
Ala	7.11±0.75[a]	6.66±0.56	8.84±0.66[a]	6.90±0.64[a]	7.37±0.75
Tyr	2.98±0.23[a]	1.74±0.11[a]	1.92±0.13[a]	4.81±0.38	4.77±0.52[a]
Pro	7.20±0.76[a]	6.37±0.64[a]	5.54±0.69[a]	7.41±0.77[a]	7.27±0.71
Val	4.45±0.25	4.96±0.43	5.07±0.38	3.91±0.39[a]	4.13±0.26[a]
Phe	5.22±0.76	5.16±0.61	4.26±0.41[a]	5.36±0.50	5.43±0.79
Ile	3.19±0.49	3.07±0.28	3.15±0.29[a]	4.15±0.49[a]	4.19±0.58[a]
Leu	9.64±0.55[a]	8.79±0.71[a]	8.18±0.77[a]	9.61±0.87	9.83±0.81
His	3.15±0.16[a]	2.67±0.18[a]	1.67±0.12[a]	2.70±0.25	2.62±0.24
Lys	3.17±0.41[a]	3.15±0.25[a]	3.57±0.38[a]	4.33±0.63[a]	4.12±0.37[a]
Met	2.56±0.28[a]	2.12±0.22	1.72±0.19	2.04±0.40	1.99±0.19
Cys	2.21±0.37	3.58±0.32	2.57±0.21	1.96±0.11	1.88±0.23

[a, b] Means the same AA between Table 2 and Table 3 with different superscripts are significantly different ($t<0.05$).

EAA: Met, Lys, His, Leu, Ile, Phe, Val, Arg, Thr. NEAA: Cys, Pro, Tyr, Ala, Ser, Glu, Gly, Asp.

[1] TAA: except for Trp.

Table 3. Duodenal CP and TAA flows (g/d) and TAA composition (g/100 g TAA) of five different feeding levels

	Exp. 1	Exp. 2	Exp. 3	Exp. 4	Exp. 5
CP (g/d)	909.11±21.50	664.61±18.21	506.78±25.28	879.47±29.37	1,106.29±21.55
TAA[1] (g/d)	741.21±18.69	503.02±15.97	339.92±12.78	729.79±24.19	863.24±30.51
TAA/CP	0.82	0.76	0.67	0.83	0.78
TAA composition (g/100 g TAA)					
TAA	100	100	100	100	100
TEAA	43.26	44.37	44.68	43.53	42.75
NEAA	56.74	55.63	55.32	56.47	57.25
Asp	9.70±0.78[b]	10.28±0.69[b]	11.01±0.91[b]	8.70±0.67[b]	8.76±0.89[b]
Ser	6.03±0.56[b]	5.68±0.67[b]	5.85±0.49[b]	4.59±0.58	4.47±0.91[b]
Glu	15.97±0.89[b]	15.78±0.81[b]	14.14±0.59[b]	16.83±0.81[b]	16.41±0.79[b]
Thr	4.61±0.52[b]	4.96±0.41[b]	5.37±0.49	4.59±0.76[b]	4.55±0.46[b]
Gly	6.12±0.38[b]	6.52±0.46[b]	6.84±0.39[b]	5.37±0.57[b]	5.74±0.45[b]
Arg	4.34±0.49[b]	4.86±0.36[b]	3.94±0.38[b]	3.89±0.43[b]	3.89±0.39[b]
Ala	6.57±0.59[b]	6.43±0.51	6.53±0.67[b]	7.60±0.75[b]	7.05±0.56
Tyr	3.42±0.39[b]	2.79±0.11[b]	3.01±0.24[b]	5.10±0.41	5.60±0.35[b]
Pro	6.73±0.47[b]	5.71±0.32[b]	5.12±0.28[b]	6.36±0.57[b]	7.05±0.72
Val	4.66±0.44	4.32±0.41	4.77±0.39	4.78±0.42[b]	4.61±0.37[b]
Phe	5.07±0.41	4.76±0.29	5.45±0.39[b]	5.35±0.46	5.29±0.64
Ile	3.12±0.30	3.69±0.36	4.15±0.29[b]	4.91±0.51[b]	4.77±0.38[b]
Leu	9.17±0.76[b]	7.99±0.49[b]	6.94±0.48[b]	9.96±0.57	9.82±0.51
His	3.88±0.45[b]	4.13±0.28[b]	4.32±0.34[b]	2.68±0.35	2.35±0.44
Lys	4.91±0.46[b]	5.53±0.36[b]	5.50±0.42[b]	5.21±0.49[b]	5.25±0.41[b]
Met	1.57±0.15[b]	1.80±0.13	2.05±0.16	2.16±0.24	2.22±0.28
Cys	2.27±0.21	2.44±0.29	2.83±0.14	2.04±0.19	2.19±0.17

