



Ability of commercially available dairy ration programs to predict duodenal flows of protein and essential amino acids in dairy cows

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ABSTRACT

The objective of this analysis was to compare the rumen submodel predictions of 4 commonly used dairy ration programs to observed values of duodenal flows of crude protein (CP), protein fractions, and essential AA (EAA). The literature was searched and 40 studies, including 154 diets, were used to compare observed values with those predicted by AminoCow (AC), Agricultural Modeling and Training Systems (AMTS), Cornell-Penn-Miner (CPM), and National Research Council 2001 (NRC) models. The models were evaluated based on their ability to predict the mean, their root mean square prediction error (RMSPE), error bias, and adequacy of regression equations for each protein fraction. The models predicted the mean duodenal CP flow within 5%, with more than 90% of the variation due to random disturbance. The models also predicted within 5% the mean microbial CP flow except CPM, which overestimated it by 27%. Only NRC, however, predicted mean rumen-undegraded protein (RUP) flows within 5%, whereas AC and AMTS underpredicted it by 8 to 9% and CPM by 24%. Regarding duodenal flows of individual AA, across all diets, CPM predicted substantially greater (>10%) mean flows of Arg, His, Ile, Met, and Lys; AMTS predicted greater flow for Arg and Met, whereas AC and NRC estimations were, on average, within 10% of observed values. Overpredictions by the CPM model were mainly related to mean bias, whereas the NRC model had the highest proportion of bias in random disturbance for flows of EAA. Models tended to predict mean flows of EAA more accurately on corn silage and alfalfa diets than on grass-based diets, more accurately on corn grain-based diets than on non-corn-based diets, and finally more accurately in the mid range of diet types. The 4 models were accurate at predicting mean dry matter intake.

The AC, AMTS, and NRC models were all sufficiently accurate to be used for balancing EAA in dairy rations under field conditions.

Key words: dairy ration program, duodenal flow, essential amino acid, protein

INTRODUCTION

For most dairy producers, protein supplementation represents a large fraction of the cost of dairy rations. Currently, many herds are fed diets containing excess CP, resulting in inefficient N use and more N excreted to the environment. Whether greater dietary protein concentrations are fed to ensure sufficient AA supply or as insurance against possible ingredient deficiency is not clear. It is possible to maintain high milk production (>40 kg/d) on diets of approximately 15% CP with a resulting reduction in N excretion compared with an 18.5% CP diet, when balanced for AA supply rather than CP level (Broderick et al., 2008). However, this result is not consistently obtained (Broderick et al., 2009), and a possible explanation may be inadequate AA supply with the low CP diet due to inaccurate estimation of the supply of total protein or digestive flow of some individual essential AA (EAA). Nutritionists are also concerned that models have been developed mostly using corn-based diets, and therefore may only predict well for high grain diets and are less accurate on low concentrate diets or diets based on forages other than corn silage and alfalfa.

Numerous models of rumen and animal metabolism with different degrees of mechanistic representation have been authored and used around the world (e.g., Baldwin et al., 1987; Dijkstra et al., 1992; Sniffen et al., 1992; Lescoat and Sauvant, 1995; Fox et al., 2004). All of these models can predict protein flow from the rumen based on ration composition and intake but, with the exception of the Cornell Net Carbohydrate-Protein System (CNCPS), are generally considered too complicated for field use. Four models, derived in various ways from the models referred to above, are designed

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to predict MP and metabolizable (or digested) AA and are widely used commercially in North America. They are (1) AminoCow (**AC**) version 3.5.2; Evonik AG Industries, Hanau, Germany; (2) Agricultural Modeling and Training Systems LLC (**AMTS**) version 2.0.15, Cortland, NY; a variation of the CNCPS; (3) Cornell-Penn-Miner (**CPM**), an earlier variation of CNCPS, version 3.0.1, published by Cornell University, Ithaca, NY; University of Pennsylvania, Philadelphia, PA; Miner Institute, Chazy, NY; and University of Maryland, College Park, cooperating; and (4) Nutrient Requirements of Dairy Cattle (NRC, 2001; 7th rev. ed., version 1.01) published by the National Research Council, Washington, DC (**NRC**). The CPM model is an early commercial version of the CNCPS (Sniffen et al., 1992; Fox et al., 2004) but is still widely used and thus is included in this evaluation. The AMTS model represents one of the newest commercially available versions of CNCPS. Despite their wide usage and published comparisons for some nutrient predictions among CNCPS (Kohn et al., 1998; Kolver et al., 1998; Von Keyserlingk et al., 1999) and other models (Bate-man et al., 2001; Yu et al., 2003; Patton, 2010), to our knowledge, these models have not been compared for their ability to predict duodenal flow of total CP, microbial CP, RUP, and EAA on a broad set of dairy rations. Despite validation of these different models by researchers before release, a straight comparison of their predictions may provide impetus for greater use of AA balance among field nutritionists should these models be proven to accurately predict the duodenal flow of protein fractions and EAA across a wide range of feeding conditions.

Therefore, the purposes of this study were (1) to compare predictions of duodenal CP, its distribution between microbial CP and RUP, and EAA flows with those reported in the literature; and (2) to identify if any diet types affected the accuracy of prediction among models.

MATERIALS AND METHODS

Google Scholar and Agricola databases were searched for studies published in refereed journals that reported treatment means of CP, microbial CP, RUP, and individual EAA flows to the duodenum. Only studies that utilized dietary treatments were included in this data set. This resulted in final identification of 40 separate studies representing 154 diets; the references are listed in the Appendix. All information for feed amounts, milk production, and BW were entered into the 4 models. When BW was not reported or could not be calculated (4 studies), default BW were taken from the NRC model for the parity reported. In studies in which

mixed parities were reported, second lactation was entered in the models. Likewise, BCS was entered when reported; otherwise, a BCS of 2.75 was assumed. Virtually all studies reported total ration CP, NDF, NE_L , and OM, or these values could be calculated from other information in the study. Nutrient composition for individual feed ingredients was entered if reported. When a nutrient of an individual feed was unreported, the NRC default values for CP, NDF, ADF, ether extract, neutral detergent insoluble CP, acid detergent insoluble CP, lignin, and ash were used. When nutritional composition of feed ingredients was not reported, forage nutrient composition was adjusted to match the total nutrient composition reported for the diets. The specific model default values were used for protein fractions, degradation rates, passage rates, and EAA composition in the case of NRC, AMTS, and CPM, except that AA content was entered in NRC when provided. For the AC model RUP and EAA, default composition was used, unless AA composition was reported. For AMTS and CPM, the AA composition of the undegradable protein was not adjusted even when AA composition of the ingredients was reported because these programs both use AA values for undegraded protein and these values are not well reported in the literature. Rather than assuming erroneous calculations, the default values were used. Nutrient content entered into each model was the same except for diets in which animal proteins were fed. In this case, the NDF as calculated by AMTS and CPM differed from that in the other models. This is because AMTS and CPM report NDF for these feeds, whereas AC and NRC do not report these feeds as having cell wall constituents. However, because AMTS and CPM need these values to function, they were left unadjusted. The AC model provides the option to adjust the calculated MP based on the amount of rumen RDP; this option was used for all diets. The energy calculations were unadjusted for each model. Our purpose in standardizing feed nutrient composition was to measure differences in the model prediction of AA flow rather than to evaluate the influence of compositional differences in the model databases. The CP flow to the small intestine for the observed values was calculated as $NAN \times 6.25$. For observed data, microbial CP was estimated as $\text{microbial N} \times 6.25$; for simplicity, observed RUP flow was calculated as $(NAN \text{ flowing to the duodenum} - \text{microbial N}) \times 6.25$, and therefore includes contribution of endogenous secretions. The definition of protein fractions contributing to duodenal CP flow differed between models. For the AMTS and CPM model, duodenal CP flow was assumed to consist only of microbial CP plus RUP, the endogenous contribution being ignored (O'Connor et al., 1993; Fox et al., 2004; Tylutki et al., 2008), whereas for the AC and

NRC models, the presence of endogenous secretions was acknowledged and RUP was therefore calculated as [duodenal CP flow - (microbial CP + endogenous flow)]. Endogenous protein was calculated as $11.87 \times \text{DMI}$ for AC (Evonik Degussa GmbH, 2007a) and as $1.9 \times \text{DMI} \times 6.25$ for the NRC model (NRC, 2001). To allow comparison of similar terms, RUP is defined in the current analysis as the model-reported RUP plus the endogenous protein for the AC and NRC models, whereas for AMTS and CPM, RUP is defined as the model-reported RUP. The AC model does not directly predict AA intestinal flow, but because of an assumed constant digestibility of duodenal AA to metabolizable AA of 80%, duodenal flow was calculated as metabolizable AA/0.8 (Evonik Degussa GmbH, 2007b). Other fractions for all models were recorded as reported by the individual models.

To investigate the effect of various ration types and ingredient types on duodenal flows, diets were grouped as follows. Diet groups based on forage types were (1) diets in which grass was the major forage (more than 50% of forage DMI) whether offered as pasture, silage or hay ($n = 23$); (2) diets in which corn silage was the major forage ($n = 68$); (3) diets in which alfalfa, offered as either silage or hay, was the major forage ($n = 36$). Diets were grouped on major source of NFC as either corn grain-based diets, including high-moisture corn, dry rolled corn, cracked corn, steam-rolled corn, and ground corn ($n = 107$), or non-corn-based diets ($n = 43$). This group contained mostly grains such as ground barley, steam-rolled barley, and ground wheat, but also contained beet pulp and molasses. Diets were also categorized according to inclusion or not of RUP source for different types of protein normally thought of as providing high RUP. A significant number of diets had no RUP source added ($n = 60$). Diets used in this study were also stratified by DMI as low ($\text{DMI} < 17$ kg/d; $n = 45$) and high ($\text{DMI} > 22$ kg/d; $n = 42$) and by protein content into low CP ($14.5 \pm 1.2\%$ DM; $n = 41$), and high CP ($18.3 \pm 0.9\%$ DM; $n = 55$). Finally, diets were stratified by NDF content into low NDF ($27.1 \pm 2.1\%$ DM; $n = 48$), and high NDF ($38.3 \pm 4.9\%$ DM; $n = 55$).

Statistical analyses similar to that reported by Bateman et al. (2001) as modified by Pacheco et al. (2006) were applied. Briefly, observed and predicted values from the 4 models were compared using regression analyses from the Mixed procedure of SAS (version 8.0; SAS Institute Inc., Cary, NC), including study as a random effect (St-Pierre, 2001). Calculations of root mean square prediction error (**RMSPE**) and the relative prediction error (**RPE**: RMSPE as a percentage of the observed mean) as well as the decomposition of the mean square prediction error (**MSPE**) into mean

bias, regression bias, and random disturbance were as described by Bibby and Toutenburg (1977), also after the study effect was removed.

