

Models for Estimating Duodenal Amino Acid Flow and Total Tract Digestibility of Starch

Robert A. Patton¹

Nittany Dairy Nutrition, Inc.

Abstract

Philosophy and usefulness of various nutritional models are discussed and comparisons among models for flow to the small intestine of protein and essential amino acids (AA) are discussed. In general terms, most models predicted with useful accuracy the flow of microbial protein, rumen undegradable protein, and AA. However, models poorly predicted both the observed ruminal starch degradation and the post ruminal starch digestion; whereas, all models tested predicted total tract starch digestion with accuracy. Predictions of dry matter intake (DMI) are also discussed and evaluated. Results suggest that more work needs to be done with diets based on starch from small grains and with consistent reporting of starch particle size in order to improve predictive accuracy for both starch degradation and AA flow.

Introduction

Over the past 30 years, the practice of establishing requirements and evaluating nutritional adequacy by use of nutritional models for dairy cattle has taken over the feed industry. Private companies, universities, governments, and even individual nutritionists have developed models. It will be the purpose of this paper to look at some concepts governing nutritional modeling, recommend some techniques for evaluating a model, and look at a few specific model comparisons.

Disclaimer

I am not a researcher or an academic. I am foremost a working nutritionist, but secondarily, I have developed several models for dairy rations. This makes me innately prejudiced—not for or against certain models, but for or against certain ways of looking at the modeling process.

About Models and Model Types

In this context, a model is a mathematical description of a physical or biological process (McNamara, 2004). For example, we might say, “A heifer grows at 1.64 lb/day.” Of course, we can quickly add that the process is more complicated than that. We know that the heifer grows at different rates at different stages of her life; we know that the energy and protein content of the diet will allow her to grow at different rates; we know that if the environment is cold, or hot or dirty, these factors will impact the actual growth rate. We even know that different heifers that all look the same and are fed the same ration will grow at different rates. Therefore, the model of heifer growth needs to be much more complex if it is to be useful.

Model complexity is basically of 2 broad types: 1) deterministic in which the mean of one modeled effect (for example, ruminal starch digestion) leads to the mean of another effect (production of volatile fatty acids [VFA]); or 2) random effect (probabilistic or stochastic) in which

¹Contact at: 9355 Buffalo Road, Mifflinburg, PA, 17844; (570) 966-4770; FAX: (570) 966-4737; Email: nittnut@aol.com.



a random portion of starch is digested ruminally and a random portion of this leads to a random amount of VFA produced. In both cases, factors known to affect the process can be added to modify the output. An example of the first model type is the NRC (2001) model, which models everything by association of linear and non-linear regression. An example of the second would be the Molly Model developed at UC-Davis by Dr. Lee Baldwin and his students, which looked at nutrient and intermediary pools and rates of reaction of basic biochemical reactions to arrive at cow performance. There is a general perception that the stochastic models are more desirable because they more clearly mimic what occurs in biology. However, the stochastic approach generally requires a more complete understanding of the biology of the cows, which may or may not exist. In other words, if there are 100 equations required to model a biological function, without the complete knowledge of how these equations relate to each other, by the laws of probability the set of equations will inevitably vary back to the average values. So while on the surface, a random model may look like it has very sophisticated knowledge, it may well be just as accurate to use a point estimate (or the average) of these effects.

Models have 2 basic uses. The original use was to describe a process so that it could be dissected, studied, and understood. The knowledge in this usage of a model is more speculative because it is in the stage of testing knowledge. The other use of a model is based on more certain knowledge and is used to manage and monitor a complicated system that can change in time or space. It is the latter approach that we want to use as working nutritionists.

Regardless of approach, all models are imperfect and all models are constantly changing. We live in a world of incomplete information and competing theories. The developer of any model must take into account these factors and make

assumptions about the relative correctness of any theory and any set of data. As model users, we need to be aware of these assumptions and understand that no matter what a modeler may select for inclusion or exclusion in a given model, it will never completely mimic animal biology. Likewise, as new research reveals more exact information, this will be added to the knowledge base of the model. Hence, we are sure that some or all of the models evaluated by our analyses have changed since the study was performed. The difficulty of updating models is, of course, to add information that really improves the accuracy of the model. On the one hand, it is important not to over react to the observations of each individual study; however, on the other hand, if one waits until all aspects are proven, the model may no longer be useful.

How to Judge a Model?