[a, b] Means the same AA between Table 2 and Table 3 with different superscripts are significantly different ($t<0.05$).
EAA: Met, Lys, His, Leu, Ile, Phe, Val, Arg, Thr. NEAA: Cys, Pro, Tyr, Ala, Ser, Glu, Gly, Asp.
[1] TAA: except for Trp.

The rate of AIA callback in fecal = (the whole AIA weight in fecal DM×the whole fecal DM/d)/the whole AIA weight in feedstuff DM

Calculation of CP, TEAA, NEAA and individual EAA flow for duodenal or ileal or fecal sample :

CP flow = DM flow×the percentage of CP in digesta DM (take CP as an example)

Quantity of proteins flowing into the small intestine : The PDI system (INRA, 1989) was used as a basis for the present model to predict the amount of true protein flowing into the small intestine (PI). The amount of PI associated with each feed was calculated as the sum of three protein fractions according to their origin: i) dietary protein undegraded in rumen (PIA); ii) microbial protein synthesized in the rumen (PIM); iii) endogenous protein from digestive secretions and cell turnover (PIendo). Intestinal flows were computed from the chemical and digestive characteristics of individual feeds:

$$PIA = CP \times 1.11 \times (1\text{-}DT)$$

$$PIM = 145 \times FOM \times 0.8$$

$$PIendo = 33 \times NDOM \times 0.5$$

$$PI = PIA + PIM + PIendo$$

Where, PIA, PIM, PIendo, PI, CP are expressed in g kg^{-1} DM; DT (g g^{-1})=proportion of CP theoretically degraded in the rumen, as assessed using the in sacco procedure and postulating a 6% h^{-1} rumen particle outflow rate; FOM (Organic Matter Fermentable in the rumen, kg kg^{-1} DM)=DOM-fat-fermentation products-by-pass dietary protein; NDOM (kg kg^{-1} DM)=OM not digested in the entire digestive tract, on the assumption that: true protein by-pass proportion =1.11×(1-DT) (INRA, 1989), microbial protein yield=145 g CP kg^{-1} FOM (INRA, 1989), endogenous protein=33 g CP kg^{-1} NDOM (INRA, 1989), AA content=0.8 for microbial protein (INRA, 1989) and 0.5 for endogenous protein (mean of values given by Guilloteau, 1986; Orskov et al., 1986).

Calculation of the amino acid profile of duodenal digesta : For a given diet, the theoretical intestinal flow of individual AA ($_tAAI$) and their proportion ($_t[AAI]$) were calculated according to the following equations (taking Lys as an example).

$$_tLys\ I = \Sigma_f\{(PI\ A_f \times [Lys\ A]_f + PIM_f \times [Lys\ M] + Piendo_f \times [Lysendo]) \times DM\ I_f\}$$

Table 4. Duodenal CP and TAA theoretical flows (g/d) and TAA composition (g/100 g TAA) of five different feeding levels