RESULTS

Three methods of evaluating models were considered: (1) the ability of models to predict the mean and standard error; (2) the size of RMSPE and RPE along with the appropriate apportionment of error into mean bias, regression or equation bias, and random bias; and (3) the linear regression of actual versus predicted values for closeness to unity. For presentation of results and discussion purposes, we are arbitrarily describing predictions within 5% of observed mean as very accurate, predictions within 10% as accurate, and predictions within 15% as acceptable. Outside this range, we considered model usefulness to be compromised. Descriptive statistics including means and ranges for production variables of animals in the studies used in the current analysis are reported in Table 1. Because the coefficient of determination (R^2) is high for all models and varies little, this will not be discussed in detail, although the R^2 will be reported for all protein fractions and EAA. Likewise, unless the models miss the mean by more than 15%, the apportionment of error will not be discussed, but will be presented in tabular form.

Across All Diets

Protein Fractions. Across all diet types, the prediction of mean CP flow to the duodenum was predicted within 5% of the observed flow with all models (Table 2). Both AC and NRC predicted slightly lower flows of microbial CP than were observed, whereas AMTS predicted slightly greater microbial CP flow. These 3 models were all very accurate, whereas CPM predicted mean microbial CP flows that were more than 25% greater than observed. All models underpredicted RUP, with NRC predicting within 5%, AC and AMTS within 10%, and CPM at 76% of observed RUP. For prediction of total CP flow, AMTS exhibited the smallest RMSPE and the highest slope parameter, indicating a slightly more robust model for prediction of CP flow; CPM displayed the largest RMSPE, and AC had the lowest slope estimate for CP passage to the duodenum (Table 3). All models displayed low mean bias (<5%) and regression bias (<7%) for CP flow prediction, with more than 93% of the variation in random disturbance. The AMTS model also displayed the smallest RMSPE for flow of microbial CP and RUP. The AC model displayed significant regression bias for microbial CP (44%), whereas CPM bias was toward the mean (57%). In accordance with an overprediction of microbial CP,

Table 1. Descriptive statistics for studies used in determination of duodenal flow of protein and essential AA of adult dairy cattle

Item	No. of diets	Mean	SD	Minimum	Maximum
DMI, kg/d	154	19.1	3.8	9.1	26.7
CP, % of DM	154	16.6	1.8	10.5	23.6
NDF, % of DM	154	32.4	5.6	21.7	53.2
Forage in diet, %	154	49.5	12.6	28.0	100.0
BW, kg	154	596	51	410	717
Milk yield, kg/d	103	29.5	6.9	13.0	41.7
Milk CP, %	103	3.12	0.22	2.69	3.69
DIM	103	135.6	58.6	50	250

CPM displayed a large mean bias (29%) for the RUP predictions and the highest RMSPE for RUP.

Individual AA. Across all diets, mean Arg was predicted very accurately by AC and NRC but over-predicted by 25% by AMTS and by 31% by CPM. The RMSPE was similar between the models, but AMTS and CPM both displayed a large mean bias for the prediction of Arg duodenal flow (40 and 53%, respectively; Table 3). Means of His flows were underpredicted by AC (4%) and NRC (8%) and overpredicted by AMTS (8%) and CPM (13%). Isoleucine was overpredicted from 6 to 13% by AC, AMTS, and CPM, but not by NRC. Leucine was underpredicted by all models but was within 5%. Lysine was also slightly overpredicted (<5%) by all models except for CPM, which predicted only acceptably. Methionine was overpredicted by 26% by CPM, acceptably by AMTS, and very accurately by AC and NRC. The AMTS model had a slight mean bias (15%) for prediction of Met, whereas CPM had a large mean bias (45%). Phenylalanine, Thr, and Val were also well predicted by all models although CPM exhibited a slight mean bias for prediction of Phe (16%). Across all AA, with the exception of Met and His, AMTS displayed the lowest RMSPE. Considering the prediction of EAA over all diets, the NRC model had the highest average percentage of random error (97%), whereas CPM had the lowest random error (72%). The CPM model displayed a mean bias for almost all AA, which on average represented 22% of the bias partition. On average, the AC model had the highest bias toward the slope and had the lowest slopes. The models displayed similar RMSPE (Table 3).

Effect of Forage Sources

Protein Fractions. All models predicted that duodenal flows of CP, microbial CP, and RUP increased as diets changed from grass-based to corn silage-based to alfalfa-based diets (Tables 4, 5, and 6). Duodenal flows of CP for the different forage diets were predicted very accurately, except for CPM in which CP flow was

overpredicted by 13 and 6% for grass-based and corn silage-based diets, respectively. It is also of interest that for diets based on corn silage and alfalfa, the flow of observed microbial CP was roughly equal to observed RUP, whereas for grass-based diets, the RUP was reduced to about 60% of the microbial CP. The proportion between microbial CP and RUP was well predicted in corn silage-based diets by AC and NRC and to a lesser extent by AMTS; the 3 models also predicted a decrease of this proportion on grass-based diets, but of smaller magnitude than the observed values. Overall, microbial CP was accurately predicted by AC, AMTS, and NRC for all diet types, except for grass-based diets for NRC in which underprediction of 12% was present. The CPM model overpredicted microbial CP flows by 14, 28, and 32% for grass-, alfalfa-, and corn silage-based diets, respectively. With the exception of NRC with corn silage-based diets, RUP was never very accurately predicted. The RUP flow of grass-based diets was overpredicted by all models, from 9 to 17%. On the other hand, RUP flow was underpredicted by all models for alfalfa-based diets, although AMTS and NRC predicted within acceptable limits. Similarly, the RUP fraction of corn silage-based diets was also underpredicted by the 4 models, with NRC having the best agreement (97%) and CPM the worst (75%). Partitioning of error for alfalfa or corn silage diets indicated that approximately 70% of error ascribed to CPM was due to a mean bias for microbial CP, whereas between 36 and 42% of the RUP error was also mean bias (Tables 4, 5, and 6).

Individual AA. For grass-based diets, only AMTS predicted Arg within 10%, and CPM within 15%. The AC and NRC underpredictions of Arg were not in a useful range (19 and 21%, respectively). All models predicted His flow to be less than observed, with only CPM predicting His flow accurately and AMTS predicting in an acceptable range. Both AC (21%) and NRC (23%) predicted His flow less than acceptably. Other than Met, which was predicted 18% high by the CPM model, predictions of other EAA were sufficiently accurate. The MSPE decomposition for Arg and His

Table 2. Means of observed and model predicted flows (g/d) of protein fractions and essential AA for all diets

Item	Observed			AC			AMTS			CPM			NRC		
	Mean	SE	Model ¹	Mean	SE	% Obs. ²	Mean	SE	% Obs.	Mean	SE	% Obs.	Mean	SE	% Obs.
CP	3,027	790		2,945	769	97.3	3,026	638	100.0	3,148	633	104.0	2,951	708	97.5
MCP ³	1,610	407		1,605	499	99.7	1,678	314	104.2	2,050	415	127.3	1,573	338	97.7
RUP	1,480	614		1,368	372	92.4	1,348	409	91.1	1,126	315	76.1	1,415	416	95.6
Arg	122	38		123	33	100.8	152	37	124.6	160	38	131.1	116	28	95.1
His	61	20		59	18	96.7	66	18	108.2	69	20	113.1	56	16	91.8
Ile	119	36		127	34	106.7	126	28	105.9	134	30	112.6	120	27	100.8
Leu	230	79		220	64	95.7	219	60	95.2	224	61	97.4	226	62	98.3
Lys	157	48		161	45	102.5	164	40	104.5	178	43	113.4	160	38	101.9
Met	47	16		48	13	102.1	53	11	112.8	59	13	125.5	47	11	100.0
Phe	129	38		128	34	99.2	134	33	103.9	140	34	108.5	126	31	97.7
Thr	123	34		124	32	100.8	120	28	97.6	127	29	103.3	120	27	97.6
Val	141	45		145	37	102.8	147	36	104.3	155	38	109.9	138	32	97.9

¹AC = AminoCow; AMTS = Agricultural Modeling and Training Systems; CPM = Cornell-Penn-Miner version of CNCPS; NRC = National Research Council (2001); see text for details on the versions used.

²Predicted value as a percentage of the observed value.

³Microbial CP.

revealed no serious bias although the mean bias was greater for these 2 AA than for all the other EAA. Apportionment of error for Met prediction indicated that the CPM model had both an 18% mean bias and an 8% regression bias (Tables 4, 5, and 6). For grass-based diets, RMSPE and R² were similar among model predictions. For these diets, CPM generally displayed the lowest RMSPE and NRC the highest.

For predictions of AA in alfalfa-based diets, Arg was overpredicted 27% by AMTS and 33% by CPM. Similarly, Met was overpredicted 17% by AMTS and 34% by CPM. Error decomposition for Arg indicated that 65% of the MSPE in AMTS and 75% in CPM were due to mean biases, whereas for Met the mean bias was 34 and 64% for AMTS and CPM, respectively. Histidine, Ile, Leu, Lys, Phe, Thr, and Val were predicted within accurate limits by the 4 models. For alfalfa-based diets, AMTS displayed the lowest MSPE and NRC the highest across all amino acids.

Duodenal flows of EAA with corn silage-based diets were all predicted within accurate limits by AC and NRC. Arginine was overpredicted by 26% by AMTS and 32% by CPM, and CPM overpredicted His by 19% and Met by 20% (Tables 4, 5, and 6). Partition of error revealed that CPM had a mean bias of 64% for Arg, 42% for His, and 38% for Met on the corn silage-based diets. The AMTS model displayed a mean bias of 52% for Arg. For corn silage diets, AC displayed the lowest RMSPE and CPM the highest.

Overall, with grass-based diets, the ratio of predicted:observed duodenal flows of EAA was always smaller than the ratio of predicted:observed CP flows, whereas the opposite was observed with alfalfa- and corn silage-based diets (except for NRC predictions of corn silage-based diets). Leucine duodenal flows were slightly (<5%) underpredicted with grass-based diets. A greater (<10%) underprediction was obtained for alfalfa- and corn silage-based diets (except NRC for corn silage).

For grass-based diets, AC displayed the lowest RMSPE for both protein fractions and EAA, whereas CPM had the highest. In alfalfa-based diets, AMTS displayed the lowest RMSPE and CPM the highest, whereas in corn silage-based diets, AMTS had the lowest RMSPE for protein fractions, but AC the lowest for EAA. In these diets, CPM displayed the largest RMSPE for both.