The single, overwhelming method of judging a model is to answer the question, "How well does the model predict animal performance?" That is to say, the model should be developed and tested with real cows and not just with in vitro studies. Permit us to give an example:

Thousands of dollars are spent each year on in vitro testing for rates of starch degradability and NDF digestibility. Both of these degradation rates are then entered into the model of Ørskov and MacDonald (1979) as below:

$$\text{Ruminal digestibility (\%)} = \text{nutrient weight} \times \left(\frac{kd}{kd + kp} \right) * 100$$

In a small trial to determine the usefulness of this test, NDF digestibilities of 22 diets were entered into the NittanyCow (**NC**) and Cornell-Miner (**CPM**) models to compare predictions of NDF digestibility to observed measurements. In this study, the NDF digestibility was adequately predicted for grass and alfalfa based diets, but NDF digestibility was over predicted for corn silage based



diets by 22% for CPM and 17% for NC (Patton, unpublished). Likewise, when we analyzed model predictions of ruminal starch degradation, they were over predicted by nearly 40% using the Ørskov and MacDonald (1979) model.

Why, then, did these sophisticated models fail to produce useful predictions that match observations of cow biology? It was at this Conference a few years ago that Dr. Mike Allen made the same observations regarding starch degradation (Allen, 2011). His suggestion was that the rate of passage (kp) was being underestimated; whereas, our suggestion was that the kd (rate of digestion) was being over predicted because of the uniform grind size in the in situ determination. In the end, it may prove that a combination of factors is responsible. Perhaps, the question that should be asked is, “Does the Ørskov equation really describe the kinetics of rumen degradation?” Regardless of one’s conclusions, this is a case when questioning the underlying assumption of the model may lead to more useful answers.

Also, it is important to keep in mind that the model should not stop with the rumen. A good model will integrate the by-products of rumen fermentation, as well as those substances that bypass rumen fermentation and integrate them with intestinal, hepatic, and mammary metabolism in order to both generate requirements and evaluate the effects of individual feeds and nutrients on the overall productivity of the animal.

Another critical (though less obvious) question is, “Has the appropriate standard been used for comparison?” This is not so simple because it is easy to miss the critical measurement.

The title of this paper is one example. In this title, the phrase “total tract digestibility of starch” is used. However, do we really care about total tract digestibility? The amount of ruminally fermented starch has the potential to produce ruminal acidosis.

Also, the relative proportion of starch fermented to propionate and other VFA compared to that absorbed as glucose in the small intestine can affect cow metabolism and productivity. Therefore, what is really important to know is: 1) what part of the starch is degraded ruminally; 2) what portion is digested in the small intestine; and 3) what portion is degraded in the hindgut (where only a small portion of the VFA could make a contribution to the overall glucose metabolism of the cow). If we look in the literature, we will find many studies that measure apparent digestibility of starch. As we will discuss, the models that we examined predicted this “total tract” digestion quite accurately. So if that was our only criterion for comparison, we could say all the models predicted spectacularly. However, because of our understanding of the biology of the animal, we know that this prediction is not very useful. We need to know how much starch was degraded in the rumen and how much was digested in the intestine. Less digestion in the rumen will mean a lower risk of acidosis and more glucose available from the starch digested in the small intestine (Reynolds, 2006). This is a case where the very accurate prediction of a measurement is not very useful because the measurement itself is not particularly descriptive of the known biology.

Once the appropriate variable has been measured, then more rigorous statistical means of evaluating the model should be used: 1) a model with a smaller mean square predicted error (**MSPE**) is more useful than one with a larger MSPE, 2) the root mean square error (**RMSE**) should be below 15% of the mean (**RPE**), and preferably less than 10%. 3) the model should predict the mean of the sample population as closely as possible to the observed, and the spread of the predicted range should match as closely as possible the observed range without over extending it, and 4) lastly, it is desirable to have an intercept of the linear equation as close to zero as possible and the slope of the equation close to one (Tedeschi, 2006). Further, it is possible to resolve the MSPE into a mean bias, a

slope (or regression) bias, and random error in order to understand where the model might be failing. Models that have mean bias and slope bias of less than 10% are more useful than those that have greater biases. Ideally, random error should account for at least 80% of the total error (Bibby and Toutenburg, 1977). Models normally display various combinations of these descriptive statistics. So one may predict the range, but over predict the mean, for example. Unfortunately in these types of studies, the correlation coefficient (R^2) is really an ineffective discriminatory technique.

The statistical technique that makes all of this possible is the development of the meta-analysis. While a description of this statistical procedure is well beyond this paper, suffice it to say that this procedure allows the combining of studies with more or less the same design or same outcome variable. By removing the effect of a study, (i.e., error and unknown factors), it is possible to aggregate all the results so that a “net effect” can be determined. Obviously, the greater number of studies which are included, the more confident one can be that the effect is real. In general, with 10 studies, trends can be detected. With 50 studies, there can be a high degree of certainty, and with 100 studies, the results are virtually assured.