	Exp. 1	Exp. 2	Exp. 3	Exp. 4	Exp. 5
CP (g/d)	935.0±14.11	730.0±10.58	482.5±16.34	951.6±15.88	1,088.5±11.75
TAA[1] (g/d)	918.2±13.72	714.83±16.38	465.66±13.19	892.13±16.95	1,005.43±20.15
TAA/CP	0.98	0.98	0.97	0.94	0.92
TAA composition (g/100 g TAA)					
TAA	100	100	100	100	100
TEAA	44.45	44.62	44.41	44.29	43.06
NEAA	55.55	55.38	55.59	55.71	56.94
Asp	9.39±0.78	10.09±0.75	11.18±0.68	10.26±0.79	10.79±0.90
Ser	4.70±0.35	4.89±0.45	5.49±0.38	5.02±0.39	5.24±0.41
Glu	16.99±0.81	16.93±0.88	15.17±0.91	16.68±0.79	17.43±0.97
Thr	4.73±0.57	4.95±0.64	5.67±0.46	4.97±0.51	5.10±0.39
Gly	4.71±0.52	4.97±0.35	5.86±0.65	4.91±0.46	5.09±0.43
Arg	4.84±0.36	5.18±0.48	4.76±0.41	4.47±0.44	4.70±0.49
Ala	7.93±0.59	7.76±0.51	8.42±0.49	7.41±0.43	7.57±0.55
Tyr	3.78±0.29	3.63±0.33	3.60±0.39	3.87±0.41	3.43±0.46
Pro	7.06±0.66	6.18±0.61	5.00±0.45	6.43±0.41	6.32±0.43
Val	5.19±0.62	5.39±0.48	5.70±0.53	5.28±0.38	3.46±0.46
Phe	5.51±0.42	5.44±0.37	4.94±0.64	5.27±0.31	5.27±0.41
Ile	4.62±0.41	4.71±0.29	4.86±0.34	4.95±0.42	5.01±0.36
Leu	9.70±0.61	8.87±0.71	8.18±0.49	9.61±0.38	9.42±0.51
His	2.43±0.28	2.30±0.21	1.97±0.19	2.39±0.15	2.34±0.16
Lys	5.03±0.23	5.41±0.32	6.21±0.34	5.19±0.42	5.51±0.39
Met	2.39±0.16	2.37±0.14	2.11±0.21	2.16±0.11	2.24±0.21
Cys	0.98±0.09	0.93±0.13	0.86±0.07	1.12±0.08	1.08±0.12

EAA: Met, Lys, His, Leu, Ile, Phe, Val, Arg, Thr. NEAA: Cys, Pro, Tyr, Ala, Ser, Glu, Gly, Asp.
[1] TAA: except for Trp.

$${}_t[\text{Lys I}] = 100\times({}_t\text{Lys I}/\Sigma_{it}\text{AA I}_i)$$

where: ${}_t$Lys I = theoretical flux of Lys in the small intestine (g d^{-1}); ${}_t$AA I = theoretical flux of each AA in the small intestine (g d^{-1}); ${}_t$[Lys I] = theoretical concentration of Lys in the small intestine (g 100 g^{-1} of AAT); [Lys A],[Lys M],[Lysendo] = assumed concentration of Lys, in protein from rumen undegraded feed (A), microbial (M), and endogenous (endo) origins respectively, (g 100 g^{-1} of AAT); PIA_f , PIM_f, $PIendo_f$ = content of rumen undegraded, microbial, and endogenous protein, respectively, for each foodstuff (g kg^{-1} DM); DMI_f = ingested DM of each foodstuff (kg d^{-1}); i = i^{th} AA; f = f^{th} foodstuff of the diet (Rulquin et al., 1998).

All the data were analyzed statistically according to the *t*-test procedure (SAS Institute, 1985). The results were expressed as means±SD, differences of $t<0.05$ were considered significant.

RESULTS

Table 2 depicts the TAA percentage of crude protein that is 0.88, 0.86, 0.62, 0.78 and 0.70 at five different diets respectively. Table 3 depicts the TAA percentage of crude protein that is 0.82, 0.76, 0.67, 0.83 and 0.78 at duodenum respectively. The TAA/CP value between diet and duodenum were affected significantly by dietary composition ($t<0.05$). In the experiment 3, the TEAA percentage of TAA between diet and duodenum was affected significantly by feeding low protein feedstuff ($t<0.05$).