Effect of Carbohydrate Sources

Protein Fractions. All models predicted CP flow of non-corn-based diets within accurate limits, whereas the CP flow of corn-based diets was estimated more precisely (Tables 7 and 8). For the non-corn-based diets,

Table 3. Model adequacy statistics for comparison of model predicted versus observed values for all diets

Model ¹	Item	RMSPE ²	RPE ²	R ²	Int. ³	Slope	MSPE bias partition ⁴		
							Mean	Slope	Random
AC	CP	175.2	5.8	0.95	854	0.73	0.3	6.5	93.5
	MCP ⁵	199.2	12.4	0.76	997	0.37	0.0	43.5	56.4
	RUP	179.6	12.1	0.91	224	0.89	5.9	1.0	93.1
	Arg	11.2	9.2	0.91	41	0.65	0.0	11.9	88.1
	His	5.6	9.2	0.92	14	0.77	1.2	10.6	88.2
	Ile	8.6	7.2	0.94	49	0.54	5.5	17.3	77.2
	Leu	17.5	7.6	0.95	40	0.75	3.6	0.6	95.8
	Lys	13.2	8.4	0.92	46	0.67	1.4	11.4	87.2
	Met	3.7	7.9	0.94	13	0.71	0.3	6.5	93.1
	Phe	9.9	7.7	0.93	28	0.77	0.1	4.6	95.3
	Thr	8.2	6.7	0.94	41	0.65	0.3	10.4	89.3
	Val	9.8	7.0	0.95	32	0.74	0.9	6.4	92.8
AMTS	CP	159.6	5.3	0.96	336	0.88	0.0	0.4	99.6
	MCP	173.5	10.8	0.81	425	0.70	3.9	6.5	89.6
	RUP	172.3	11.6	0.92	154	0.94	4.3	1.3	94.3
	Arg	11.2	9.2	0.91	29	0.61	39.7	11.8	48.5
	His	5.7	9.3	0.92	6	0.83	8.2	11.8	80.1
	Ile	8.4	7.1	0.94	31	0.69	4.4	9.4	86.2
	Leu	15.7	6.8	0.96	23	0.94	3.6	0.2	96.1
	Lys	12.4	7.9	0.93	23	0.81	3.5	4.4	92.0
	Met	3.9	8.3	0.94	11	0.67	15.9	5.7	78.5
	Phe	9.4	7.3	0.93	17	0.82	4.4	3.3	92.3
	Thr	7.7	6.3	0.95	25	0.82	1.7	3.2	95.1
	Val	8.4	6.0	0.95	23	0.80	2.3	7.0	90.8
CPM	CP	202.2	6.7	0.93	462	0.80	4.9	0.7	94.6
	MCP	178.6	11.1	0.80	531	0.52	56.9	10.1	33.0
	RUP	245.2	16.6	0.84	812	0.55	29.4	0.4	70.2
	Arg	11.4	9.3	0.91	32	0.56	53.0	9.4	37.6
	His	5.8	9.5	0.92	11	0.70	17.9	14.7	67.4
	Ile	9.0	7.6	0.93	36	0.61	19.3	7.0	73.7
	Leu	16.9	7.3	0.95	31	0.89	1.4	0.3	98.3
	Lys	14.0	8.9	0.91	41	0.64	25.9	5.6	68.5
	Met	3.9	8.3	0.94	9	0.64	45.3	4.9	49.9
	Phe	10.2	7.9	0.92	26	0.73	16.0	4.2	79.9
	Thr	8.4	6.8	0.94	36	0.68	2.6	4.7	92.7
	Val	10.2	7.6	0.95	19	0.78	12.6	6.7	80.7
NRC	CP	180.9	6.0	0.95	571	0.82	2.4	2.0	95.6
	MCP	179.6	11.2	0.80	551	0.67	1.0	11.8	87.2
	RUP	198.5	13.4	0.84	14	0.68	2.3	0.2	97.5
	Arg	11.2	9.2	0.91	26	0.82	4.3	3.2	92.5
	His	5.8	9.5	0.92	6	0.96	6.9	3.6	89.4
	Ile	9.1	7.6	0.92	28	0.76	0.0	3.2	96.8
	Leu	16.9	7.3	0.95	17	0.94	0.6	0.0	99.4
	Lys	13.1	8.3	0.92	13	0.89	0.9	0.8	98.4
	Met	3.8	8.1	0.94	6	0.86	0.1	1.4	98.6
	Phe	11.4	8.8	0.92	23	0.83	1.5	0.6	97.9
	Thr	8.2	6.7	0.94	27	0.79	0.8	1.6	97.6
	Val	10.2	7.2	0.95	11	0.94	0.9	0.3	98.8

¹AC = AminoCow; AMTS = Agricultural Modeling and Training Systems; CPM = Cornell-Penn-Miner version of CNCPS; NRC = National Research Council (2001); see text for details on the versions used.

²RMSPE = root mean square prediction error; RPE = relative prediction error RMSPE as a percentage of the observed mean.

³Intercept.

⁴MSPE = mean square prediction error with percentage due to mean, regression, and random disturbance biases.

⁵Microbial CP.

CPM predicted microbial CP to be 19% greater than was observed, AMTS was very precise (1%), whereas AC and NRC underpredicted the flow of microbial CP but within an acceptable range. The decomposition of

error revealed 36% mean bias as well as 19% regression bias for the CPM prediction of microbial CP. In contrast, for corn-based diets, all models predicted more microbial CP than was observed, but within 5% except

Table 5. Observed and predicted duodenal flows (g/d), and statistical adequacy of 4 programs¹ for rations of alfalfa-based diets (n = 36)

Item	AC						AMTS									
	Observed		MSPE bias partition ³				Observed		MSPE bias partition							
	Mean	SE	Mean	SE	RMSPE ²	R ²	Mean	SE	RMSPE	R ²	Mean	Slope	Random			
CP	3,354	874	3,231	562	190.3	0.95	5.1	6.5	88.5	3,236	423	153.2	0.97	3.3	9.3	87.4
MCP ⁴	1,742	331	1,874	400	151.2	0.77	11.1	36.4	52.5	1,784	230	147.5	0.78	1.5	16.4	82.1
RUP	1,622	718	1,357	255	109.6	0.97	20.2	29.2	50.5	1,452	266	99.0	0.98	9.6	29.0	61.5
Arg	132	34	131	21	8.3	0.94	0.0	1.2	98.8	168	20	7.1	0.95	64.8	0.1	35.1
His	66	19	63	12	5.1	0.92	3.6	2.7	93.8	72	11	3.0	0.97	16.2	0.1	83.7
Ile	133	38	142	24	6.7	0.96	7.4	3.3	89.3	140	17	6.1	0.97	3.6	1.0	95.4
Leu	258	82	235	44	14.6	0.97	13.1	4.9	82.0	234	38	10.8	0.98	11.5	3.6	84.9
Lys	180	48	181	30	12.4	0.93	0.1	0.0	99.9	182	24	8.6	0.97	0.1	2.1	97.8
Met	47	13	52	9	3.2	0.93	15.7	2.8	81.5	55	8	2.7	0.95	33.9	0.5	65.6
Phe	148	38	139	24	8.9	0.94	14.2	4.8	81.1	147	21	6.1	0.97	0.2	1.6	98.1
Thr	140	35	138	23	7.4	0.95	0.9	3.3	95.8	132	17	6.3	0.96	7.1	1.2	91.7
Val	156	45	158	26	9.3	0.95	0.4	0.0	99.6	161	22	6.6	0.98	1.5	1.4	97.1
			CPM				NRC									
CP			3,334	441	208.6	0.94	0.1	5.9	94.0	3,182	531	157.0	0.96	10.7	16.9	72.4
MCP			2,236	288	158.9	0.75	68.7	6.5	24.9	1,774	218	160.6	0.74	1.5	0.8	97.8
RUP			1,098	242	199.2	0.92	42.2	3.1	54.7	1,408	334	118.4	0.97	16.4	21.1	62.5
Arg			175	23	8.0	0.94	75.0	0.0	25.0	126	20	7.7	0.94	6.5	10.6	83.0
His			75	13	4.1	0.95	31.8	0.0	68.0	61	12	5.0	0.92	16.4	6.2	77.4
Ile			147	19	7.6	0.96	15.6	0.2	84.2	130	21	7.3	0.96	0.5	3.1	96.0
Leu			238	41	13.1	0.97	8.5	2.6	88.9	240	46	12.5	0.97	9.3	10.2	80.5
Lys			198	29	12.4	0.93	18.2	0.1	81.7	178	27	11.6	0.94	0.5	8.3	91.2
Met			63	9	3.2	0.93	64.0	3.1	32.8	51	8	3.4	0.92	13.6	0.0	86.4
Phe			151	23	7.7	0.95	1.2	2.6	96.2	134	22	12.9	0.87	24.0	4.8	71.2
Thr			139	19	7.7	0.95	0.1	3.4	96.5	132	20	7.4	0.95	7.0	0.2	92.9
Val			169	25	8.6	0.96	9.0	1.5	89.5	150	24	8.3	0.96	4.2	4.6	91.2

¹AC = AminoCow; AMTS = Agricultural Modeling and Training Systems; CPM = Cornell-Penn-Miner version of CNCPS; NRC = National Research Council (2001); see text for details on the versions used.

²RMSPE = root mean square prediction error.

³MSPE = mean square prediction error with percentage due to mean, regression, and random disturbance biases.

⁴Microbial CP.

Table 6. Observed and predicted duodenal flows (g/d), and statistical adequacy of 4 programs¹ for rations of corn silage-based diets (n = 68)

Item	AC						AMTS										
	Observed		MSPE bias partition ³						MSPE bias partition								
	Mean	SE	Mean	SE	RMSPE ²	R ²	Mean	Slope	Random	Mean	SE	RMSPE	R ²	Mean	Slope	Random	
CP	3,007	688	3,011	691	146.5	0.95	0.0	14.9	85.1	3,060	550	150.6	0.95	1.1	1.9	97.0	
MCP ⁴	1,524	404	1,543	513	153.0	0.85	0.1	47.4	52.4	1,676	292	98.6	0.94	20.2	1.5	78.4	
RUP	1,568	550	1,464	334	163.4	0.91	2.9	0.1	96.9	1,383	353	150.0	0.92	0.0	0.2	99.8	
Arg	122	35	128	33	12.3	0.87	55.1	14.4	80.5	154	36	12.3	0.87	51.6	10.3	38.1	
His	59	16	61	16	5.8	0.86	2.2	12.8	85.0	67	16	5.9	0.85	28.6	10.8	60.5	
Ile	125	33	129	33	9.3	0.92	1.3	21.4	77.3	126	24	9.7	0.91	0.2	3.1	96.7	
Leu	250	66	231	55	18.6	0.92	16.8	0.5	82.8	226	49	17.8	0.92	28.3	1.4	70.2	
Lys	157	47	162	45	12.0	0.93	2.3	12.5	85.2	165	38	13.3	0.92	6.4	1.5	92.1	
Met	49	15	49	12	3.4	0.94	0.5	6.1	93.5	53	10	4.0	0.92	10.5	4.3	85.2	
Phe	131	34	132	30	10.5	0.90	0.3	4.3	95.5	136	27	10.8	0.89	4.9	0.3	94.8	
Thr	125	30	127	29	7.5	0.94	0.3	10.9	88.8	121	24	7.7	0.93	3.8	1.0	95.2	
Val	147	45	148	33	10.3	0.94	0.2	0.8	99.0	142	28	11.1	0.94	0.3	0.1	99.5	
			CPM				NRC										
CP			3,178	543	190.5	0.92	11.4	0.9	87.7	3,049	616	171.0	0.94	1.0	3.0	96.1	
MCP			2,022	369	100.3	0.94	70.2	3.2	26.6	1,539	340	111.9	0.92	0.2	15.2	84.6	
RUP			1,182	301	200.1	0.86	36.3	1.9	61.8	1,517	384	176.9	0.89	0.0	0.3	99.7	
Arg			161	35	13.0	0.85	64.4	6.7	28.9	120	25	12.6	0.86	0.4	0.9	98.7	
His			70	17	6.6	0.82	41.5	13.0	45.5	58	13	6.5	0.82	0.5	4.2	95.3	
Ile			134	26	10.6	0.89	10.4	2.2	87.3	123	24	10.3	0.90	1.1	3.4	93.5	
Leu			229	51	20.9	0.90	22.5	0.6	76.8	239	51	20.5	0.90	5.9	0.1	94.0	
Lys			176	40	15.4	0.89	28.5	1.7	69.8	162	35	13.3	0.92	2.6	0.0	97.4	
Met			59	11	4.3	0.91	37.8	2.9	59.3	48	10	3.8	0.93	0.8	0.9	98.3	
Phe			141	28	12.6	0.85	17.4	1.1	81.5	131	27	12.0	0.87	0.0	0.3	99.7	
Thr			128	25	9.2	0.90	1.2	0.8	98.0	123	24	8.2	0.92	1.1	0.8	98.2	
Val			156	32	12.0	0.93	7.9	0.0	92.1	142	28	11.6	0.93	2.5	1.2	96.3	

¹AC = AminoCow; AMTS = Agricultural Modeling and Training Systems; CPM = Cornell-Penn-Miner version of CNCPS; NRC = National Research Council (2001); see text for details on the versions used.