Model Comparisons

Duodenal flows of protein and essential AA

The final dataset that we used for assessing protein and AA flow consisted of 40 studies that represented 154 individual dietary means which were gleaned from all studies in milking cows that had sufficient data on body weight (**BW**), milk production, and ration ingredients such that the ration could be reconstructed and where actual DMI was reported (Pacheco et al., 2012). All studies were conducted in doubly cannulated cows (i.e., at both the rumen and the duodenum) and were of short duration (usually less than 4 weeks). Diets were

entered into AminoCow version 3.5.2 (**AC**; RP Nutrients, Springfield, NJ), Agricultural Model and Training Systems version 2.0.15 (**AMTS**; Cortland, NY); Cornell-Penn-Miner version 3.0.1 (**CPM**; Cornell University, Ithaca, NY), and the 2001 model of the National Research Council (**NRC**). These models were selected because at the time of the study, they were readily available and widely used commercially. When ingredient composition was given in the study, this composition was used. When the ingredient analysis was not provided, the NRC values for each feedstuff were used. This occurred mainly for grains and for small inclusion ingredients. When only the nutrient composition of the total diet was given, the forages in the diet were adjusted so that the total ration agreed with the reported nutrient density. Therefore, all models contained the same exact dietary information, including crude protein, but the information on protein fractions, degradation rates, and passage rates were entered as program defaults. Comparisons were between the flow of CP, microbial protein (**MCP**), rumen undegradable protein (**RUP**), and essential AA (Arg, His, Ile, Leu, Lys, Met, Phe, Thr and Val) reported for each diet and that predicted by the models. Treatments were further segmented into dietary forage sources (grass, corn silage, and alfalfa based diets), carbohydrate source (corn versus non-corn based diets), RUP source (added versus no RUP source), high (> 48.5 lb/day) and low DMI (< 37.5 lb/day), low CP ($14.6 \pm 1.2\%$) or high CP ($18.3 \pm 0.95\%$), as well as high ($38.3 \pm 4.9\%$) and low ($27.1 \pm 2.1\%$) dietary NDF.

The ability of each model to predict the mean of protein and AA flows across the total dataset is presented in Table 1. All models predicted the flow of total CP accurately. The CPM over predicted microbial crude protein (27%), and under predicted the flow of RUP (24%), while the other models predicted these flows within 10% of observed. CPM over predicted the flow of Met (25%), Lys (13%), and Arg (31%), while AMTS over

predicted the flow of Met (12%) and Arg (24%). For both models, other AA were within 10% of what was observed; whereas, AC and NRC predicted the flow of all AA within 10%.

Statistical evaluation for predictions across all diets is presented in Table 2 for MCP, RUP, Met, Lys, His and Arg. Briefly, with the exception of the AC prediction of MCP and NRC and CPM for predictions of RUP, the RMSPE errors are remarkably similar. Generally, the NRC model displayed the lowest intercept and the slope closest to 1, suggesting that this was the most useful model. The CPM had a random disturbance term lower than 75% and generally had a large mean bias for those components investigated. Overall, except for CPM, the other models provided useful predictions across all diet types for these nutrients.

The data look slightly less encouraging when looking at different diet scenarios. Tables 3 and 4 present a summary of all diet types tested and lists the models that predicted within 5% of the mean (i.e., was accurate) and whose RPE was less than 10% (i.e., was precise). It should be obvious that there was no perfect model. It is particularly disturbing that neither model predicted non-corn rations well nor did any model accurately predict the amount of RUP flow for any diet combination. Across all possible combinations in this study (168), the best model was accurate and precise only 50.6% of the time. But, clearly all models are useful for diet construction - even CPM, which although not accurate, is precise. Because the bias in CPM tends to be a mean bias, as long as the user is aware that the model over predicts flows of MCP and AA, the model can be adjusted in order to achieve satisfactory performance.