Intakes, flow and essential AA (EAA) and nonessential AA in the small intestine are presented in Table 3. The overall profile of AA flow to the duodenum was affected significantly by rumen degradation and microbial synthesis. The Asp, Thr, Gly, Tyr, His and Lys percentage of TAA to the duodenum was higher than dietary individual AA percentage of TAA with diets supplemented with cotton meal ($t<0.05$) (Exp. 1 and Exp. 2). On the contrary, The Glu, Arg, Pro and Leu percentage of TAA to the duodenum was lower than dietary individual AA percentage of TAA. For the soybean meal diet (Exp. 4 and Exp. 5), The Thr, Gly, Val, Ile and Lys percentage of TAA to the duodenum was higher than dietary individual AA percentage of TAA ($t<0.05$). Similarly, The Asp, Glu and Arg percentage of TAA to the duodenum was lower than dietary individual AA percentage of TAA.

Table 4 showed the duodenal CP and TAA theoretical flows (g/d) and TAA composition (g/100 g TAA) of five different feeding levels, and Table 5 depicted the regression equations between theoretical and experimental concentration of AA in duodenal digesta. The results

Table 5. Theoretical and experimental concentration of AA in duodenal digesta (g/100 g TAA)

	Theoretical concentration	Experimental concentration	Regression equation
CP (g/d)	837.51±20.13	813.25±18.24	y_{cp}= 0.9647x_{cp}+5.2998 (R^2=0.9636, n=5)
TAA[1] (g/d)	799.25±11.56	634.36±10.28	y_{TAA}= 0.9667x_{TAA}-138.26 (R^2=0.9761, n=5)
TEAA	44.17	43.70	y_{TEAA}= 1.0852x_{TEAA}-4.0195(R^2=0.7698, n=5)
NEAA	55.83	56.30	y_{NEAA}= 0.9281x_{NEAA}+4.4674 (R^2=0.887, n=5)
Asp	10.34±0.67	9.69±0.56	y_{Asp}= 0.7275x_{Asp}+2.8943 (R^2=0.9964, n=5)
Ser	5.07±0.41	5.32±0.38	y_{Ser}= -3.1577x_{Ser}+20.864 (R^2=0.8474, n=5)
Glu	16.64±0.76	15.83±0.65	y_{Glu}= 0.9993x_{Glu}-1.0355 (R^2=0.995, n=5)
Thr	5.08±0.42	4.82±0.38	y_{Thr}= 0.8055x_{Thr}+0.7977 (R^2=0.8381, n=5)
Gly	5.11±0.23	6.12±0.32	y_{Gly}= 0.5563x_{Gly}+3.6117 (R^2=0.8692, n=5)
Arg	4.79±0.41	4.18±0.21	y_{Arg}= 1.5039x_{Arg}-3.0157 (R^2=0.8366, n=5)
Ala	7.82±0.35	6.84±0.46	y_{Ala}= -0.9182x_{Ala}+14.018 (R^2=0.5247, n=5)
Tyr	3.66±0.29	3.98±0.34	y_{Tyr}= 6.9071x_{Tyr}-22.162 (R^2=0.8235, n=5)
Pro	6.20±0.31	6.20±0.41	y_{Pro}= 0.7962x_{Pro}+1.0732 (R^2=0.9207, n=5)
Val	5.01±0.24	4.63±0.51	$y_{Va;}$= 0.0758$x_{Va;}$+4.3453 (R^2=0.5597, n=5)
Phe	5.29±0.42	5.18±0.38	y_{Phe}= -0.6437x_{Phe}+8.6589 (R^2=0.9308, n=5)
Ile	4.83±0.28	4.13±0.21	y_{Ile}= 4.4403x_{Ile}-17.329 (R^2=0.9509, n=5)
Leu	9.16±0.52	8.78±0.43	y_{Leu}= 1.8759x_{Leu}-8.4109 (R^2=0.8723, n=5)
His	2.29±0.15	3.47±0.18	y_{His}= 16.142x_{His}-35.564 (R^2=0.8962, n=5)
Lys	5.47±0.35	5.28±0.36	y_{Lys}= 0.2726x_{Lys}+3.7932 (R^2=0.9252, n=5)
Met	2.25±0.21	1.96±0.18	y_{Met}= 1.2476x_{Met}-0.6167 (R^2=0.7573, n=5)
Cys	0.99±0.08	2.35±0.15	y_{Cys}= -2.571x_{Cys}+4.911 (R^2=0.8702, n=5)

Abbreviations used: R^2, coefficient of determination.
EAA: Met, Lys, His, Leu, Ile, Phe, Val, Arg, Thr. NEAA: Cys, Pro, Tyr, Ala, Ser, Glu, Gly, Asp. [1] TAA: except for Trp.