²RMSPE = root mean square prediction error.

³MSPE = mean square prediction error with percentage due to mean, regression, and random disturbance biases.

⁴Microbial CP.

for the CPM model, which predicted excessively high (31%). Error decomposition suggested that this was due largely to mean biases of 67 and 32%, respectively.

For both sources of dietary carbohydrate, the RUP fraction was systematically underpredicted: within acceptable limits for the non-corn-based diets, except for the CPM model, which underpredicted it by 20%, and by 10% for the corn diets, except for the CPM model, in which the overprediction of microbial CP resulted in underprediction of the RUP flow by 24%. The error was mainly associated with a mean bias of 25 and 32% for non-corn-based and corn-based diets, respectively. For both diet types, AMTS generally displayed the lowest RMSPE and CPM the highest for all protein fractions.

Individual AA. Predictions of EAA flow to the duodenum were more variable for non-corn-based diets compared with corn-based diets (Tables 7 and 8). For the non-corn-based diets, Arg flow was overpredicted outside of an acceptable limit by AMTS and CPM but underpredicted within accurate range for the other 2 models. Histidine was underpredicted by 16% by AC and 22% by NRC. This was due to a 21% mean bias for AC and a 28% mean bias for NRC. Isoleucine was overpredicted by all models, with AC (17%), AMTS (22%), and CPM (28%) predicting unacceptably high. Only NRC predicted Ile in a useful range for non-corn-based diets. This error decomposition suggested strong mean bias for all models for prediction of Ile flow to the duodenum, being 60, 51, 50, and 65% for AC, AMTS, CPM, and NRC, respectively. Leucine, Lys, Met, and Val were predicted within acceptable limits by AC, AMTS, and NRC, except for Met with AMTS, which was overpredicted by 29%. Flows of these AA were overpredicted by more than 15% by CPM, with Met being overpredicted by 43% on non-corn-based diets (Tables 7 and 8). Error associated with Met flow from non-corn-based diets consisted of 52% mean bias and 11% regression bias for the CPM model and 29% mean bias and 19% regression bias for the AMTS model. Prediction of the flows of Leu, Lys, and Val by the CPM model displayed mean bias (25, 19, and 38%, respectively) and regression bias (21, 26, and 29%, respectively).

On the corn-based diets, Arg was overpredicted by 25% by AMTS and 32% for CPM. This error was 49 and 67% mean bias, respectively (Tables 7 and 8). Although all models underpredicted Leu flow and overpredicted Lys flow, these were all within 10% of mean observed values. Predicted flows of other AA were all accurate with the exceptions of His and Met flow by CPM, which were overpredicted by 17 and 21%, respectively. Apportionment of error for these AA in CPM indicated that Met overprediction was mainly due to

mean bias, but that His was due to a mixture of mean and regression bias.

For non-corn-based diets, although CPM did not predict the mean accurately, it did predict precisely as evidenced by the lowest RMSPE. The NRC model, which was the most accurate for predicting mean flows, had the highest RMSPE overall. Overall, with non-corn-based diets, the ratio of predicted:observed duodenal flows of EAA was always greater than the ratio of predicted:observed CP flows, whereas for corn-based diets, the prediction of total EAA followed more closely the prediction of CP flow.

Effect of RUP

Protein Fractions. For diets with no source of proteins considered to be high in RUP (Tables 9 and 10), CP flow was very accurately estimated by the 4 models. Microbial CP flow was estimated within 5% by AC, AMTS, and NRC, whereas CPM overestimated microbial CP flow by 26%. All models underestimated mean RUP flow but, with the exception of CPM (27%), they were underestimated within acceptable limits. The CPM underprediction was mainly due to mean bias of 35%. In fact, all models displayed more mean bias for predictions of RUP than would be desirable for the low RUP diets (Tables 9 and 10). The predictions of the protein fraction flows were similar for rations with RUP added as for the non-RUP rations. The AC, AMTS, and NRC models predicted both microbial CP and RUP within 5% of observed, whereas CPM overpredicted microbial CP (28%) and underpredicted RUP (22%).

Individual AA. All EAA of low RUP diets were predicted by AC, AMTS, and NRC within 10% of observed mean, except Arg and Met, which were overpredicted by 20 and 11%, respectively by AMTS. The CPM model overpredicted the flow of all EAA except Leu and Thr, but within acceptable limits except for Arg and Met, which were overpredicted by 26 and 24%, respectively, in low RUP diets. Error for Arg for both AMTS and CPM in these diets was due to a mix of mean bias and regression bias, whereas the Met error for CPM was due mainly to mean bias (Tables 9 and 10). For diets where RUP was added, EAA flows were predicted accurately with AC and NRC models. The AMTS model, on average, predicted greater flows, with His, Ile, and Met being acceptable and Arg, which was predicted to be 27% greater than observed with 47% mean bias (Tables 9 and 10). The CPM model overpredicted Arg (34%), His (16%), Ile (17%), and Met (24%). Except for His, which was a mix of mean and regression bias, all other errors were attributable to mean bias (Tables 9 and 10). When diets were evalu-

Table 9. Observed and predicted duodenal flows (g/d), and statistical adequacy of 4 programs¹ for rations without added RUP sources (n = 60)

Item	AC						AMTS										
	Observed		MSPE bias partition ³				MSPE bias partition										
	Mean	SE	Mean	SE	RMSPE ²	R ²	Mean	Slope	Random	Mean	SE	RMSPE	R ²	Mean	Slope	Random	
CP	3,002	828	2,890	863	128.5	0.98	4.5	13.0	82.5	2,918	648	117.5	0.98	3.7	2.1	94.2	
MCP ⁴	1,671	377	1,731	532	148.6	0.84	1.3	56.6	42.1	1,715	295	144.3	0.84	2.2	5.4	92.4	
RUP	1,422	616	1,209	319	103.2	0.97	23.0	18.2	58.8	1,204	200	75.5	0.98	14.7	13.7	71.6	
Arg	123	40	119	36	6.8	0.97	1.3	13.8	84.9	147	38	6.5	0.97	29.4	13.2	57.4	
His	59	20	55	17	3.0	0.98	4.4	10.8	84.8	61	17	2.7	0.98	2.0	10.5	87.5	
Ile	125	35	128	37	6.4	0.96	0.9	21.0	78.1	123	29	6.1	0.97	0.5	4.0	95.5	
Leu	222	74	205	63	12.3	0.97	15.5	0.1	84.4	201	54	10.0	0.98	20.5	3.1	76.4	
Lys	162	45	161	48	9.0	0.96	0.3	19.4	80.3	161	38	9.4	0.95	0.3	2.7	97.0	
Met	45	14	46	14	2.8	0.96	0.8	22.2	77.0	50	10	2.1	0.97	16.4	3.8	79.8	
Phe	127	38	123	37	6.3	0.97	4.9	5.5	89.6	126	32	5.8	0.96	0.4	0.0	99.6	
Thr	125	34	123	35	5.5	0.97	0.5	17.9	81.6	117	28	5.4	0.97	11.1	2.0	86.9	
Val	140	43	140	40	6.2	0.98	0.1	8.4	91.5	138	33	6.4	0.98	0.4	0.5	99.1	
			CPM				NRC										
CP			3,081	660	184.7	0.95	2.9	0.3	96.8	2,841	786	116.4	0.98	13.7	2.0	84.3	
MCP			2,107	441	159.7	0.81	56.5	15.2	28.3	1,627	357	147.3	0.84	1.5	20.3	78.2	
RUP			1,033	262	179.1	0.91	34.8	0.4	64.8	1,277	419	86.6	0.98	14.5	5.9	79.6	
Arg			155	41	6.7	0.97	43.4	12.2	44.4	113	33	6.4	0.97	8.3	7.3	84.4	
His			64	17	3.2	0.97	8.8	10.1	81.1	53	16	3.0	0.98	11.6	5.7	82.7	
Ile			131	32	6.9	0.96	6.4	6.1	87.5	118	31	6.2	0.97	7.0	3.7	89.3	
Leu			205	55	11.3	0.98	15.7	3.6	80.7	209	63	10.1	0.98	12.4	0.6	87.0	
Lys			174	43	12.3	0.92	12.5	7.7	79.8	158	41	10.2	0.94	2.3	5.7	92.0	
Met			56	13	2.6	0.96	50.3	7.8	41.9	45	12	2.6	0.96	0.1	12.6	87.3	
Phe			131	33	6.5	0.97	3.4	0.1	96.5	120	34	6.0	0.97	13.8	0.2	86.0	
Thr			124	31	6.1	0.96	0.2	6.2	93.6	118	31	5.7	0.97	7.7	5.4	86.9	
Val			146	36	7.2	0.97	4.2	1.2	94.6	133	34	6.4	0.98	7.9	0.1	92.0	

¹AC = AminoCow; AMTS = Agricultural Modeling and Training Systems; CPM = Cornell-Penn-Miner version of CNCPS; NRC = National Research Council (2001); see text for details on the versions used.

²RMSPE = root mean square prediction error.

³MSPE = mean square prediction error with percentage due to mean, regression, and random disturbance biases.

⁴Microbial CP.