Ruminal degradation and total tract digestion of starch

Like the protein dataset, studies were gathered from all sources that reported sufficient

data to reconstruct the diet, production, BW and both ruminal and total tract starch digestion. Diets on a DM basis were entered into models using the same technique as described above. The model entitled 'OFF' was constructed as an Excel spreadsheet using the equations of Offner and Sauvant (2004), while that labeled SM_NC is a 'simple method,' also calculated as an Excel spreadsheet. Briefly, the SM_NC method considers that any given starch source can contribute at most all the degradable starch up to the total reported degradability, or at the very least the amount of starch remaining after considering all other starch sources are 100% digestible. These values then establish the minimum and maximum possible starch digestibility of a given source in a given diet. Then, the average of these 2 values was entered as the predicted starch digestibility for the source under investigation (see Patton et al., 2012, for a full description of this process). In the end, there were 41 studies with 161 diets. Two of the studies were with dry cows. Starch sources included 83 diets based on corn, 58 diets based on small grain (barley, oats, and wheat), and only 8 diets based on sorghum.

Ability to predict the mean observed total tract, rumen, and post-ruminal digestion (total intestinal) for all diets is presented in Table 5, as well as corn, small grain and sorghum based diets separately. Please notice that for each diet type, the predictions of total tract starch digestion are rather close to observed for all the models, except that starch digestion of sorghum in which the observed digestion was over estimated by all models. The AMTS and CPM models considerably over predicted (25 to 40%) the amount of starch degraded in the rumen, and because of this, under predicted starch digested post ruminally. The OFF model closely predicted the mean ruminal degradation across all diets and for the sorghum diets, but considerably over-predicted degradation in corn and small grain based diets. The SM_NC closely predicted ruminal digestion across all diets

and for corn and sorghum based diets but considerably under predicted starch degradation in diets whose starch source was small grain. This model also over predicted the amount of post-ruminal starch digested for small grains and sorghum. No model captured in a useful way the range in either rumen degradation or post-ruminal digestion.

Model statistical comparisons are present in Table 6 for all diets for total tract, rumen, and post-rumen digestion, but rumen and post-rumen data only for corn, small grain and sorghum diets. What this clearly shows is that none of the models tested are really useful for predicting anything except total tract starch digestion. All of the models have huge inaccuracies in terms of intercepts, slopes, and the amount of error due to random disturbance.

There were several more things of interest brought out in this study. First, we found that ruminal starch degradation was depressed across all diet types, from 75% when starch consumption was less than 2 lb to about 60% when starch intake was greater than 10 lb. We also could find no effect of DMI per se, but only the amount of starch in the diet (e.g., not as a percent of starch, but weight of starch). This result is contrary to the studies of Firkins et al. (2001) and Offner et al. (2003). More studies will be required in order to separate these effects.

As reported by both Nocek and Tamminga (1991) and Firkins et al. (2001), starch particle size has the biggest effect on the variability of starch digestion. Yet, starch particle size data were rarely reported in the studies assembled in the dataset for this study, and when particle size was reported, it was not on a consistent basis. At least a portion of the failure of models to adequately predict starch degradation could be due to the lack of consistent particle size data. It is clear that if researchers want to adequately study ruminal starch degradation, they must develop a uniform particle size separation criterion and report particle size data in feeding studies. In any case, it seems futile for nutritionists

to ask for tests of starch degradability when we really do not have fruitful ways of using these data in existing models.

The DMI Dilemma

While it is fair and correct to evaluate models, the misuse of these same models is far more perplexing. This is especially true in the case of DMI predictions, and unfortunately, most nutritionists are still using model generated DMI consumption when balancing rations. We looked at DMI predictions in the study of Pacheco et al. (2012) and found that the actual DMI was within 3.3 lb of observed only 61, 50, 49, and 58% of the time for intake predicted by AC, AMTS, CP and NRC, respectively. In other words, regardless of model, 40 to 50% of the time we miss the DMI by more than 3 lb! Because of the effect of this much DM difference on the flow of nutrients to the rumen and to the duodenum, as well as on the production of MCP, it seems a bit disingenuous to try to pick “the best” model when the difference between actual and predicted DMI would more than overwhelm differences predicted by models. If nutritionists are serious about using the technology of AA balance and ruminal starch degradation, they must first stop using default prediction of DMI and endeavor to determine the true DMI for the groups of cows for which they are balancing rations. Using a single herd TMR, where DMI is widely divergent, may be one reason that AA balance technology has not greatly advanced (Patton, 2009), in spite of relatively good accuracy of prediction of AA flows by various models.

Final Considerations

There seems to be a growing sentiment that the more complicated and the more inputs a model requires, the better it will predict a given biological outcome. If we take a look only at the models for protein and AA flows, 3 levels of complexity are represented: AC, which uses only 1 term to describe



the amount of RUP and rumen escape AA; NRC, which uses 3 terms (totally degraded, totally undegraded, and potentially degraded); and the CNCPS model, which uses 5 fractions (a totally degraded, a totally undegraded and a potential degraded fraction that is subdivided into 3 parts). Given the results in hand, it does not appear that adding greater protein fractionation is providing better prediction of RUP flow, MCP, or AA flow. In the future, it may turn out that more fractions are needed, but at present, it seems to be adding unneeded complexity. Likewise, adding additional effects to carbohydrate modeling, such as starch vitreousness and protein coating, while they may be valid, cannot improve models until the particle size issue is resolved.