Abbreviation

TAA: Total amino acid
EAA: Essential amino acid
NEAA: Non-essential amino acid
PI: Protein intestine
TDN: Total digestible nutrient
Ala: Alanine
Cys: Cystine
His: Histidine
Lys: Lysine
Pro: Proline
Trp: Tryptophan
FOM: Fermentation organic matter
TEAA: Total essential amino acid
DM: Dry matter
OM: Organic matter
UDP: Undegraded protein
Arg: Arginine
Glu: Glutamate
Ile: Isoleucine
Met: Methionine
Ser: Serine
Tyr: Tyrosine
NDOM: Non-digestible organic matter
ADG: Average daily gains
CP: Crude protein
NDF: Neutral detergent fibre
AIA: Acid insoluble ash
Asp: Aspartate
Gly: Glycine
Leu: Leucine
Phe: Phenylalanine
Thr: Threonine
Val: Valine

showed that the duodenal CP and TAA theoretical flows tended to be slightly higher than those of experimental flows on the average.

The theoretical concentration of Ser, Gly, Tyr, His and Cys was higher than that of experimental concentration. The theoretical concentration of Asp, Glu, Thr, Arg, Ala, Val, Phe, Ile, Leu, Lys and Met was lower than that of experimental concentration (Table 5). The theoretical concentration of Pro was identical to that of experimental concentration. Except for Ala and Val, individual AA of experimental data was predicted with a high degree of confidence ($0.7573<R^2<0.9964$).

DISCUSSION

Amount of AA passing into the small intestine

As we all know, the amount of AA passing into the small intestine includes three parts of protein resources (microbial protein, undegraded feed protein and endogenous protein).

Microbial amino acid profile

Given the large amount of microbial CP that passes into the small intestine (34 to 89% of duodenal NAN in dairy cows) (Clark et al., 1992), the AA composition of ruminal microorganisms is decisive to the determination of the AA profile of intestinal proteins. For instance, with high levels of DMI, the flow of microbial proteins would be underestimated (Ramangasoavina and Sauvant, 1993). It has long been recognized that the AA profile of bacteria isolated from the rumen was remarkably constant (Bergen et al., 1968; Storm and Orskov, 1983; Arambel et al., 1987). However, recent reports (Clark et al., 1992) have indicated large variations in the AA composition of bacteria. These variations are mainly due to the chemical and physical

methods used to characterize bacteria, but they may arise from the distribution of bacterial species in the rumen. In this study, amino acid composition of intestinal microbial (Le Hénaff, 1991) was used.

Amino acid profile of undegraded feed protein : Data recently estimated by YAN et al. (2003) revealed a change in the AA profile of feeds induced by ruminal fermentation and this change would probably also vary between feeds. Indeed, there is good agreement between studies using the nylon bag technique (Titgemeyer et al., 1989; Le Hénaff, 1991; Erasmus et al., 1994; Yan et al., 2003) on the fact that protein residues in nylon bag have generally higher contents of branched chain AA, Thr and lower contents of His and Arg than original proteins. These differences can explain a part of the average underestimation of Leu and Ile and overestimation Arg observed with the factorial approach (Rulquin et al., 1998). In this model, experimental data of AA profile of each original feed residue using nylon bag technique were used. The AA profile of endogenous protein (Orskov et al., 1986) was used.

Overall, the high R^2-values for regression equation imply that the model performed adequately in predicting observed duodenal essential amino acids and non-essential amino acids.

IMPLICATIONS

A model has been presented for predicting the supply of absorbed amino acids at the proximal duodenum in growing beef cattle (Table 5). So nutrition scientists can formulate the better diet fed to beef cattle according to the profile AA of the each feedstuff. This study demonstrated that development of an accurate theoretical model needs more research on AA composition of microbial and by-pass protein. Effective supplementation of limiting amino acids (such as Met or Lys) may result in the following benefits to the cattle industry: 1) increased weight gains for growing beef cattle, 2) increases in the efficiency of protein utilization, and 3) lowered feed costs lower protein contents of diets.

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