Table 10. Observed and predicted duodenal flows (g/d), and statistical adequacy of 4 programs¹ for rations with added RUP sources (n = 94)

Item	AC						AMTS									
	Observed		MSPE bias partition ³						MSPE bias partition							
	Mean	SE	Mean	SE	RMSPE ²	R ²	Mean	Slope	Random	Mean	SE	RMSPE	R ²	Mean	Slope	Random
CP	3,044	769	2,981	705	174.1	0.95	1.2	8.0	90.8	3,094	626	159.5	0.92	0.8	2.2	97.0
MCP ⁴	1,572	423	1,525	463	233.9	0.68	1.1	32.7	66.2	1,655	326	193.3	0.78	5.0	7.6	87.4
RUP	1,515	614	1,463	370	191.7	0.90	1.2	0.2	98.6	1,439	366	176.2	0.91	1.6	0.1	98.3
Arg	122	38	125	31	11.8	0.90	0.6	9.8	89.6	155	36	12.2	0.89	46.6	10.2	43.2
His	62	21	61	18	5.8	0.92	0.2	9.5	90.3	69	19	6.3	0.90	13.9	10.6	75.5
Ile	116	36	127	32	8.9	0.94	9.2	16.8	74.0	128	28	8.6	0.94	11.6	11.3	77.1
Leu	235	82	230	62	17.6	0.95	0.8	0.5	98.7	231	60	16.1	0.96	0.5	0.9	98.6
Lys	153	50	162	43	12.5	0.93	4.5	7.8	87.7	166	41	11.6	0.94	9.5	4.6	85.9
Met	48	17	49	12	3.7	0.95	0.1	1.2	98.7	55	12	4.1	0.94	16.1	6.1	77.8
Phe	130	38	132	32	10.6	0.92	0.5	3.2	96.3	140	32	10.1	0.92	11.6	4.1	84.3
Thr	122	34	126	30	8.7	0.93	1.9	5.7	92.4	122	27	8.1	0.94	0.0	3.4	96.6
Val	142	46	148	35	10.4	0.95	2.4	5.0	92.6	153	37	10.6	0.95	6.2	9.0	84.8
			CPM				NRC									
CP			3,190	615	187.7	0.94	6.3	2.5	91.2	3,022	634	190.9	0.94	0.2	1.4	98.4
MCP			2,014	397	195.1	0.78	57.1	7.4	35.5	1,539	324	199.8	0.77	0.8	7.9	91.3
RUP			1,181	332	250.8	0.83	26.3	1.2	72.5	1,494	395	216.5	0.87	0.2	0.0	99.8
Arg			163	36	11.9	0.90	59.3	7.3	33.4	117	25	12.1	0.89	2.3	0.6	97.1
His			72	20	5.9	0.92	24.3	15.0	60.7	58	15	6.0	0.91	4.5	2.0	93.5
Ile			136	28	8.9	0.94	27.9	6.8	65.3	120	24	9.9	0.92	2.3	2.8	94.9
Leu			236	62	16.7	0.96	0.0	1.0	99.0	237	59	18.2	0.95	0.2	0.0	99.8
Lys			180	44	12.4	0.94	34.6	4.2	61.2	161	35	12.6	0.94	5.0	0.0	95.0
Met			61	13	4.0	0.94	42.9	3.5	53.6	49	10	4.0	0.94	0.0	0.2	99.8
Phe			145	34	10.5	0.92	24.9	4.9	70.2	130	28	13.1	0.87	0.0	0.4	99.6
Thr			129	28	8.5	0.93	7.9	3.1	89.0	122	24	8.9	0.93	0.1	0.0	99.9
Val			161	38	10.5	0.95	18.1	8.0	73.9	142	30	11.2	0.94	0.0	0.2	99.8

¹AC = AminoCow; AMTS = Agricultural Modeling and Training Systems; CPM = Cornell-Penn-Miner version of CNCPS; NRC = National Research Council (2001); see text for details on the versions used.

²RMSPE = root mean square prediction error.

³MSPE = mean square prediction error with percentage due to mean, regression, and random disturbance biases.

⁴Microbial CP.

ated as no added RUP and added RUP, the RMSPE for average EAA flows was smallest for AMTS across both diet types and greatest for CPM on diets with no added RUP and greatest for NRC in diets with added RUP.

Effect of Intake Level

Protein Fractions. At low intake level, the AC, AMTS, and NRC models predicted CP flow very accurately, whereas CPM overpredicted CP flow by 13%, mainly due to a mean bias. Despite this accuracy in total CP flow, microbial CP was underpredicted by AC (19%), AMTS (1%), and NRC (14%), whereas CPM overpredicted microbial CP (16%) flow (Tables 11 and 12). Therefore, RUP was overpredicted by all models, but within acceptable limits for the low intake diets. At high intake level, CP flows were predicted very accurately by all models. All models overpredicted the microbial CP fraction within an acceptable limit except CPM, which overestimated it by 35% due to a large mean bias (75% of the error). In contrast, RUP was underestimated by all models but within acceptable limits except for CPM, which underestimated it by 29%. For predictions on both intake levels, AMTS displayed the lowest RMSPE for protein fractions, and CPM displayed the highest.

Individual AA. All AA were predicted within an acceptable range on low intake diets by all models, except for CPM, which overpredicted Arg (20%) and Met (16%), and NRC, which underpredicted His (17%) passage to the duodenum (Tables 11 and 12). On high intake diets, AMTS overpredicted Arg (32%) and His (20%), whereas CPM overpredicted Arg (39%), His (26%), and Met (27%). For predictions on low DMI diets, CPM displayed the lowest RMSPE for EAA and NRC the highest, whereas on high intake levels, AC displayed the lowest RMSPE and CPM the highest (Tables 11 and 12).

Effect of Dietary CP Level

Protein Fractions. Flows of CP for cows consuming low CP diets ($14.6 \pm 1.2\%$ DM; range 10.5–15.8%) were predicted within acceptable limits by the 4 models (Tables 13 and 14). Microbial CP, however, was underpredicted by AC (18%) and overpredicted by CPM (26%). The CPM model again underpredicted RUP (18%), whereas the other 3 models predicted it very accurately. Error partitioning indicated that the microbial prediction by AC was a combination of mean and regression biases, whereas the error in the CPM predictions was mainly due to a mean bias (Tables 13 and 14). Predictions of duodenal flow of CP and CP

fractions of cows on high CP diets by AC, AMTS, and NRC were all acceptable. The CPM model underpredicted RUP (31%) and overpredicted microbial CP (25%), with the significant error assigned to mean bias. Model predictions of low CP diets by AMTS had the lowest RMSPE for CP fractions, whereas NRC had the highest RMSPE. However, for high protein diets, NRC displayed the lowest RMSPE for protein fractions and CPM had the highest RMSPE (Tables 13 and 14).

Individual AA. Flows of EAA in cows consuming low CP diets followed the same trend as total CP flow. They were predicted accurately by the AC, AMTS, and NRC models, except that AMTS overpredicted Arg (23%) and Met (17%) flows. The CPM model overpredicted the flow of most EAA and was outside acceptable limits for Arg (31%), Lys (16%), and Met (31%). Error partitioning indicated the presence of mean bias in the predictions of AMTS and CPM (Tables 13 and 14). Predictions of EAA flows of high CP diets by AC, AMTS, and NRC were all within acceptable limits, except for Arg prediction by AMTS, which was 25% greater than observed. The CPM model overpredicted Arg (25%) and Met (23%). All of the significant errors for high CP diets were attributable to mean bias. Model predictions of low CP diets by CPM displayed the lowest RMSPE for EAA and AC the highest. However, for high protein diets, AC displayed the lowest RMSPE for EAA, whereas CPM had the highest RMSPE (Tables 13 and 14).

Effect of NDF Level

Protein Fractions. Prediction of total CP flow was accurate for all models for diets that were low in NDF ($27.1 \pm 2.1\%$ DM; range 21.7–29.4), although all models predicted smaller RUP flow than the observed values: within acceptable limits for AC (12%), AMTS (14%), and NRC (11%) but outside acceptable limits for CPM (30%; Tables 15 and 16). In addition, microbial CP was overpredicted by CPM (21%). The error was partitioned between mean and slope biases for AC, AMTS, and NRC, whereas it was mainly due to mean bias for CPM. For high NDF diets, prediction of total CP flow by all models were highly accurate (Tables 15 and 16). The AC, AMTS, and NRC models also very accurately predicted the flow of microbial CP, whereas CPM overpredicted microbial CP by 19%. The high microbial flow predicted by CPM was due to a mix of mean and regression biases. The RUP flows were very accurately predicted, except for the CPM prediction, which was barely within acceptable limits. Predictions for low and high NDF diets resulted in AMTS having, on average, the lowest RMSPE for protein fractions.

Table 11. Observed and predicted duodenal flows (g/d), and statistical adequacy of 4 programs¹ for rations at low (<17 kg/d) DMI (n = 45)

Item	AC						AMTS									
	Observed		MSPE bias partition ³						MSPE bias partition							
	Mean	SE	Mean	SE	RMSPE ²	R ²	Mean	Slope	Random	Mean	SE	RMSPE	R ²	Mean	Slope	Random
CP	2,175	557	2,094	507	131.9	0.94	2.5	15.4	82.1	2,267	462	119.7	0.95	4.5	4.6	90.9
MCP ⁴	1,368	462	1,103	298	143.8	0.90	21.0	5.50	73.5	1,355	266	140.7	0.90	0.5	4.6	94.9
RUP	898	396	1,024	345	118.2	0.90	17.1	4.00	78.9	912	325	99.0	0.93	4.4	2.1	93.5
Arg	97	49	87	22	10.4	0.95	4.6	0.5	94.9	109	28	10.2	0.95	6.6	2.3	91.1
His	48	27	42	14	3.8	0.98	6.2	0.1	93.7	46	14	4.6	0.97	0.4	1.1	98.5
Ile	93	32	91	24	6.7	0.95	0.7	16.7	82.6	93	21	6.2	0.96	0.2	0.9	98.9
Leu	159	65	156	47	14.4	0.95	0.8	0.2	99.0	157	48	14.0	0.95	0.4	2.4	97.2
Lys	115	33	115	27	8.1	0.94	0.0	22.5	77.5	119	31	7.8	0.94	1.3	10.9	87.8
Met	37	17	33	8	3.8	0.94	8.0	0.4	91.6	40	8	3.8	0.94	2.4	3.2	94.4
Phe	92	33	92	23	8.8	0.92	0.0	0.5	99.5	98	25	8.7	0.92	8.1	0.1	91.8
Thr	96	34	89	19	7.0	0.95	4.5	0.4	95.1	87	20	6.5	0.96	9.6	1.3	89.1
Val	104	37	105	25	7.8	0.95	0.1	6.2	93.7	102	19	7.7	0.95	2.3	3.0	94.7
							CPM			NRC						
CP			2,448	474	141.8	0.93	31.3	3.0	65.7	2,127	425	144.4	0.93	1.1	5.1	93.8
MCP			1,581	306	149.2	0.89	38.5	0.4	61.1	1,182	206	148.5	0.89	13.4	3.0	83.6
RUP			912	300	137.5	0.88	0.2	4.2	95.6	978	312	111.8	0.91	8.7	0.4	90.9
Arg			116	27	10.6	0.95	15.6	1.1	83.3	83	18	10.8	0.95	8.6	0.2	91.2
His			49	15	4.2	0.97	0.5	0.3	99.2	40	11	4.0	0.97	11.1	3.6	85.3
Ile			99	21	5.8	0.96	3.7	0.6	95.7	88	15	8.4	0.92	4.4	0.4	95.2
Leu			162	47	12.8	0.96	0.6	5.2	94.2	161	45	15.7	0.92	0.1	0.7	99.2
Lys			130	29	7.4	0.95	20.4	9.9	69.7	117	21	8.4	0.93	0.4	8.7	90.9
Met			43	9	3.6	0.95	17.8	2.0	80.2	34	6	3.7	0.95	5.6	2.1	92.3
Phe			103	25	8.6	0.92	21.9	0.0	78.1	91	20	9.2	0.91	0.0	0.1	99.9
Thr			94	21	6.6	0.96	0.6	0.4	99.0	89	16	7.2	0.95	4.1	0.1	95.8
Val			115	29	6.5	0.97	14.0	1.8	84.2	102	19	8.8	0.94	0.3	0.1	99.6

¹AC = AminoCow; AMTS = Agricultural Modeling and Training Systems; CPM = Cornell-Penn-Miner version of CNCPS; NRC = National Research Council (2001); see text for details on the versions used.