Conclusions

Available models, excepting perhaps CPM, can be usefully accurate and precise at predicting the flow of protein and AA to the small intestine. However, competing models are reasonably poor at predicting ruminal and total tract starch digestion with precision. Significant work needs to be performed with small grain based diets in terms of improving prediction of both AA flow and starch degradation. Starch digestion trials must report starch particle size on a consistent basis if progress toward more accurate predictions will be made.

References

- Allen, M.S. 2011. Mind over models. Pages 29-43 in Proceeding of Tri-State Dairy Nutrition Conference, Fort Wayne, IN. Published by The Ohio State University, Columbus.
- Bibby, J., and H. Toutenburg. 1977. Chapter 1: Basic ideas. Pages 16-19 in Prediction and Improved Estimation in Linear Models. John Wiley and Sons, London, UK.
- Firkins, J.L., M.L. Eastridge, N.R. St-Pierre, and S.M. Nofstger. 2001. Effects of grain variability and processing on starch utilization by lactating dairy cattle. *J. Anim. Sci.* 79(E. Suppl):E219-E238.
- McNamara, J.P. 2004. Research, improvement and application of mechanistic, biochemical dynamic models of metabolism in lactating dairy cattle. *Anim. Feed Sci. Technol.* 112:155-176.
- Nocek, J.E., and S. Tamminga. 1991. In situ and other methods to estimate ruminal protein and energy digestibility: A review. *J. Dairy Sci.* 74:3598-3629.
- NRC. 2001. Nutrient Requirements of Dairy Cattle. 7th rev. ed. Natl. Acad. Sci., Washington, DC.
- Offner, A., A. Bach, and D. Sauvant. 2003. Quantitative review of in situ starch degradation in the rumen. *Anim. Feed Sci. Technol.* 106:81-93.
- Offner, A., and D. Sauvant. 2003. Prediction of in vivo starch digestion in cattle from in situ data. *Animal Feed Sci. Technol.* 111:41-56.
- Ørskov, E.R., and I. McDonald. 1979. The estimation of protein degradability in the rumen from incubation measurements weighted according to rate of passage. *J. Agric. Sci. (Camb.)* 92:499-503.
- Pacheco, D., R.A. Patton, C. Parys, and H. Lapierre. 2012. Ability of commercially available dairy ration programs to predict duodenal flows of protein and essential amino acids in dairy cows. *J. Dairy Sci.* 95:937-963.
- Patton, R.A. 2009. The strategic use of ruminally protected amino acids in dairy nutrition. Proceeding of 2009 Florida Ruminant Nutrition Symposium, Pages 39-51. University of Florida, Gainesville.



Patton, R.A., J.R. Patton, and S.E. Boucher. 2012. Defining ruminal and total-tract starch degradation for adult dairy cattle using in vivo data. *J. Dairy Sci.* 95:765-782.

Reynolds, C.K. 2006. Production and metabolic effects of site of starch digestion in dairy cattle. *Anim. Feed Sci. Technol.* 130:78-94.

Tedeschi, L.O. 2006. Assessment of the adequacy of mathematical models. *Agric. Syst.* 89:225-247.



Table 1. Ability of models to predict the mean observed value across all diet types.¹

Model ²	Flow (g/day)	Mean	±SE	% observed	Flow (g/day)	Mean	±SE	% observed
Observed	CP	3027	790	--	MCP	1610	407	--
AC		2945	769	97.3		1605	499	99.7
AMTS		3026	638	100		1678	314	104.2
CPM		3148	633	104		2050	145	127.3
NRC		2951	708	97.5		1573	416	97.7
Observed	RUP	1480	614	--	Arg	122	38	--
AC		1368	372	92.4		123	33	100.8
AMTS		1348	409	91.1		152	37	124.6
CPM		1126	315	76.1		160	38	131.1
NRC		1415	416	95.6		116	28	95.1
Observed	His	61	20	--	Ile	119	36	--
AC		59	18	96.7		127	34	106.7
AMTS		66	18	108.2		126	28	105.9
CPM		69	20	113.1		134	30	112.6
NRC		56	16	91.8		120	27	100.8
Observed	Leu	230	79	--	Lys	157	48	--
AC		220	64	95.7		161	45	102.5
AMTS		219	60	95.2		164	40	104.5
CPM		224	61	97.4		178	43	113.4
NRC		226	62	98.3		160	38	101.9
Observed	Met	47	16	--	Phe	129	38	--
AC		48	13	102.1		128	34	99.2
AMTS		53	11	112.8		134	33	103.9
CPM		59	13	125.5		140	34	108.5
NRC		47	11	100.0		126	31	97.7
Observed	Thr	123	34	--	Val	141	45	--
AC		124	32	100.8		145	37	102.8
AMTS		120	28	97.6		147	36	104.8
CPM		127	29	103.3		155	38	109.9
NRC		120	27	97.6		138	32	97.9