²RMSPE = root mean square prediction error.

³MSPE = mean square prediction error with percentage due to mean, regression, and random disturbance biases.

⁴Microbial CP.

Table 12. Observed and predicted duodenal flows (g/d), and statistical adequacy of 4 programs¹ for rations at high (>22 kg/d) DMI (n = 42)

Item	AC							AMTS								
	Observed		MSPE bias partition ³									MSPE bias partition				
	Mean	SE	Mean	SE	RMSPE ²	R ²	Mean	Slope	Random	Mean	SE	RMSPE	R ²	Mean	Slope	Random
CP	3,671	416	3,739	386	171.5	0.82	1.8	34.8	63.4	3,639	286	176.4	0.81	0.4	34.8	64.8
MCP ⁴	1,833	268	2,092	308	105.1	0.83	35.1	30.3	34.6	1,927	181	108.7	0.82	7.0	39.4	53.6
RUP	1,842	379	1,647	249	178.3	0.84	20.5	9.7	69.8	1,712	279	171.6	0.78	10.8	7.0	82.2
Arg	141	22	155	16	9.3	0.81	24.1	15.9	60.0	186	14	10.1	0.78	77.5	4.2	18.3
His	69	10	76	14	6.0	0.65	17.9	41.0	41.1	83	14	5.0	0.75	48.4	26.4	25.2
Ile	141	30	160	18	8.4	0.91	27.5	8.7	63.8	152	10	9.7	0.88	10.1	10.3	79.6
Leu	293	46	278	41	17.5	0.84	7.7	24.6	67.7	269	38	16.6	0.86	17.1	22.3	60.6
Lys	193	34	208	24	14.2	0.81	14.5	15.2	70.3	202	21	12.9	0.85	7.7	6.4	85.9
Met	56	11	60	6	3.1	0.92	10.8	6.5	82.7	62	6	3.4	0.90	21.7	2.8	75.5
Phe	158	19	161	20	10.5	0.68	1.5	46.0	52.5	164	19	11.0	0.65	4.0	47.6	48.4
Thr	150	20	158	16	7.6	0.85	12.7	14.8	72.5	147	12	7.4	0.86	2.4	10.2	87.4
Val	173	29	183	21	10.0	0.88	9.2	20.3	70.5	180	21	11.1	0.85	3.4	36.1	60.5
			CPM							NRC						
CP			3,776	350	206.7	0.73	3.1	51.0	45.9	3,695	334	187.9	0.78	0.3	22.3	77.4
MCP			2,471	171	111.6	0.81	75.2	13.8	11.0	1,943	112	110.8	0.82	13.5	9.1	77.4
RUP			1,305	284	226.1	0.62	60.9	10.2	28.9	1,751	295	193.3	0.72	5.9	12.5	81.6
Arg			196	12	10.4	0.76	80.8	6.7	12.5	145	11	9.7	0.80	3.4	5.7	90.9
His			87	16	5.3	0.72	52.4	31.0	16.6	71	10	5.5	0.71	4.4	30.7	64.9
Ile			162	11	9.9	0.88	30.8	11.6	57.6	148	11	9.2	0.90	5.5	1.8	92.7
Leu			274	44	17.9	0.84	9.1	35.5	55.4	282	37	17.7	0.84	4.6	19.1	76.3
Lys			222	25	16.7	0.74	37.5	13.5	49.0	201	16	13.1	0.84	6.5	1.3	92.2
Met			71	6	3.2	0.92	66.8	1.0	32.2	58	5	3.3	0.91	3.8	1.3	94.9
Phe			171	22	11.5	0.61	14.1	53.5	32.4	157	16	11.2	0.63	0.3	34.9	64.8
Thr			157	13	8.2	0.83	7.3	27.2	65.5	150	11	8.2	0.82	0.0	5.4	94.6
Val			191	26	11.2	0.84	16.4	40.7	42.9	172	18	10.5	0.86	0.2	16.7	83.1

¹AC = AminoCow; AMTS = Agricultural Modeling and Training Systems; CPM = Cornell-Penn-Miner version of CNCPS; NRC = National Research Council (2001); see text for details on the versions used.

²RMSPE = root mean square prediction error.

³MSPE = mean square prediction error with percentage due to mean, regression, and random disturbance biases.

⁴Microbial CP.

Table 13. Observed and predicted duodenal flows (g/d), and statistical adequacy of 4 programs¹ for rations with low CP concentration (CP = 14.6 ± 1.2%; n = 41)

Item	AC						AMTS									
	Observed		MSPE bias partition ³						MSPE bias partition							
	Mean	SE	Mean	SE	RMSPE ²	R ²	Mean	Slope	Random	Mean	SE	RMSPE	R ²	Mean	Slope	Random
CP	2,634	780	2,330	653	150.4	0.96	26.5	1.4	72.1	2,461	625	105.7	0.98	0.0	0.9	99.1
MCP ⁴	1,526	450	1,244	423	198.2	0.79	21.9	26.6	51.5	1,599	102	100.6	0.95	6.9	0.8	92.3
RUP	1,151	536	1,154	314	130.8	0.94	0.0	0.9	99.1	1,120	321	118.0	0.95	0.7	3.3	96.0
Arg	105	42	98	29	8.5	0.96	4.6	0.3	95.1	129	36	9.0	0.95	34.3	4.1	61.6
His	51	17	46	14	4.6	0.93	12.3	0.8	86.9	54	16	3.8	0.95	11.0	2.8	86.2
Ile	105	37	102	30	6.9	0.96	1.1	10.7	88.2	109	28	6.1	0.97	1.8	0.7	97.5
Leu	190	80	172	51	16.3	0.96	10.5	2.4	87.1	183	56	10.2	0.98	2.6	4.4	93.0
Lys	135	49	128	38	9.0	0.96	2.8	7.2	90.0	141	40	9.1	0.96	2.5	0.9	96.6
Met	41	17	39	11	3.8	0.95	4.3	1.4	94.3	48	12	4.1	0.94	23.6	0.0	76.4
Phe	105	37	101	28	9.2	0.94	2.6	0.1	97.3	113	30	7.6	0.96	9.6	0.0	90.4
Thr	101	32	100	27	6.6	0.96	0.4	6.8	92.8	102	26	5.4	0.97	0.1	0.4	99.5
Val	121	44	115	31	8.4	0.96	3.2	1.2	95.6	124	32	8.6	0.96	0.9	0.0	99.1
							CPM							NRC		
CP			2,809	693	140.3	0.96	15.6	0.4	84.0	2,483	614	188.8	0.94	6.9	1.1	92.0
MCP			1,930	448	119.8	0.92	60.4	5.2	34.4	1,380	320	177.4	0.83	12.6	34.6	52.8
RUP			943	307	182.8	0.87	15.3	2.4	82.3	1,177	358	157.9	0.91	0.0	14.8	85.2
Arg			138	39	6.8	0.97	56.3	3.0	40.7	96	25	8.2	0.96	7.5	1.1	91.4
His			58	17	2.9	0.97	32.1	5.1	62.8	46	13	4.7	0.92	16.8	0.6	82.6
Ile			118	31	5.0	0.98	24.0	0.5	75.5	101	23	7.1	0.96	2.0	0.9	97.1
Leu			189	57	10.3	0.98	0.1	9.3	90.6	185	52	12.4	0.97	1.4	7.3	91.3
Lys			156	41	7.3	0.98	31.6	0.8	67.6	135	32	9.3	0.96	0.0	0.0	100.0
Met			54	14	3.5	0.96	62.0	0.0	38.0	41	10	3.9	0.94	0.2	6.5	93.3
Phe			119	32	7.2	0.96	36.2	0.0	63.8	104	26	9.2	0.93	0.2	2.3	97.5
Thr			110	29	4.8	0.98	19.1	0.8	80.1	102	24	6.5	0.96	0.2	0.0	99.8
Val			133	35	6.6	0.98	18.8	0.1	81.1	116	26	8.6	0.96	2.7	3.5	93.8

¹AC = AminoCow; AMTS = Agricultural Modeling and Training Systems; CPM = Cornell-Penn-Miner version of CNCPS; NRC = National Research Council (2001); see text for details on the versions used.

²RMSPE = root mean square prediction error.

³MSPE = mean square prediction error with percentage due to mean, regression, and random disturbance biases.

⁴Microbial CP.

Table 14. Observed and predicted duodenal flows (g/d), and statistical adequacy of 4 programs¹ for rations with high CP concentration (CP = 18.3 ± 0.9%; n = 55)

Item	AC						AMTS									
	Observed		MSPE bias partition ³						MSPE bias partition							
	Mean	SE	Mean	SE	RMSPE ²	R ²	Mean	Slope	Random	Mean	SE	RMSPE	R ²	Mean	Slope	Random
CP	3,428	671	3,462	520	155.7	0.94	0.5	1.6	97.9	3,352	489	165.2	0.94	2.1	1.3	96.6
MCP ⁴	1,719	329	1,912	326	203.7	0.59	30.6	15.9	53.5	1,750	254	211.5	0.56	1.4	16.6	82.0
RUP	1,787	596	1,562	328	227.3	0.85	16.4	0.1	83.5	1,629	294	224.3	0.85	9.4	0.5	90.1
Arg	138	29	144	25	12.4	0.81	5.6	13.8	80.6	172	28	12.6	0.80	56.5	10.9	32.6
His	68	15	69	15	6.7	0.80	0.5	18.3	81.2	75	16	6.9	0.78	20.7	17.7	61.6
Ile	133	34	151	23	9.7	0.92	31.6	0.0	68.4	142	21	9.8	0.92	6.0	8.1	85.9
Leu	260	78	260	54	16.3	0.95	0.7	0.2	99.1	250	53	16.1	0.95	0.8	2.5	96.7
Lys	173	40	191	31	10.9	0.92	27.3	1.6	71.1	184	31	11.6	0.91	8.4	8.7	82.9
Met	52	14	56	9	3.0	0.95	14.8	0.2	85.0	58	9	3.2	0.94	16.8	12.5	70.7
Phe	148	31	152	26	9.5	0.90	3.4	1.3	95.3	152	26	9.8	0.89	3.0	9.9	87.1
Thr	140	27	146	22	7.9	0.91	7.3	3.7	89.0	134	21	8.2	0.90	5.0	8.6	86.4
Val	159	43	169	28	9.6	0.95	33.2	5.5	61.3	164	29	10.2	0.94	1.8	8.3	89.9
			CPM						NRC							
CP			3,378	475	192.5	0.91	0.8	3.4	95.8	3,345	525	142.8	0.95	2.9	1.3	95.8
MCP			2,157	317	211.3	0.56	57.2	14.8	28.0	1,738	240	198.2	0.61	1.2	8.7	90.1
RUP			1,234	263	285.0	0.76	47.2	2.1	50.7	1,622	350	231.2	0.84	10.8	0.0	89.2
Arg			178	29	13.4	0.77	63.0	10.5	26.5	133	22	13.2	0.78	3.1	7.7	89.2
His			77	18	7.4	0.75	27.3	24.9	47.8	64	13	7.0	0.78	7.5	9.4	83.1
Ile			149	22	10.4	0.90	19.3	4.9	75.8	137	21	10.0	0.91	2.0	0.6	97.4
Leu			252	58	17.9	0.94	0.4	4.6	95.0	261	54	17.3	0.95	0.9	0.1	99.0
Lys			197	35	13.7	0.87	29.5	10.2	60.3	182	28	11.2	0.92	8.1	0.2	91.7
Met			64	10	3.1	0.95	47.6	5.1	47.3	53	8	3.1	0.95	2.3	0.5	97.2
Phe			156	29	11.0	0.86	8.7	16.1	75.2	144	25	13.0	0.81	1.9	4.2	93.9
Thr			141	23	8.9	0.89	0.1	13.5	86.4	137	21	8.2	0.90	2.8	1.7	95.5
Val			171	32	10.4	0.94	10.1	7.5	82.4	157	25	10.0	0.94	0.6	1.4	98.0