¹CP = crude protein, MCP = microbial crude protein, and RUP = rumen undegradable protein.

²Models tested: AminoCow (AC), Agricultural Modeling and Training System (AMTS), Cornell-Penn-Miner (CPM), and National Research Council (NRC).

Table 2. Model adequacy statistics for microbial crude protein (**MCP**), rumen undegradable protein (**RUP**), Arg, His, Lys and Met.

Item	Model ¹	RMSE ²	RPE ³	Intercept	Slope	MSPE bias partition (%)		
						Mean	Slope	Random
MCP	AC	199.2	12.4	997	0.37	0	43.5	56.4
	AMTS	173.5	10.8	425	0.70	3.9	6.5	89.6
	CPM	178.6	11.1	531	0.52	56.9	10.1	33.0
	NRC	179.6	11.2	551	0.67	1	11.8	87.2
RUP	AC	179.6	12.1	224	0.89	5.9	1	93.1
	AMTS	172.3	11.6	154	0.94	4.3	1.3	94.3
	CPM	245.2	16.6	812	0.55	29.4	0.4	70.2
	NRC	198.5	13.4	314	0.68	2.3	0.2	97.5
Arg	AC	11.2	9.2	41	0.65	0	11.9	88.1
	AMTS	11.2	9.2	29	0.61	39.7	11.8	48.5
	CPM	11.4	9.3	32	0.56	53	9.4	37.6
	NRC	11.2	9.2	26	0.82	4.3	3.2	92.5
His	AC	5.6	9.2	14	0.77	1.2	10.6	88.2
	AMTS	5.7	9.3	6	0.83	8.2	11.8	80.1
	CPM	5.8	9.5	11	0.70	17.9	14.7	67.4
	NRC	5.8	9.5	6	0.96	6.9	3.6	89.4
Lys	AC	13.2	8.4	46	0.67	1.4	11.4	87.2
	AMTS	12.4	7.9	23	0.81	3.5	4.4	92.0
	CPM	14.0	8.9	41	0.64	25.9	5.6	68.5
	NRC	13.1	8.3	13	0.89	0.9	0.8	98.4
Met	AC	3.7	7.9	13	0.71	0.3	6.5	93.1
	AMTS	3.9	8.3	11	0.67	15.9	5.7	78.5
	CPM	3.9	8.3	9	0.64	45.3	4.9	49.9
	NRC	3.8	8.1	6	0.86	0.1	1.4	98.6

¹Models tested: AminoCow (AC), Agricultural Modeling and Training System (AMTS), Cornell-Penn-Miner (CPM), and National Research Council (NRC).

²RMSE = root mean square prediction error.

³RPE = Percent of mean of RMSE.

Table 3. Summary of the evaluation of 4 dairy ration programs¹ to predict duodenal flows of total CP, microbial protein (MCP), rumen undegradable (RUP), and essential amino acids for all fractions, forage source, grain source and RUP amount.

Flow (g/day)	Database	Forage Basis			Grain Basis			RUP	
		Grass	Alfalfa	Corn Silage	Non-corn	Corn	Not added	Added	
CP	All	AC, AMTS, NRC	AC, AMTS, CPM	AC, AMTS, NRC	AMTS, CPM	All	AC	All	
MCP	None	None	AMTS, NRC	NRC	None	AC, NRC	AC	None	
RUP	None	None	None	None	None	None	None	None	
Arg	AC, NRC	AMTS	AC, NRC	None	None	AC, NRC	AC	AC, NRC	
His	AC	None	AC	AC	None	AC, NRC	AMTS	AC	
Ile	NRC	AC, AMTS	NRC	AC, AMTS, NRC	None	AC, AMTS, NRC	AC, AMTS, CPM	NRC	
Leu	ALL	All	None	NRC	None	None	None	All	
Lys	AC, AMTS, NRC	AC, NRC	AC, AMTS, NRC	AC, NRC	NRC	AC, AMTS, NRC	AMTS, CPM, NRC	None	
Met	AC, NRC	None	None	AC, NRC	None	AC, NRC	AC, NRC	AC, NRC	
Phe	AC, AMTS, NRC	AC, AMTS, NRC	AMTS, CPM	AC, AMTS, NRC	AC	AC, AMTS, NRC	AC, AMTS, CPM	AC	
Thr	All	AC, AMTS, NRC	AMTS, CPM	All	AMTS, NRC	AC, CPM, NRC	AC, CPM	AC, AMTS, NRC	
Val	AC, AMTS, NRC	AC, CPM	AC, AMTS, NRC	AC, AMTS, NRC	NRC	AC, AMTS, NRC	AC, AMTS, CPM	AC, NRC	