¹AC = AminoCow; AMTS = Agricultural Modeling and Training Systems; CPM = Cornell-Penn-Miner version of CNCPS; NRC = National Research Council (2001); see text for details on the versions used.²RMSPE = root mean square prediction error.³MSPE = mean square prediction error with percentage due to mean, regression, and random disturbance biases.⁴Microbial CP.

On low NDF diets, CPM had the largest RMSPE for protein fractions, whereas for high NDF diets, NRC had the largest.

Individual AA. For diets that were low in NDF, EAA flows were underpredicted within acceptable limits by AC, AMTS, and NRC, with predictions for Leu by AC and Arg by ATMS just barely useful. Arginine (21%) was overpredicted by CPM, and Met was just on the limit (15%) for acceptability. For high NDF diets, AC and NRC predicted all AA within acceptable limits. The AMTS model overpredicted Arg (29%) and Met (23%). The CPM model overpredicted Arg (36%), His (20%), Ile (17%), Met (38%), and Val (17%). Most of these inaccuracies were associated with a mean bias, but errors for Met in AMTS and His in CPM were due to a combination of mean and regression biases for high NDF diets (Tables 15 and 16). Predictions for low NDF diets resulted in AC having, on average, the lowest RMSPE for EAA, whereas CPM had the largest RMSPE. For high NDF diets, NRC had the largest RMSPE, whereas the 3 other models had very similar values.

DMI

Because many nutritionists use the respective model default DMI prediction without adjustment to balance dairy rations, we wanted to investigate the accuracy of model prediction of DMI for this data set using the same statistical model as for protein flows. The observed DMI averaged 19.1 ± 3.8 kg/d. The prediction of DMI by AC was 18.9 ± 2.6 kg/d; AMTS and CPM predicted 18.2 and 18.0 ± 2.5 kg/d, respectively; and NRC predicted 19.5 ± 2.9 kg/d. The RMSPE was low for all diets, averaging 0.97, 0.98, 1.00, and 0.89 for AC, AMTS, CPM, and NRC, respectively.

DISCUSSION

Models are an attempt to describe mathematically a real-world situation (McNamara, 2004). To predict the duodenal flow of CP fractions and EAA of adult dairy cows, the models evaluated here had to estimate complex rumen processes of microbial protein synthesis, ruminal escape of dietary protein and their AA concentrations, and where calculated, the flow of endogenous protein and its AA pattern. From dietary constituents and cow data such as BW and DMI, these models of rumen digestion use different assumptions: many of these are based upon models that have been previously developed and include features of Molly (Baldwin et al., 1987), INRA (1989), and various editions of NRC (1978, 1989). Models also emphasize different aspects of studies and employ different approaches and equations to arrive at predictions, for example factorial

summations versus empirical equations for estimating AA duodenal flows (discussed by Pacheco et al., 2006). As different models may require many or fewer inputs, the evaluation of a model by a working nutritionist may not necessarily assess which is best in absolute terms, but which is best in terms of resources spent and the accuracy obtained.

The primary differences between this study and previous evaluations of rumen CP and AA flows include the evaluation of models across a wide diversity of forage and concentrate ingredients as well as feeding levels and management. In addition, in all studies used in the current analysis, the duodenal protein fractions and EAA flows were measured in the same cows. The models evaluated in this study were reasonably robust when diets included corn as the primary grain and combinations of corn and alfalfa as the forage base. For diets based on other forages or on non-corn energy sources, the partition of CP duodenal flows into microbial CP and RUP was shifted among models. Generally, the AC, AMTS, and NRC models behaved similarly. Within grass-based diets, although the CP flows were estimated very accurately, a systematic underestimation of microbial CP was found, leading to an increased contribution of RUP, which tended to yield lower EAA flows. In contrast to non-corn-based diets, in corn-based diets a trend was observed for lower total CP and microbial CP flows for AC and NRC models and lower RUP flows for AC, AMTS, and NRC models. However, on average, the EAA flows were not underestimated and were even overestimated by AMTS. This may be due to the flow or to the prediction of EAA composition of different protein fractions, or to both (Lanzas et al., 2007). It was sobering to note that none of the models could be considered accurate and precise at same time for RUP and various EAA (this information is summarized in Table 17). Possible reasons underlying these differences will be discussed by model.

CNCPS Models

The AMTS and CPM models are both developed from the CNCPS system and thus share many characteristics. Briefly, both models assume 2 types of rumen bacteria: those that ferment fiber and those that ferment nonstructural carbohydrate (Fox et al., 2004; Tylutki et al., 2008). Dietary proteins are divided into 5 fractions depending on protein solubility determined from laboratory procedures in both models, where the first fraction (A) is NPN and contributes N only to RDP and to microbial synthesis, and the last fraction (C) is completely undegradable in the rumen. Flow of RUP to the duodenum is determined by the relative rate of degradation (**kd**) and rate of passage (**kp**) of

Table 16. Observed and predicted duodenal flows (g/d), and statistical adequacy of 4 programs¹ for rations with high NDF concentration (NDF = 38.3 ± 4.9%; n = 55)

Item	AC						AMTS									
	Observed		MSPE bias partition ³						MSPE bias partition							
	Mean	SE	Mean	SE	RMSPE ²	R ²	Mean	Slope	Random	Mean	SE	RMSPE	R ²	Mean	Slope	Random
CP	2,791	837	2,760	831	142.7	0.97	0.5	8.0	91.5	2,772	778	129.4	0.97	0.2	2.5	97.3
MCP ⁴	1,561	485	1,590	494	139.7	0.91	0.6	17.2	82.2	1,534	387	138.0	0.91	0.5	3.5	96.0
RUP	1,235	583	1,239	374	202.2	0.87	2.5	0.4	97.1	1,212	380	181.6	0.90	0.4	1.0	98.6
Arg	106	42	111	36	8.7	0.96	2.6	8.5	88.9	137	45	9.3	0.95	37.6	16.9	45.5
His	51	20	53	19	5.2	0.92	2.2	10.7	87.1	58	21	5.4	0.92	19.9	17.0	63.1
Ile	104	39	120	36	7.8	0.96	18.0	14.1	67.9	115	34	7.6	0.96	9.0	16.7	74.3
Leu	188	78	196	66	14.1	0.96	2.4	2.2	95.4	191	64	14.4	0.96	0.3	2.2	97.5
Lys	144	55	154	48	9.9	0.96	6.7	4.1	89.2	150	49	9.1	0.97	2.2	5.1	92.7
Met	39	14	44	13	3.2	0.94	19.8	12.0	68.2	48	14	3.1	0.94	39.7	12.9	47.4
Phe	112	41	118	37	9.2	0.95	5.0	2.5	92.5	121	39	9.1	0.95	10.1	4.3	85.6
Thr	110	39	117	35	6.6	0.97	4.7	6.4	88.9	108	34	6.6	0.97	0.5	4.1	95.4
Val	119	47	135	41	7.6	0.97	14.9	6.5	78.6	132	43	7.3	0.97	9.1	12.6	78.3
							CPM			NRC						
CP			2,921	758	161.9	0.96	6.8	2.1	91.1	2,721	774	176.4	0.95	2.7	1.4	95.9
MCP			1,864	483	135.7	0.92	35.9	11.2	52.9	1,478	381	167.2	0.87	5.6	1.0	93.4
RUP			1,060	345	217.0	0.85	14.4	0.2	85.4	1,270	432	181.9	0.90	0.6	0.0	99.4
Arg			144	45	8.7	0.95	49.5	12.6	37.9	105	31	9.3	0.95	0.0	2.0	98.0
His			61	22	5.2	0.93	30.0	16.6	53.4	50	17	6.0	0.90	0.2	2.2	97.6
Ile			122	34	7.2	0.96	21.8	12.1	66.1	111	30	9.6	0.93	4.4	7.5	88.1
Leu			195	63	18.0	0.94	1.4	1.5	97.1	200	64	18.0	0.94	5.0	1.1	93.9
Lys			163	50	8.3	0.98	20.8	4.2	75.0	149	42	11.4	0.95	2.1	0.0	97.9
Met			54	15	2.9	0.95	61.6	10.9	27.5	43	12	3.9	0.91	14.3	8.4	77.3
Phe			125	39	9.0	0.95	22.2	3.3	74.5	115	34	11.0	0.92	1.1	0.0	98.9
Thr			115	34	6.0	0.97	2.6	5.0	92.4	112	30	8.1	0.95	0.2	1.5	98.3
Val			139	43	6.7	0.98	20.8	10.0	69.2	127	36	9.8	0.95	5.1	1.7	93.2

¹AC = AminoCow; AMTS = Agricultural Modeling and Training Systems; CPM = Cornell-Penn-Miner version of CNCPS; NRC = National Research Council (2001); see text for details on the versions used.

²RMSPE = root mean square prediction error.

³MSPE = mean square prediction error with percentage due to mean, regression, and random disturbance biases.

⁴Microbial CP.

Table 17. Summary of the evaluation of 4 dairy ration programs to predict duodenal flows of total CP, microbial protein (MCP), RUP, and essential AA¹

Flow	Database	Type of diet												
		Forage base			Grain base		RUP		DMI		CP		NDF	
		Grass	Alfalfa	Corn silage	Non-corn	Corn	Not added	Added	Low	High	Low	High	Low	High
CP	All	AC, AMTS, NRC	AC, AMTS, CPM	AC, AMTS, NRC	AMTS, CPM	All	AC	All	AC, AMTS, NRC	All	None	All	AMTS, CPM	All
MCP	None	None	AMTS, NRC	NRC	None	AC, NRC	AC	None	None	None	None	AMTS	None	AMTS, NRC, AC, AMTS
RUP Arg	None AC, NRC	None AMTS	None AC, NRC	None None	None None	None AC, NRC	None AC	None AC, NRC	None None	None AC, NRC	None None	None AC, NRC	None None	None AC, NRC
His	AC	None	AC	AC	None	AC, NRC	AMTS	AC	AMTS, CPM	AC	None	AC	AMTS	None
Ile	NRC	AC, AMTS	NRC	AC, AMTS, NRC	None	AC, AMTS, NRC	AC, AMTS, CPM	NRC	AC, AMTS	NRC	AC, AMTS, NRC	NRC	AMTS, CPM	None
Leu	All	All	None	NRC	None	None	None	All	All	All	AMTS, CPM, NRC	All	None	AC, AMTS, CPM, AMTS, NRC
Lys	AC, AMTS, NRC	AC, NRC	AC, AMTS, NRC	AC, NRC	NRC	AC, AMTS, NRC	AC, AMTS, NRC	None	AC, AMTS, NRC	None	AMTS, NRC	None	AC, AMTS, NRC	None
Met	AC, NRC	None	None	AC, NRC	None	AC, NRC	AC, NRC	AC, NRC	None	AC, NRC	AC, NRC	NRC	AMTS	None
Phe	AC, AMTS, NRC	AC, AMTS, NRC	AMTS, CPM	AC, AMTS, NRC	AC	AC, AMTS, NRC	AC, AMTS, CPM	AC	AC	AC	AC, NRC	AC, AMTS, NRC	AMTS, CPM	NRC
Thr	All	AC, CPM, NRC	AC, CPM	All	AMTS, NRC	AC, CPM, NRC	AC, CPM	AC, AMTS, NRC	CPM	AC, AMTS, NRC	AC, AMTS, NRC	All	CPM	AMTS, CPM, NRC
Val	AC, AMTS, NRC	AC, CPM	AC, AMTS, NRC	AC, AMTS, NRC	NRC	AC, AMTS, NRC	AC, AMTS, CPM	AC, AMTS, NRC	AC, AMTS, NRC	AC, AMTS, NRC	AC, NRC	AMTS, NRC	CPM	None

¹Models with very accurate prediction of the mean (within 5% of the observed values) and relative prediction error less than 10% are listed for each of the dietary types and feed management conditions evaluated. AC = AminoCow; AMTS = Agricultural Modeling and Training Systems; CPM = Cornell-Penn-Miner version of CNCPS; NRC = National Research Council (2001); see text for details on the versions used.

the B₁, B₂, and B₃ fractions. The rate of degradation is defined by the in sacco procedure and rate of passage is calculated by the model. Microbial CP is also determined from kd and kp. Predicted deficiency in ammonia levels will reduce the amount of microbial CP synthesized proportionally. Predicted levels of rumen peptides are considered stimulatory to non-fiber-fermenting bacteria (Fox et al., 2004) and some provision is made in AMTS for urea recycling (Tylutki et al., 2008). Rates of passage are modified by effective NDF (peNDF) and rates of fermentation are modified by predicted rumen pH (Fox et al., 2004). The AA composition of RUP is determined as the AA composition of the undegraded protein. A large difference between these 2 models is the changes in kd for protein fractions as well as smaller changes in kp (Tylutki et al., 2008). Neither model attempts to account for the presence of endogenous protein in duodenal CP flow.

On average, CPM slightly overpredicted duodenal CP flows because of considerable overprediction of microbial CP on most ration types investigated. In this study, of the 13 types of rations studied, only in diets where grass was the major forage was microbial CP overpredicted within acceptable limits (14%). The overprediction of microbial CP by more than 25% across all diet types resulted in smaller predictions of RUP than were observed, resulting in systematic overpredictions of various EAA compared with the reported values; only Leu flows were underpredicted on average. This situation has been largely corrected in the latest CNCPS model (AMTS). In fact, the AMTS model predicted within 3% of observed microbial CP and did it with the lowest RMSPE of all the models and the highest partition of MSPE in random disturbance, indicating a very robust and precise model for microbial CP synthesis. A similar situation exists for RUP, with AMTS having the smallest RMSPE of all models for this protein fraction. Overall, AMTS predicted a slightly greater flow for total EAA, but that mainly originated from overprediction of Arg and, to a lesser extent, Met. In 10 of the 13 ration types, AMTS overpredicted Arg outside acceptable limits, and this was by an average of 26%. Methionine was overpredicted in 4 ration types (alfalfa-based, non-corn-based, low CP, and high NDF diets) and was just barely acceptable in 4 other ration types (no added RUP, added RUP, high DMI, and high CP) and equal to CPM for having the highest RMSPE for Met. It is not possible from the data in hand to understand why the prediction of Arg and Met should behave in this manner, although because the percentage of microbial CP is different for these diets, we suggest that the assumed concentration of Arg and Met in RUP of ingredient(s) might have been overestimated.

AC Model

The AC model requires fewer inputs than the other models. Dietary protein is broken into RDP and RUP similar to the sixth revised edition of NRC (1989), but using the RDP as determined by the *Streptomyces griseus* assay (Evonik Industries GmbH, 2007b) and assuming that RDP plus RUP percentages equal to 100% of CP. The RUP arriving at the duodenum is calculated as CP amount times the RUP percentage, with an adjustment for DMI. The AA composition of RUP is assumed to be the same as for the feed ingredient protein. Microbial CP is considered one homogeneous mass and is predicted from the truly digestible nutrients of the entire daily diet, as described in the seventh edition of NRC (2001). No provision is made for urea recycling, a peptide effect, or asynchrony between carbohydrates and rumen N. However, a deduction of microbial CP is taken when predicted RDP supply is negative. This deduction is curvilinear, with greater deductions as the calculated RDP deficiency becomes greater. Endogenous protein is calculated, and an AA composition of this protein is assumed as constant (Evonik Industries GmbH, 2007a).

Although AC predicted RUP with acceptable accuracy, it underestimated microbial CP on 2 diet types (low DMI and low CP diets). Inspection of these rations indicated that the deduction made on microbial CP might be too large when the model-calculated RDP deficiency was greater than -0.54 kg. Additionally, AC underpredicted His flow by more than 10% on grass-based, non-corn-based starch, low intake, low CP, and low NDF diets. These diets were generally of low intake, suggesting that AC may not account appropriately for the His contribution from microbial CP. Arginine on grass-based diets was also underpredicted, but because it was not underpredicted on other low DMI diets, this could reflect an error in the Arg concentration assumed for grasses.

NRC Model

The NRC model may be looked at as intermediate in complexity between the CNCPS models and the AC model. The NRC model uses 3 fractions of CP, based on in situ ruminal protein degradation (NRC, 2001). Protein fraction A is completely rumen degradable, fraction C is completely undegradable in the rumen, yielding fraction B, which is potentially degradable in the rumen. Fractions are determined by curve peeling of individual ingredients by the in sacco technique. Degradation constants are determined in a similar manner. Passage rates are calculated depending on whether the

ingredient is concentrate or forage (dry or wet). Microbial CP yield is calculated from discounted total digestible nutrients. Essential AA of feeds are considered to be the same for the RUP fraction. Endogenous CP is calculated, but like microbial CP, the AA composition is not reported. The EAA flows are determined by regression equations relating the percentage of AA in duodenal flow to percentage of each EAA in RUP and percentage of RUP in duodenal flow, and then multiplying the percentage of EAA in duodenal flow by CP duodenal flow (NRC, 2001).

The NRC model predicted mean microbial CP and RUP closer to observed values than the other models, although generally with greater RMSPE than either AC or AMTS. The predictions of AA were, on average, slightly underestimated, but NRC had the lowest slope bias compared with the other models. On average, flows of Arg and His were underpredicted to a greater degree under "low" supply conditions compared with their "high" counterpart (i.e., grass-based vs. corn silage-based diets; non-corn-based vs. corn-based diets; no added vs. added RUP; low vs. high intake; low vs. high protein; low vs. high NDF). Because AC and NRC use a common data set for AA composition of feeds and because RUP flows were predicted close to observed, the Arg underprediction could be due to underestimation in feed protein, whereas the His underprediction occurs as a result of underestimation in both feed and microbial protein. Other than underprediction of Arg and His, the NRC model proved to be very robust across the different diet groups, with smaller mean and slope biases than the other models.

Other Considerations

It is interesting to note the close approximation of model-predicted DMI to that actually observed. However, model predictions of DMI were within 1.5 kg of measured in only 61, 50, 49, and 58% of the diets (by AC, AMTS, CPM, and NRC, respectively). This suggests that accurately balancing AA in dairy rations may not be easy to achieve unless actual DMI is determined. Using the estimated DMI values from the models to provide protein supply could result in both over- and underfeeding of protein in practical situations. It is also interesting to note that individual diets that had a poor prediction of DMI in one model seemed to have a poor predictions in other models. Likewise, in general terms, all models tended to have more problems accurately predicting some AA than others. This was particularly noticeable for Arg, His, Ile, and Met, which appear to be predicted with more biases than Leu, Lys, Val, Thr, and Phe. This may suggest that applying similar constants (i.e., similar biology) to all

AA may be in error. For example, across all diets, Leu was underpredicted by all models (Table 2). However, this underprediction by all models was not present with non-corn-based diets but was consistently present with corn-based diets. This suggests that Leu, present in high concentration in corn protein, might have greater concentrations than those used in the model database, or Leu is less degraded in the rumen than the other AA in these types of diet. It is also of interest that in terms of mean prediction and RMSPE, adding more protein fractions did not greatly increase the precision or accuracy of RUP prediction. This may mean less variation in RUP of specific proteins or a lack of basic knowledge as to how proteins are actually degraded by various rumen populations.

Finally, the results of this study must be viewed with some caution. For example, NRC may appear to be best at predicting the means of the measured protein fractions with the lowest bias because unreported feed ingredient values were taken from NRC. In addition, it should be acknowledged that data necessary for the full function of the CNCPS models was not available. It may well be that adding these inputs would improve the accuracy or reduce the RMSPE of the CNCPS-based models. However, except for CPM, the other models appeared to predict with sufficient accuracy and without bias except in those situations already detailed. With the exception of those AA already noted, the models appear adequate for use in routine ration work if the actual DMI is determined. It is encouraging that AC, AMTS, and NRC accurately predicted the means of observed AA flow and predicted as close to each other as they did, and that the RMSPE and error partitioning were also close. This implies that nutritionists have tools available so that AA balance and subsequent protein savings should begin in earnest.

CONCLUSIONS

No model was clearly superior to the others; all have areas where significant improvements can be achieved, as summarized in Table 17. With the possible exception of CPM, commercially available nutritional models can accurately predict the flow of EAA to the duodenum, although EAA flows are better predicted on corn-based diets than on other diet types. Although all models need improvement, some of which were detailed in this analysis, it is clear that model errors in the prediction of duodenal EAA flows are not a large barrier for adoption of EAA balance in diets for dairy cattle.

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APPENDIX

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