¹Models with both 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; Models are: AminoCow (AC), Agricultural Modeling and Training Systems (AMTS), Cornell-Penn-Miner version of CNCPS (CPM), and National Research Council (NRC, 2001).

Table 4. Summary of the evaluation of 4 dairy ration programs¹ to predict duodenal flows of total CP, microbial protein (**MCP**), rumen undegradable protein (**RUP**) and essential amino acids for cows of high and low DMI, high and low CP, and high and low NDF.

Flow (g/day)	DMI		CP		NDF	
	Low	High	Low	High	Low	High
CP	AC, AMTS, NRC	All	None	All	AMTS, CPM	All
MCP	None	None	AMTS	None	AMTS, NRC	AC, AMTS
RUP	None	None	None	None	None	None
Arg	None	AC, NRC	None	AC, NRC	None	AC, NRC
His	AMTS, CPM, NRC	AC	None	AC, AMTS, NRC	AMTS	None
Ile	AC, AMTS	NRC	AC, AMTS, CPM	NRC	AMTS, CPM	None
Leu	All	All	AMTS, CPM, NRC	All	None	AC, AMTS, CPM
Lys	AMTS, CPM, NRC	None	AMTS, NRC	None	AC, AMTS, NRC	AMTS, NRC
Met	None	AC, NRC	AC, NRC	NRC	AMTS	None
Phe	AC	AC	AC, NRC	AC, AMTS, NRC	AMTS, CPM	NRC
Thr	CPM	AC, AMTS, NRC	AC, AMTS, NRC	All	CPM	AMTS, CPM, NRC
Val	AC, AMTS, NRC	AC, NRC	AC, AMTS, NRC	AMTS, NRC	CPM	None

¹Models with both 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; Models are: AminoCow (**AC**); Agricultural Modeling and Training Systems (**AMTS**), Cornell-Penn-Miner version of CNCPS (**CPM**); National Research Council (2001:NRC).

Table 5. Ability of models to predict the mean observed starch degradation and total tract starch digestion.

Model	Starch	Mean Total			Mean			Mean Post		
		Tract (%)	±SE	% observed	Rumen (%)	±SE	% observed	Rumen (%)	±SE	% observed
Observed	All	92.8	7.4	—	61.8	20.6	—	30.9	19.2	—
AMTS		96.0	2.2	103.4	81.2	6.6	131.4	14.8	4.8	47.9
CPM		96.3	2.6	103.8	82.4	6.9	133.3	14.0	5.1	45.3
Offner		92.9	3.5	100.1	64.9	8.1	105.0	27.8	5.3	90.0
SM_NC		91.8	3.5	98.9	60.2	6.6	97.4	31.6	4.5	102.3
Observed	Corn	92.3	6.2	—	54.6	18.5	—	37.7	17.7	—
AMTS	n = 82	95.8	2.3	103.8	79.9	5.9	146.3	15.9	4.1	42.2
CPM		96.1	2.5	104.1	80.5	5.7	147.4	15.6	3.6	41.4
Offner		91.5	3.2	99.1	70.1	13.1	128.4	29.4	4.8	78.0
SM_NC		92.0	3.0	99.7	58.9	6.5	107.9	33.1	4.5	87.8
Observed	Small grain	94.6	5.4	—	76.4	15.4	—	18.2	13.0	—
AMTS	n = 58	96.9	0.9	102.4	85.4	3.2	111.8	11.5	2.8	63.2
CPM		97.1	2.0	102.6	86.7	3.0	113.5	10.5	2.7	57.7
Offner		95.6	2.3	101.1	85.4	8.1	111.8	24.3	4.2	133.4
SM_NC		92.5	2.9	97.8	63.4	4.6	83.0	29.9	3.4	164.2
Observed	Sorghum	80.4	17.7	—	54.0	17.5	—	26.3	12.7	—
AMTS	n=8	93.2	3.7	115.9	68.6	8.9	127.0	24.6	5.2	93.5
CPM		93.5	3.7	116.3	69.9	8.9	129.4	23.6	5.3	89.7
Offner		89.9	1.2	111.8	56.8	2.6	105.2	33.0	1.6	125.5
SM_NC		87.5	7.4	108.8	56.1	12.4	103.9	31.4	5.0	119.4

¹Models evaluated were Agricultural Modeling and Training System (AMTS), Cornell-Penn-Miner version of CNCPS (CPM), the model proposed by Offner and Sauvant (2004: OFF), and a simple method used in NittanyCow (SM_NC).

Table 6. Model adequacy statistics for rumen and post ruminal starch digestion.

Item	Model ¹	MSPE ²	RPE, % ³	Intercept	Slope	MSPE bias partition (%)		
						Mean	Slope	Random
All	AMTS	9.09	3.2	-75.30	1.75	18.8	1.9	79.3
Total	CPM	11.95	3.8	-37.10	1.35	22.0	0.4	77.6
Tract	OFF	14.95	4.2	0.10	0.99	3.1	4.4	92.5
	SM_NC	11.54	3.7	10.20	0.90	2.1	0.8	97.1
All Rumen	AMTS	95.55	15.8	8.70	0.65	51.1	0.2	48.7
	CPM	100.91	16.2	27.70	0.41	53.8	0.1	46.1
	OFF	70.76	13.8	-27.90	1.38	3.2	7.4	89.4
	SM_NC	35.32	9.6	-29.10	1.50	0.7	0.3	99.0
All Post Rumen	AMTS	76.09	28.2	32.20	-0.08	43.4	0.0	56.6
	CPM	71.66	27.4	37.50	-0.46	45.2	0.1	54.7
	OFF	67.12	26.5	-4.40	1.27	3.1	4.4	92.5
	SM_NC	49.94	22.9	-16.80	1.52	0.1	0.2	99.7
Corn Rumen	AMTS	50.75	13.0	27.20	0.36	66.0	0.6	33.4
	CPM	50.57	13.0	19.90	0.45	67.9	0.1	32.0
	OFF	43.93	12.1	11.60	0.72	16.9	0.0	83.1
	SM_NC	28.32	9.8	-8.60	1.08	5.4	1.1	93.5
Corn Post Rumen	AMTS	30.16	14.6	43.70	-0.49	61.0	0.3	38.7
	CPM	30.09	14.5	45.00	-0.58	38.2	35.9	25.9
	OFF	33.24	15.3	33.40	0.09	1.4	10.5	88.1
	SM_NC	28.84	14.2	11.80	0.74	6.3	1.0	92.7
Small Grain Rumen	AMTS	22.52	6.2	64.60	0.11	26.3	0.2	73.5
	CPM	22.18	6.2	26.50	0.55	33.5	1.0	65.5
	OFF	22.96	6.3	45.30	0.41	21.4	18.6	24.3
	SM_NC	16.96	5.4	14.30	0.93	38.2	9.4	52.4
Small Grain Post Rumen	AMTS	51.92	13.3	-46.40	1.47	62.2	5.0	32.8
	CPM	33.64	10.7	-52.40	1.54	67.7	5.8	26.5
	OFF	45.98	12.6	-233.20	5.08	3.5	28.7	67.8
	SM (NC)	16.03	22.0	25.10	-0.18	34.9	27.7	37.4
Sorghum Rumen	AMTS	51.92	13.3	-46.40	1.47	62.2	5.0	32.8
	CPM	33.64	10.7	-52.40	1.54	67.7	5.8	26.5
	OFF	45.98	12.6	-233.20	5.08	3.5	28.7	67.8
	SM_NC	31.74	10.4	-11.70	1.19	24.7	29.5	47.8
Sorghum Post Rumen	AMTS	41.47	24.5	5.60	0.73	1.9	11.4	86.7
	CPM	31.34	21.4	0.65	0.96	4.6	2.5	92.9
	OFF	32.45	21.7	-82.50	3.20	25.6	5.7	68.7
	SM_NC	37.49	23.3	-4.40	0.89	14.1	8.5	77.5

¹Models evaluated were Agricultural Modeling and Training System (AMTS), Cornell-Penn-Miner version of CNCPS (CPM), the model proposed by Offner and Sauvant (2004: OFF), and a simple method used in NittanyCow (SM_NC).

²MSPE = Means square prediction error and RPE = percent of mean of MSPE.

